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Departamento de Agronomía, Biotecnología y Alimentación

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REGULACIÓN POSTRADUCCIONAL DE LA RESPUESTA DE LAS PLANTAS A VOLÁTILES EMITIDOS POR HONGOS FITOPATÓGENOS

Tesis Doctoral para optar al título de Doctora, presentada por:

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El Dr. **Javier Pozueta Romero**, Profesor de Investigación del Consejo Superior de Investigaciones Científicas y la Dra. **Edurne Baroja Fernández**, Científico Titular del Consejo Superior de Investigaciones Científicas,

CERTIFICAN:

Que el trabajo titulado "Regulación postraduccional de la respuesta de las plantas a volátiles emitidos por hongos fitopatógenos" recogido en la presente memoria, ha sido realizado por Kinia Ameztoy del Amo en el Instituto de Agrobiotecnología (UPNA/CSIC/Gobierno de Navarra) bajo su supervisión y que cumple las condiciones exigidas por la legislación vigente para optar al grado de Doctora. Kinia Ameztoy del Amo ha disfrutado de una beca predoctoral de la Universidad Pública de Navarra. Este trabajo ha sido financiado por el proyecto BIO2016-78747-P de la Comisión Interministerial de Ciencia y Tecnología and Fondo Europeo de Desarrollo Regional y los proyectos P1044 AGROESTI and P1004 PROMEBIO del Gobierno de Navarra.

Y para que así conste, firman la presente en Pamplona, a __ de _____de 2020.

Fdo. Javier Pozueta Romero Fdo. Edurne Baroja Fernández

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A mis padres Carthy y Mari Carmen, por hacerlo posible

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RESUMEN

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Las plantas han desarrollado mecanismos que les permiten adaptar su crecimiento, desarrollo y metabolismo a estímulos externos. Los microorganismos de la fitosfera emiten sustancias (ej. azúcares, proteínas, ácidos grasos, ácidos orgánicos, aminoácidos y hormonas) que alteran el crecimiento y el desarrollo de la planta (Philippot et al., 2013; De-la-Peña and Loyola-Vargas, 2014; Backer et al., 2018). Estos microorganismos también emiten compuestos volátiles (VCs) que juegan un papel fundamental en la comunicación con las plantas. VCs emitidos por microorganismos beneficiosos fomentan el crecimiento, la captación de nutrientes y la fotosíntesis, modulan la arquitectura de la raíz, activan la respuesta de defensa de la planta e incrementan su resistencia al estrés salino y la sequía (Ryu et al., 2003; Zhang et al., 2008; Splivallo et al., 2009; Zhang et al., 2009; Gutiérrez-Luna et al., 2010; Kanchiswamy et al., 2015; Park et al., 2015; Ledger et al., 2016). Estudios llevados a cabo por el grupo de investigación en el que he realizado mi tesis doctoral demostraron que los VCs emitidos por una amplia gama de bacterias y hongos fitopatógenos también poseen propiedades bioestimulantes (Ezquer et al., 2010; Sánchez-López et al., 2016b; Sánchez-López et al., 2016a). Cambios inducidos por VCs emitidos por hongos fitopatógenos están asociados a variaciones en el transcriptoma y el proteoma de la planta y en el estado redox de proteínas plastidiales relacionadas con el metabolismo del almidón. Tales cambios sugieren que la regulación de la respuesta de la planta a los VCs microbianos está regulada tanto a nivel transcripcional como no-transcripcional. Con el fin de profundizar en los mecanismos que median la relación entre la planta y los microorganismos, en este trabajo investigué el papel que juegan dos formas de regulación postraduccional en la respuesta de las plantas a los VCs emitidos por el hongo fitopatógeno *Alternaria alternata*: la regulación redox y la proteostasis.

En el trabajo presentado en el capítulo 1 investigué el papel que juega la tiorredoxina reductasa C dependiente de NADPH (NTRC) en la respuesta de las plantas a los VCs microbianos. Para ello, analicé la respuesta en el desarrollo, en el metabolismo y en el redox proteoma de plantas *wild type* (WT) y un mutante *knock out* de NTRC (*ntrc*) a VCs emitidos por *A. alternata*. En plantas WT, el tratamiento con VCs fúngicos fomentó el crecimiento, dio lugar a cambios en la arquitectura de la raíz, alteró la expresión de genes regulados por CK y ABA y aumentó la capacidad fotosintética de la planta. Tales cambios fueron muy reducidos en plantas *ntrc*, pero notables en plantas *ntrc-Δ2cp* con expresión reducida en una proteína que media en la acción de NTRC y que es determinante del estado redox plastidial, la 2-Cys peroxirredoxina. Análisis redox-

proteómicos revelaron que los VCs promueven una reducción global del redox proteoma (especialmente de las proteínas relacionadas con la fotosíntesis) en plantas WT, pero una oxidación en plantas *ntrc*. Globalmente, los resultados presentados en este capítulo muestran que NTRC juega un papel importante en la respuesta de las plantas a los VCs microbianas a través de mecanismos que involucran cambios globales en el redox proteoma que afectan a la fotosíntesis.

Tras hipotetizar que la respuesta de las plantas a VCs microbianos implica una regulación postraduccional de la expresión de las enzimas involucradas en la ruta 2-C-methyl-D-erythritol 4-phosphate (MEP) y del shikimato a través de mecanismos que implican una señalización de la activación redox de la fotosíntesis, en el trabajo presentado en el **segundo capítulo** comparé las respuestas a VCs fúngicos de plantas de Arabidopsis WT y un mutante *cfbp1* que no expresa la isoforma de la enzima fructosa-1,6-bisfosfatasa del ciclo de Calvin-Benson que posee regulación redox. Estos estudios mostraron que, contrariamente a lo que ocurre en plantas WT, los VCs microbianos no fomentan el crecimiento y la fotosíntesis, ni tampoco cambios metabólicos y proteómicos en plantas *cfbp1*. En plantas WT, pero no en plantas *cfbp1*, los VCs microbianos disminuyeron los niveles de transcritos y proteínas del sistema proteasa Clp estromático y aumentaron los de las chaperoninas y co-chaperoninas plastidiales. Consistentemente, los VCs fúngicos incrementaron los niveles de proteínas diana de Clp, tales como enzimas de las rutas MEP y del shikimato en plantas WT. Mutantes con actividad proteolítica disminuida de Clp respondieron débilmente a VCs fúngicos. Globalmente, los resultados presentados en este capítulo demuestran que la respuesta de las plantas a los VCs fúngicos implica una activación redox de la fotosíntesis y una posterior señalización retrógrada del cloroplasto al núcleo para la regulación proteostática de las rutas MEP y del shikimato.

SUMMARY

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Plants have developed mechanisms that allow them to adapt their growth, development and metabolism to external stimuli. Microorganisms in the phytosphere emit substances (e.g. sugars, proteins, fatty acids, organic acids, amino acids and hormones) that alter the growth and development of the plant (Philippot et al., 2013; De-la-Peña and Loyola-Vargas, 2014; Backer et al., 2018). These microorganisms also synthesize and emit many volatile compounds (VCs) that play a fundamental role in communication with plants. VCs emitted by beneficial microorganisms promote growth, nutrient uptake, and photosynthesis, modulate root architecture, activate the plant's defense response, and increase its resistance to salt stress and drought (Ryu et al., 2003; Zhang et al., 2008; Splivallo et al., 2009; Zhang et al., 2009; Gutiérrez-Luna et al., 2010; Kanchiswamy et al., 2015; Park et al., 2015; Ledger et al., 2016). Studies carried out by the research group where I have developed my doctoral thesis showed that VCs emitted by a wide range of bacteria and phytopathogenic fungi promote growth, photosynthesis and starch accumulation in many plant species (Ezquer et al., 2010; Sánchez-López et al., 2016b; Sánchez-López et al., 2016a). These changes are associated with variations in the transcriptome, proteome and redox state of proteins related to starch metabolism that suggest that the regulation of the plant response to VCs emitted by phytopathogenic microorganisms is mediated by transcriptional and non-transcriptional mechanisms. In this work I have investigated the role played by two post-translational regulatory mechanisms (e.g. redox regulation and proteostatic regulation) in the response of plants to the VCs emitted by the phytopathogenic fungus *Alternaria alternata*.

In **Chapter I** of this work I hypothesized that plants´ responses to microbial VCs involve post-translational modifications of the thiol redox proteome through action of the plastidial NADPH-dependent thioredoxin reductase C (NTRC), which regulates chloroplast redox status via its functional relationship with 2-Cys peroxiredoxins. To test this hypothesis, I analyzed developmental, metabolic, hormonal, genetic and redox proteomic responses of wild type (WT) plants and a NTRC knock out mutant (*ntrc*) to VCs emitted by *A. alternata*. Fungal VC-promoted growth, changes in root architecture, shifts in expression of VC-responsive CK- and ABA-regulated genes, and increases in photosynthetic capacity were substantially weaker in *ntrc* plants than in WT plants. As in WT plants, fungal VCs strongly promoted growth, chlorophyll accumulation and photosynthesis in *ntrc-Δ2cp* plants with reduced 2-Cys peroxiredoxin expression. OxiTRAQ-based quantitative and site-specific redox-proteomic analyses revealed that

VCs promote global reduction of the thiol redox proteome (especially of photosynthesis-related proteins) of WT leaves, but its oxidation in *ntrc* leaves. Findings presented in this chapter show that NTRC is an important mediator of plant responses to microbial VCs through mechanisms involving global thiol redox proteome changes that affect photosynthesis.

In **Chapter II**, I hypothesized that plants' responses to microbial VCs involve post-translational modulation of the expression of enzymes of the 2-C-methyl-D-erythritol 4-phosphate (MEP) and shikimate pathways via mechanisms involving redox-activated photosynthesis signaling. To test this hypothesis, I compared the growth, metabolic, and proteomic responses in wild-type (WT) Arabidopsis plants and a *cfbp1* mutant defective in a redox-regulated isoform of the Calvin-Benson cycle enzyme fructose-1,6-bisphosphatase to VCs emitted by *A. alternata*. Fungal VC-promoted growth and photosynthesis, as well as metabolic and proteomic changes, were substantially weaker in *cfbp1* plants than in WT plants. In WT plants, but not in *cfbp1* plants, fungal VCs reduced the levels of both transcripts and proteins of the stromal Clp protease system and enhanced those of plastidial chaperonins and co-chaperonins. Consistently, fungal VCs promoted the accumulation of putative Clp protease clients such as MEP and shikimate pathway enzymes in WT plants. Mutants with decreased Clp proteolytic capacity responded weakly to fungal VCs. Findings presented in this chapter provide evidence that plant responses to fungal VCs involve chloroplast-to-nucleus retrograde signaling of redox-activated photosynthesis leading to proteostatic regulation of the MEP and shikimate pathways.

INTRODUCCIÓN

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Cómo alimentar a la población mundial de modo eco-sostenible y saludable es un reto que la humanidad debe afrontar y superar con éxito. El incremento de la producción mundial de alimentos experimentado durante las últimas décadas fue posible gracias a la revolución verde, basada en el uso de variedades de cultivos de alto rendimiento, fertilizantes inorgánicos y fitosanitarios (http://iofacturo.mx/ecologia/que-es-la-revolucion-verde). Algunas de estas prácticas agrícolas infringen un gran daño al medioambiente y a la salud humana ya que están asociadas a la utilización de sustancias tóxicas que pueden acumularse en elevadas concentraciones en el suelo, la atmósfera y el agua de los ríos, mares y acuíferos (Savci, 2012). A estos efectos adversos hay que añadir los derivados del cambio climático, un fenómeno global que ha dado lugar a cambios en la cantidad, distribución e intensidad de las lluvias y a frecuentes y prolongados periodos de sequía que limitan la disponibilidad de nutrientes para las plantas y, por tanto, el rendimiento de los cultivos (Pareek, 2017). Para evitar los problemas de salud pública y medioambientales derivados del empleo abusivo de agroquímicos es imprescindible diseñar nuevas estrategias respetuosas con el medio ambiente que garanticen el elevado rendimiento de los cultivos y satisfagan las crecientes demandas de la población mundial. Una de estas estrategias está basada en el empleo de bioestimulantes, definidos como sustancias o microorganismos que, aplicados en bajas dosis sobre la planta, estimulan la eficiencia en la nutrición de estas, las hacen más resistentes al estrés y, así, mejoran el rendimiento de los cultivos y la calidad de sus productos (Calvo et al., 2014; du Jardin, 2015; Ahmad et al., 2018; Rouphael and Colla, 2018; Rouphael and Colla, 2020).

1. LOS MICROORGANISMOS EMITEN COMPUESTOS VOLÁTILES QUE FOMENTAN EL CRECIMIENTO DE LAS PLANTAS

Los microorganismos presentes en la filosfera, rizosfera y endosfera sintetizan y emiten compuestos tales como carbohidratos, proteínas, lípidos, aminoácidos, hormonas, etc. que modulan el crecimiento y el desarrollo de la planta (Bhattacharyya and Jha, 2012; De-la-Peña and Loyola-Vargas, 2014; Ahmad et al., 2018; Sammauria et al., 2020). Además, los microorganismos sintetizan y emiten compuestos volátiles (VCs) que son capaces de difundir a través del suelo y el aire y que juegan un papel importante en la comunicación entre la planta y el microorganismo (Schulz and Dickschat, 2007; Kanchiswamy et al., 2015). Estudios pioneros llevados a cabo por Ryu y colaboradores (2003) mostraron que los VCs emitidos por algunos aislados de bacterias beneficiosas del género *Bacillus* fomentan el crecimiento de plantas de *Arabidopsis thaliana*. Trabajos posteriores mostraron que esta respuesta es debida a la activación de mecanismos que facilitan la absorción de nutrientes y fomentan la fotosíntesis (Zhang et al., 2008; Zhang et al., 2009). Desde entonces se han realizado numerosos estudios para identificar VCs microbianos bioactivos y sus modos de acción sobre la planta (Hung et al., 2013; Delaplace et al., 2015; Ditengou et al., 2015; Garnica-Vergara et al., 2016; Cordovez et al., 2018). Investigaciones realizadas por el grupo en el que he realizado mi trabajo de tesis demostraron que los microorganismos fitopatógenos también emiten VCs que estimulan el crecimiento de las plantas (Sánchez-López et al., 2016a; Sánchez-López et al., 2016b). La exposición de plantas a VCs emitidos por el hongo fitopatógeno *Alternaria alternata* conlleva un notable incremento de la fotosíntesis y un aumento de los niveles de fotosintatos primarios (almidón, azucares solubles, aminoácidos y gliceraldehido 3-fosfato (GAP)) y compuestos isoprenoides derivados de la ruta 2-C-metil-D-eritritol 4-fosfato (MEP) tales como clorofilas, carotenoides y citoquininas (CKs) (Ezquer et al., 2010; Sánchez-López et al., 2016a; Sánchez-López et al., 2016b). Estos cambios están asociados a su vez a numerosas alteraciones en el transcriptoma de la planta que indujeron a pensar que la respuesta de la planta a VCs microbianos está regulada a nivel transcripcional (Ezquer et al., 2010; Sánchez-López et al., 2016b). Recientemente, Sánchez-López et al. (2016b) y García-Gómez et al. (2019) mostraron que gran parte de las variaciones del transcriptoma de plantas inducidas por VCs emitidos por *A. alternata* son similares a las inducidas por VCs emitidos por microorganismos beneficiosos y por factores que fomentan la fotosíntesis tales como la exposición a alta intensidad lumínica o a elevadas concentraciones de CO_2. Sin embargo, la respuesta fenotípica y metabólica de la planta a estos estímulos es muy diferente a la desencadenada por los VCs fúngicos. Por otro lado, análisis proteómicos de hojas expuestas a la acción de VCs emitidos por *A. alternata* revelaron que un elevado porcentaje de las proteínas diferencialmente expresadas por los VCs fúngicos están codificadas por genes que no responden a estos compuestos (Sánchez-López et al., 2016a; Sánchez-López et al., 2016b). Finalmente, Li et al. (2011) observaron que los VCs emitidos por *A. alternata* fomentan la acumulación de almidón a través de mecanismos que implican la activación redox de la enzima ADP-glucosa pirofosforilasa (AGPasa) mediados por la tiorredoxina (Trx) plastidial NTRC. Todo ello indica que, tal y como se ilustra en el modelo metabólico de la **Figura 1**, la respuesta de las plantas a VCs microbianos implica mecanismos de regulación

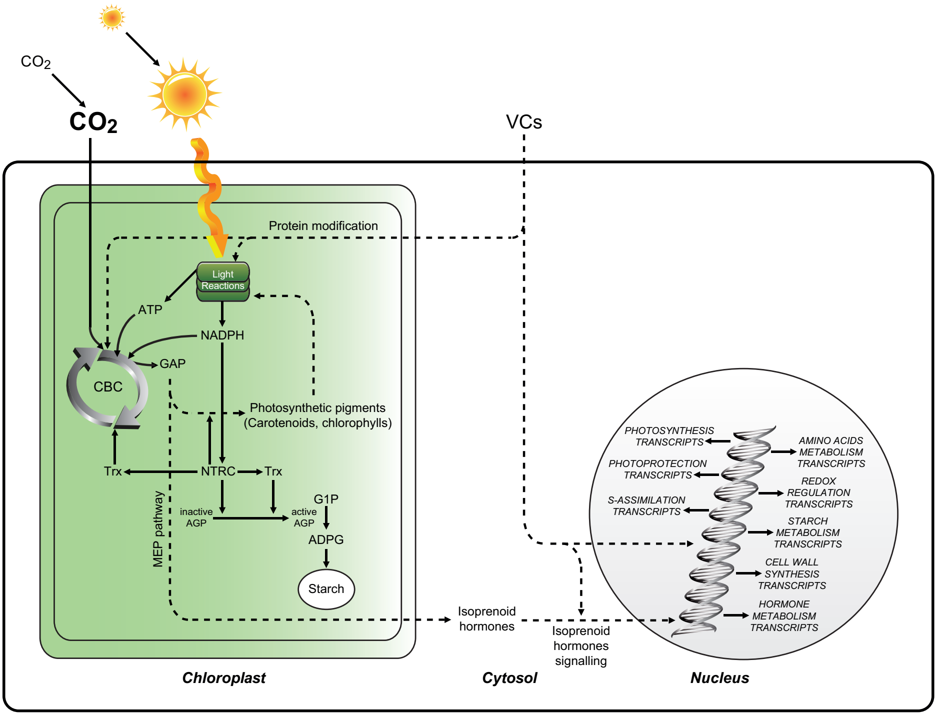


Figura 1: Modelo integrativo que ilustra los mecanismos que regulan la respuesta de las plantas a VCs microbianos.

transcripcional y no-transcripcional. Según este modelo, los VCs microbianos generarían señales inductoras de cambios rápidos en la expresión de genes determinantes del crecimiento, fotosíntesis, metabolismo del almidón, etc. (Sánchez-López et al., 2016b; García-Gómez et al., 2019). Alternativa y/o adicionalmente, los VCs microbianos modificarían y activarían proteínas implicadas en la fotosíntesis. Al igual que ocurre en plantas puntualmente expuestas a alta intensidad lumínica o a elevadas concentraciones de CO_2, tal activación de la maquinaria fotosintética conllevaría un aumento de la fijación del CO_2 atmosférico que daría lugar a un incremento de la producción de GAP. Este intermediario metabólico del ciclo de Calvin-Benson (CBC) actúa como sustrato de la ruta MEP implicada en la producción de compuestos isoprenoides tales como clorofilas, carotenoides y hormonas. El incremento de la producción de pigmentos fotosintéticos resultante contribuiría a fomentar la fotosíntesis mientras que el incremento de los niveles de hormonas isoprenoides activaría una serie de reacciones de señalización que alterarían la expresión de genes involucrados en diferentes procesos que afectan al crecimiento, desarrollo y metabolismo de la planta. Mecanismos no-transcripcionales adicionales de regulación de la expresión génica tales como los implicados en el control de la calidad y la estabilidad de las proteínas determinarían el perfil proteómico final de la planta. El aumento de la producción fotosintética de NADPH aportaría más poder reductor para las reacciones del CBC y favorecería la activación redox mediada por Trxs de enzimas del CBC, la ruta MEP y de síntesis de almidón.

A continuación, presentaré algunos de los actores principales de este modelo de regulación de la respuesta de la planta a los VCs microbianos, concretamente la fotosíntesis, la regulación redox del metabolismo mediada por tiorredoxinas y la regulación de la producción de isoprenoides derivados de la ruta MEP (especialmente a través de procesos de homeostasis proteica).

2. FOTOSÍNTESIS

Las plantas, algas y cianobacterias realizan el proceso químico denominado fotosíntesis oxigénica que implica la conversión de agua y CO_2 atmosférico en carbohidratos y en O_2 haciendo uso de la energía lumínica. La fotosíntesis en las plantas tiene lugar en los cloroplastos a través de (i) reacciones fotoquímicas, en las que la energía lumínica es convertida en compuestos ricos en energía (ATP) y poder reductor (NADPH) y (ii) reacciones de fijación del CO_2 atmosférico, que utilizan esa energía para la síntesis de carbohidratos que utilizará la planta para su crecimiento y desarrollo.

2.1. Reacciones implicadas en la fotosíntesis

Las reacciones fotoquímicas de la fotosíntesis tienen lugar en los tilacoides, donde la energía lumínica de los fotones es captada por los fotosistemas I y II (PSI y PSII, respectivamente) y transferida a una cadena de transporte de electrones para generar ATP y NADPH (**Figura 2**) (Johnson, 2016). Los fotosistemas son complejos proteicos transmembrana que se componen de un complejo antena (LHC) que capta y transfiere la energía de excitación a los centros de reacción donde se dan las reacciones fotoquímicas. Los LHC de los fotosistemas se asocian con moléculas de clorofila (Chl) *a* y *b* y con carotenoides. Las reacciones fotoquímicas de la fotosíntesis comienzan en el PSII que usa la energía lumínica para oxidar una molécula de agua a oxígeno y producir plastoquinol (PQH_2) tras la reducción de un aceptor de electrones que se encuentra en la membrana tilacoidal llamado plastoquinona (PQ). El PQH_2 transfiere los electrones obtenidos de la fotólisis del agua hasta un complejo de membrana llamado citocromo b_6f (cytb_6f). El cytb_6f oxida al PQH_2 a PQ y reduce a una pequeña molécula transportadora de electrones llamada plastocianina (PC) que se encuentra en el lumen. Una segunda reacción iniciada por la luz tiene lugar en el PSI. El PSI oxida a la PC y reduce a una proteína trasportadora de electrones que se encuentra en el estroma, la ferredoxina (Fd). Los electrones transferidos a la Fd son usados por la FNR para reducir el NADP+ a NADPH. Los protones generados por la fotólisis del agua junto con el flujo de electrones acoplado al movimiento de los protones a través de la membrana tilacoidal generan un gradiente de energía libre que es usado por la ATP sintasa (ATPasa) para producir ATP (**Figura 2**) (Johnson, 2016). En plantas y algas existe una ruta alternativa de transferencia de electrones, llamada *cyclic electron flow* que implica la transferencia de electrones de la Fd a la PQ. En esta ruta no se produce NADPH, pero sí ATP ya que los protones transferidos al lumen por la oxidación del PQH_2 a través del complejo cytb_6f son usados por la ATPasa. Esta ruta alternativa permite a los organismos fotosintéticos controlar la relación NADPH/ATP según sus necesidades metabólicas.

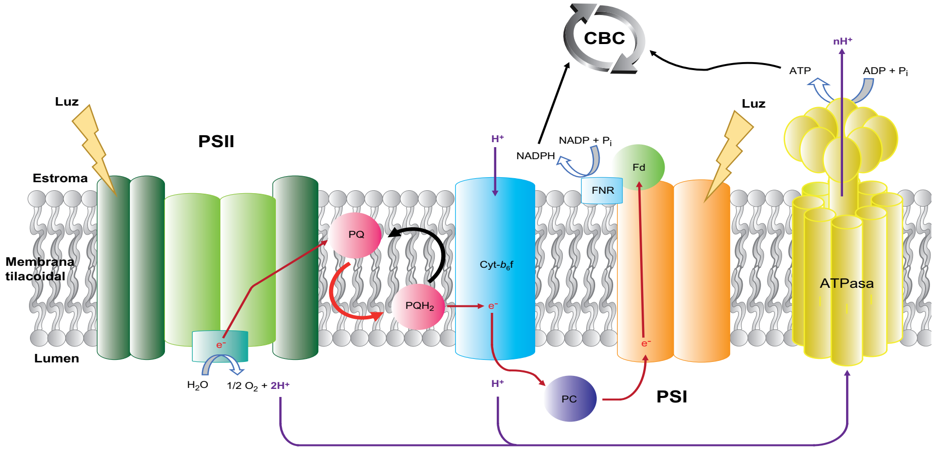


Figura 2: Reacciones fotoquímicas que tienen lugar en el tilacoide. Las reacciones fotoquímicas comienzan con la captación de energía lumínica por el PSI y PSII y la obtención de electrones y protones que pasan por una cadena de transporte dando lugar a la síntesis de NADPH y ATP. (Figura adaptada de Johnson (2016))

Las reacciones de fijación del CO_2 atmosférico tienen lugar en el estroma del cloroplasto en el CBC. Esta ruta metabólica fija el CO_2 atmosférico consumiendo el ATP y el NADPH generado en las reacciones fotoquímicas. En la primera reacción de este ciclo la enzima ribulosa-1,5-bisfosfato carboxilasa/oxigenasa (RuBisCO) cataliza la carboxilación de la ribulosa-1,5-bisfosfato (RuBP) (**Figura 3**). Esta reacción produce 3-fosfoglicerato (3-PGA) que es fosforilado a 1,3-bisfosfoglicerato y GAP por la acción acoplada de las enzimas 3-fosfoglicerato quinasa y GAP deshidrogenasa (GAPDH) usando ATP y NADPH. Por cada tres moléculas de CO_2 iniciales se generan seis moléculas de GAP. Sin embargo, solo una de estas moléculas de GAP se considera

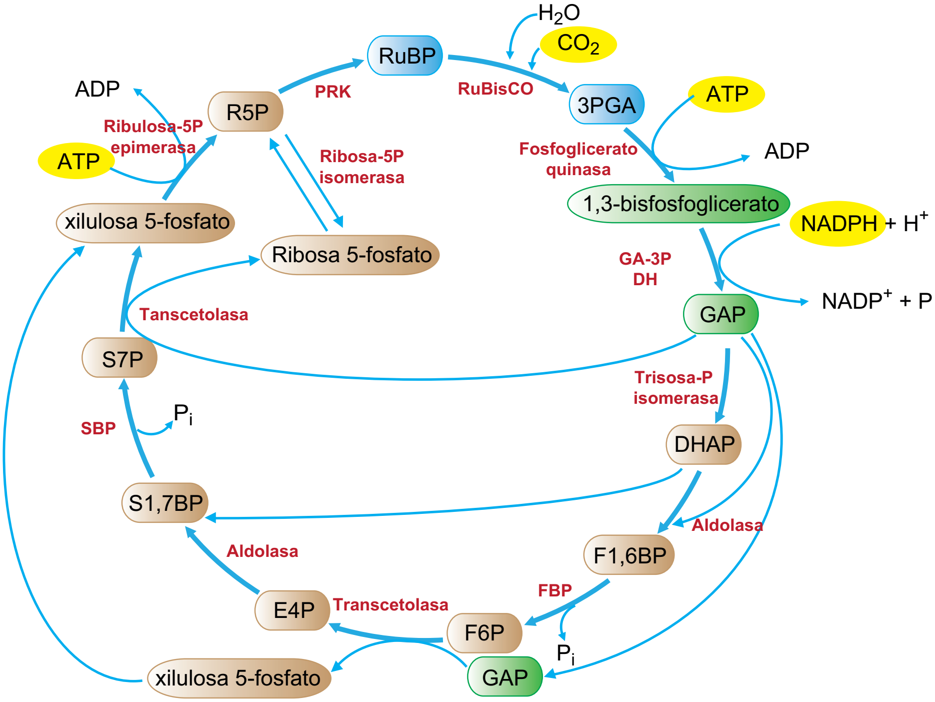


Figura 3: Ciclo de Calvin-Benson. Esquema de las reacciones enzimáticas que tienen lugar en el CBC. En rojo se destacan las enzimas implicadas. Los intermediarios involucrados en las etapas de fijación, reducción y regeneración están destacados en azul, verde y marrón, respectivamente. Ribulosa-1,5-bisfosfato carboxilasa/oxigenasa, RuBisCO; gliceraldehido 3-fosfato deshidrogenasa, GA-3P DH; fructosa 1,6-bifosfatasa, FBP; Sedoheptulosa 1,7-bisfosfatasa, SBP; fosforibuloquinasa, PRK; gliceraldehido 3-fosfato, GAP; dihidroacetona fosfato, DHAP; fructosa 1,6-bifosfato, F1,6BP; fructosa 6-fosfato, F6P; eritrosa 4-fosfato, E4P; sedoheptulosa 1,7-bifosfato, S1,7BP; sedoheptulosa 7-fosfato, S7P; ribulosa 5-fosfato, R5P; ribulosa-1,5-bisfosfato, RuBP.

producto del CBC. Las cinco moléculas restantes se utilizan para la regeneración de la RuBP que comienza con la conversión de una molécula de GAP en dihidroacetona fosfato (DHAP) mediante una triosa fosfato isomerasa. La DHAP junto con otra molécula de GAP generan fructosa 1,6-bisfosfato y fructosa 6-fosfato (F6P) por la acción acoplada de la aldolasa y la fructosa 1,6-bisfosfatasa (FBP). La F6P y una molécula de GAP generan eritrosa 4-fosfato (E4P) y xilulosa 5-fosfato. A partir de E4P se forma sedoheptulosa 7-bisfosfato mediante reacciones acopladas de las enzimas aldolasa y sedoheptulosa 1,7-bisfosfatasa (SBP). Finalmente, la regeneración termina con una serie de reacciones que dan lugar a la RuBP consumiendo ATP y en las que están implicadas las enzimas transcetolasa, ribulosa 5-fosfato epimerasa y fosforibuloquinasa (PRK). Las moléculas de GAP producidas en el CBC que no se usan para la regeneración de la RuBP son utilizadas en diferentes rutas metabólicas como la ruta MEP y la ruta del shikimato, que darán lugar a metabolitos importantes para el desarrollo de la planta tales como los aminoácidos, ácidos grasos, compuestos isoprenoides, fenilpropanoides, etc.

2.2. Regulación de la fotosíntesis

La fotosíntesis funciona de forma integrada con diferentes rutas metabólicas en un entorno sujeto a variaciones de temperatura, intensidad lumínica, disponibilidad de nutrientes y agua, etc. Este proceso químico está finamente regulado, tanto a nivel de la cadena de transporte electrónico como a nivel del CBC.

El transporte de electrones requiere una regulación continua para mantener el equilibrio entre la disponibilidad de luz y las demandas metabólicas. La distribución de proteínas en la membrana tilacoidal no es uniforme (Melis, 1991). Mientras que el complejo cytb_6f aparece distribuido más o menos uniformemente por toda la membrana, cada fotosistema se concentra en una zona distinta; el PSII es más abundante en los tilacoides apilados, mientras que el PSI abunda más en los tilacoides sin apilar (Johnson, 2016). Ambos fotosistemas son móviles, de modo que los tilacoides constituyen un sistema dinámico regulado por la cantidad y la calidad de la luz que incide sobre ellos. Si bien la luz es esencial para la fotosíntesis, un exceso de luz puede dañar el aparato fotosintético provocando una acumulación de fotones y electrones que deben ser disipados para evitar el deterioro de la maquinaria fotosintética (Eberhard et al., 2008; Rochaix, 2011; Alboresi et al., 2019). El aparato fotosintético es capaz de responder a variaciones de irradiancia mediante mecanismos que actúan de manera coordinada. En torno al PSII se desencadena toda una serie de desacoplamientos y desactivaciones, que permiten maximizar la disipación de energía y minimizar el daño global sobre el aparato fotosintético. Así, un exceso de energía en el PSII desencadena la fosforilación de sus complejos LHCII que provoca a su vez la migración de estos al PSI y una mayor absorción de luz en el PSI. Por otro lado, un exceso de activación del PSI provoca que los complejos LHCII vuelvan hacia el PSII (Foyer and Harbinson, 1997; Ohad et al., 2006; Johnson, 2016).

La regulación de la actividad de las enzimas implicadas en el CBC es también clave para el correcto funcionamiento de la fotosíntesis. Las variaciones de pH estromático y los niveles de moléculas auxiliares no proteicas conocidas como cofactores (ej. Fe^{2+} y Mg^{2+}) son esenciales para el correcto funcionamiento de las enzimas y la regulación del CBC (Johnson, 2016; Jensen et al., 2017). El proceso de inhibición por retroalimentación (según el cual el producto final de una vía metabólica actúa sobre la enzima reguladora de esa vía para evitar sobreproducción del producto final) es otra medida de regulación de las enzimas del CBC (Paul and Pellny, 2003; Johnson, 2016). Otro mecanismo de regulación de esta ruta metabólica está basado en la modulación de la actividad de sus enzimas por cambios en la concentración de sus sustratos (Jensen et al., 2017; Heyneke and Fernie, 2018). Por otro lado, enzimas del CBC tales como la PRK, la SBP, la GAPDH y la FBP, están reguladas por cambios en su estado redox mediados por el sistema Fd/Trx (Michelet et al., 2013; Nikkanen et al., 2016; Yoshida and Hisabori, 2016; Ojeda et al., 2017). Tal y como se explicará más detalladamente en la siguiente sección, los electrones necesarios para la reducción de los residuos de cisteína de la proteína diana proceden de la cadena de transporte de electrones y son cedidos a las enzimas del CBC mediante el sistema Fd/Trx (Buchanan, 1980; Schürmann and Buchanan, 2008). Dado que el poder reductor necesario para la activación de las enzimas del CBC proviene de la cadena de transporte electrónico, se considera que la regulación redox de estas enzimas depende de la luz (Buchanan and Balmer, 2005; Michelet et al., 2013; Nikkanen et al., 2016).

3. REGULACIÓN REDOX MEDIADA POR TIORREDOXINAS

Los cambios en el estado redox de las proteínas constituyen un mecanismo de regulación postraduccional que consiste en reacciones bioquímicas reversibles de reducción/oxidación. Uno de los mecanismos de acción de la regulación redox consiste en la formación de enlaces disulfuro entre grupos tiol de residuos de cisteínas de las proteínas. Existen tres tipos de enlaces disulfuro: intramolecular, intermolecular y mixto. El enlace intramolecular es el que ocurre entre dos cisteínas de un mismo péptido que se encuentran próximas una vez la proteína está plegada. El enlace intermolecular ocurre entre dos aminoácidos que se encuentran en diferentes péptidos y conlleva a la formación de un dímero. En el mixto, una cisteína reacciona con una molécula de glutatión. Todos estos enlaces disulfuro son reversibles, pasando de una forma oxidada a una reducida y viceversa (Buchanan and Balmer, 2005; Oelze et al., 2008; Schürmann and Buchanan, 2008).

Las proteínas encargadas de realizar estas modificaciones en el estado redox de otras proteínas son las Trx. Estas proteínas de la familia disulfuro oxidorreductasas poseen un motivo estructural característico formado por 4 hélices-α que rodean una lámina-β compuesta de 5 hebras y poseen un centro activo muy conservado WC(G/P)PC. Las Trxs reducen los puentes disulfuro de sus proteínas diana, ya sean intramoleculares o intermoleculares (Schürmann and Buchanan, 2008; Nikkanen et al., 2017). El mecanismo de acción de las Trxs implica dos pasos (**Figura 4**) (Holmgren, 1985). En el primero, el grupo tiol de una de las cisteínas del centro activo de la Trx reducida realiza un ataque nucleófilo sobre uno de los átomos de azufre del puente disulfuro de su proteína diana oxidada, dejando una cisteína reducida y otra formando un enlace covalente con la Trx. En el siguiente paso, la cisteína reducida que queda libre en el centro activo de la Trx rompe el enlace disulfuro entre Trx y proteína diana, quedando la proteína diana reducida y la Trx oxidada.

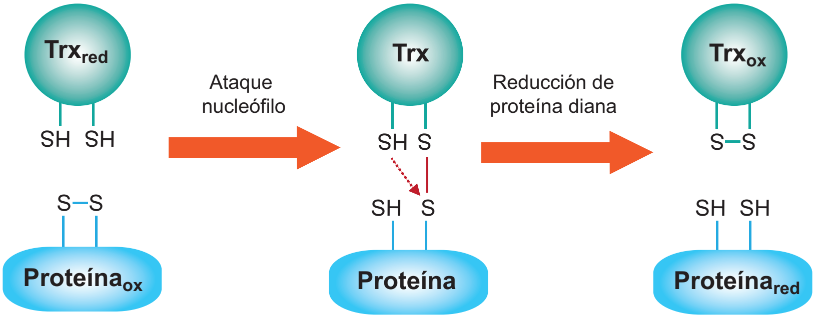


Figura 4: Mecanismo de acción de las Trxs. El grupo tiol N-terminal de la Trx ataca al puente disulfuro de la proteína diana, (i) liberándose un grupo tiol y (ii) formando un puente disulfuro con la segunda cisteína de la proteína diana. Este nuevo puente disulfuro es eliminado por el grupo tiol C-terminal de la Trx, dando lugar a la proteína diana reducida y la Trx oxidada.

Existen múltiples Trxs y la mayoría de ellas se localizan en el plastidio. Las Trx plastidiales se clasifican en típicas (*f*, *m*, *x*, *y*, *z*) y atípicas entre las que cabe destacar la Trx reductasa C dependiente de NADPH (NTRC). La Trx *f* está involucrada en la regulación redox de enzimas del CBC, metabolismo del almidón, síntesis de lípidos, ruta oxidativa de las pentosas fosfato (OPPP), síntesis de clorofilas y ATP (Thormählen et al., 2015; Geigenberger et al., 2017). La Trx *m* regula los mismos procesos que la Trx *f*, aunque es más específica en la regulación de proteínas involucradas en la asimilación del nitrógeno y en mecanismos de defensa frente a estrés oxidativo (Balmer et al., 2003; Rey et al., 2013). Las Trx *x*, *y*, *z* juegan un papel importante en la regulación de proteínas involucradas en la defensa frente al estrés oxidativo (Geigenberger et al., 2017). Entre las Trxs extraplastidiales cabe mencionar la Trx *o* y la Trx *h*. La primera se localiza en la mitocondria y su función se relaciona principalmente con la defensa contra las especies reactivas de oxígeno (Yoshida et al., 2013), la regulación del ciclo de Krebs (Daloso et al., 2015) y la defensa frente a la sequía o el estrés osmótico (da Fonseca-Pereira et al., 2019). La Trx *h* se localiza en múltiples compartimentos (citosol, núcleo, retículo endoplasmático y mitocondria) y está involucrada en la protección contra el estrés oxidativo, en particular durante la germinación de semillas (Gelhaye et al., 2004). La Trx atípica NTRC está localizada en el estroma de plastidios de órganos autotróficos y heterotróficos (Serrato et al., 2004; Kirchsteiger et al., 2012). Es una enzima bimodular formada por un dominio NTR en su extremo N-terminal y un dominio Trx en su extremo C-terminal (**Figura 5**) (Serrato et al., 2004; Cejudo et al., 2012). Desde su descubrimiento en 2004 (Serrato et al., 2004) se ha avanzado mucho en el conocimiento de las propiedades de NTRC, se ha caracterizado su modo de acción y se han identificado los procesos que regula. NTRC forma parte de la maquinaria antioxidante del cloroplasto ya que regula el estado redox de una peroxirredoxina (2-Cys-Prx) a la que se le ha atribuido un papel importante en la detoxificación de H_2O_2 en el cloroplasto (Pérez-Ruiz et al., 2006; Puerto-Galán et al., 2015). Además, NTRC juega un papel importante en el control de la fotosíntesis a través de la regulación del estado redox de la Mg-quelatasa implicada en la producción de clorofilas (Richter et al., 2013; Pérez-Ruiz et al., 2014; Richter et al., 2016), de la ATP sintasa (Carrillo et al., 2016; Nikkanen et al., 2016) y de la Trx *f* (Thormählen et al., 2015; Nikkanen et al., 2016; Yoshida and Hisabori, 2016; Ojeda et al., 2017). También juega un papel determinante en la biosíntesis de almidón mediante la modificación del estado redox de la AGPasa (Michalska et al.,

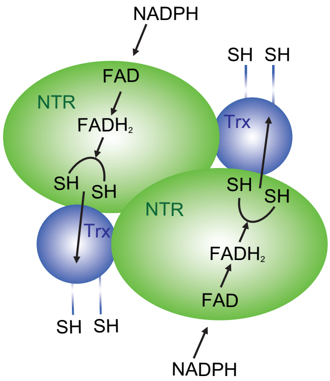
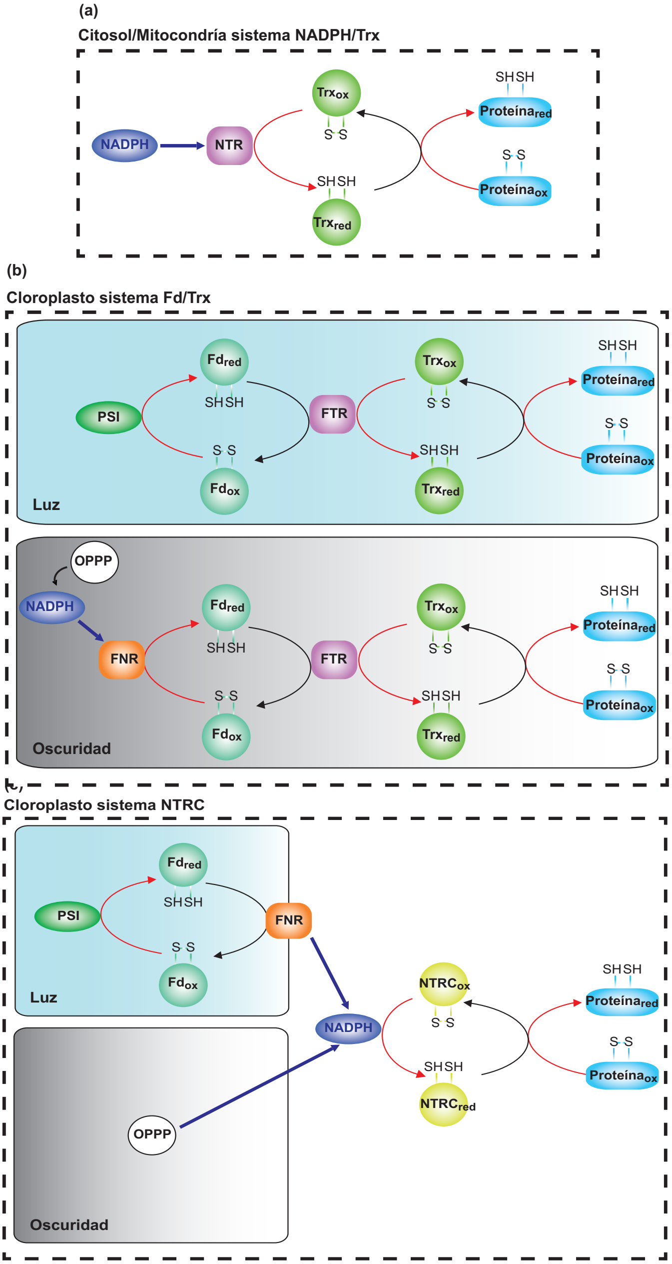


Figura 5: Mecanismo de acción de NTRC. El NADPH dona sus electrones al cofactor FAD del dominio NTR de cada subunidad de NTRC y seguidamente los electrones se transfieren a los residuos de cisteínas que se encuentran en el sitio activo del dominio Trx. (Figura adaptada de Cejudo et al. (2012)).

2009; Valerio et al., 2010; Li et al., 2011; Lepistö et al., 2013). Además NTRC participa en la formación de raíces laterales a través de la regulación de la síntesis de auxinas por mecanismos aún desconocidos (Kirchsteiger et al., 2009) y juega un papel importante en el control del non-photochemical quenching (NPQ) a través de su control del estado redox de la violaxantina de-epoxidasa (Naranjo et al., 2016).

Los sistemas de reducción de proteínas mediados por Trxs extraplastidiales y plastidiales son diferentes (**Figura 6**). En el caso de las Trxs citosólicas y mitocondriales el poder reductor necesario para la reducción de la proteína diana proviene del NADPH, que transfiere sus electrones a la proteína Trx reductasa dependiente de NADPH (NTR) que es a su vez la encargada de reducir a la Trx para que esta reduzca a la proteína diana. Este mecanismo se denomina sistema NADPH/Trx (**Figura 6a**) (Buchanan and Balmer, 2005). En cambio, las Trxs plastidiales pueden utilizar dos mecanismos de reducción: uno dependiente de Trx y otro dependiente de NTRC. El sistema Fd/Trx puede recibir el poder reductor a través del PSI en condiciones de luz o través de la OPPP mediante el sistema Fd-$NADP^+$ reductasa (FNR) en condiciones de oscuridad. En ambas condiciones los electrones son cedidos a la Fd que los transfiere a la proteína Fd-Trx-reductasa (FTR), que finalmente reduce a las Trxs (**Figura 6b**). El sistema NTRC utiliza NADPH como poder reductor para la regulación redox en el cloroplasto. Durante el día, cuando los niveles de Fd reducida son elevados, NTRC juega un papel complementario al sistema Fd/Trx, y obtiene el poder reductor vía Fd y FNR. Sin embargo, durante la



(a) Citosol/Mitocondría sistema NADPH/Trx

(b) Cloroplasto sistema Fd/Trx

(c) Cloroplasto sistema NTRC

Figura 6: Sistemas de reducción de las tiorredoxinas. (a) El sistema NADPH/Trx de las mitocondrias y del citosol usa el poder reductor del NADPH y transfiere los electrones a NTR. (b) En el sistema Fd/Trx de los plastidios la Fd puede ser reducida por los electrones provenientes de la OPPP o del PSI. (c) El sistema NTRC de los plastidios utiliza el poder reductor que proviene de la cadena de transporte de electrones vía FNR o de la OPPP.

noche, cuando los niveles de Fd reducida y NADPH provenientes de las reacciones fotoquímicas son bajos, NTRC obtiene el poder reductor desde el NADPH producido por la OPPP (Pérez-Ruiz et al., 2006; Cejudo et al., 2012) (**Figura 6c**).

4. LA RUTA MEP Y LA SÍNTESIS DE ISOPRENOIDES EN EL PLASTIDIO

Los isoprenoides, también llamados terpenoides, son el grupo de metabolitos secundarios más abundante y diverso, tanto estructural como funcionalmente, en procariotas y eucariotas. Participan en múltiples procesos tales como las modificaciones postraduccionales a través de prenilación y glicosilación, la biosíntesis de la pared celular, el transporte de electrones, la fotosíntesis, la señalización intracelular y la degradación de proteínas (Pulido et al., 2012; Banerjee and Sharkey, 2014; Frank and Groll, 2017).

En las plantas, los compuestos precursores de los isoprenoides (el isopentenil disfosfato (IPP) y el dimetilalil difosfato (DMAPP)) se sintetizan a través de dos rutas: la ruta del mevalonato (que tiene lugar en el citosol) y la ruta MEP (que tiene lugar en el plastidio) (Pulido et al., 2012; Banerjee and Sharkey, 2014). Los isoprenoides que se sintetizan en el plastidio participan en procesos tan esenciales como la regulación del crecimiento y el desarrollo (síntesis de CKs, giberelinas, ácido abscísico) y la fotosíntesis (síntesis de carotenoides, clorofilas, plastoquinonas, tocoferoles) (**Figura 7**) (Joyard et al., 2009; Tzin and Galili, 2010; Czarnecki and Grimm, 2012; Pulido et al., 2012; Vranová et al., 2012; Banerjee and Sharkey, 2014). Los isoprenoides plastidiales también participan en las vías de señalización del desarrollo del plastidio o en la producción de moléculas señal tales como los tocoferoles que forman parte de una red compleja de señalización modulada por ROS, antioxidantes y las hormonas ABA, ácido salicílico y jasmónico (Munné-Bosch and Alegre, 2002; Rodríguez-Concepción, 2002; Munné-Bosch, 2005; Phillips et al., 2008; Joyard et al., 2009; Pulido et al., 2012).

La ruta MEP comienza con la reacción irreversible catalizada por la enzima 1-deoxy-D-xylulosa-5-fosfato sintasa (DXS) que utiliza piruvato y GAP, y finaliza con la producción de los precursores de los isoprenoides IPP y DMAPP (Phillips et al., 2008; Cordoba et al., 2009) (**Figura 7**). Todas las enzimas que forman parte de esta ruta están codificadas por el genoma nuclear (Rodríguez-Concepción, 2002; Cordoba et al., 2009; Joyard et al., 2009; Kato and Sakamoto, 2010; Lee et al., 2013). La ruta MEP utiliza ATP y poder reductor (NADPH) para su actividad. En cloroplastos iluminados, la ruta MEP

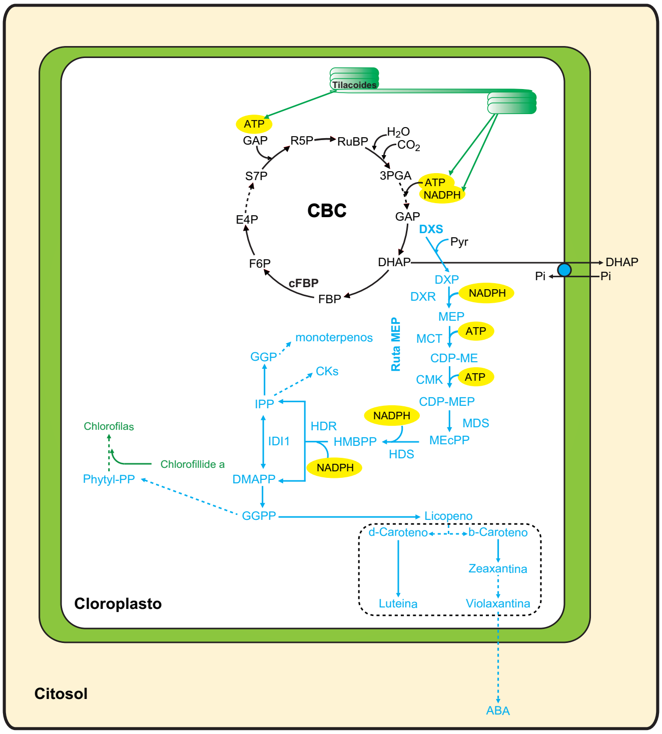


Figura 7: Esquema de la síntesis de isoprenoides en el cloroplasto. En azul se destaca la ruta MEP en la que se produce el IPP y DMAPP necesarios para la síntesis de isoprenoides plastidiales.

obtiene el poder reductor a partir de la cadena de transporte de electrones del cloroplasto, mientras que en cloroplastos no iluminados y en plastidios fotosintéticamente inactivos, el poder reductor lo obtiene de la glucólisis o de la OPPP. La ruta MEP está regulada a través de diferentes mecanismos: (i) la disponibilidad de GAP, que en el caso de las hojas depende de la actividad fotosintética (Ghirardo et al., 2010; Banerjee and Sharkey, 2014; Pokhilko et al., 2015); (ii) la retroalimentación negativa ejercida por IPP y DMAPP sobre la enzima DXS (Cordoba et al., 2009; Pokhilko et al., 2015) y la (iii) regulación postraduccional a través del control de la estabilidad (y por tanto de la actividad) de DXS mediante el sistema de control de calidad de proteínas que implica la acción del complejo Clp, la chaperona Hsp70 y la proteína J20 (Banerjee et al., 2013; Ghirardo et al., 2014; Wright et al., 2014; Pokhilko et al., 2015; Pulido et al., 2016; Rodríguez-Concepción et al., 2019).

5. CONTROL DE CALIDAD DE LAS PROTEÍNAS

La maquinaria implicada en el control de calidad de las proteínas incluye peptidasas, chaperonas, co-chaperonas y proteasas que son las encargadas del adecuado procesamiento proteolítico, recorte y maduración de las proteínas codificadas tanto en el núcleo, como en el plastidio y en la mitocondria (Kato and Sakamoto, 2010; Olinares et al., 2011). La mayoría de las proteínas plastidiales se codifican en el núcleo, se sintetizan en el citosol como pre-proteínas que contienen péptidos de tránsito al plastidio y se transportan al interior del estroma del cloroplasto a través del complejo proteico TOC/TIC localizado en las membranas externa e interna del cloroplasto (**Figura 8**) (Jarvis and López-Juez, 2013; Nishimura et al., 2017a). Una vez que las pre-proteínas entran en el estroma del cloroplasto, el péptido de tránsito es eliminado por una peptidasa y la proteína madura resultante es plegada por una chaperona localizada en el estroma (Kato and Sakamoto, 2010). Aquellas proteínas que ejercen su función en el interior del tilacoide deben sufrir un procesamiento adicional mediado por chaperonas (encargadas de ayudar al plegamiento de otras proteínas recién sintetizadas o dañadas y/o de dirigir la degradación proteolítica de las proteínas irreversiblemente dañadas) y proteasas. Entre los diferentes tipos de chaperonas existentes en la célula, las pertenecientes a la

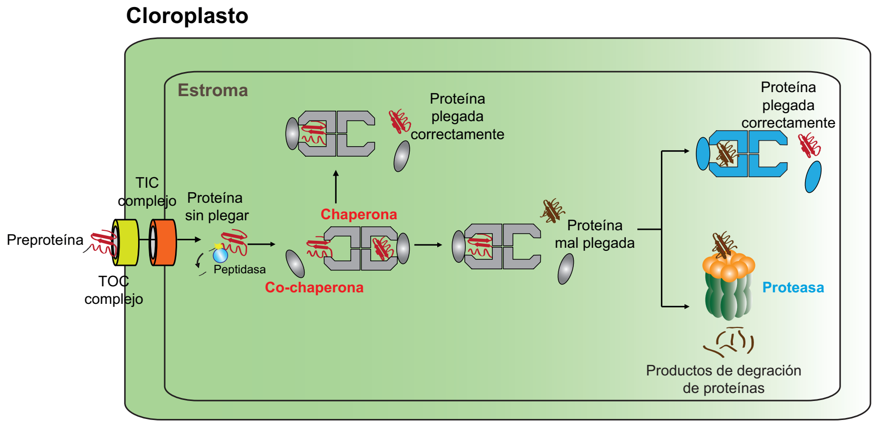


Figura 8: Sistema de estabilización de proteínas en el interior del cloroplasto. El sistema incluye el complejo TOC/TIC de entrada de proteínas al interior del cloroplasto, las peptidasas encargadas de eliminar el péptido de tránsito y el sistema de chaperonas, co-chaperonas y proteasas encargados del correcto plegamiento o eliminación de las proteínas.

familia de proteínas de choque térmico (Hsp) es la más abundante e incluye las proteínas Hsp60, Hsp70, Hsp90 y Hsp100 que se clasifican según su peso molecular: (Zhao and Liu, 2018). Estas chaperonas requieren la ayuda de co-chaperonas (Cpn10, Cpn20, Cpn60) y la presencia de ATP y Mg^{2+}.

Entre los 18 tipos de proteasas existentes en el cloroplasto, las dependientes de ATP (Clp y FstH) juegan un papel muy importante en la homeostasis proteica plastidial. Las FstH desempeñan un papel crítico en la biogénesis de la membrana tilacoidal y en el control de calidad de las proteínas de dicha membrana. Las proteasas Clp actúan en el estroma del cloroplasto eliminando proteínas dañadas (Kato and Sakamoto, 2018) (**Figura 8**). El complejo de proteasa Clp actúa en coordinación con chaperonas plastidiales codificadas nuclearmente para controlar los niveles y el adecuado plegado de las proteínas (Olinares et al., 2011; Nishimura and Van Wijk, 2015).

6. HIPÓTESIS DE TRABAJO

Las hipótesis que justificaron la ejecución de este trabajo de investigación fueron las siguientes:

- *Hipótesis relacionada con el papel que juega NTRC en la regulación postraduccional de la respuesta de la planta a volátiles microbianos:* Estudios previos llevados a cabo por el grupo de investigación en el que he realizado mi tesis doctoral demostraron que el incremento de los niveles de almidón en respuesta a los VCs fúngicos implica una activación redox de la AGPasa mediada por NTRC (Li et al., 2011). Estos antecedentes permitieron elaborar la hipótesis de que la respuesta de la planta a VCs microbianos implica cambios globales en el redox-proteoma de la planta en los que NTRC juega un papel fundamental. Para explorar esta hipótesis, comparé el crecimiento, el desarrollo, el metabolismo y el redox proteoma de plantas WT y *ntrc* cultivadas en presencia o ausencia de VC emitidos por *A. alternata*.

- *Hipótesis relacionada con el papel que juegan la regulación redox de la fotosíntesis y la homeostasis de enzimas de la ruta MEP en la respuesta de la planta a volátiles microbianos:* La síntesis de isoprenoides plastidiales implicados en el crecimiento y el desarrollo de la planta y en su relación con el entorno está finamente regulada por la provisión de GAP por parte del CBC y por mecanismos proteostáticos que regulan la expresión de enzimas de la ruta MEP. Investigaciones llevadas a cabo por mi grupo de investigación antes de comenzar mi trabajo demostraron que los VCs microbianos (i) fomentan la producción de GAP fotosintético y pigmentos fotosintéticos y (ii) dan lugar a cambios en el transcriptoma y proteoma de la planta mediados por hormonas derivadas de isoprenoides plastidiales (Sánchez-López et al., 2016a; Sánchez-López et al., 2016b). Estos antecedentes sentaron las bases para elaborar una hipótesis según la cual la respuesta de las plantas a VCs microbianos es debida a una activación de la ruta MEP como consecuencia de un incremento de la provisión de GAP fotosintético y/o de la expresión de enzimas de la ruta MEP. Para explorar esta hipótesis comparé la respuesta en el metabolismo, niveles de hormonas y proteoma de plantas WT y un mutante *knock out* de la isoforma plastidial de la cFBP1 (*cfbp1*). Arabidopsis expresa dos isoformas de FBP plastidial: cFBP1 y cFBP2. Contrariamente a lo que ocurre con cFBP2, la actividad de cFBP1 está sujeta a cambios en su estado redox (Serrato et al., 2009; Rojas-González et al., 2015). Teniendo en cuenta que (i) el CBC está regulado por las variaciones del estado redox de las enzimas implicadas en esta ruta (Michelet et al., 2013) y (ii) los VCs microbianos alteran el estado redox de estas enzimas (Ameztoy et al., 2019), es concebible que si la respuesta promovida por VCs microbianos en la planta es debida a una activación redox del CBC, la respuesta de las plantas *cfbp1* a los VCs fúngicos debería ser más débil que la de las plantas WT. Por el contrario, si la activación redox de la fotosíntesis no juega un papel importante en la respuesta de la planta a los VCs microbianos, la respuesta de las *cfbp1* a los VCs microbianos debería ser similar a la observada en plantas WT.

OBJETIVOS

El objetivo general de esta tesis es profundizar en el conocimiento de los mecanismos que regulan la respuesta de las plantas a los VCs microbianos. Para ello me planteé los siguientes objetivos específicos:

Objetivo #1: estudiar el papel que juega NTRC en la regulación de la respuesta de plantas de Arabidopsis a la acción de VCs emitidos por *A. alternata*.

Objetivo #2: estudiar el papel que juegan la regulación redox de la fotosíntesis y la homeostasis de enzimas de la ruta MEP en la respuesta de la planta a VCs microbianos.

CAPÍTULO I

Plant responses to fungal volatiles involve global post-translational thiol redox proteome changes that affect photosynthesis

INTRODUCTION

It is well known that volatile compounds (VCs) emitted by beneficial rhizosphere bacteria and fungi can promote plant growth (Ryu et al., 2003; Hung et al., 2013; Kanchiswamy et al., 2015; Piechulla et al., 2017) and root developmental changes (Gutierrez-Luna et al., 2010; Delaplace et al., 2015; Ditengou et al., 2015; Garnica-Vergara et al., 2016). However, recent studies have shown that pathogens may also release growth-promoting VCs (Sánchez-López et al., 2016b). Promotion of growth and developmental changes by microbial VCs has frequently been associated with lipophilic carbon-containing compounds with molecular masses less than 300 Da and high equilibrium vapor pressures, known as volatile organic compounds (VOCs) (Kanchiswamy et al., 2015). In addition to VOCs, microorganisms also release volatile inorganic compounds (VICs) with molecular masses less than 45 Da. When exogenously applied in discrete forms and low concentrations, some of these compounds can act as signaling molecules that promote plant growth, photosynthesis and developmental changes through thiol redox modifications (He et al., 2008; Chen et al., 2011; Takahashi et al., 2014). Using a "box-in-box" co-cultivation system in which plants are grown in the vicinity of microbial cultures covered with VOCs-adsorbing charcoal filters, we have recently provided evidence that VOCs with molecular masses less than 45 Da and/or VICs other than CO_2 are strong determinants of plants´ responses to microbial VCs (García-Gómez et al., 2019).

In Arabidopsis plants exposed to VCs emitted by various microbes, growth promotion is accompanied by increases in photosynthesis rates, levels of cytokinins (CKs) derived from the 2-C-methyl-D-erythritol 4-phosphate (MEP) pathway, and starch in leaves, together with reductions in abscisic acid (ABA) contents, and distinct changes in shoot and root development (Zhang et al., 2008; Ezquer et al., 2010; Li et al., 2011; Sánchez-López et al., 2016b; García-Gómez et al., 2019). Mutants with reduced CK and ABA sensitivity have been found to respond weakly to microbial VCs, indicating that plant responses to microbial VCs involve CK and ABA signaling (Zhang et al., 2008; Sánchez-López et al., 2016b). Several studies have also found similarities in transcriptional changes in plants exposed to VCs emitted by different microorganisms, despite substantial differences in induced developmental changes in roots and shoots (Sánchez-López et al., 2016b; García-Gómez et al., 2019). These findings suggest that regulation of some plant responses to microbial VCs is primarily post-transcriptional

(García-Gómez et al., 2019). This hypothesis is supported by reports that fungal VCs do not affect the transcription of genes encoding most proteins that are differentially expressed following plants´ exposure to VCs (Sánchez-López et al., 2016b), and microbial VCs promote post-translational reductive activation of starch biosynthetic enzymes (García-Gómez et al., 2019).

Reversible reduction-oxidation (redox) thiol modifications of cysteines (such as disulfide bond formation, S-glutathionylation, S-nitrosylation and S-sulfenylation) provide fundamental post-translational "switches" that play important roles in the regulatory mechanisms of metabolism, growth and development that allow plants to adjust to continuously changing environmental constraints (Buchanan and Balmer, 2005; Couturier et al., 2013; Akter et al., 2015; Hu et al., 2015; Keech et al., 2017). Therefore, identification of reactive cysteine residues is crucial not only for understanding protein functions but also for obtaining insights into the mechanisms involved in plants´ responses to environmental changes. To assist such efforts, increasing numbers of mass spectrometry (MS)-based large-scale redox proteomic techniques have been developed recently to identify proteins that undergo reversible oxidative modifications (Fares et al., 2011; Guo et al., 2014; Liu et al., 2014; Akter et al., 2015; De Smet et al., 2019). The results obtained using these approaches indicate that almost any metabolic pathway may be subject to thiol-based redox regulation.

Important components of plants´ thiol redox regulation machinery include thioredoxins (Trx) proteins that mediate disulfide-dithiol exchange of cysteine residues, thereby modulating activities of target proteins. Plant chloroplasts have a versatile set of Trxs, which receive reducing equivalents from the photosystem I (PSI) electron acceptor ferredoxin (Fdx), with participation of a Fdx-dependent Trx reductase (FTR) (Schürmann and Buchanan, 2008). In addition, plastids contain an NADPH-dependent Trx reductase (NTR) with a joint Trx domain, called NTRC, which uses NADPH produced by the oxidative pentose phosphate pathway (OPPP) and photosynthetic electron transport (PET) as a source of reducing power (Serrato et al., 2004). In Arabidopsis, NTRC is the most efficient reductant of two H_2O_2-detoxifying 2-Cys peroxiredoxins (Prxs) A and B, suggesting that it plays an important role in avoidance of toxic levels of reactive oxygen species (ROS) (Pérez-Ruiz et al., 2006; Kirchsteiger et al., 2009; Pulido et al., 2010; Puerto-Galán et al., 2015). Biochemical and genetic studies have provided evidence that NTRC participates in regulation of the redox status of stromal target proteins, including starch metabolism enzymes (Valerio et al., 2010; Lepistö et al., 2013), ATP synthase (Carrillo et al., 2016; Nikkanen et al., 2016) and diverse Trxs that control the redox status of Calvin-Benson cycle (CBC) enzymes such as plastidial fructose-1,6-bisphosphatase (cFBP1), phosphoribulokinase (PRK), sedoheptulose-1,7-bisphosphatase (SBP) and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (Nikkanen et al., 2016; Yoshida and Hisabori, 2016; Ojeda et al., 2017). NTRC also regulates the redox status of Mg-protoporfirin IX methyltransferase (CHLM), which is involved in chlorophyll biosynthesis (Richter et al., 2013; Da et al., 2017), and CHLI (Pérez-Ruiz et al., 2014), which is the subunit of the Mg-chelatase complex involved in chlorophyll biosynthesis and ABA signaling (Tsuzuki et al., 2011 ; Du et al., 2012). Furthermore, recent studies have shown that NTRC plays important roles in control of non-photochemical quenching (NPQ) and PET (Carrillo et al., 2016; Naranjo et al., 2016a).

Arabidopsis NTRC knock out (*ntrc*) mutants show a strong photoperiod-dependent phenotype of stunted growth and low chlorophyll content, highlighting the enzyme´s crucial roles in chloroplast functions, photosynthesis and growth (Pérez-Ruiz et al., 2006; Lepistö et al., 2009). NTRC is localized in plastids of both photosynthetic and non-photosynthetic tissues, prompting the hypothesis that it acts as a general molecular switch capable of converting reducing power in the form of NADPH into redox signals that coordinate redox regulation in the whole plant (Kirchsteiger et al., 2012). Growth is dramatically inhibited in Arabidopsis mutants combining deficiencies of NTRC and Trxs *f* and *x* (Ojeda et al., 2017), suggesting that NTRC and the Fdx-FTR-Trxs systems act in concert. Recent studies have shown that the *ntrc* phenotype is suppressed by decreased expression of 2-Cys Prxs (Pérez-Ruiz et al., 2017; Ojeda et al., 2018). These findings led to the proposal that 2-Cys Prxs are crucial to maintain the redox status of the pool of plastidial Trxs and, consequently, the light-dependent reduction of photosynthesis-related proteins (Pérez-Ruiz et al., 2017; Ojeda et al., 2018). Accordingly, it has been suggested that the phenotype of *ntrc* plants is due to impairment of the redox regulation of chloroplastic growth- and photosynthesis-related processes rather than ROS over-accumulation as a consequence of 2-Cys Prxs inactivation (Pérez-Ruiz et al., 2017).

Microbial VCs induce smaller increases in starch contents in *ntrc* plants than in wild type (WT) plants (Li et al., 2011). Since NTRC plays a central role in redox-regulation of various plastidial processes involved in metabolism, growth and development, we hypothesized that NTRC could be involved in plants´ overall responses to VCs. To test the potential importance of post-translational thiol modifications of proteins in plant responses to microbial VCs, and investigate NTRC´s contribution to these responses, we compared developmental, metabolic, hormonal and redox-proteomic responses of WT and *ntrc* plants to VCs emitted by the fungal phytophathogen *Alternaria alternata*. Our findings show that NTRC is an important mediator of plant responses to fungal VCs and provide a broad quantitative picture of redox-mediated responses of the thiol proteome in Arabidopsis to VCs, allowing us to infer potential redox switches.

MATERIAL AND METHODS

Plants, growth conditions and sampling

The work was carried out using *Arabidopsis thaliana* L. (Heynh) ecotype Columbia (Col-0), the *ntrc* mutant (Pulido et al., 2010), the *Δ2cp* and *ntrc*-*Δ2cp* mutants with severe reduction of 2-Cys Prxs expression (Pérez-Ruiz et al., 2017), the ADPglucose pyrophosphorylase null *aps1* mutant (SALK_040155) and the *gwd* (SALK_077211) mutant. Microorganisms used in this study were also used by Sánchez-López et al. (2016b). Unless otherwise indicated, the plants were cultured in Petri dishes (92 x 16 mm, Sarstedt, Ref. 82.1472.001) containing sucrose-free half-strength solid Murashige and Skoog (MS) (Phytotechlab M519) medium in growth chambers providing ‘long day’ 16 h light (90 µmol photons sec^{-1} m^{-2}), 22 ºC /8 h dark, 18 ºC cycles. Fungi were cultured in small Petri dishes (35x10 mm, Sarstedt, Ref. 82.1135.500) containing solid MS medium supplemented with 90 mM sucrose. Bacteria were cultured in small Petri dishes containing solid M9 minimal (95 mM Na_2HPO_4/44 mM KH_2PO_4/17 mM NaCl/37 mM NH_4Cl/0.1 mM $CaCl_2$/2 mM $MgSO_4$, 1.5% bacteriological agar) medium supplemented with 50 mM glucose. M9 medium for *Bacillus subtilis* culture was supplemented with 7 µM each of $MnSO_4$, $FeSO_4$ and $ZnSO_4$ and 1 µM thiamine. Effects of microbial VCs on plants were investigated using the “box-in-box” co-cultivation system as described in (García-Gómez et al., 2019). Briefly, microbial cultures in unlidded Petri dishes with a top layer of VOCs-adsorbing activated charcoal filters and plant cultures of 14 days after sowing were placed together in sterile plastic boxes (200 x 150 x 50 mm IT200N Instrument Trays; AW Gregory, UK) sealed with polyvinyl chloride plastic wrap. As negative controls, Petri dishes containing plant cultures were incubated in sealed boxes together with Petri dishes containing sterile microbial culture media and a charcoal filter.

At the indicated incubation periods, leaves were harvested, immediately freeze-clamped and ground to a fine powder in liquid nitrogen with a pestle and mortar.

Determination of gas exchange rates and photosynthetic parameters

Gas exchange rates were determined as described by Sánchez-López et al. (2016b) using a LI-COR 6400 gas exchange portable photosynthesis system (LI-COR, Lincoln, NE, USA). The net rate of CO_2 assimilation (A_n) was calculated using equations developed by von Caemmerer and Farquhar (1981). The maximum rate of carboxylation by Rubisco (V_{cmax}), triose phosphate use (*TPU*) and maximum electron transport demand for RuBP regeneration (J_{max}) values were calculated from A_n/C_i curves (where C_i is the intracellular CO_2 concentration) according to Long and Bernacchi (2003). Photosynthetic electron transport (ETR) values were calculated according to Krall and Edwards (1992) as Φ_{PSII} x PPFD x 0.84 x 0.5, where PPFD is the photosynthetic photon flux density incident on the leaf, Φ_{PSII} is the photosystem II (PSII) operating efficiency, 0.5 was used as the fraction of excitation energy distributed to PSII (Ögren and Evans, 1993) and 0.84 as the fractional light absorbance (Morales et al., 1991). Chlorophyll fluorescence emission parameters were determined using a PlantScreenTM XYZ System (Photon Systems Instruments, Brno, Czech Republic). The phenotyping system was equipped with a FluorCam unit for pulse amplitude modulated measurement of chlorophyll fluorescence. After 20 min of dark adaptation the standardized measurement protocol was applied, as described by Humplík et al. (2015). The maximum quantum yields of PSII in the dark-adapted state (Φ_{Po}) (also referred to as Fv/Fm), Φ_{PSII} and non-photochemical quenching Φ_{NPQ}) were calculated from the measured parameters according to Lazár (2015).

Root morphological analysis

Numbers and lengths of roots of plants grown on vertical square Petri dishes (10 x 10 x 2 cm, Sarstedt, Ref. 82.9923.422) were measured using a MVX10 stereomicroscope and microphotographs were captured with a DP72 video camera equipped with Cell D software (all supplied by Olympus, Japan).

Analytical procedures

For sucrose, glucose and fructose measurements, a 0.1 g aliquot of the frozen powders (see above) were resuspended in 1 ml of 90% ethanol, incubated at 70 ^{o}C for 90 min and centrifuged at 13000 x g for 10 min. Sugar contents in the supernatants were then determined by HPLC with pulsed amperometric detection using a ICS-3000 Dionex system as described by Bahaji et al. (2015). NADP and NADPH contents were measured as described by Queval and Noctor (2007). Recovery percentages of the analytes were estimated from differences in measured amounts in samples of frozen tissue slurry with and without spiking by standards immediately after addition of extraction solutions. All presented concentrations of these metabolites were corrected for losses during extraction. Starch was measured using an amyloglucosydase–based test kit (Boehringer Mannheim, Germany), and chlorophyll contents were quantified according to Lichtenthaler (1987). To determine levels of CKs, portions of the frozen leaves (prepared as described above) were lyophilized and CKs were quantified following Novák et al. (2008). ABA contents were determined as described by Floková et al. (2014).

ROS staining

ROS were semi-quantitatively detected in rosettes essentially as described by Nguyen et al. (2017). Briefly, superoxide anion was detected by staining rosettes for 15 min with 0.05% nitro blue tetrazolium (NBT) (w/v) in 50 mM potassium phosphate, pH 7.0, and H_2O_2 by staining for 5 h with 0.1% 3,3′-diaminobenzidine (DAB) in 10 mM potassium phosphate, pH 7.0.

Real-time quantitative PCR

Total RNA was extracted from frozen Arabidopsis leaves of *in vitro* cultured plants using the Trizol method according to the manufacturer’s recommendations (Invitrogen), following treatment with RNAase-free DNAase (Takara). RNA (1.5 µg) was reverse-transcribed using polyT primers and an Expand Reverse Transcriptase kit (Roche) according to the manufacturer’s instructions. RT-PCR amplification was performed as described by Sánchez-López el al. (2016b) using primers listed in **Table S1**, and their specificity was checked by separating the obtained products on 1.8% agarose gels.

Identification of redox-sensitive cysteines

Protein extraction and tagging

Proteins were extracted and tagged essentially as described by Guo et al. (2014) with some modifications. Briefly, 0.5 g of plant tissue was ground in liquid nitrogen, mixed with 2 mL extraction buffer (20 mM HEPES, 0.5 mM EDTA, 0.5% Triton X-100, 100 mM NaCl, 1% SDS) supplemented with 100 mM N-ethylmaleimide (NEM) to block the free thiol groups, and incubated for 1 h at room temperature. The mixture was centrifuged at 4 ºC for 10 min at 10,000 x g. Proteins were precipitated and washed to remove any free NEM by adding of 5 volumes of iced acetone and incubating overnight at -20 ºC. After centrifugation, the supernatant was discarded and the protein pellet was recovered by centrifugation at 10,000 x g and 4 ºC for 10 min, rinsed with cold acetone three times, and air-dried. Urea solution (8 M) was added to dissolve the pellet, and brief intermittent sonication was applied until the pellet dissolved. The resulting protein-containing solution was incubated with 10 mM dithiothreitol (DTT) at 37 ºC for 30 min to reduce oxidized thiols. DTT was then removed with PD-10 desalting columns (GE Healthcare). The protein concentration of each preparation was determined using a Pierce™ 660 nm protein Assay Kit (Thermo Fisher Scientific), and a portion containing 500 µg of proteins was used for the subsequent enrichment experiment. The samples were alkylated with 1 M of 2-iodoacetamide (IAM) (Wako) for 1 h at 37 °C in the dark to tag the DTT-reduced thiols by carbamidomethylation. Proteins were acetone-precipitated, re-solubilized in 8 M urea, digested with lysine (Sigma) for 3 h and trypsin (Sigma) overnight at 37 ºC at a 1:40 trypsin-to-protein mass ratio, desalted using Sep-Pak C18 cartridges, and dried in a SpeedVac.

iTRAQ labeling of peptides and strong cation exchange fractionation

Peptides from samples of non-VC-treated WT plants, VC-treated WT plants, non-VC-treated *ntrc* plants and VC-treated *ntrc* plants were labeled at room temperature for 2 h with iTRAQ reporter reagents 114, 115, 116 and 117, respectively, according to the iTRAQ manual (SCIEX). All four samples were then mixed in a single tube and dried in a SpeedVac (Eppendorf). Peptides were subsequently fractionated by strong cation exchange columns (SCIEX, USA) and then lyophilized to dryness.

Liquid chromatography–mass spectrometry (LC-MS/MS) analysis

Proteomic profiles of three technical replicates of samples were quantitatively analyzed as described by Fukao et al. (2011) and Shiraya et al. (2015) using a coupled DiNA-A (KYA Tech., Tokyo, Japan) and LTQ-Orbitrap XL (Thermo Fisher Scientific) liquid chromatography-MS/MS system. The ionization voltage and capillary transfer temperature at the electrospray ionization nano-stage were set to 1.7–2.5 kV and 200

°C, respectively. iTRAQ-labelled peptides were separated in a Mono Cap C18 High Resolution 2000 column (GL Sciences), using a mobile phase consisting of a 240-min linear gradient of 2-26.7% acetonitrile in water (with a 10 min wash with 80% acetonitrile, v/v, and 15 min re-equilibration between each run, maintaining 0.1% formic acid, v/v, throughout). Peptides that eluted from the column were introduced directly into the mass at a flow rate of 300 nL/min. Divalent or trivalent ions were subjected to MS/MS analysis in Top-3 data-dependent acquisition mode. CID and HCD settings for all MS/MS analyses were 35 and 45 eV, respectively.

MS data analysis

Raw MS data files were submitted to Proteome Discoverer 1.4 with the SEQUEST algorithm (Thermo Scientific Inc., Bremen, Germany) and MsAmanda (Dorfer et al., 2014) to search for matches in the Gene Ontology (GO) Arabidopsis database. Percolator was set to a target false discovery rate (FDR) of 0.05. Peptides were quantified using the iTRAQ4plex reporter ion method, and identified from database search results with the following criteria: enzyme, trypsin; maximum missed cleavage sites, 2; peptide charge, 2+ or 3+; MS tolerance, 5 ppm; MS/MS tolerance, ±0.6 Da; dynamic modification, oxidation (H, M, W), iTRAQ 4-plex (K, Y, N-terminus). Variable modifications for the search included carbamidomethylation and NEM at cysteines, iTRAQ (4-plex) at tyrosines, and oxidation at methionines (mass shifts: 57.02, 125.05, 144.10 and 15.99, respectively). The fixed modification was iTRAQ (4-plex) reagent labeling at N-terminal and lysine.

OxiTRAQ data analysis

Amounts of detected peptides were normalized using total intensities of their assigned mass spectra according to the SEQUEST searching results, and peptide ratios were calculated accordingly from medians of the normalized intensities. Log_2-transformed treated/control ratios were subjected to Student's t-test (two-tailed). Differences in concentrations of peptides between samples with fold changes greater than 1.9 or less than 0.5, and $P<0.05$, were considered significantly changed. The isobaric tags for relative and absolute quantitation (iTRAQ) data (Parker et al., 2012) were searched using the database mentioned above to generate information about changes in total protein levels. The same set of samples were analyzed in another MS run and used as technical replicates to determine possible variation caused by MS analysis. Student's t-test was applied to peak intensity values of all spectra of corresponding peptides from control and treated samples in the same MS run.

Statistical analysis

Presented data are means (± SE) obtained from 3-4 independent experiments, with 3-5 replicates for each experiment. The significance of differences between WT and *ntrc* plants not exposed to VCs, and plants exposed and not exposed to *A. alternata* VCs was statistically evaluated with Student´s t-test using the SPSS software. Differences were considered significant if $P<0.05$.

RESULTS

ntrc plants poorly respond to *A. alternata* VCs

Using the box-in-box co-cultivation system described by García-Gómez et al. (2019) we compared growth and developmental responses of WT and *ntrc* plants grown in the vicinity of *A. alternata* cultures covered with VOCs-adsorbing charcoal filters. We also analyzed the growth response to fungal VCs of near starch-less *aps1* plants impaired in starch biosynthesis, and starch-excess *gwd* plants impaired in starch breakdown (Caspar et al., 1991; Ventriglia et al., 2008; Baslam et al., 2017). In the absence of VOCs-depleted fungal VCs, rosettes and roots of the *ntrc* mutant were slightly smaller and lighter than those of WT plants (**Figure 1a, b**), as reported by Lepistö et al. (2009) and Li et al. (2011). *ntrc* plants produced shorter primary roots and fewer first and second order lateral roots (LRs) than WT plants (**Figure 1a, c**), as found by Kirchsteiger et al. (2012). In keeping with findings by Sánchez-López et al. (2016b) and García-Gómez et al. (2019), VOCs-depleted fungal VCs promoted rosette and root growth, elongation of the primary root and formation of first and second order LRs in WT plants (**Figure 1**), thereby increasing the density of the root system (**Figure 1c**). As in WT plants, VOCs-depleted fungal VCs promoted rosette and root growth in *aps1* and *gwd* plants (**Figure 2**). Notably, fungal VC-promoted rosette and root growth was substantially weaker in *ntrc* plants than in WT plants (**Figure 1a, b**). Furthermore, unlike in WT plants, VOCs-depleted fungal VCs did not promote primary root elongation or LR formation and did not enhance the root system density in the *ntrc* mutant (**Figure 1c**). Fungal VCs promoted root hair elongation in both WT and *ntrc* plants (**Figure 3**).

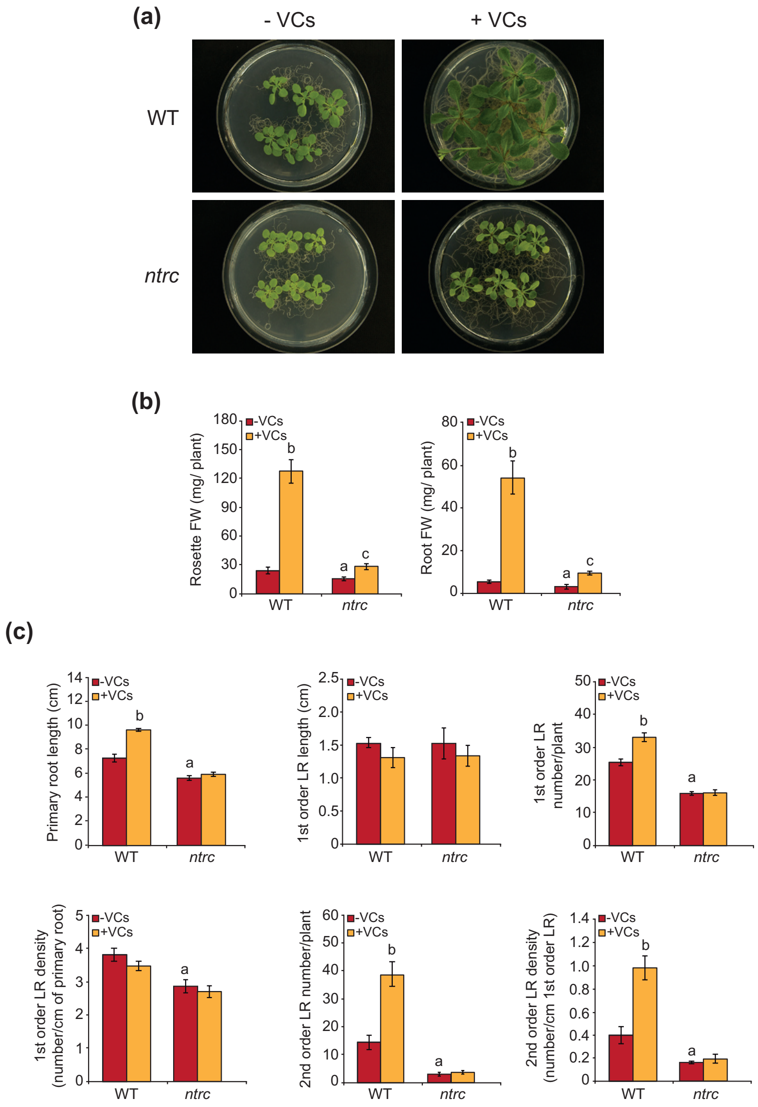


Figure 1. *ntrc* plants weakly respond to *A. alternata* VCs. (a) external phenotypes, (b) rosette and root FW and (c) root architecture parameters of WT and *ntrc* plants cultured in the absence or continuous presence of VCs emitted by adjacent *A. alternata* cultures covered with VOCs-adsorbing charcoal filters for one week. Values in panels (b) and (c) are means ± SE for three biological replicates (each a pool of 12 plants) obtained from four independent experiments. Letters "a", "b" and "c" indicate significant differences, according to Student´s t-test ($P<0.05$), between: "a" WT and *ntrc* plants cultured without fungal VC treatment, "b" VC-treated and non-treated WT plants, and "c" VC-treated and non-treated *ntrc* plants. Plants providing data shown in (c) were grown on vertical plates.

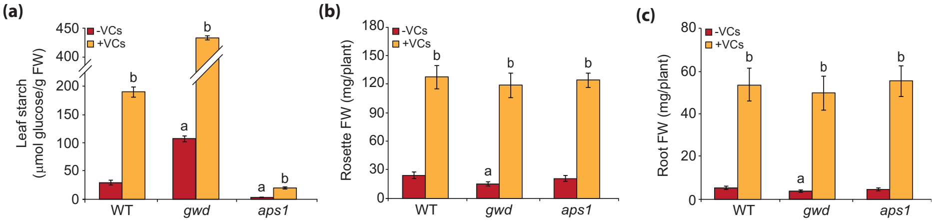


Figure 2. **Growth responses of starch excess (*gwd*) and starch deficient (*aps1*) mutants to fungal VCs are comparable to those of WT plants.** (a) Leaf starch content, (b) rosette FW and (c) root FW of WT, *aps1* and *gwd* plants cultured in the absence or continuous presence of VCs emitted by adjacent cultures of *A. alternata* for one week. Values are means ± SE for three biological replicates (each pool of 12 plants) obtained from 4 independent experiments. Letters "a" and "b" indicate significant differences, according to Student´s t-test ($p<0.05$), between: "a" WT and *gwd* or *aps1* plants cultured without fungal VC treatment, and "b" VC-treated and nontreated plants.

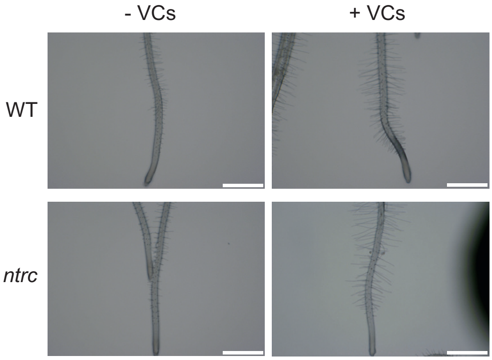


Figure 3. External root phenotypes of WT and *ntrc* plants cultured in the absence or continuous presence of VCs emitted by adjacent *A. alternata* cultures for one week. Scale bars = 1 mm.

It is known that VCs emitted by diverse types of microorganisms promote growth of WT plants (Sánchez-López et al., 2016b). To assess further the growth responses of *ntrc* plants to microbial VCs we grew plants in the presence of adjacent cultures of phylogenetically diverse species of fungi and bacteria with or without a top layer of VOCs-adsorbing charcoal filter. As shown in **Figure 4**, growth promoted by VOCs-depleted VCs of tested microorganisms was substantially weaker in *ntrc* plants than in WT plants. In keeping with García-Gómez et al. (2019), the responses of WT and *ntrc* plants grown in the vicinity of microbial cultures not covered with charcoal filters were identical to those of plants grown with adjacent fungal cultures covered with charcoal filters (not shown).

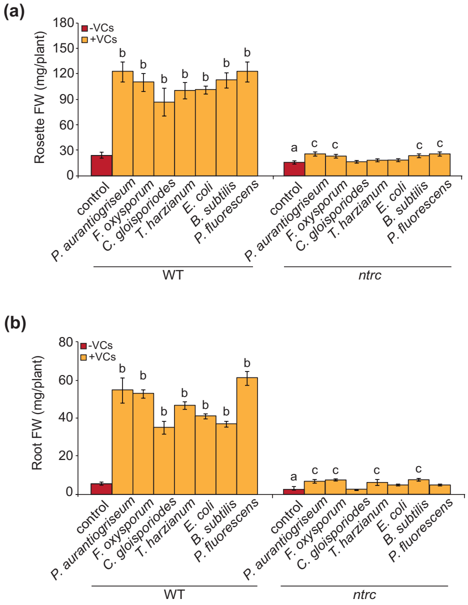


Figure 4. *ntrc* plants weakly respond to VCs emitted by phylogenetically diverse microorganisms. (a) rosette FW and (b) root FW of WT and *ntrc* plants cultured in the absence or continuous presence of VCs emitted by adjacent cultures of the indicated microorganisms for one week. Values are means ± SE for three biological replicates (each pool of 12 plants) obtained from 4 independent experiments. Letters “a”, “b” and “c” indicate significant differences, according to Student´s t-test ($p<0.05$), between: “a” WT and *ntrc* plants cultured without fungal VC treatment, “b” VC-treated and non-treated WT plants, and “c” VC-treated and non-treated *ntrc* plants.

A. alternata VCs reduce ABA content and increase levels of plastidial CKs, but weakly alter expression of ABA- and CK-responsive genes in *ntrc* plants

Having established NTRC´s involvement in plants´ response to fungal VCs, we compared their effects on ABA and CK contents and signaling in *ntrc* and WT plants. For this, we measured the contents of ABA and CKs in mature leaves of *ntrc* plants cultured in the absence or continuous presence of VCs emitted by adjacent *A. alternata* cultures for 3 days. We also analyzed expression levels of a selected group of CK- and ABA-responsive genes (Nemhauser et al., 2006; Bhargava et al., 2013; Brenner and Schmülling, 2015) that are sensitive to fungal VCs (cf. Table 3 in Sánchez-López et al., (2016b)) by qRT-PCR.

In the absence of fungal VCs, *ntrc* leaves had higher ABA content than WT leaves (209 ± 16 and 352 ± 8 pmol g^{-1} DW in WT and *ntrc* plants, respectively), but similar CK contents (**Table S2, Figure S1**). *A. alternata* VCs caused a significant reduction in

ABA contents in leaves of both WT and *ntrc* plants (86.1 ± 19.7 and 94.7 ± 25.4 pmol g^{-1} DW, respectively) and increases in levels of precursors, active and transport forms of plastidial CKs (**Table S2, Figure S1**). Notably, changes in levels of expression of ABA- and CK-responsive genes in response to VC treatment were substantially weaker in *ntrc* leaves than in WT leaves (**Figure 5**).

Fungal VCs weakly increase photosynthetic capacities of exposed *ntrc* plants

NTRC plays an important role in photosynthesis (Naranjo et al., 2016a; Nikkanen et al., 2016; Ojeda et al., 2017). To investigate whether *ntrc* plants´ weak responses to VCs could be due to non-responsiveness of photosynthesis to fungal VCs we compared key photosynthetic parameters of WT and *ntrc* plants cultured in the absence or continuous presence of VCs emitted by adjacent *A. alternata* cultures.

As shown in **Figure 6a**, and previously recorded (Pérez-Ruiz et al., 2006), leaves of *ntrc* plants that were not exposed to fungal VCs accumulated lower levels of chlorophyll than those of WT plants. In keeping with previous reports (Lepistö et al., 2009; Naranjo et al., 2016a), Φ_{Po}, Φ_{PSII} and photochemical quenching (qP) were lower in *ntrc* plants

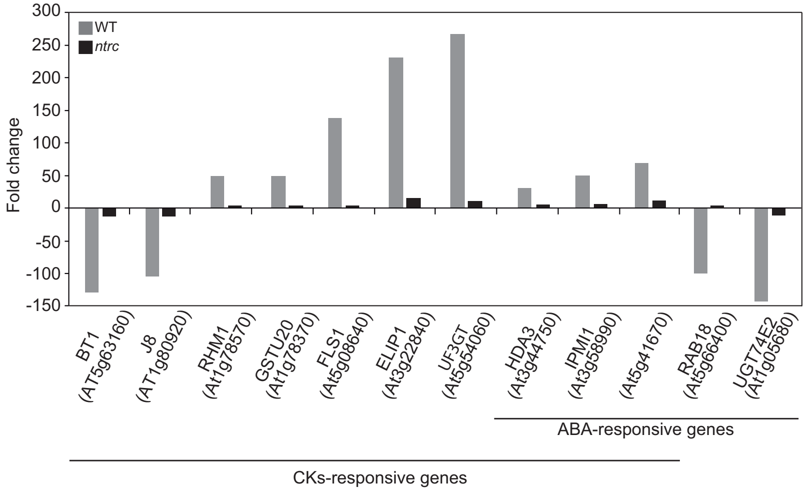


Figure 5. ***A. alternata* VCs weakly alter expression of ABA- and CK-responsive genes in *ntrc* plants.** Relative abundance of transcripts of CK- and ABA-responsive genes in leaves of WT and *ntrc* plants (gray and black, respectively) cultured in the absence or continuous presence of VCs emitted by adjacent *A. alternata* cultures for three days. Fold change values are differences in levels of transcripts (measured by quantitative RT-PCR) in leaves of plants cultured in the presence of VCs and harvested at the end of the light period for 16 h, relative to those of control leaves of plants cultured in the absence of VCs.

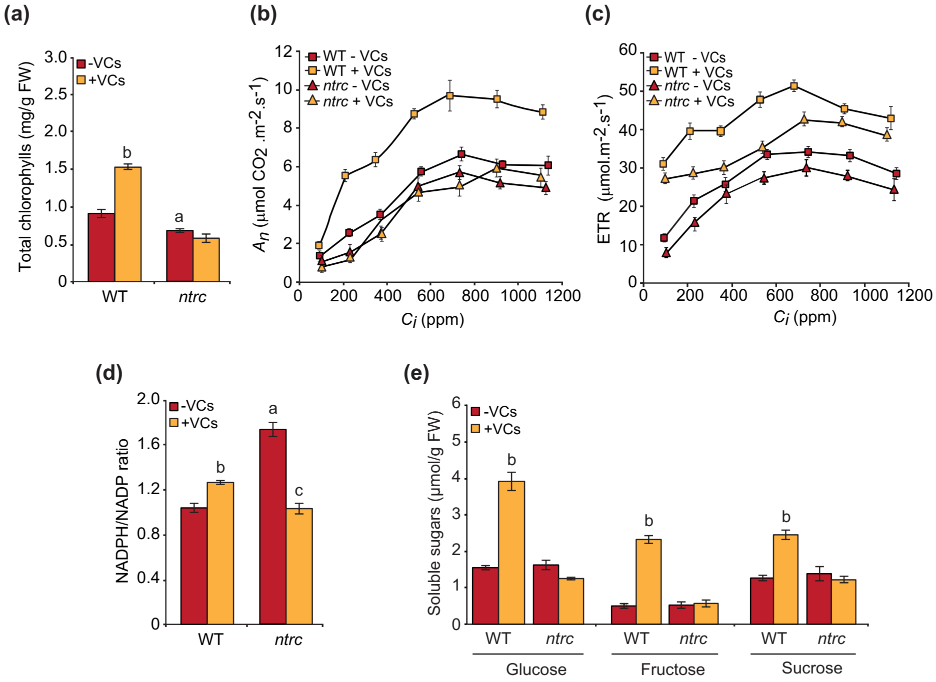


Figure 6. **Fungal VCs poorly increase photosynthetic capacities of exposed *ntrc* plants.** (a) Total chlorophyll contents, curves of (b) net CO_2 assimilation rate (A_n) and (c) photosynthetic electron transport (ETR) versus intercellular CO_2 concentration (C_i), (d) NADPH/NADP ratio and (e) levels of primary photosynthates (soluble sugars) in leaves of WT and *ntrc* plants cultured in the absence or continuous presence of VCs emitted by adjacent *A. alternata* cultures for one week. VC treatment started 28 days after sowing plants. Values in panels (a), (d) and (e) are means ± SE for three biological replicates (each a pool of 12 plants) obtained from four independent experiments. Letters “a”, “b” and “c” indicate significant differences, according to Student´s t-test ($P<0.05$), between: “a” WT and *ntrc* plants cultured without fungal VC treatment, “b” VC-treated and non-treated WT plants, and “c” VC-treated and non-treated *ntrc* plants.

than in WT plants (**Table 1, Figure 7**). Accordingly, A_n and ETR at all C_i levels (**Figure 6b, c**) as well as V_{cmax}, *TPU* and J_{max} values (**Table 1**) were lower in *ntrc* plants than in WT plants. Nonphotochemical quenching of chlorophyll fluorescence (Φ_{NPQ}) was higher in *ntrc* plants than in WT plants (**Table 1**), as previously reported by Naranjo et al. (2016a). The NADPH/NADP ratio was higher in *ntrc* leaves than in WT leaves (**Figure 6d**), as observed by Thormählen et al. (2015). Leaves of VC-exposed WT plants accumulated substantially higher levels of chlorophyll than those of non-treated plants (**Figure 6a**). Φ_{PSII} was higher and Φ_{NPQ} lower in VC-treated WT plants than in non-treated controls (**Table 1**), as found by Sánchez-López et al. (2016b). Accordingly,

Table 1. Photosynthetic parameters of leaves of WT and *ntrc* plants cultured in the absence or continuous presence of VCs emitted by adjacent *A. alternata* cultures for three days. Values are means ± SE of determinations in three independent experiments. Superscripts a, b and c indicate significant differences, according to Student´s t-test ($P<0.05$), between: (a) WT and *ntrc* plants cultured without fungal VC treatment, (b) VC-treated and non-treated WT plants, and (c) VC-treated and non-treated *ntrc* plants

Treatment	ϕ_{Po}	ϕ_{PSII}	ϕ_{NPQ}	***qP***	J_{max} (µmol e⁻ m⁻² s⁻¹)	V_{cmax} (µmol CO_2 m⁻² s⁻¹)	***TPU*** (µmol Pi m⁻² s⁻¹)
WT - VCs	0.830 ± 0.002	0.710 ± 0.001	0.243 ± 0.002	0.722 ± 0.008	33.1 ± 1.7	12.8 ± 0.9	1.82 ± 0.09
WT + VCs	0.831 ± 0.000	0.718 ± 0.002^{b}	0.215 ± 0.002^{b}	0.770 ± 0.002^{b}	53.7 ± 1.3^{b}	20.4 ± 2.0^{b}	2.79 ± 0.04^{b}
ntrc - VCs	0.815 ± 0.001^{a}	0.688 ± 0.003^{a}	0.311 ± 0.004^{a}	0.543 ± 0.010^{a}	28.6 ± 2.1^{a}	11.3 ± 0.8^{a}	1.44 ± 0.05^{a}
ntrc + VCs	0.795 ± 0.002^{c}	0.696 ± 0.004	0.304 ± 0.009	0.362 ± 0.013^{c}	29.0 ± 2.3	11.6 ± 0.7	1.36 ± 0.02

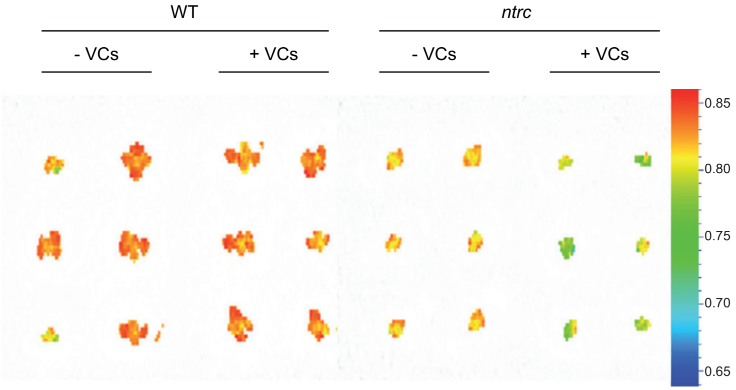


Figure 7. Chlorophyll-a fluorescence images of WT and *ntrc* plants cultured in the absence or presence of VCs emitted by adjacent cultures of *A. alternata* for one day. The color scale indicates the numeric values of Φ_{Po} (F_v/F_m).

leaves of VC-treated WT plants had higher A_n and ETR values than controls at all C_i levels (**Figure 6b, c**). VC-treated WT leaves also had higher V_{cmax}, J_{max} and *TPU* values than non-treated controls (**Table 1**), higher NADPH/NADP ratios (**Figure 6d, Figure 8**) and higher levels of primary photosynthates (e.g. glucose, fructose and sucrose) (**Figure 6e**). In contrast, *A. alternata* VCs caused a non-significant reduction in chlorophyll contents in leaves of *ntrc* plants (**Figure 6a**). Moreover, VCs had a negative effect on Φ_{Po} and *qP* and did not significantly alter Φ_{NPQ} in *ntrc* plants (**Table 1)**. Furthermore, no significant differences were observed in *An* values between VC-treated and non-treated *ntrc* leaves at any C_i levels (**Figure 6b**). Accordingly, no significant differences in V_{cmax}, J_{max} and *TPU* were observed between VC-treated and non-treated *ntrc* leaves (**Table 1**). Finally, NADPH/NADP ratios were lower in leaves of VC-treated *ntrc* plants than in controls (**Figure 6d, Figure 8**) and levels of primary photosynthates were not significantly altered by *A. alternata* VCs in the *ntrc* mutant (**Figure 6e**). Fungal VCs enhanced ETR at all C_i levels and Φ_{PSII} in leaves of *ntrc* plants (**Table 1, Figure 6c**).

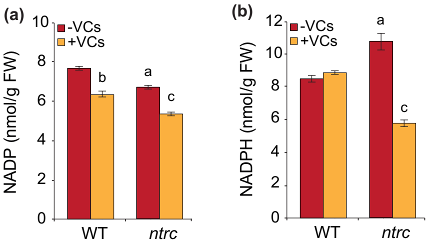


Figure 8. Levels of (a) NADP and (b) NADPH in leaves of WT and *ntrc* plants cultured in the absence or continuous presence of VCs emitted by adjacent *A. alternata* cultures for one week. Letters "a", "b" and "c" indicate significant differences, according to Student´s t-test ($P<0.05$), between: "a" WT and *ntrc* plants cultured without fungal VC treatment, "b" VC-treated and non-treated WT plants, and "c" VC-treated and non-treated *ntrc* plants.

The weak response to fungal VCs of *ntrc* plants is suppressed by decreased 2-Cys Prx expression

Pérez-Ruiz et al. (2017) have recently reported that reduction of 2-Cys Prx expression suppresses the *ntrc* phenotype, and proposed that NTRC regulates chloroplast redox status via its functional relationship with 2-Cys Prxs. To investigate the possible involvement of the NTRC-2Cys-Prxs tandem in the plant response to fungal VCs we characterized *Δ2cp* and *ntrc-Δ2cp* plants cultured in the absence or continuous presence of charcoal-filtered VCs emitted by adjacent *A. alternata* cultures for one week. As shown in **Figure 9a**, VC-exposed *Δ2cp*, *ntrc-Δ2cp* and WT plants had similar sizes and were much larger than the non-treated controls. Leaves of VC-exposed *Δ2cp* and *ntrc-Δ2cp* plants accumulated higher levels of chlorophyll, had higher A_n values and accumulated higher levels of primary photosynthates (starch and soluble sugars) than leaves of non-treated plants (**Figure 9b, c, d**). These findings clearly indicate that the suppressor effect of the *ntrc* phenotype by decreased levels of 2-Cys Prxs is also exerted on the plant´s response to VOCs-depleted fungal VCs. To test whether the weak responsiveness to VOCs-depleted fungal VCs of *ntrc* plants could be due to ROS over-accumulation in leaves we examined their superoxide anion and H_2O_2 contents by NBT and DAB staining, respectively. No significant differences in ROS contents were found between leaves of WT, *ntrc*, *Δ2cp* and *ntrc-Δ2cp* plants and VC-treated and -untreated plants (**Figure 10**).

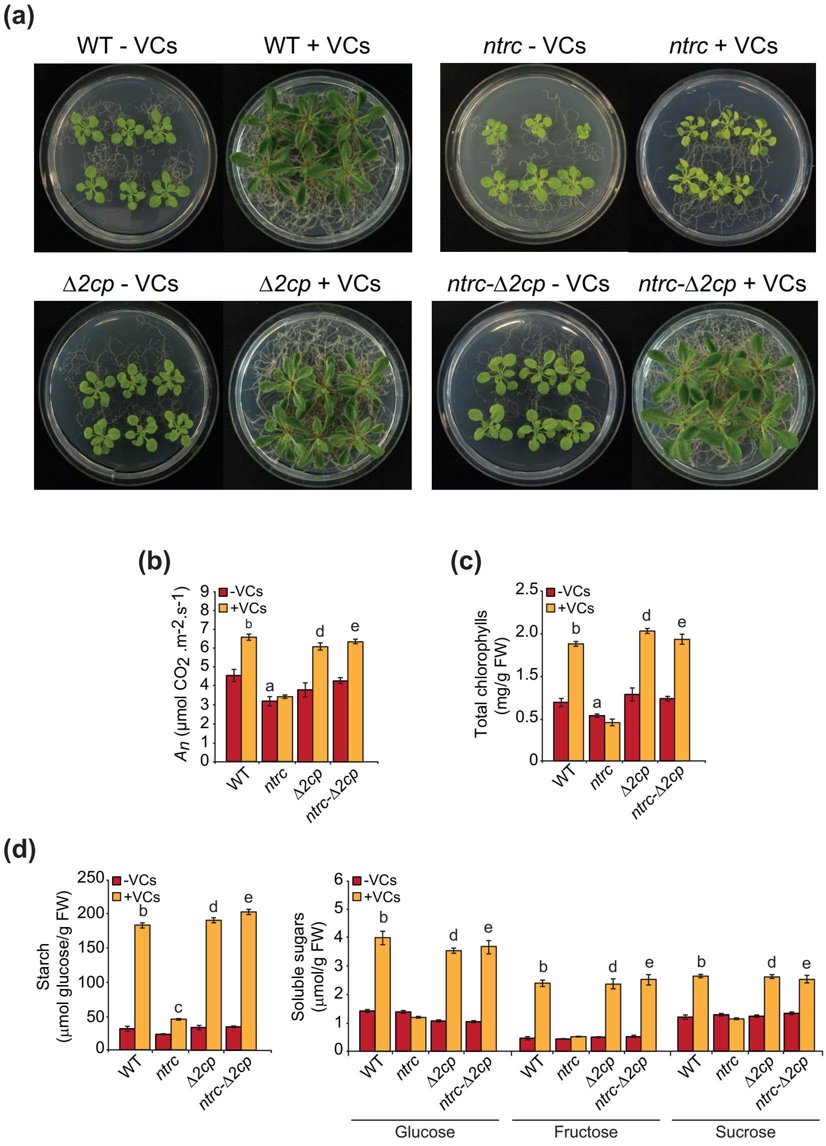


Figure 9. Reducing 2-Cys Prx activity restores ntrc plants´ responses to fungal VCs. (a) external phenotype, (b) net CO$_2$ assimilation rate (A_n), (c) total chlorophyll content and (d) contents of primary photosynthates (starch, sucrose, glucose and fructose) in leaves of WT, *ntrc*, *Δ2cp* and *ntrc-Δ2cp* plants cultured in the absence or continuous presence of VCs emitted by adjacent *A. alternata* cultures for one week. Values in panels (b), (c) and (d) are means ± SE of three biological replicates (each a pool of 12 plants) obtained from four independent experiments. Letters "a-e" indicate significant differences, according to Student´s t-test (P<0.05), between: "a" WT and *ntrc*, *Δ2cp* and *ntrc-Δ2cp* plants cultured without fungal VC treatment, "b" VC-treated and non-treated WT plants, "c" VC-treated and non-treated *ntrc* plants, "d" VC-treated and non-treated *Δ2cp* plants, and "e" VC-treated and non-treated *ntrc-Δ2cp* plants

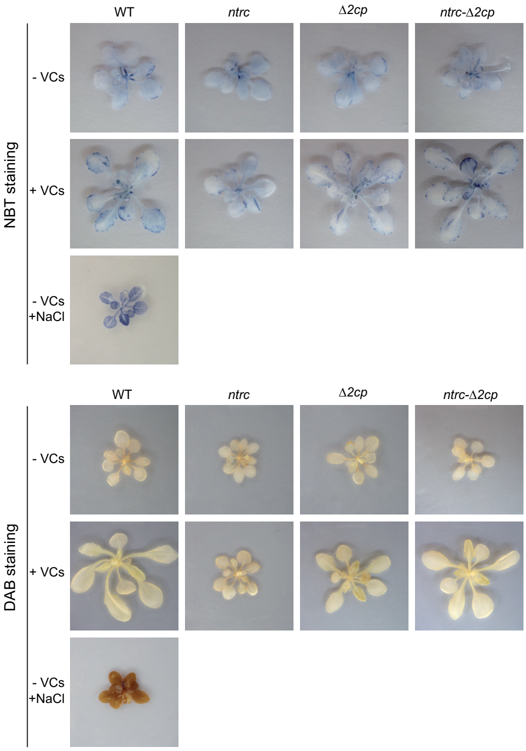


Figure 10. ROS staining of rosettes of WT and *ntrc* plants cultured in the absence or presence for five days of adjacent cultures of *A. alternata* covered with VOC-adsorbing charcoal filters. NBT and DAB staining was used to assess the accumulation of superoxide anion and H_2O_2, respectively. WT plants cultured in MS supplemented with 100 mM NaCl were used as controls of ROS accumulation.

A. alternata VCs promote global reduction and oxidation of the thiol redox proteomes of WT and *ntrc* leaves, respectively

The weak response to VCs of the *ntrc* mutant suggested that thiol-dependent post-translational modifications play an important role in plant responses to VCs. Thus, we next addressed the possibility that the different responses to *A. alternata* VCs observed in WT and *ntrc* plants include (and are partially due to) differences in oxidative modifications of protein cysteine residues. Because of the complexity of the multiple forms of cysteine redox modifications (e.g. disulfide, S-nitrosylation, S-glutathionylation, S-cyanylation, persulfidation or S-sulfenylation) this study focused on the quantification of total reversible thiol oxidation in leaves of WT and *ntrc* plants cultured in the absence or continuous presence of VCs emitted by nearby fungal cultures for three days using

OxiTRAQ-based quantitative redox proteomics. This approach is based on differential labeling of reduced and oxidized cysteines and only quantifies reversibly oxidized thiols that are DTT-reducible (for further details, see Materials and Methods).

In total, 782 unique cysteine-containing peptides from 747 distinct proteins obtained from WT leaves, and 781 unique cysteine-containing peptides from 746 distinct proteins obtained from *ntrc* leaves were identified in this study (data not shown). A peptide whose abundance differed by more than 1.9-fold or less than 0.5 with a $P<0.05$, was considered to be redox-sensitive in this report. Applying this criterion, 113 cysteine-containing peptides from 110 distinct proteins, and 87 cysteine-containing peptides from 87 distinct proteins were found to be redox-sensitive in response to VCs in WT and *ntrc* plants, respectively (**Tables S3 and S4**). Of the VC-responsive redox-sensitive proteins, nearly 15% have been shown to be redox-sensitive in other studies (**Tables S3 and S4**). Among the 113 VC-responsive redox-sensitive peptides of WT leaves, 74 cysteines in 71 different proteins were in a more reduced state in the VC-treated than in non-treated plants, while 49 cysteines in 47 different proteins were more oxidized in the VC-treated than in non-treated plants (**Table S3**). Furthermore, of the 87 VC-responsive redox-sensitive peptides of *ntrc* plants, 56 cysteines in 44 different proteins were in a more oxidized state in the VC-treated than in non-treated plants, whereas 44 cysteines in 41 different proteins were more reduced in VC-treated than in non-treated plants (**Table S4**).

Predicted locations of the VC-responsive, redox-sensitive proteins of WT and *ntrc* plants obtained using the SUBA4 Arabidopsis protein subcellular localization database included almost all cellular compartments, but the highest proportions had predicted plastidial, nuclear and mitochondrial locations (**Tables S3 and S4, Figure S2**). Using DiANNA software (http://clavius.bc.edu/~clotelab/DiANNA/), 50% and 60% of the redox-sensitive peptides of WT and *ntrc* plants, respectively, were predicted to form intramolecular disulfide bonds (**Tables S3 and S4**). It should be noted that formation of disulfide bridges represents only one possibility of thiol modifications (Buchanan and Balmer, 2005; Couturier et al., 2013), and other modifications such as glutathionylation, nitrosylation, and oxidation to sulfenic acid are also chemically reversible by DTT, which was used to reduce oxidized thiols before the reaction with thiol-reactive IAM. Therefore, some of the VC-promoted reversible thiol modifications identified in this study could be due to any of those types.

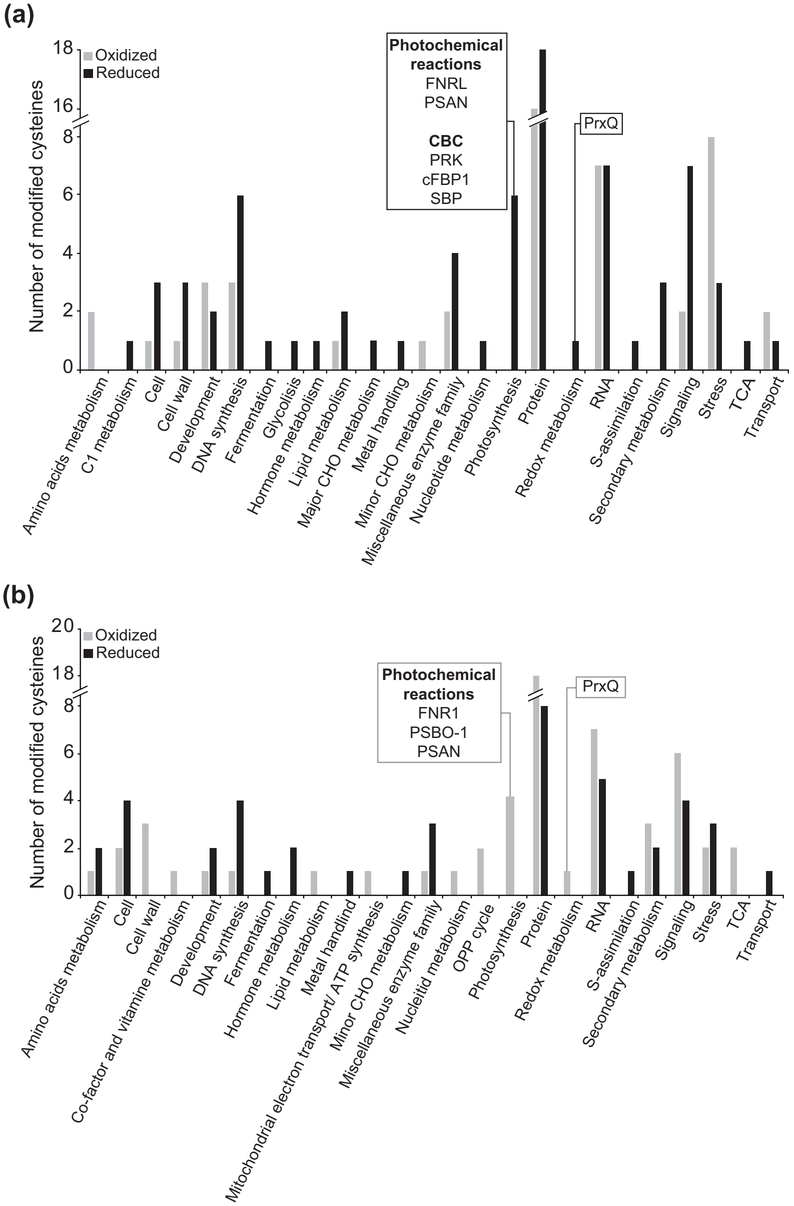


Figure 11. ***A. alternata*** **VCs promote global reduction and oxidation of the thiol redox proteomes of WT leaves and** ***ntrc*** **leaves, respectively.** The graphics represent functional categorizations of VC-responsive redox sensitive proteins in (a) WT and (b) *ntrc* plants, sorted according to putative functional categories assigned by MapMan software. Numbers of oxidized and reduced cysteines in each categorical group are indicated by gray and black bars, respectively. Proteins discussed in the text are boxed.

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Using broad characterizations outlined by the MapMan tool (Thimm et al., 2004) (http://gabi.rzpd.de/projects/MapMan/), the VC-responsive, redox-sensitive proteins were assembled into functional groups. Most were assigned to protein, RNA, signaling and stress response functional categories (**Tables S3 and S4, Figure 11**). Notably, VC exposure resulted in reduction of cysteine residues of several CBC enzymes (e.g. cFBP1, PRK and SBP), proteins involved in photochemical reactions of photosynthesis (e.g. FNRL and PSAN) and PrxQ in WT leaves (**Table S3, Figure 11a**). In addition, fungal VC exposure of *ntrc* plants resulted in oxidation of cysteine residues of proteins involved in photochemical reactions of photosynthesis (e.g. FNR1, PSAN and PSBO-1) and PrxQ (**Table S4, Figure 11b**). All these cysteine residues are highly conserved throughout land plants and algae (**Figure S3**).

DISCUSSION

NTRC is an important mediator of plant responses to microbial VCs

VCs emitted by *A. alternata* and other microbial species had weak stimulatory effects on growth and development of *ntrc* plants (**Figure 1a, b, Figure 4**), strongly indicating that NTRC plays an important role in plant responses to microbial VCs. The weak response of *ntrc* plants to fungal VCs cannot be ascribed to altered starch metabolism since growth responses of the starch-deficient *aps1* and the starch-excess *gwd* plants were comparable to those of WT plants (**Figure 2**).

Unlike in WT plants, chlorophyll content did not increase upon fungal VC treatment in *ntrc* plants (**Figure 6a**), indicating that NTRC is a major determinant of chlorophyll biosynthesis in VC-exposed plants and no other reductant system(s) can functionally replace NTRC in promoting photosynthetic pigment production under VC exposure. Also, Φ_{NPQ} did not vary and *qP* did not increase upon fungal VC treatment in *ntrc* plants (**Table 1**), indicating that, unlike in WT plants, VCs do not improve the efficiency of light use in *ntrc* leaves and, hence, do not improve photosynthetic CO_2 fixation. This inference was supported by the finding that fungal VCs did not alter V_{cmax}, J_{max} and *TPU* values of *ntrc* plants, but increased those of WT plants (**Table 1**). These observations suggest that NTRC is a major mediator of the plants´ responses to VCs, probably due to its regulatory action on photosynthesis-related mechanisms.

Previous reports have shown that microbial VCs can induce changes in root development (Molina-Favero et al., 2008; Ditengou et al., 2015; Garnica-Vergara et

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al., 2016; García-Gómez et al., 2019). Furthermore, Kirchsteiger et al. (2012) reported that NTRC is involved in LR formation in Arabidopsis seedlings by unidentified mechanisms. Here we found that, unlike in WT plants, VCs did not promote formation of LR in *ntrc* plants (**Figure 1c**), strongly indicating that NTRC is an important determinant of LR formation in response to *A. alternata* VCs. CKs and ABA are major regulators of photosynthesis, growth and development (Moore et al., 2003; Rolland et al., 2006; Cortleven and Valcke, 2012; Kieber and Schaller, 2014). In WT plants, microbial VCs promote reduction of ABA levels and increases in plastidial CK contents (Zhang et al., 2008; Sánchez-López et al., 2016b), which are accompanied by changes in the expression of ABA and CK-responsive genes (Zhang et al., 2008; Sánchez-López et al., 2016a; Sánchez-López et al., 2016b). Arabidopsis mutants with CK deficiency, and/or reduced endogenous ABA and CK receptor sensitivity, weakly respond to microbial VCs (Zhang et al., 2008; Sánchez-López et al., 2016b), indicating that plant responses to microbial VCs involve endogenous ABA and CK signaling. NTRC is a good reductant of CHLI (Pérez-Ruiz et al., 2014), which together with the putative ABA receptor CHLH (Shen et al., 2006; Wu et al., 2009; Shang et al., 2010; Du et al., 2012) is involved in ABA signaling in processes such as stomatal movement, seed development and seedling growth (Tsuzuki et al., 2011; Du et al., 2012). Moreover, NTRC is an important determinant of post-translational regulation of CHLI expression, as impairment of the NTRC-mediated redox regulation of CHLI destabilizes the protein (Pérez-Ruiz et al., 2014). Notably, here we found that responses in expression of ABA-responsive genes to VC treatment were substantially weaker in *ntrc* plants than in WT plants (**Figure 5**). This suggests that NTRC affects ABA signaling in VC-exposed plants through its action on CHLI redox status. Therefore, the non-responsiveness of ABA-responsive genes in *ntrc* plants to fungal VCS could be due, at least partly, to the lack of active CHLI. As responses in expression of CK-responsive genes to VC treatment were weaker in *ntrc* plants than in WT plants (**Figure 5**), it is tempting to speculate that NTRC participates in CK signaling in VC-exposed plants through unidentified mechanisms involving regulation of the redox status of proteins that mediate this signal pathway. Clearly, further experiments are needed to test this hypothesis.

Weak responses of *ntrc* plants to microbial VCs are not due to ROS over-accumulation

Photosynthesis involves transport of electrons in the presence of oxygen and, thus, is a major source of ROS. When high levels accumulate under stress conditions in which PET rates exceed photosynthetic capacity, ROS over-accumulation may cause photooxidative damage (Apel and Hirt, 2004; Stenbaek et al., 2008). Microbial VCs enhance photosynthetic ETR in *ntrc* plants (**Figure 6c**) but have no effect on A_n (**Figure 6b**), thereby creating conditions that promote ROS production. In Arabidopsis, NTRC is a good reductant of the two H_2O_2 detoxifying 2-Cys Prxs, hence suggesting it plays an important role in preventing excessive ROS accumulation (Kirchsteiger et al., 2009; Pérez-Ruiz et al., 2006; Pulido et al., 2010; Puerto-Galán et al., 2015). Notably, as in WT plants, VCs strongly promoted photosynthesis and growth of *ntrc-Δ2cp* plants (**Figure 9**). Furthermore, leaves of VC-treated and non-treated WT, *ntrc*, *Δ2cp* and *ntrc-Δ2cp* plants accumulated comparable ROS levels (**Figure 10**). These findings indicate that *ntrc* plants´ weak responses to VCs are not due to ROS over-accumulation as a consequence of 2-Cys Prxs inactivation. They also indicate that the stimulatory effect of microbial VCs on plant performance requires an appropriate chloroplast redox homeostasis through mechanisms wherein the NTRC-2-Cys-Prx tandem plays a central function.

A. alternata VCs promote changes in the thiol redox-proteome of WT plants that could account for the observed plants´ responses

The redox-proteomic analyses conducted here provide an in-depth report of thiol-based redox proteins that are responsive to microbial VCs in plants. Our results show that microbial VCs promote global reduction of the thiol redox proteome of WT leaves, especially of proteins involved in cell wall metabolism, nucleotide metabolism, photosynthesis, protein synthesis and processing, redox metabolism, secondary metabolism and signaling (**Figure 11**), which could partly explain the stimulatory growth responses of plants to VCs. Notably, microbial VCs promote global changes in the redox status of proteins distributed in all cellular compartments, but especially in plastids, mitochondria and the nucleus (**Figure 11, Tables S3 and S4, Figure S2)**, indicating that interorganellar redox crosstalk is involved in maintenance of whole cells´ redox balance. The results highlight a redox switching mechanism in VC signaling,

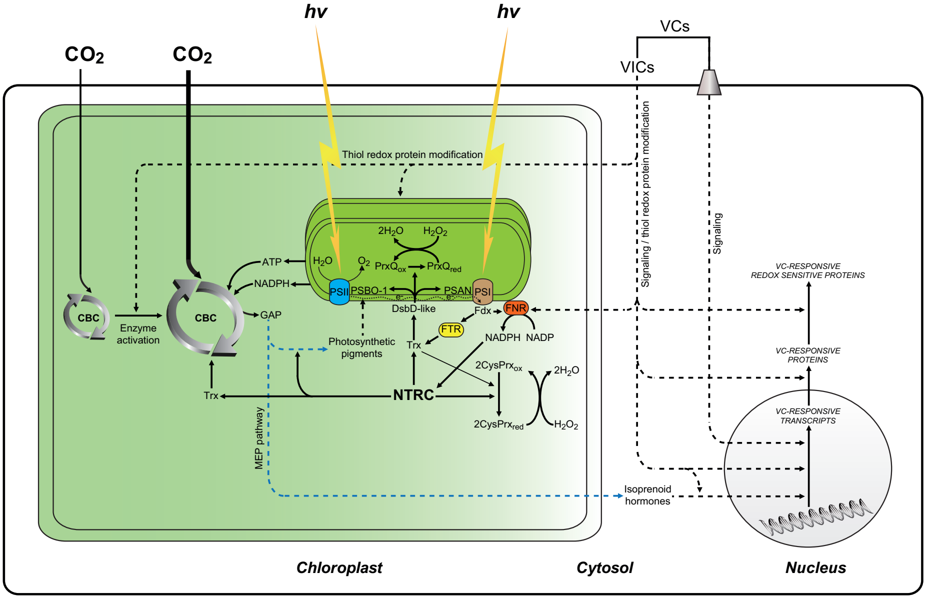

Figure 12. Suggested model for regulation of plants´ responses to microbial VCs involving post-translational thiol redox proteome changes and NTRC. According to this model, interactions between VCs and unidentified plasma membrane receptors generate signals that rapidly promote changes in expression of VC-responsive genes. Additionally, and/or alternatively, reactive VICs penetrating cells may induce thiol redox modifications of proteins and/or signaling reactions that promote reductive activation of photosynthesis-related proteins (e.g. FNR1, cFBP1, SBP, PRK, PSBO-1, and PSAN). The resulting augmentation of photosynthetic activity enhances synthesis of GAP, which enters the MEP pathway, fueling production of isoprenoid hormones that initiate a cascade of redox-regulated signaling reactions resulting in changes in the expression of genes whose translation is subject to redox regulation. Reductive activation of enzymes involved in photochemical reactions enhances NADPH production, thereby influencing whole cells´ redox balance, reduction of NTRC and NTRC´s target enzymes involved in processes such as synthesis of photosynthetic pigments, H_2O_2 detoxification, and CBC.

and provide additional confirmation of the hypothesis that, as illustrated in **Figure 12**, microbial VC signaling operates at multiple (including transcriptional, translational and post-translational) levels (Sánchez-López et al., 2016b; García-Gómez et al., 2019).

Redox regulation is inextricably associated with the PET chain and CBC enzymes in plants. Besides the earliest studied CBC enzymes (e.g. cFBP1, PRK, SBP and GAPDH), recent biochemical and proteomic studies have provided evidence that all CBC enzymes may undergo redox regulation through multiple redox post-translational modifications (Michelet et al., 2013). We found that fungal VCs promote reduction of cysteine residues of CBC enzymes in WT plants (e.g. Cys154 of cFBP1, Cys150 of SBP and Cys295 of PRK) (**Figure 11a, Table S3**). Although highly conserved throughout land plants and algae (**Figure S3**), these cysteine residues are not located in the proposed regulatory Trx redox or catalytic domains of cFBP1, PRK and SBP (Villeret et al., 1995; Brandes et al., 1996; Dunford et al., 1998; Chiadmi et al., 1999). However, it should be noted that, besides the structural role of disulfide bonds, redox changes in proteins´ cysteine residues can have diverse effects. They can participate in regulatory, protective, catalytic and signaling mechanisms by influencing subcellular localization or protein-protein interactions, and promoting conformational changes that affect the modified proteins´ biological activities. Therefore, the redox status of Cys154 of cFBP1, Cys150 of SBP and Cys295 of PRK could play roles in the respective enzymes´ stability, subcellular localization and/or formation of protein complexes in response to varying environmental conditions. In addition, reduction of some of these cysteine residues may be involved in the VC-promoted enhancement of photosynthesis in WT plants.

The redox-proteomic analysis of WT plants performed in this study also showed that VCs promote reduction of cysteine residues of two proteins involved in photochemical reactions of photosynthesis: PSAN and FNRL. These cysteine residues (e.g. Cys155 of PSAN and Cys141 of FNRL) are highly conserved in land plants and algae (**Figure S3**), highlighting the importance of their roles throughout a very long period of evolutionary history. PSAN is essential for efficient interaction between the plastocyanin and P700 reaction center of the PSI complex and thus participates in optimization of electron flow (Haldrup et al., 1999). FNRL is an FAD-containing NADP+ oxidoreductase likely involved in PET (Koskela et al., 2018). It is tempting to speculate that VC-promoted ETR enhancement (**Figure 6c**) is at least partly due to reductive activation of PSAN and FNRL.

The *ntrc* mutant shows global oxidation of its redox proteome, especially photosynthesis-related proteins

In contrast to WT plants, fungal VCs promoted global oxidation of the redox-proteome of leaves of *ntrc* plants, especially of proteins related to cell wall metabolism, nucleotide metabolism, photosynthesis, protein synthesis and processing, redox metabolism, secondary metabolism and signaling (**Figure 11, Table S4**), which could partly explain the weak responses of *ntrc* plants to VCs. As microbial VC-promoted global oxidation of the redox-proteome involved proteins distributed in all subcellular compartments in *ntrc* plants (**Figure S2**), NTRC conceivably plays an important role in maintaining whole cell´s redox homeostasis in VC-exposed plants.

Fungal VCs promoted oxidation of Cys155 of PSAN in *ntrc* plants (**Table S4**), which became more reduced in WT plants exposed to fungal VCs (see above). This indicates that PSAN is subject to redox regulation in VC-exposed plants through mechanisms involving NTRC. In addition, fungal VCs promoted oxidation of Cys114 of one of the two PSBO isoforms (e.g. PSBO-1) in *ntrc* plants (**Table S4**), which is a component of the PSII involved in water oxidation and formation of molecular oxygen (Murakami et al., 2005). Like Cys155 of PSAN, Cys114 of PSBO-1 is highly conserved in land plants and algae (**Figure S3**). It is tempting to speculate that weak VC-promoted ETR enhancement in *ntrc* plants (**Figure 6c**) could be at least partly due to reduced electron flow as a consequence of PSAN and PSBO-1 oxidation.

Microbial VCs also promoted oxidation of Cys178 and Cys183 of FNR1, both of which are highly conserved in land plants and algae (**Figure S3**). FNR1 is one of the two isoforms of leaf Fdx:NADP$^+$(H) oxidoreductase (FNR) that oxidize the final reduced product of PET, thereby generating the NADPH required for stromal redox regulation, reduction of NTRC and its target proteins, and enzymes involved in diverse metabolic pathways, including the CBC (Ceccarelli et al., 2004). Leaf FNR is also implicated in cyclic electron transfer around PSI, which generates a proton gradient across the thylakoid membrane, resulting in ATP production (Johnson, 2005). FNR1-lacking plants grow slowly and accumulate low levels of chlorophyll (Lintala et al., 2007). Notably, Cys178 is essential for FNR1 enzymatic activity (Aliverti et al., 1993). Thus, NTRC expression seems to be necessary to prevent FNR1 oxidation in VC-exposed plants. Moreover, the reduced FNR1 activity might contribute to the lack of enhancement of photosynthetic capacity, reduction of the NADPH/NADP ratios and global oxidation of the redox-proteome in VC-exposed *ntrc* plants (**Table 1, Figure 6, Figure 8, Table S4**).

In vitro, PrxQ is a good target of NTRC (Yoshida and Hisabori, 2016). In WT plants, fungal VCs promoted reduction of Cys116 of this Prx (**Table S3, Figure 11a**), which is conserved throughout land plants and algae (**Figure S3**). In contrast, fungal VCs promoted oxidation of the same cysteine residue in *ntrc* plants (**Table S4, Figure 11b**), suggesting that PrxQ is subject to redox regulation in VC-exposed plants to prevent excessive H_2O_2 accumulation through mechanisms involving NTRC as schematically illustrated in **Figure 12**. Both PSAN and PrxQ are luminal proteins (Petersson et al., 2006), although there are indications that PrxQ may associate with PSII in the grana stacks (Lamkemeyer et al., 2006) or thylakoids on the stromal side (Rouhier et al., 2004). Putative interactions between NTRC, located in the stroma, and PSAN and PrxQ might occur through the DsbD-like transmembrane pathway for disulfide-thiol exchange, which accepts electrons from stromal Trx-*m* and transfers these reducing equivalents to luminal proteins (Motohashi and Hisabori, 2006; Karamoko et al., 2013) (**Figure 12**).

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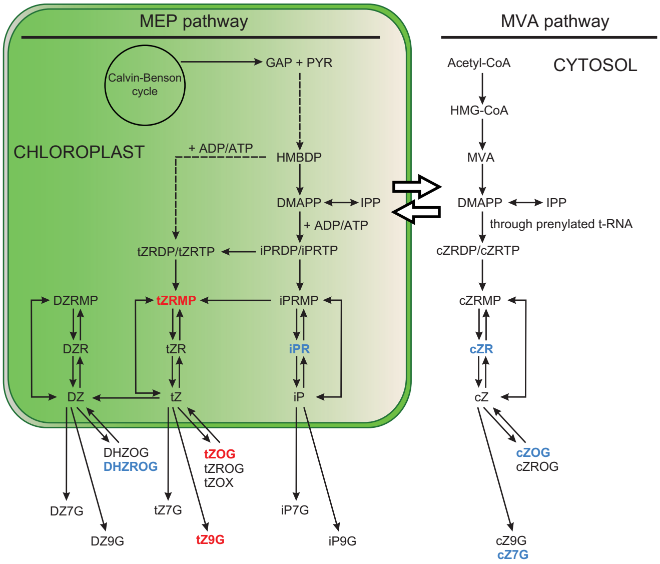
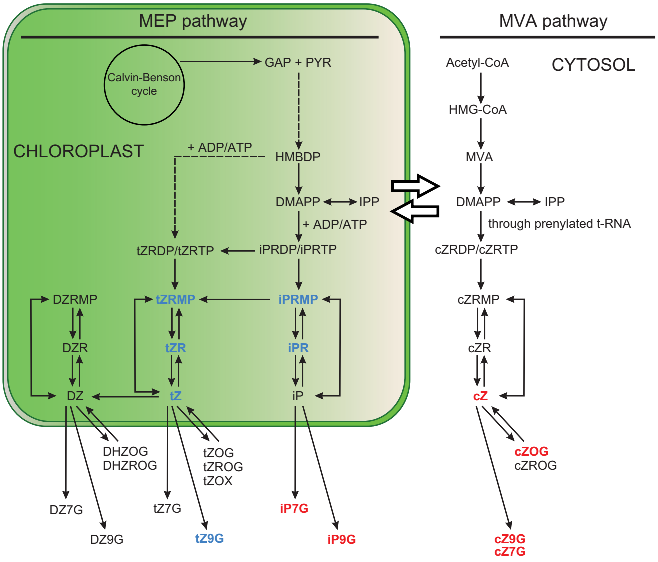
SUPPLEMENTAL MATERIAL

(a)



(b)



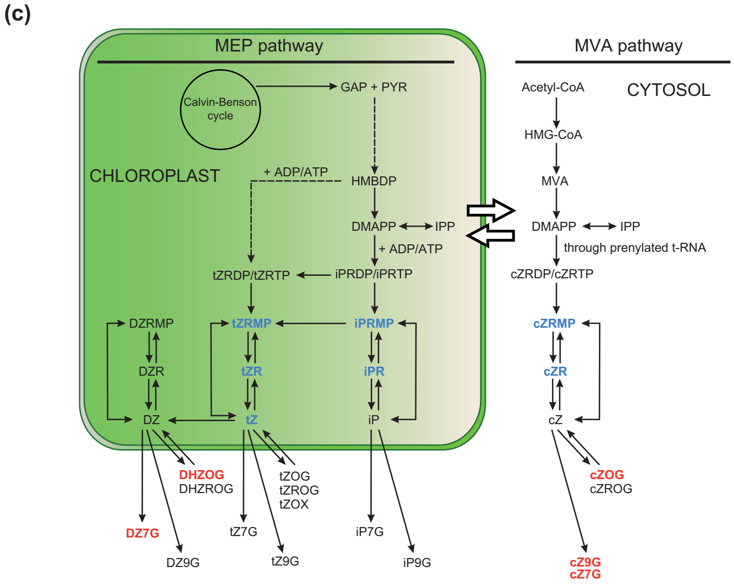


Figure S1. VCs emitted by *A. alternata* promote augmentation of the levels of CKs in leaves of WT and *ntrc* plants**.** Schemes representing pathways of CK biosynthesis through the plastidic MEP and cytosolic MVA pathways in leaves. In (a), CKs whose levels are higher in *ntrc* than in WT leaves are highlighted in blue, and CKs whose levels are lower in *ntrc* than in WT leaves are highlighted in red. In (b) and (c), CKs whose levels are enhanced by VCs in WT and *ntrc* plants, respectively, are highlighted in blue. CKs whose levels are decreased by VCs are highlighted in red. Data from **Table S2**. Black arrows show the biosynthesis, interconversions and metabolic flow of CKs in Arabidopsis cell. Multistep reactions are depicted with hollow arrows.

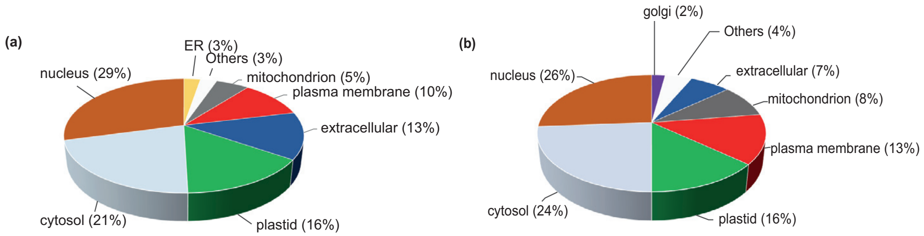


Figure S2. Categorization of VC-responsive redox-sensitive proteins in (a) WT and (b) *ntrc* plants according to their subcellular localization. Data from **Table S3** and **Table S4.**

FNR1

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Arabidopsis thaliana     MAAAISAAVSLPSSKSSSLLTKISSV-SPQRIFLKKSTVCYR------RVVSVKAQVTTDTTEAPP-V--KVVKESKKQE  70
Oryza sativa             MAAVNTVSSL-PCSKAGAAVAGGAPRPSTCSVFYPPRC---WSKRSSGNGVRAQASTTETTAAPAAEVTTKVEKVSKKQV  76
Spinacia oleracea        MTTAVTAAVSFPSTKTTSLSARSSSVISPDKISYKKVPLYYRNVSATGKMGPIRAQIASDVEAPPP-APAKVEKHSKKME  79
Triticum aestivum        MAAQLTAALP-SYSPATTKAAAGGSSPSSHFLAYPSRP---RNVR---NGVRAQVSTTEPTAEPAPAAPAKPVKISKKQD  73
Zea mays                 MATVMAAAVS-SFPSSSAVVAKASPASPCAAPHF--RP---RAVRA---AIRAQASAVEAPA------TAKAKKESKKQE  65
Chlamydomonas reinhardtii MQTVRAPA-------ASGVATRVAG----------RRMC-RPVAAT------KASTAVTTDMSKRTVPTKL------EE  49

Arabidopsis thaliana     EGIVVNKFKPKNPYTGRCLLNTKITGDDAPGETWHIVFTTEGEVPYREGQSIGVIPEGIDKNGK----PHKLRLYSIASS  146
Oryza sativa             DGVVTNKYRPKEPYTGRCLLNTRITGDDAPGETWHMVFSTDGEIPYREGQSIGVIPDGIDKNGK----PHKLRLYSIASS  152
Spinacia oleracea        EGITVNKFKPKTPYVGRCLLNTKITGDDAPGETWHMVFSHEGEIPYREGQSVGVIPDGEDKNGK----PHKLRLYSIASS  155
Triticum aestivum        EGVVTNKYRPKEPYVGRCLLNTRLTGDNAPGETWHMVFSTEGEVPYREGQSIGVIADGEDKNGK----PHKLRLYSIASS  149
Zea mays                 EGVVTNLYKPKEPYVGRCLLNTKITGDDAPGETWHMVFSTEGKIPYREGQSIGVIADGVDKNGK----PHKVRLYSIASS  141
Chlamydomonas reinhardtii GEMPLNTYSNKAPFKAKVRSVEKITGPKATGETCHIIIETEGKIPFWEGQSYGVIPPGTKINSKGKEVPHGTRLYSIASS  129

Arabidopsis thaliana     AIGDFGDSKTVSLCVKRLVY----TNDGGEIVKGVCSNFLCDLKPGDEAKITGPVGKEMLMPKDPNATIIMLGTGTGIAP  222
Oryza sativa             AIGDFADSKTVSLCVKRLVY----TNDQGEIVKGVCSNFLCDLKPGSDVKITGPVGKEMLMPKDPNATIIMLGTGTGIAP  228
Spinacia oleracea        ALGDFGDAKSVSLCVKRLIY----TNDAGETIKGVCSNFLCDLKPGAEVKLTGPVGKEMLMPKDPNATIIMLGTGTGIAP  231
Triticum aestivum        ALGDFGDSKTVSLCVKRLVY----TNDAGEVVKGVCSNFLCDLKPGSEVKITGPVGKKMLMPKDPNATIIMLATGTGIAP  225
Zea mays                 AIGDFGDSKTVSLCVKRLIY----TNDAGEIVKGVCSNFLCDLQPGDNVQITGPVGKEMLMPKDPNATIIMLATGTGIAP  217
Chlamydomonas reinhardtii RYGDDFDGQTASLCVRRAVYVDPETGKEDPAKKGLCSNFLCDATPGTEISMTGPTGKVLLLPADANAPLICVATGTGIAP  209

Arabidopsis thaliana     FRSFLWKMFFEEHEDYKFNGLAWLFLGVPTSSSLLYKEEFEKMKEKNPDNFRLDFAVSREQTNEKGEKMYIQTRMAEYAE  302
Oryza sativa             FRSFLWKMFFEEHDDYKFNGLAWLFLGVPTSSTLLYREEFERMKEIAPERFRLDFAVSREQTNAAGEKMYIQTRMAEYKD  308
Spinacia oleracea        FRSFLWKMFFEKHDDYKFNGLAWLFLGVPTSSSLLYKEEFEKMKEKAPDNFRLDFAVSREQTNEKGEKMYIQTRMAQYAV  311
Triticum aestivum        FRSFLWKMFFEEHEDYKFNGLAWLFLGVPTSDTLLYKEEFEKMVEIGGENFRLDFAVSREQTNAAGEKMYIQTRMAEYKE  305
Zea mays                 FRSFLWKMFFEKHDDYKFNGLGWLFLGVPTSSSLLYKEEFGKMKERAPENFRVDYAVSREQTNAAGERMYIQTRMAEYKE  297
Chlamydomonas reinhardtii FRSFWRRCFIENVPSYKFTGLFWLFMGVANSDAKLYDEELQAIAKAYPGQFRLDYALSREQNNRKGGKMYIQDKVEEYAD  289

Arabidopsis thaliana     ELWELLKKDNTFVYMCGLKGMEKGIDDIMVSLAAKDGIDWLEYKKQLKRSEQWNVEVY                         360
Oryza sativa             ELWELLKKDNTYVYMCGLKGMEKGIDDIMIDLAAKDGIDWLDYKKQLKKSEQWNVEVY                         366
Spinacia oleracea        ELWEMLKKDNTYVYMCGLKGMEKGIDDIMVSLAAAEGIDWIEYKRQLKKAEQWNVEVY                         369
Triticum aestivum        ELWEMLKKDNTYVYMCGLKGMEKGIDDIMVDLAAKDGIDWIDYKKQLKKAEQWNVEVY                         363
Zea mays                 ELWELLKKDNTYVYMCGLKGMEKGIDDIMVSLAEKDGIDWFDYKKQLKRGDQWNVEVY                         355
Chlamydomonas reinhardtii EIFDLLD-NGAHMYFCGLKGMMPGIQDMLERVAKEKGLNYEEWVEGLKHKNQWHVEVY                         346
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FNRL

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Arabidopsis thaliana     MST-----LPFAP-------------SV--THAHFSHSLSPMFILRHLP-------LTRHLRLSRNNRVASVVSAAAVR  52
Oryza sativa             MAAVA-NTVTTLP-------------LLPSPHAFAVPAMGSLPFLR--------------RRMRSRRL------AAVQ  44
Spinacia oleracea        MSICSLSPLPHIS-------------PLHRPHAHLHLPTRSMSFFRHLT-------LP--LRRHNKRRLFSVV-ASAVR  56
Triticum aestivum        M-------------------------------LLRSPPRRLHLLR-----------PHRLRALSNAA---AAALAGPP  33
Zea mays                 M-------------------------------ILRSAPRRLHLLR-----------PHHLRLLSAAALASAVPVPAPA  36
Chlamydomonas reinhardtii MQHTLMRANSYPAGAACSGRASQRRAQPVTVCSGASRTPQQGIAPMRGSSACGASGRLPAPFSSAAASRPTAAGRRGAVR  80

Arabidopsis thaliana     QDASLWTPA----PLSLIESAAE--SLFHISIDISNAPDLVASYTRPGQYLQIRVPDVE--KPSFMAIASPPS-------  117
Oryza sativa             QDAAVWTPA----PVSSFGPATADGSLVHFSVDLSDATDLAASYTTPGQYLLIRVPGEDELKPAFMAIASPPG-------  113
Spinacia oleracea        QDTTLFTPS----PISLIEPAAE--SLFHVSIDVSDAPDIASSYTRAGQYLQLKVPDSP--KPSFLAIASPPS-------  121
Triticum aestivum        PAPTEWTEA----PVASVRAATADASLFHVSLDLSAHGPLLASHVAAGQFLPFRLPSAP--YPIFLAISSPPPASSS---  104
Zea mays                 QSPTEWAEA----PLASVRPATADASLFHVSLDLSAHRGLLASHTAAGQFLRFRLPASP--YHIFLAIASPPPPPALEAL  110
Chlamydomonas reinhardtii VQAN-WGAPVEFQPAKVVSNSPAAAGPLH-KVVIDVGAPLAAGYTVPGQFVQVKVGDS---KPGFFAIASAPGAHA----  151

Arabidopsis thaliana     -LASSRGAFEFLVKSIAGSTAEILCGLKKGETVELSS-VMGNGFNIDLIDPPEEYPTVLIFATGSGISPIRSLIESGFGA  195
Oryza sativa             -GAA----FEFLVKTVPGTTAEKLCGLRDGDVLELGA-IMGNGFPISRINPPDEAQTVLLFATGTGISPVRSLIEFGFAA  187
Spinacia oleracea        -LAAVRGEFHFLVKSVAGSTAELLCALKKGDVVELSS-VMGNGFDVDRLSPAEEFPTVLIFATGSGISPIRSLIESGFVV  199
Triticum aestivum        --GSPPKSFDFLVKRLPGTPSARLCDLRPGDLVPVGGSVVGRGFEVSRIA---DARDVLVFATGSGISPIRSLIESGFGE  179
Zea mays                 ALAGPPSCFEFLVKRLPGTPSARLCDLRPGDLVHVGASVVGRGFDVARIS---DARDVLVFATGSGISPIRSLIESGFAE  187
Chlamydomonas reinhardtii ----GSGQLEFLIKGAPGSTAELLCNASAGDPVSVSP-VMGKGFALDRL-PASTTRAVLLFATGSGISPLRAVIDSGALA  225

Arabidopsis thaliana     DRRSDVRLYYGARNLNRMAYQEKFKEWESAGVKVVPVLSQPDDGWKGETGYVQAAFAR----AKQLSAPKATGAVLCGQK  271
Oryza sativa             DQRADVRLYYGARNLQTMAYQDRFTNWESTGLKIIPVLSRADDSWKGERGYVQDAFLK----AQNIANHFSTGAVLCGQK  263
Spinacia oleracea        DKRSDVRLYYGARNLQRMAYQDRFKDWESSGVKIVPVLSQPDEGWTGETGYVQAAFCR----SKNISNPNSTGVVLCGQK  275
Triticum aestivum        SEKIDVSLFYGVRNLQRMAYQERFSDWESRGIKIIPVLSRPDDQWTGQRGYVQNAFSR----AKKVINPSSTGAILCGHK  255
Zea mays                 NKKTDVRLFYGVRNLQRMAYQERFEDWESRGVKIVPVLSRPDGQWTGERGYVQNVFSR----MKSTVNPPSVGVILCGHK  263
Chlamydomonas reinhardtii GR--DVTLYYGTRNPESTAYSELLPQWTAAGVKVVSVYSESKQ------GYVHDVFEREGLAALPADAASSVGAMLCGHK  297

Arabidopsis thaliana     QMAEEITSMLVADGVSNDKLLKNF                                                         295
Oryza sativa             QMSEEITSALVADGVSPDKILTNY                                                         287
Spinacia oleracea        QMTEEITCILTENGVSTDKILKNF                                                         299
Triticum aestivum        QMTEEITRALVADGMSKDKILTNF                                                         279
Zea mays                 QMSEEITRVLVADGLSKDRILTNF                                                         287
Chlamydomonas reinhardtii GMCQAVTALLTAKGVPPEKILLNF                                                         321
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PSBO-1

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Arabidopsis thaliana         MAAS----------------------------------------LQSTATFLQSAKIATAPSRGS-SHLRSTQAVGKSFG  39
Oryza sativa                 MAAS----------------------------------------LQAAATLMQPAKLGGRASSAALPS-RPSSHVARAFG  39
Spinacia oleracea            MAAS----------------------------------------LQASTTFLQPTKVASRNTL----QLRSTQNVCKAFG  36
Triticum aestivum            MAAS----------------------------------------LQAAATLM-PAKIGGRASSA-----RPSSHVARAFG  34
Zea mays                     MATNSPALTKRPSRHAPTHQTDRGEEKGQKATPPATTTMAASLQVQAAATLMQPAKIGGRAPSASLPSSRPSSQLARAFG  80
Chlamydomonas reinhardtii    MA------------------------------------------LRAA----QSAKAGVRAARPN----RATAVVCKAQK  30

Arabidopsis thaliana         LE-TSSA-RLTCSFQSDFKDFTGKCSDAVKIAGFALATSALVVSGASAEGAPKRLTYDEIQSKTYMEVKGTGTANQCPTI  117
Oryza sativa                 VD-TGAAGRITCSLQSDIREVANKCADAAKLAGFALATSALLVSGASAEGVPRRLTFDEIQSKTYMEVKGTGTANQCPTV  118
Spinacia oleracea            VESASSGGRLSLSLQSDLKELANKCVDATKLAGLALATSALIASGANAEGG-KRLTYDEIQSKTYLEVKGTGTANQCPTV  115
Triticum aestivum            VD-AGA--RITCSLQSDIREVASKCADAAKMAGFALATSALLVSGASAEGAPKRLTFDEIQSKTYMEVKGTGTANQCPTI  111
Zea mays                     VD-AGAA-RITCSLQSDVRDVASKCVDAAKLAGFALATSALLVSGASAEGTPKRLTYDEIQSKTYLEVKGTGTANQCPTI  158
Chlamydomonas reinhardtii    VGQAAAAAALATAM---------------------------------VAGSANALTFDEIQGLTYLQVKGSGIANTCPVL  77

Arabidopsis thaliana         DGGSETFS-FKPGKYAGKKFCFEPTSFTVKADSVSKNAPPEFQNTKLMTRLTYTLDEIEGPFEVASDGSVNFKEEDGIDY  196
Oryza sativa                 EGGVDSFA-FKAGKYNMKKFCLEPTSFTVKAEGVAKNAPPEFQKTKLMTRLTYTLDEIEGPLEVSSDGTIKFEEKDGIDY  197
Spinacia oleracea            EGGVDSFA-FKPGKYTAKKFCLEPTKFAVKAEGISKNSGPDFQNTKLMTRLTYTLDEIEGPFEVSSDGTVKFEEKDGIDY  194
Triticum aestivum            DGGVDSFP-FKAGKYEMKKFCLEPTSFTVKAEGIQKNEPPAFQKTKLMTRLTYTLDEMEGPLEVGADGTLKFEEKDGIDY  190
Zea mays                     DGGVDSFP-FKPGKYQMKKLCLEPTSFTVKAEGIAKNAPPEFQKTKLMTRLTYTLDEIEGPLEVASDGTLKFEEKDGIDY  237
Chlamydomonas reinhardtii    ESGTTNLKELKAGSYKLENFCIEPTSFTVKEESQFKGGETEFVKTKLMTRLTYTLDAMSGSFKVGSDGSAELKEDDGIDY  157

Arabidopsis thaliana         AAVTVQLPGGERVPFLFTVKQLDASGKPDSFTGKFLVPSYRGSSFLDPKGRGGSTGYDNAVALPAGGRGDEEELVKENVK  276
Oryza sativa                 AAVTVQLPGGERVPFLFTIKNLVATGKPESFGGPFLVPSYRGSSFLDPKGRGGSTGYDNAVALPAGGRGDEEELAKENVK  277
Spinacia oleracea            AAVTVQLPGGERVPFLFTIKQLVASGKPESFSGDFLVPSYRGSSFLDPKGRGGSTGYDNAVALPAGGRGDEEELQKENNK  274
Triticum aestivum            AAVTVQLPGGERVPFLFTVKQLVATGKPESFSGPFLVPSYRGSSFLDPKGRGGSTGYDNAVALPAGGRGDEEELAKENVK  270
Zea mays                     AAVTVQLPGGERVPFLFTVKQLVATGKPDSFGGPFLVPSYRGSSFLDPKGRGGSTGYDNAVALPAGGRGDEEELQKENIK  317
Chlamydomonas reinhardtii    AATTVQLPGGERVAFLFTIKQFDGKGTLDNIKGDFLVPSYRGSSFLDPKGRGGSTGYDNAVALPA--RADAEELLKENVK  235

Arabidopsis thaliana         NTAASVGEITLKVTKSKPETGEVIGVFESLQPSDTDLGAKVPKDVKIQGVWYGQLE                         332
Oryza sativa                 NASSSTGNITLSVTKSKPETGEVIGVFESVQPSDTDLGAKVPKDVKIQGVWYAQLE                         333
Spinacia oleracea            NVASSKGTITLSVTSSKPETGEVIGVFQSLQPSDTDLGAKVPKDVKIEGVWYAQLE-Q                       331
Triticum aestivum            NASSSTGNITLSVTKSKPETGEVIGVFESVQPSDTDLGAKAPKDVKIQGVWYAQLESN                       328
Zea mays                     NAASSTGNITLSVTKSNPDTGEVIGVFESVQPSDTDLGAKAPKDVKIQGVWYAQLE                         373
Chlamydomonas reinhardtii    ITKALKGSAVFSVAKVDPVTGEIAGVFESIQPSDTDLGAKPPKDIKVTGLWYAQL--K                       291
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PRK

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Arabidopsis thaliana         MAVSTIYSTQALNS--THFLTSSSSSKQVFLYR---------RQPQTNRRFNTLITCA-QE------TIVIGLAADSGCGKSTFMRRLTS  72
Oryza sativa                 MA------ARSFSSASTT----------TILL-----RSGRWRRTMRAAAFPFRVSCSAAAAAAAGGTVVIGLAADSGCGKTTFVRRLTS  69
Spinacia oleracea            MAVCTVYTI-----PTTTHLGSSFNQNNKQVFFNYKRSSSSNNTLFTTRP-SYVITCSQQQ------TIVIGLAADSGCGKSTFMRRLTS  78
Triticum aestivum            MAFCSPHSTTSLRSPCTTIPNSGFRQNQVILFTTRSSRRSNTRH--GARTFQ--VSCAVEQ------PIVIGLAADSGCGKSTFMRRLTS  80
Zea mays                     MAICSAHTTTSLRSPCTTVSNAGLRQKQVI-FVTSNRRSGGGRRHGGARSFQ--VSCSVDK------PVVIGLAADSGCGKSTFMRRLTS  81
Chlamydomonas reinhardtii    MAF-------TMRAPA--------------------PRATAQSRVTANRARRSLVVRADKDK-----TVVIGLAADSGCGKSTFMRRMTS  58

Arabidopsis thaliana         VFGG----AAKPPKGGNPDSNTLISDTTTVICLDDYHSLDRYGRKEQKVTALDPRANDFDLMYEQVKALKNGIAVEKPIYNHVTGLLDPP  158
Oryza sativa                 VLGAGTAAAAAPPWGGNPGSNTLLGDAATVICLDDYHSLDRAGRKERGVTALDPRANDFDLMYRQLKAIKEGRAVAKPIYNHATGLLDPP  159
Spinacia oleracea            VFGG----AAEPPKGGNPDSNTLISDTTTVICLDDFHSLDRNGRKVEKVTALDPKANDFDLMYEQVKALKEGKAVDKPIYNHVSGLLDPP  164
Triticum aestivum            VFGG----AAEPPKGGNPDSNTLISDTTTVICLDDYHSLDRTGRKEKGVTALDPKANDFDLMYEQVKAIKEGKAIEKPIYNHVTGLLDPA  166
Zea mays                     VFGG----AAEPPKGGNPDSNTLISDTTTVICLDDYHSLDRNGRKEKGVTALDPRANNFDLMYEQVKAIKEGQAVEKPIYNHVTGLLDPP  167
Chlamydomonas reinhardtii    IFGG----VPKPPAGGNPDSNTLISDMTTVICLDDYHCLDRNGRKVKGVTALAPEAQNFDLMYNQVKALKEGKSVDKPIYNHVSGLIDAP  144

Arabidopsis thaliana         ELIQPPKILVIEGLHPMFDERVRDLLDFSIYLDISNEVKFAWKIQRDMAERGHSLESIKASIEARKPDFDAFIDPQKQYADAVIEVLPTT  248
Oryza sativa                 ELITPPKILVVEGLHPMYDERVRGLLDFSIYLDISSDIKFAWKIQRDMAERGHSLESIKASIEARKPDFDAYIDPQKQYADAVIEVLPTR  249
Spinacia oleracea            ELIQPPKILVIEGLHPMYDARVRELLDFSIYLDISNEVKFAWKIQRDMKERGHSLESIKASIESRKPDFDAYIDPQKQHADVVIEVLPTE  254
Triticum aestivum            ELIQPPKIFVIEGLHPMYDERVRELLDFSIYLDISNEVKFAWKIQRDMAERGHSLESIKASIEARKPDFDAFIGPQKQYADAVIEVLPTQ  256
Zea mays                     ELIAPPKIFVIEGLHPMFDERVRDLLDFSIYLDISDEVKFAWKIQRDMAERGHSLESIKASIEARKPDFDAFIDPQKQYADAVIEVLPTQ  257
Chlamydomonas reinhardtii    EKIESPPILVIEGLHPFYDKRVAELLDFKIYLDISDDIKFAWKIQRDMAERGHSLESIKSSIAARKPDFDAYIDPQKKDADMIIQVLPTQ  234

Arabidopsis thaliana         LIP----DDNEGKVLRVRLIMKEGVKYFSPVYLFDEGSTISWIPCGRKLTCSYPGIKFNYEPDSYFDHEVSVLEMDGQFDRLDELIYVES  334
Oryza sativa                 LIAAADDDGDEGKVLRVKLIMKEGVEHFAPAYLFDEGSTISWIPCGRKLSCSYPGIKFSYFPDTYFGHEVSVLEMDGKFDKLDELIYVES  339
Spinacia oleracea            LIP----DDDEGKVLRVRMIQKEGVKFFNPVYLFDEGSTISWIPCGRKLTCSYPGIKFSYGPDTFYGNEVTVVEMDGMFDRLDELIYVES  340
Triticum aestivum            LIP----DDNEGKVLRVKLIMKEGIKFFNPVYLFDEGSTINWIPCGRKLTCSYPGIKFSYGPDTYFGQEVSVLEMDGQFDRLDELIYVES  342
Zea mays                     LIP----DDNEGKVLRVKLIMKEGVKNFNPVYLFDEGSTISWVPCGRKLTCSYPGIKFSYGPDTYFGNEVSVLEMDGQFDRLDELIYVES  343
Chlamydomonas reinhardtii    LVP-----DDKGQYLRVRLIMKEGSKMFDPVYLFDEGSTISWIPCGRKLTCSFPGIKMFYGPDTWYGQEVSVLEMDGQFDKLEELIYVES  319

Arabidopsis thaliana         HLSNLSTKFYGEVTQQMLKHADFPGSNNGTGLFQTIVGLKIRDLYEQLIANKATARAE-A-KA                            395
Oryza sativa                 HLSNLSTKYYGEVTQQMLKHADFPGSNNGTGLFQTIVGLKIRDLYEQVVAERAASPPALAAVA                            402
Spinacia oleracea            HLSNLSTKFYGEVTQQMLKHQNFPGSNNGTGFFQTIIGLKIRDLFEQLVASRSTATAT-AAKA                            402
Triticum aestivum            HLSNLSTKFYGEVTQQMLKHADFPGSNNGTGLFQTIVGLKIRDLYEQIIAERAGVPAE-AAKV                            404
Zea mays                     HLSNLSTKFYGEVTQQMLKHADFPGSNNGTGLFQTIIGLKIRDLYEQIVAERAGVPAE-AAKV                            405
Chlamydomonas reinhardtii    HLSNTSAKFYGEITQQMLKNSGFPGSNNGTGLFQTIVGLKVREVYERIV-KKDVVP------V                            375
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cFBP1

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Arabidopsis thaliana       MAATA-ATTTSSHLLLSSSRHVASSSQPSILSPRSL---FSNNGKRAPTGVRNHQYASGVRCMAVAADAAE-TKTAARKKSGYELQTLTG  85
Oryza sativa               MAA---AATTSSHLLLLSRQQAAASLQCG--------LSFRRQPGRLAGGSS----APSVRCMAAVDTASAPAATEASKKSSYEITTLTT  75
Spinacia oleracea          MASIG-PATTTAVKL----RSSIFNPQSSTLSPSQQCITFTKSLHSFPTATR-HNVASGVRCMAAVGEAA--TETKARTRSKYEIETLTG  82
Triticum aestivum          MDH---AADTFRTDLMTITRHV--------------------------------------------------------------------  19
Zea mays                   MDH---AADAHRTDLMTITRHV--------------------------------------------------------------------  19
Chlamydomonas reinhardtii  MAATMLRSSTQSGIAAKAGRKEAVSVRAVAQPQRQ-----AGAASVFSSSSSGAAARRGV--VAQATAVATPAAKPAAKTSQYELFTLTT  83

Arabidopsis thaliana       WLLRQEMKGEIDAELTIVMSSISLACKQIASLVQRAGISNLTGVQGAVNIQGEDQKKLDVISNEVFSNCLRSSGRTGIIASEEEDVPVAV  175
Oryza sativa               WLLKQEQAGTIDGEMTIVLASISTACKQIASLVQRAPISNLTGVQGAVNVQGEDQKKLDVVSNEVFSNCLKSSGRTGVIASEEEDVPVAV  165
Spinacia oleracea          WLLKQEMAGVIDAELTIVLSSISLACKQIASLVQRAGISNLTGIQGAVNIQGEDQKKLDVVSNEVFSSCLRSSGRTGIIASEEEDVPVAV  172
Triticum aestivum          -LNEQSRHPESRGDLTILLSHIVLGCKFVASAVNKAGLAKLTGLAGETNVQGEEQKKLDVLSNEVFVNALVSSGRTCVLVSEEDEKATFV  108
Zea mays                   -LNEQSRNPESRGDFTILLSHIVLGCKFVASAVNKAGLAQLIGLAGETNVQAKEQKKLDVLSNEVFVKALVSSGRTCVLVSEEDEEATFV  108
Chlamydomonas reinhardtii  WLLKEEMKGTIDGELATVISSVSLACKQIASLVNRAGISNLTGVAGNQNVQGEDQKKLDVVSNEVFKNCLASCGRTGVIASEEEDQPVAV  173

Arabidopsis thaliana       EESYSGNYVVVFDPLDGSSNIDAAVSTGSIFGIYSPNDECIVD-DSDDISALGSEEQRCIVNVCQPGNNLLAAGYCMYSSSVIFVLTLGK  264
Oryza sativa               EESYSGNYIVVFDPLDGSSNIDAAVSTGSIFGIYSPNDECLADIADDQ--NLDQVEQRCIVSVCQPGSNLLAAGYCMYSSSVIFVLTIGT  253
Spinacia oleracea          EESYSGNYIVVFDPLDGSSNIDAAVSTGSIFGIYSPNDECIVDSDHDDESQLSAEEQRCVVNVCQPGDNLLAAGYCMYSSSVIFVLTIGK  262
Triticum aestivum          DPKLRGKYCVCFDPLDGSSNIDCGVSIGTIFGIY----------------MIKNQDTVTLEEVLQPGKDMIAAGYCMYGSSCTLVLSTGN  182
Zea mays                   DPKLRGRYCVCFDPLDGSSNIDCGVSIGTIFGIY----------------IIKDKDNVTLEDVLQPGKNMLAAGYCMYGSSCTLVLSTGT  182
Chlamydomonas reinhardtii  EETYSGNYIVVFDPLDGSSNIDAGISVGSIFGIYEPSEECPIDAMDDPQKMM----EQCVMNVCQPGSRLKCAGYCLYSSSTIMVLTIGN  259

Arabidopsis thaliana       GVFSFTLDPMYGEFVLTQENIEIPKAGRIYSFNEGNYQMWDDKLKKYIDDLKDPGP-TGKPYSARYIGSLVGDFHRTLLYGGIYGYPRDA  353
Oryza sativa               GVYVFTLDPMYGEFVLTQEKVQIPKAGKIYAFNEGNYALWDDKLKSYMDSLKEPGP-SGKPYSARYIGSLVGDFHRTLLYGGIYGYPRDQ  342
Spinacia oleracea          GVYAFTLDPMYGEFVLTSEKIQIPKAGKIYSFNEGNYKMWDDKLKKYMDDLKEPGE-SQKPYSSRYIGSLVGDFHRTLLYGGIYGYPRDA  351
Triticum aestivum          GVNGFTLDPSLGEFIMTHPDIKIPPKGKIYSVNEGNAKNWDTPTAKYVEKCKYPTD-GSSPKSLRYIGSMVADVHRTLLYGGIFLYPADK  271
Zea mays                   GVNGFTLDPSLGEFILTHPDIKIPKKGKIYSVNEGNAKNWDAPVAKFVEKCKYPKD-GSPPRSLRYIGSMVADVHRTLLYGGVFLYPADE  271
Chlamydomonas reinhardtii  GVFGFTLDPLVGEFVLTHPNVQIPEVGKIYSFNEGNYGLWDDSVKAYMDSLKDPKKWDGKPYSARYIGSLVGDFHRTLLYGGIYGYPGDA  349

Arabidopsis thaliana       KSKNGKLRLLYECAPMSFIVEQAGGKGSDGHSRVLDIQPTEIHQRVPLYIGSTEEVEKLEKYLA                            417
Oryza sativa               KSKNGKLRLLYECAPMSFIVEQAGGKGSDGHQRILDIMPTEIHQRVPLYIGSVEEVEKVEKFLA                            406
Spinacia oleracea          KSKNGKLRLLYECAPMSFIVEQAGGKGSDGHQRILDIQPTEIHQRVPLYIGSVEEVEKLEKYLA                            415
Triticum aestivum          KSPSGKLRVMYEVFPMSFLMEEAGGQSFTGKGRSLDLIPTDIHERSPIFLGSSDDVEEIKALYAEEAKKEG-SA                  344
Zea mays                   KNPNGKLRILYEVFPMSFLMEQAGGQSFTGKERALDLVPTKIHDRSPIFLGSYDDVEEIKALYAEQAKSSSASS                  345
Chlamydomonas reinhardtii  KNKNGKLRLLYECAPMSFIAEQAGGLGSTGQERVLDVNPEKVHQRVPLFIGSKKEVEYLESFTKKH                          415
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SBP

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Arabidopsis thaliana       -SIACYSRGILPPSVSSQRSSTLVSPPSYSTSSSFKRLKSSSIFGDSLRL-APKSQLKATKAKSNGA--STVTKCEIGQSLE  81
Oryza sativa                AAASYTRG--AATRSPACCAAMSFSQSYRPKAARPP---STFYGESLRVNTAR-SLPSGRQSKAASRAALSTRCEIGDSLE  79
Spinacia oleracea          -SMACCSRSIVLPRVSPQHSSALVPS-----SINLKSLKSSSLFGESLRM-TTKSSVRVNKAKN--S--SLVTKCELGDSLE  74
Triticum aestivum           AAAGYARG--AATRSPACCAAMSFSQSYRPKAARPA---TSFYGESLRANTARTSFPAGRQSKAASRAALTTRCAIGDSLE  80
Zea mays                    A-----------TRSPACCAAVSFSQSYRPKASRPP---TTFYGESVRVNTAR-PLSARRQSKAASRAALSARCEIGDSLE  70
Chlamydomonas reinhardtii  MMMRQKVAGAIAGERRSAVAPKMGRAAT--APVVVASANASAFKGAAV---TARVKRSTRAARVQSRRTAVLTQAKIGDSLA  80

Arabidopsis thaliana       LAQATPDKGLRTLLMCMGEALRTIAFKVRTASCGGTACVNSFGDEQLAVDMLADKLLFEALQYSHVCKYACSEEVPELQDMGG  166
Oryza sativa               LTKATPDKNLIRLLICMGEAMRTISFKVRTASCGGTACVNSFGDEQLAVDMLADKLLFEALEYSHVCKYACSEEVPELQDMGG  164
Spinacia oleracea          LAKATTDKGLIRLMMCMGEALRTIGFKVRTASCGGTQCVNTFGDEQLAIDVLADKLLFEALNYSHFCKYACSEELPELQDMGG  159
Triticum aestivum          LTKATPDKNLIRLLICMGEAMRTIAFKVRTASCGGTACVNSFGDEQLAVDMLADKLLFEALEYSHVCKYACSEEVPELQDMGG  165
Zea mays                   LTKATPDKNLIRLLICMGEAMRTIAFKVRTASCGGTACVNSFGDEQLAVDMLANKLLFEALEYSHVCKYACSEEVPELQDMGG  155
Chlamydomonas reinhardtii  LVEATPDPKLRQLMMSMAEATRTIAHKVRTASCAGTACVNSFGDEQLAVDMVADKLLFEALKYSHVCKLACSEEVPEPVDMGG  165

Arabidopsis thaliana       GGFSVAFDPLDGSSIVDTNFTVGTIFGVWPGDKLTGITGGDQVAAAMGIYGPRTTYVLAVKGFPGTHEFLLLDEGKWQHVKE  251
Oryza sativa               GGFSVAFDPLDGSSIVDTNFTVGTIFGVWPGDKLTGVTGGDQVAAAMGIYGPRTTYIIALKDCPGTHEFLLLDEGKWQHVKD  249
Spinacia oleracea          GGFSVAFDPLDGSSIVDTNFSVGTIFGVWPGDKLTGVTGRDQVAAAMGIYGPRTTYVLALKDYPGTHEFLLLDEGKWQHVKE  244
Triticum aestivum          GGFSVAFDPLDGSSIVDTNFTVGTIFGVWPGDKLTGVTGGDQVAAAMGIYGPRTTFVVALKDCPGTHEFLLLDEGKWQHVKD  250
Zea mays                   GGFSVAFDPLDGSSIVDTNFTVGTIFGVWPGDKLTGVTGGDQVAAAMGIYGPRTTYIVALKDCPGTHEFLLLDEGKWQHVKD  240
Chlamydomonas reinhardtii  EGFCVAFDPLDGSSIVDTNFAVGTIFGVWPGDKLTNITGREQVAAGMGIYGPRTVFCIALKDAPGCHEFLLMDDGKWMHVKE  247

Arabidopsis thaliana       IAEGKMFSPGNLRATFDNSEYSKLIDYYVKEKYTLRYTGGMVPDVNQIIVKEKGIFTNVTSPTAKAKLRLLFEVAPLGLLIE  336
Oryza sativa               IGEGKMFSPGNLRATFDNPEYDKLINYYVKEKYTLRYTGGMVPDVNQIIVKEKGIFTNVTSPTAKAKLRLLFEVAPLGFLIE  334
Spinacia oleracea          INEGKLFCPGNLRATSDNADYAKLIQYYIKEKYTLRYTGGMVPDVNQIIVKEKGIFTNVISPTAKAKLRLLFEVAPLGFLIE  329
Triticum aestivum          IGEGKMFSPGNLRATFDNPDYDKLVNYYVKEKYTLRYTGGMVPDVNQIIVKEKGIFTNVTSPTAKAKLRLLFEVAPLGFLIE  335
Zea mays                   IGEGKMFSPGNLRATFDNPEYDKLINYYVKEKYTLRYTGGMVPDVNQIIVKEKGIFTNVTSPTAKAKLRLLFEVAPLGFLME  325
Chlamydomonas reinhardtii  IGEGKMFAPGNLRATFDNPAYERLINFYLGEKYTLRYTGGMVPDVFQIIVKEKGVFTNVTSPTTKAKLRILFEVAPLALLIE  332

Arabidopsis thaliana       GGFSS-DGHK-SVLDKTIINLDDRTQVAYGSKNEIIRFEETLYGTS-RLKN-VPIGVTA                         392
Oryza sativa               GGYSS-DGKQ-SVLDKVINNLDERTQVAYGSKNEIIRFEETLYGSS-RLTAGATVGAAA                         392
Spinacia oleracea          GGHSS-EGTK-SVLDIEVKNLDDRTQVAYGSLNEIIRFEKTLYGSS-RLEEPVPVGAAA                         387
Triticum aestivum          GGHSS-DGKQ-SVLDKVISVLDERTQVAYGSKNEIIRFEETLYGSS-RLAASATVGATA                         393
Zea mays                   GGYSS-DGKQ-SVLDRVINELDERTQVAYGSKNEIIRFEETLYGSS-RLAASATATARALI                       385
Chlamydomonas reinhardtii  GGASSCDGKAVSALDIPILVCDQRTQICYGSIGEVRRFEEYMYGTSPRFSEKVAA                             389
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PrxQ

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Arabidopsis thaliana          MAASSSSFTLCNHTTLRTLPLR---KTLVTKTQFSVPTKSSESNFFGSTLTHSS-------YISPVSSSSLKGLIF-AKVNKGQA  74
Oryza sativa                  MAFAVSTAC--RPSLL--LPPRQRSSPPRP---RPLLCTPSTAAFRRGALSATT---TPTPARAALPSTTGRNRIVCGKVSKGSA  75
Spinacia oleracea             MA----SLSLPKHSLISTLPTQTQTRKPISSQNLCILSNATQSQFCGLKLSHTS------PLSSPFTSRSSKLSVI-AKVKEGTL  74
Triticum aestivum             MAFAASTAC-CEPSVL--LAPRASS---LSSSQARLCRPSTSAAFHGLRAPASAFALTPAPRRRAASTG-----IVCGKVSKGSV  74
Zea mays                      MAFTPATAC-CKASLA--LAPRASPRSPAACAQAALLCTPSTSVFRGLRAPASA---APAPRRRRSAASTG---IVCGKVAKGSV  74
Chlamydomonas reinhardtii     MQ----------------TIRAPARAPVASSRRV-------ATFR-------A---APRVSRTPVVVVRAELKV----GEKLED  47

Arabidopsis thaliana          APDF--TLKDQNGKPVSLKKYKGK-PVVLYFYPADETPGCTKQACAFRDSYEKFKKAGAEV-------------IGISGDDSASH  143
Oryza sativa                  APNF--TLRDQDGRAVSLSKFKGR-PVVVYFYPADETPGCTKQACAFRDSYEKFKKAGAEV-------------IGISGDDAASH  144
Spinacia oleracea             APAF--SLKDQDGRNVSLSKFKGK-PVVVYFYPADESPGCTKQACSFRDSYEKFKKAGAEV-------------IGISVNDPSSH  143
Triticum aestivum             PPNF--TLKDQDGKTVSLSKFKGK-PVVLYFYPADETPGCTKQIIR-QKTFSPLGSAGASSPLGSRILSKRHGSTTIQASLSSPN  155
Zea mays                      PPNF--TLKDQNGKPVSLNKFKGK-PVVVYFYPADETPGCTKQACAFRDSYEKFKKAGAEV-------------IGISGDDAASH  145
Chlamydomonas reinhardtii     YPNYYKVLKTSEGKTISLSSYKGKQPIVLFFYPKAATPGCTKEACRFRDEYSRFTAAGAVV-------------FGISSDSPADN  119

Arabidopsis thaliana          KAFASKYKLPYTLLSDE---GNKVRKDWGVPGDLFGALPGRQT------------------------------------------  183
Oryza sativa                  KEFKKKYKLPFTLLSDE---GNKVRKEWGVPADLFGTLPGRQT------------------------------------------  184
Spinacia oleracea             KAFKEKYRLPYTLLSDE---DNSVRKEWGIPSDLFGALPGRQT------------------------------------------  183
Triticum aestivum             PAPRQQKHLAMTIPSQEITEAATPRRQQPIEEELVGNGGGRTCELPTWALIGGVTVGVALALSLSVDAGPAMALGPEGPLLEEFW  240
Zea mays                      KAFAQKYRLPFTLLSDE---GNRVRKEWGVPADLFGTLPGRQT------------------------------------------  185
Chlamydomonas reinhardtii     AAFGKANNLPYPLVTDE---NSILRKTFGIKGDFLGLLPGRQT------------------------------------------  159

Arabidopsis thaliana          --------YVLDKN-----GVVQLIYNNQFQPEKHI-------DETLKFLKAA                                216
Oryza sativa                  --------YVLDKN-----GVVQYIYNNQFQPEKHI-------GETLKILQSL                                217
Spinacia oleracea             --------YVLDKN-----GVVQLVYNNQFQPEKHI-------NETLKFLESL                                216
Triticum aestivum             DNMRRYGLYALTVSTGFAWALVQPIYELLRNPITAVLIIVVMAGGAVLTVQVINAMAGNSDFVYMYEQ                 308
Zea mays                      --------YVLDKQ-----GVVQYVYNNQFQPEKHI-------GETLKILQTL                                218
Chlamydomonas reinhardtii     --------YVIDVN-----GKCVMAFNDQLNVEQHV-------DEALKVLASVKVAA                            196
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PSAN

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Arabidopsis thaliana     MAAMNSSVLTCSYAIAGSGSVELNQKVGLVN--SSVGFGQKKQMIMPVIKAQRVVGDDVDGSNGRRSAMVFLAATLFSTAAVSASANAGV  88
Oryza sativa             MAGVNNSL------------VGLKPAAAVPQSAGSPALPKRVHVAAPPKLSRAAAG--------------------APRCWAGQARAGV  57
Spinacia oleracea        MASMNSSVLACSYAMSGAGGLELSSKASSVSCVAPSSLGGSEKLTM--IKAQAQNSQQDKAVEGRRAALFGLAAALVATS-FSSNANAGV  87
Triticum aestivum        MAGVNTSV------------VGLKPAAAVPQSASPAA-AKRVQVAPA---------------KDRRSALLGLAAVFAVTAASAGSARASV  62
Zea mays                 MAGVNSSV------------VGLKPAAAVPQAAAASSPAKRVQLAAP---------------EGRRAALLGLAAVFAVTATT-GSAKATI  62

Arabidopsis thaliana     IDEYLERSKTNKELNDKKRLATSGANFARAFTVQFGSCKFPENFTGCQDLAKQKKVPFISEDIALECEGKDKYKCGSNVFWKW          171
Oryza sativa             FDEYLEKSKANK-----VRM                                                                        72
Spinacia oleracea        IDEYLEKSKANKELNDRKRLATSGANFARANTVQFGTCNFPLNFTGCQDLAKQKKVPFISEDIELECEGKDKFKCGSNVFWKW          170
Triticum aestivum        FDEYLEKSKLNKELNDKKRAATSGANFARAYTVQFGSCKFPYNFTGCQDLAKQKKVPFITDDLEIECEGKEKFKCGSNVFWKW          145
Zea mays                 FDEYLEKSKANKELNDKKRLATSGANFARAYTVEFGSCQFPYNFTGCQDLAKQKKVPFISDDLEIECEGKEKFKCGSNVFWKW          145
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Figure S3. Alignment of mature forms of FNR1, FNRL, PSBO-1, PRK, SBP, cFBP1, PrxQ and PSAN from indicated land plants (e.g. *Arabidopsis thaliana, Oryza sativa, Spinacia oleracea, Triticum aestivum* and *Zea mays*) and algae (e.g. *Chlamydomonas reinhardtii*).

Table S1. Primers used in qRT-PCR

Gene		Sequence
EF-1 alfa	Forward	TTCGTCTCCCACTTCAGGAT
At1g07940	Reverse	GGAGCAAAGGTCACAACCAT
ELIP1	Forward	GTCCAGCACCAGAGAGGATT
At3g22840	Reverse	ACCGTCGGAGATCTGAGCTA
UF3GT	Forward	TTGATGGCAAGGAAATGTCA
At5g54060	Reverse	CCACACGAAACTCAGGGATT
RHM1	Forward	TGGGATGGTCAGAGAGAACC
At1g78570	Reverse	AGGAAGCAATGCTCCAGAAA
GSTU20	Forward	TAGAGTTGCGTTGCGAGAGA
At1g78370	Reverse	CGGGATTTTCTTGTGAATGG
IPMI1	Forward	CAGGCGAGTCAATAACCAGAG
At3g58990	Reverse	GAAGGGATGAGAGTGCCGTA
FLS1	Forward	ACAACATTCCGAGGTCCAAC
At5g08640	Reverse	AATAGCCCCCATTCTTCACTC
At5g41670	Forward	TCAGAACACAGAGCGACGAA
	Reverse	GCATAAGAGAAGGACCATTACGA
HDA3	Forward	GATGATTCTGATGGTGAGGATTC
At3g44750	Reverse	CAGGTGCTTTAGGGGTAGTTTC
BT1	Forward	ATCTTGCCGTGTCCCTCTTT
At5g63160	Reverse	GCAGACGCTACTCTTCTCACC
J8	Forward	TACCCCACAATTGCTTCCTC
At1g80920	Reverse	TTAAGATCCGACCCGATTCA
RAB18	Forward	CGCTTGAGCTTGACCAGACT
At5g66400	Reverse	TAGCTCGGAGGATGATGGAC
UGT74E2	Forward	CACAAGCTTTGGACCCATTT
At1g05680	Reverse	TGTGGTGGATCAGCTCTCAA

Table S2. CK content (pmol g^{-1} DW) in leaves of WT and *ntrc* plants cultured in solid MS medium in the absence or presence of VCs emitted by *A. alternata* for 3 days. Values represent the mean ± SE of determinations on 3 independent experiments. Superscripts a, b and c indicate significant differences, according to Student´s t-test ($P<0.05$), between: (a) WT and *ntrc* plants cultured without fungal VC treatment, (b) VC-treated and non-treated WT plants, and (c) VC-treated and non-treated *ntrc* plants. iPRMP, *N^{6}-isopentenyladenosine-5'-monophosphate*; tZRMP, *tZ-riboside-5'-monophosphate*; iPR, *N^{6}-isopentenyladenosine*; tZR, *tZ-riboside*; DZR, *dihydrozeatin-riboside*; iP, *isopentenyladenine*; tZ, *trans-zeatin*; DZ, *dihydrozeatin*; iP7G, N^{6}-isopentenyladenosine-7-glucoside; iP9G, *N^{6}-isopentenyladenosine-9-glucoside*; tZOG, *trans-zeatin-O-glucoside*; tZROG, *trans-zeatin-O-glucoside riboside*; cZRMP, *cis-zeatin riboside-5'-monophosphate*; DHZROG, *dihydrozeatin-riboside-O-glucoside*; DHZOG, *dihydrozeatin-O-glucoside*; tZ7G, *trans-zeatin-7-glucoside*; DZ7G, *dihydrozeatin7-glucoside*; tZ9G, *trans-zeatin-9-glucoside*; cZR, *cis-zeatin ribosides*; cZ, *cis-zeatin*; cZ7G, *cis-zeatin-7-glucoside*; cZOG, *cis-zeatin-O-glucoside*; cZROG, *tZ-riboside-O-glucoside*.

		MEP pathway (plastid) derived CKs				**MVA pathway (cytosol) derived CKs**				
		WT-VCs	WT+VCs	*ntrc*-VCs	*ntrc*+VCs		WT-VCs	WT+VCs	*ntrc*-VCs	*ntrc*+VCs
Precursors	**iPRMP**	51.45 ± 1.01	132.35 ± 5.50^{b}	49.83 ± 1.9	76.63 ± 2.29^{c}	**cZRMP**	17.62 ± 1.9	22.45 ± 4.02	13.03 ± 2.39	29.52 ± 2.79^{c}
	tZRMP	5.66 ± 0.43	53.01 ± 2.83^{b}	2.93 ± 0.12^{a}	8.75 ± 0.48^{c}					
	∑	57.11	185.36	52.76	85.38	∑	17.62	22.45	13.03	29.52
Transport forms	**iPR**	8.32 ± 0.18	13.28 ± 0.22^{b}	14.51 ± 1.66^{a}	68.73 ± 7.36^{c}	**cZR**	1.41 ± 0.08	2.12 ± 0.58	3.63 ± 0.17^{a}	36.53 ± 6.20^{c}
	tZR	1.60 ± 0.08	12.96 ± 12.06^{b}	1.45 ± 0.04	6.89 ± 0.54^{c}					
	DZR	2.47 ± 0.13	2.44 ± 0.21	2.95 ± 0.32	3.96 ± 0.52					
	∑	12.39	43.62	18.91	79.58	∑	1.41	2.12	3.63	36.53
Active forms	**iP**	16.16 ± 0.48	15.07 ± 1.26	19.25 ± 2.76	21.67 ± 2.37	**cZ**	6.22 ± 0.24	3.9 ± 0.17^{b}	7.94 ± 1.13	7.02 ± 1.07
	tZ	13.70 ± 1.83	24.01 ± 1.34^{b}	15.97 ± 2.72	21.68 ± 3.55					
	DZ	0.71 ± 0.15	0.65 ± 0.09	0.89 ± 0.20	0.77 ± 0.1					
	∑	36.06	39.73	36.11	44.12	∑	6.22	3.99	7.94	7.02
Glycosylated (inactive) forms	**iP7G**	2853.32 ± 322.11	1571.17 ± 181.21^{b}	3295.7 ± 84.16	2972.54 ± 299.28	**cZ7G**	1015,39 ± 158,01	299,77 ± 54,21^{b}	1745,44 ± 56,51^{a}	662,50 ± 70,21^{c}
	tZ7G	1003.49 ± 86.38	1267.03 ± 105.57	828.8 ± 10.18	872.56 ± 67.65					
	DZ7G	63.43 ± 8.39	55.64 ± 4.26	58.31 ± 3.64	46.33 ± 1.90^{c}	**cZ9G**	10.79 ± 0.69	2.85 ± 0.13^{b}	13.04 ± 0.85	9.19 ± 0.66^{c}
	iP9G	78.33 ± 3.2	40.95 ± 2.22^{b}	83.08 ± 10.07	85.6 ± 9.53					
	tZ9G	186.93 ± 2.94	293.38 ± 21.13^{b}	149.7 ± 10.93^{a}	206.22 ± 19.87					
	tZOG	85.73 ± 2.22	93.76 ± 6.67	69.62 ± 2.32^{a}	71.17 ± 9.02	**cZOG**	24.19 ± 1.15	9.07 ± 0.03^{b}	31.82 ± 0.67^{a}	18.30 ± 0.69^{c}
	DHZOG	1.66 ± 0.09	1.39 ± 0.12	1.96 ± 0.07	1.29 ± 0.08^{c}					
	tZROG	8.09 ± 0.32	10.63 ± 0.70	7.68 ± 0.14	13.52 ± 4.55	**cZROG**	17.0 ± 4.95	11.29 ± 2.90	23.41 ± 3.10	18.21 ± 1.89
	DHZROG	0.30 ± 0.04	0.47 ± 0.04	0.62 ± 0.07^{a}	0.53 ± 0.03					
	∑	4281.3	3114.53	4494.13	4059.41	∑	1066.98	322.98	1813.71	708.2
TOTAL	∑	4386.86	3343.24	4601.91	4268.49	∑	1092.23	351.54	1838.31	781.27

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Table S3. List of VC-responsive redox-sensitive peptides in leaves of WT plants identified in the redox-proteomic analysis. Proteins are assembled into functional groups according to the Mapman tool. The asterisk symbol (*) highlights the position of NEM-tagged cysteine residues. The symbol (^) highlights the position of cysteine carbamidomethylation tagging due to the reaction with IAM. The column "Cys redox status" shows the redox status of cysteine residues in VC-treated plants with respect to that of the same cysteine residues in VC non-treated plants. Peptides whose cysteines are oxidized in response to the VC treatment are highlighted in gray. The column "Ref" includes the references of previous studies showing redox sensitiveness of the protein. (1) Fares et al., (2011); (2) Wang et al., (2012); (3) Dixon et al., (2005); (4) Marchand et al., (2010); (5) Liu et al., (2014); (6) Liu et al., (2015); (7) Muthuramalingam et al., (2013); (8) Zhu et al., (2014); (9) Buchanan and Balmer (2005); (10) Akter et al., (2015); (11) De Smet et al., (2019).

Accession number	Protein description	Subcellular location	Peptide sequence	Cys site	Cys redox status	Fold change (log2)	Disulfide bond formation prediction (DiANNA)	Ref.
Amino acids metabolism								
AT1G55880	Pyridoxal-5'-phosphate-dependent enzyme family protein	ER	C*FLIDPPGSGLYNK	277	oxi	0,448	No	
AT5G57890	Glutamine amidotransferase type 1 family protein	plastid	MAATTLYNSC*LLQPK	10	oxi	0,318	Yes	
C1-metabolism								
AT5G56260	Ribonuclease E inhibitor RraA/Dimethylmenaquinone methyltransferase	cytosol	RC^FSGPIVTLK	37	red	0,465	-	
Cell								
AT3G44730	Kinesin-like protein 1	nucleus	GC*LHLVDLAGSERVEK	606	red	2,206	-	
AT4G39050	Kinesin motor family protein	plastid	SSPSC^SNKAVSGEYADELKK	727	red	0,460	-	
AT5G67530	Plant U-box 49	cytosol	TTGNVFC^YEAIKELNIKTK	127	red	0,260	No	
AT5G67530	Plant U-box 49	cytosol	TTGNVFC*YEAIKELNIK	127	oxi	0,497	No	

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Cell wall								
AT1G65570	Pectin lyase-like superfamily protein	extracellular	NLMVDGITC*GPGHGISIGSLAK	242	oxi	0,493	-	
AT2G20750	Expansin B1	extracellular	C^LDKTIC^SK	98/104	red/red	0,405	Yes	
AT5G60920	COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored protein family	Plasma membrane	YKGNIPHC^CKK	116	red	0,281	Yes	
Development								
AT1G69440	Argonaute family protein	cytosol	EIQRAASNNLQLIIC^VMEK	652	red	0,381	-	
AT3G24560	Adenine nucleotide alpha hydrolases-like superfamily protein	mitochondrion, plasma membrane	YEMISNVC^FR	189	red	0,326	-	
AT1G76580	Squamosa promoter-binding protein-like (SBP domain) transcription factor family protein	nucleus	VC*EVHSKATK	136	oxi	0,398	-	
AT1G02220	NAC domain containing protein 3	nucleus	DVAWC*FFRPKENK	64	oxi	0,487	-	
AT1G34180	NAC domain containing protein 16	nucleus	C*KNAKEYYALYK	151	oxi	0,400	Yes	
DNA synthesis								
AT1G60930	RECQ helicase L4B	nucleus	C^VTDNWNMPRDYLVSK	398	red	0,446	-	
AT2G19120	P-loop containing nucleoside triphosphate hydrolases superfamily protein	nucleus	FC^VGVYMHLQKTLKSLGAGK	917	red	0,405	-	
AT2G32000	DNA topoisomerase, type IA, core	nucleus	LYQYVC^QHFLGTVSPNCK	408	red	0,446	-	
AT5G44800	Chromatin remodeling 4	nucleus	YGTAVINIC^EDKWK	596	red	0,395	-	
AT5G46920	Intron maturase, type II family protein	mitochondrion	IVNFC^SYIIRGSLAK	557	red	0,305	-	
AT1G06670	Nuclear DEIH-boxhelicase	nucleus	C^QAGICYHLYSKLR	693	red	0,241	-	
AT3G10010	Demeter-like 2	nucleus	LHC*SHVAIRTK	1319	oxi	0,410	-	
AT3G47460	Structural maintenance of chromosomes (SMC) family protein	nucleus	NC*SVKVDK	922	oxi	0,444	-	

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AT3G14890	Phosphoesterase	nucleus	SC*SNKIAVKSLR	65	oxi	0,427	No	
Fermentation								
AT1G77120	Alcohol dehydrogenase 1	cytosol	FDQAKEFGVTEC^VNPK	243	red	0,382	No	1, 2, 3, 9
Glycolisis								
AT1G22170	Phosphoglycerate mutase family protein (PGM)	plastid	KTNFC^KIK	45	red	0,412	Yes	9
Hormone metabolism								
AT3G07900	O-fucosyltransferase family protein	plastid	KLAGLC^PLNAK	408	red	0,496	Yes	
Lipid metabolism								
AT2G15090	3-ketoacyl-CoA synthase 8 (KCS8)	Plasma membrane	SLNLGGMGC^SAGVIAVDVAK	213	red	0,442	Yes	
AT5G22420	fatty acid reductase 7 (FAR7)	cytosol	KC^VKPK	78	red	0,437	No	
AT1G06520	Glycerol-3-phosphate acyltransferase 1	mitochondrion	LPKEMTC*AGGK	540	oxi	0,144	Yes	
Major CHO metabolism								
AT1G05610	ADP-glucose pyrophosphorylase small subunit 2	plastid	LLREC*LIK	274	red	1,934	No	
Metal handling								
AT5G08730	IBR domain-containing protein	nucleus	LEISTTC^TGNHFDGFIK	426	red	0,447	No	
Minor CHO metabolism								
AT1G04420	NAD(P)-linked oxidoreductase superfamily protein	plastid	DKIVLATKVC^GYSER	143	oxi	2,235	No	

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Miscellaneous enzyme family								
AT2G34500	Cytochrome P450, family 710, subfamily A, polypeptide 1	extracellular	LGETLGIC^AGKSK	245	red	0,301	-	
AT3G50400	GDSL-like Lipase/Acylhydrolase superfamily protein	extracellular	QC*VDLANK	249	oxi	0,392	No	
AT4G33355	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	extracellular	QLPAKCGVNIGVPFSKTVDC*NR	115	red	5,952	Yes	
AT4G37530	Peroxidase superfamily protein	extracellular	AKEAVDAVPNC^RNK	119	oxi	1,917	Yes	
AT5G16960	Zinc-binding dehydrogenase family protein	cytosol	IAAC^GMISQYNLK	255	red	0,450	No	
AT5G56870	Beta-galactosidase 4	extracellular	DKSCIFLAILCC^LSLSCIVK	18	red	0,323	Yes	
Nucleotide metabolism								
AT3G46940	DUTP-PYROPHOSPHATASE-LIKE	nucleus	MAC^VNEPSPKLQK	3	red	0,343	-	10
Photosynthesis								
AT1G15140	FAD/NAD(P)-binding oxidoreductase (FNRL)	plastid	SIAGSTAEILC^GLKK	141	red	0,463	Yes	
AT3G54050	Fructose-1,6-bisphosphatase (cFBP1)	plastid	KLDVISNEVFSNC^LR	154	red	0,325	Yes	9
AT1G32060	Phosphoribulokinase (PRK)	plastid	KLTC^SYPGIK	295	red	0,487	-	1, 8, 10
AT3G55800	sedoheptulose-bisphosphatase (SBP)	plastid	LLFEALQYSHVC^K	150	red	0,420	No	7, 8, 9, 11
AT5G64040	Photosystem I reaction center subunit PSI-N, chloroplast, putative / PSI-N, putative (PSAN)	plastid	KVPFISEDIALEC^EGK	155	red	0,483	Yes	
AT5G64040	Photosystem I reaction center subunit PSI-N, chloroplast, putative / PSI-N, putative (PSAN)	plastid	KVPFISEDIALEC*EGK	155	red	2,321	Yes	

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Protein								
AT1G02010	Secretory 1A	cytosol	ILIMDRVTVKVMSQSC^K	62	red	0,459	-	
AT1G10730	Clathrin adaptor complexes medium subunit family protein	cytosol	MRTYLSGMPEC^KLGLNDR	212	red	0,464	-	
AT1G12960	Ribosomal protein L18e/L15 superfamily protein	cytosol	FYC*QIVNLDK	51	red	3,984	-	
AT1G19160	F-box family protein	Plasma membrane	GVC*THGVLYYGAYTGDGAK	185	oxi	0,493	Yes	
AT1G21160	Eukaryotic translation initiation factor 2 (eIF-2) family protein	cytosol	MGVKIFCDDTIYC^LFDK	930	oxi	2,180	-	
AT1G22780	Ribosomal protein S13/S18 family	cytosol	GIGRRLANIVC*K	45	oxi	0,410	-	
AT1G26630	Eukaryotic translation initiation factor 5A-1 (eIF-5A 1) protein	cytosol	KGGHIVIKNRPC*K	39	oxi	0,302	No	8
AT1G28350	Nucleotidylyl transferase superfamily protein	cytosol	AYCPPKTVEGNPC^LEYVK	661	red	2,035	-	
AT1G67180	Zinc finger (C3HC4-type RING finger) family protein / BRCT domain-containing protein	nucleus	SITHLVC^WK	43	red	0,234	No	
AT1G75370	Sec14p-like phosphatidylinositol transfer family protein	cytosol	EFEKTVNIKLPAC*C*IAAK	218/219	oxi/oxi	0,448	No	
AT2G01735	RING-finger protein for embryogenesis	plastid	MRATCPLC^KYNILK	347	red	0,497	Yes	
AT2G04842	Threonyl-tRNA synthetase, putative / threonine--tRNA ligase, putative	plastid, mitochondrion	HTC*AHVMAMAVQK	86	oxi	0,482	-	11
AT2G22980	Serine carboxypeptidase-like 13	extracellular	IC^KGNYVK	240	red	0,308	Yes	
AT2G37150	RING/U-box superfamily protein	nucleus	CAIC*LEEYK	548	oxi	0,223	-	
AT2G39660	Botrytis-induced kinase1	Plasma membrane	MGSC*FSSRVK	4	oxi	0,484	-	
AT3G13680	F-box and associated interaction domains-containing protein	cytosol	AIRSTC^QKWNSLSK	31	red	0,479	No	

AT3G17265	F-box and associated interaction domains-containing protein	cytosol	VPATFLKELQTTC^K	30	red	0,229	Yes	
AT3G43180	RING/U-box superfamily protein	cytosol	SC*ANLLTPKTK	117	oxi	0,427	Yes	
AT3G44620	Protein tyrosine phosphatases;protein tyrosine phosphatases	plastid	VKLMC*SYC^KK	218/221	oxi/red	0,398	No	
AT4G08455	BTB/POZ domain-containing protein	nucleus	SYC^ERFLVTK	158	red	0,432	-	
AT4G22390	F-box associated ubiquitination effector family protein	cytosol	FPC^PVEVKVFSLK	170	red	0,153	Yes	
AT5G01020	Protein kinase superfamily protein	Plasma membrane	AC*SLAYYC*LSQNPK	322/328	oxi/oxi	0,470	-	
AT5G05670	Signal recognition particle binding	ER	IPVLLCC*NK	176	oxi	0,295	No	
AT5G11400	Protein kinase superfamily protein	cytosol	MGNC^LKHFK	4	red	0,361	-	
AT5G15250	FTSH protease 6	plastid	FDRQVC^WLILKPNK	390	red	0,477	-	
AT5G35210	Metalloendopeptidases;zinc ion binding;DNA binding	nucleus	GC^MLNAAVAGATKGAMK	719	red	0,405	-	
AT5G45570	Ulp1 protease family protein	nucleus	DYKQFQPDYRC^FK	739	red	0,332	-	
AT5G49940	NIFU-like protein 2	plastid	VKLQGAC*GSCPSSTMTMK	126	oxi	0,371	No	
AT5G54940	Translation initiation factor SUI1 family protein	cytosol	DLKKDFC*C^NGNVVQDK	67/68	red/oxi	2,254	No	
AT5G67380	Casein kinase alpha 1	ER	C^IIKILKPVK	136	red	0,498	-	
Redox metabolism								
AT3G26060	Peroxiredoxin Q (PrxQ)	plastid	QAC^AFRDSYEK	116	red	0,481	No	8
RNA								
AT1G09620	ATP binding;leucine-tRNA ligases;aminoacyl-tRNA ligases	cytosol	C*NGHIMLNSEKMSK	705	red	2,300	-	5, 6,10
AT1G09770	Cell division cycle 5	nucleus	QAEIGGTEVEC^FKALK	752	red	0,234	-	
AT1G09920	TRAF-type zinc finger-related	nucleus	C*KICGDMVPKK	38	oxi	0,394	Yes	
AT2G31180	myb domain protein 14	nucleus	HAGLLRC*GK	49	oxi	1,975	No	
AT3G05430	Tudor/PWWP/MBT superfamily prot	nucleus	SENC^PPEPKKK	539	red	0,472	-	

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AT4G10920	Transcriptional coactivator p15 (PC4) family protein (KELP)	nucleus	EYENSQVNKEEEDGDKDC^GK	83	oxi	3,390	No	
AT4G12920	Eukaryotic aspartyl protease family protein	extracellular	IC*TYQQHYLDETNIK	133	oxi	0,345	-	
AT4G20280	TBP-associated factor 11	nucleus	IGMPMIIVAC^GIAK	155	red	0,469	No	
AT4G21030	Dof-type zinc finger domain-containing protein	nucleus	SQPRYKC^K	48	red	0,400	Yes	
AT4G29000	Tesmin/TSO1-like CXC domain-containing protein	nucleus	FRDC*LNRLISYAEIK	510	oxi	0,446	-	
AT5G40880	WD-40 repeat family protein / zfwd3 protein (ZFWD3)	nucleus	QHIGTVTSLLC^WDK	360	red	0,485	-	
AT5G46190	RNA-binding KH domain-containing protein	nucleus	VIC*SSSKIGRVIGK	323	oxi	0,457	No	
AT5G49330	Myb domain protein 111	nucleus	KSC^SSSSGAKNNNK	140	red	0,329	No	
AT5G61190	Putative endonuclease or glycosyl hydrolase with C2H2-type zinc finger domain	nucleus	KIC*GTLESSVK	605	oxi	0,489	-	
S-assimilation								
AT1G62180	5'adenylylphosphosulfate reductase 2 (APR2)	plastid	AKEC^GLHKGNIK	314	red	0,463	No	9
Secondary metabolism								
AT1G33750	Terpenoid cyclases/Protein prenyltransferases superfamily protein	mitochondrion	STKLNLC^VK	52	red	0,386	No	
AT5G26000	Thioglucoside glucohydrolase 1	peroxisome	RIDYLC^SHLC^FLSK	445/449	red/red	0,410	No	7, 8
Signaling								
AT1G07550	Leucine-rich repeat protein kinase family protein	Plasma membrane	NC^YSLNVK	92	red	0,361	-	
AT1G48050	Ku80 family protein	nucleus	RMC^LITNAAC^PTK	124/131	red/red	0,391	No	

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AT2G14440	Leucine-rich repeat protein kinase family protein	Plasma membrane	VLRYFPEGIRNC*YSLSVK	93	oxi	0,351	-	
AT3G22170	Far-red elongated hypocotyls 3 (FHY3)	nucleus	FEKC^IYK	400	red	0,450	Yes	
AT4G36080	Phosphotransferases,alcohol group as acceptor	cytosol	SGVHC^LALFK	543	red	0,358	-	
AT5G01890	Leucine-rich receptor-like protein kinase family protein	Plasma membrane	NWFSGDVPSDIGRC^SSLK	236	red	0,482	-	
AT5G37770	EF hand calcium-binding protein family	cytosol	ELHSVMKNLGEKC*SVQDC^K	126/131	oxi/red	0,337	No	
Stress								
AT1G56520	Disease resistance protein (TIR-NBS-LRR class) family	mitochondrion	AFKKMC*NLLILK	554	oxi	0,344	-	
AT1G56520	Disease resistance protein (TIR-NBS-LRR class) family	mitochondrion	NQTGDFGIAFKETC*AHK	128	red	2,097	-	
AT1G60989	SCR-like 7	extracellular	QQVFRGSC*SDDGGQK	45	oxi	0,306	Yes	
AT1G68905	Defensin-like (DEFL) family protein	extracellular	AEVNC*IGGK	36	oxi	0,461	Yes	
AT2G32680	Receptor like protein 23	extracellular	LPRSFVNC*SSLK	575	oxi	0,497	-	
AT2G36800	Don-glucosyltransferase 1	Plasma membrane	AERGNKSDIDQDEC*LK	277	oxi	0,463	No	
AT2G43550	Scorpion toxin-like knottin superfamily protein	extracellular	FIC*VVEYGGDVGPTFCNPK	33	oxi	0,315	Yes	
AT3G10980	PLAC8 family protein	Plasma membrane	FYHLVLLC^RWKHDDITK	197	red	0,359	Yes	
AT4G07820	CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein)	extracellular	VKC^NNGGFLAICSYDPSVILSERPF	138	oxi	3,632	No	
AT4G29033	Defensin-like (DEFL) family protein	extracellular	IANC^NQTC*IESQFLGGK	44/48	oxi/red	2,059	Yes	

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TCA								
AT1G59900	Pyruvate dehydrogenase complex E1 alpha subunit	mitochondrion	DC^PMPEPSELFTNVYVK	355	red	0,342	No	9
Transport								
AT2G29650	Phosphate transporter 4;1 (PHT4)	plastid	KLIADNC^ASK	303	red	0,318	No	
AT1G02520	P-glycoprotein 11	Plasma membrane	VMQMYKKQC*EGPIK	921	oxi	0,306	-	
AT2G37010	Non-intrinsic ABC protein 12	Plasma membrane	DEATTVHVKPNINC*NLAK	139	oxi	0,409	-	

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Table S4. List of VC-responsive redox-sensitive peptides in *ntrc* plants identified in the redox-proteomic analysis. Proteins are assembled into functional groups according to the MapMan tool. The asterisk symbol (*) highlights the position of NEM-tagged cysteine residues. The symbol (^) highlights the position of cysteine carbamidomethylation tagging due to the reaction with IAM. The column "Cys redox status" shows the redox status of cysteine residues in VC-treated *ntrc* plants with respect to that of the same cysteine residues in VC non-treated plants. Peptides whose cysteines are oxidized by the VC treatment are highlighted in gray. The column "Ref" includes the references of previous studies showing redox sensitiveness of the protein. (1) Fares et al., (2011); (2) Wang et al., (2012); (3) Dixon et al., (2005); (4) Marchand et al., (2010); (5) Liu et al., (2014); (6) Liu et al., (2015); (7) Hu et al., (2014); (8) Muthuramalingam et al., (2013); (9) Guo et al., (2014); (10) Zhu et al., (2014); (11) Buchanan and Balmer (2005); (12) Lindahl and Kieselbach (2009); (13) Akter et al., (2015); (14) De Smet et al., (2019).

Accession number	Protein description	Subcellular location	Peptide sequence	Cys site	Cys redox status	Fold change (log2)	Disulfide bond formation prediction (DiANNA)	Ref.
Amino acids metabolism								
AT1G69040	ACT domain repeat 4	cytosol	MNPPRVVIDNDSC*K	30	oxi	0,364	Yes	
AT5G48060	C2 calcium/lipid-binding plant phosphoribosyltransferase	cytosol	GSTNAYC^VAKYGQK	652	red	0,422	-	
AT5G17920	Cobalamin-independent synthase family protein	cytosol	C*VKPPVIYGDVSRPK	522	red	2,704	-	3, 4, 10
Cell								
AT1G03670	Ankyrin repeat family protein	plasma membrane	IIKEFLKHC*PDSR	310	oxi	0,340	-	
AT4G16340	Guanyl-nucleotide exchange factors;GTPase binding;GTP binding	golgi	SQELQQLIAALLEFMAVC*K	1786	oxi	0,481	-	
AT5G27000	Kinesin 4	cytosol	SGIVLC*NVLNK	86	red	5,772	-	
AT2G02300	Phloem protein 2-B5	cytosol	KC^VMLSAKK	127	red	0,461	No	
AT5G67530	Plant U-box 49	cytosol	TTGNVFC^YEAIKELNIKTK	127	red	0,369	No	
AT3G49650	P-loop containing nucleoside triphosphate hydrolases	cytosol	KTTTLTVAVKC*RPLMEK	21	red	1,932	No	

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Cell wall								
AT3G29810	COBRA-like protein 2 precursor	plasma membrane	FKGNIPHC*CK	109	oxi	0,454	Yes	
AT3G45970	Expansin-like A1	extracellular	C^KNPKLCSTK	80	oxi	2,567	No	
AT1G57590	Pectinacetylesterase family protein	extracellular	GGAKLIDC*AYPCDK	429	oxi	0,499	Yes	
Co-factor and vitamine metabolism								
AT2G29630	ThiaminC (THIC1)	plastid	MAASVHC^TLMSVVCNNK	7	oxi	1,929	No	14
Development								
AT1G69440	Argonaute family protein	cytosol	EIQRAASNNLQLIIC^VMEK	652	red	0,496	-	
AT1G76580	Squamosa promoter-binding protein-like (SBP domain)	nucleus	VC*EVHSKATK	136	oxi	0,468	-	
AT5G52820	WD-40 repeat family protein / notchless protein, putative	nucleus	KSIICLSGHTLAVTC*VK	236	red	1,907	-	
DNA synthesis								
AT3G10010	demeter-like 2	nucleus	LHC*SHVAIRTK	1319	oxi	0,448	-	
AT1G22275	Myosin heavy chain-related protein	nucleus	GHLILQC^NENEK	505	red	0,462	-	
AT4G25120	P-loop containing nucleoside triphosphate hydrolases	nucleus	SPEQC^RKMGNEIGAK	917	red	0,410	-	
AT3G20540	Polymerase gamma 1	nucleus	FRNWASKHC^PDAK	540	red	0,476	-	
AT3G47460	Structural maintenance of chromosomes (SMC) family protein	nucleus	NC*SVKVDK	922	red	2,134	-	

Fermentation								
AT1G77120	Alcohol dehydrogenase 1	cytosol	FDQAKEFGVTEC^VNPK	243	red	0,346	No	1, 2, 3, 11
Hormone metabolism								
AT2G30810	Gibberellin-regulated family protein	extracellular	CSATSHRKPC^LFFC^NK	65/69	red/red	0,419	Yes	
Lipid metabolism								
AT1G06520	Glycerol-3-phosphate acyltransferase 1	mitochondrion	LPKEMTC*AGGK	540	oxi	0,266	Yes	
Metal handling								
AT5G23980	Ferric reduction oxidase 4 (FRO4)	plasma membrane	HEVAKIC^SSGLAK	682	red	0,355	-	
Michocondrial electron transport								
ATMG00640	Hydrogen ion transporting ATP synthases	mitochondrion	KMLFAAILSIC*ALSSK	22	oxi	0,499	Yes	5
Minor CHO metabolism								
AT1G04420	NAD(P)-linked oxidoreductase superfamily protein	plastid	DKIVLATKVC^GYSER	143	red	0,400	No	
Miscellaneous enzyme family								
AT5G56870	Beta-galactosidase 4	extracellular	DKSCIFLAILCC^LSLSCIVK	18	red	0,431	Yes	
AT4G33355	Bifunctional inhibitor/lipid-transfer protein	extracellular	QLPAKCGVNIGVPFSKTVDC*NR	115	red	2,126	Yes	
AT1G63450	Root hair specific 8	mitochondrion	KKPGSC^EGK	279	red	0,494	No	
AT2G18560	UDP-Glycosyltransferase	golgi	EPMKIPGC*KPVGPK	82	oxi	0,435	No	

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Nucleotide metabolism								
AT4G30530	Class I glutamine amidotransferase-like superfamily protein	cytosol	C*HQDEVLVLPETAK	154	oxi	0,461	-	
OPP cycle								
AT1G30510	Root FNR 2	plastid	NGVC*SNFLC*DSKPGDK	200/ 205	oxi/oxi	0,405	Yes	5
Photosynthesis								
AT5G66190	Ferredoxin-NADP(+)-oxidoreductase 1 (FNR1)	plastid	GVC^SNFLC^DLKPGDEAK	178/ 183	oxi/oxi	1,977	Yes	8, 9
AT5G64040	Photosystem I reaction center subunit PSI-N, chloroplast, putative / PSI-N, putative (PSAN)	plastid	KVPFISEDIALEC^EGK	155	oxi	2,791	Yes	
AT5G66570	PS II oxygen-evolving complex 1 (PSBO-1)	plastid	GTGTANQC^PTIDGGSETFSFKPGK	114	oxi	2,361	Yes	7, 8, 9, 10
Protein								
AT1G09620	ATP binding;leucine-tRNA ligases;aminoacyl-tRNA ligases	cytosol	C*NGHIMLNSEKMSK	705	red	2,305	-	5, 6, 13
AT5G25350	EIN3-binding F box protein 2	nucleus	GMTDVGLEAVGNGC*PDLKHVSLNK	350	oxi	0,468	-	
AT3G17480	F-box and associated interaction domains-containing protein	cytosol	ELNLKGLLC^NSGK	101	oxi	1,977	Yes	
AT3G47030	F-box and associated interaction domains-containing protein	mitochondrion	VC^PPILGLICCKSSK	141	red	0,458	Yes	
AT4G22390	F-box associated ubiquitination effector family protein	cytosol	FPC^PVEVKVFSLK	170	red	0,379	Yes	
AT1G32375	F-box/RNI-like/FBD-like	plasma	MLLSNC^PVLEDLVVK	178	oxi	2,458	Yes	

	domains-containing protein	membrane						
AT5G02980	Galactose oxidase/kelch repeat superfamily protein	cytosol	FLYIC^LNLTK	70	oxi	4,945	Yes	
AT1G02170	Metacaspase 1	cytosol	FSRHELKGC^INDAK	99	red	0,372	No	
AT5G35210	Metalloendopeptidases;zinc ion binding;DNA binding	nucleus	GC^MLNAAVAGATKGAMK	719	red	0,471	-	
AT5G49940	NIFU-like protein 2	plastid	VKLQGAC*GSCPSSTMTMK	126	oxi	0,408	No	
AT5G38510	Rhomboid-related intramembrane serine protease family protein	plasma membrane	DC^RMKSYMK	45	oxi	2,385	Yes	
AT1G48350	Ribosomal L18p/L5e family protein	plastid	KVGEVIAKSC*LEK	135	oxi	0,422	Yes	
ATCG00830	Ribosomal protein L2	plastid	NAYIC^LIHYGDGEK	90	oxi	2,036	No	
AT1G67430	Ribosomal protein L22p/L17e family protein	nucleus, cytosol	INPYMSNPC^HIELILSEK	145	oxi	2,054	-	
AT1G22780	Ribosomal protein S13/S18 family	cytosol	GIGRRLANIVC*K	45	red	2,507	-	
AT5G54990	RING/U-box superfamily protein	nucleus	VDVEQWVRIDC^C^C^KQK	159/ 160/ 161	oxi/oxi/ oxi	2,228	Yes	
AT3G43180	RING/U-box superfamily protein	cytosol	SC*ANLLTPKTK	117	red	5,113	Yes	
AT4G31450	RING/U-box superfamily protein	nucleus	FNSNSCKVPIC*SDEK	38	oxi	0,329	Yes	
AT2G21540	SEC14-like 3	cytosol	TKLC*SLKK	29	oxi	0,355	-	
AT1G75370	Sec14p-like phosphatidylinositol transfer family protein	cytosol	EFEKTVNIKLPAC*C*IAAK	218/ 219	oxi/oxi	0,420	No	
AT1G11330	S-locus lectin protein kinase family protein	plasma membrane	ITFSSPIKDSESETLLC*K	49	oxi	0,446	-	
AT1G65130	Ubiquitin carboxyl-terminal hydrolase-related protein	plastid	GERDDGKNLVC^K	411	oxi	1,942	-	
AT2G36170	Ubiquitin supergroup;Ribosomal protein L40e	nucleus, cytosol	C*GHSNQLRPK	115	red	2,548	No	

Redox metabolism								
AT3G26060	Peroxiredoxin Q (PrxQ)	plastid	QAC^AFRDSYEK	116	oxi	2,972	No	10
RNA								
AT4G36540	BR enhanced expression 2	nucleus	KMKC^LQDIVPGC^NK	169/ 177	red/red	0,454	Yes	
AT5G56200	C2H2 type zinc finger transcription factor family	nucleus	KHICC^EC*GKR	82/84	oxi/red	2,446	-	
AT1G63100	GRAS family transcription factor	nucleus	TKTSGC*SLKQNIK	85	oxi	0,492	Yes	
AT4G03430	Pre-mRNA splicing factor-related	nucleus	KEVVAKC*VACEPK	986	oxi	0,396	-	
AT3G52100	RING/FYVE/PHD-type zinc finger family protein	nucleus	KTGVTNSTSC*DVSK	474	oxi	0,314	-	
AT4G35800	RNA polymerase II large subunit	nucleus	TVLSIMRC*VC*FNCSK	104/ 106	oxi/oxi	0,407	-	
AT5G15270	RNA-binding KH domain-containing protein	nucleus	IGC*ILGK	383	oxi	1,928	-	5
AT4G29000	Tesmin/TSO1-like CXC domain-containing protein	nucleus	FRDC*LNRLISYAEIK	510	red	3,030	Yes	
S-assimilation								
AT1G62180	5'adenylylphosphosulfate reductase 2 (APR2)	plastid	AKEC^GLHKGNIK	314	red	0,427	No	11
Secondary metabolism								
AT1G33750	Terpenoid cyclases/Protein prenyltransferases superfamily protein	mitochondrion	STKLNLC^VK	52	red	0,476	No	
AT3G14490	Terpenoid cyclases/Protein prenyltransferases superfamily	plastid	LNFNYC^QLHYIQELK	30	red	0,264	Yes	

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AT3G14520	Terpenoid cyclases/Protein prenyltransferases superfamily protein	plastid	HHLVC*VRSTK	49	oxi	0,372	Yes	
AT5G26000	thioglucoside glucohydrolase 1	peroxisome	RIDYLC^SHLC^FLSK	445/ 449	oxi/oxi	2,568	No	8, 10
Signaling								
AT4G33050	Calmodulin-binding family protein	nucleus, cytosol	QC^IRYLGPMER	228	oxi	1,951	Yes	
AT1G48050	Ku80 family protein	nucleus	KRMC*LITNAACPTK	124	oxi	0,417	No	
AT1G07550	Leucine-rich repeat protein kinase family protein	plasma membrane	NC^YSLNVK	92	oxi	2,957	-	
AT2G19230	Leucine-rich repeat transmembrane protein kinase protein	plasma membrane	VGGNPDLC^VSDSCRNKK	502	oxi	2,065	-	
AT4G36080	Phosphotransferases, alcohol group as acceptor	cytosol	MLDAGKSLC^SLLK	543	oxi	1,929	-	
AT3G26490	Phototropic-responsive NPH3 family protein	plasma membrane	LC*RILDC^K	470/ 475	oxi/red	0,389	Yes	
AT1G35467	RALF-like 5	extracellular	DC*GGLSTWKK	71	red	2,120	-	
AT3G22020	Receptor-like protein kinase-related family protein	mitochondrion	LYAMVQC^TLDIFHCK	176	red	0,481	No	
Stress								
AT2G36800	Don-glucosyltransferase 1	plasma membrane	AERGNKSDIDQDEC*LK	227	oxi	0,347	No	
AT1G56280	Drought-induced 19	nucleus	NVC^PVCSLKVGVDIVAHK	69	red	0,483	Yes	
AT1G50180	NB-ARC domain-containing disease resistance protein	cytosol	C*LIVLDDIWGK	270	oxi	0,488	-	
AT3G21210	Zinc ion binding	nucleus	CNFVVHKEC^VYFPC^IIK	416/ 421	red/red	0,404	Yes	

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TCA								
AT1G48030	Mitochondrial lipoamide dehydrogenase 1	mitochondrion	RGALGGTC^LNVGC^IPSK	82/87	oxi/oxi	2,077	-	10, 13
Transport								
AT2G19110	Heavy metal atpase 4	plasma membrane	KVVENVC^LSIILK	661	red	0,369	-	

CAPÍTULO II

Proteostatic regulation of MEP and shikimate pathways by redox-activated photosynthesis signaling in plants exposed to microbial volatiles

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INTRODUCTION

Microbes can produce volatile compounds (VCs) that promote plant growth, photosynthesis and developmental changes (Ryu et al., 2003; Zhang et al., 2008; Kanchiswamy et al., 2015; Ditengou et al., 2015; Garnica-Vergara et al., 2016; Sánchez-López et al., 2016b; García-Gómez et al., 2020). In Arabidopsis, promotion of growth and photosynthesis by microbial VCs is associated with enhanced levels of soluble sugars, starch resulting from the activation of non-canonical biosynthetic pathway(s), anthocyanins and photosynthetic pigments (Zhang et al., 2008; Ezquer et al., 2010; Sánchez-López et al., 2016a; Sánchez-López et al., 2016b; Ameztoy et al., 2019; García-Gómez et al., 2019). This response is also associated with reduction in the contents in leaves of abscisic acid (ABA), and enhancement of cytokinins (CKs) derived from the plastid-localized 2-C-methyl-D-erythritol 4-phosphate (MEP) pathways (Zhang et al., 2008; Sánchez-López et al., 2016b; Ameztoy et al., 2019). Transcriptomic changes induced by microbial VCs are similar to those occurring in plants cultured under conditions that enhance photosynthesis such as exposure to elevated CO_2 and increased irradiance (García-Gómez et al., 2019), despite substantial differences in induced developmental and metabolic changes (Sánchez-López et al., 2016b; García-Gómez et al., 2019). This suggests that (i) transcriptional changes in microbial VC-exposed plants are mainly due to enhanced photosynthesis signaling, and (ii) regulation of some plant responses to fungal VCs is primarily non-transcriptional (García-Gómez et al., 2019). This hypothesis is supported by recent quantitative and site-specific redox-proteomic analyses showing that microbial VCs promote global thiol redox proteome changes including the reduction of highly conserved Cys residues of redox-regulated Calvin-Benson cycle (CBC) enzymes (e.g. phosphoribulokinase, sedoheptulose-1,7-bisphosphatase and one of the two isoforms of plastid-localized fructose-1,6-bisphosphatase [cFBP1]), and proteins involved in photochemical reactions of photosynthesis (Ameztoy et al., 2019).

The carbon fixed by the CBC can be used for sucrose and starch biosynthesis, and is also essential to provide substrates for the synthesis of secondary compounds that are important for growth and development (e.g. phenylpropanoids and isoprenoids) via the plastid-localized shikimate and MEP pathways. Modulation of the metabolic flux towards the shikimate pathway involves substrate (e.g. erythrose-4-phosphate, E4P) provision by the CBC (Henkes et al., 2001), and feedback allosteric inhibition and redox regulation of the first enzyme of the pathway (e.g. phospho-2-dehydro-3-deoxyheptonate aldolase [DHS]) (Entus et al., 2002; Tzin et al., 2012). Nishimura et al. (2013) reported that DHS is recognized by the Clp protease system, and suggested that Clp-regulated proteolysis could provide a mechanism of control of the shikimate pathway activity. The MEP pathway uses pyruvate and glyceraldehyde 3-phosphate (GAP) to produce the universal prenyl diphosphate precursors of isoprenoid compounds. Works centered on the identification of the mechanisms that control the metabolic flux through the MEP pathway in leaves indicate multiple levels of regulation. One level reflects the dependence of the MEP pathway on the availability of GAP, which in turn depends on photosynthetic activity (Ghirardo et al., 2010; Pokhilko et al., 2015). Another level involves coarse control by transcriptional regulation of the expression of MEP pathway genes (Carretero-Paulet et al., 2002; Cordoba et al., 2009; Vranová et al., 2013) whereas fine regulation involves post-translational control of the first enzymatic step of the MEP pathway, which is catalyzed by 1-deoxy-D-xylulose-5-phosphate synthase (DXS). Consistent with its major contribution to the control of the MEP pathway flux (Wright et al., 2014) DXS abundance and activity are regulated by post-translational mechanisms including (i) degradation or activation through a pathway involving the J-protein adaptor J20, Hsp70 chaperones, the Hsp100 chaperones ClpB3 and ClpC1 and the Clp protease complex (Pulido et al., 2013; Pulido et al., 2016; Llamas et al., 2017; Rodríguez-Concepción et al., 2019), and (ii) allosteric inhibition by MEP pathway products (Banerjee et al., 2013; Ghirardo et al., 2014).

Fungal VCs-promoted accumulation of chlorophylls and plastidial CKs in leaves is not associated with enhanced expression of genes encoding enzymes directly involved in the synthesis of these compounds (Sánchez-López et al., 2016b). As there is a strong direct dependence of the MEP pathway flux on photosynthetically produced GAP, this indicates that enhanced MEP pathway-derived metabolism in response to microbial VCs can be due, at least partly, to enhanced photosynthetic activity (García-Gómez et al., 2019). Alternatively and/or additionally, enhancement of MEP pathway-derived metabolism by microbial VCs can be due to non-transcriptional up-regulation of the expression of enzymes of the MEP pathway caused by signaling of redox-activated photosynthesis. To test these hypotheses, and to obtain insights into the mechanisms involved in the plant responses to microbial VCs, we compared proteomic, metabolic and hormonal responses of wild-type (WT) Arabidopsis plants and a cFBP1 knock out mutant (*cfbp1*) to VCs emitted by the fungal phytopathogen *Alternaria alternata*. Arabidopsis expresses two plastidial fructose-1,6-bisphosphatases: cFBP1, which is redox-regulated by light, and cFBP2, which is not redox-regulated (Serrato et al., 2009, Rojas-González et al., 2015). As the CBC is subject to redox control (Michelet et al., 2013) and appears to be redox-activated by microbial VCs (Ameztoy et al., 2019), we reasoned that if the microbial VC-promoted response is subject to control by substrate provision and/or non-transcriptional regulation of CBC-related pathways by enhanced photosynthesis, the response of *cfbp1* plants to fungal VCs should be weaker than that of WT plants. Conversely, if redox-activation of photosynthesis does not play an important role in regulation of CBC-related pathways that are important for growth and development, the responses of WT and *cfbp1* plants to microbial VCs should be similar. The results presented in this work are consistent with the former scenario and provide evidence that the response of plants to fungal VCs is subject to post-translational regulation of the homeostasis of enzymes of the MEP and shikimate pathways by the plastid protein quality control (PQC) system. Our results also show that investigating the response of plants to microbial VCs constitutes an excellent system to obtain knowledge on the fundamental mechanisms involved in plant-microbe interactions and metabolic regulation in plants.

MATERIALS AND METHODS

Plant and microbial cultures, growth conditions and sampling

The work was carried out using *Arabidopsis thaliana* L. (Heynh) ecotype Columbia (Col-0), the *cfbp1* mutant (Rojas-González et al., 2015), the *cfbp2* mutant (SALK_053799) and the *clpc1* and *clpr1-2* mutants (Pulido et al., 2016). Plants were cultured in Petri dishes (92 x 16 mm, Sarstedt, Ref. 82.1472.001) containing half-strength solid Murashige and Skoog (MS) (Phytotechlab M519) medium in growth chambers providing 'long day' 16 h light (90 µmol photons sec^{-1} m^{-2}), 22 ºC /8 h dark, 18 ºC cycles. Fungi were cultured in Petri dishes containing solid MS medium supplemented with 90 mM sucrose. Effects of microbial VCs on plants were investigated using the "box-in-box" co-cultivation system in which plants are grown in the vicinity of fungal cultures covered with volatile organic compounds-adsorbing charcoal filters as described in (García-Gómez et al., 2019). At the indicated incubation periods, leaves were harvested, immediately freeze-clamped and ground to a fine powder in liquid nitrogen with a pestle and mortar.

Determination of gas exchange rates and photosynthetic parameters

Gas exchange rates were determined as described by Sánchez-López et al. (2016b) using a LI-COR 6400 gas exchange portable photosynthesis system (LI-COR, Lincoln, NE, USA). The net rate of CO_2 assimilation (A_n) was calculated as described by von Caemmerer and Farquhar (1981). The maximum rate of carboxylation by Rubisco (V_{cmax}), triose phosphate use (*TPU*) and maximum electron transport demand for RuBP regeneration (J_{max}) values were calculated from A_n/C_i curves (where C_i is the intracellular CO_2 concentration) according to Long and Bernacchi (2003). To avoid miscalculation of A_n and C_i because of leakage into the gasket of the gas analyser, we performed CO_2 response curves using an empty chamber. The values obtained for A_n and C_i in the empty chamber were compared with those of the chamber filled with a leaf and subtracted from the values obtained with the empty chamber. The rate of mitochondrial respiration in the dark necessary for *TPU* calculation was determined by measuring the rate of CO_2 evolution in the dark.

Analytical procedures

Tocopherols were extracted according to Kobayashi and DellaPenna (2008) and quantified by fluorescence HPLC (Kanwischer et al., 2005). Flavonols (e.g. quercetin and kaempferol) were measured according to Yin et al. (2012). Levels of CKs and ABA were determined following Novák et al. (2008) and Floková et al. (2014), respectively. IAA and IAA conjugates contents were determined essentially as described by Stirk et al. (2004). Recovery experiments were carried out by adding known amounts of metabolite standards to the frozen slurry immediately after the addition of extraction solutions. The difference between the measurements from samples with and without added standards was used as an estimate of the percentage recovery. All presented concentrations of these metabolites were corrected for losses during extraction. Total photosynthetic pigments and anthocyanins contents were quantified according to Lichtenthaler (1987) and Teow et al. (2007), respectively.

Real-time quantitative PCR

Total RNA was extracted from frozen Arabidopsis leaves of *in vitro* cultured plants using the Trizol method according to the manufacturer's recommendations (Invitrogen), following treatment with RNAase-free DNAase (Takara). RNA (1.5 µg) was reverse-transcribed using polyT primers and an Expand Reverse Transcriptase kit (Roche) according to the manufacturer's instructions. RT-PCR amplification was performed as described by Sánchez-López et al. (2016b) using primers listed in **Table S1**, and their specificity was checked by separating the obtained products on 1.8% agarose gels.

Label-free proteomic analysis

Protein sample extraction

Samples were prepared by grinding 200 mg of leaf material into a fine powder under liquid nitrogen using a precooled mortar and pestle. The powder was then mixed with chaotropic lysis buffer containing 8.4 M urea (USB Corporation, Cleveland, OH), 2.4 M thiourea (Sigma-Aldrich), 5 % CHAPS (Sigma-Aldrich), 5 mM TCEP (Sigma-Aldrich) and a protease inhibitor cocktail (Sigma-Aldrich), and incubated for 15 min on ice. Homogenization of the pellet was achieved by ultrasonication for 5 min on ultrasonic bath Branson 2510 (Marshall Scientific, New Hampshire, USA). The homogenate was centrifuged at 20000 × g for 10 min at 4 °C, and the supernatant containing the solubilized proteins was used for further analysis. Samples were then precipitated by methanol/ chloroform method and re-suspended in 100 µl of multichaotropic sample solution UTT buffer (7 M Urea, 2 M thiourea, 100 mM TEAB (Sigma-Aldrich)). Twenty µg of sample quantified by colorimetric method Pearse was reduced with 2 µL of 50 mM TCEP, pH 8.0, at 37 °C for 60 min, followed by addition of 1 µL of 200 mM cysteine-blocking reagent MMTS (SCIEX, Foster City, CA) for 10 min at room temperature. Sample was diluted to 100 µL to reduce the urea concentration with 25 mM TEAB. Finally, digestion was initiated by adding 1 µg of Pierce MS-grade trypsin (Thermo-Fisher Scientific Inc.) to each sample in a ratio 1 :20 (w/w), and then incubated at 37 °C overnight on a shaker. Sample digestion was evaporated to dryness in a vacuum concentrator.

Liquid chromatography and mass spectrometer analysis

Digested sample was desalted using Stage-Tips with Empore 3M C18 disks (Sigma-Aldrich). A 1 µg aliquot of each digested sample was subjected to 1D-nano LC ESI-MSMS analysis using a nano liquid chromatography system (Eksigent Technologies nanoLC Ultra 1D plus, SCIEX, Foster City, CA) coupled to high speed Triple TOF 5600 mass spectrometer (SCIEX, Foster City, CA) with a Nanospray III source. The analytical column used was a silica-based reversed phase Acquity UPLC® M-Class

Peptide BEH C18 Column, 75 µm × 150 mm, 1.7 µm particle size and 130 Å pore size (Waters). The trap column was a C18 Acclaim PepMapTM 100 (Thermo Scientific), 100 µm × 2 cm, 5 µm particle diameter, 100 Å pore size, switched on-line with the analytical column. The loading pump delivered a solution of 0.1% formic acid in water at 2 µl/min. The nano-pump provided a flow-rate of 250 nl/min and was operated under gradient elution conditions. Peptides were separated using a 250 minutes gradient ranging from 2% to 90% mobile phase B (mobile phase A: 2% acetonitrile, 0.1% formic acid; mobile phase B: 100% acetonitrile, 0.1% formic acid). Injection volume was 5 µl.

Data acquisition was performed with a Triple Time of Flight (TOF) 5600 System (SCIEX, Foster City, CA). Data was acquired using an ion spray voltage floating (ISVF) of 2300 V, a curtain gas (CUR) of 35, an interface heater temperature (IHT) of 150, an ion source gas 1 (GS1) of 25 and a declustering potential (DP) of 100 V. All data was acquired using information-dependent acquisition (IDA) mode with Analyst TF 1.7 software (SCIEX, USA). For IDA parameters, 0.25s MS survey scan in the mass range of 350–1250 Da were followed by 35 MS/MS scans of 100ms in the mass range of 100–1800 (total cycle time: 4 s). Switching criteria were set to ions greater than mass to charge ratio (m/z) 350 and smaller than m/z 1250 with charge state of 2–5 and an abundance threshold of more than 90 counts (cps). Former target ions were excluded for 15s. IDA rolling collision energy (CE) parameters script was used for automatically controlling the CE.

Data analysis and quantification

The mass spectrometry data obtained were processed using PeakView® 2.2 Software (SCIEX, Foster City, CA) and exported as mgf files. Proteomics data analysis were performed by using four search engines (Mascot Server v.2.6.1, OMSSA, X!Tandem and Myrimatch) and a target/decoy database built from sequences in the Solanum tuberosum proteome at Uniprot Knowledgebase. All search engines were configured to match potential peptide candidates to recalibrated spectra with mass error tolerance of 10 ppm and fragment ion tolerance of 0.02 Da, allowing for up to two missed tryptic cleavage sites and a maximum isotope error (^{13}C) of 1, considering fixed MMTS modification of cysteine and variable oxidation of methionine, pyroglutamic acid from glutamine or glutamic acid at the peptide N-terminus. Score distribution models were used to compute peptide-spectrum match p-values1, and spectra recovered by a false discovery rate (FDR) ≤ 0.01 (peptide-level) filter were selected for quantitative analysis.

Differential regulation was measured using linear models2, and statistical significance was measured using q-values (FDR). All analyses were conducted using software from Proteobotics (Madrid, Spain).

Statistical analysis

Unless otherwise indicated, presented data are means (± SE) obtained from 3-4 independent experiments, with 3-5 replicates for each experiment. The significance of differences between plants not exposed to VCs, and plants exposed and not exposed to *A. alternata* VCs was statistically evaluated with Student´s t-test using the SPSS software. Differences were considered significant if $P<0.05$.

RESULTS

Fungal VCs do not promote growth of *cfbp1* plants

Using a "box-in-box" co-cultivation system in which plants are grown in the vicinity of microbial cultures covered with charcoal filters (García-Gómez et al., 2019), we compared growth responses of in vitro cultured WT, *cfbp1* and *cfbp2* plants to VCs emitted by adjacent *A. alternata* cultures. In the absence of fungal VCs, shoots of the c*fbp2* mutant displayed a WT growth phenotype (**Figure 1**). In keeping with Rojas-González et al. (2015), *cfbp1* plants were smaller than those of WT plants, a phenotype that could be rescued by sucrose supplementation (**Figure 1**). As in WT plants, fungal VCs promoted growth of *cfbp2* plants cultured in MS with or without sucrose supplementation (**Figure 1**). In contrast, regardless of the inclusion of sucrose in the culture medium, fungal VCs did not promote growth of *cfbp1* plants (**Figure 1**). Fungal VCs did not promote growth in WT plants cultured in sucrose containing medium under dark conditions (**Figure 2**), strongly indicating that photosynthesis plays an important role in the response of plants to fungal VCs.

Fungal VCs do not increase photosynthetic capacities of exposed *cfbp1* plants

Whether the imperturbability of *cfbp1* plants to fungal VCs could be due to non-responsiveness of photosynthesis to fungal VCs was investigated by comparing key photosynthetic parameters of fully developed WT and *cfbp1* plants cultured in the absence or continuous presence of adjacent fungal cultures. Under non-induced conditions, A_n at all C_i levels as well as V_{cmax}, J_{max} and *TPU* values were lower in *cfbp1*

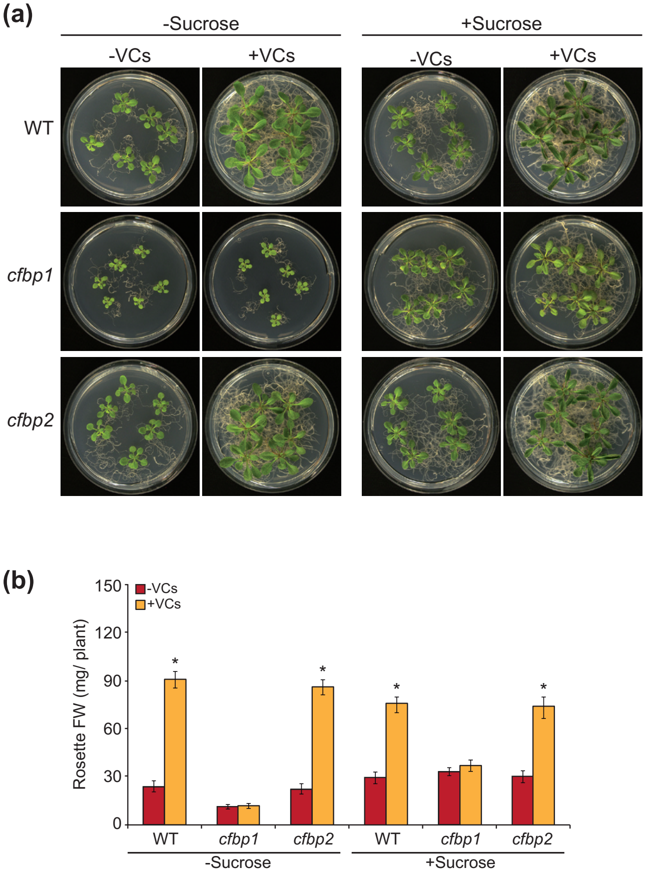

Figure 1. Fungal VCs do not promote growth of *cfbp1* plants. (a) External phenotypes and (b) rosette FW of WT, *cfbp1* and *cfbp2* plants cultured in the absence or continuous presence of adjacent *A. alternata* cultures covered with VOC-adsorbing charcoal filters for one week. Values in "B" are means ± SE for three biological replicates (each a pool of 12 plants) obtained from four independent experiments. Asterisks indicate significant differences relative to plants not cultured with adjacent fungal cultures based on Student´s t-test ($P<0.05$).

plants than in WT plants (**Figure 3, Table 1**), which is consistent with Rojas-González et al. (2015). Leaves of fungal VC-treated WT plants had higher A_n values than controls at all C_i levels (**Figure 3**) as found by Sánchez-López et al. (2016b). Fungal VC-treated WT leaves also had higher V_{cmax}, *TPU* and J_{max} values than non-treated controls (**Table 1**). In contrast, no significant differences were observed in A_n values between fungal VC-treated and non-treated *cfbp1* leaves at any C_i levels (**Figure 3**). Consistently, no significant differences in V_{cmax}, *TPU* and J_{max} values were observed between VC-treated and non-treated *cfbp1* leaves (**Table 1**).

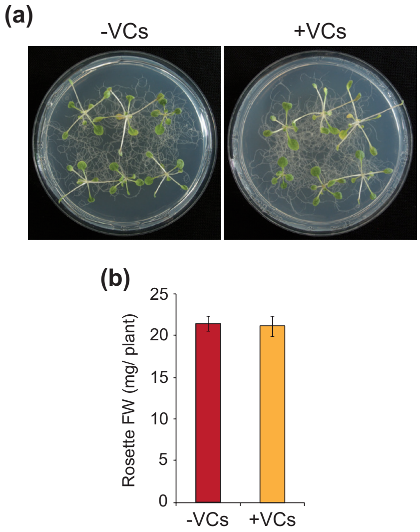

Figure 2. Light is an essential component of the response of plants to fungal VCs. (a) External phenotypes and (b) rosette FW of WT plants cultured in darkness in solid MS medium supplemented with sucrose in the absence or continuous presence of adjacent *A. alternata* cultures covered with VOC-adsorbing charcoal filters for one week. Values in "B" are means ± SE for three biological replicates (each a pool of 12 plants) obtained from four independent experiments.

Fungal VCs exposure do not alter the levels of MEP and shikimate pathways-derived compounds in *cfbp1* leaves.

We next compared the effects of fungal VCs on contents of MEP pathway-derived compounds (e.g. ABA, CK, tocopherols, chlorophylls and carotenoids) and shikimate pathway-derived compounds such as phenylpropanoids (e.g. flavonols and anthocyanins) and indole acetic acid (IAA) and IAA conjugates in mature leaves of WT and *cfbp1* plants. In the absence of fungal VCs, *cfbp1* leaves had similar to WT contents of CK, ABA, γ-tocopherol, flavonols (e.g. kaempherol and quercetin) and total anthocyanins, higher levels of IAA and IAA conjugates than WT leaves, and lower levels of α-tocopherol than WT plants (**Figure 4, Figure 5, Table S2**). In keeping with Rojas-González et al. (2015), *cfbp1* leaves accumulated lower levels of total chlorophylls and carotenoids than WT leaves (**Figure 4**). As shown in **Figure 4** and **Figure 5**, *A. alternata* VCs caused a significant increase in contents of chlorophylls, carotenoids, anthocyanins and flavonols, and a reduction in contents of ABA, tocopherols and IAA conjugates in WT leaves, but had no effect in *cfbp1* leaves. Moreover, fungal VCs enhanced the contents of precursors, active and transport forms of plastidial CKs in leaves of both WT and *cfbp1* plants (**Table S2**).

Fungal VCs exposure weakly alter the proteome of c*fbp1* leaves

We carried out high-throughput differential proteomic analysis of leaves of WT and *cfbp1* Arabidopsis plants cultured in the absence or presence for 3 days of VCs emitted by adjacent *A. alternata* cultures. As some responses promoted by fungal VCs can be

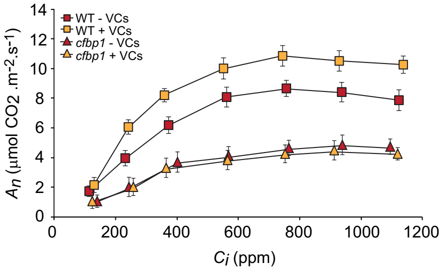

Figure 3. Fungal VCs do not increase photosynthetic capacities of exposed *cfbp1* plants. Curve of net CO_2 assimilation rate (A_n) versus intercellular CO_2 concentration (C_i) in leaves of WT and *cfbp1* plants cultured in the absence or continuous presence of adjacent *A. alternata* cultures covered with charcoal filters for three days. Treatment started 28 days after sowing plants. Values are means ± SE for four plants.

due to fine regulation of the proteome, this analysis was conducted using a label-free-based (spectral counting and ion intensity-based) strategy, which is known to provide the deepest proteome coverage for identification of differentially expressed proteins (DEPs) among available quantitative proteomic methods (Megger et al., 2014).

As shown in **Table S3** and **Table S4**, 1054 and 68 out of the 3135 proteins identified in the study of WT plants were proteins with known functions that were differentially expressed by fungal VCs with statistical significance levels of “confident” (established at qvalue levels ≤ 0.01) and “likely” (established at qvalue levels ≥ 0.01 and ≤ 0.05), respectively. Among the population of 1054 proteins differentially expressed by VCs in WT plants at a “confident” statistical significance level, 569 were up-regulated and 485 were down-regulated (**Table S3**). Unlike in WT plants, fungal VCs did not promote changes in the expression of proteins at “confident” statistical significance level in *cfbp1* plants, and only 298 out of the 3168 proteins identified in the study plants were differentially expressed with a “likely” statistical significance level (**Table S5**). Proteomic analysis of leaves of WT and *cfbp1* plants not exposed to fungal VCs revealed that knocking out cFBP1 causes important changes in the leaf proteome, including

Table 1. Photosynthetic parameters of leaves of WT and *cfbp1* plants cultured in the absence or continuous presence of VCs emitted by adjacent *A. alternata* cultures covered with charcoal filters for three days. Values are means ± SE for three biological replicates (each a pool of 4 plants) obtained from four independent experiments. Asterisks indicate significant differences relative to plants not cultured with adjacent fungal cultures according to Student´s t-test (P<0.05)..

	***V*cmax** (µmol CO_2 m^{-2} s^{-1})	***J*max** (µmol e^- m^{-2} s^{-1})	***TPU*** (µmol Pi m^{-2} s^{-1})
WT	20,2 ± 0,4	50,2 ± 1,3	1,11 ± 0,17
WT + VCs	25,4 ± 0,6*	63,9 ± 1,7*	1,54 ± 0,05*
cfbp1	11,7 ± 0,6	28,3 ± 3,4	0,67 ± 0,13
***cfbp1* + VCs**	12,3 ± 0,3	29,5 ± 2,5	0,68 ± 0,09

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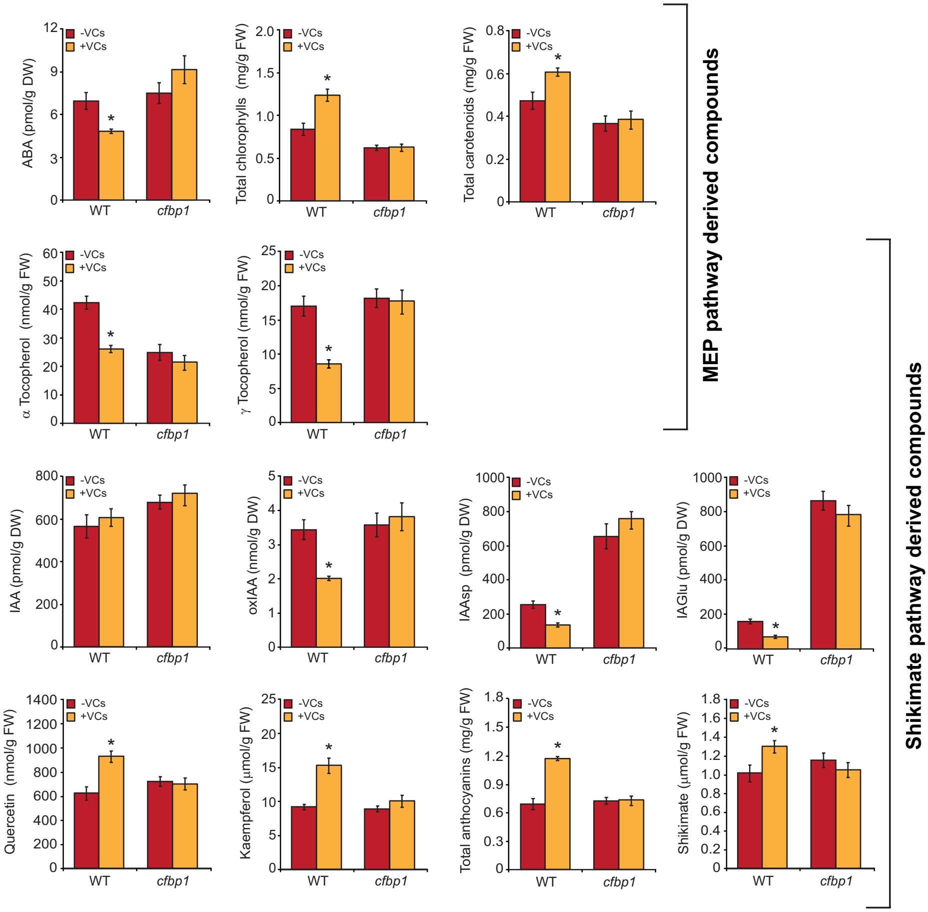


Figure 4. Fungal VCs do not alter the contents of some MEP and shikimate pathways-derived compounds in leaves of *cfbp1* plants. The graphics represent the contents of MEP and shikimate pathways-derived compounds in leaves of WT and *cfbp1* plants cultured in solid MS medium without sucrose supplementation in the absence or continuous presence of adjacent *A. alternata* cultures covered with charcoal filters for 3 days. Values are means ± SE for three biological replicates (each a pool of 12 plants) obtained from four independent experiments. Asterisks indicate significant differences relative to plants not cultured with adjacent fungal cultures according to Student´s t-test ($P<0.05$).

disturbance of the expression of proteins involved in the plastidial PQC system and down-regulation of the expression of plastidial thioredoxins and MEP pathway- and photosynthesis related enzymes (**Figure 6**, **Table S6**).

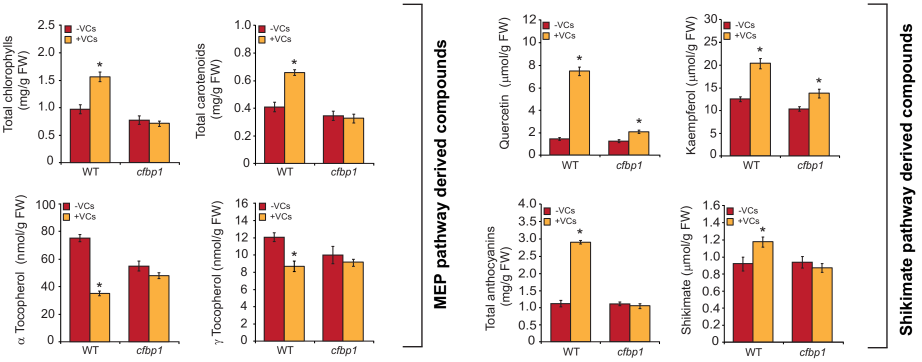


Figure 5. Fungal VCs do not alter the contents of some MEP and shikimate pathways-derived compounds in leaves of *cfbp1* plants. The graphics represent the contents of MEP and shikimate pathways-derived compounds in leaves of WT and *cfbp1* plants cultured in solid MS medium supplemented with sucrose in the absence or continuous presence of adjacent *A. alternata* cultures covered with charcoal filters for 3 days. Values are means ± SE for three biological replicates (each a pool of 12 plants) obtained from four independent experiments. Asterisks indicate significant differences relative to plants not cultured with adjacent fungal cultures according to Student´s t-test (P<0.05).

Fungal VCs alter the expression of enzymes of the MEP and shikimate pathways and of proteins involved in the plastid proteostasis in WT plants

Using the broad characterizations outlined by the MapMan tool (https://mapman.gabipd.org/) (Thimm et al., 2004), the 1054 proteins differentially expressed by fungal VCs in WT leaves were assembled into 33 functional groups according to the Mapman tool (**Figure 7**). Predicted locations of these proteins obtained using the SUBA4 Arabidopsis protein subcellular localization database included almost all cellular compartments, but the highest proportions had predicted plastidial location (**Table S3, Figure S1**). Fungal VCs enhanced the expression of plastidial proteins including redox enzymes (e.g. TRXM2, TRXM4, TRXF1 and NTR2), MEP pathway enzymes (e.g. DXS, DXR, HDR and IDI1), enzymes involved in the synthesis of chlorophyll (e.g. GSA2, HEMA1, HEMC, CPX1, CHLI1, CHLI2, CHLM, GUN5, CRD1, PORB, PORC, GUN4 and CHLP) and carotenoids (e.g. LUT2), shikimate pathway enzymes (e.g. DHS1 and DHS2) and phenylpropanoid pathway enzymes (e.g. PAL1, CHS, F3PE, FLS1 and UGT74C1) (**Figure 7, Table S3**). Fungal VCs also down-regulated the expression of enzymes involved in carotenoid breakdown (e.g. CCD4), the synthesis of ABA from carotenoids (e.g. ZEP) and the conversion of chorismate into tocopherols (e.g. VTE1) and IAA and IAA conjugates (e.g. ASA2, At1g70570, NIT2 and UGT75B1) (**Figure 7,**

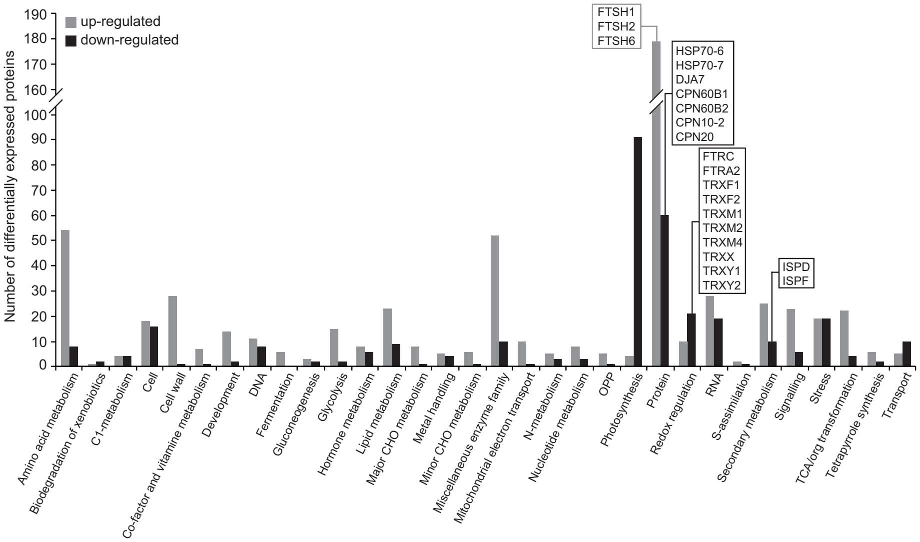


Figure 6. Knocking out cFBP1 reduces the expression of enzymes of the MEP pathways and of proteins involved in the plastidial proteostasis. The graphic represents the functional categorization of the proteins that are differentially expressed by knocking out cFBP1. The proteins that are down- and up-regulated by the lack of cFBP1 expression were sorted according to the putative functional category assigned by MapMan software. The number of up- and down-regulated proteins in each categorical group is indicated by gray and black bars, respectively. Almost 1100 out of the 3140 proteins identified in this proteomic study were proteins with known functions that were differentially expressed by the lack of cFBP1 with "confident" statistical significance levels (**Table S6**). Among these proteins, 669 were up-regulated and 425 were down-regulated (**Table S6**). Note that knocking down cFBP1 reduced the expression of enzymes that control the redox status of plastidial proteins (e.g. FTRC, FTRA2, TRXF1, TRXF2, TRXM1, TRXM2, TRXM4, TRXX, TRXY1 and TRXY2) and MEP pathway enzymes (e.g. ISPD and ISPF). The lack of cFBP1 also enhanced the expression of 3 out of the 9 plastidial ATP-dependent zinc metalloproteases (e.g. FTSH1, FTSH2 and FTSH6), and reduced the expression of the 2 plastidial Hsp70 chaperones (e.g. HSP70-6 and HSP70-7), one Hsp40/DnaJ family chaperone member (e.g. DJA7), 2 out of the 6 plastidial chaperonins (e.g. CPN60B1 and CPN60B2) and 2 out of the 3 plastidial co-chaperonins (e.g. CPN10-2 and CPN20) that are expressed in Arabidopsis.

Table S3). Except CCD4, ZEP, F3PE, PAL1, FLS1 and CHS, none of the above proteins are encoded by fungal VC responsive genes (cf. Supplemental Table 3 in Sánchez-López et al., 2016b), indicating that changes in the leaf proteome promoted by fungal VCs are subject to non-transcriptional regulation. No changes in the expression of enzymes directly involved in CK metabolism could be observed upon fungal VC treatment.

Fungal VC exposure also altered the expression of proteins of the plastidial PQC system. Thus, fungal VCs reduced the expression of 4 plastidial ATP-dependent zinc metalloproteases (e.g. FTSH1, FTSH2, FTSH5 and FTSH8), one serine protease (e.g. SPPA), several subunits of the proteolytic core of the ATP-dependent serine-type Clp protease complex (e.g. ClpP5, ClpP6 and ClpR3) and the Clp stabilizer ClpT2

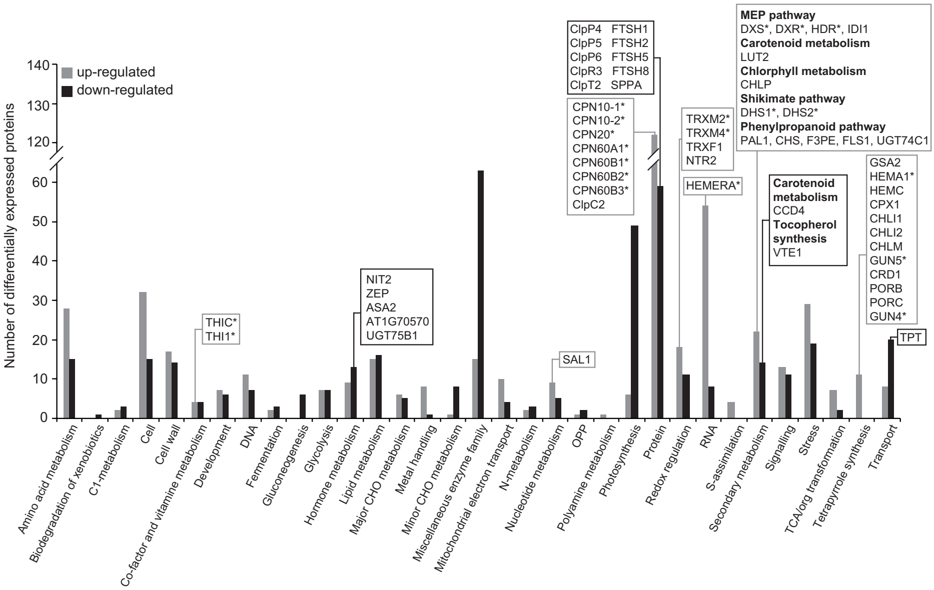


Figure 7. Fungal VCs alter the expression of enzymes of the MEP and shikimate pathways and of proteins involved in the plastidial proteostasis in WT plants. The graphic represents the functional categorization of DEPs in leaves of WT plants cultured in the presence of adjacent cultures of *A. alternata* covered with charcoal filters for 3 days. The proteins that were significantly down- and up-regulated following VC exposure were sorted according to the putative functional category assigned by MapMan software. The number of up- and down-regulated proteins in each categorical group is indicated by gray and black bars, respectively. Proteins discussed here are boxed, and putative Clp clients are indicated with asterisks. Data obtained from **Table S3**.

(**Figure 7, Table S3**). VC exposure also augmented the expression of chaperones that are implicated in the folding and onward guidance of newly imported plastid proteins into their native states, including 4 out of the 6 plastidial chaperonins (e.g. CPN60A1, CPN60B1, CPN60B2 and CPN60B3) and the 3 plastidial co-chaperonins of Arabidopsis (e.g. CPN20, CPN10-1 and CPN10-2) (Kessler and Blobel 1996; Zhao and Liu 2018) (**Figure 7, Table S3**).

Fungal VCs alter the expression of genes encoding proteins of the PQC system in WT plants

Regulation of the MEP pathway requires chloroplast-to-nucleus communication that involves Clp protease-regulated expression of nuclear genes encoding plastid-targeted chaperones (Llamas et al., 2017; Rodríguez-Concepción et al., 2019). Changes in the

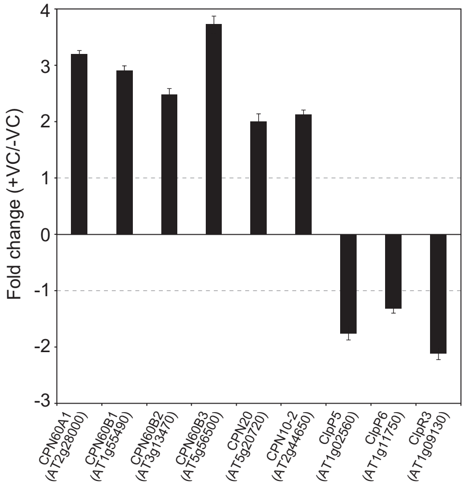


Figure 8. Fungal VCs alter the expression of genes encoding proteins of the PQC system in WT plants. Relative abundance of transcripts encoding PQC system proteins differentially expressed by fungal VCs in WT leaves. Fold change values are differences in levels of transcripts (measured by quantitative RT-PCR) in leaves of WT plants cultured in the presence of fungal VCs for 3 days relative to those of leaves of plants cultured in the absence of VCs. Gray dashed lines indicate the threshold of log2-fold change = 1 (2-fold change) to consider genes as significantly regulated by fungal VCs. Values are means ± SE for three biological replicates

levels of Clp protease components, and plastidial chaperonins and co-chaperonins promoted by fungal VCs in WT plants, but not in *cfbp1* plants, suggested chloroplast-to-nucleus signaling of enhanced photosynthesis. To test this hypothesis we analyzed by qRT-PCR levels of transcripts encoding fungal VC-responsive proteins of the PQC system in WT and *cfbp1* plants cultured in the absence or presence of fungal VCs. These analyses revealed that fungal VCs up-regulated the expression of CPN60A1, CPN60B1, CPN60B2, CPN60B3, CPN20 and CPN10-2, and down-regulated the expression of ClpP4, ClpP5 and ClpR3 in WT plants (**Figure 8**). As shown in **Figure 9**, fungal VCs did not enhance the expression of plastidial chaperonin and co-chaperonin encoding genes in *cfbp1* plants.

Plants with disrupted plastidial proteostasis weakly respond to fungal VCs

Plants with decreased Clp proteolytic capacity accumulate high levels of DXS, DXR, HDR, DHS1, DHS2, THIC, THI1, HEMERA, HEMA1, GUN4, GUN5, TRXM2, TRXM4, SKL2, ClpC2, CPN60A1, CPN60B1, CPN60B2, CPN60B3, CPN20, CPN10-

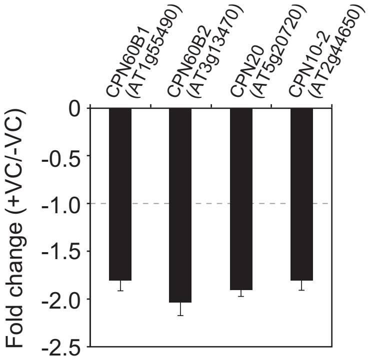


Figure 9. Fungal VCs do not enhance the expression of genes encoding plastidial chaperones in *cfbp1* plants. Relative abundance of transcripts encoding plastidial chaperones differentially expressed by fungal VCs in *cfbp1* leaves. Fold change values are differences in levels of transcripts (measured by quantitative RT-PCR) in leaves of *cfbp1* plants cultured in the presence of fungal VCs for 3 days relative to those of leaves of plants cultured in the absence of VCs. Gray dashed lines indicate the threshold of log2-fold change = 1 (2-fold change) to consider genes as significantly regulated by fungal VCs. Values are means ± SE for three biological replicates.

1 and CPN10-2 (Rudella et al., 2006; Zybailov et al., 2009; Nishimura et al., 2013; Pulido et al., 2016; Moreno et al., 2018; Rodríguez-Concepción et al., 2019). Up-regulation of these proteins and down-regulation of ClpP5, ClpP6, ClpR3 and ClpT2 promoted by fungal VCs (**Figure 7, Table S3**) suggested that fine regulation of plastid proteostasis plays important roles in the response of plants to microbial VCs. To test this hypothesis we characterized the response of *clpr1-2* and *clpc1* mutants defective in Clp protease activity and in the Hsp100 chaperone ClpC1 that delivers the protein clients to the Clp catalytic core, respectively. In the absence of fungal VCs both *clpr1-2* and *clpc1* plants were slightly smaller and accumulated less photosynthetic pigments than WT plants (**Figure 10**), as reported by Welsch et al. (2018). Notably, fungal VC-promoted growth was substantially weaker in the two mutants than in WT plants (**Figure 10**). Furthermore, unlike in WT plants, VCs did not enhance total chlorophylls and carotenoids in the mutants (**Figure 10**).

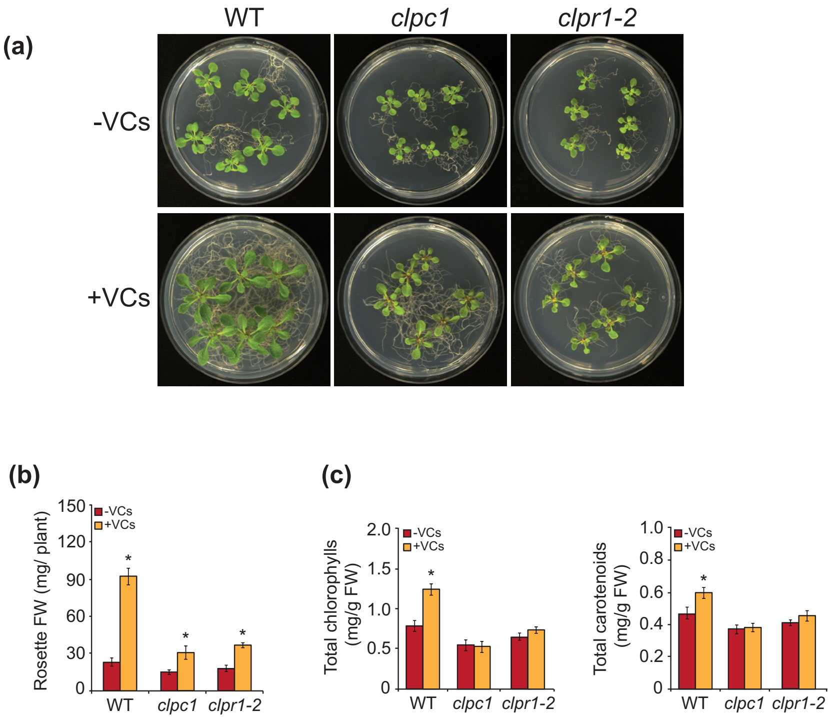


Figure 10. Plants with disrupted plastidial proteostasis weakly respond to fungal VCs. (a) External phenotypes and (b) rosette FW of WT, *clpc1* and *clpr1-2* plants cultured in the absence or continuous presence of adjacent *A. alternata* cultures for one week. (c) Total contents of total chlorophylls and carotenoids in leaves of WT, *clpc1* and *clpr1-2* plants cultured in the absence or continuous presence of adjacent *A. alternata* cultures for 3 days. Values in "a" and "c" are means ± SE for three biological replicates (each a pool of 12 plants) obtained from four independent experiments. Asterisks indicate significant differences relative to plants not cultured with adjacent fungal cultures according to Student´s t-test ($P<0.05$).

DISCUSSION

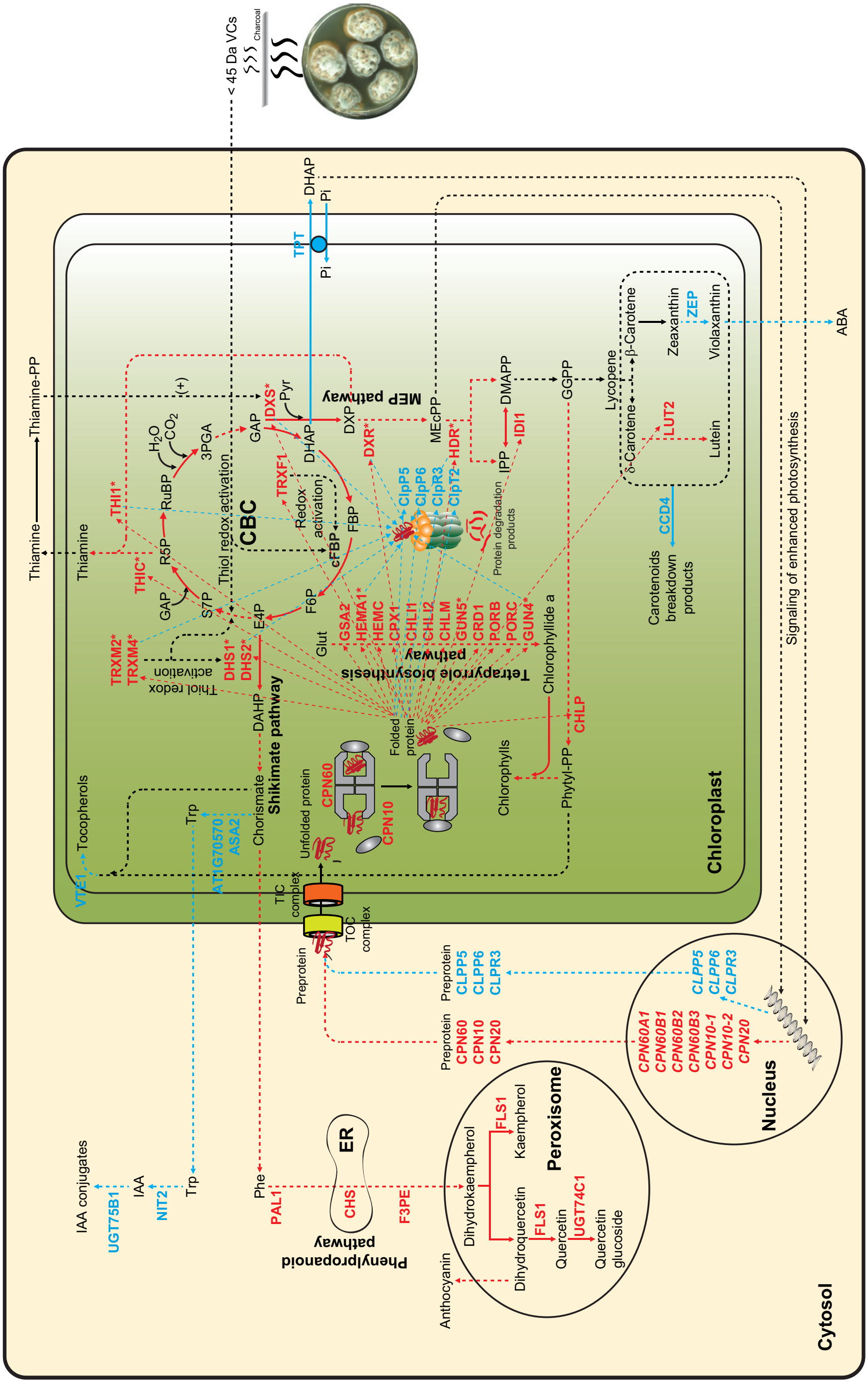
Redox activation of photosynthetic CO_2 fixation is an important determinant of plant responses to microbial VCs

We have recently shown that microbial VCs promote global reduction of the thiol redox proteome of WT leaves, especially of CBC enzymes, which could partly explain the stimulatory growth and photosynthetic responses of plants to VCs (Ameztoy et al., 2019). Here we found that, unlike in WT and redox sensitive cFBP1-expressing *cfbp2* plants, fungal VCs did not stimulate growth and photosynthesis in redox insensitive cFBP2-expressing *cfbp1* plants (**Figure 1, Figure 3, Table 1**). Furthermore, fungal VCs did not alter the contents of some phenylpropanoid and MEP pathways-derived compounds in *cfbp1* leaves (**Figure 4, Figure 5**). Moreover, unlike in WT plants, fungal VCs weakly promoted changes in the proteome of *cfbp1* leaves (**Figure 7, Table S3, Table S5**). Finally, fungal VCs did not promote growth of WT plants cultured in sucrose containing medium under dark conditions (**Figure 2**). These observations indicate that enhancement of photosynthetic CO_2 fixation through light-dependent redox-activation of CBC enzymes is an important determinant of the plants´ growth, proteomic and metabolic responses to fungal VCs.

Proteome changes triggered by fungal VCs can account for many of the changes in the contents of MEP and shikimate pathways-derived compounds promoted by VCs

Data presented in this work indicate that fungal VC-promoted changes in the levels of MEP and shikimate pathways-derived compounds in WT plants are due, at least in part, to proteome and redox-proteome resetting as schematically illustrated in **Figure 11**. Enhanced photosynthetic CO_2 fixation promoted by fungal VCs (**Figure 3**) could potentially be due to redox activation of the CBC caused by up-regulation of TRXM2, TRXM4 and TRXF1 (**Figure 7, Figure 11, Table S3**) as these thioredoxins are major determinants of the light-dependent redox activation of the CBC enzymes (Okegawa and Motohashi 2015; Naranjo et al., 2016b). Fungal VC-promoted photosynthesis can

Figure 11. Suggested model for regulation of plants´ responses to microbial VCs. According to this model, the response of plants to fungal VCs involves post-translational regulatory mechanisms wherein signaling of VC-promoted redox-activation of the photosynthetic machinery and subsequent PQC-mediated proteostatic up-regulation of enzymes of the MEP and shikimate pathways play important roles. Thiol redox activation of photosynthesis-related proteins promoted by microbial VCs augments the production of GAP and E4P, which enter the MEP and shikimate pathways, respectively, to fuel the production of compounds that initiate a cascade of signaling reactions that result in changes in the expression of nuclear encoded plastidial PQC functions. Reduced protease (e.g. FTSH and Clp) activity and enhanced expression of chaperones in the chloroplast increases the stability and activity of enzymes of the MEP, shikimate and tetrapyrrole biosynthesis pathways, which guarantees high metabolic flux towards the production of secondary metabolites that are important for growth and development including hormones, photosynthetic pigments, ROS scavengers, etc. The high chaperone-to-protease balance also promotes the accumulation of active thioredoxins, which in turn redox activate CBC and shikimate enzymes. Enzymatic activities that are up-regulated by fungal VCs are highlighted with red letters, whereas enzymatic activities and pathways that are down-regulated by fungal VCs are highlighted with blue letters. Multistep enzymatic reactions and signaling cascades are depicted with dashed arrows.


< 45 Da VCs
Charcoal
Cytosol
Chloroplast
Nucleus
Peroxisome
ER
CBC
MEP pathway
Shikimate pathway
Tetrapyrrole biosynthesis pathway
Phenylpropanoid pathway
Thiamine-PP
Thiamine
THI1*
THIC*
RuBP
R5P
GAP
S7P
E4P
F6P
FBP
cFBP
3PGA
H_2O
CO_2
(+)
IDXS*
Pyr
DHAP
DXP
DXR*
MEcPP
HDR*
IPP
IDI1
DMAPP
GGPP
Lycopene
δ-Carotene
β-Carotene
LUT2
Lutein
Zeaxanthin
ZEP
Violaxanthin
ABA
CCD4
Carotenoids breakdown products
TPT
Pi
TRXF1
Redox activation
Thiol redox activation
ClpP5
ClpP6
ClpR3
ClpT2
Protein degradation products
TRXM2*
TRXM4*
DHS1*
DHS2*
DAHP
Chorismate
Trp
AT1G70570
ASA2
Tocopherols
VTE1
Glut
GSA2
HEMA1*
HEMC
CPX1
CHLI1
CHLI2
CHLM
GUN5*
CRD1
PORB
PORC
GUN4*
Chlorophyllide a
Chlorophylls
Phytyl-PP
CHLP
Folded protein
Unfolded protein
CPN60
CPN10
TIC complex
TOC complex
Preprotein
CLPP5
CLPP6
CLPR3
CPN20
CPN60A1
CPN60B1
CPN60B2
CPN60B3
CPN10-1
CPN10-2
Signaling of enhanced photosynthesis
Phe
PAL1
CHS
F3PE
Dihydrokaempherol
FLS1
Kaempherol
Dihydroquercetin
Quercetin
UGT74C1
Quercetin glucoside
Anthocyanin
NIT2
IAA
UGT75B1
IAA conjugates

also be ascribed to enhanced production of chlorophylls and carotenoids (**Figure 4**) caused by (i) down-regulation of carotenoid degradation enzymes, (ii) up-regulation of MEP pathway enzymes, and enzymes involved in the synthesis of tetrapyrroles, phytyl-PP and carotenoids, and (iii) up-regulation of TRXM2 and TRXM4, as these thioredoxins activate enzymes of the tetrapyrrole biosynthetic pathway (Da et al., 2017) (**Figure 7, Figure 11, Table S3**). Enhanced contents of flavonols and anthocyanins promoted by fungal VCs (**Figure 4**) could at least partly be due to (i) redox activation of the shikimate pathway caused by increased expression of TRXM2 and TRXM4, as these thioredoxins redox activate the main regulatory enzymes of this pathway (e.g. DHS1 and DHS2) (Entus et al., 2002), and (ii) up-regulation of the expression of DHS1 and DHS2 and phenylpropanoid pathway enzymes (e.g. PAL1, CHS, F3PE and FLS1) (**Figure 7, Figure 11, Table S3**). In addition, fungal VC-promoted reduction of the levels of tocopherols and IAA conjugates (**Figure 4**) can be ascribed to down-regulation of the expression of enzymes involved in the conversion of chorismate into tocopherol (e.g. VTE1), and IAA and IAA conjugates (e.g. ASA2, At1g70570, NIT2 and UGT75B1). Reduction of the ABA content promoted by fungal VCs (**Figure 4**) is consistent with the down-regulation of ZEP expression (**Figure 7, Table S3**).

Augmented cytokinin levels promoted by fungal VCs is not due to enhanced flux from the CBC to the MEP pathway

We previously proposed that fungal VC-promoted enhancement of active MEP pathway derived CKs in leaves could be at least partly due to enhanced metabolic flux from the CBC to the MEP pathway (Sánchez-López et al., 2016a,b). However, here we found that, as in WT plants, fungal VCs increased the levels of plastidial CKs in exposed *cfbp1* plants (**Table S2**) despite exerting weak or null stimulatory effect on photosynthesis (**Figure 3, Table 1**). As in *cfbp1* plants, fungal VCs exerted weak stimulatory effects on growth and photosynthesis in *ntrc* plants impaired in NADPH-dependent thioredoxin reductase C (NTRC), a particular type of plastidial thioredoxin that participates in regulation of the redox status of stromal target proteins including cFBP1 and other CBC enzymes (Ameztoy et al., 2019). In addition, fungal VC exposed *ntrc* plants accumulated higher levels of MEP pathway-derived CKs than controls (Ameztoy et al., 2019). Because (i) VCs do not alter the expression of CK metabolism-related enzymes in leaves (this work) but enhance the expression of enzymes involved in CK biosynthesis in roots (García-

Gómez et al., 2020), (ii) VCs do not promote photosynthesis in *cfpb1* and *ntrc* plants, and (iii) plastidial MEP pathway derived CKs are mainly synthesized in vascular tissues of roots and transported to the aerial parts of the plant (Miyawaki et al., 2004; Ko et al., 2014) we now propose that VC-promoted enhancement of CK content in leaves of *cfbp1* and *ntrc* mutants is not due to enhanced flux from the CBC to the MEP pathway, but mainly to up-regulation of the CK biosynthetic pathway in vascular tissues of roots and subsequent transport to leaves.

The plastid protein quality control system mediates changes in the chloroplast proteome in response to fungal VCs

Proteases (including Clp, FtsH, Lon and Deg) and chaperones (including HSP70/DnaJ, HSP90, Hsp100 and CPN60/CPN10) are essential components of the PQC system in chloroplasts, and are important for fine regulation of photosynthesis, metabolism and signaling pathways as well as viability of cells and chloroplasts (Nishimura et al., 2017b; Zhao and Liu 2018; Rodríguez-Concepción et al., 2019). Enzymes of the MEP and shikimate pathways, enzymes involved in the synthesis of tetrapyrroles, carotenoids and thiamine, and plastidial proteins involved in phytochrome signaling and redox regulation are putative clients of the Clp protease system (Zybailov et al., 2009; Nishimura et al., 2013; Nishimura et al., 2015; Pulido et al., 2016; Rodríguez-Concepción et al., 2019). Using highly sensitive label-free high-throughput differential proteomic analysis here we found that fungal VCs reduce the expression of proteins of the Clp protease system (e.g. ClpP5, ClpP6, ClpR3 and ClpT2) (**Figure 7, Table S3**). This was surprising as these proteins are constitutively expressed and show only minor changes in expression under long-term stress conditions (Zheng et al., 2002). We also found that plastidial proteins that accumulate to higher levels in Clp-defective mutants than in WT plants (including enzymes involved in the MEP pathway [e.g. DXS, DXR and HDR], the shikimate pathway [e.g. DHS1 and DHS2], thiamine-PP synthesis [THIC and THI1], phytochrome signaling [e.g. HEMERA], tetrapyrrole synthesis [HEMA1, GUN4 and GUN5], redox regulation [e.g. TRXM2 and TRXM4] and folding and assembly of newly imported plastid proteins [e.g. ClpC2, CPN60A1, CPN60B1, CPN60B2, CPN60B3, CPN20, CPN10-1 and CPN10-2]) (Rudella et al., 2006; Zybailov et al., 2009; Nishimura et al., 2013; Pulido et al., 2016; Rodríguez-Concepción et al., 2019) also accumulate to higher levels in fungal VC-treated plants than in controls (**Figure 7,**

Table S3). This indicates that the adaptation of the chloroplast proteome to fungal VCs is mediated by mechanisms of regulation of the plastidial PQC system wherein dynamic balances between the expression of chaperones and the Clp protease complex and other proteases play important roles. That *clpc1* and *clpr1-2* plants with disrupted plastidial protein homeostasis weakly respond to fungal VCs (**Figure 11**) strongly indicates that plant´s response to fungal VCs requires a finely regulated plastidial PQC system.

Plant responses to fungal VCs involve chloroplast-to-nucleus retrograde signaling

Chloroplast-to-nucleus retrograde signaling is important to instruct the nuclear genome about the physiological and functional state of the chloroplast under varying environmental cues, and to adjust the chloroplast proteome to its needs through mechanisms involving the PQC system (Chan et al., 2016; Hernández-Verdeja and Strand 2018). Accumulation of nuclear gene-encoded stromal chaperones in mutants with reduced Clp proteolytic activity is a response that involves chloroplast retrograde signaling, as protein folding stress in the chloroplasts of plants with decreased Clp activity sends as-yet unidentified signal(s) to the nucleus that up-regulate the expression of genes encoding plastidial chaperones (Llamas et al., 2017; Perlaza et al., 2019). In WT leaves, reduction of the expression of proteins of the Clp protease system (e.g. ClpP5, ClpP6, ClpR3 and ClpT2) promoted by fungal VCs was associated with down-regulation of ClpP5, ClpP6 and ClpR3 transcript levels, and enhanced levels of CPN60A1, CPN60B1, CPN60B2, CPN60B3, CPN20, CPN10-1 and CPN10-2 (**Figure 7, Table S3**) and their encoding transcripts (**Figure 8**). No such increases in the expression of plastidial chaperonines and co-chaperonines occurred in leaves of *cfbp1* plants (**Figure 9, Table S5**) or in roots of WT plants exposed to fungal VCs (García-Gómez et al., 2020). This indicates that, as illustrated in **Figure 11,** plastid proteome adaptation to fungal VCs in leaves involves photosynthesis-driven chloroplast-to-nucleus retrograde signaling mechanisms wherein transcriptional up-regulation of plastidial chaperones and down-regulation of the Clp protease system play important roles. The photosynthetic activity as a trigger for retrograde signals in VC-exposed plants is supported by the fact that, contrary to the effect of fungal VCs on the plastidial proteome of WT plants, knocking out cFBP1 results in decreased photosynthetic activity and down-regulation of the expression of plastidial chaperonins, co-chaperonins, MEP pathway enzymes and thioredoxins in leaves (**Figure 6, Table S6**).

Fungal VCs did not alter the expression of chaperones involved in DXS turnover (e.g. ClpC1, Hsp70 and ClpB3) (**Table S3**). Therefore, chloroplast-to-nucleus retrograde signaling pathways operating in VC-exposed plants appear to be different to those reported for the control of the expression of the model protein DXS in plants with reduced Clp activity (Pulido et al., 2013; Pulido et al., 2016; Llamas et al., 2017).

Signals involved in chloroplast-to-nucleus retrograde signaling range from reactive oxygen species (ROS) generated by photosynthesis, tetrapyrroles, the by-product of the sulfur metabolism 3´-phosphoadenosine 5´-phosphate (PAP), the MEP pathway intermediate 2-C-methyl-D-erythritol-2,4-cyclopyrophosphate (MEcPP), isoprenes and the CBC intermediate dehydroxyacetone phosphate (DHAP) (Estavillo et al., 2011; Xiao et al., 2012; Vogel et al., 2014; Chan et al., 2016). Fungal VCs do not promote changes in ROS levels in leaves (Ameztoy et al., 2019), which would indicate that these compounds are not involved in retrograde signaling of redox-activated photosynthesis promoted by fungal VCs. DHAP produced by the CBC can be exported to the cytosol through the triose-phosphate/phosphate translocator (TPT) where it can activate protein phosphorylation signaling cascades (Estavillo et al., 2011). Fungal VCs down-regulated TPT expression (**Figure 7, Table S3**), indicating that retrograde signaling of redox-activated photosynthesis promoted by fungal VCs does not involve enhanced TPT-mediated transport of DHAP to the cytosol. In contrast, fungal VCs up-regulated the expression of MEP pathway enzymes and SAL1 (**Figure 7, Table S3**), a plastidial enzyme that controls the intracellular levels of PAP (Estavillo et al., 2011; Phua et al., 2018) (**Figure 7, Table S3**). Therefore, it is likely that chloroplast-to-nucleus retrograde signaling of enhanced photosynthesis promoted by fungal VCs involves PAP and/or MEP pathway intermediates such as MEcPP. An alternative or additional candidate to participate in this process is HEMERA, which expression is up-regulated by fungal VCs (**Figure 7, Table S3**). This transcription factor shows dual localization in chloroplast nucleoids and nucleus (Chen et al., 2010; Melonek et al., 2016) and is abundant in plants with decreased Clp activity, which suggests that its accumulation in chloroplast might cause its translocation to the nucleus to regulate nuclear gene expression (Moreno et al., 2018). HEMERA participates in phytochrome signaling (Chen et al., 2010). Notably, accumulation of exceptionally high levels of starch promoted by fungal VCs is subject to phytochrome signaling (Li et al., 2011), which would support the idea that translocation of HEMERA could be involved in the chloroplast-to-nucleus retrograde signaling of fungal VCs.

Proposal of an integrative model of regulation of the plant response to microbial VCs involving proteostatic modulation of MEP and shikimate pathways by redox-activated photosynthesis signaling

Results presented in this and previous works (Ameztoy et al., 2019; García-Gómez et al., 2019) provide evidence that the response of plants to fungal VCs involves post-translational regulatory mechanisms wherein signaling of redox-activated photosynthesis and subsequent PQC system-mediated proteostatic up-regulation of thioredoxins and enzymes of the MEP, shikimate and tetrapyrrole biosynthesis pathways play important roles. According to this view schematically illustrated in **Figure 11**, rapid thiol redox activation of CBC enzymes promoted by microbial VCs augments the photosynthetic production of GAP and E4P, which enter the MEP and shikimate pathways, respectively, to fuel the production of compounds that initiate a cascade of signaling reactions that result in changes in the expression of nuclear encoded plastidial PQC system functions. Reduced protease activity and enhanced expression of chaperones in the chloroplast increases the stability and activity of enzymes of the MEP, shikimate and tetrapyrrole biosynthesis pathways, which guarantees high metabolic flux from the CBC towards the production of secondary metabolites that are important for growth and development including hormones, photosynthetic pigments, ROS scavengers, etc. The high chaperone-to-protease balance also promotes the accumulation of active thioredoxins, which in turn redox activate enzymes of the CBC, shikimate and tetrapyrrole biosynthesis pathways enzymes (**Figure 11**).

SUPPLEMENTAL MATERIAL

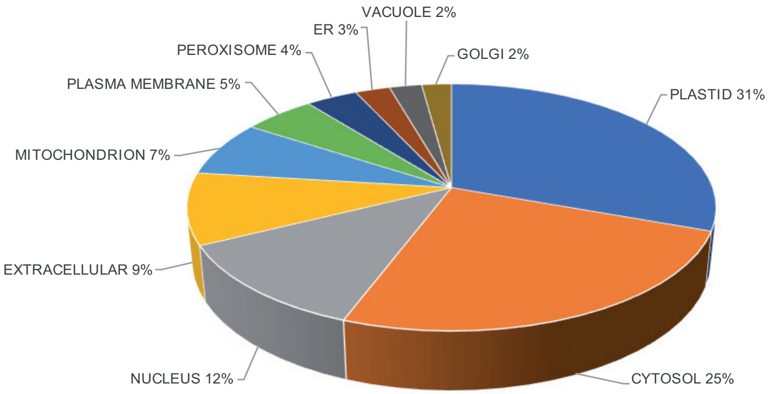


Figure S1. Categorization of fungal VC-responsive proteins according to their subcellular localizations**.** Data from **Table S3**.

Table S1. Primers used in qRT-PCR

Gene		Sequence
EF-1 alfa	Forward	TTCGTCTCCCACTTCAGGAT
At1g07940	Reverse	GGAGCAAAGGTCACAACCAT
CPN60A1	Forward	TCGTGAGGTTGCGAGTAAGA
At2g28000	Reverse	CCAGAAGTGACGCTCAACAA
CPN60B1	Forward	CAAGCTCGCAGATCTTGTTG
At1g55490	Reverse	TTGCAACAGTCACACCATCA
CPN60B2	Forward	GCAAGTATGGATCCCCAAGA
At3g13470	Reverse	GCTTGCCTTACAAGCTTTGC
CPN60B3	Forward	ACGGTCGCTAGAGAGGTTGA
At5g56500	Reverse	CGTTGTTCCATCACCAGCTA
CPN20	Forward	AGTTCCGTCGTTTGGTTGTC
At5g20720	Reverse	GCCTCCTTGATCTTCACCAA
CPN10-2	Forward	TAAATGGGAACCGACAAAGG
At2g44650	Reverse	CACAGCTGCTTTAGGCAACA
ClpP5	Forward	CGTCTCCTCAAGGAGTTTGG
At1g02560	Reverse	CTTGCACCATAGGAGGTGGT
ClpP6	Forward	TGGAGTGATAGAGGCGAAAAA
At1g11750	Reverse	TGCGGTTACGGAATAACACA
ClpR3	Forward	GCCGCCATATCTTGACATCT
At1g09130	Reverse	GTCTGGTGGAGGAGTTCTCG

Table S2. CK content (pmol g^{-1} DW) in leaves of WT and *cfbp1* plants cultured in solid MS medium in the absence or presence of VCs emitted by *A. alternata* for 3 days. Values represent the mean ± SE of determinations on 3 independent experiments. Asterisks indicate statistically significant difference in the VC treatments versus the controls in a paired Student's t-test (*, **, and *** correspond to P-values of $0.05 > p > 0.01$, $0.01 > p > 0.001$, and $p < 0.001$, respectively). *in-riboside*; iP, *isopentenyladenine*; tZ, *trans-zeatin*; DZ, *dihydrozeatin*; iP7G, N^6-isopentenyladenosine-7-glucoside; iP9G, *N^6-isopentenyladenosine-9-glucoside*; tZOG, *trans-zeatin-O-glucoside*; tZROG, *trans-zeatin-O-glucoside riboside*; cZRMP, *cis-zeatin riboside-5'-monophosphate*; DHZROG, *dihydrozeatin-riboside-O-glucoside*; DHZOG, *dihydrozeatin-O-glucoside*; tZ7G, *trans-zeatin-7-glucoside*; DZ7G, *dihydrozeatin7-glucoside*; tZ9G, *trans-zeatin-9-glucoside*; cZR, *cis-zeatin ribosides*; cZ, *cis-zeatin*; cZ7G, *cis-zeatin-7-glucoside*; cZOG, *cis-zeatin-O-glucoside*; cZROG, *tZ-riboside-O-glucoside*.

		MEP pathway (plastid) derived CKs				**MVA pathway (cytosol) derived CKs**				
		WT-VCs	WT+VCs	*cfbp1*-VCs	*cfbp1*+VCs		WT-VCs	WT+VCs	*cfbp1*-VCs	*cfbp1*+VCs
Precursors	**iPRMP**	48.8 ± 7.4	158 ± 10***	79.2 ± 2.0	116 ± 5***	**cZRMP**	122 ± 12	108 ± 6	111 ± 5	114 ± 7.9
	tZRMP	36.3 ± 4.3	232 ± 13***	38.7 ± 2.0	127 ± 8***					
	DHZRMP	1.7 ± 0.5	2.3 ± 0.3**	1.8 ± 0.4	1.8 ± 0.5					
	∑	86.8	392	119	245	∑	122	108	111	114
Transport forms	**iPR**	2.6 ± 0.3	7.0 ± 1.7***	6.8 ± 1.2	10.4 ± 1.1**	**cZR**	3.8 ± 0.4	3.1 ± 0.9	4.0 ± 0.3	4.6 ± 0.4
	tZR	2.8 ± 0.2	18.5 ± 2.4***	4.2 ± 0.6	15.9 ± 0.2***					
	DHZR	0.2 ± 0.1	0.55 ± 0.12***	0.27 ± 0.05	0.64 ± 0.13***					
	∑	5.7	26.0	11.25	26.97	∑	3.8	3.1	4.0	4.6
Active forms	**iP**	3.4 ± 0.2	3.8 ± 0.6	3.5 ± 0.3	3.4 ± 0.1	**cZ**	12.4 ± 1.0	5.9 ± 0.7***	9.1 ± 1.8	7.2 ± 0.3
	tZ	10.2 ± 0.8	18.4 ± 2.4***	7.3 ± 1.2	14.7 ± 2.4***					
	DHZ	--	--	--	--					
	∑	13.6	22.2	10.7	18.2	∑	12.4	5.9	9.1	7.2
Glycosylated (inactive) forms	**iP7G**	524 ± 23	332 ± 8***	607 ± 26	461 ± 82*	**cZ7G**	322 ± 11	109 ± 8***	368 ± 33	279 ± 19***
	tZ7G	284 ± 9	352 ± 15***	188 ± 14	263 ± 21***					
	DHZ7G	124 ± 6	63.5 ± 3.8***	111 ± 6	67 ± 6***					
	iP9G	43.4 ± 1.9	25.6 ± 1.8***	48.4 ± 6.5	107 ± 118	**cZ9G**	5.4 ± 0.8	1.1 ± 0.1***	6.5 ± 0.7	4.2 ± 0.2***
	tZ9G	91.3 ± 5.3	141 ± 10***	68.6 ± 6.1	107 ± 4***					
	DHZ9G	2.7 ± 0.3	2.0 ± 0.3***	2.2 ± 0.4	2.4 ± 0.1					
	tZOG	105.3 ± 24.1	222 ± 46**	182 ± 30	269 ± 22**	**cZOG**	33.5 ± 3.4	27.6 ± 6.0	89.6 ± 20.6	81.4 ± 7.2
	DHZOG	2.6 ± 0.1	2.0 ± 0.1***	2.0 ± 0.3	2.0 ± 0.1					
	tZROG	8.2 ± 0.3	9.0 ± 0.8	7.9 ± 0.8	11.2 ± 1.4**	**cZROG**	39.9 ± 2.1	20.7 ± 3.5***	59.8 ± 7.9	53.8 ± 10.6
	DHZROG	1.6 ± 0.3	1.3 ± 0.1*	1.9 ± 0.6	1.9 ± 0.3					
	∑	1,189	1,153	1,220	1,295	∑	401	158	524	418
TOTAL	∑	1,295	1,594	1,362	1,585	∑	539	276	649	545

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Table S3: List of proteins that are differentially expressed by VOCs-depleted VCs of *A. alternata* in leaves of WT plants with a "confident" statistical significance level (fungal VC-treated vs. non-treated plants).DEPs are classified according to their functions. DEPs that are discussed in the main text are highlighted in yellow. DEPs that are clients of Clp are highlighted in orange. DEPs encoded by fungal FV-responsive genes (cf. Supplemental Table 3 in Sánchez-López et al., 2016b)

Accesion number	Protein ID	Fold change (log2)	qValue (FDR)	Subcellular location	Description
Aminoacids metabolism					
AT5G54080	Q9ZRA2	-1,811	0,001	cytosol	Homogentisate 1,2-dioxygenase OS=Arabidopsis thaliana GN=HGO PE=2 SV=2
AT3G45300	Q9SWG0	-1,757	0,001	mitochondrion	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Arabidopsis thaliana GN=IVD PE=1 SV=2
AT1G03090	Q42523	-1,169	0,001	mitochondrion	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Arabidopsis thaliana GN=MCCA PE=1 SV=2
AT2G13360**	Q56YA5	-1,127	0,001	peroxisome	Serine--glyoxylate aminotransferase OS=Arabidopsis thaliana GN=AGT1 PE=1 SV=2
AT2G41040	Q0WPT7	-1,02	0,001	plastid	Uncharacterized methyltransferase At2g41040, chloroplastic OS=Arabidopsis thaliana GN=At2g41040 PE=1 SV=1
AT1G68010**	Q9C9W5	-0,932	0,001	peroxisome	Glycerate dehydrogenase HPR, peroxisomal OS=Arabidopsis thaliana GN=HPR PE=1 SV=1
AT5G11520	P46644	-0,902	0,001	peroxisome	Aspartate aminotransferase 3, chloroplastic OS=Arabidopsis thaliana GN=ASP3 PE=1 SV=1
AT1G23310**	Q9LR30	-0,876	0,001	peroxisome	Glutamate--glyoxylate aminotransferase 1 OS=Arabidopsis thaliana GN=GGAT1 PE=1 SV=1
AT2G39800**	P54887	-0,869	0,001	peroxisome	Delta-1-pyrroline-5-carboxylate synthase A OS=Arabidopsis thaliana GN=P5CSA PE=1 SV=1
AT3G22200	Q94CE5	-0,81	0,001	mitochondrion	Gamma-aminobutyrate transaminase POP2, mitochondrial OS=Arabidopsis thaliana GN=POP2 PE=1 SV=1
AT1G70580**	Q9S7E9	-0,74	0,002	peroxisome	Glutamate--glyoxylate aminotransferase 2 OS=Arabidopsis thaliana GN=GGAT2 PE=1 SV=1
AT3G19480	Q9LT69	-0,72	0,001	plastid	D-3-phosphoglycerate dehydrogenase 3, chloroplastic OS=Arabidopsis thaliana GN=PGDH3 PE=1 SV=1
AT5G52100	Q9FJ82	-0,706	0,002	plastid	Dihydrodipicolinate reductase-like protein CRR1, chloroplastic OS=Arabidopsis thaliana GN=DAPB3 PE=2 SV=1
AT4G14880	P47998	-0,369	0,008	cytosol	Cysteine synthase 1 OS=Arabidopsis thaliana GN=OASA1 PE=1 SV=2
AT1G70570	F4I5H7	-0,366	0,01	plastid	Anthranilate phosphoribosyltransferase OS=Arabidopsis thaliana GN=At1g70570 PE=4 SV=1
AT2G29690	P32069	-0,359	0,004	plastid	Anthranilate synthase alpha subunit 2, chloroplastic OS=Arabidopsis thaliana GN=ASA2 PE=2 SV=1
AT5G63890	Q9C5U8	0,354	0,001	plastid	Histidinol dehydrogenase, chloroplastic OS=Arabidopsis thaliana GN=HISN8 PE=2 SV=1
AT3G48560	P17597	0,361	0,002	plastid	Acetolactate synthase, chloroplastic OS=Arabidopsis thaliana GN=ALS PE=1 SV=1
AT3G53580	Q9LFG2	0,423	0,001	plastid	Diaminopimelate epimerase, chloroplastic OS=Arabidopsis thaliana GN=DAPF PE=1 SV=1
AT1G31230**	Q9SA18	0,426	0,001	plastid	Bifunctional aspartokinase/homoserine dehydrogenase 1, chloroplastic OS=Arabidopsis thaliana GN=AKHSDH1 PE=1 SV=1
AT2G35500	O82290	0,456	0,001	plastid	Probable inactive shikimate kinase like 2, chloroplastic OS=Arabidopsis thaliana GN=SKL2 PE=2 SV=2
AT4G19710	O81852	0,472	0,002	plastid	Bifunctional aspartokinase/homoserine dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=AKHSDH2 PE=1 SV=1
AT3G59760	Q43725	0,476	0,001	mitochondrion	Cysteine synthase, mitochondrial OS=Arabidopsis thaliana GN=OASC PE=1 SV=3
AT5G05730	P32068	0,495	0,001	plastid	Anthranilate synthase alpha subunit 1, chloroplastic OS=Arabidopsis thaliana GN=ASA1 PE=1 SV=1
AT2G36230	O82782	0,529	0,005	plastid	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase, chloroplastic OS=Arabidopsis thaliana GN=HISN3 PE=2 SV=1
AT4G35630	Q96255	0,539	0,002	plastid	Phosphoserine aminotransferase 1, chloroplastic OS=Arabidopsis thaliana GN=PSAT1 PE=1 SV=1
AT3G26900	Q9LW20	0,555	0,001	plastid	Probable inactive shikimate kinase like 1, chloroplastic OS=Arabidopsis thaliana GN=SKL1 PE=2 SV=1
AT1G22410	Q9SK84	0,556	0,004	plastid	Phospho-2-dehydro-3-deoxyheptonate aldolase OS=Arabidopsis thaliana GN=At1g22410 PE=3 SV=1
AT5G48880**	Q570C8	0,566	0,002	peroxisome	3-ketoacyl-CoA thiolase 5, peroxisomal OS=Arabidopsis thaliana GN=KAT5 PE=1 SV=2
AT1G18500	Q9LPR4	0,588	0,001	plastid	2-isopropylmalate synthase 1, chloroplastic OS=Arabidopsis thaliana GN=IPMS1 PE=1 SV=2
AT2G17630**	Q9SHP0	0,589	0,002	plastid	Phosphoserine aminotransferase 2, chloroplastic OS=Arabidopsis thaliana GN=PSAT2 PE=1 SV=1
AT5G08100	P50287	0,594	0,004	cytosol	Isoaspartyl peptidase/L-asparaginase 1 OS=Arabidopsis thaliana GN=At5g08100 PE=1 SV=2
AT5G04740	Q9LZ23	0,597	0,001	plastid	ACT domain-containing protein ACR12 OS=Arabidopsis thaliana GN=ACR12 PE=2 SV=1
AT3G49680**	Q9M401	0,607	0,001	plastid	Branched-chain-amino-acid aminotransferase 3, chloroplastic OS=Arabidopsis thaliana GN=BCAT3 PE=1 SV=1
AT4G33150	F4JVY8	0,646	0,003	cytosol	reversed Lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme OS=Arabidopsis thaliana GN=LKR PE=4 SV=1
AT4G08900	P46637	0,71	0,002	mitochondrion	reversed Arginase 1, mitochondrial OS=Arabidopsis thaliana GN=ARGAH1 PE=1 SV=1
AT1G18640	O82796	0,74	0,001	plastid	Phosphoserine phosphatase, chloroplastic OS=Arabidopsis thaliana GN=PSP PE=1 SV=2
AT1G09795	Q8GSJ1	0,762	0,002	plastid	ATP phosphoribosyltransferase 2, chloroplastic OS=Arabidopsis thaliana GN=HISN1B PE=1 SV=1
AT1G58080	Q9S762	0,782	0,001	plastid	ATP phosphoribosyltransferase 1, chloroplastic OS=Arabidopsis thaliana GN=HISN1A PE=1 SV=1
AT1G17745	O04130	0,827	0,002	plastid	D-3-phosphoglycerate dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=PGDH2 PE=1 SV=2
AT1G74040	Q9C550	0,929	0,002	plastid	2-isopropylmalate synthase 2, chloroplastic OS=Arabidopsis thaliana GN=IPMS2 PE=1 SV=1
AT5G16290	Q9FFF4	1,068	0,002	plastid	Acetolactate synthase small subunit 1, chloroplastic OS=Arabidopsis thaliana GN=VAT1 PE=1 SV=1
AT5G14200**	Q9FMT1	1,645	0,002	plastid	3-isopropylmalate dehydrogenase 3, chloroplastic OS=Arabidopsis thaliana GN=IMDH3 PE=1 SV=1
AT3G19710**	Q9LE06	2,429	0,001	cytosol	Methionine aminotransferase BCAT4 OS=Arabidopsis thaliana GN=BCAT4 PE=1 SV=1
Biodegradation of Xenobiotics					
AT1G53580	Q9C8L4	-0,556	0,001	mitochondrion	Persulfide dioxygenase ETHE1 homolog, mitochondrial OS=Arabidopsis thaliana GN=GLY3 PE=1 SV=3

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C1- metabolism					
AT5G14780**	Q9S7E4	-0,794	0,001	mitochondrion	Formate dehydrogenase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=FDH1 PE=1 SV=1
AT2G26080	O80988	-0,519	0,001	mitochondrion	Glycine dehydrogenase (decarboxylating) 2, mitochondrial OS=Arabidopsis thaliana GN=GLDP2 PE=1 SV=1
AT4G33010**	Q94B78	-0,466	0,001	mitochondrion	Glycine dehydrogenase (decarboxylating) 1, mitochondrial OS=Arabidopsis thaliana GN=GLDP1 PE=1 SV=2
AT3G02770	Q9M8R9	0,408	0,004	cytosol	Putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase 1 OS=Arabidopsis thaliana GN=At3g02770 PE=2 SV=1
AT5G16450	Q9FFE0	0,679	0,003	cytosol	Putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase 2 OS=Arabidopsis thaliana GN=At5g16450 PE=1 SV=1
Cell					
AT4G22240	O49629	-1,822	0,003	plastid	Probable plastid-lipid-associated protein 2, chloroplastic OS=Arabidopsis thaliana GN=PAP2 PE=1 SV=1
AT4G04020	O81439	-1,644	0,001	plastid	Probable plastid-lipid-associated protein 1, chloroplastic OS=Arabidopsis thaliana GN=PAP1 PE=1 SV=1
AT2G46910	Q8W4F1	-1,184	0,001	plastid	Probable plastid-lipid-associated protein 10, chloroplastic OS=Arabidopsis thaliana GN=PAP10 PE=1 SV=1
AT1G42550	Q9C8E6	-0,873	0,002	cytosol	Protein PLASTID MOVEMENT IMPAIRED 1 OS=Arabidopsis thaliana GN=PMI1 PE=1 SV=1
AT3G26070	Q9LU85	-0,78	0,001	plastid	Probable plastid-lipid-associated protein 4, chloroplastic OS=Arabidopsis thaliana GN=PAP4 PE=1 SV=1
AT3G23400	Q9LW57	-0,535	0,001	plastid	Plastid-lipid-associated protein 6, chloroplastic OS=Arabidopsis thaliana GN=PAP6 PE=1 SV=1
AT3G12110	P53496	-0,517	0,002	cytosol	Actin-11 OS=Arabidopsis thaliana GN=ACT11 PE=1 SV=1
AT1G07660	P59259	-0,506	0,001	nucleus	Histone H4 OS=Arabidopsis thaliana GN=At1g07660 PE=1 SV=2
AT4G11380	Q9SUS3	-0,503	0,005	plasma membrane	Beta-adaptin-like protein B OS=Arabidopsis thaliana GN=BETAB-AD PE=1 SV=1
AT5G10470	Q9LX99	-0,473	0,001	cytosol	Kinesin-like protein KIN-14A OS=Arabidopsis thaliana GN=KIN14A PE=1 SV=1
AT3G18780	Q96292	-0,443	0,001	cytosol	Actin-2 OS=Arabidopsis thaliana GN=ACT2 PE=1 SV=1
AT1G71270	Q94KD3	-0,42	0,008	golgi	Vacuolar protein sorting-associated protein 52 A OS=Arabidopsis thaliana GN=VPS52 PE=1 SV=1
AT2G35490	O82291	-0,384	0,001	plastid	Probable plastid-lipid-associated protein 3, chloroplastic OS=Arabidopsis thaliana GN=PAP3 PE=1 SV=1
AT3G09740	Q9SF29	-0,374	0,005	plasma membrane	Syntaxin-71 OS=Arabidopsis thaliana GN=SYP71 PE=1 SV=1
AT2G21280	Q9SJU9	-0,364	0,01	plastid	Epimerase family protein SDR39U1 homolog, chloroplastic OS=Arabidopsis thaliana GN=GC1 PE=2 SV=2
AT2G26210	Q8VZ34	0,375	0,01	cytosol	Ankyrin repeat family protein OS=Arabidopsis thaliana GN=At2g26210 PE=2 SV=1
AT4G29350	Q42418	0,376	0,002	cytosol	Profilin-2 OS=Arabidopsis thaliana GN=PRO2 PE=2 SV=1
AT5G44340	P24636	0,38	0,001	cytosol	Tubulin beta-4 chain OS=Arabidopsis thaliana GN=TUBB4 PE=2 SV=2
AT1G15730	Q9LMR1	0,399	0,004	plastid	At1g15730/F7H2_7 OS=Arabidopsis thaliana GN=At1g15730 PE=1 SV=1
AT1G21380	Q9LPL6	0,416	0,002	nucleus	TOM1-like protein 3 OS=Arabidopsis thaliana GN=TOL3 PE=1 SV=1
AT5G65020	Q9XEE2	0,437	0,001	plasma membrane,cytosol	Annexin D2 OS=Arabidopsis thaliana GN=ANN2 PE=1 SV=1
AT2G34560	B9DGC0	0,452	0,007	cytosol	AT2G34560 protein OS=Arabidopsis thaliana GN=CCP1 PE=1 SV=1
AT2G18040	Q9SL42	0,464	0,006	cytosol	Peptidyl-prolyl cis-trans isomerase Pin1 OS=Arabidopsis thaliana GN=PIN1 PE=1 SV=1
AT1G20010	P29513	0,468	0,005	cytosol	Tubulin beta-5 chain OS=Arabidopsis thaliana GN=TUBB5 PE=2 SV=1
AT4G14960	P29511	0,48	0,005	cytosol	Tubulin alpha-6 chain OS=Arabidopsis thaliana GN=TUBA6 PE=1 SV=1
AT2G36250	O82533	0,482	0,002	plastid	Cell division protein FtsZ homolog 2-1, chloroplastic OS=Arabidopsis thaliana GN=FTSZ2-1 PE=1 SV=2
AT2G29960	Q8LDP4	0,487	0,003	endoplasmic reticulum	Peptidyl-prolyl cis-trans isomerase CYP19-4 OS=Arabidopsis thaliana GN=CYP19-4 PE=1 SV=2
AT3G04710	Q9SR03	0,487	0,005	cytosol	Ankyrin repeat family protein OS=Arabidopsis thaliana GN=TPR10 PE=2 SV=1
AT5G55230	Q9FLP0	0,503	0,001	cytosol	65-kDa microtubule-associated protein 1 OS=Arabidopsis thaliana GN=MAP65-1 PE=1 SV=1
AT5G62690	Q56YW9	0,513	0,001	cytosol	Tubulin beta-2 chain OS=Arabidopsis thaliana GN=TUBB2 PE=2 SV=2
AT5G19940	Q941D3	0,516	0,003	plastid	Probable plastid-lipid-associated protein 8, chloroplastic OS=Arabidopsis thaliana GN=PAP8 PE=1 SV=1
AT4G11740	F4JPR7	0,52	0,005	nucleus	Plant UBX domain-containing protein 8 OS=Arabidopsis thaliana GN=PUX8 PE=1 SV=1
AT2G19760	Q42449	0,521	0,001	cytosol	Profilin-1 OS=Arabidopsis thaliana GN=PRO1 PE=1 SV=1
AT1G50010	B9DGT7	0,542	0,001	cytosol	Tubulin alpha-2 chain OS=Arabidopsis thaliana GN=TUBA2 PE=2 SV=2
AT3G52750	Q9LXJ0	0,558	0,002	plastid	Cell division protein FtsZ homolog 2-2, chloroplastic OS=Arabidopsis thaliana GN=FTSZ2-2 PE=1 SV=1
AT3G10220	Q67Z52	0,56	0,004	cytosol	Tubulin-folding cofactor B OS=Arabidopsis thaliana GN=TFCB PE=1 SV=1
AT1G35720	Q9SYT0	0,574	0,001	peroxisome	Annexin D1 OS=Arabidopsis thaliana GN=ANN1 PE=1 SV=1
AT1G47200	Q9C500	0,576	0,004	nucleus	WPP domain-containing protein 2 OS=Arabidopsis thaliana GN=WPP2 PE=1 SV=1
AT2G16600	Q38900	0,589	0,002	cytosol	Peptidyl-prolyl cis-trans isomerase CYP19-1 OS=Arabidopsis thaliana GN=CYP19-1 PE=1 SV=1
AT5G53400	Q9LV09	0,61	0,001	cytosol	Protein BOBBER 1 OS=Arabidopsis thaliana GN=BOB1 PE=1 SV=1
AT1G26550	Q9FE18	0,668	0,001	nucleus	Peptidyl-prolyl cis-trans isomerase OS=Arabidopsis thaliana GN=At1g26550 PE=2 SV=1
AT5G48580	Q38936	0,733	0,001	endoplasmic reticulum	Peptidyl-prolyl cis-trans isomerase FKBP15-2 OS=Arabidopsis thaliana GN=FKBP15-2 PE=2 SV=2
AT4G34870	Q42406	0,752	0,001	cytosol	Peptidyl-prolyl cis-trans isomerase CYP18-4 OS=Arabidopsis thaliana GN=CYP18-4 PE=1 SV=1
AT3G25220	Q38935	0,817	0,002	endoplasmic reticulum	Peptidyl-prolyl cis-trans isomerase FKBP15-1 OS=Arabidopsis thaliana GN=FKBP15-1 PE=2 SV=2
AT5G12250	P29514	0,975	0,006	cytosol	Tubulin beta-6 chain OS=Arabidopsis thaliana GN=TUBB6 PE=2 SV=1
AT1G79830	Q0WVL7	0,997	0,004	golgi	Golgin candidate 5 OS=Arabidopsis thaliana GN=GC5 PE=1 SV=1
AT5G13850	Q6ICZ8	1,006	0,001	cytosol	Nascent polypeptide-associated complex subunit alpha-like protein 3 OS=Arabidopsis thaliana GN=At5g13850 PE=1 SV=1
Cell wall					
AT5G49360**	Q9FGY1	-2,805	0,001	extracellular	Beta-D-xylosidase 1 OS=Arabidopsis thaliana GN=BXL1 PE=1 SV=1
AT4G30270	P24806	-1,946	0,001	extracellular	Xyloglucan endotransglucosylase/hydrolase protein 24 OS=Arabidopsis thaliana GN=XTH24 PE=1 SV=2
AT5G06860**	Q9M5J9	-1,763	0,001	extracellular	Polygalacturonase inhibitor 1 OS=Arabidopsis thaliana GN=PGIP1 PE=1 SV=1
AT5G44130	Q9FFH6	-1,219	0,001	tracellular,plasma membra	Fasciclin-like arabinogalactan protein 13 OS=Arabidopsis thaliana GN=FLA13 PE=1 SV=1

AT1G03870	Q9ZWA8	-0,85	0,003	plasma membrane	Fasciclin-like arabinogalactan protein 9 OS=Arabidopsis thaliana GN=FLA9 PE=1 SV=1
AT1G12780	Q42605	-0,807	0,001	cytosol	Bifunctional UDP-glucose 4-epimerase and UDP-xylose 4-epimerase 1 OS=Arabidopsis thaliana GN=UGE1 PE=1 SV=2
AT3G60900	Q9LZX4	-0,731	0,002	plasma membrane	Fasciclin-like arabinogalactan protein 10 OS=Arabidopsis thaliana GN=FLA10 PE=1 SV=1
AT2G45470	O22126	-0,698	0,001	tracellular,plasma membra	Fasciclin-like arabinogalactan protein 8 OS=Arabidopsis thaliana GN=FLA8 PE=1 SV=1
AT3G10740**	Q9SG80	-0,533	0,004	extracellular	Alpha-L-arabinofuranosidase 1 OS=Arabidopsis thaliana GN=ASD1 PE=1 SV=1
AT5G57560	Q38857	-0,47	0,006	extracellular	Xyloglucan endotransglucosylase/hydrolase protein 22 OS=Arabidopsis thaliana GN=XTH22 PE=1 SV=1
AT5G64570**	Q9FLG1	-0,462	0,001	extracellular	Beta-D-xylosidase 4 OS=Arabidopsis thaliana GN=BXL4 PE=1 SV=1
AT4G16130	O23461	-0,435	0,003	cytosol	L-arabinokinase OS=Arabidopsis thaliana GN=ARA1 PE=1 SV=1
AT1G11580	Q1JPL7	-0,423	0,009	extracellular	Pectinesterase/pectinesterase inhibitor 18 OS=Arabidopsis thaliana GN=PME18 PE=1 SV=3
AT2G15880	Q9XIL9	-0,371	0,009	extracellular	reversed Pollen-specific leucine-ricrepeat extensin-like protein 3 OS=Arabidopsis thaliana GN=PEX3 PE=2 SV=1
AT2G27860	Q9ZUY6	0,445	0,007	cytosol	UDP-D-apiose/UDP-D-xylose synthase 1 OS=Arabidopsis thaliana GN=AXS1 PE=1 SV=1
AT1G53500	Q9LPG6	0,455	0,002	cytosol	Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM2 OS=Arabidopsis thaliana GN=RHM2 PE=1 SV=1
AT2G45790	O80840	0,48	0,001	mitochondrion,cytosol	Phosphomannomutase OS=Arabidopsis thaliana GN=PMM PE=1 SV=1
AT3G51160	P93031	0,499	0,005	cytosol	GDP-mannose 4,6 dehydratase 2 OS=Arabidopsis thaliana GN=MUR1 PE=1 SV=3
AT2G06850	Q39099	0,511	0,005	extracellular	Xyloglucan endotransglucosylase/hydrolase protein 4 OS=Arabidopsis thaliana GN=XTH4 PE=1 SV=1
AT5G59290	Q9FIE8	0,52	0,001	cytosol	UDP-glucuronic acid decarboxylase 3 OS=Arabidopsis thaliana GN=UXS3 PE=1 SV=1
AT1G08200	Q9SGE0	0,544	0,001	cytosol	UDP-D-apiose/UDP-D-xylose synthase 2 OS=Arabidopsis thaliana GN=AXS2 PE=2 SV=1
AT1G78570**	Q9SYM5	0,613	0,003	cytosol	Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM1 OS=Arabidopsis thaliana GN=RHM1 PE=1 SV=1
AT5G15490	Q9LF33	0,637	0,003	extracellular	UDP-glucose 6-dehydrogenase 3 OS=Arabidopsis thaliana GN=UGD3 PE=1 SV=1
AT5G16510	Q9FFD2	0,798	0,001	extracellular,cytosol	Probable UDP-arabinopyranose mutase 5 OS=Arabidopsis thaliana GN=RGP5 PE=1 SV=1
AT3G12145	Q9LH52	0,803	0,001	extracellular	Leucine-ricrepeat protein FLOR 1 OS=Arabidopsis thaliana GN=FLR1 PE=1 SV=1
AT4G37800	Q8LER3	0,821	0,001	extracellular	Probable xyloglucan endotransglucosylase/hydrolase protein 7 OS=Arabidopsis thaliana GN=XTH7 PE=2 SV=2
AT1G63000	Q9LQ04	0,825	0,002	cytosol	Bifunctional dTDP-4-dehydrorhamnose 3,5-epimerase/dTDP-4-dehydrorhamnose reductase OS=Arabidopsis thaliana GN=NRS/ER PE=1 SV=1
AT1G65310	O80803	0,967	0,001	extracellular	Probable xyloglucan endotransglucosylase/hydrolase protein 17 OS=Arabidopsis thaliana GN=XTH17 PE=1 SV=1
AT5G39320	Q9FM01	1,034	0,001	extracellular	UDP-glucose 6-dehydrogenase 4 OS=Arabidopsis thaliana GN=UGD4 PE=1 SV=1
AT3G29360	Q9LIA8	1,068	0,001	extracellular	UDP-glucose 6-dehydrogenase 2 OS=Arabidopsis thaliana GN=UGD2 PE=1 SV=1
AT3G44990**	P93046	1,243	0,001	tracellular,plasma membra	Xyloglucan endotransglucosylase/hydrolase protein 31 OS=Arabidopsis thaliana GN=XTH31 PE=1 SV=2
Co-factor and vitamin metabolism					
AT3G14990**	Q9FPF0	-1,325	0,001	golgi	Protein DJ-1 homolog A OS=Arabidopsis thaliana GN=DJ1A PE=1 SV=1
AT2G38230**	O80448	-0,889	0,001	cytosol	Pyridoxal 5'-phosphate synthase subunit PDX1.1 OS=Arabidopsis thaliana GN=PDX11 PE=1 SV=1
AT2G44050	O80575	-0,733	0,001	plastid	6,7-dimethyl-8-ribityllumazine synthase, chloroplastic OS=Arabidopsis thaliana GN=At2g44050 PE=2 SV=1
AT5G60540	Q8LAD0	-0,363	0,01	cytosol	Probable pyridoxal 5'-phosphate synthase subunit PDX2 OS=Arabidopsis thaliana GN=PDX2 PE=1 SV=1
AT5G54770	Q38814	0,36	0,001	plastid	Thiamine thiazole synthase, chloroplastic OS=Arabidopsis thaliana GN=THI1 PE=1 SV=1
AT5G15530	Q9LLC1	0,457	0,007	plastid	Biotin carboxyl carrier protein of acetyl-CoA carboxylase 2, chloroplastic OS=Arabidopsis thaliana GN=BCCP2 PE=1 SV=1
AT5G20990	Q39054	0,502	0,003	cytosol	Molybdopterin biosynthesis protein CNX1 OS=Arabidopsis thaliana GN=CNX1 PE=1 SV=2
AT5G44720**	O48588	0,965	0,001	cytosol	Molybdenum cofactor sulfurase family protein OS=Arabidopsis thaliana GN=T19K24.17 PE=2 SV=1
AT2G29630	O82392	1,571	0,001	plastid	Phosphomethylpyrimidine synthase, chloroplastic OS=Arabidopsis thaliana GN=THIC PE=1 SV=1
Development					
AT2G26560	O48723	-2,106	0,003	cytosol	Patatin-like protein 2 OS=Arabidopsis thaliana GN=PLP2 PE=1 SV=1
AT5G06760	Q9FG31	-0,73	0,002	peroxisome	Late embryogenesis abundant protein 46 OS=Arabidopsis thaliana GN=LEA46 PE=2 SV=1
AT5G44020	Q9FNC4	-0,693	0,001	cytosol	HAD superfamily, subfamily IIIB acid phosphatase OS=Arabidopsis thaliana GN=MRH10.13 PE=2 SV=1
AT4G12420	Q9SU40	-0,436	0,002	plasma membrane	Monocopper oxidase-like protein SKU5 OS=Arabidopsis thaliana GN=SKU5 PE=1 SV=1
AT2G03440	Q9ZQ80	-0,391	0,002	nucleus	Nodulin-related protein 1 OS=Arabidopsis thaliana GN=NRP1 PE=1 SV=1
AT4G24220	Q9STX2	-0,361	0,008	cytosol	3-oxo-Delta(4,5)-steroid 5-beta-reductase OS=Arabidopsis thaliana GN=VEP1 PE=1 SV=1
AT2G33430	O22793	0,464	0,005	plastid	Multiple organellar RNA editing factor 2, chloroplastic OS=Arabidopsis thaliana GN=MORF2 PE=1 SV=1
AT1G08780	Q9M4B5	0,473	0,002	nucleus	Probable prefoldin subunit 4 OS=Arabidopsis thaliana GN=AIP3 PE=1 SV=3
AT2G44060	O80576	0,529	0,001	cytosol	At2g44060 OS=Arabidopsis thaliana GN=late embryogenesis abundant 26 PE=2 SV=1
AT2G42840	Q9S728	0,538	0,004	extracellular	Protodermal factor 1 OS=Arabidopsis thaliana GN=PDF1 PE=2 SV=1
AT1G11430	Q9LPZ1	0,561	0,001	plastid	Multiple organellar RNA editing factor 9, chloroplastic OS=Arabidopsis thaliana GN=MORF9 PE=1 SV=1
AT3G51280	Q9SD20	0,639	0,003	nucleus	reversed Protein POLLENLESS 3-LIKE 2 OS=Arabidopsis thaliana GN=At3g51280 PE=2 SV=1
AT3G02180	Q9S7P8	0,682	0,001	plasma membrane	Protein SPIRAL1-like 3 OS=Arabidopsis thaliana GN=SP1L3 PE=1 SV=1
DNA					
AT5G27670	Q94F49	-1,16	0,004	nucleus	Probable histone H2A.5 OS=Arabidopsis thaliana GN=At5g27670 PE=1 SV=1
AT4G09730	Q56X76	-1,11	0,001	plastid	DEAD-box ATP-dependent RNA helicase 39 OS=Arabidopsis thaliana GN=RH39 PE=2 SV=2
AT1G08880	O04848	-0,649	0,003	nucleus	Probable histone H2AXa OS=Arabidopsis thaliana GN=At1g08880 PE=1 SV=1
AT2G28560	Q9SK02	-0,643	0,003	nucleus	DNA repair protein RAD51 homolog 2 OS=Arabidopsis thaliana GN=RAD51B PE=2 SV=2
AT3G54560	O23628	-0,641	0,003	nucleus	Histone H2A variant 1 OS=Arabidopsis thaliana GN=H2AV PE=1 SV=1
AT2G45810	Q94BV4	-0,585	0,003	nucleus	DEAD-box ATP-dependent RNA helicase 6 OS=Arabidopsis thaliana GN=RH6 PE=2 SV=2

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AT3G15950	Q9LSB4	-0,362	0,001	endoplasmic reticulum	TSA1-like protein OS=Arabidopsis thaliana GN=NAI2 PE=1 SV=1
AT5G38470	Q84L30	0,478	0,002	cytosol	Ubiquitin receptor RAD23d OS=Arabidopsis thaliana GN=RAD23D PE=1 SV=2
AT3G04880	Q05212	0,528	0,005	cytosol	DNA damage-repair/toleration protein DRT102 OS=Arabidopsis thaliana GN=DRT102 PE=1 SV=2
AT5G39770	F4KFU8	0,553	0,004	cytosol	reversed Restriction endonuclease, type II-like superfamily protein OS=Arabidopsis thaliana GN=MKM21.10 PE=4 SV=1
AT2G47450	O22265	0,576	0,001	plastid	Signal recognition particle 43 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=CAO PE=1 SV=2
AT3G19130	Q0WW84	0,847	0,002	nucleus	Polyadenylate-binding protein RBP47B OS=Arabidopsis thaliana GN=RBP47B PE=2 SV=1
AT1G18800	Q8LC68	1,014	0,001	nucleus	NAP1-related protein 2 OS=Arabidopsis thaliana GN=NRP2 PE=1 SV=2
AT5G07460**	Q9LY15	1,074	0,001	nucleus	Peptide methionine sulfoxide reductase A2 OS=Arabidopsis thaliana GN=MRSA2 PE=1 SV=1
AT4G26110	Q9SZI2	1,227	0,001	nucleus	Nucleosome assembly protein 1;1 OS=Arabidopsis thaliana GN=NAP1;1 PE=1 SV=1
AT2G19480	Q9ZUP3	1,442	0,001	nucleus	Nucleosome assembly protein 1;2 OS=Arabidopsis thaliana GN=NAP1;2 PE=1 SV=1
AT5G56950	Q94K07	1,645	0,001	nucleus	Nucleosome assembly protein 1;3 OS=Arabidopsis thaliana GN=NAP1;3 PE=1 SV=1
AT1G20960	Q9SYP1	1,994	0,001	nucleus	reversed DExH-box ATP-dependent RNA helicase DExH12 OS=Arabidopsis thaliana GN=BRR2A PE=1 SV=1
Fermentation					
AT1G54100	Q9SYG7	-1,226	0,001	cytosol	Aldehyde dehydrogenase family 7 member B4 OS=Arabidopsis thaliana GN=ALDH7B4 PE=2 SV=3
AT5G17380	Q9LF46	-0,606	0,001	peroxisome	2-hydroxyacyl-CoA lyase OS=Arabidopsis thaliana GN=HACL PE=1 SV=1
AT3G48000	Q9SU63	-0,481	0,001	mitochondrion	Aldehyde dehydrogenase family 2 member B4, mitochondrial OS=Arabidopsis thaliana GN=ALDH2B4 PE=1 SV=1
AT3G24503	Q56YU0	0,425	0,001	cytosol	Aldehyde dehydrogenase family 2 member C4 OS=Arabidopsis thaliana GN=ALDH2C4 PE=1 SV=2
AT4G36250	Q70E96	0,627	0,003	cytosol	Aldehyde dehydrogenase family 3 member F1 OS=Arabidopsis thaliana GN=ALDH3F1 PE=2 SV=2
Gluconeogenesis					
AT3G58750	Q9LXS6	-1,05	0,008	peroxisome	Citrate synthase 2, peroxisomal OS=Arabidopsis thaliana GN=CSY2 PE=2 SV=1
AT2G22780	O82399	-1,002	0,001	peroxisome	Malate dehydrogenase 1, peroxisomal OS=Arabidopsis thaliana GN=PMDH1 PE=1 SV=1
AT5G09660**	Q9ZP05	-0,909	0,001	peroxisome	Malate dehydrogenase 2, peroxisomal OS=Arabidopsis thaliana GN=PMDH2 PE=1 SV=1
AT4G15530	O23404	-0,837	0,001	plastid,cytosol	Pyruvate, phosphate dikinase 1, chloroplastic OS=Arabidopsis thaliana GN=PPDK PE=1 SV=2
AT2G42790	Q9SJH7	-0,535	0,004	peroxisome	Citrate synthase 3, peroxisomal OS=Arabidopsis thaliana GN=CSY3 PE=2 SV=1
AT3G16910	Q8VZF1	-0,519	0,002	peroxisome	Acetate/butyrate--CoA ligase AE7, peroxisomal OS=Arabidopsis thaliana GN=AE7 PE=1 SV=1
Glycolisis					
AT4G26530**	O65581	-1,091	0,001	cytosol	Fructose-bisphosphate aldolase 5, cytosolic OS=Arabidopsis thaliana GN=FBA5 PE=1 SV=1
AT1G70820	Q9SSL0	-0,904	0,001	plastid	At1g70820 OS=Arabidopsis thaliana GN=At1g70820 PE=2 SV=1
AT1G07110	Q9MB58	-0,841	0,001	cytosol	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase OS=Arabidopsis thaliana GN=FKFBP PE=1 SV=1
AT4G26270	Q94AA4	-0,69	0,01	cytosol	ATP-dependent 6-phosphofructokinase 3 OS=Arabidopsis thaliana GN=PFK3 PE=1 SV=1
AT1G43670	Q9MA79	-0,688	0,001	cytosol	Fructose-1,6-bisphosphatase, cytosolic OS=Arabidopsis thaliana GN=CYFBP PE=1 SV=1
AT5G22620	Q9FNJ9	-0,428	0,003	plastid	Probable 2-carboxy-D-arabinitol-1-phosphatase OS=Arabidopsis thaliana GN=At5g22620 PE=1 SV=1
AT1G32440	Q93Z53	-0,358	0,006	plastid	Plastidial pyruvate kinase 3, chloroplastic OS=Arabidopsis thaliana GN=PKP3 PE=1 SV=1
AT1G66430	Q9C524	0,358	0,001	plastid	Probable fructokinase-6, chloroplastic OS=Arabidopsis thaliana GN=At1g66430 PE=2 SV=1
AT1G12000	Q8W4M5	0,393	0,002	golgi	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta 1 OS=Arabidopsis thaliana GN=PFP-BETA1 PE=1 SV=1
AT1G13440	Q9FX54	0,455	0,002	nucleus,cytosol	Glyceraldehyde-3-phosphate dehydrogenase GAPC2, cytosolic OS=Arabidopsis thaliana GN=GAPC2 PE=1 SV=1
AT3G08590	Q9M9K1	0,487	0,001	cytosol	Probable 2,3-bisphosphoglycerate-independent phosphoglycerate mutase 2 OS=Arabidopsis thaliana GN=At3g08590 PE=1 SV=1
AT2G36460	Q9SJQ9	0,638	0,001	cytosol	Fructose-bisphosphate aldolase 6, cytosolic OS=Arabidopsis thaliana GN=FBA6 PE=1 SV=1
AT3G52930	Q9LF98	0,654	0,001	cytosol	Fructose-bisphosphate aldolase 8, cytosolic OS=Arabidopsis thaliana GN=FBA8 PE=1 SV=1
AT2G31390	Q9SID0	0,689	0,001	cytosol	Probable fructokinase-1 OS=Arabidopsis thaliana GN=At2g31390 PE=2 SV=1
AT2G29560	Q9ZW34	0,8	0,002	cytosol	Cytosolic enolase 3 OS=Arabidopsis thaliana GN=ENO3 PE=1 SV=1
AT1G09780	O04499	0,848	0,001	cytosol	2,3-bisphosphoglycerate-independent phosphoglycerate mutase 1 OS=Arabidopsis thaliana GN=PGM1 PE=2 SV=3
Hormone metabolism					
AT2G33830**	P93017	-2,42	0,001	peroxisome	Dormancy-associated protein homolog 1 OS=Arabidopsis thaliana GN=DRMH1 PE=1 SV=1
AT4G27450	Q93V62	-2,344	0,001	cytosol	AT4g27450/F27G19_50 OS=Arabidopsis thaliana GN=At4g27450 PE=1 SV=1
AT3G02480	Q9M892	-1,84	0,001	cytosol	AT3g02480/F16B3_11 OS=Arabidopsis thaliana GN=At3g02480 PE=2 SV=1
AT3G44300	P32962	-1,665	0,002	cytosol	Nitrilase 2 OS=Arabidopsis thaliana GN=NIT2 PE=1 SV=1
AT1G05560**	Q9LR44	-1,551	0,001	plastid	UDP-glycosyltransferase 75B1 OS=Arabidopsis thaliana GN=UGT75B1 PE=1 SV=1
AT4G19170**	O49675	-1,499	0,001	plastid	Probable carotenoid cleavage dioxygenase 4, chloroplastic OS=Arabidopsis thaliana GN=CCD4 PE=1 SV=1
AT1G76680**	Q8LAH7	-0,773	0,001	cytosol	12-oxophytodienoate reductase 1 OS=Arabidopsis thaliana GN=OPR1 PE=1 SV=2
AT5G67030**	Q9FGC7	-0,652	0,001	plastid	Zeaxanthin epoxidase, chloroplastic OS=Arabidopsis thaliana GN=ZEP PE=1 SV=1
AT5G13370	Q8GZ29	-0,636	0,005	cytosol	At5g13370 OS=Arabidopsis thaliana GN=At5g13370 PE=2 SV=1
AT1G52100	Q5XF82	-0,538	0,001	cytosol	Jacalin-related lectin 11 OS=Arabidopsis thaliana GN=JAL11 PE=2 SV=1
AT4G30610	Q9M099	-0,419	0,006	extracellular	Serine carboxypeptidase 24 OS=Arabidopsis thaliana GN=SCPL24 PE=1 SV=1
AT5G42650	Q96242	-0,392	0,001	plastid	Allene oxide synthase, chloroplastic OS=Arabidopsis thaliana GN=CYP74A PE=1 SV=3
AT3G07390	Q94BT2	-0,387	0,004	plasma membrane	Auxin-induced in root cultures protein 12 OS=Arabidopsis thaliana GN=AIR12 PE=1 SV=3
AT5G14920	Q9LFR3	0,435	0,007	extracellular	Gibberellin-regulated protein 14 OS=Arabidopsis thaliana GN=GASA14 PE=1 SV=1

AT2G36880	Q9SJL8	0,636	0,001	cytosol	S-adenosylmethionine synthase 3 OS=Arabidopsis thaliana GN=METK3 PE=1 SV=1
AT2G46280	Q38884	0,637	0,001	cytosol	Eukaryotic translation initiation factor 3 subunit I OS=Arabidopsis thaliana GN=TIF3I1 PE=2 SV=2
AT2G42680	Q9SJI8	0,663	0,003	nucleus	Multiprotein-bridging factor 1a OS=Arabidopsis thaliana GN=MBF1A PE=2 SV=1
AT1G62380	Q41931	0,738	0,001	golgi	1-aminocyclopropane-1-carboxylate oxidase 2 OS=Arabidopsis thaliana GN=ACO2 PE=1 SV=2
AT1G05010	Q06588	0,777	0,001	golgi	1-aminocyclopropane-1-carboxylate oxidase 4 OS=Arabidopsis thaliana GN=ACO4 PE=1 SV=2
AT1G02500	P23686	0,859	0,002	cytosol	S-adenosylmethionine synthase 1 OS=Arabidopsis thaliana GN=SAM1 PE=1 SV=2
AT4G01850	P17562	0,987	0,001	nucleus,cytosol	S-adenosylmethionine synthase 2 OS=Arabidopsis thaliana GN=SAM2 PE=1 SV=1
AT3G17390	Q9LUT2	1,024	0,001	nucleus,plasma membrane	S-adenosylmethionine synthase 4 OS=Arabidopsis thaliana GN=METK4 PE=1 SV=1
Lipid metabolism					
AT5G59310	Q9LLR6	-1,553	0,001	extracellular	Non-specific lipid-transfer protein 4 OS=Arabidopsis thaliana GN=LTP4 PE=3 SV=1
AT5G16370	Q9FFE6	-1,037	0,001	peroxisome	Probable acyl-activating enzyme 5, peroxisomal OS=Arabidopsis thaliana GN=AE5 PE=1 SV=1
AT5G59320	Q9LLR7	-0,956	0,002	extracellular	Non-specific lipid-transfer protein 3 OS=Arabidopsis thaliana GN=LTP3 PE=3 SV=1
AT4G26690	Q9SZ11	-0,9	0,001	plasma membrane	Glycerophosphodiester phosphodiesterase GDPDL3 OS=Arabidopsis thaliana GN=GDPDL3 PE=1 SV=3
AT3G51840	Q96329	-0,887	0,001	peroxisome	Acyl-coenzyme A oxidase 4, peroxisomal OS=Arabidopsis thaliana GN=ACX4 PE=1 SV=1
AT5G54500	Q9LSQ5	-0,885	0	plasma membrane	NAD(P)dehydrogenase (quinone) FQR1 OS=Arabidopsis thaliana GN=FQR1 PE=1 SV=1
AT3G51600	Q9XFS7	-0,77	0,002	extracellular	Non-specific lipid-transfer protein 5 OS=Arabidopsis thaliana GN=LTP5 PE=1 SV=1
AT1G27950	Q9C7F7	-0,702	0,002	tracellular,plasma membra	Non-specific lipid transfer protein GPI-anchored 1 OS=Arabidopsis thaliana GN=LTPG1 PE=1 SV=1
AT1G66970	Q7Y208	-0,695	0,002	plasma membrane	Glycerophosphodiester phosphodiesterase GDPDL1 OS=Arabidopsis thaliana GN=GDPDL1 PE=1 SV=2
AT5G10160	Q9LX13	-0,69	0,002	plastid	(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase-like protein OS=Arabidopsis thaliana GN=At5g10160 PE=2 SV=1
AT5G55480	Q9FJ62	-0,649	0,003	plasma membrane	Glycerophosphodiester phosphodiesterase GDPDL4 OS=Arabidopsis thaliana GN=GDPDL4 PE=1 SV=1
AT4G16760	O65202	-0,452	0,001	peroxisome	Peroxisomal acyl-coenzyme A oxidase 1 OS=Arabidopsis thaliana GN=ACX1 PE=1 SV=1
AT2G22230	Q9SIE3	-0,442	0,003	plastid	At2g22230/T26C19.11 OS=Arabidopsis thaliana GN=At2g22230 PE=2 SV=2
AT2G05990	Q9SLA8	-0,414	0,001	plastid	Enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic OS=Arabidopsis thaliana GN=MOD1 PE=1 SV=1
ATCG00500	P56765	-0,407	0,005	plastid	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic OS=Arabidopsis thaliana GN=accD PE=1 SV=2
AT1G80460	Q9M8L4	-0,352	0,007	cytosol	Glycerol kinase OS=Arabidopsis thaliana GN=GLPK PE=1 SV=1
AT1G54630	P25702	0,392	0,007	plastid	Acyl carrier protein 3, chloroplastic OS=Arabidopsis thaliana GN=ACP3 PE=1 SV=2
AT4G33030	O48917	0,395	0,001	plastid	UDP-sulfoquinovose synthase, chloroplastic OS=Arabidopsis thaliana GN=SQD1 PE=1 SV=1
AT1G45201**	A0A1P8AVY3	0,453	0,001	golgi	Triacylglycerol lipase-like 1 OS=Arabidopsis thaliana GN=TLL1 PE=4 SV=1
AT3G55360	Q9M2U2	0,601	0,006	ısmic reticulum,plasma me	Very-long-chain enoyl-CoA reductase OS=Arabidopsis thaliana GN=ECR PE=1 SV=1
AT2G38540	Q42589	0,608	0,001	extracellular	Non-specific lipid-transfer protein 1 OS=Arabidopsis thaliana GN=LTP1 PE=2 SV=1
AT2G33470	O22797	0,609	0,002	golgi	Glycolipid transfer protein 1 OS=Arabidopsis thaliana GN=GLTP1 PE=2 SV=1
AT5G42890	Q9FMN0	0,727	0,005	peroxisome	Sterol carrier protein 2 OS=Arabidopsis thaliana GN=SCP2 PE=2 SV=1
AT4G30950	P46312	0,809	0,002	plastid	Omega-6 fatty acid desaturase, chloroplastic OS=Arabidopsis thaliana GN=FAD6 PE=1 SV=2
AT2G43710	O22832	0,847	0,001	plastid	Stearoyl-[acyl-carrier-protein] 9-desaturase 7, chloroplastic OS=Arabidopsis thaliana GN=FAB2 PE=1 SV=1
AT3G08770	Q9LDB4	0,893	0,001	extracellular	Non-specific lipid-transfer protein 6 OS=Arabidopsis thaliana GN=LTP6 PE=3 SV=1
AT5G20060	Q8L9X1	0,941	0,002	mitochondrion	Alpha/beta-Hydrolases superfamily protein OS=Arabidopsis thaliana GN=At5g20060 PE=1 SV=1
AT1G48600	Q944H0	1,187	0,001	cytosol	Phosphomethylethanolamine N-methyltransferase OS=Arabidopsis thaliana GN=NMT2 PE=2 SV=2
AT1G79750	Q9CA83	1,288	0,001	plastid	NADP-dependent malic enzyme 4, chloroplastic OS=Arabidopsis thaliana GN=NADP-ME4 PE=1 SV=1
AT1G54580	P25701	1,337	0,001	plastid	Acyl carrier protein 2, chloroplastic OS=Arabidopsis thaliana GN=ACP2 PE=1 SV=2
AT1G73600**	Q9C6B9	3,175	0,001	cytosol	Phosphoethanolamine N-methyltransferase 3 OS=Arabidopsis thaliana GN=NMT3 PE=2 SV=2
Major CHO metabolism					
AT1G12240	Q39041	-0,891	0,001	vacuole	Acid beta-fructofuranosidase 4, vacuolar OS=Arabidopsis thaliana GN=BFRUCT4 PE=1 SV=2
AT1G62660	Q43348	-0,785	0,001	vacuole	Acid beta-fructofuranosidase 3, vacuolar OS=Arabidopsis thaliana GN=BFRUCT3 PE=2 SV=1
AT3G13790	Q43866	-0,667	0,003	extracellular	Beta-fructofuranosidase, insoluble isoenzyme CWINV1 OS=Arabidopsis thaliana GN=CWINV1 PE=1 SV=1
AT5G19220	P55229	-0,549	0,004	plastid	Glucose-1-phosphate adenylyltransferase large subunit 1, chloroplastic OS=Arabidopsis thaliana GN=ADG2 PE=1 SV=3
AT5G17310**	P57751	-0,538	0,001	extracellular	UTP--glucose-1-phosphate uridylyltransferase 1 OS=Arabidopsis thaliana GN=UGP1 PE=2 SV=1
AT3G29320**	Q9LIB2	0,371	0,001	plastid	Alpha-glucan phosphorylase 1 OS=Arabidopsis thaliana GN=PHS1 PE=1 SV=1
AT3G52180**	Q9FEB5	0,608	0,001	plastid	Phosphoglucan phosphatase DSP4, chloroplastic OS=Arabidopsis thaliana GN=DSP4 PE=1 SV=1
AT1G69830	Q94A41	0,694	0,001	plastid	Alpha-amylase 3, chloroplastic OS=Arabidopsis thaliana GN=AMY3 PE=1 SV=1
AT1G32900**	Q9MAQ0	0,781	0,001	plastid	Granule-bound starch synthase 1, chloroplastic/amyloplastic OS=Arabidopsis thaliana GN=GBSS1 PE=1 SV=1
Metal handling					
AT1G02335	Q9FZ27	-0,382	0,005	extracellular	Germin-like protein subfamily 2 member 2 OS=Arabidopsis thaliana GN=At1g02335 PE=2 SV=1
AT4G14040**	Q93WN0	0,496	0,001	cytosol	Selenium-binding protein 2 OS=Arabidopsis thaliana GN=SBP2 PE=1 SV=1
AT4G14030	O23264	0,498	0,001	cytosol	Selenium-binding protein 1 OS=Arabidopsis thaliana GN=SBP1 PE=1 SV=1
AT1G56430**	Q9C7X5	0,529	0,009	cytosol	Probable nicotianamine synthase 4 OS=Arabidopsis thaliana GN=NAS4 PE=2 SV=1
AT3G56090	Q9LYN2	0,589	0,003	plastid	Ferritin-3, chloroplastic OS=Arabidopsis thaliana GN=FER3 PE=2 SV=1
AT1G30470	F4I6B2	0,619	0,006	golgi	SIT4 phosphatase-associated family protein OS=Arabidopsis thaliana GN=At1g30470 PE=1 SV=1
AT1G66240	Q94BT9	0,644	0,001	plasma membrane	Copper transport protein ATX1 OS=Arabidopsis thaliana GN=ATX1 PE=1 SV=2

AT4G14710	Q8W108	0,738	0,001	cytosol	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase 3 OS=Arabidopsis thaliana GN=ARD3 PE=2 SV=1
AT5G19140	Q94BR2	0,846	0,001	plasma membrane	Aluminum induced protein wiYGL and LRDR motifs OS=Arabidopsis thaliana GN=AILP1 PE=2 SV=1
Minor CHO metabolism					
AT5G20250**	Q8RX87	-2,472	0,002	plastid	Probable galactinol--sucrose galactosyltransferase 6 OS=Arabidopsis thaliana GN=RFS6 PE=2 SV=2
AT5G57655**	Q9FKK7	-1,322	0,01	endoplasmic reticulum	Xylose isomerase OS=Arabidopsis thaliana GN=XYLA PE=2 SV=2
AT2G37760	O80944	-0,891	0,007	cytosol	Aldo-keto reductase family 4 member C8 OS=Arabidopsis thaliana GN=AKR4C8 PE=1 SV=2
AT3G47800	Q9STT3	-0,866	0,001	extracellular	Aldose 1-epimerase OS=Arabidopsis thaliana GN=T23J7.130 PE=2 SV=1
AT2G37770**	Q0PGJ6	-0,745	0,002	plastid	NADPH-dependent aldo-keto reductase, chloroplastic OS=Arabidopsis thaliana GN=AKR4C9 PE=1 SV=1
AT1G06690	Q94A68	-0,649	0,001	plastid	Uncharacterized oxidoreductase At1g06690, chloroplastic OS=Arabidopsis thaliana GN=At1g06690 PE=1 SV=1
AT5G51970**	Q9FJ95	-0,525	0,001	cytosol	Sorbitol dehydrogenase OS=Arabidopsis thaliana GN=SDPE=1 SV=1
AT5G37850	Q8W1X2	-0,425	0,003	plastid	Pyridoxal kinase OS=Arabidopsis thaliana GN=PK PE=1 SV=2
AT3G17940	Q9LVH6	0,727	0,001	cytosol	Aldose 1-epimerase OS=Arabidopsis thaliana GN=At3g17940 PE=3 SV=1
Miscelaneous					
AT2G39330	O80948	-3,353	0,001	cytosol	Jacalin-related lectin 23 OS=Arabidopsis thaliana GN=JAL23 PE=1 SV=1
AT5G63800**	Q9FFN4	-3,021	0,002	extracellular	Beta-galactosidase 6 OS=Arabidopsis thaliana GN=BGAL6 PE=2 SV=1
AT3G51000	Q9SD45	-2,259	0,001	cytosol	AT3g51000/F24M12_40 OS=Arabidopsis thaliana GN=F24M12.40 PE=2 SV=1
AT3G04000**	Q9SQR2	-2,222	0,001	plastid	NADPH-dependent aldehyde reductase 2, chloroplastic OS=Arabidopsis thaliana GN=ChlADR2 PE=1 SV=1
AT4G12480	Q39176	-2,118	0,001	extracellular	Lipid transfer protein EARLI 1 OS=Arabidopsis thaliana GN=EARLI1 PE=1 SV=1
AT3G13750**	Q9SCW1	-1,832	0,001	extracellular	Beta-galactosidase 1 OS=Arabidopsis thaliana GN=BGAL1 PE=2 SV=1
AT5G56870**	Q9SCV8	-1,728	0,001	extracellular	Beta-galactosidase 4 OS=Arabidopsis thaliana GN=BGAL4 PE=1 SV=1
AT5G16990	Q39173	-1,66	0,002	cytosol	NADP-dependent alkenal double bond reductase P2 OS=Arabidopsis thaliana GN=P2 PE=2 SV=2
AT5G16970**	Q39172	-1,361	0,001	cytosol	NADPH-dependent oxidoreductase 2-alkenal reductase OS=Arabidopsis thaliana GN=AER PE=1 SV=1
AT5G16980**	F4KFK3	-1,271	0,001	cytosol	Zinc-binding dehydrogenase family protein OS=Arabidopsis thaliana GN=At5g16980 PE=4 SV=1
AT5G64120	Q43387	-1,246	0,001	extracellular	Peroxidase 71 OS=Arabidopsis thaliana GN=PER71 PE=1 SV=1
AT4G22513	A8MQX6	-1,153	0,001	extracellular	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein OS=Arabidopsis thaliana GN=At4g22513 PE=4 SV=1
AT4G13180	Q9SVQ9	-1,1	0,001	plastid	AT4g13180/F17N18_70 OS=Arabidopsis thaliana GN=At4g13180 PE=1 SV=1
AT2G43820**	O22822	-0,983	0,001	tracellular,plasma membra	UDP-glycosyltransferase 74F2 OS=Arabidopsis thaliana GN=UGT74F2 PE=1 SV=1
AT5G64250	Q9FMG0	-0,98	0,001	cytosol	2-nitropropane dioxygenase-like protein OS=Arabidopsis thaliana GN=MSJ1.9 PE=1 SV=1
AT4G12470	Q9SU35	-0,922	0,006	golgi	pEARLI1-like lipid transfer protein 1 OS=Arabidopsis thaliana GN=AZI1 PE=1 SV=1
AT4G21580	O65423	-0,875	0,001	cytosol	AT4g21580/F18E5_200 OS=Arabidopsis thaliana GN=F18E5.200 PE=2 SV=1
AT4G20860	Q9SUC6	-0,866	0,001	extracellular	Berberine bridge enzyme-like 22 OS=Arabidopsis thaliana GN=FAD-OXR PE=2 SV=1
AT3G48460	Q9STM6	-0,861	0,006	extracellular	GDSL esterase/lipase At3g48460 OS=Arabidopsis thaliana GN=At3g48460 PE=2 SV=1
AT4G20830	Q9SVG4	-0,86	0,001	extracellular	Berberine bridge enzyme-like 19 OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2
AT3G32980	Q9LHB9	-0,84	0,001	extracellular	Peroxidase 32 OS=Arabidopsis thaliana GN=PER32 PE=1 SV=3
AT1G02920	Q9SRY5	-0,802	0,002	cytosol	Glutathione S-transferase F7 OS=Arabidopsis thaliana GN=GSTF7 PE=2 SV=3
AT2G31750	Q9SKC5	-0,798	0,001	plastid	UDP-glycosyltransferase 74D1 OS=Arabidopsis thaliana GN=UGT74D1 PE=1 SV=1
AT3G09260	Q9SR37	-0,792	0,001	endoplasmic reticulum	Beta-glucosidase 23 OS=Arabidopsis thaliana GN=BGLU23 PE=1 SV=1
AT1G71500	Q9C9I7	-0,789	0,001	plastid	Rieske (2Fe-2S) domain-containing protein OS=Arabidopsis thaliana GN=PSB33 PE=2 SV=1
AT2G45180	Q42044	-0,787	0,001	vacuole	At2g45180 OS=Arabidopsis thaliana GN=At2g45180 PE=2 SV=2
AT1G59700	Q9XIF8	-0,747	0,002	cytosol	Glutathione S-transferase U16 OS=Arabidopsis thaliana GN=GSTU16 PE=2 SV=1
AT2G26740	Q42566	-0,734	0,001	cytosol	TsEOS=Arabidopsis thaliana GN=ATsEPE=2 SV=1
AT1G54000	Q1H583	-0,727	0,002	vacuole	GDSL esterase/lipase 22 OS=Arabidopsis thaliana GN=GLL22 PE=1 SV=1
AT1G12090	O65369	-0,724	0,002	extracellular	At1g12090/T28K15.14 OS=Arabidopsis thaliana GN=ELP PE=2 SV=1
AT4G15550**	O23406	-0,721	0,001	plastid	UDP-glycosyltransferase 75D1 OS=Arabidopsis thaliana GN=UGT75D1 PE=2 SV=2
AT4G27520	Q9T076	-0,636	0,001	plasma membrane	Early nodulin-like protein 2 OS=Arabidopsis thaliana GN=At4g27520 PE=1 SV=1
AT4G15490	O23401	-0,635	0,002	golgi,cytosol	UDP-glycosyltransferase 84A3 OS=Arabidopsis thaliana GN=UGT84A3 PE=1 SV=1
AT4G00165	Q8RW93	-0,617	0,003	extracellular	Putative lipid-binding protein At4g00165 OS=Arabidopsis thaliana GN=At4g00165 PE=2 SV=1
AT2G38380	P24102	-0,615	0,001	extracellular	Peroxidase 22 OS=Arabidopsis thaliana GN=PER22 PE=1 SV=2
AT3G08920	Q9SR92	-0,612	0,001	plastid	Rhodanese-like domain-containing protein 10 OS=Arabidopsis thaliana GN=STR10 PE=2 SV=1
AT1G78380	Q9ZRW8	-0,565	0,001	cytosol	Glutathione S-transferase U19 OS=Arabidopsis thaliana GN=GSTU19 PE=1 SV=1
AT1G71695	Q96520	-0,563	0,001	extracellular	Peroxidase 12 OS=Arabidopsis thaliana GN=PER12 PE=1 SV=1
AT2G10940	Q9SKI0	-0,563	0,001	vacuole	At2g10940/F15K19.1 OS=Arabidopsis thaliana GN=At2g10940 PE=2 SV=1
AT2G29450	P46421	-0,562	0,001	cytosol	Glutathione S-transferase U5 OS=Arabidopsis thaliana GN=GSTU5 PE=2 SV=1
AT4G22010	O65449	-0,559	0,004	extracellular	At4g22010 OS=Arabidopsis thaliana GN=sks4 PE=1 SV=1
AT4G19880	F4JU03	-0,541	0,001	plastid	Glutathione S-transferase family protein OS=Arabidopsis thaliana GN=At4g19880 PE=1 SV=1
AT4G22490	Q9SUX0	-0,54	0,002	extracellular	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein OS=Arabidopsis thaliana GN=At4g22490 PE=2 SV=1
AT4G27700	Q94A65	-0,539	0,001	plastid	Rhodanese-like domain-containing protein 14, chloroplastic OS=Arabidopsis thaliana GN=At4g27700 PE=2 SV=1
AT5G06060	Q9LHT0	-0,531	0,005	cytosol	Tropinone reductase homolog At5g06060 OS=Arabidopsis thaliana GN=At5g06060 PE=2 SV=1

AT1G08980**	Q9FR37	-0,503	0,001	cytosol	Amidase 1 OS=Arabidopsis thaliana GN=AMI1 PE=1 SV=1
AT3G12800	Q9LTV6	-0,494	0,003	peroxisome	Peroxisomal 2,4-dienoyl-CoA reductase OS=Arabidopsis thaliana GN=At3g12800 PE=2 SV=1
AT1G10360	Q9FUS9	-0,459	0,008	cytosol	Glutathione S-transferase U18 OS=Arabidopsis thaliana GN=GSTU18 PE=2 SV=1
AT4G22485	A8MRQ5	-0,457	0,005	extracellular	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein OS=Arabidopsis thaliana GN=At4g22485 PE=4 SV=2
AT1G09010	Q75W54	-0,444	0,008	vacuole	Mannosylglycoprotein endo-beta-mannosidase OS=Arabidopsis thaliana GN=EBM PE=1 SV=3
AT4G02520**	P46422	-0,442	0,001	cytosol	Glutathione S-transferase F2 OS=Arabidopsis thaliana GN=GSTF2 PE=1 SV=3
AT1G49670	F4I3C3	-0,439	0,003	peroxisome	RP protein (REF) OS=Arabidopsis thaliana GN=NQR PE=4 SV=1
AT3G26720	P94078	-0,429	0,004	extracellular	Alpha-mannosidase At3g26720 OS=Arabidopsis thaliana GN=At3g26720 PE=1 SV=1
AT5G42100	Q9FHX5	-0,417	0,006	extracellular	Glucan endo-1,3-beta-glucosidase 10 OS=Arabidopsis thaliana GN=At5g42100 PE=1 SV=1
AT5G41210	Q9ZRT5	-0,41	0,003	peroxisome	Glutathione S-transferase T1 OS=Arabidopsis thaliana GN=GSTT1 PE=2 SV=1
AT2G29260	Q9ZW12	-0,407	0,007	plastid	Tropinone reductase homolog At2g29260, chloroplastic OS=Arabidopsis thaliana GN=At2g29260 PE=2 SV=1
AT1G78830**	Q9ZVA2	-0,388	0,001	extracellular	EP1-like glycoprotein 2 OS=Arabidopsis thaliana GN=At1g78830 PE=1 SV=1
AT4G30140	Q9SZW7	-0,386	0,002	extracellular	GDSL esterase/lipase At4g30140 OS=Arabidopsis thaliana GN=At4g30140 PE=2 SV=1
AT1G02930	P42760	-0,381	0,007	cytosol	Glutathione S-transferase F6 OS=Arabidopsis thaliana GN=GSTF6 PE=2 SV=2
AT2G42220	O48529	-0,381	0,002	plastid	Rhodanese-like domain-containing protein 9, chloroplastic OS=Arabidopsis thaliana GN=STR9 PE=2 SV=1
AT3G18080	Q9LV33	-0,37	0,002	extracellular	Beta-glucosidase 44 OS=Arabidopsis thaliana GN=BGLU44 PE=2 SV=1
AT2G47730	Q96266	-0,365	0,001	plastid	Glutathione S-transferase F8, chloroplastic OS=Arabidopsis thaliana GN=GSTF8 PE=1 SV=3
AT5G13980	Q8LPJ3	-0,365	0,001	extracellular	Probable alpha-mannosidase At5g13980 OS=Arabidopsis thaliana GN=At5g13980 PE=2 SV=1
AT4G18970	Q93YW8	0,393	0,004	extracellular	GDSL esterase/lipase At4g18970 OS=Arabidopsis thaliana GN=At4g18970 PE=2 SV=1
AT1G29660**	Q9C7N5	0,449	0,001	extracellular	GDSL esterase/lipase At1g29660 OS=Arabidopsis thaliana GN=At1g29660 PE=1 SV=1
AT2g32520	A0A1P8AZN3	0,451	0,002	cytosol	Alpha/beta-Hydrolases superfamily protein OS=Arabidopsis thaliana GN=At2g32520 PE=4 SV=1
AT5G63840	Q9FN05	0,472	0,005	endoplasmic reticulum	Probable glucan 1,3-alpha-glucosidase OS=Arabidopsis thaliana GN=PSL5 PE=1 SV=1
AT2G30860	O80852	0,487	0,001	cytosol	Glutathione S-transferase F9 OS=Arabidopsis thaliana GN=GSTF9 PE=1 SV=1
AT1G78360	F4IA73	0,571	0,003	ısmic reticulum,plasma me	Glutathione S-transferase U21 OS=Arabidopsis thaliana GN=GSTU21 PE=3 SV=1
AT1G32550	Q9C7Y4	0,611	0,003	plastid	Ferredoxin OS=Arabidopsis thaliana GN=FdC2 PE=2 SV=1
AT5G03455	Q8GY31	0,626	0,003	mitochondrion	Dual specificity phosphatase Cdc25 OS=Arabidopsis thaliana GN=CDC25 PE=1 SV=1
AT4G14890	O23344	0,634	0,003	plastid	Ferredoxin OS=Arabidopsis thaliana GN=dl3485w PE=2 SV=1
AT3G22120	A0A1I9LSA3	0,667	0,001	tracellular,plasma membra	Cell wall-plasma membrane linker protein OS=Arabidopsis thaliana GN=CWLP PE=4 SV=1
AT4G11290	Q9SUT2	0,677	0,005	extracellular	Peroxidase 39 OS=Arabidopsis thaliana GN=PER39 PE=1 SV=1
AT5G19370	Q93WI0	0,684	0,001	plastid	Rhodanese-like/PpiC domain-containing protein 12, chloroplastic OS=Arabidopsis thaliana GN=At5g19370 PE=1 SV=1
AT4G21960	Q9SB81	1,202	0,001	extracellular	Peroxidase 42 OS=Arabidopsis thaliana GN=PER42 PE=1 SV=2
AT1G78370**	Q8L7C9	1,44	0,005	peroxisome	Glutathione S-transferase U20 OS=Arabidopsis thaliana GN=GSTU20 PE=1 SV=1
AT1G48750	Q94AQ3	1,761	0,001	extracellular	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein OS=Arabidopsis thaliana GN=At1g48750 PE=2 SV=1
Mitochondrial electron transport					
ATMG00160	P93285	-0,701	0,002	mitochondrion	Cytochrome c oxidase subunit 2 OS=Arabidopsis thaliana GN=COX2 PE=1 SV=2
ATMG01080	P60112	-0,7	0,002	mitochondrion	ATP synthase subunit 9, mitochondrial OS=Arabidopsis thaliana GN=ATP9 PE=2 SV=2
AT5G08740	Q8GXR9	-0,435	0,001	plastid,mitochondrion	Alternative NAD(P)H-ubiquinone oxidoreductase C1, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=NDC1 PE=1 SV=2
AT3G54110	O81845	-0,413	0,004	mitochondrion	Mitochondrial uncoupling protein 1 OS=Arabidopsis thaliana GN=PUMP1 PE=1 SV=1
AT3G52300	Q9FT52	0,356	0,001	mitochondrion	ATP synthase subunit d, mitochondrial OS=Arabidopsis thaliana GN=At3g52300 PE=1 SV=3
AT5G37510	Q9FGI6	0,369	0,001	mitochondrion	NADdehydrogenase [ubiquinone] iron-sulfur protein 1, mitochondrial OS=Arabidopsis thaliana GN=EMB1467 PE=1 SV=2
AT2G21870**	Q9SJ12	0,381	0,001	mitochondrion	Probable ATP synthase 24 kDa subunit, mitochondrial OS=Arabidopsis thaliana GN=At2g21870 PE=1 SV=1
AT5G67590	Q9FJW4	0,403	0,003	mitochondrion	NADdehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial OS=Arabidopsis thaliana GN=FRO1 PE=1 SV=1
AT1G47260	Q9C6B3	0,412	0,001	mitochondrion	Gamma carbonic anhydrase 2, mitochondrial OS=Arabidopsis thaliana GN=GAMMACA2 PE=1 SV=1
AT5G52840	Q9FLX7	0,423	0,001	mitochondrion	Probable NADdehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5, mitochondrial OS=Arabidopsis thaliana GN=At5g52840 PE=1 SV=1
AT5G66510	Q94AU7	0,426	0,003	mitochondrion	Gamma carbonic anhydrase 3, mitochondrial OS=Arabidopsis thaliana GN=GAMMACA3 PE=1 SV=1
AT1G22450	Q9S7L9	0,434	0,001	mitochondrion	Cytochrome c oxidase subunit 6b-1 OS=Arabidopsis thaliana GN=COX6B-1 PE=1 SV=1
AT3G15640	Q9LW15	0,469	0,005	mitochondrion	Cytochrome c oxidase subunit 5b-1, mitochondrial OS=Arabidopsis thaliana GN=COX5B-1 PE=1 SV=1
AT4G37830	Q9T070	0,864	0,002	mitochondrion	Cytochrome c oxidase subunit 6a, mitochondrial OS=Arabidopsis thaliana GN=COX6A PE=3 SV=1
N- metabolism					
AT5G07440	Q38946	-1,04	0,001	mitochondrion	Glutamate dehydrogenase 2 OS=Arabidopsis thaliana GN=GDH2 PE=1 SV=1
AT5G18170	Q43314	-0,579	0,002	mitochondrion	Glutamate dehydrogenase 1 OS=Arabidopsis thaliana GN=GDH1 PE=2 SV=1
AT5G57440	Q8VZP1	-0,577	0,003	mitochondrion	(DL)-glycerol-3-phosphatase 2 OS=Arabidopsis thaliana GN=GPP2 PE=1 SV=1
AT5G37600	Q56WN1	0,547	0,002	cytosol	Glutamine synthetase cytosolic isozyme 1-1 OS=Arabidopsis thaliana GN=GLN1-1 PE=1 SV=2
AT5G53460	Q9LV03	0,568	0,001	plastid	Glutamate synthase 1 [NADH], chloroplastic OS=Arabidopsis thaliana GN=GLT1 PE=1 SV=2
Nucleotide metabolism					
AT3G17810	Q9LVI9	-0,649	0,003	plastid	Dihydropyrimidine dehydrogenase (NADP(+)), chloroplastic OS=Arabidopsis thaliana GN=PYD1 PE=1 SV=1
AT2G37690	Q84TI2	-0,635	0,001	plastid	Phosphoribosylaminoimidazole carboxylase like protein OS=Arabidopsis thaliana GN=At2g37690 PE=2 SV=1
AT4G34740	Q9STG9	-0,567	0,002	plastid	Amidophosphoribosyltransferase 2, chloroplastic OS=Arabidopsis thaliana GN=ASE2 PE=1 SV=1

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AT3G46940	Q9STG6	-0,367	0,009	nucleus	Deoxyuridine 5'-triphosphate nucleotidohydrolase OS=Arabidopsis thaliana GN=DUT PE=1 SV=1
AT5G35170	Q8VYL1	-0,367	0,001	plastid	Adenylate kinase 5, chloroplastic OS=Arabidopsis thaliana GN=At5g35170 PE=1 SV=1
AT5G50370	Q9FK35	0,369	0,002	mitochondrion	Adenylate kinase 3 OS=Arabidopsis thaliana GN=ADK2 PE=1 SV=1
AT1G16350	Q9SA34	0,373	0,002	peroxisome	Inosine-5'-monophosphate dehydrogenase 2 OS=Arabidopsis thaliana GN=At1g16350 PE=1 SV=1
AT4G22570	Q9SUW2	0,463	0,006	cytosol	Adenine phosphoribosyltransferase 3 OS=Arabidopsis thaliana GN=APT3 PE=1 SV=1
AT5G63400	O82514	0,479	0,001	mitochondrion	Adenylate kinase 4 OS=Arabidopsis thaliana GN=ADK1 PE=1 SV=2
AT3G09820**	Q9SF85	0,597	0,003	cytosol	Adenosine kinase 1 OS=Arabidopsis thaliana GN=ADK1 PE=1 SV=1
AT2G18230	P21216	0,605	0,001	cytosol	Soluble inorganic pyrophosphatase 2 OS=Arabidopsis thaliana GN=PPA2 PE=2 SV=2
AT5G63980	Q42546	0,653	0,001	plastid	SAL1 phosphatase OS=Arabidopsis thaliana GN=SAL1 PE=1 SV=1
AT4G30530	Q9M0A7	0,703	0,001	cytosol	Gamma-glutamyl peptidase 1 OS=Arabidopsis thaliana GN=GGP1 PE=1 SV=1
AT5G26667	O04905	0,928	0,001	cytosol	UMP-CMP kinase 3 OS=Arabidopsis thaliana GN=UMK3 PE=1 SV=1
OPP					
AT4G05390	Q9M0V6	0,791	0,001	plastid	Ferredoxin--NADP reductase, root isozyme 1, chloroplastic OS=Arabidopsis thaliana GN=RFNR1 PE=2 SV=2
Polyamine metabolism					
AT1G70310	O48661	0,463	0,001	cytosol	Spermidine synthase 2 OS=Arabidopsis thaliana GN=SPDSYN2 PE=1 SV=2
Photosyntesis					
AT1G29930	P04778	-1,126	0,001	plastid	Chlorophyll a-b binding protein 1, chloroplastic OS=Arabidopsis thaliana GN=LHCB1.3 PE=1 SV=1
AT3G01500**	P27140	-1,122	0,001	plastid	Beta carbonic anhydrase 1, chloroplastic OS=Arabidopsis thaliana GN=BCA1 PE=1 SV=2
ATCG00700	P62113	-1,099	0,002	plastid	Protein PsbN OS=Arabidopsis thaliana GN=psbN PE=3 SV=1
AT5G02120	O81208	-0,989	0,001	plastid	Light-harvesting complex-like protein OHP1, chloroplastic OS=Arabidopsis thaliana GN=OHP1 PE=1 SV=1
AT2G05070	Q9S7J7	-0,91	0,002	plastid	Chlorophyll a-b binding protein 2.2, chloroplastic OS=Arabidopsis thaliana GN=LHCB2.2 PE=1 SV=1
AT2G05100	Q9SHR7	-0,9	0,002	plastid	Chlorophyll a-b binding protein 2.1, chloroplastic OS=Arabidopsis thaliana GN=LHCB2.1 PE=1 SV=1
AT5G38410	B3H5S2	-0,686	0,001	plastid	Ribulose bisphosphate carboxylase small chain OS=Arabidopsis thaliana GN=RBCS3B PE=3 SV=1
AT3G26650**	P25856	-0,662	0,001	plastid	Glyceraldehyde-3-phosphate dehydrogenase GAPA1, chloroplastic OS=Arabidopsis thaliana GN=GAPA1 PE=1 SV=3
AT5G14740**	P42737	-0,658	0,001	plastid	Isoform 2 of Beta carbonic anhydrase 2, chloroplastic OS=Arabidopsis thaliana GN=BCA2
AT2G34430**	Q39142	-0,653	0,001	plastid	Chlorophyll a-b binding protein, chloroplastic OS=Arabidopsis thaliana GN=Lhb1B1 PE=1 SV=1
AT1G34000	Q9FEC1	-0,633	0,001	plastid	Light-harvesting complex-like protein OHP2, chloroplastic OS=Arabidopsis thaliana GN=OHP2 PE=2 SV=1
ATCG00420	P56754	-0,627	0,004	plastid	NAD(P)H-quinone oxidoreductase subunit J, chloroplastic OS=Arabidopsis thaliana GN=ndhJ PE=3 SV=1
AT3G56650	Q9LXX5	-0,609	0,001	plastid	PsbP domain-containing protein 6, chloroplastic OS=Arabidopsis thaliana GN=PPD6 PE=1 SV=1
AT5G58260	Q9LVM2	-0,567	0,004	plastid	NAD(P)H-quinone oxidoreductase subunit N, chloroplastic OS=Arabidopsis thaliana GN=ndhN PE=2 SV=1
AT1G15820	Q9LMQ2	-0,554	0,001	plastid	Chlorophyll a-b binding protein, chloroplastic OS=Arabidopsis thaliana GN=CHLOROPHYLL PROTEIN 24 PE=1 SV=1
AT2G46820	Q8LCA1	-0,54	0,001	plastid	Protein CURVATURE THYLAKOID 1B, chloroplastic OS=Arabidopsis thaliana GN=CURT1B PE=1 SV=2
AT2G28605	Q8VY52	-0,536	0,002	plastid	PsbP domain-containing protein 2, chloroplastic OS=Arabidopsis thaliana GN=PPD2 PE=1 SV=1
AT2G06520	Q9SKI3	-0,528	0,005	plastid	Expressed protein OS=Arabidopsis thaliana GN=PSBX PE=1 SV=1
AT1G51400	Q9SYE2	-0,514	0,003	plastid	At1g51400/F5D21_10 OS=Arabidopsis thaliana GN=F11M15.26 PE=2 SV=1
AT4G10340	Q9XF89	-0,514	0,001	plastid	Chlorophyll a-b binding protein CP26, chloroplastic OS=Arabidopsis thaliana GN=LHCB5 PE=1 SV=1
AT2G40100	Q9S7W1	-0,509	0,002	plastid	Chlorophyll a-b binding protein CP29.3, chloroplastic OS=Arabidopsis thaliana GN=LHCB4.3 PE=2 SV=1
ATCG00540	P56771	-0,508	0	plastid	Cytochrome f OS=Arabidopsis thaliana GN=petA PE=3 SV=1
AT3G12780**	Q9LD57	-0,489	0,001	plastid	Phosphoglycerate kinase 1, chloroplastic OS=Arabidopsis thaliana GN=PGK1 PE=1 SV=1
AT5G01530	Q07473	-0,48	0,003	plastid	Chlorophyll a-b binding protein CP29.1, chloroplastic OS=Arabidopsis thaliana GN=LHCB4.1 PE=1 SV=1
AT5G54270	Q9S7M0	-0,479	0,001	plastid	Chlorophyll a-b binding protein 3, chloroplastic OS=Arabidopsis thaliana GN=LHCB3 PE=1 SV=1
AT2G26500**	O48717	-0,478	0,002	plastid	At2g26500 OS=Arabidopsis thaliana GN=At2g26500 PE=2 SV=1
AT2G45290	F4IW47	-0,469	0,001	plastid	Transketolase-2, chloroplastic OS=Arabidopsis thaliana GN=TKL-2 PE=1 SV=1
ATCG00630	P56769	-0,467	0,002	plastid	Photosystem I reaction center subunit IX OS=Arabidopsis thaliana GN=psaJ PE=3 SV=1
AT1G56190	P50318	-0,458	0,001	plastid	Phosphoglycerate kinase 2, chloroplastic OS=Arabidopsis thaliana GN=At1g56190 PE=1 SV=3
AT4G04640	Q01908	-0,453	0,001	plastid	ATP synthase gamma chain 1, chloroplastic OS=Arabidopsis thaliana GN=ATPC1 PE=1 SV=1
AT2G39730**	P10896	-0,449	0	plastid	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic OS=Arabidopsis thaliana GN=RCA PE=1 SV=2
ATCG00350	P56766	-0,432	0,002	plastid	Photosystem I P700 chlorophyll a apoprotein A1 OS=Arabidopsis thaliana GN=psA PE=2 SV=1
AT1G79040	P27202	-0,431	0,003	plastid	Photosystem II 10 kDa polypeptide, chloroplastic OS=Arabidopsis thaliana GN=PSBR PE=1 SV=1
ATCG00470	P09468	-0,429	0,001	plastid	ATP synthase epsilon chain, chloroplastic OS=Arabidopsis thaliana GN=atpE PE=1 SV=2
AT3G60750	Q8RWV0	-0,422	0,001	plastid	Transketolase-1, chloroplastic OS=Arabidopsis thaliana GN=TKL-1 PE=1 SV=1
ATCG00120	P56757	-0,422	0,001	plastid	ATP synthase subunit alpha, chloroplastic OS=Arabidopsis thaliana GN=atpA PE=1 SV=1
AT3G55330	P82538	-0,413	0,001	plastid	PsbP-like protein 1, chloroplastic OS=Arabidopsis thaliana GN=PPL1 PE=1 SV=1
AT1G20020	Q8W493	-0,405	0,001	plastid	Ferredoxin--NADP reductase, leaf isozyme 2, chloroplastic OS=Arabidopsis thaliana GN=LFNR2 PE=1 SV=1
ATCG01110	P56753	-0,395	0,002	plastid	NAD(P)H-quinone oxidoreductase subunit H, chloroplastic OS=Arabidopsis thaliana GN=ndhPE=1 SV=1
ATCG00560	P60129	-0,394	0,009	plastid	Photosystem II reaction center protein L OS=Arabidopsis thaliana GN=psbL PE=1 SV=1
ATCG00340	P56767	-0,392	0,002	plastid	Photosystem I P700 chlorophyll a apoprotein A2 OS=Arabidopsis thaliana GN=psaB PE=3 SV=1
AT1G55670	Q9S7N7	-0,389	0,004	plastid	Photosystem I reaction center subunit V, chloroplastic OS=Arabidopsis thaliana GN=PSAG PE=1 SV=1

ATCG00130	P56759	-0,377	0,001	plastid	ATP synthase subunit b, chloroplastic OS=Arabidopsis thaliana GN=atpF PE=3 SV=1
AT1G77090	O49292	-0,375	0,002	plastid	PsbP domain-containing protein 4, chloroplastic OS=Arabidopsis thaliana GN=PPD4 PE=1 SV=2
AT3G54890	Q01667	-0,367	0,001	plastid	Chlorophyll a-b binding protein 6, chloroplastic OS=Arabidopsis thaliana GN=LHCA1 PE=1 SV=1
AT1G44575	Q9XF91	-0,366	0,001	plastid	Photosystem II 22 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=PSBS PE=2 SV=1
ATCG00430	P56756	-0,366	0,006	plastid	NAD(P)H-quinone oxidoreductase subunit K, chloroplastic OS=Arabidopsis thaliana GN=ndhK PE=3 SV=1
AT4G32260	Q42139	-0,361	0,001	plastid	AT4g32260/F10M6_100 OS=Arabidopsis thaliana GN=PDE334 PE=1 SV=2
AT3G47470	P27521	-0,356	0,001	plastid	Chlorophyll a-b binding protein 4, chloroplastic OS=Arabidopsis thaliana GN=LHCA4 PE=1 SV=1
ATCG00710	P56780	0,449	0,002	plastid	Photosystem II reaction center protein OS=Arabidopsis thaliana GN=psbPE=1 SV=2
AT4G05180	Q41932	0,61	0,001	plastid	Oxygen-evolving enhancer protein 3-2, chloroplastic OS=Arabidopsis thaliana GN=PSBQ2 PE=1 SV=2
AT1G79530**	Q9SAJ6	0,708	0,001	plastid	Glyceraldehyde-3-phosphate dehydrogenase GAPCP1, chloroplastic OS=Arabidopsis thaliana GN=GAPCP1 PE=1 SV=1
AT3G52720	O04846	1,817	0,001	plastid	Alpha carbonic anhydrase 1, chloroplastic OS=Arabidopsis thaliana GN=ACA1 PE=1 SV=2
Protein					
AT5G65620	Q94AM1	-1,308	0,006	plastid	Organellar oligopeptidase A, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=OOP PE=1 SV=1
AT1G06430	Q8W585	-1,235	0,001	plastid	ATP-dependent zinc metalloprotease FTS8, chloroplastic OS=Arabidopsis thaliana GN=FTSH8 PE=1 SV=1
AT1G03220	Q9ZVS4	-1,17	0,001	extracellular	Eukaryotic aspartyl protease family protein OS=Arabidopsis thaliana GN=At1g03220 PE=2 SV=1
AT2G45740**	O80845	-1,155	0,001	peroxisome	Peroxisomal membrane protein 11D OS=Arabidopsis thaliana GN=PEX11D PE=1 SV=2
AT2G18710	Q38885	-1,097	0,002	plastid	Preprotein translocase subunit SCY1, chloroplastic OS=Arabidopsis thaliana GN=SCY1 PE=1 SV=2
AT1G65590	Q8L7S6	-1,026	0,001	tracellular,plasma membra	Beta-hexosaminidase 3 OS=Arabidopsis thaliana GN=HEXO3 PE=1 SV=1
ATCG00830	P56791	-1,014	0,001	plastid	50S ribosomal protein L2, chloroplastic OS=Arabidopsis thaliana GN=rpl2-A PE=3 SV=1
AT2G42810	Q84XU2	-1,008	0,009	nucleus,cytosol	Serine/threonine-protein phosphatase 5 OS=Arabidopsis thaliana GN=PAPP5 PE=1 SV=1
AT2G26140	O80983	-0,988	0,001	mitochondrion	ATP-dependent zinc metalloprotease FTS4, mitochondrial OS=Arabidopsis thaliana GN=FTSH4 PE=1 SV=2
AT2G41620	O22224	-0,985	0,001	nucleus	Nuclear pore complex protein NUP93A OS=Arabidopsis thaliana GN=NUP93A PE=1 SV=2
AT5G24490**	Q94K97	-0,914	0,001	plastid	30S ribosomal protein OS=Arabidopsis thaliana GN=At5g24490 PE=1 SV=1
AT4G36195	Q94CC6	-0,838	0,001	extracellular	Prolyl carboxypeptidase like protein OS=Arabidopsis thaliana GN=At4g36195 PE=2 SV=1
AT1G03230**	Q9ZVS5	-0,714	0,001	extracellular	Eukaryotic aspartyl protease family protein OS=Arabidopsis thaliana GN=At1g03230 PE=2 SV=1
AT5G43010	Q9SEI3	-0,699	0,002	nucleus,cytosol	26S proteasome regulatory subunit 10B homolog A OS=Arabidopsis thaliana GN=RPT4A PE=1 SV=1
AT4G04350	Q9XEA0	-0,665	0,003	plastid	Leucine--tRNA ligase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=EMB2369 PE=2 SV=1
AT5G47040**	O64948	-0,662	0,005	peroxisome	Lon protease homolog 2, peroxisomal OS=Arabidopsis thaliana GN=LON2 PE=2 SV=1
AT5G49030	Q8RXK8	-0,659	0,001	plastid	Isoleucine--tRNA ligase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=OVA2 PE=2 SV=1
AT1G50250	Q39102	-0,651	0,005	plastid	ATP-dependent zinc metalloprotease FTS1, chloroplastic OS=Arabidopsis thaliana GN=FTSH1 PE=1 SV=2
AT1G51930	Q6AWX4	-0,617	0,003	plasmic reticulum,extrace	reversed At1g51930 OS=Arabidopsis thaliana GN=At1g51930 PE=2 SV=1
AT3G11910	Q84WU2	-0,609	0,003	cytosol	Ubiquitin carboxyl-terminal hydrolase 13 OS=Arabidopsis thaliana GN=UBP13 PE=1 SV=1
AT5G47190	Q8RXX5	-0,602	0,002	plastid	50S ribosomal protein L19-2, chloroplastic OS=Arabidopsis thaliana GN=At5g47190 PE=2 SV=1
AT3G25800	Q38950	-0,598	0,002	cytosol	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Arabidopsis thaliana GN=PP2A2 PE=1 SV=2
AT1G67700	Q8LDL0	-0,588	0,001	plastid	Protein HHL1, chloroplastic OS=Arabidopsis thaliana GN=HHL1 PE=1 SV=1
AT4G17300	O48593	-0,585	0,002	plastid	Asparagine--tRNA ligase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=SYNO PE=2 SV=3
AT2G30950	O80860	-0,584	0,001	plastid	ATP-dependent zinc metalloprotease FTS2, chloroplastic OS=Arabidopsis thaliana GN=FTSH2 PE=1 SV=1
AT1G73990	Q9C9C0	-0,58	0,002	plastid	Serine protease SPPA, chloroplastic OS=Arabidopsis thaliana GN=SPPA PE=2 SV=1
AT2G33450	O22795	-0,564	0,007	plastid	50S ribosomal protein L28, chloroplastic OS=Arabidopsis thaliana GN=RPL28 PE=2 SV=2
AT4G26300	O23247	-0,556	0,002	plastid	Arginine--tRNA ligase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=EMB1027 PE=1 SV=1
AT5G37680	Q8W4C8	-0,556	0,004	plasma membrane	reversed ADP-ribosylation factor-like protein 8c OS=Arabidopsis thaliana GN=ARL8C PE=2 SV=1
AT3G17250	Q9LUU7	-0,553	0,004	mitochondrion	Probable protein phosphatase 2C 43 OS=Arabidopsis thaliana GN=At3g17250 PE=2 SV=1
AT1G47128**	P43297	-0,541	0,001	extracellular	Cysteine proteinase RD21A OS=Arabidopsis thaliana GN=RD21A PE=1 SV=1
AT3G10060	Q9SR70	-0,533	0,001	plastid	Peptidyl-prolyl cis-trans isomerase FKBP16-4, chloroplastic OS=Arabidopsis thaliana GN=FKBP16-4 PE=1 SV=1
AT2G24820	Q9SK50	-0,523	0,001	plastid	Protein TIC 55, chloroplastic OS=Arabidopsis thaliana GN=TIC55 PE=1 SV=1
AT4G03080	Q8L7U5	-0,523	0,005	nucleus	Serine/threonine-protein phosphatase BSL1 OS=Arabidopsis thaliana GN=BSL1 PE=1 SV=2
AT1g50380	A0A1P8ATN7	-0,517	0,005	cytosol	Prolyl oligopeptidase family protein OS=Arabidopsis thaliana GN=At1g50380 PE=4 SV=1
AT5G23120	O82660	-0,497	0,001	plastid	Photosystem II stability/assembly factor HCF136, chloroplastic OS=Arabidopsis thaliana GN=HCF136 PE=1 SV=1
AT2G34480	P51418	-0,486	0,002	cytosol	60S ribosomal protein L18a-2 OS=Arabidopsis thaliana GN=RPL18AB PE=1 SV=2
ATCG00790	P56793	-0,478	0,006	plastid	50S ribosomal protein L16, chloroplastic OS=Arabidopsis thaliana GN=rpl16 PE=3 SV=1
AT3G55260	A7WM73	-0,46	0,007	extracellular	Beta-hexosaminidase 1 OS=Arabidopsis thaliana GN=HEXO1 PE=1 SV=1
AT4G30690	Q94B52	-0,459	0,001	plastid	Translation initiation factor IF3-4, chloroplastic OS=Arabidopsis thaliana GN=IF3-4 PE=2 SV=1
ATCG00750	P56802	-0,456	0,002	plastid	30S ribosomal protein S11, chloroplastic OS=Arabidopsis thaliana GN=rps11 PE=3 SV=1
AT4G27690	Q9T091	-0,436	0,009	golgi	Vacuolar protein sorting-associated protein 26B OS=Arabidopsis thaliana GN=VPS26B PE=2 SV=2
AT2G25840	Q8RXE9	-0,432	0,009	plastid	Tryptophan--tRNA ligase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=OVA4 PE=1 SV=1
AT5G43970	Q9FNC9	-0,431	0,009	mitochondrion	Mitochondrial import receptor subunit TOM9-2 OS=Arabidopsis thaliana GN=TOM9-2 PE=1 SV=3
AT5G10360	P51430	-0,43	0,002	cytosol	40S ribosomal protein S6-2 OS=Arabidopsis thaliana GN=RPS6B PE=1 SV=3
AT3G62910	Q8RX79	-0,428	0,007	plastid	Peptide chain release factor APG3, chloroplastic OS=Arabidopsis thaliana GN=APG3 PE=2 SV=1
AT5G60160	Q9LST0	-0,425	0,003	vacuole	AT5g60160/f15I12_20 OS=Arabidopsis thaliana GN=At5g60160 PE=2 SV=1
AT1G21720	Q9XI05	-0,419	0,002	nucleus,cytosol	Proteasome subunit beta type-3-A OS=Arabidopsis thaliana GN=PBC1 PE=1 SV=2

AT5G43960	Q9FND0	-0,408	0,01	nucleus	AD20086.1 OS=Arabidopsis thaliana GN=MRH10.6 PE=1 SV=1
AT3G09630	Q9SF40	-0,403	0,002	cytosol	60S ribosomal protein L4-1 OS=Arabidopsis thaliana GN=RPL4A PE=1 SV=1
AT3G19760	Q94A52	-0,401	0,004	nucleus	Eukaryotic initiation factor 4A-III homolog OS=Arabidopsis thaliana GN=EIF4A3 PE=1 SV=2
AT4G20850	F4JVN6	-0,385	0,001	plastid	Tripeptidyl-peptidase 2 OS=Arabidopsis thaliana GN=TPP2 PE=1 SV=1
AT1G02560	Q9S834	-0,384	0,002	plastid	ATP-dependent Clp protease proteolytic subunit 5, chloroplastic OS=Arabidopsis thaliana GN=CLPP5 PE=1 SV=1
AT5G42270	Q9FH02	-0,384	0,001	plastid	ATP-dependent zinc metalloprotease FTSH 5, chloroplastic OS=Arabidopsis thaliana GN=FTSH5 PE=1 SV=1
AT1G09130	Q8L770	-0,374	0,002	plastid	ATP-dependent Clp protease proteolytic subunit-related protein 3, chloroplastic OS=Arabidopsis thaliana GN=CLPR3 PE=1 SV=1
AT1G58380	Q8L8Y0	-0,37	0,004	cytosol	40S ribosomal protein S2-1 OS=Arabidopsis thaliana GN=RPS2A PE=2 SV=2
AT2G43440	A8MS20	-0,368	0,01	cytosol	reversed F-box protein At2g43440 OS=Arabidopsis thaliana GN=At2g43440 PE=2 SV=1
AT2G22990**	Q8RUW5	-0,364	0,004	extracellular	Serine carboxypeptidase-like 8 OS=Arabidopsis thaliana GN=SCPL8 PE=1 SV=2
AT2G18190	F4IQG2	-0,36	0,009	plasma membrane	A-ATPase At2g18190 OS=Arabidopsis thaliana GN=At2g18190 PE=2 SV=1
AT4G12060	Q8GW78	-0,358	0,004	plastid	ATP-dependent Clp protease ATP-binding subunit CLPT2, chloroplastic OS=Arabidopsis thaliana GN=CLPT2 PE=1 SV=1
AT1G63770	Q8H0S9	-0,358	0,001	plastid	Puromycin-sensitive aminopeptidase OS=Arabidopsis thaliana GN=MPA1 PE=2 SV=1
AT1G02780	Q9SRX2	-0,356	0,005	cytosol	60S ribosomal protein L19-1 OS=Arabidopsis thaliana GN=RPL19A PE=2 SV=1
AT1G11750	Q9SAA2	-0,354	0,006	plastid	ATP-dependent Clp protease proteolytic subunit 6, chloroplastic OS=Arabidopsis thaliana GN=CLPP6 PE=1 SV=1
AT5G23210	Q0WPR4	-0,352	0,005	extracellular	Serine carboxypeptidase-like 34 OS=Arabidopsis thaliana GN=SCPL34 PE=2 SV=2
AT5G45390	Q94B60	-0,342	0,002	plastid	ATP-dependent Clp protease proteolytic subunit 4, chloroplastic OS=Arabidopsis thaliana GN=CLPP4 PE=1 SV=1
AT5G20720**	O65282	0,351	0,001	plastid	20 kDa chaperonin, chloroplastic OS=Arabidopsis thaliana GN=CPN20 PE=1 SV=2
AT1G14980**	P34893	0,353	0,002	mitochondrion	10 kDa chaperonin, mitochondrial OS=Arabidopsis thaliana GN=CPN10 PE=1 SV=1
AT2G04390	P49205	0,354	0,002	cytosol	40S ribosomal protein S17-1 OS=Arabidopsis thaliana GN=RPS17A PE=2 SV=3
AT5G20920	Q41969	0,363	0,01	cytosol	Eukaryotic translation initiation factor 2 subunit beta OS=Arabidopsis thaliana GN=EIF2B PE=1 SV=3
AT5G58290	Q9SEI4	0,363	0,003	nucleus,cytosol	26S proteasome regulatory subunit 6B homolog OS=Arabidopsis thaliana GN=RPT3 PE=1 SV=1
AT3G09500	Q9SF53	0,378	0,01	cytosol	60S ribosomal protein L35-1 OS=Arabidopsis thaliana GN=RPL35A PE=2 SV=1
AT3G46560	Q9XGX9	0,378	0,006	mitochondrion	Mitochondrial import inner membrane translocase subunit TIM9 OS=Arabidopsis thaliana GN=TIM9 PE=1 SV=2
AT3G51800	Q96327	0,378	0,001	nucleus	ERBB-3 BINDING PROTEIN 1 OS=Arabidopsis thaliana GN=EBP1 PE=1 SV=1
AT1G75350	Q9FWS4	0,38	0,001	plastid	50S ribosomal protein L31, chloroplastic OS=Arabidopsis thaliana GN=RPL31 PE=2 SV=1
AT1G27970	Q9C7F5	0,382	0,002	nucleus	Nuclear transport factor 2B OS=Arabidopsis thaliana GN=NTF2B PE=1 SV=1
AT3G08740	Q8VZW6	0,386	0,001	plastid	Elongation factor P (EF-P) family protein OS=Arabidopsis thaliana GN=At3g08740 PE=1 SV=1
AT2G27710**	Q9SLF7	0,387	0,002	cytosol	60S acidic ribosomal protein P2-2 OS=Arabidopsis thaliana GN=RPP2B PE=1 SV=1
AT5G17870	Q9FKP0	0,387	0,01	plastid	50S ribosomal protein 6, chloroplastic OS=Arabidopsis thaliana GN=PSRP6 PE=3 SV=1
AT1G61570	Q9XH48	0,389	0,007	mitochondrion	Mitochondrial import inner membrane translocase subunit TIM13 OS=Arabidopsis thaliana GN=TIM13 PE=1 SV=2
AT5G02240	Q94EG6	0,39	0,001	cytosol	Uncharacterized protein At5g02240 OS=Arabidopsis thaliana GN=At5g02240 PE=1 SV=1
AT4G16143	F4JL11	0,391	0,008	nucleus	Importin subunit alpha-2 OS=Arabidopsis thaliana GN=IMPA2 PE=1 SV=1
AT2G44650	O80504	0,392	0,007	plastid	10 kDa chaperonin 2, chloroplastic OS=Arabidopsis thaliana GN=CPN10-2 PE=2 SV=1
AT1G29990	Q2HIK4	0,394	0,001	cytosol	At1g29990 OS=Arabidopsis thaliana GN=PFD6 PE=2 SV=1
AT1G53850	O81149	0,394	0,008	nucleus,cytosol	Proteasome subunit alpha type-5-A OS=Arabidopsis thaliana GN=PAE1 PE=1 SV=1
AT2G36060	Q9SJ44	0,395	0,004	cytosol	Ubiquitin-conjugating enzyme E2 variant 1C OS=Arabidopsis thaliana GN=UEV1C PE=1 SV=1
AT3G56150	O49160	0,399	0,002	nucleus,cytosol	Eukaryotic translation initiation factor 3 subunit C OS=Arabidopsis thaliana GN=TIF3C1 PE=1 SV=2
AT5G20890	Q940P8	0,4	0,001	cytosol	T-complex protein 1 subunit beta OS=Arabidopsis thaliana GN=CCT2 PE=1 SV=1
AT1G48900	P49967	0,402	0,01	cytosol	Signal recognition particle 54 kDa protein 3 OS=Arabidopsis thaliana GN=SRP-54C PE=2 SV=2
AT3G55620	Q9M060	0,403	0,002	cytosol	Eukaryotic translation initiation factor 6-2 OS=Arabidopsis thaliana GN=EIF6-2 PE=2 SV=1
AT1G48350	Q9SX68	0,406	0,002	plastid	50S ribosomal protein L18, chloroplastic OS=Arabidopsis thaliana GN=RPL18 PE=2 SV=1
AT1G27420	Q9FZJ3	0,414	0,008	plastid	Putative F-box/kelch-repeat protein At1g27420 OS=Arabidopsis thaliana GN=At1g27420 PE=4 SV=2
AT5G54600	P92959	0,414	0,001	plastid	50S ribosomal protein L24, chloroplastic OS=Arabidopsis thaliana GN=RPL24 PE=2 SV=2
AT4G26720	P48529	0,415	0,009	cytosol	Serine/threonine-protein phosphatase PP-X isozyme 1 OS=Arabidopsis thaliana GN=PPX1 PE=1 SV=1
AT3G26400	Q9LIN5	0,416	0,007	cytosol	Eukaryotic translation initiation factor 4B1 OS=Arabidopsis thaliana GN=EIF4B1 PE=1 SV=1
AT5G55220	Q8S9L5	0,423	0,001	plastid	Trigger factor-like protein TIG, Chloroplastic OS=Arabidopsis thaliana GN=TIG PE=1 SV=1
AT2G30050	O64740	0,424	0,003	nucleus,cytosol	Protein transport protein SEC13 homolog B OS=Arabidopsis thaliana GN=SEC13B PE=1 SV=1
AT1G13690	Q0WRA3	0,427	0,003	nucleus	ATPase E1 OS=Arabidopsis thaliana GN=ATE1 PE=1 SV=1
AT2G28000**	P21238	0,428	0,001	plastid	Chaperonin 60 subunit alpha 1, chloroplastic OS=Arabidopsis thaliana GN=CPN60A1 PE=1 SV=2
AT3G56190	Q9SPE6	0,429	0,002	vacuole	Alpha-soluble NSF attachment protein 2 OS=Arabidopsis thaliana GN=ASNAP2 PE=1 SV=1
AT5G46210	Q8LGH4	0,431	0,006	cytosol	Cullin-4 OS=Arabidopsis thaliana GN=CUL4 PE=1 SV=1
AT5G27770	Q9FE58	0,433	0,003	cytosol	60S ribosomal protein L22-3 OS=Arabidopsis thaliana GN=RPL22C PE=2 SV=1
AT3G57810	Q8LBZ4	0,435	0,007	mitochondrion	OTU domain-containing protein At3g57810 OS=Arabidopsis thaliana GN=At3g57810 PE=2 SV=1
AT1G30230	P48006	0,438	0,005	cytosol	Elongation factor 1-delta 1 OS=Arabidopsis thaliana GN=At1g30230 PE=1 SV=2
AT1G50670	Q9LPT6	0,445	0,002	cytosol	F11F12.1 protein OS=Arabidopsis thaliana GN=F11F12.1 PE=1 SV=1
AT3G49910	P51414	0,457	0,001	cytosol	60S ribosomal protein L26-1 OS=Arabidopsis thaliana GN=RPL26A PE=2 SV=2
AT2G44120	P60039	0,458	0,002	cytosol	60S ribosomal protein L7-3 OS=Arabidopsis thaliana GN=RPL7C PE=2 SV=1
AT5G67360	O65351	0,459	0,001	extracellular	Subtilisin-like protease SBT1.7 OS=Arabidopsis thaliana GN=SBT1.7 PE=1 SV=1
AT1G01100**	Q8LCW9	0,462	0,001	cytosol	60S acidic ribosomal protein P1-1 OS=Arabidopsis thaliana GN=RPP1A PE=3 SV=2
AT1G13950	Q9XI91	0,463	0,006	cytosol	Eukaryotic translation initiation factor 5A-1 OS=Arabidopsis thaliana GN=ELF5A-1 PE=1 SV=1

AT3G22480	Q9LJ98	0,466	0,006	nucleus	Probable prefoldin subunit 2 OS=Arabidopsis thaliana GN=At3g22480 PE=2 SV=1
AT3G12390	Q9LHG9	0,469	0,002	nucleus	Nascent polypeptide-associated complex subunit alpha-like protein 1 OS=Arabidopsis thaliana GN=At3g12390 PE=1 SV=1
AT4G31700	O48549	0,469	0,005	cytosol	40S ribosomal protein S6-1 OS=Arabidopsis thaliana GN=RPS6A PE=1 SV=2
AT1G12310	Q94AZ4	0,474	0,002	cytosol	Probable calcium-binding protein CML13 OS=Arabidopsis thaliana GN=CML13 PE=2 SV=1
AT3G10090	Q9SR73	0,476	0,004	cytosol	40S ribosomal protein S28-1 OS=Arabidopsis thaliana GN=RPS28A PE=3 SV=1
AT4G04210	Q8RWU7	0,482	0,005	nucleus	Plant UBX domain-containing protein 4 OS=Arabidopsis thaliana GN=PUX4 PE=1 SV=1
AT5G40950	Q9FLN4	0,482	0,002	plastid	50S ribosomal protein L27, chloroplastic OS=Arabidopsis thaliana GN=RPL27 PE=2 SV=1
AT1G79340	O64517	0,493	0,001	cytosol	Metacaspase-4 OS=Arabidopsis thaliana GN=AMC4 PE=1 SV=1
AT3G27160	A0A1I9LRJ3	0,493	0,004	plastid	Ribosomal protein S21 family protein OS=Arabidopsis thaliana GN=GHS1 PE=3 SV=1
AT3G48870	Q9SXJ7	0,497	0,001	plastid	Chaperone protein ClpC2, chloroplastic OS=Arabidopsis thaliana GN=CLPC2 PE=1 SV=1
AT3G16480	O04308	0,5	0,001	mitochondrion	Probable mitochondrial-processing peptidase subunit alpha-2, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=MPPA2 PE=1 SV=1
AT3G14290	Q42134	0,501	0,003	nucleus,cytosol	Proteasome subunit alpha type-5-B OS=Arabidopsis thaliana GN=PAE2 PE=1 SV=2
AT2G27720	P51407	0,503	0,002	cytosol	60S acidic ribosomal protein P2-1 OS=Arabidopsis thaliana GN=RPP2A PE=3 SV=2
AT2G19730	O82204	0,506	0,004	cytosol	60S ribosomal protein L28-1 OS=Arabidopsis thaliana GN=RPL28A PE=1 SV=1
AT5G36170	Q9LVY0	0,507	0,002	plastid	Peptide chain release factor PrfB1, chloroplastic OS=Arabidopsis thaliana GN=PRFB1 PE=2 SV=1
AT3G02560	Q9M885	0,508	0,004	cytosol	40S ribosomal protein S7-2 OS=Arabidopsis thaliana GN=RPS7B PE=2 SV=1
AT4G00810**	O23095	0,509	0,001	cytosol	60S acidic ribosomal protein P1-2 OS=Arabidopsis thaliana GN=RPP1B PE=1 SV=2
AT5G47930**	Q8L953	0,51	0,002	cytosol	40S ribosomal protein S27-3 OS=Arabidopsis thaliana GN=RPS27D PE=2 SV=2
AT5G48760	Q9FKC0	0,51	0,004	cytosol	60S ribosomal protein L13a-4 OS=Arabidopsis thaliana GN=RPL13AD PE=2 SV=1
AT5G57290	Q9LVC9	0,511	0,002	cytosol	60S acidic ribosomal protein P3-2 OS=Arabidopsis thaliana GN=RPP3B PE=2 SV=1
AT3G05530	Q9SEI2	0,516	0,001	nucleus,cytosol	26S proteasome regulatory subunit 6A homolog A OS=Arabidopsis thaliana GN=RPT5A PE=1 SV=1
AT3G07110	Q9SFU1	0,518	0,001	cytosol	60S ribosomal protein L13a-1 OS=Arabidopsis thaliana GN=RPL13A PE=2 SV=1
AT3G11400	F4J6A1	0,529	0,001	cytosol	Eukaryotic translation initiation factor 3 subunit G OS=Arabidopsis thaliana GN=EIF3G1 PE=3 SV=1
AT2G20630	Q9SIU8	0,537	0,001	cytosol	Probable protein phosphatase 2C 20 OS=Arabidopsis thaliana GN=PPC3-1.2 PE=1 SV=3
AT2G24200	P30184	0,545	0,001	cytosol	Leucine aminopeptidase 1 OS=Arabidopsis thaliana GN=LAP1 PE=1 SV=1
AT2G27600	Q9ZNT0	0,545	0,002	cytosol	Protein SUPPRESSOR OF K(+) TRANSPORT GROWDEFECT 1 OS=Arabidopsis thaliana GN=SKD1 PE=1 SV=1
AT1G55490	P21240	0,547	0,001	plastid	Chaperonin 60 subunit beta 1, chloroplastic OS=Arabidopsis thaliana GN=CPN60B1 PE=1 SV=3
AT5G28060	Q8LC83	0,548	0,008	cytosol	40S ribosomal protein S24-2 OS=Arabidopsis thaliana GN=RPS24B PE=2 SV=2
AT1G04850	Q9MAT3	0,554	0,004	nucleus	F13M7.16 protein OS=Arabidopsis thaliana GN=At1g04850 PE=2 SV=1
AT2G18110	Q9SI20	0,562	0,002	cytosol	Elongation factor 1-delta 2 OS=Arabidopsis thaliana GN=At2g18110 PE=1 SV=1
AT1G15930	Q9S9P1	0,573	0,002	cytosol	40S ribosomal protein S12-1 OS=Arabidopsis thaliana GN=RPS12A PE=2 SV=1
AT5G53140	Q94AT1	0,573	0,002	mitochondrion	Probable protein phosphatase 2C 76 OS=Arabidopsis thaliana GN=At5g53140 PE=2 SV=1
AT4G26840	P55852	0,587	0,001	nucleus	Small ubiquitin-related modifier 1 OS=Arabidopsis thaliana GN=SUMO1 PE=1 SV=2
AT1G14400	P25865	0,588	0,003	nucleus	Ubiquitin-conjugating enzyme E2 1 OS=Arabidopsis thaliana GN=UBC1 PE=1 SV=1
AT5G64350	Q8LGG0	0,59	0,001	cytosol	Peptidyl-prolyl cis-trans isomerase FKBP12 OS=Arabidopsis thaliana GN=FKBP12 PE=1 SV=2
AT1G51690	Q38821	0,601	0,004	nucleus	Serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Arabidopsis thaliana GN=PP2AB1 PE=1 SV=2
AT2G19750	P49689	0,603	0,003	nucleus,cytosol	40S ribosomal protein S30 OS=Arabidopsis thaliana GN=RPS30A PE=3 SV=3
AT5G35680	F4K1D3	0,605	0,002	cytosol	Nucleic acid-binding, OB-fold-like protein OS=Arabidopsis thaliana GN=MXH1.2 PE=3 SV=1
AT1G23100**	Q8LDC9	0,613	0,002	mitochondrion	GroES-like family protein OS=Arabidopsis thaliana GN=At1g23100 PE=2 SV=1
AT3G45030	P49200	0,613	0,001	cytosol	40S ribosomal protein S20-1 OS=Arabidopsis thaliana GN=RPS20A PE=2 SV=2
AT5G47700**	Q8LEQ0	0,617	0,001	cytosol	60S acidic ribosomal protein P1-3 OS=Arabidopsis thaliana GN=RPP1C PE=1 SV=2
AT5G37475	Q8GRX2	0,624	0,002	cytosol	Eukaryotic translation initiation factor 3 subunit J OS=Arabidopsis thaliana GN=At5g37475 PE=1 SV=1
AT2G17190	Q9SII9	0,63	0,002	nucleus	Ubiquitin domain-containing protein DSK2a OS=Arabidopsis thaliana GN=DSK2A PE=1 SV=2
AT2G32850	Q8H0Z0	0,633	0,003	nucleus	Protein kinase superfamily protein OS=Arabidopsis thaliana GN=At2g32850 PE=2 SV=1
AT5G19510	Q9SCX3	0,635	0,001	cytosol	Elongation factor 1-beta 2 OS=Arabidopsis thaliana GN=At5g19510 PE=1 SV=1
AT4G18100	P49211	0,646	0,002	cytosol	60S ribosomal protein L32-1 OS=Arabidopsis thaliana GN=RPL32A PE=2 SV=2
AT3G13470	Q9LJE4	0,648	0,001	plastid	Chaperonin 60 subunit beta 2, chloroplastic OS=Arabidopsis thaliana GN=CPN60B2 PE=1 SV=1
AT5G20290	Q93VG5	0,655	0,001	nucleus,cytosol	40S ribosomal protein S8-1 OS=Arabidopsis thaliana GN=RPS8A PE=1 SV=1
AT5G54940	Q9FFT6	0,66	0,003	cytosol	AT5g54940/MBG8_21 OS=Arabidopsis thaliana GN=MBG8.21 PE=2 SV=1
AT1G75950	Q39255	0,661	0,001	cytosol	SKP1-like protein 1A OS=Arabidopsis thaliana GN=SKP1A PE=1 SV=1
AT3G62940	Q9LYC7	0,661	0,003	nucleus	Cysteine proteinases superfamily protein OS=Arabidopsis thaliana GN=T20O10_40 PE=2 SV=1
AT4G01940	Q93W77	0,663	0,001	plastid	NifU-like protein 1, chloroplastic OS=Arabidopsis thaliana GN=NIFU1 PE=1 SV=1
AT5G54760	Q9FFV1	0,664	0,003	cytosol	At5g54760 OS=Arabidopsis thaliana GN=MBG8.2 PE=1 SV=1
AT1G26630	Q93VP3	0,683	0,001	cytosol	Eukaryotic translation initiation factor 5A-2 OS=Arabidopsis thaliana GN=ELF5A-2 PE=1 SV=1
AT5G56500**	C0Z361	0,684	0,002	plastid	Chaperonin 60 subunit beta 3, chloroplastic OS=Arabidopsis thaliana GN=CPN60B3 PE=1 SV=1
AT3G47370	Q9STY6	0,691	0,001	cytosol	40S ribosomal protein S20-2 OS=Arabidopsis thaliana GN=RPS20B PE=2 SV=1
AT2G46290	F4II66	0,693	0,001	cytosol	Eukaryotic translation initiation factor 3 subunit I OS=Arabidopsis thaliana GN=At2g46290 PE=3 SV=1
AT3G53890	Q9M337	0,693	0,001	cytosol	40S ribosomal protein S21-1 OS=Arabidopsis thaliana GN=RPS21B PE=1 SV=1
AT5G64140	P34789	0,696	0,002	cytosol	40S ribosomal protein S28-2 OS=Arabidopsis thaliana GN=RPS28C PE=3 SV=1
AT2G32060**	Q9SKZ3	0,708	0,009	cytosol	40S ribosomal protein S12-2 OS=Arabidopsis thaliana GN=RPS12C PE=1 SV=1
AT2G05920	Q9ZUF6	0,713	0,001	extracellular	Subtilisin-like protease SBT1.8 OS=Arabidopsis thaliana GN=SBT1.8 PE=1 SV=1

AT2G21270	A8MQW3	0,717	0,002	cytosol	AT2G21270 protein OS=Arabidopsis thaliana GN=UFD1 PE=2 SV=1
AT2G29530**	Q9ZW33	0,722	0,003	mitochondrion	Mitochondrial import inner membrane translocase subunit TIM10 OS=Arabidopsis thaliana GN=TIM10 PE=1 SV=1
AT2G40660	Q93VB0	0,722	0,001	cytosol	Nucleic acid-binding, OB-fold-like protein OS=Arabidopsis thaliana GN=At2g40660 PE=2 SV=1
AT2G30410	O04350	0,793	0,007	cytosol	Tubulin-folding cofactor A OS=Arabidopsis thaliana GN=TFCA PE=1 SV=2
AT5G12110**	Q84WM9	0,796	0,001	cytosol	Elongation factor 1-beta 1 OS=Arabidopsis thaliana GN=At5g12110 PE=2 SV=2
AT2G04160	Q9ZSP5	0,815	0,002	extracellular	Subtilisin-like protease SBT5.3 OS=Arabidopsis thaliana GN=AIR3 PE=2 SV=1
AT1G13270	Q9FV52	0,829	0,001	plastid	Methionine aminopeptidase 1B, chloroplastic OS=Arabidopsis thaliana GN=MAP1B PE=2 SV=2
AT5G20160	F4K455	0,884	0,002	nucleus	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein OS=Arabidopsis thaliana GN=At5g20160 PE=4 SV=1
AT4G15410	Q7Y175	0,9	0,002	nucleus	Plant UBX domain-containing protein 5 OS=Arabidopsis thaliana GN=PUX5 PE=1 SV=1
AT4G10480	Q9SZY1	0,915	0,001	cytosol	Nascent polypeptide-associated complex subunit alpha-like protein 4 OS=Arabidopsis thaliana GN=At4g10480 PE=1 SV=1
AT3G44590**	Q9LXM8	0,927	0,001	cytosol	60S acidic ribosomal protein P2-4 OS=Arabidopsis thaliana GN=RPP2D PE=3 SV=1
AT2G39460	Q8LD46	0,941	0,001	cytosol	60S ribosomal protein L23a-1 OS=Arabidopsis thaliana GN=RPL23A PE=2 SV=2
AT5G56710	P51420	0,945	0,002	cytosol	60S ribosomal protein L31-3 OS=Arabidopsis thaliana GN=RPL31C PE=3 SV=2
AT2G47110	P59232	1,028	0,001	cytosol	Ubiquitin-40S ribosomal protein S27a-2 OS=Arabidopsis thaliana GN=RPS27AB PE=2 SV=2
AT4G25890**	Q9SVZ6	1,124	0,001	cytosol	60S acidic ribosomal protein P3-1 OS=Arabidopsis thaliana GN=RPP3A PE=3 SV=1
AT1G33040	Q8LGC6	1,159	0,001	nucleus	Nascent polypeptide-associated complex subunit alpha-like protein 5 OS=Arabidopsis thaliana GN=At1g33040 PE=2 SV=2
AT5G08260	Q9LEY1	1,225	0,001	extracellular	Serine carboxypeptidase-like 35 OS=Arabidopsis thaliana GN=SCPL35 PE=2 SV=1
AT3G60210	Q9M1C2	1,583	0,001	plastid	10 kDa chaperonin 1, chloroplastic OS=Arabidopsis thaliana GN=CPN10-1 PE=2 SV=1
AT2G36070	Q5XF06	2,52	0,001	mitochondrion	Mitochondrial import inner membrane translocase subunit TIM44-2 OS=Arabidopsis thaliana GN=TIM44-2 PE=1 SV=1
Redox metabolism					
AT4G35090**	P25819	-1,621	0,001	peroxisome	Catalase-2 OS=Arabidopsis thaliana GN=CAT2 PE=1 SV=3
AT1G45145	Q39241	-1,073	0,001	cytosol	Thioredoxin H5 OS=Arabidopsis thaliana GN=TRX5 PE=1 SV=1
AT2G25080**	P52032	-0,928	0,001	plastid	Phospholipid hydroperoxide glutathione peroxidase 1, chloroplastic OS=Arabidopsis thaliana GN=GPX1 PE=2 SV=2
AT2G31570	O04922	-0,697	0,001	cytosol	Probable glutathione peroxidase 2 OS=Arabidopsis thaliana GN=GPX2 PE=1 SV=1
AT4G35000	Q42564	-0,675	0,001	peroxisome	L-ascorbate peroxidase 3 OS=Arabidopsis thaliana GN=APX3 PE=1 SV=1
AT4G11600	O48646	-0,587	0,001	mitochondrion	Probable phospholipid hydroperoxide glutathione peroxidase 6, mitochondrial OS=Arabidopsis thaliana GN=GPX6 PE=2 SV=2
AT2G28190**	O78310	-0,561	0,009	plastid	Superoxide dismutase [Cu-Zn] 2, chloroplastic OS=Arabidopsis thaliana GN=CSD2 PE=1 SV=2
AT5G28840	Q93VR3	-0,554	0,001	cytosol	GDP-mannose 3,5-epimerase OS=Arabidopsis thaliana GN=At5g28840 PE=1 SV=1
AT5G37830	Q9FIZ7	-0,498	0,001	cytosol	5-oxoprolinase OS=Arabidopsis thaliana GN=OXP1 PE=1 SV=1
AT1G20630**	Q96528	-0,452	0,006	peroxisome	Catalase-1 OS=Arabidopsis thaliana GN=CAT1 PE=1 SV=3
AT3G54660	P42770	-0,438	0,001	plastid	Glutathione reductase, chloroplastic OS=Arabidopsis thaliana GN=EMB2360 PE=2 SV=1
AT4G03520	Q9SEU8	0,351	0,003	plastid	Thioredoxin M2, chloroplastic OS=Arabidopsis thaliana GN=TRXM2 PE=1 SV=2
AT2G17420	Q39242	0,361	0,007	plastid	Thioredoxin reductase 2 OS=Arabidopsis thaliana GN=NTR2 PE=2 SV=2
AT1G19570**	Q9FWR4	0,369	0,001	peroxisome	Glutathione S-transferase DHAR1, mitochondrial OS=Arabidopsis thaliana GN=DHAR1 PE=1 SV=1
AT3G06050	Q9M7T0	0,371	0,001	mitochondrion	Peroxiredoxin-2F, mitochondrial OS=Arabidopsis thaliana GN=PRXIIF PE=1 SV=2
AT1G65980	Q9XEX2	0,386	0,001	cytosol	Peroxiredoxin-2B OS=Arabidopsis thaliana GN=PRXIIB PE=1 SV=1
AT3G48890	Q9M2Z4	0,389	0,004	endoplasmic reticulum	Membrane steroid-binding protein 2 OS=Arabidopsis thaliana GN=MSBP2 PE=1 SV=1
AT5G20080	P83291	0,411	0,001	mitochondrion	NADH-cytochrome b5 reductase-like protein OS=Arabidopsis thaliana GN=CBR2 PE=1 SV=2
AT3G15360	Q9SEU6	0,455	0,001	plastid	Thioredoxin M4, chloroplastic OS=Arabidopsis thaliana GN=TRXM4 PE=2 SV=2
AT2G24940	Q9SK39	0,462	0,001	nucleus	Probable steroid-binding protein 3 OS=Arabidopsis thaliana GN=MP3 PE=1 SV=1
AT3G02730	Q9XFH8	0,484	0,001	plastid	Thioredoxin F1, chloroplastic OS=Arabidopsis thaliana GN=At3g02730 PE=1 SV=2
AT3G15660	Q8LBK6	0,487	0,001	mitochondrion	Monothiol glutaredoxin-S15, mitochondrial OS=Arabidopsis thaliana GN=GRXS15 PE=1 SV=2
AT1G20620	Q42547	0,565	0,004	peroxisome	Catalase-3 OS=Arabidopsis thaliana GN=CAT3 PE=1 SV=3
AT5G60640	Q9FF55	0,589	0,001	endoplasmic reticulum	Protein disulfide isomerase-like 1-4 OS=Arabidopsis thaliana GN=PDIL1-4 PE=1 SV=1
AT2G47470	O22263	0,641	0,001	endoplasmic reticulum	Protein disulfide-isomerase like 2-1 OS=Arabidopsis thaliana GN=PDIL2-1 PE=2 SV=1
AT1G77510	Q9SRG3	0,67	0,001	endoplasmic reticulum	Protein disulfide isomerase-like 1-2 OS=Arabidopsis thaliana GN=PDIL1-2 PE=2 SV=1
AT1G21750	Q9XI01	0,727	0,001	endoplasmic reticulum	Protein disulfide isomerase-like 1-1 OS=Arabidopsis thaliana GN=PDIL1-1 PE=1 SV=1
AT5G20500	Q8LFQ6	0,781	0,001	vacuole	Glutaredoxin-C4 OS=Arabidopsis thaliana GN=GRXC4 PE=2 SV=2
AT3G54960	Q8VX13	0,788	0,002	endoplasmic reticulum	Protein disulfide isomerase-like 1-3 OS=Arabidopsis thaliana GN=PDIL1-3 PE=2 SV=1
AT1G07960	Q8GYD1	0,882	0,002	extracellular	Protein disulfide-isomerase 5-1 OS=Arabidopsis thaliana GN=PDIL5-1 PE=2 SV=1
AT2G16060**	O24520	1,506	0,001	cytosol	Non-symbiotic hemoglobin 1 OS=Arabidopsis thaliana GN=AHB1 PE=1 SV=1
RNA					
AT3G61260	Q9M2D8	-1,34	0,001	plasma membrane	Uncharacterized protein At3g61260 OS=Arabidopsis thaliana GN=At3g61260 PE=1 SV=1
AT3G15790	Q9LW00	-1,271	0,004	nucleus	Methyl-CpG-binding domain-containing protein 11 OS=Arabidopsis thaliana GN=MBD11 PE=1 SV=1
AT3G07670	Q9S7D2	-1,014	0,002	plastid	Putative ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I OS=Arabidopsis thaliana GN=F17A17.1 PE=1 SV=1
AT1G34410	Q9C8N9	-0,541	0,004	nucleus	reversed Putative auxin response factor 21 OS=Arabidopsis thaliana GN=ARF21 PE=3 SV=2
AT1G55970	Q9LG11	-0,505	0,005	nucleus	reversed Histone acetyltransferase HAC4 OS=Arabidopsis thaliana GN=HAC4 PE=2 SV=2
AT1G76010	Q93VA8	-0,399	0,004	nucleus	Alba DNA/RNA-binding protein OS=Arabidopsis thaliana GN=At1g76010 PE=2 SV=1
AT1G15340	Q9XI36	-0,363	0,002	nucleus	Methyl-CpG-binding domain-containing protein 10 OS=Arabidopsis thaliana GN=MBD10 PE=1 SV=1

AT5G14260	Q8VZB5	-0,354	0,001	plastid	Rubisco methyltransferase family protein OS=Arabidopsis thaliana GN=At5g14260 PE=1 SV=1
AT3G20390	Q94JQ4	0,354	0,001	plastid	Reactive Intermediate Deaminase A, chloroplastic OS=Arabidopsis thaliana GN=RIDA PE=1 SV=1
AT2G34640	F4IHY7	0,363	0,004	plastid	Protein PLASTID TRANSCRIPTIONALLY ACTIVE 12/HEMERA, chloroplastic OS=Arabidopsis thaliana GN=PTAC12 PE=1 SV=1
AT4G29160	Q9SZE4	0,364	0,004	nucleus	Vacuolar protein sorting-associated protein 32 homolog 2 OS=Arabidopsis thaliana GN=VPS32.2 PE=1 SV=1
AT1G47500	Q9SX80	0,389	0,008	nucleus	Polyadenylate-binding protein RBP47C' OS=Arabidopsis thaliana GN=RBP47C' PE=2 SV=1
AT4G24770	Q04836	0,391	0,001	plastid	31 kDa ribonucleoprotein, chloroplastic OS=Arabidopsis thaliana GN=CP31A PE=1 SV=1
AT3G26420	Q9LIN3	0,392	0,007	nucleus	Glycine-ricRNA-binding protein RZ1A OS=Arabidopsis thaliana GN=RZ1A PE=1 SV=1
AT3G52380	Q39061	0,399	0,001	plastid	RNA-binding protein CP33, chloroplastic OS=Arabidopsis thaliana GN=CP33 PE=2 SV=1
AT1G65700	Q8VYI0	0,404	0,004	nucleus	Sm-like protein LSM8 OS=Arabidopsis thaliana GN=LSM8 PE=1 SV=1
AT2G06530	Q9SKI2	0,41	0,008	golgi	Vacuolar protein sorting-associated protein 2 homolog 1 OS=Arabidopsis thaliana GN=VPS2.1 PE=1 SV=2
AT4G27000	Q93W34	0,441	0,003	nucleus	Polyadenylate-binding protein RBP45C OS=Arabidopsis thaliana GN=RBP45C PE=2 SV=1
AT2G15430	Q39211	0,449	0,006	nucleus	DNA-directed RNA polymerases II, IV and V subunit 3 OS=Arabidopsis thaliana GN=NRPB3 PE=1 SV=1
AT1G60650	O22703	0,456	0,007	nucleus	Glycine-ricRNA-binding protein RZ1B OS=Arabidopsis thaliana GN=RZ1B PE=2 SV=1
AT5G23290	P57742	0,456	0,003	cytosol	Probable prefoldin subunit 5 OS=Arabidopsis thaliana GN=At5g23290 PE=2 SV=1
AT2G29570	Q9ZW35	0,458	0,003	nucleus	Proliferating cell nuclear antigen 2 OS=Arabidopsis thaliana GN=PCNA2 PE=1 SV=1
AT5G07350	Q8VZG7	0,471	0,001	nucleus	Ribonuclease TUDOR 1 OS=Arabidopsis thaliana GN=TSN1 PE=1 SV=1
ATCG00170	P56764	0,473	0,006	plastid	DNA-directed RNA polymerase subunit beta'' OS=Arabidopsis thaliana GN=rpoC2 PE=3 SV=1
AT4G04830	Q9ZS91	0,479	0,003	cytosol	Peptide methionine sulfoxide reductase B5 OS=Arabidopsis thaliana GN=MSRB5 PE=1 SV=1
AT1G49760	Q9FXA2	0,484	0,001	cytosol	Polyadenylate-binding protein 8 OS=Arabidopsis thaliana GN=PAB8 PE=1 SV=1
AT3G05060	Q9MAB3	0,486	0,003	nucleus	Probable nucleolar protein 5-2 OS=Arabidopsis thaliana GN=NOP5-2 PE=1 SV=1
AT2G23350**	O22173	0,488	0,001	cytosol	Polyadenylate-binding protein 4 OS=Arabidopsis thaliana GN=PAB4 PE=1 SV=1
AT5G47210	Q9LVT8	0,495	0,001	nucleus	RGG repeats nuclear RNA binding protein C OS=Arabidopsis thaliana GN=RGGC PE=1 SV=1
AT2G33410	O22791	0,498	0,002	nucleus	Putative RNA-binding protein OS=Arabidopsis thaliana GN=At2g33410 PE=2 SV=1
AT4G16830	O23523	0,524	0,002	cytosol	RGG repeats nuclear RNA binding protein A OS=Arabidopsis thaliana GN=RGGA PE=1 SV=1
AT1G17880	Q9SMW7	0,543	0,001	nucleus	Basic transcription factor 3 OS=Arabidopsis thaliana GN=BTF3 PE=1 SV=1
AT4G35570	O49597	0,549	0,007	nucleus	Higmobility group B protein 5 OS=Arabidopsis thaliana GN=HMGB5 PE=2 SV=1
AT3G53340	Q67XJ2	0,552	0,004	nucleus	Nuclear transcription factor Y subunit B-10 OS=Arabidopsis thaliana GN=NFYB10 PE=1 SV=1
AT2G33845	Q8RYC3	0,559	0,003	nucleus	Expressed protein OS=Arabidopsis thaliana GN=At2g33845 PE=2 SV=1
AT1G60000	Q9ZUJ3	0,566	0,002	plastid	AT1G60000 protein OS=Arabidopsis thaliana GN=At1g60000 PE=2 SV=1
AT2G19830	O82197	0,568	0,003	golgi	Vacuolar protein sorting-associated protein 32 homolog 1 OS=Arabidopsis thaliana GN=VPS32.1 PE=1 SV=1
AT1G68730	Q9S7X9	0,58	0,003	plastid	F24J5.3 OS=Arabidopsis thaliana GN=F14K14.16 PE=2 SV=1
AT4G17520	O23593	0,595	0,001	nucleus	RGG repeats nuclear RNA binding protein B OS=Arabidopsis thaliana GN=RGGB PE=1 SV=1
AT1G26761	Q93ZE3	0,608	0,003	plastid	Arabinanase/levansucrase/invertase OS=Arabidopsis thaliana GN=At1g26761 PE=2 SV=1
AT4G14300	Q8W034	0,618	0,001	nucleus	Heterogeneous nuclear ribonucleoprotein 1 OS=Arabidopsis thaliana GN=RNP1 PE=1 SV=1
AT1G17680	Q8GUP0	0,621	0,003	nucleus	Tetratricopeptide repeat (TPR)-containing protein OS=Arabidopsis thaliana GN=At1g17680 PE=2 SV=1
AT1G77640	Q9CAP4	0,633	0,003	plastid	Ethylene-responsive transcription factor ERF013 OS=Arabidopsis thaliana GN=ERF013 PE=2 SV=1
AT5G19350	Q8VXZ9	0,633	0,003	cytosol	Polyadenylate-binding protein RBP47B' OS=Arabidopsis thaliana GN=RBP47B' PE=2 SV=1
AT2G21660	Q03250	0,676	0,001	nucleus	Glycine-ricRNA-binding protein 7 OS=Arabidopsis thaliana GN=RBG7 PE=1 SV=1
AT1G74230	Q9C909	0,678	0,002	mitochondrion	Glycine-ricRNA-binding protein 5, mitochondrial OS=Arabidopsis thaliana GN=RBG5 PE=1 SV=1
AT1G10200	Q94JX5	0,713	0,002	cytosol	LIM domain-containing protein WLIM1 OS=Arabidopsis thaliana GN=WLIM1 PE=1 SV=1
AT2G03870	Q9SI54	0,727	0,002	cytosol	Sm-like protein LSM7 OS=Arabidopsis thaliana GN=LSM7 PE=1 SV=1
AT4G34110	P42731	0,749	0,002	nucleus	Polyadenylate-binding protein 2 OS=Arabidopsis thaliana GN=PAB2 PE=1 SV=1
AT3G03920	Q8VZT0	0,755	0,002	nucleus	Putative H/ACA ribonucleoprotein complex subunit 1-like protein 1 OS=Arabidopsis thaliana GN=At3g03920 PE=2 SV=1
AT2G20490	Q93XX8	0,756	0,001	nucleus	H/ACA ribonucleoprotein complex subunit 3-like protein OS=Arabidopsis thaliana GN=At2g20490 PE=3 SV=2
AT5G61780	Q9FLT0	0,761	0,001	nucleus	Ribonuclease TUDOR 2 OS=Arabidopsis thaliana GN=TSN2 PE=1 SV=1
AT4G13850	Q9SVM8	0,784	0,001	mitochondrion	Glycine-ricRNA-binding protein 2, mitochondrial OS=Arabidopsis thaliana GN=RBG2 PE=1 SV=1
AT1G02080	F4HVV6	0,809	0,003	golgi	Transcription regulator OS=Arabidopsis thaliana GN=At1g02080 PE=4 SV=1
AT5G54900	Q9FPJ8	0,824	0,001	nucleus	Polyadenylate-binding protein RBP45A OS=Arabidopsis thaliana GN=RBP45A PE=2 SV=1
AT3G07810	F4JFN7	0,903	0,002	nucleus	RNA-binding (RRM/RBD/RNP motifs) family protein OS=Arabidopsis thaliana GN=At3g07810 PE=1 SV=1
AT5G61030	Q9FNR1	0,925	0,001	mitochondrion	Glycine-ricRNA-binding protein 3, mitochondrial OS=Arabidopsis thaliana GN=RBG3 PE=1 SV=1
AT3G53460	Q43349	0,927	0,001	plastid	29 kDa ribonucleoprotein, chloroplastic OS=Arabidopsis thaliana GN=CP29A PE=2 SV=2
AT1G73230	Q9CAT7	0,935	0,001	nucleus	Nascent polypeptide-associated complex subunit beta OS=Arabidopsis thaliana GN=At1g73230 PE=2 SV=1
AT2G20280	Q9SK74	1,027	0,001	nucleus	Zinc finger CCCdomain-containing protein 21 OS=Arabidopsis thaliana GN=At2g20280 PE=4 SV=1
AT1G49600	F4I3B3	1,03	0,002	nucleus	Polyadenylate-binding protein RBP47A OS=Arabidopsis thaliana GN=RBP47A PE=2 SV=1
AT5G46420	Q9FHG3	1,96	0,001	plastid	16S rRNA processing protein RimM family OS=Arabidopsis thaliana GN=At5g46420 PE=3 SV=1
S-assimilation					
AT1G19920	Q43870	0,583	0,001	plastid	ATP sulfurylase 2 OS=Arabidopsis thaliana GN=APS2 PE=1 SV=1
AT3G22890	Q9LIK9	0,992	0,001	plastid,cytosol	ATP sulfurylase 1, chloroplastic OS=Arabidopsis thaliana GN=APS1 PE=1 SV=1
AT4G14680**	O23324	1,112	0,001	plastid	ATP-sulfurylase 3, chloroplastic OS=Arabidopsis thaliana GN=APS3 PE=1 SV=1
AT2G14750**	Q43295	1,28	0,001	plastid	Adenylyl-sulfate kinase 1, chloroplastic OS=Arabidopsis thaliana GN=APK1 PE=1 SV=1

Secondary metabolism					
AT1G72680**	Q9CAI3	-1,458	0,001	cytosol	Probable cinnamyl alcohol dehydrogenase 1 OS=Arabidopsis thaliana GN=CAD1 PE=2 SV=1
AT1G57770	Q9FVR9	-0,778	0,001	plastid	FAD/NAD(P)-binding oxidoreductase family protein OS=Arabidopsis thaliana GN=At1g57770 PE=2 SV=1
AT2G29290**	Q9ZW13	-0,738	0,002	plasma membrane,golgi	Tropinone reductase homolog At2g29290 OS=Arabidopsis thaliana GN=At2g29290 PE=2 SV=1
AT3G63520	O65572	-0,652	0,001	vacuole	Carotenoid 9,10(9',10')-cleavage dioxygenase 1 OS=Arabidopsis thaliana GN=CCD1 PE=1 SV=2
AT2G25450**	Q9SKK4	-0,623	0,001	golgi	Probable 2-oxoacid dependent dioxygenase OS=Arabidopsis thaliana GN=GSL-OPE=2 SV=1
AT4G32770	Q94FY7	-0,602	0,001	plastid	Tocopherol cyclase, chloroplastic OS=Arabidopsis thaliana GN=VTE1 PE=1 SV=1
AT1G17050	Q76FS5	-0,57	0,002	plastid	Solanesyl diphosphate synthase 2, chloroplastic OS=Arabidopsis thaliana GN=SPS2 PE=1 SV=1
AT4G05160	Q9M0X9	-0,549	0,004	peroxisome	4-coumarate--CoA ligase-like 7 OS=Arabidopsis thaliana GN=4CLL7 PE=1 SV=1
AT5G25980	Q9C5C2	-0,464	0,001	extracellular	Myrosinase 2 OS=Arabidopsis thaliana GN=TGG2 PE=1 SV=1
AT1G54010	Q8W4H8	-0,448	0,001	vacuole	Inactive GDSL esterase/lipase-like protein 23 OS=Arabidopsis thaliana GN=GLL23 PE=1 SV=1
AT2G29340	F4IKM1	-0,417	0,002	cytosol	Tropinone reductase homolog At2g29340 OS=Arabidopsis thaliana GN=At2g29340 PE=2 SV=1
AT3G19450	P48523	-0,4	0,001	cytosol	Cinnamyl alcohol dehydrogenase 4 OS=Arabidopsis thaliana GN=CAD4 PE=1 SV=1
AT1G08550**	Q39249	-0,36	0,002	plastid	Violaxanthin de-epoxidase, chloroplastic OS=Arabidopsis thaliana GN=VDE1 PE=1 SV=1
AT5G26000	P37702	-0,356	0,01	peroxisome	Myrosinase 1 OS=Arabidopsis thaliana GN=TGG1 PE=1 SV=1
AT4G15560	Q38854	0,357	0,01	plastid	1-deoxy-D-xylulose-5-phosphate synthase, chloroplastic OS=Arabidopsis thaliana GN=DXS PE=1 SV=2
AT5G62790	Q9XFS9	0,36	0,002	plastid	1-deoxy-D-xylulose 5-phosphate reductoisomerase, chloroplastic OS=Arabidopsis thaliana GN=DXR PE=2 SV=2
AT1G74470	Q9CA67	0,36	0,002	plastid	Geranylgeranyl diphosphate reductase, chloroplastic OS=Arabidopsis thaliana GN=CHLP PE=1 SV=1
AT1G74090**	Q9C9C9	0,363	0,009	cytosol	Cytosolic sulfotransferase 18 OS=Arabidopsis thaliana GN=SOT18 PE=1 SV=1
AT4G34350	Q94B35	0,409	0,001	plastid	4-hydroxy-3-methylbut-2-enyl diphosphate reductase, chloroplastic OS=Arabidopsis thaliana GN=ISPH/ISPPE/HDR=2 SV=1
AT5G16440	Q38929	0,511	0,003	plastid	Isopentenyl-diphosphate Delta-isomerase I, chloroplastic OS=Arabidopsis thaliana GN=IPP1/IDI1 PE=2 SV=3
AT5G57030	Q38932	0,521	0,005	plastid	Lycopene epsilon cyclase, chloroplastic OS=Arabidopsis thaliana GN=LUT2 PE=1 SV=2
AT4G34050	O49499	0,543	0,001	cytosol	Caffeoyl-CoA O-methyltransferase 1 OS=Arabidopsis thaliana GN=CCOAOMT1 PE=1 SV=1
AT4G11820	P54873	0,546	0,002	cytosol	Hydroxymethylglutaryl-CoA synthase OS=Arabidopsis thaliana GN=HMGS PE=1 SV=2
AT4G39980	P29976	0,601	0,003	plastid	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic OS=Arabidopsis thaliana GN=DHS1 PE=2 SV=2
AT3G51240**	Q9S818	0,615	0,001	cytosol	Naringenin,2-oxoglutarate 3-dioxygenase OS=Arabidopsis thaliana GN=F3PE=1 SV=1
AT1G74100	Q9C9D0	0,745	0,002	cytosol	Cytosolic sulfotransferase 16 OS=Arabidopsis thaliana GN=SOT16 PE=1 SV=1
AT2G31790	Q9SKC1	0,811	0,001	mitochondrion	UDP-glycosyltransferase 74C1 OS=Arabidopsis thaliana GN=UGT74C1 PE=2 SV=1
AT4G33510	Q00218	0,853	0,001	plastid	Phospho-2-dehydro-3-deoxyheptonate aldolase 2, chloroplastic OS=Arabidopsis thaliana GN=DHS2 PE=2 SV=2
AT2G37040**	P35510	0,914	0,001	cytosol	Phenylalanine ammonia-lyase 1 OS=Arabidopsis thaliana GN=PAL1 PE=1 SV=3
AT4G13430	Q94AR8	0,964	0,001	plastid	3-isopropylmalate dehydratase large subunit, chloroplastic OS=Arabidopsis thaliana GN=IIL1 PE=1 SV=1
AT5G08640**	Q96330	0,987	0,001	peroxisome	Flavonol synthase/flavanone 3-hydroxylase OS=Arabidopsis thaliana GN=FLS1 PE=1 SV=1
AT3G14210**	Q9LJG3	1,004	0,001	vacuole	GDSL esterase/lipase ESM1 OS=Arabidopsis thaliana GN=ESM1 PE=1 SV=1
AT1G80560	P93832	1,03	0,001	plastid	3-isopropylmalate dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=IMDH2 PE=1 SV=1
AT5G23010**	Q9FG67	1,031	0,001	plastid	Methylthioalkylmalate synthase 1, chloroplastic OS=Arabidopsis thaliana GN=MAM1 PE=1 SV=1
AT2G20610	Q9SIV0	1,06	0,001	cytosol	S-alkyl-thiohydroximate lyase SUR1 OS=Arabidopsis thaliana GN=SUR1 PE=1 SV=1
AT5G13930**	P13114	2,302	0,001	endoplasmic reticulum	Chalcone synthase OS=Arabidopsis thaliana GN=CHS PE=1 SV=1
AT3G58990**	Q9LYT7	2,992	0,001	plastid	3-isopropylmalate dehydratase small subunit 2 OS=Arabidopsis thaliana GN=IPMI1 PE=1 SV=1
AT2G43100**	Q9ZW84	3,008	0,001	plastid	3-isopropylmalate dehydratase small subunit 1 OS=Arabidopsis thaliana GN=IPMI2 PE=1 SV=1
Signalling					
AT5G09440**	Q9FY71	-1,827	0,001	extracellular	Protein EXORDIUM-like 4 OS=Arabidopsis thaliana GN=EXL4 PE=2 SV=1
AT3G22060	Q9LRJ9	-1,229	0,001	extracellular	Cysteine-ricrepeat secretory protein 38 OS=Arabidopsis thaliana GN=CRRSP38 PE=2 SV=1
AT3G48530	Q8LBB2	-1,131	0,008	cytosol	SNF1-related protein kinase regulatory subunit gamma-1 OS=Arabidopsis thaliana GN=KING1 PE=1 SV=2
AT2G33380	O22788	-0,853	0,006	cytosol	Probable peroxygenase 3 OS=Arabidopsis thaliana GN=PXG3 PE=1 SV=1
AT4G02080	O04834	-0,845	0,003	plasma membrane	GTP-binding protein SAR1A OS=Arabidopsis thaliana GN=SAR1A PE=2 SV=1
AT4G18130	P42498	-0,751	0,008	nucleus	Phytochrome E OS=Arabidopsis thaliana GN=PHYE PE=1 SV=2
AT4G20260	Q96262	-0,588	0,001	plasma membrane	Plasma membrane-associated cation-binding protein 1 OS=Arabidopsis thaliana GN=PCAP1 PE=1 SV=1
AT1G49340	Q9SXA1	-0,475	0,005	plasma membrane	Phosphatidylinositol 4-kinase alpha 1 OS=Arabidopsis thaliana GN=PI4KA1 PE=1 SV=2
AT1G52280	Q9C820	-0,447	0,007	sma membrane,golgi,vacu	Ras-related protein RABG3d OS=Arabidopsis thaliana GN=RABG3D PE=2 SV=1
AT4G18810	F4JRN8	-0,431	0,001	plastid	NAD(P)-binding Rossmann-fold superfamily protein OS=Arabidopsis thaliana GN=At4g18810 PE=4 SV=1
AT5G65430	P48348	-0,356	0,001	nucleus	14-3-3-like protein GF14 kappa OS=Arabidopsis thaliana GN=GRF8 PE=1 SV=2
AT1G07140	Q9LMK7	0,379	0,002	cytosol	Ran-binding protein 1 homolog a OS=Arabidopsis thaliana GN=RANBP1A PE=1 SV=1
AT5G38480	P42644	0,384	0,002	cytosol	14-3-3-like protein GF14 psi OS=Arabidopsis thaliana GN=GRF3 PE=1 SV=2
AT1G22300**	P48347	0,42	0,001	cytosol	14-3-3-like protein GF14 epsilon OS=Arabidopsis thaliana GN=GRF10 PE=1 SV=1
AT2G30060	Q8RWG8	0,45	0,005	nucleus	Ran-binding protein 1 homolog b OS=Arabidopsis thaliana GN=RANBP1B PE=1 SV=2
AT5G61790	P29402	0,513	0,004	endoplasmic reticulum	Calnexin homolog 1 OS=Arabidopsis thaliana GN=CNX1 PE=1 SV=1
AT5G58590	P92985	0,629	0,003	nucleus	Ran-binding protein 1 homolog c OS=Arabidopsis thaliana GN=RANBP1C PE=2 SV=1
AT5G56360	Q9FM96	0,648	0,009	endoplasmic reticulum	Glucosidase 2 subunit beta OS=Arabidopsis thaliana GN=PSL4 PE=2 SV=1
AT1G48630	Q9C4Z6	0,652	0,001	cytosol	Receptor for activated C kinase 1B OS=Arabidopsis thaliana GN=RACK1B PE=1 SV=1

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AT4G09000	P42643	0,677	0,003	cytosol	14-3-3-like protein GF14 chi OS=Arabidopsis thaliana GN=GRF1 PE=1 SV=3
AT5G19320	Q9M651	0,688	0,003	nucleus,cytosol	RAN GTPase-activating protein 2 OS=Arabidopsis thaliana GN=RANGAP2 PE=1 SV=2
AT1G09210	Q38858	0,785	0,001	endoplasmic reticulum	Calreticulin-2 OS=Arabidopsis thaliana GN=CRT2 PE=1 SV=3
AT1G56340	O04151	0,886	0,001	endoplasmic reticulum	Calreticulin-1 OS=Arabidopsis thaliana GN=CRT1 PE=1 SV=1
AT3G15680	Q9LW11	1,264	0,001	nucleus	At3g15680 OS=Arabidopsis thaliana GN=At3g15680 PE=2 SV=1
Stress					
AT2G36800**	Q9ZQ94	-1,614	0,001	plasma membrane	UDP-glycosyltransferase 73C5 OS=Arabidopsis thaliana GN=UGT73C5 PE=2 SV=1
AT2G43620	O22841	-1,123	0,001	extracellular	Endochitinase At2g43620 OS=Arabidopsis thaliana GN=At2g43620 PE=3 SV=1
AT1G72610**	P94040	-1,005	0,001	extracellular	Germin-like protein subfamily 3 member 1 OS=Arabidopsis thaliana GN=GLP1 PE=1 SV=1
AT2G43590	O24658	-0,981	0,002	extracellular	Endochitinase At2g43590 OS=Arabidopsis thaliana GN=At2g43590 PE=2 SV=1
AT3G25760	Q9LS03	-0,959	0,001	plastid	Allene oxide cyclase 1, chloroplastic OS=Arabidopsis thaliana GN=AOC1 PE=1 SV=1
AT1G23130	O49304	-0,954	0,001	cytosol	At1g23130/T26J12_10 OS=Arabidopsis thaliana GN=At1g23130 PE=2 SV=1
AT2G42540	Q42512	-0,868	0,001	plastid	Protein COLD-REGULATED 15A, chloroplastic OS=Arabidopsis thaliana GN=COR15A PE=1 SV=1
AT1G30360**	Q9C8G5	-0,8	0,001	plasma membrane	CSC1-like protein ERD4 OS=Arabidopsis thaliana GN=ERD4 PE=2 SV=1
AT1g33590	A0A1P8AWX	-0,674	0,001	extracellular	Leucine-ricrepeat (LRR) family protein OS=Arabidopsis thaliana GN=At1g33590 PE=4 SV=1
AT4G02100	Q84VX5	-0,661	0,002	nucleus	reversed At4g02100 OS=Arabidopsis thaliana GN=At4g02100 PE=2 SV=1
AT1G17860	Q9LMU2	-0,651	0,001	extracellular	Kunitz trypsin inhibitor 2 OS=Arabidopsis thaliana GN=KTI2 PE=2 SV=1
AT1G09560	P94014	-0,649	0,003	extracellular	Germin-like protein subfamily 2 member 1 OS=Arabidopsis thaliana GN=GLP4 PE=2 SV=2
AT5G20630**	P94072	-0,628	0,001	extracellular	Germin-like protein subfamily 3 member 3 OS=Arabidopsis thaliana GN=GER3 PE=1 SV=1
AT3G25070	Q8GYN5	-0,574	0,004	plasma membrane	RPM1-interacting protein 4 OS=Arabidopsis thaliana GN=RIN4 PE=1 SV=1
AT4G37000	Q8LDU4	-0,562	0,001	plastid	Red chlorophyll catabolite reductase, chloroplastic OS=Arabidopsis thaliana GN=RCCR PE=1 SV=2
AT3G12580	Q9LHA8	-0,534	0,001	cytosol	Probable mediator of RNA polymerase II transcription subunit 37c OS=Arabidopsis thaliana GN=MED37C PE=1 SV=1
AT5G52640	P27323	-0,465	0,003	cytosol	Heat shock protein 90-1 OS=Arabidopsis thaliana GN=HSP90-1 PE=1 SV=3
AT5G21430	Q84VQ4	-0,411	0,002	plastid	NAD(P)H-quinone oxidoreductase subunit U, chloroplastic OS=Arabidopsis thaliana GN=ndhU PE=1 SV=1
AT2G47710	O82240	-0,374	0,004	cytosol	Adenine nucleotide alpha hydrolases-like superfamily protein OS=Arabidopsis thaliana GN=At2g47710 PE=2 SV=1
AT5G54430	Q8VYN9	0,353	0,002	cytosol	Universal stress protein PHOS32 OS=Arabidopsis thaliana GN=PHOS32 PE=1 SV=1
AT1G20440	P31168	0,371	0,009	nucleus	Dehydrin COR47 OS=Arabidopsis thaliana GN=COR47 PE=1 SV=2
AT5G39730	Q9FIX1	0,382	0,004	cytosol	AIG2-like protein B OS=Arabidopsis thaliana GN=AIG2LB PE=1 SV=1
AT1G75310	A0A1P8AND	0,383	0,009	nucleus	reversed Auxin-like 1 protein OS=Arabidopsis thaliana GN=AUL1 PE=4 SV=1
AT4G23670	Q9SUR0	0,391	0,001	cytosol	AT4G23670 protein OS=Arabidopsis thaliana GN=At4g23670 PE=2 SV=1
AT3G18165	Q949S9	0,394	0,008	nucleus	Pre-mRNA-splicing factor SPF27 homolog OS=Arabidopsis thaliana GN=MOS4 PE=1 SV=1
AT3G15700	Q9LW09	0,412	0,009	cytosol	Putative disease resistance protein At3g15700 OS=Arabidopsis thaliana GN=At3g15700 PE=3 SV=1
AT1G33950	Q9C8V2	0,414	0,01	nucleus	reversed Immune-associated nucleotide-binding protein 7 OS=Arabidopsis thaliana GN=IAN7 PE=2 SV=1
AT3G17210	Q9LUV2	0,427	0,001	cytosol	Stress-response A/B barrel domain-containing protein HS1 OS=Arabidopsis thaliana GN=HS1 PE=1 SV=1
AT5G02500	P22953	0,447	0,001	cytosol	Probable mediator of RNA polymerase II transcription subunit 37e OS=Arabidopsis thaliana GN=MED37E PE=1 SV=3
AT4G36020	O65639	0,461	0,002	nucleus	Cold shock protein 1 OS=Arabidopsis thaliana GN=CSP1 PE=1 SV=1
AT4G16660	F4JMJ1	0,471	0,001	endoplasmic reticulum	Heat shock 70 kDa protein 17 OS=Arabidopsis thaliana GN=HSP70-17 PE=2 SV=1
AT1G54410	Q9SLJ2	0,49	0,005	cytosol	Dehydrin HIRD11 OS=Arabidopsis thaliana GN=HIRD11 PE=1 SV=1
AT1G14930	Q96274	0,5	0,004	cytosol	AMajor latex homologue type2 OS=Arabidopsis thaliana GN=MLP2 PE=2 SV=1
AT1G70840	Q941R6	0,525	0,004	cytosol	MLP-like protein 31 OS=Arabidopsis thaliana GN=MLP31 PE=2 SV=2
AT3G28940	Q9MBH2	0,536	0,001	cytosol	Protein AIG2 B OS=Arabidopsis thaliana GN=AIG2B PE=2 SV=1
AT1G70890	Q9SSK5	0,552	0,002	peroxisome	MLP-like protein 43 OS=Arabidopsis thaliana GN=MLP43 PE=1 SV=1
AT4G37910	Q8GUM2	0,563	0,001	mitochondrion	Heat shock 70 kDa protein 9, mitochondrial OS=Arabidopsis thaliana GN=HSP70-9 PE=1 SV=1
AT4G24190	Q9STX5	0,567	0,001	endoplasmic reticulum	Endoplasmin homolog OS=Arabidopsis thaliana GN=HSP90-7 PE=1 SV=1
AT4G00860	Q38842	0,569	0,004	mitochondrion	protein OS=Arabidopsis thaliana GN=ATOZI1 PE=2 SV=1
AT1G62740	Q5XEP2	0,6	0,001	nucleus	Hsp70-Hsp90 organizing protein 2 OS=Arabidopsis thaliana GN=HOP2 PE=1 SV=1
AT5G28540	Q9LKR3	0,713	0,001	endoplasmic reticulum	Mediator of RNA polymerase II transcription subunit 37a OS=Arabidopsis thaliana GN=MED37A PE=1 SV=1
AT1G76180	P42763	0,794	0,001	peroxisome	Dehydrin ERD14 OS=Arabidopsis thaliana GN=ERD14 PE=1 SV=1
AT1G28290	Q9FZA2	0,8	0,001	extracellular	Non-classical arabinogalactan protein 31 OS=Arabidopsis thaliana GN=AGP31 PE=1 SV=1
AT5G42020	Q39043	0,823	0,002	endoplasmic reticulum	Mediator of RNA polymerase II transcription subunit 37f OS=Arabidopsis thaliana GN=MED37F PE=1 SV=2
AT5G55530	Q5HZ03	0,902	0,005	nucleus	At5g55530 OS=Arabidopsis thaliana GN=MTE17.25 PE=1 SV=1
AT1G20450	P42759	0,917	0,001	plasma membrane,cytosol	Dehydrin ERD10 OS=Arabidopsis thaliana GN=ERD10 PE=1 SV=1
AT1G24020**	Q93VR4	1,148	0,001	golgi	MLP-like protein 423 OS=Arabidopsis thaliana GN=MLP423 PE=2 SV=1
AT1G70830	Q9SSK9	1,66	0,001	golgi	MLP-like protein 28 OS=Arabidopsis thaliana GN=MLP28 PE=1 SV=1
TCA/org transformation					
AT4G35830	Q42560	-0,745	0,001	mitochondrion,cytosol	Aconitate hydratase 1 OS=Arabidopsis thaliana GN=ACO1 PE=1 SV=2
AT1G09430	O80526	-0,67	0,001	cytosol	ATP-citrate synthase alpha chain protein 3 OS=Arabidopsis thaliana GN=ACLA-3 PE=2 SV=1
AT3G13930	Q8RWN9	0,373	0,001	mitochondrion	Dihydrolipoyllysine-residue acetyltransferase component 2 of pyruvate dehydrogenase complex, mitochondrial OS=Arabidopsis thaliana GN=At3g13930 PE=1 SV=2
AT5G08300	P68209	0,382	0,003	mitochondrion	Succinate--CoA ligase [ADP-forming] subunit alpha-1, mitochondrial OS=Arabidopsis thaliana GN=At5g08300 PE=1 SV=1

AT1G54220	Q5M729	0,427	0,008	mitochondrion	Dihydrolipoyllysine-residue acetyltransferase component 3 of pyruvate dehydrogenase complex, mitochondrial OS=Arabidopsis thaliana GN=At1g54220 PE=1 SV=1
AT1G10670	Q9SGY2	0,474	0,003	cytosol	ATP-citrate synthase alpha chain protein 1 OS=Arabidopsis thaliana GN=ACLA-1 PE=1 SV=1
AT1G04410	P93819	0,596	0,001	vacuole	Malate dehydrogenase 1, cytoplasmic OS=Arabidopsis thaliana GN=MDH1 PE=1 SV=2
AT5G40650	Q8LB02	0,604	0,001	mitochondrion	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit 2, mitochondrial OS=Arabidopsis thaliana GN=SDH2-2 PE=1 SV=2
AT5G43330	P57106	0,855	0,001	cytosol	Malate dehydrogenase 2, cytoplasmic OS=Arabidopsis thaliana GN=MDH2 PE=1 SV=1
Tetrapyrrole synthesis					
AT4G25080	Q9SW18	0,355	0,001	plastid	Magnesium protoporphyrin IX methyltransferase, chloroplastic OS=Arabidopsis thaliana GN=CHLM PE=1 SV=1
AT1G03475	Q9LR75	0,359	0,001	plastid	Coproporphyrinogen-III oxidase 1, chloroplastic OS=Arabidopsis thaliana GN=CPX1 PE=2 SV=1
AT3G48730	Q42522	0,374	0,002	plastid	Glutamate-1-semialdehyde 2,1-aminomutase 2, chloroplastic OS=Arabidopsis thaliana GN=GSA2 PE=2 SV=2
AT3G56940	Q9M591	0,421	0,001	plastid	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplastic OS=Arabidopsis thaliana GN=CRD1 PE=1 SV=2
AT4G18480	P16127	0,468	0,001	plastid	Magnesium-chelatase subunit ChlI-1, chloroplastic OS=Arabidopsis thaliana GN=CHLI1 PE=1 SV=1
AT5G08280	Q43316	0,47	0,001	plastid	Porphobilinogen deaminase, chloroplastic OS=Arabidopsis thaliana GN=HEMC PE=1 SV=1
AT3G59400	Q9LX31	0,512	0,005	plastid	Tetrapyrrole-binding protein, chloroplastic OS=Arabidopsis thaliana GN=GUN4 PE=1 SV=1
AT5G13630	Q9FNB0	0,646	0,001	plastid	Magnesium-chelatase subunit ChlH, chloroplastic OS=Arabidopsis thaliana GN=CHLPE/GUN5=1 SV=1
AT5G45930	Q5XF33	0,677	0,001	plastid	Magnesium-chelatase subunit ChlI-2, chloroplastic OS=Arabidopsis thaliana GN=CHLI2 PE=1 SV=1
AT1G58290	P42804	1,306	0,001	plastid	Glutamyl-tRNA reductase 1, chloroplastic OS=Arabidopsis thaliana GN=HEMA1 PE=1 SV=2
AT1G03630	O48741	1,754	0,004	plastid	Protochlorophyllide reductase C, chloroplastic OS=Arabidopsis thaliana GN=PORC PE=1 SV=1
AT4G27440	P21218	2,478	0,001	plastid	Protochlorophyllide reductase B, chloroplastic OS=Arabidopsis thaliana GN=PORB PE=1 SV=3
Transport					
AT1G72150**	Q56WK6	-1,763	0,001	plasma membrane	Patellin-1 OS=Arabidopsis thaliana GN=PATL1 PE=1 SV=2
AT5G64290	Q9FMF7	-1,134	0,001	plastid	Dicarboxylate transporter 2.1, chloroplastic OS=Arabidopsis thaliana GN=DIT2-1 PE=1 SV=1
AT4G35100	P93004	-1,018	0,001	plasma membrane	Aquaporin PIP2-7 OS=Arabidopsis thaliana GN=PIP2-7 PE=1 SV=2
AT4G09160	Q9M0R2	-1,012	0,001	nucleus	Patellin-5 OS=Arabidopsis thaliana GN=PATL5 PE=1 SV=2
AT1G22530	Q56ZI2	-0,991	0,001	plasma membrane,cytosol	Patellin-2 OS=Arabidopsis thaliana GN=PATL2 PE=1 SV=2
AT3G26520	Q41963	-0,979	0,001	vacuole	Aquaporin TIP1-2 OS=Arabidopsis thaliana GN=TIP1-2 PE=1 SV=2
AT5G46110**	Q9ZSR7	-0,84	0,002	plastid	Triose phosphate/phosphate translocator TPT, chloroplastic OS=Arabidopsis thaliana GN=TPT PE=1 SV=1
AT2G45960**	Q06611	-0,793	0,001	plasma membrane	Aquaporin PIP1-2 OS=Arabidopsis thaliana GN=PIP1-2 PE=1 SV=1
AT4G02620	Q9ZQX4	-0,697	0,002	vacuole	V-type proton ATPase subunit F OS=Arabidopsis thaliana GN=VHA-F PE=2 SV=1
AT4G25450	Q8LPQ6	-0,693	0,001	plastid	ABC transporter B family member 28 OS=Arabidopsis thaliana GN=ABCB28 PE=2 SV=1
AT1G15690	P31414	-0,672	0,001	vacuole	Pyrophosphate-energized vacuolar membrane proton pump 1 OS=Arabidopsis thaliana GN=AVP1 PE=1 SV=1
AT5G12860	Q9LXV3	-0,596	0,003	plastid	Dicarboxylate transporter 1, chloroplastic OS=Arabidopsis thaliana GN=DIT1 PE=1 SV=1
AT5G22830	Q058N4	-0,595	0,003	plastid	Magnesium transporter MRS2-11, chloroplastic OS=Arabidopsis thaliana GN=MRS2-11 PE=1 SV=1
AT2G36830	P25818	-0,535	0,001	vacuole	Aquaporin TIP1-1 OS=Arabidopsis thaliana GN=TIP1-1 PE=1 SV=1
AT4G00430	Q39196	-0,535	0,008	plasma membrane	Probable aquaporin PIP1-4 OS=Arabidopsis thaliana GN=PIP1.4 PE=1 SV=1
AT3G16240**	Q41951	-0,532	0,001	vacuole	Aquaporin TIP2-1 OS=Arabidopsis thaliana GN=TIP2-1 PE=1 SV=2
AT3G53420**	P43286	-0,513	0,001	plasma membrane	Aquaporin PIP2-1 OS=Arabidopsis thaliana GN=PIP2-1 PE=1 SV=1
AT4G39080	Q8W4S4	-0,423	0,007	vacuole	V-type proton ATPase subunit a3 OS=Arabidopsis thaliana GN=VHA-a3 PE=1 SV=1
AT3G42050	Q9LX65	-0,388	0,001	vacuole,golgi	V-type proton ATPase subunit OS=Arabidopsis thaliana GN=VHA-PE=1 SV=1
AT2G18960	P20649	-0,367	0,002	plasma membrane	ATPase 1, plasma membrane-type OS=Arabidopsis thaliana GN=AHA1 PE=1 SV=3
AT1G32500	Q9LQK7	0,356	0,002	plastid	Protein ABCI7, chloroplastic OS=Arabidopsis thaliana GN=ABCI7 PE=1 SV=1
AT3G01280	Q9SRH5	0,389	0,001	mitochondrion	Mitochondrial outer membrane protein porin 1 OS=Arabidopsis thaliana GN=VDAC1 PE=1 SV=3
AT1G72660	Q9CAI1	0,479	0,006	cytosol	Developmentally-regulated G-protein 2 OS=Arabidopsis thaliana GN=DRG2 PE=2 SV=1
AT2G38270	Q8H7F6	0,488	0,001	plastid	Bifunctional monothiol glutaredoxin-S16, chloroplastic OS=Arabidopsis thaliana GN=GRXS16 PE=1 SV=2
AT2G25600	Q8GXE6	0,494	0,005	cytosol	reversed Potassium channel AKT6 OS=Arabidopsis thaliana GN=AKT6 PE=1 SV=2
AT1G44790	Q84QC1	0,505	0,002	peroxisome	Gamma-glutamylcyclotransferase 2-3 OS=Arabidopsis thaliana GN=GGCT2;3 PE=1 SV=1
AT5G57490	Q9FKM2	0,505	0,004	mitochondrion	Mitochondrial outer membrane protein porin 4 OS=Arabidopsis thaliana GN=VDAC4 PE=1 SV=1
AT4G23710	O82629	0,688	0,003	vacuole,golgi	V-type proton ATPase subunit G2 OS=Arabidopsis thaliana GN=VHA-G2 PE=1 SV=2
Not assigned					
AT4g01870**	A0A1P8B8B4	-2,756	0,001	cytosol	protein-like protein OS=Arabidopsis thaliana GN=At4g01870 PE=4 SV=1
AT2G05380**	Q9ZSJ6	-2,179	0,001	extracellular	Glycine-ricprotein 3 short isoform OS=Arabidopsis thaliana GN=GRP3S PE=1 SV=2
AT3G27570	F4IWK4	-1,563	0,002	mitochondrion	Sucrase/ferredoxin-like family protein OS=Arabidopsis thaliana GN=At3g27570 PE=1 SV=1
AT5G05200	Q9ASX5	-1,515	0,001	plastid	Uncharacterized ArF domain-containing protein kinase At5g05200, chloroplastic OS=Arabidopsis thaliana GN=At5g05200 PE=1 SV=1
AT5G48540	Q9LV60	-1,357	0,001	extracellular	Cysteine-ricrepeat secretory protein 55 OS=Arabidopsis thaliana GN=CRRSP55 PE=2 SV=1
AT5g26280	A0A1P8BA53	-1,322	0,001	extracellular	TRAF-like family protein OS=Arabidopsis thaliana GN=At5g26280 PE=4 SV=1
AT2G42975	Q8RXT7	-1,283	0,003	plastid	Myosin-G heavy chain-like protein OS=Arabidopsis thaliana GN=At2g42975 PE=2 SV=1
AT3G21965	Q9LRL2	-1,193	0,001	extracellular	Putative cysteine-ricrepeat secretory protein 25 OS=Arabidopsis thaliana GN=CRRSP25 PE=5 SV=2
AT4G02370	O81296	-1,185	0,001	extracellular	AT4g02370 protein OS=Arabidopsis thaliana GN=At4g02370 PE=2 SV=1
AT3G20370	Q9LTQ5	-1,154	0,001	extracellular	AT3g20370/MQC12_13 OS=Arabidopsis thaliana GN=At3g20370 PE=2 SV=1

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AT3G24190	Q9LRN0	-1,033	0,001	plastid	AT3g24190/MUJ8_17 OS=Arabidopsis thaliana GN=At3g24190 PE=2 SV=1
AT4G24350	Q94K59	-1,027	0,008	extracellular	Phosphorylase superfamily protein OS=Arabidopsis thaliana GN=At4g24350 PE=2 SV=1
AT5G58770**	Q56Y11	-1,023	0,001	plastid	Dehydrodolichyl diphosphate synthase 2 OS=Arabidopsis thaliana GN=At5g58770 PE=2 SV=2
AT5G19860	Q7XA63	-0,987	0,001	extracellular	At5g19860 OS=Arabidopsis thaliana GN=At5g19860 PE=2 SV=1
AT3G14420**	Q9LRR9	-0,946	0,001	peroxisome	(S)-2-hydroxy-acid oxidase GLO1 OS=Arabidopsis thaliana GN=GLO1 PE=1 SV=1
AT1G16720**	A0A1P8AWU	-0,846	0,001	plastid	Higchlorophyll fluorescence phenotype 173 OS=Arabidopsis thaliana GN=HCF173 PE=4 SV=1
AT2G21960	Q9SJ03	-0,846	0,003	plastid	Expressed protein OS=Arabidopsis thaliana GN=At2g21960 PE=2 SV=2
AT1G32220	Q9FVR6	-0,835	0,001	plastid	Uncharacterized protein At1g32220, chloroplastic OS=Arabidopsis thaliana GN=At1g32220 PE=1 SV=1
AT4G35250	O65502	-0,814	0,001	plastid	AT4g35250/F23E12_190 OS=Arabidopsis thaliana GN=HCF244 PE=1 SV=1
AT3G14415	Q9LRS0	-0,791	0,001	peroxisome	(S)-2-hydroxy-acid oxidase GLO2 OS=Arabidopsis thaliana GN=GLO2 PE=1 SV=1
AT1G14345	Q949S6	-0,774	0,002	plastid	NAD(P)-linked oxidoreductase superfamily protein OS=Arabidopsis thaliana GN=At1g14345 PE=2 SV=1
AT5G63620	F4KAS6	-0,747	0,003	mitochondrion	GroES-like zinc-binding alcohol dehydrogenase family protein OS=Arabidopsis thaliana GN=MBK5.9 PE=4 SV=1
AT5G57170	F4KAK0	-0,745	0,002	plastid	Tautomerase/MIF superfamily protein OS=Arabidopsis thaliana GN=MUL3.12 PE=4 SV=1
AT1G58270	Q9SLV3	-0,725	0,001	extracellular	At1g58270/F19C14_8 OS=Arabidopsis thaliana GN=ZW9 PE=2 SV=1
AT3G09350	Q84J81	-0,712	0,001	cytosol	Fes1A OS=Arabidopsis thaliana GN=Fes1A PE=2 SV=1
AT2G43945	F4IT21	-0,71	0,002	plastid	Uncharacterized protein OS=Arabidopsis thaliana GN=At2g43945 PE=4 SV=1
AT5G63440	Q8GWQ6	-0,707	0,009	cytosol	UPF0235 protein At5g63440 OS=Arabidopsis thaliana GN=At5g63440 PE=1 SV=1
AT5G51720**	Q9FLI7	-0,705	0,001	plastid	CDGSiron-sulfur domain-containing protein NEET OS=Arabidopsis thaliana GN=NEET PE=1 SV=1
AT3G12345**	Q9LHH3	-0,703	0,003	plastid	FKBP-type peptidyl-prolyl cis-trans isomerase OS=Arabidopsis thaliana GN=At3g12345 PE=1 SV=1
AT5G38520	F4KBJ3	-0,697	0,002	plastid	Alpha/beta-Hydrolases superfamily protein OS=Arabidopsis thaliana GN=MBB18.5 PE=4 SV=1
AT1G09340**	Q9SA52	-0,696	0,001	plastid	Chloroplast stem-loop binding protein of 41 kDa b, chloroplastic OS=Arabidopsis thaliana GN=CSP41B PE=1 SV=1
AT3G28270**	Q9LHD9	-0,695	0,001	plasma membrane	UPF0496 protein At3g28270 OS=Arabidopsis thaliana GN=At3g28270 PE=2 SV=1
AT3G44100	Q9LXQ2	-0,686	0,001	extracellular	At3g44100 OS=Arabidopsis thaliana GN=F26G5_50 PE=2 SV=1
AT5G65560	Q9LSL9	-0,685	0,002	mitochondrion	Pentatricopeptide repeat-containing protein At5g65560 OS=Arabidopsis thaliana GN=At5g65560 PE=2 SV=1
AT1G15130	F4HXZ1	-0,68	0,005	nucleus	Vacuolar-sorting protein BRO1 OS=Arabidopsis thaliana GN=BRO1 PE=1 SV=1
AT1G15200	F4HZI8	-0,679	0,005	nucleus	Protein-protein interaction regulator family protein OS=Arabidopsis thaliana GN=At1g15200 PE=4 SV=1
AT2G37970	F4IRX7	-0,678	0,002	plasma membrane	SOUL heme-binding family protein OS=Arabidopsis thaliana GN=SOUL-1 PE=1 SV=2
AT3G63160	Q9M1X3	-0,673	0,001	plastid	AT3g63160/F16M2_10 OS=Arabidopsis thaliana GN=F16M2_10 PE=1 SV=1
AT2G34460	Q8H124	-0,646	0,001	plastid	Uncharacterized protein At2g34460, chloroplastic OS=Arabidopsis thaliana GN=At2g34460 PE=1 SV=1
AT3G57180	Q8W4I6	-0,641	0,003	plastid	GTP-binding protein BRASSINAZOLE INSENSITIVE PALE GREEN 2, chloroplastic OS=Arabidopsis thaliana GN=BPG2 PE=1 SV=1
AT4G29590	Q9SU88	-0,639	0,003	plastid	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein OS=Arabidopsis thaliana GN=At4g29590 PE=4 SV=1
AT5G62140	Q9FIS4	-0,637	0,003	plastid	ATP-dependent Clp protease ATP-binding subunit OS=Arabidopsis thaliana GN=MTG10.17 PE=2 SV=1
AT1G32080	Q9FVQ4	-0,6	0,002	plastid	Plastidal glycolate/glycerate translocator 1, chloroplastic OS=Arabidopsis thaliana GN=PLGG1 PE=1 SV=1
AT1G50450	Q94BZ0	-0,584	0,002	plastid	At1g50450/F11F12_20 OS=Arabidopsis thaliana GN=At1g50450 PE=2 SV=1
AT2G17120	O23006	-0,581	0,003	plasma membrane	LysM domain-containing GPI-anchored protein 2 OS=Arabidopsis thaliana GN=LYM2 PE=1 SV=1
AT2G45990	O82790	-0,581	0,002	plastid	AT2G45990 protein OS=Arabidopsis thaliana GN=At2g45990 PE=1 SV=1
AT1G69840	Q9CAR7	-0,578	0,004	vacuole	Hypersensitive-induced response protein 2 OS=Arabidopsis thaliana GN=HIR2 PE=1 SV=1
AT3G52230	Q9SUY2	-0,556	0,004	plastid	AT3g52230/F4F15_340 OS=Arabidopsis thaliana GN=F4F15.340 PE=1 SV=1
AT4G30720	F4JQE2	-0,551	0,005	plastid	reversed FAD/NAD(P)-binding oxidoreductase family protein OS=Arabidopsis thaliana GN=PDE327 PE=4 SV=1
AT3G02720	Q9M8R4	-0,549	0,003	plasma membrane	Protein DJ-1 homolog D OS=Arabidopsis thaliana GN=DJ1D PE=1 SV=1
AT1G21670**	Q9XI11	-0,543	0,001	extracellular	ADPP6 amino-terminal domain protein OS=Arabidopsis thaliana GN=At1g21670 PE=2 SV=1
AT4G38225	F4JTL0	-0,536	0,004	plastid	Glycerol kinase OS=Arabidopsis thaliana GN=At4g38225 PE=4 SV=1
AT5G57460	Q9FKM4	-0,534	0,005	cytosol	At5g57460 OS=Arabidopsis thaliana GN=MUA2.4 PE=1 SV=1
AT1G33600	Q9FW48	-0,531	0,001	extracellular	Leucine-ricrepeat (LRR) family protein OS=Arabidopsis thaliana GN=At1g33600 PE=4 SV=1
AT4G31530	F4JSP1	-0,523	0,002	plastid	NAD(P)-binding Rossmann-fold superfamily protein OS=Arabidopsis thaliana GN=At4g31530 PE=1 SV=1
AT3G59870	Q9M1Y7	-0,512	0,005	plastid	Uncharacterized protein F24G16.140 OS=Arabidopsis thaliana GN=F24G16.140 PE=4 SV=1
AT3G48420	Q94K71	-0,509	0,001	plastid	CBBY-like protein OS=Arabidopsis thaliana GN=CBBY PE=1 SV=1
AT1G02475	Q94K52	-0,501	0,005	plastid	Polyketide cyclase/dehydrase and lipid transport superfamily protein OS=Arabidopsis thaliana GN=At1g02475 PE=2 SV=1
AT1G61090	B3H4X2	-0,495	0,004	nucleus	reversed Uncharacterized protein OS=Arabidopsis thaliana GN=At1g61090 PE=4 SV=1
AT1G52510	Q8VZ57	-0,494	0,001	plastid	Alpha/beta-Hydrolases superfamily protein OS=Arabidopsis thaliana GN=At1g52510 PE=2 SV=1
AT1G15980	Q9S9N6	-0,478	0,002	plastid	Photosynthetic NDsubunit of subcomplex B 1, chloroplastic OS=Arabidopsis thaliana GN=PNSB1 PE=2 SV=1
AT1G60420	O80763	-0,471	0,005	cytosol	Probable nucleoredoxin 1 OS=Arabidopsis thaliana GN=At1g60420 PE=1 SV=1
AT2G47910	O82258	-0,458	0,008	plastid	Protein CHLORORESPIRATORY REDUCTION 6, chloroplastic OS=Arabidopsis thaliana GN=CRR6 PE=2 SV=1
AT4G10300	Q9SV91	-0,454	0,002	plastid	At4g10300 OS=Arabidopsis thaliana GN=F24G24.100 PE=2 SV=1
AT1G28150	Q9FZ89	-0,453	0,006	plastid	UPF0426 protein At1g28150, chloroplastic OS=Arabidopsis thaliana GN=At1g28150 PE=1 SV=1
AT2G42130	Q8S9M1	-0,447	0,001	plastid	RAIsoform 3 of Probable plastid-lipid-associated protein 13, chloroplastic OS=Arabidopsis thaliana GN=PAP13
AT2G45060	Q94AZ5	-0,447	0,008	mitochondrion	Alanine-tRNA ligase OS=Arabidopsis thaliana GN=At2g45060 PE=1 SV=1
AT1G76850	Q8S3U9	-0,438	0,007	plasma membrane	Exocyst complex component SEC5A OS=Arabidopsis thaliana GN=SEC5A PE=1 SV=1
AT4G24930	Q9SW33	-0,435	0,003	plastid	Thylakoid lumenal 17.9 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=At4g24930 PE=1 SV=1
AT1G54780**	Q9ZVL6	-0,427	0,001	plastid	UPF0603 protein At1g54780, chloroplastic OS=Arabidopsis thaliana GN=At1g54780 PE=1 SV=1
AT2G44640	O80503	-0,425	0,007	plastid	Expressed protein OS=Arabidopsis thaliana GN=At2g44640 PE=4 SV=2

AT1G55980	F4I3I1	-0,42	0,008	cytosol	FAD/NAD(P)-binding oxidoreductase family protein OS=Arabidopsis thaliana GN=At1g55980 PE=4 SV=2
AT5G20090	Q949R9	-0,418	0,007	mitochondrion	Mitochondrial pyruvate carrier 1 OS=Arabidopsis thaliana GN=MPC1 PE=3 SV=1
AT2G44920**	O22160	-0,402	0,001	plastid	Thylakoid lumenal 15 kDa protein 1, chloroplastic OS=Arabidopsis thaliana GN=At2g44920 PE=1 SV=2
AT1G64770	Q94AQ8	-0,399	0,004	plastid	Photosynthetic NDsubunit of subcomplex B 2, chloroplastic OS=Arabidopsis thaliana GN=PNSB2 PE=2 SV=1
AT3G60950	F4JD16	-0,398	0,008	mitochondrion	C2 calcium/lipid-binding endonuclease/exonuclease/phosphatase OS=Arabidopsis thaliana GN=At3g60950 PE=4 SV=1
AT1G14310	Q9M9T1	-0,396	0,008	mitochondrion	F14L17.7 protein OS=Arabidopsis thaliana GN=At1g14310 PE=4 SV=1
AT3G59780	F4J9G2	-0,376	0,002	plastid	Rhodanese/Cell cycle control phosphatase superfamily protein OS=Arabidopsis thaliana GN=At3g59780 PE=4 SV=1
AT1G52315	F4ICV8	-0,375	0,009	mitochondrion	Regulator of Vps4 activity in the MVB pathway protein OS=Arabidopsis thaliana GN=At1g52315 PE=4 SV=1
AT5G48790	Q94F50	-0,374	0,009	plastid	AT5g48790/K24G6_12 OS=Arabidopsis thaliana GN=At5g48790 PE=2 SV=1
AT1G16080	Q9S9M7	-0,37	0,001	plastid	Nuclear protein OS=Arabidopsis thaliana GN=At1g16080 PE=1 SV=1
AT4G15545**	Q93W28	-0,369	0,001	nucleus	Uncharacterized protein At4g15545 OS=Arabidopsis thaliana GN=At4g15545 PE=1 SV=1
AT4G09670	Q9SZ83	-0,366	0,001	cytosol	Uncharacterized oxidoreductase At4g09670 OS=Arabidopsis thaliana GN=At4g09670 PE=1 SV=1
AT5G38660	Q2HIR7	-0,362	0,001	plastid	Acclimation of photosynthesis to environment OS=Arabidopsis thaliana GN=APE1 PE=1 SV=1
AT1g21350	A0A1P8ATZ7	-0,359	0,004	plastid	Thioredoxin superfamily protein OS=Arabidopsis thaliana GN=At1g21350 PE=4 SV=1
AT3G58010	Q9M2P7	-0,352	0,002	plastid	Probable plastid-lipid-associated protein 9, chloroplastic OS=Arabidopsis thaliana GN=PAP9 PE=1 SV=1
AT5G27390	A0A1P8BEU1	-0,35	0,007	plastid	Tagatose-6-phosphate ketose/aldose isomerase, putative (Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein) OS=Arabidopsis thaliana GN=At5g27390 PE=4 SV=1
AT4G03150	Q944G6	0,356	0,007	plastid	AT4g03150/F4C21_7 OS=Arabidopsis thaliana GN=At4g03150 PE=2 SV=1
AT5G39570	Q9FKA5	0,356	0,002	nucleus	Uncharacterized protein At5g39570 OS=Arabidopsis thaliana GN=At5g39570 PE=1 SV=1
AT4g15790	A0A1I9LNC0	0,357	0,01	nucleus	Uveal autoantigen wicoiled-coil/ankyrin OS=Arabidopsis thaliana GN=At4g15790 PE=1 SV=1
AT2G26340	F4IUJ0	0,36	0,002	plastid	Uncharacterized protein OS=Arabidopsis thaliana GN=At2g26340 PE=4 SV=1
AT4G27500	O23144	0,375	0,005	ısmic reticulum,plasma me	Proton pump-interactor 1 OS=Arabidopsis thaliana GN=PPI1 PE=1 SV=2
AT1G27385	F4HSW0	0,381	0,008	mitochondrion	Phosphoribosylformylglycinamidine synthase OS=Arabidopsis thaliana GN=At1g27385 PE=4 SV=1
AT1G27090	Q9LFX8	0,394	0,004	nucleus	Glycine-ricprotein OS=Arabidopsis thaliana GN=At1g27090 PE=1 SV=1
AT5G02050	Q9LZM6	0,397	0,006	mitochondrion	At5g02050 OS=Arabidopsis thaliana GN=At5g02050 PE=2 SV=1
AT3G04550	Q9SR19	0,399	0,002	plastid	Rubisco accumulation factor 1.2, chloroplastic OS=Arabidopsis thaliana GN=RAF1.2 PE=1 SV=1
AT3G07480	Q9SRR8	0,408	0,002	mitochondrion	2Fe-2S ferredoxin-like superfamily protein OS=Arabidopsis thaliana GN=F21O3.19 PE=2 SV=1
AT2G21160	P45434	0,422	0,009	endoplasmic reticulum	Translocon-associated protein subunit alpha OS=Arabidopsis thaliana GN=At2g21160 PE=2 SV=3
AT4G13200	Q8LDV3	0,427	0,002	plastid	Uncharacterized protein At4g13200, chloroplastic OS=Arabidopsis thaliana GN=At4g13200 PE=1 SV=2
AT2G38740	Q9ZVJ5	0,44	0,008	cytosol	Haloacid dehalogenase-like hydrolase domain-containing protein Sgpp OS=Arabidopsis thaliana GN=SGPP PE=1 SV=2
AT3G63540	P82658	0,451	0,001	plastid	Thylakoid lumenal 19 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=At3g63540 PE=1 SV=2
AT2g16980	A0A1P8B0Q4	0,458	0,005	plasma membrane	reversed Major facilitator superfamily protein OS=Arabidopsis thaliana GN=At2g16980 PE=4 SV=1
AT3G05540	Q9M9V9	0,472	0,002	cytosol	Translationally controlled tumor protein 2 OS=Arabidopsis thaliana GN=TCTP2 PE=1 SV=1
AT1G77710	Q9CA23	0,473	0,003	nucleus	Ubiquitin-fold modifier 1 OS=Arabidopsis thaliana GN=At1g77710 PE=3 SV=1
AT1G21065	Q9LPU1	0,476	0,003	plastid	Secondary thiamine-phosphate synthase enzyme OS=Arabidopsis thaliana GN=T22I11.11 PE=2 SV=1
AT1G64980**	Q9XIP8	0,495	0,001	cytosol	Protein CDI OS=Arabidopsis thaliana GN=CDI PE=2 SV=1
AT1G68930	Q9CAA8	0,496	0,005	cytosol	reversed Putative pentatricopeptide repeat-containing protein At1g68930 OS=Arabidopsis thaliana GN=PCMP-H22 PE=3 SV=1
AT4G16390	Q8GWE0	0,507	0,002	plastid	Pentatricopeptide repeat-containing protein At4g16390, chloroplastic OS=Arabidopsis thaliana GN=P67 PE=1 SV=3
AT1G47420	Q9SX77	0,51	0,001	mitochondrion	Succinate dehydrogenase subunit 5, mitochondrial OS=Arabidopsis thaliana GN=SDH5 PE=1 SV=1
AT4G32330	Q94C48	0,51	0,003	nucleus	Protein WVD2-like 5 OS=Arabidopsis thaliana GN=WDL5 PE=1 SV=1
AT5G16730	Q9LFE4	0,511	0,004	cytosol	WEB family protein At5g16730, chloroplastic OS=Arabidopsis thaliana GN=At5g16730 PE=1 SV=1
AT5G52970	Q9LVV5	0,512	0,002	plastid	Thylakoid lumenal 15.0 kDa protein 2, chloroplastic OS=Arabidopsis thaliana GN=At5g52970 PE=1 SV=2
AT1G69510	Q9C787	0,517	0,004	nucleus	Uncharacterized protein At1g69510 OS=Arabidopsis thaliana GN=At1g69510 PE=1 SV=1
AT1G19130	Q8GYZ3	0,523	0,002	nucleus	RmlC-like jelly roll fold protein OS=Arabidopsis thaliana GN=At1g19130 PE=2 SV=1
AT2G07340	Q94AF7	0,524	0,001	nucleus	At2g07350/T13E11.12 OS=Arabidopsis thaliana GN=PFD1 PE=2 SV=1
AT3G54600**	Q9M1G8	0,526	0,004	plasma membrane	DJ-1 protein homolog F OS=Arabidopsis thaliana GN=DJ1F PE=1 SV=1
AT2G35810	Q8VZP3	0,529	0,009	cytosol	Uncharacterized protein At2g35810 OS=Arabidopsis thaliana GN=At2g35810 PE=2 SV=1
AT2G31890	Q8VZE7	0,53	0,005	plastid	RAP domain-containing protein, chloroplastic OS=Arabidopsis thaliana GN=RAP PE=1 SV=1
AT1G62780	Q8VY70	0,54	0,001	plastid	Dimethylallyl, adenosine tRNA methylthiotransferase OS=Arabidopsis thaliana GN=At1g62780 PE=2 SV=1
AT2G32840	Q8GYK6	0,543	0,004	nucleus	reversed Proline-ricfamily protein OS=Arabidopsis thaliana GN=At2g32840 PE=2 SV=1
AT2G14880	O82326	0,546	0,002	plastid	Expressed protein OS=Arabidopsis thaliana GN=At2g14880 PE=1 SV=1
AT3G15000	Q9LKA5	0,558	0,001	mitochondrion	Multiple organellar RNA editing factor 8, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=MORF8 PE=1 SV=1
AT1G21440**	Q501F7	0,563	0,001	plastid	At1g21440 OS=Arabidopsis thaliana GN=At1g21440 PE=2 SV=1
AT3G01310	F4J8C6	0,581	0,003	golgi	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase VIP1 OS=Arabidopsis thaliana GN=VIP1 PE=1 SV=1
AT2G35605	Q93W30	0,605	0,002	mitochondrion	Expressed protein OS=Arabidopsis thaliana GN=At2g35605 PE=2 SV=1
AT4G32915	F4JV80	0,611	0,003	plastid	Glutamyl-tRNA(Gln) amidotransferase subunit C, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=GATC PE=1 SV=1
AT2G46540	Q9ZPY5	0,613	0,003	mitochondrion	At2g46540/F11C10.23 OS=Arabidopsis thaliana GN=At2g46540 PE=2 SV=2
AT1G29350	F4I1G1	0,614	0,001	nucleus	RNA polymerase II degradation factor-like protein (DUF1296) OS=Arabidopsis thaliana GN=At1g29350 PE=4 SV=1
AT1G78150	F4IA48	0,617	0,001	nucleus	N-lysine methyltransferase OS=Arabidopsis thaliana GN=At1g78150 PE=1 SV=1
AT2G20760	Q9SKU1	0,617	0,001	plasma membrane	Clathrin light chain 1 OS=Arabidopsis thaliana GN=At2g20760 PE=2 SV=1
AT5G18980	Q93ZV0	0,621	0,003	plasma membrane	RM repeat superfamily protein OS=Arabidopsis thaliana GN=At5g18980 PE=2 SV=1
AT2G35120	O82179	0,638	0,002	mitochondrion	Glycine cleavage system protein 2, mitochondrial OS=Arabidopsis thaliana GN=GDH2 PE=2 SV=1

AT1G51730	Q9C8I1	0,643	0,002	nucleus	Ubiquitin-conjugating enzyme family protein OS=Arabidopsis thaliana GN=At1g51730 PE=2 SV=1
AT3G18420	Q9LS48	0,643	0,001	plastid	protein SLOW GREEN 1, chloroplastic OS=Arabidopsis thaliana GN=SG1 PE=1 SV=1
AT5G24460	Q9FGE4	0,649	0,001	extracellular	RING-H2 zinc finger protein OS=Arabidopsis thaliana GN=At5g24460 PE=2 SV=1
AT1G10590	Q93W05	0,661	0,002	cytosol	At1g10590/F20B24_1 OS=Arabidopsis thaliana GN=At1g10590 PE=1 SV=1
AT1G50900	Q8VY88	0,678	0,001	plastid	Protein LHCP TRANSLOCATION DEFECT OS=Arabidopsis thaliana GN=LTD PE=1 SV=1
AT4G22670	Q93YR3	0,679	0,001	cytosol	FAM10 family protein At4g22670 OS=Arabidopsis thaliana GN=At4g22670 PE=1 SV=1
AT4G12340	Q9STH7	0,688	0,003	mitochondrion	AT4g12340/T4C9_180 OS=Arabidopsis thaliana GN=At4g12340 PE=2 SV=1
AT5G63560	Q9FFQ7	0,693	0,004	cytosol	Fatty alcohol:caffeoyl-CoA acyltransferase OS=Arabidopsis thaliana GN=FACT PE=2 SV=1
AT5G09620	Q9LXC6	0,702	0,01	nucleus	Gb|AD14519.1 OS=Arabidopsis thaliana GN=At5g09620 PE=1 SV=1
AT2G22125	F4IIM1	0,712	0,003	plasma membrane	Protein CELLULOSE SYNTHASE INTERACTIVE 1 OS=Arabidopsis thaliana GN=CSI1 PE=1 SV=1
AT5G53620	Q93XY1	0,714	0,002	nucleus	At5g53620 OS=Arabidopsis thaliana GN=MNC6.16 PE=1 SV=1
AT4G15802	Q8GW48	0,723	0,001	nucleus	At4g15810 OS=Arabidopsis thaliana GN=HSBP PE=2 SV=1
AT2G43090	Q9ZW85	0,741	0,001	plastid	3-isopropylmalate dehydratase small subunit 3 OS=Arabidopsis thaliana GN=At2g43090 PE=1 SV=1
AT5G10840	F4KIB2	0,757	0,002	golgi	Transmembrane 9 superfamily member 8 OS=Arabidopsis thaliana GN=TMN8 PE=2 SV=1
AT1G22630	Q9SKA5	0,759	0,002	vacuole	At1g22630/F12K8_2 OS=Arabidopsis thaliana GN=At1g22630 PE=2 SV=1
AT4G38710	Q9SZP8	0,786	0,001	nucleus	Eukaryotic translation initiation factor 4B3 OS=Arabidopsis thaliana GN=EIF4B3 PE=1 SV=1
AT1G24050	Q8L466	0,817	0,002	cytosol	At1g24050/T23E23_11 OS=Arabidopsis thaliana GN=At1g24050 PE=1 SV=1
AT1G56580	Q9FXB0	0,819	0,002	cytosol	At1g56580/F25P12_18 OS=Arabidopsis thaliana GN=SMALLER WIVARIABLE BRANCHES PE=2 SV=1
AT1G69230	Q9LE54	0,825	0,002	plasma membrane	Protein SPIRAL1-like 2 OS=Arabidopsis thaliana GN=SP1L2 PE=2 SV=1
AT3G53560	Q9LFG3	0,825	0,001	plastid	Tetratricopeptide repeat (TPR)-like superfamily protein OS=Arabidopsis thaliana GN=F4P12_260 PE=4 SV=1
AT5G51110	Q9LU63	0,839	0,001	plastid	AT5g51110/MWD22_5 OS=Arabidopsis thaliana GN=pdl1 PE=2 SV=1
AT3G57320	A8MQN7	0,869	0,005	nucleus	Threonine-tRNA ligase 2 OS=Arabidopsis thaliana GN=At3g57320 PE=4 SV=2
AT3G07460	F4JEG0	0,881	0,002	extracellular	Uncharacterized protein OS=Arabidopsis thaliana GN=At3g07460 PE=4 SV=1
AT1G42480	F4I9G7	0,889	0,002	extracellular	TLR4 regulator/MIR-interacting MSAP protein OS=Arabidopsis thaliana GN=At1g42480 PE=4 SV=1
AT3G62530	Q94K48	0,9	0,001	mitochondrion	RM repeat superfamily protein OS=Arabidopsis thaliana GN=At3g62530 PE=2 SV=1
AT1G10522	Q9XIK0	0,929	0,001	plastid	Protein PLASTID REDOX INSENSITIVE 2, chloroplastic OS=Arabidopsis thaliana GN=PRIN2 PE=1 SV=1
AT4G36910	O23193	0,941	0,001	plastid	CBS domain-containing protein CBSX1, chloroplastic OS=Arabidopsis thaliana GN=CBSX1 PE=1 SV=2
AT5G64130	A8MS32	0,942	0,001	nucleus	AT5G64130 protein OS=Arabidopsis thaliana GN=MHJ24.11 PE=1 SV=1
AT3G21200	Q9LU39	0,964	0,001	plastid	Glutamyl-tRNA reductase-binding protein, chloroplastic OS=Arabidopsis thaliana GN=GLUTRBP PE=1 SV=1
AT3G62810	Q9LZI4	1,002	0,001	mitochondrion	At3g62810 OS=Arabidopsis thaliana GN=F26K9_240 PE=2 SV=1
AT5G01590	Q7Y1W1	1,004	0,005	plastid	Protein TIC 56, chloroplastic OS=Arabidopsis thaliana GN=TIC56 PE=1 SV=1
AT4G21210	O49562	1,024	0,001	plastid	Pyruvate, phosphate dikinase regulatory protein 1, chloroplastic OS=Arabidopsis thaliana GN=RP1 PE=1 SV=1
AT2G25670	Q9SL96	1,118	0,001	cytosol	Expressed protein OS=Arabidopsis thaliana GN=At2g25670 PE=2 SV=1
AT3G49140	Q0WMN5	1,191	0,001	plastid	Uncharacterized protein At3g49140 OS=Arabidopsis thaliana GN=At3g49140 PE=1 SV=2
AT1G09310	Q9ZPZ4	1,351	0,001	cytosol	AT31J12.3 protein OS=Arabidopsis thaliana GN=At1g09310 PE=1 SV=1
AT5G22580	Q9FK81	1,546	0,001	vacuole	Stress-response A/B barrel domain-containing protein At5g22580 OS=Arabidopsis thaliana GN=At5g22580 PE=1 SV=1
AT1G36320	Q9C8X8	3,739	0,001	plastid	At1g36320/F7F23_4 OS=Arabidopsis thaliana GN=At1g36320 PE=2 SV=1

Table S4: list of proteins that are differentially expressed by VOCs-depleted VCs of *A. alternata* in leaves of WT plants with a “likely” statistical significance level (fungal VC-treated vs. non-treated plants). DEPs are classified according to their functions.

Accesion number	Protein ID	Fold change (log2)	qValue (FDR)	Subcellular location	Description
Aminoacids metabolism					
AT2G22250	Q9SIE1	-0,622	0,013	plastid	Bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase OS=Arabidopsis thaliana GN=PAT PE=1 SV=2
AT5G21060	F4K6Y8	-0,595	0,012	cytosol	Homoserine dehydrogenase OS=Arabidopsis thaliana GN=At5g21060 PE=3 SV=1
AT2G14170	Q0WM29	-0,412	0,02	mitochondrion	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Arabidopsis thaliana GN=ALDH6B2 PE=1 SV=2
Cell wall					
AT1G69530	Q9C554	-0,702	0,016	extracellular	Expansin-A1 OS=Arabidopsis thaliana GN=EXPA1 PE=2 SV=1
AT2G28950	Q38865	0,393	0,021	extracellular	Expansin-A6 OS=Arabidopsis thaliana GN=EXPA6 PE=2 SV=2
Co-factor and vitamin metabolism					
AT2G23420	Q84WV8	-0,694	0,016	cytosol	Nicotinate phosphoribosyltransferase 2 OS=Arabidopsis thaliana GN=NAPRT2 PE=2 SV=1
AT1G22940	Q5M731	-0,45	0,011	plastid	Thiamine biosynthetic bifunctional enzyme TH1, chloroplastic OS=Arabidopsis thaliana GN=TH1 PE=1 SV=1
Development					
AT1G50600	Q8H125	-0,525	0,036	nucleus	Scarecrow-like protein 5 OS=Arabidopsis thaliana GN=SCL5 PE=2 SV=1
AT1G56220	Q8LD26	0,521	0,036	nucleus	Dormancy-associated protein homolog 3 OS=Arabidopsis thaliana GN=At1g56220 PE=1 SV=1
DNA					
AT1G06670	F4IDQ6	-1,309	0,043	nucleus	reversed DExH-box ATP-dependent RNA helicase DExH2 OS=Arabidopsis thaliana GN=NIPE=1 SV=1
AT1G79650	Q84L33	-0,473	0,013	nucleus	Ubiquitin receptor RAD23b OS=Arabidopsis thaliana GN=RAD23B PE=1 SV=3
AT1G51060	Q9C681	0,375	0,012	nucleus	Probable histone H2A.1 OS=Arabidopsis thaliana GN=At1g51060 PE=1 SV=1
Lipid metabolism					
AT2G20900	Q9C5E5	1,775	0,038	cytosol	reversed Diacylglycerol kinase 5 OS=Arabidopsis thaliana GN=DGK5 PE=2 SV=1
Minor CHO metabolism					
AT4G28706	F4JM15	1,192	0,029	plastid	PfkB-like carbohydrate kinase family protein OS=Arabidopsis thaliana GN=At4g28706 PE=3 SV=1
Miscelaneous					
AT2G29420	Q9ZW24	-1,407	0,023	cytosol	Glutathione S-transferase U7 OS=Arabidopsis thaliana GN=GSTU7 PE=2 SV=1
AT4G02340	O81299	-0,46	0,016	peroxisome	AT4g02340 protein OS=Arabidopsis thaliana GN=At4g02340 PE=2 SV=1
AT3G12270	Q0WVD6	-0,405	0,011	nucleus	reversed Probable protein arginine N-methyltransferase 3 OS=Arabidopsis thaliana GN=PRMT3 PE=2 SV=1
AT5G61510	A1L4Y4	-0,387	0,013	mitochondrion	At5g61510 OS=Arabidopsis thaliana GN=At5g61510 PE=2 SV=1
AT3G01510	F4J117	-0,361	0,036	plastid	reversed Phosphoglucan phosphatase LSF1, chloroplastic OS=Arabidopsis thaliana GN=LSF1 PE=1 SV=1
AT4G38990	Q9SVJ4	0,355	0,013	extracellular	Endoglucanase 22 OS=Arabidopsis thaliana GN=GH9B16 PE=3 SV=1
AT5G06580	Q94AX4	0,361	0,012	mitochondrion	D-lactate dehydrogenase [cytochrome], mitochondrial OS=Arabidopsis thaliana GN=DLD PE=1 SV=1
AT3G07320	Q9SRT4	0,406	0,02	extracellular	O-Glycosyl hydrolases family 17 protein OS=Arabidopsis thaliana GN=F21O3.3 PE=2 SV=1
Mitochondrial electron transport					
AT1G51650	Q96253	0,373	0,021	mitochondrion	ATP synthase subunit epsilon, mitochondrial OS=Arabidopsis thaliana GN=At1g51650 PE=1 SV=3
OPP					
AT1G30510	Q9S9P8	-0,551	0,034	plastid	Ferredoxin--NADP reductase, root isozyme 2, chloroplastic OS=Arabidopsis thaliana GN=RFNR2 PE=1 SV=1
Protein					
AT2G20890	Q9SKT0	-0,609	0,033	plastid	Protein THYLAKOID FORMATION 1, chloroplastic OS=Arabidopsis thaliana GN=THF1 PE=1 SV=1
AT5G44090	Q9XGR4	-0,604	0,013	cytosol	Serine/threonine protein phosphatase 2A regulatory subunit B''alpha OS=Arabidopsis thaliana GN=B''ALPHA PE=1 SV=1
AT2G45770	O80842	-0,584	0,014	plastid	Cell division protein FtsY homolog, chloroplastic OS=Arabidopsis thaliana GN=CPFTSY PE=1 SV=2
AT3G20320	Q9LTR2	-0,499	0,018	plastid	Protein TRIGALACTOSYLDIACYLGLYCEROL 2, chloroplastic OS=Arabidopsis thaliana GN=TGD2 PE=1 SV=1
AT1G14320	Q93VT9	-0,474	0,013	cytosol	60S ribosomal protein L10-1 OS=Arabidopsis thaliana GN=RPL10A PE=1 SV=1
AT3G23710	F4J469	-0,444	0,032	plastid	Protein TIC 22-like, chloroplastic OS=Arabidopsis thaliana GN=TIC22L PE=3 SV=1
AT5G52520	Q9FYR6	-0,397	0,033	plastid	Proline--tRNA ligase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=OVA6 PE=2 SV=1
AT2G03640	F4IT98	-0,352	0,033	nucleus	Nuclear transport factor 2 (NTF2) family protein wiRNA binding (RRM-RBD-RNP motifs) domain-containing protein OS=Arabidopsis thaliana GN=At2g03640 PE=4 SV=1

AT1G18170	Q9LDY5	-0,35	0,016	plastid	Peptidyl-prolyl cis-trans isomerase FKBP17-2, chloroplastic OS=Arabidopsis thaliana GN=FKBP17-2 PE=1 SV=1
AT1G66070	Q9C8D8	0,369	0,015	cytosol	Eukaryotic translation initiation factor 3 subunit J OS=Arabidopsis thaliana GN=At1g66070 PE=2 SV=1
AT3G53430	Q9LFH5	0,389	0,025	cytosol	60S ribosomal protein L12-2 OS=Arabidopsis thaliana GN=RPL12B PE=1 SV=1
AT1G45000	Q9MAK9	0,39	0,011	nucleus, cytosol	26S proteasome regulatory subunit S10B homolog B OS=Arabidopsis thaliana GN=RPT4B PE=1 SV=1
AT5G02490	P22954	0,532	0,036	cytosol	Probable mediator of RNA polymerase II transcription subunit 37c OS=Arabidopsis thaliana GN=MED37D PE=1 SV=2
AT4G24730	Q9SB68	0,59	0,011	cytosol	Manganese-dependent ADP-ribose/CDP-alcohol diphosphatase OS=Arabidopsis thaliana GN=At4g24730 PE=2 SV=1
AT1G11480	Q94C21	0,794	0,013	cytosol	At1g11480/T23J18_15 OS=Arabidopsis thaliana GN=At1g11480 PE=1 SV=1
AT3G15260	Q9LDA7	0,868	0,049	cytosol	Probable protein phosphatase 2C 39 OS=Arabidopsis thaliana GN=At3g15260 PE=2 SV=1
Redox metabolism					
AT1G08830	P24704	-0,351	0,013	cytosol	Superoxide dismutase [Cu-Zn] 1 OS=Arabidopsis thaliana GN=CSD1 PE=1 SV=2
RNA					
AT5G04290	F4JW79	-1,058	0,042	nucleus	Protein RNA-directed DNA methylation 3 OS=Arabidopsis thaliana GN=RDM3 PE=1 SV=1
AT4G12750	F4JRF5	-0,527	0,014	nucleus	reversed Homeobox-DDT domain protein RLT3 OS=Arabidopsis thaliana GN=RLT3 PE=3 SV=1
AT5G26210	O81488	-0,384	0,012	nucleus	PHD finger protein ALFIN-LIKE 4 OS=Arabidopsis thaliana GN=AL4 PE=1 SV=2
AT2G04530	Q8L633	-0,363	0,015	plastid	tRNase Z TRZ2, chloroplastic OS=Arabidopsis thaliana GN=TRZ2 PE=2 SV=1
AT1G21600	Q9XI19	0,355	0,012	plastid	AT1G21600 protein OS=Arabidopsis thaliana GN=F8K7.1 PE=2 SV=1
AT3G12130	Q9C7C3	0,383	0,012	nucleus	Zinc finger CCCdomain-containing protein 36 OS=Arabidopsis thaliana GN=At3g12130 PE=2 SV=1
AT1G20110	Q9ASS2	0,472	0,018	nucleus	Protein FREE1 OS=Arabidopsis thaliana GN=FREE1 PE=1 SV=1
Secondary metabolism					
AT4G14210	Q07356	-0,437	0,011	plastid	15-cis-phytoene desaturase, chloroplastic/chromoplastic OS=Arabidopsis thaliana GN=PDS PE=1 SV=1
Signalling					
AT3G26740	Q96500	0,387	0,012	plastid	Light-regulated protein 1, chloroplastic OS=Arabidopsis thaliana GN=LIR1 PE=1 SV=1
AT5G07340	Q38798	0,366	0,011	ER	Calnexin homolog 2 OS=Arabidopsis thaliana GN=At5g07340 PE=2 SV=2
Stress					
AT5G38940	Q9FMA8	-0,477	0,011	extracellular	Germin-like protein subfamily 1 member 11 OS=Arabidopsis thaliana GN=At5g38940 PE=2 SV=1
Not assigned					
AT3G62360	Q9LZQ4	-0,837	0,012	ER	Carbohydrate-binding-like fold OS=Arabidopsis thaliana GN=T12C14_60 PE=4 SV=1
AT1G18270	F4IAP5	-0,674	0,015	cytosol	Ketose-bisphosphate aldolase class-II family protein OS=Arabidopsis thaliana GN=At1g18270 PE=4 SV=1
AT2G34070	O22960	-0,668	0,013	extracellular	Protein trichome birefringence-like 37 OS=Arabidopsis thaliana GN=TBL37 PE=2 SV=2
AT1G04080	F4I448	-0,449	0,04	nucleus	Tetratricopeptide repeat (TPR)-like superfamily protein OS=Arabidopsis thaliana GN=PRP39 PE=1 SV=1
AT2G47960	O82263	-0,431	0,011	golgi	At2g47960/T9J23.10 OS=Arabidopsis thaliana GN=At2g47960 PE=2 SV=2
AT3G01660	Q9SS89	-0,384	0,05	mitochondrion	At3g01660 OS=Arabidopsis thaliana GN=At3g01660 PE=2 SV=1
AT5G39590	Q9FKA3	-0,383	0,012	golgi	TLD-domain containing nucleolar protein OS=Arabidopsis thaliana GN=MIJ24.8 PE=4 SV=1
AT4G34260	Q8L7W8	-0,354	0,011	extracellular	Alpha-L-fucosidase 2 OS=Arabidopsis thaliana GN=FUC95A PE=1 SV=1
AT4G34215	Q8L9J9	0,355	0,011	cytosol	Probable carbohydrate esterase At4g34215 OS=Arabidopsis thaliana GN=At4g34215 PE=1 SV=2
AT2G03420	Q9ZQ78	0,361	0,011	plastid	Uncharacterized protein At2g03420 OS=Arabidopsis thaliana GN=At2g03420 PE=2 SV=2
AT5G12240	Q6NQD2	0,362	0,011	cytosol	At5g12240 OS=Arabidopsis thaliana GN=MXC9.20 PE=2 SV=1
AT2G30695	Q945Q5	0,394	0,013	plastid	At2g30700/T11J7.9 OS=Arabidopsis thaliana GN=At2g30695 PE=2 SV=1
AT2G36835	Q8W455	0,427	0,016	plastid	Expressed protein OS=Arabidopsis thaliana GN=At2g36835 PE=2 SV=1
AT3G48500	F4JF21	0,587	0,025	plastid	Protein PLASTID TRANSCRIPTIONALLY ACTIVE 10 OS=Arabidopsis thaliana GN=PTAC10 PE=1 SV=1
AT5G10010	A2RVJ8	0,697	0,019	nucleus	Protein HEAT INTOLERANT 4 OS=Arabidopsis thaliana GN=HIT4 PE=1 SV=1
AT1G53645	Q9C8L9	1,025	0,044	mitochondrion	At1g53640/F22G10.8 OS=Arabidopsis thaliana GN=F22G10.8 PE=2 SV=1

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Table S5: List of proteins that are differentially expressed by VOCs-depleted VCs of *A. alternata* in leaves of *cfbp1* plants with a “likely” statistical significance level (fungal VC-treated vs. non-treated plants). DEPs are classified according to their functions.

Accesion number	Protein ID	Fold change (log2)	qValue (FDR)	Subcellular location	Description
Aminoacids metabolism					
AT5G52100	Q9FJ82	-0,632	0,018	plastid	Dihydrodipicolinate reductase-like protein CRR1, chloroplastic OS=Arabidopsis thaliana GN=DAPB3 PE=2 SV=1
AT3G47340	P49078	-0,503	0,022	cytosol	Asparagine synthetase [glutamine-hydrolyzing] 1 OS=Arabidopsis thaliana GN=ASN1 PE=2 SV=2
AT3G45300	Q9SWG0	-0,493	0,014	mitochondrion	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Arabidopsis thaliana GN=IVD PE=1 SV=2
AT3G06850	Q9M7Z1	-0,466	0,024	mitochondrion	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=Arabidopsis thaliana GN=BCE2 PE=1 SV=1
AT5G54080	Q9ZRA2	-0,433	0,028	cytosol	Homogentisate 1,2-dioxygenase OS=Arabidopsis thaliana GN=HGO PE=2 SV=2
AT4G35630	Q96255	0,352	0,019	plastid	Phosphoserine aminotransferase 1, chloroplastic OS=Arabidopsis thaliana GN=PSAT1 PE=1 SV=1
AT1G31230	Q9SA18	0,369	0,014	plastid	Bifunctional aspartokinase/homoserine dehydrogenase 1, chloroplastic OS=Arabidopsis thaliana GN=AKHSDH1 PE=1 SV=1
AT4G19710	O81852	0,379	0,017	plastid	Bifunctional aspartokinase/homoserine dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=AKHSDH2 PE=1 SV=1
AT5G19550	P46645	0,384	0,013	cytosol	Aspartate aminotransferase, cytoplasmic isozyme 1 OS=Arabidopsis thaliana GN=ASP2 PE=1 SV=2
AT4G33150	F4JVY8	0,387	0,03	cytosol	reversed Lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme OS=Arabidopsis thaliana GN=LKR PE=4 SV=1
AT1G75330	O50039	0,412	0,016	plastid	Ornithine carbamoyltransferase, chloroplastic OS=Arabidopsis thaliana GN=OTC PE=1 SV=2
AT1G02500	P23686	0,467	0,024	cytosol	S-adenosylmethionine synthase 1 OS=Arabidopsis thaliana GN=SAM1 PE=1 SV=2
AT2G36230	O82782	0,486	0,024	plastid	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase, chloroplastic OS=Arabidopsis thaliana GN=HISN3 PE=2 SV=1
AT5G46180	Q9FNK4	0,521	0,036	mitochondrion	Ornithine aminotransferase, mitochondrial OS=Arabidopsis thaliana GN=DELTA-OAT PE=1 SV=1
AT5G13280	Q9LYU8	0,548	0,018	plastid	Aspartokinase 1, chloroplastic OS=Arabidopsis thaliana GN=AK1 PE=1 SV=1
AT1G17745	O04130	0,726	0,016	plastid	D-3-phosphoglycerate dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=PGDH2 PE=1 SV=2
C1- metabolism					
AT1G76730	Q9SRE0	-1,344	0,025	mitochondrion	5-formyltetrahydrofolate cyclo-ligase-like protein COG0212 OS=Arabidopsis thaliana GN=COG0212 PE=2 SV=1
Cell					
AT2G46910	Q8W4F1	-0,62	0,014	plastid	Probable plastid-lipid-associated protein 10, chloroplastic OS=Arabidopsis thaliana GN=PAP10 PE=1 SV=1
AT5G15970	P31169	-0,619	0,013	cytosol	Stress-induced protein KIN2 OS=Arabidopsis thaliana GN=KIN2 PE=2 SV=1
AT2G38730	Q9ZVJ4	-0,571	0,019	cytosol	Peptidyl-prolyl cis-trans isomerase CYP22 OS=Arabidopsis thaliana GN=CYP22 PE=2 SV=1
AT3G52750	Q9LXJ0	-0,376	0,02	plastid	Cell division protein FtsZ homolog 2-2, chloroplastic OS=Arabidopsis thaliana GN=FTSZ2-2 PE=1 SV=1
AT2G27970	Q9SJJ5	1,542	0,013	nucleus	Cyclin-dependent kinases regulatory subunit 2 OS=Arabidopsis thaliana GN=CKS2 PE=1 SV=1
AT1G06210	Q9LNC6	-1,527	0,016	nucleus	TOM1-like protein 2 OS=Arabidopsis thaliana GN=TOL2 PE=1 SV=1
Cell wall					
AT3G60900	Q9LZX4	-1,214	0,013	plasma membrane	Fasciclin-like arabinogalactan protein 10 OS=Arabidopsis thaliana GN=FLA10 PE=1 SV=1
AT5G49360	Q9FGY1	-0,99	0,034	extracellular	Beta-D-xylosidase 1 OS=Arabidopsis thaliana GN=BXL1 PE=1 SV=1
AT5G57560	Q38857	-0,946	0,014	extracellular	Xyloglucan endotransglucosylase/hydrolase protein 22 OS=Arabidopsis thaliana GN=XTH22 PE=1 SV=1
AT1G65310	O80803	-0,709	0,016	extracellular	Probable xyloglucan endotransglucosylase/hydrolase protein 17 OS=Arabidopsis thaliana GN=XTH17 PE=1 SV=1
AT4G30270	P24806	-0,613	0,013	extracellular	Xyloglucan endotransglucosylase/hydrolase protein 24 OS=Arabidopsis thaliana GN=XTH24 PE=1 SV=2
AT1G69530	Q9C554	-0,579	0,034	extracellular	Expansin-A1 OS=Arabidopsis thaliana GN=EXPA1 PE=2 SV=1
AT2G45470	O22126	-0,514	0,014	ma membrane, extracellu	Fasciclin-like arabinogalactan protein 8 OS=Arabidopsis thaliana GN=FLA8 PE=1 SV=1
AT5G44130	Q9FFH6	-0,395	0,016	ma membrane, extracellu	Fasciclin-like arabinogalactan protein 13 OS=Arabidopsis thaliana GN=FLA13 PE=1 SV=1
AT5G64570	Q9FLG1	-0,356	0,013	extracellular	Beta-D-xylosidase 4 OS=Arabidopsis thaliana GN=BXL4 PE=1 SV=1
AT1G78570	Q9SYM5	0,361	0,025	cytosol	Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM1 OS=Arabidopsis thaliana GN=RHM1 PE=1 SV=1
AT1G63000	Q9LQ04	0,389	0,035	cytosol	Bifunctional dTDP-4-dehydrorhamnose 3,5-epimerase/dTDP-4-dehydrorhamnose reductase OS=Arabidopsis thaliana GN=NRS/ER PE=1 SV=1
AT3G02230	Q9SRT9	0,428	0,015	cytosol	UDP-arabinopyranose mutase 1 OS=Arabidopsis thaliana GN=RGP1 PE=1 SV=1
AT1G53500	Q9LPG6	0,482	0,014	cytosol	Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM2 OS=Arabidopsis thaliana GN=RHM2 PE=1 SV=1
AT3G44990	P93046	0,495	0,024	ma membrane, extracellu	Xyloglucan endotransglucosylase/hydrolase protein 31 OS=Arabidopsis thaliana GN=XTH31 PE=1 SV=2
Co-factor and vitamin metabolism					
AT2G29630	O82392	0,717	0,013	plastid	Phosphomethylpyrimidine synthase, chloroplastic OS=Arabidopsis thaliana GN=THIC PE=1 SV=1
Development					
AT1G30610	Q9SA76	-0,466	0,025	plastid	reversed Pentatricopeptide repeat-containing protein At1g30610, chloroplastic OS=Arabidopsis thaliana GN=EMB2279 PE=3 SV=1
AT3G47650	Q9SN73	-0,359	0,035	plastid	DnaJ/Hsp40 cysteine-ricdomain superfamily protein OS=Arabidopsis thaliana GN=F1P2.200 PE=2 SV=1
AT2G44060	O80576	0,366	0,019	cytosol	At2g44060 OS=Arabidopsis thaliana GN=late embryogenesis abundant 26 PE=2 SV=1
AT1G02090	Q94JU3	1,712	0,021	nucleus, cytosol	COP9 signalosome complex subunit 7 OS=Arabidopsis thaliana GN=CSN7 PE=1 SV=1

DNA					
AT4G09730	Q56X76	-0,51	0,022	plastid	DEAD-box ATP-dependent RNA helicase 39 OS=Arabidopsis thaliana GN=RH39 PE=2 SV=2
AT2G19480	Q9ZUP3	0,46	0,015	nucleus	Nucleosome assembly protein 1;2 OS=Arabidopsis thaliana GN=NAP1;2 PE=1 SV=1
AT3G15950	Q9LSB4	0,47	0,021	ER	TSA1-like protein OS=Arabidopsis thaliana GN=NAI2 PE=1 SV=1
AT5G56950	Q94K07	0,584	0,019	nucleus	Nucleosome assembly protein 1;3 OS=Arabidopsis thaliana GN=NAP1;3 PE=1 SV=1
AT1G20960	Q9SYP1	1,162	0,014	nucleus	reversed DExH-box ATP-dependent RNA helicase DExH12 OS=Arabidopsis thaliana GN=BRR2A PE=1 SV=1
AT1G79650	Q84L33	1,337	0,016	nucleus	Ubiquitin receptor RAD23b OS=Arabidopsis thaliana GN=RAD23B PE=1 SV=3
Gluconeogenesis					
AT2G22780	O82399	-0,418	0,019	peroxisome	Malate dehydrogenase 1, peroxisomal OS=Arabidopsis thaliana GN=PMDH1 PE=1 SV=1
Glycolisis					
AT2G36580	Q9SJQ0	0,429	0,03	:ytosol, plasma membran	Pyruvate kinase OS=Arabidopsis thaliana GN=At2g36580 PE=1 SV=2
Hormone metabolism					
AT2G33830	P93017	-0,916	0,014	peroxisome	Dormancy-associated protein homolog 1 OS=Arabidopsis thaliana GN=DRMH1 PE=1 SV=1
AT3G44300	P32962	-0,752	0,016	cytosol	Nitrilase 2 OS=Arabidopsis thaliana GN=NIT2 PE=1 SV=1
AT4G19170	O49675	-0,641	0,015	plastid	Probable carotenoid cleavage dioxygenase 4, chloroplastic OS=Arabidopsis thaliana GN=CCD4 PE=1 SV=1
AT1G30100	Q9C6Z1	-0,532	0,021	plastid	reversed Probable 9-cis-epoxycarotenoid dioxygenase NCED5, chloroplastic OS=Arabidopsis thaliana GN=NCED5 PE=1 SV=1
AT3G44860	Q9FYC4	-0,507	0,021	cytosol	Farnesoic acid carboxyl-O-methyltransferase OS=Arabidopsis thaliana GN=FAMT PE=1 SV=1
AT3G07390	Q94BT2	-0,398	0,018	plasma membrane	Auxin-induced in root cultures protein 12 OS=Arabidopsis thaliana GN=AIR12 PE=1 SV=3
AT1G22400	Q9SK82	-0,355	0,036	cytosol	UDP-glycosyltransferase 85A1 OS=Arabidopsis thaliana GN=UGT85A1 PE=2 SV=1
AT3G16450	O04311	0,432	0,013	cytosol	Jacalin-related lectin 33 OS=Arabidopsis thaliana GN=JAL33 PE=1 SV=1
AT4G27450	Q93V62	0,607	0,018	cytosol	AT4g27450/F27G19_50 OS=Arabidopsis thaliana GN=At4g27450 PE=1 SV=1
Lipid metabolism					
AT5G55480	Q9FJ62	-0,648	0,017	plasma membrane	Glycerophosphodiester phosphodiesterase GDPDL4 OS=Arabidopsis thaliana GN=GDPDL4 PE=1 SV=1
AT3G51600	Q9XFS7	-0,411	0,027	extracellular	Non-specific lipid-transfer protein 5 OS=Arabidopsis thaliana GN=LTP5 PE=1 SV=1
AT1G66970	Q7Y208	-0,397	0,028	plasma membrane	Glycerophosphodiester phosphodiesterase GDPDL1 OS=Arabidopsis thaliana GN=GDPDL1 PE=1 SV=2
AT4G13050	Q9SV64	-0,368	0,045	plastid	Oleoyl-acyl carrier protein thioesterase 2, chloroplastic OS=Arabidopsis thaliana GN=FATA2 PE=2 SV=1
AT4G33030	O48917	0,477	0,02	plastid	UDP-sulfoquinovose synthase, chloroplastic OS=Arabidopsis thaliana GN=SQD1 PE=1 SV=1
AT1G54580	P25701	0,545	0,02	plastid	Acyl carrier protein 2, chloroplastic OS=Arabidopsis thaliana GN=ACP2 PE=1 SV=2
AT3G55360	Q9M2U2	0,597	0,019	ER, plama membrane	Very-long-chain enoyl-CoA reductase OS=Arabidopsis thaliana GN=ECR PE=1 SV=1
AT1G48600	Q944H0	0,639	0,016	cytosol	Phosphomethylethanolamine N-methyltransferase OS=Arabidopsis thaliana GN=NMT2 PE=2 SV=2
AT1G73600	Q9C6B9	1,149	0,013	cytosol	Phosphoethanolamine N-methyltransferase 3 OS=Arabidopsis thaliana GN=NMT3 PE=2 SV=2
AT3G18000	Q9FR44	2,464	0,021	golgi	Phosphoethanolamine N-methyltransferase 1 OS=Arabidopsis thaliana GN=NMT1 PE=1 SV=1
Major CHO metabolism					
AT1G11720	F4IAG2	-0,508	0,021	plastid	Starcsynthase 3, chloroplastic/amyloplastic OS=Arabidopsis thaliana GN=SS3 PE=1 SV=1
AT2G31390	Q9SID0	0,412	0,015	cytosol	Probable fructokinase-1 OS=Arabidopsis thaliana GN=At2g31390 PE=2 SV=1
AT3G29320	Q9LIB2	0,422	0,024	plastid	Alpha-glucan phosphorylase 1 OS=Arabidopsis thaliana GN=PHS1 PE=1 SV=1
AT1G32900	Q9MAQ0	0,498	0,013	plastid	Granule-bound starcsynthase 1, chloroplastic/amyloplastic OS=Arabidopsis thaliana GN=GBSS1 PE=1 SV=1
Metal handling					
AT5G44070	Q9S7Z3	-0,398	0,039	cytosol	Glutathione gamma-glutamylcysteinyltransferase 1 OS=Arabidopsis thaliana GN=PCS1 PE=1 SV=1
AT1G56430	Q9C7X5	0,432	0,034	cytosol	Probable nicotianamine synthase 4 OS=Arabidopsis thaliana GN=NAS4 PE=2 SV=1
Minor CHO metabolism					
AT5G20250	Q8RX87	-0,683	0,014	plastid	Probable galactinol--sucrose galactosyltransferase 6 OS=Arabidopsis thaliana GN=RFS6 PE=2 SV=2
AT5G53850	Q9FN41	0,48	0,015	plastid	Probable bifunctional methylthioribulose-1-phosphate dehydratase/enolase-phosphatase E1 OS=Arabidopsis thaliana GN=At5g53850 PE=1 SV=1
Miscelaneous					
AT3G13750	Q9SCW1	-0,911	0,014	extracellular	Beta-galactosidase 1 OS=Arabidopsis thaliana GN=BGAL1 PE=2 SV=1
AT5G56870	Q9SCV8	-0,783	0,016	extracellular	Beta-galactosidase 4 OS=Arabidopsis thaliana GN=BGAL4 PE=1 SV=1
AT1G09010	Q75W54	-0,714	0,016	vacuole	Mannosylglycoprotein endo-beta-mannosidase OS=Arabidopsis thaliana GN=EBM PE=1 SV=3
AT4G22490	Q9SUX0	-0,671	0,014	extracellular	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein OS=Arabidopsis thaliana GN=At4g22490 PE=2 SV=1
AT4G31840	Q9SZ51	-0,535	0,016	extracellular	Early nodulin-like protein 15 OS=Arabidopsis thaliana GN=ENODL15 PE=2 SV=1
AT1G12090	O65369	-0,513	0,02	extracellular	At1g12090/T28K15.14 OS=Arabidopsis thaliana GN=ELP PE=2 SV=1
AT4G20860	Q9SUC6	-0,494	0,016	extracellular	Berberine bridge enzyme-like 22 OS=Arabidopsis thaliana GN=FAD-OXR PE=2 SV=1
AT4G22513	A8MQX6	-0,477	0,016	extracellular	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein OS=Arabidopsis thaliana GN=At4g22513 PE=4 SV=1
AT4G22485	A8MRQ5	-0,474	0,022	extracellular	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein OS=Arabidopsis thaliana GN=At4g22485 PE=4 SV=2

AT1G31690	F4IAX0	-0,473	0,024	extracellular	Amine oxidase OS=Arabidopsis thaliana GN=At1g31690 PE=3 SV=1
AT4G22505	F4JLV7	-0,466	0,021	extracellular	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein OS=Arabidopsis thaliana GN=At4g22505 PE=4 SV=1
AT4G30140	Q9SZW7	-0,452	0,014	extracellular	GDSL esterase/lipase At4g30140 OS=Arabidopsis thaliana GN=At4g30140 PE=2 SV=1
AT1G78340	Q8GYM1	-0,432	0,027	cytosol	Glutathione S-transferase U22 OS=Arabidopsis thaliana GN=GSTU22 PE=1 SV=1
AT1G28580	Q9FXJ2	-0,413	0,034	extracellular	GDSL esterase/lipase At1g28580 OS=Arabidopsis thaliana GN=At1g28580 PE=2 SV=1
AT5G62350	Q9LVA4	-0,398	0,015	extracellular	Plant invertase/pectin methylesterase inhibitor superfamily protein OS=Arabidopsis thaliana GN=MMI9.18 PE=2 SV=1
AT3G22120	A0A1I9LSA3	-0,385	0,019	ma membrane, extracellu	Cell wall-plasma membrane linker protein OS=Arabidopsis thaliana GN=CWLP PE=4 SV=1
AT3G45190	F4J5I0	-0,376	0,039	plasma membrane	SIT4 phosphatase-associated family protein OS=Arabidopsis thaliana GN=At3g45190 PE=1 SV=1
AT4G27520	Q9T076	-0,358	0,013	plasma membrane	Early nodulin-like protein 2 OS=Arabidopsis thaliana GN=At4g27520 PE=1 SV=1
AT2G10940	Q9SKI0	-0,352	0,014	vacuole	At2g10940/F15K19.1 OS=Arabidopsis thaliana GN=At2g10940 PE=2 SV=1
AT4G38990	Q9SVJ4	-0,35	0,039	extracellular	Endoglucanase 22 OS=Arabidopsis thaliana GN=GH9B16 PE=3 SV=1
AT1G52400	Q9SE50	0,384	0,024	peroxisome	Beta-D-glucopyranosyl abscisate beta-glucosidase OS=Arabidopsis thaliana GN=BGLU18 PE=1 SV=2
AT5G57850	Q8L493	0,445	0,017	plastid	D-amino-acid transaminase, chloroplastic OS=Arabidopsis thaliana GN=DAAT PE=1 SV=1
AT3G16420	O04314	0,452	0,019	cytosol	PYK10-binding protein 1 OS=Arabidopsis thaliana GN=PBP1 PE=1 SV=1
AT1G02930	P42760	0,473	0,013	cytosol	Glutathione S-transferase F6 OS=Arabidopsis thaliana GN=GSTF6 PE=2 SV=2
AT1G78360	F4IA73	0,554	0,02	ER, plama membrane	Glutathione S-transferase U21 OS=Arabidopsis thaliana GN=GSTU21 PE=3 SV=1
AT5G16990	Q39173	0,566	0,037	cytosol	ADP-dependent alkenal double bond reductase P2 OS=Arabidopsis thaliana GN=P2 PE=2 SV=2
AT2G39330	O80948	0,954	0,034	cytosol	Jacalin-related lectin 23 OS=Arabidopsis thaliana GN=JAL23 PE=1 SV=1
AT5G63800	Q9FFN4	0,967	0,025	extracellular	Beta-galactosidase 6 OS=Arabidopsis thaliana GN=BGAL6 PE=2 SV=1
Mitochondrial electron transport					
AT1G52710	Q9SSS5	-0,459	0,023	mitochondrion	reversed Putative cytochrome c oxidase subunit 5b-like OS=Arabidopsis thaliana GN=At1g52710 PE=3 SV=2
AT5G13440	Q9LYR2	-0,356	0,036	mitochondrion	Cytochrome b-c1 complex subunit Rieske-2, mitochondrial OS=Arabidopsis thaliana GN=UCR1-2 PE=1 SV=1
ATMG00640	Q04613	0,428	0,029	mitochondrion	ATP synthase protein MI25 OS=Arabidopsis thaliana GN=AtMg00640 PE=1 SV=2
AT2G20530	Q9SIL6	0,54	0,021	mitochondrion	Prohibitin-6, mitochondrial OS=Arabidopsis thaliana GN=PHB6 PE=1 SV=1
N- metabolism					
AT5G37600	Q56WN1	0,503	0,016	cytosol	Glutamine synthetase cytosolic isozyme 1-1 OS=Arabidopsis thaliana GN=GLN1-1 PE=1 SV=2
Nucleotide metabolism					
AT3G09820	Q9SF85	0,528	0,021	cytosol	Adenosine kinase 1 OS=Arabidopsis thaliana GN=ADK1 PE=1 SV=1
AT3G46940	Q9STG6	-0,397	0,026	nucleus	Deoxyuridine 5'-triphosphate nucleotidohydrolase OS=Arabidopsis thaliana GN=DUT PE=1 SV=1
Photosyntesis					
AT5G38410	B3H5S2	-0,897	0,016	plastid	Ribulose bisphosphate carboxylase small chain OS=Arabidopsis thaliana GN=RBCS3B PE=3 SV=1
ATCG01060	P62090	-0,553	0,013	plastid	Photosystem I iron-sulfur center OS=Arabidopsis thaliana GN=psaC PE=3 SV=2
ATCG00630	P56769	-0,535	0,015	plastid	Photosystem I reaction center subunit IX OS=Arabidopsis thaliana GN=psaJ PE=3 SV=1
ATCG00680	P56777	-0,506	0,02	plastid	Photosystem II CP47 reaction center protein OS=Arabidopsis thaliana GN=psbB PE=1 SV=1
AT4G26530	O65581	-0,467	0,018	plastid	Fructose-bisphosphate aldolase 5, cytosolic OS=Arabidopsis thaliana GN=FBA5 PE=1 SV=1
ATCG00280	P56778	-0,465	0,022	plastid	Photosystem II CP43 reaction center protein OS=Arabidopsis thaliana GN=psbC PE=1 SV=3
ATCG00270	P56761	-0,457	0,019	plastid	Photosystem II D2 protein OS=Arabidopsis thaliana GN=psbD PE=1 SV=3
ATCG00560	P60129	-0,451	0,028	plastid	Photosystem II reaction center protein L OS=Arabidopsis thaliana GN=psbL PE=1 SV=1
ATCG00430	P56756	-0,446	0,021	plastid	NAD(P)H-quinone oxidoreductase subunit K, chloroplastic OS=Arabidopsis thaliana GN=ndhK PE=3 SV=1
AT5G58260	Q9LVM2	-0,444	0,025	plastid	NAD(P)H-quinone oxidoreductase subunit N, chloroplastic OS=Arabidopsis thaliana GN=ndhN PE=2 SV=1
AT3G21055	Q39195	-0,397	0,018	plastid	Photosystem II 5 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=PSBT PE=3 SV=2
AT4G21280	Q9XFT3	-0,386	0,013	plastid	Isoform 2 of Oxygen-evolving enhancer protein 3-1, chloroplastic OS=Arabidopsis thaliana GN=PSBQ1
ATCG00020	P83755	-0,383	0,015	plastid	Photosystem II protein D1 OS=Arabidopsis thaliana GN=psbA PE=1 SV=2
AT5G64040	P49107	-0,373	0,013	plastid	Photosystem I reaction center subunit N, chloroplastic OS=Arabidopsis thaliana GN=PSAN PE=1 SV=2
AT3G55330	P82538	-0,368	0,013	plastid	PsbP-like protein 1, chloroplastic OS=Arabidopsis thaliana GN=PPL1 PE=1 SV=1
ATCG00720	P56773	-0,366	0,016	plastid	Cytochrome b6 OS=Arabidopsis thaliana GN=petB PE=1 SV=1
AT3G16140	Q9SUI7	-0,361	0,034	plastid	Photosystem I reaction center subunit VI-1, chloroplastic OS=Arabidopsis thaliana GN=PSAH1 PE=2 SV=1
AT1G67090	P10795	-0,36	0,018	plastid	Ribulose bisphosphate carboxylase small chain 1A, chloroplastic OS=Arabidopsis thaliana GN=RBCS-1A PE=1 SV=2
AT1G51400	Q9SYE2	-0,352	0,027	plastid	At1g51400/F5D21_10 OS=Arabidopsis thaliana GN=F11M15.26 PE=2 SV=1
AT2G35120	O82179	0,371	0,029	mitochondrion	Glycine cleavage system protein 2, mitochondrial OS=Arabidopsis thaliana GN=GDH2 PE=2 SV=1
AT2G05100	Q9SHR7	0,523	0,02	plastid	Chlorophyll a-b binding protein 2.1, chloroplastic OS=Arabidopsis thaliana GN=LHCB2.1 PE=1 SV=1
Protein					
AT5G66140	O24616	-3,941	0,025	nucleus, cytosol	Proteasome subunit alpha type-7-B OS=Arabidopsis thaliana GN=PAD2 PE=1 SV=2
AT2G42810	Q84XU2	-1,217	0,029	nucleus, cytosol	Serine/threonine-protein phosphatase 5 OS=Arabidopsis thaliana GN=PAPP5 PE=1 SV=1
AT5G02490	P22954	-1,032	0,024	cytosol	Probable mediator of RNA polymerase II transcription subunit 37c OS=Arabidopsis thaliana GN=MED37D PE=1 SV=2
AT5G46430	Q9FHG2	-0,821	0,042	cytosol	60S ribosomal protein L32-2 OS=Arabidopsis thaliana GN=RPL32B PE=2 SV=1

AT1G51930	Q6AWX4	-0,647	0,02	ER, extracellular	reversed At1g51930 OS=Arabidopsis thaliana GN=At1g51930 PE=2 SV=1
AT5G37680	Q8W4C8	-0,585	0,019	plasma membrane	reversed ADP-ribosylation factor-like protein 8c OS=Arabidopsis thaliana GN=ARL8C PE=2 SV=1
AT4g17100	F4JNE0	-0,573	0,018	cytosol	Poly(U)-specific endoribonuclease-B protein OS=Arabidopsis thaliana GN=At4g17100 PE=4 SV=1
AT3G17250	Q9LUU7	-0,571	0,02	mitochondrion	Probable protein phosphatase 2C 43 OS=Arabidopsis thaliana GN=At3g17250 PE=2 SV=1
AT3G11910	Q84WU2	-0,557	0,019	cytosol	Ubiquitin carboxyl-terminal hydrolase 13 OS=Arabidopsis thaliana GN=UBP13 PE=1 SV=1
ATCG00380	P56799	-0,53	0,022	plastid	30S ribosomal protein S4, chloroplastic OS=Arabidopsis thaliana GN=rps4 PE=3 SV=1
AT5G27700	Q3E902	-0,494	0,04	cytosol	40S ribosomal protein S21-2 OS=Arabidopsis thaliana GN=RPS21C PE=1 SV=2
AT5G15250	Q1PDW5	-0,484	0,039	plastid	ATP-dependent zinc metalloprotease FTS6, chloroplastic OS=Arabidopsis thaliana GN=FTSH6 PE=2 SV=1
AT1G03230	Q9ZVS5	-0,483	0,017	extracellular	Eukaryotic aspartyl protease family protein OS=Arabidopsis thaliana GN=At1g03230 PE=2 SV=1
AT1G20810	Q9LM71	-0,472	0,015	plastid	Peptidyl-prolyl cis-trans isomerase FKBP18, chloroplastic OS=Arabidopsis thaliana GN=FKBP18 PE=1 SV=2
AT5G43010	Q9SEI3	-0,468	0,025	nucleus, cytosol	26S proteasome regulatory subunit 10B homolog A OS=Arabidopsis thaliana GN=RPT4A PE=1 SV=1
AT1G64510	Q8VY91	-0,453	0,014	plastid	30S ribosomal protein S6 alpha, chloroplastic OS=Arabidopsis thaliana GN=RPS6 PE=2 SV=1
ATCG00840	P61845	-0,449	0,025	plastid	50S ribosomal protein L23, chloroplastic OS=Arabidopsis thaliana GN=rpl23-A PE=3 SV=1
AT1G50250	Q39102	-0,435	0,027	plastid	ATP-dependent zinc metalloprotease FTS1, chloroplastic OS=Arabidopsis thaliana GN=FTSH1 PE=1 SV=2
AT4G30910	Q8RX72	-0,423	0,029	plastid	Leucine aminopeptidase 3, chloroplastic OS=Arabidopsis thaliana GN=LAP3 PE=2 SV=1
ATCG00790	P56793	-0,42	0,031	plastid	50S ribosomal protein L16, chloroplastic OS=Arabidopsis thaliana GN=rpl16 PE=3 SV=1
AT4G39710	Q9SCY3	-0,417	0,016	plastid	Photosynthetic NDsubunit of lumenal location 4, chloroplastic OS=Arabidopsis thaliana GN=PNSL4 PE=1 SV=1
ATCG01120	P56805	-0,398	0,03	plastid	30S ribosomal protein S15, chloroplastic OS=Arabidopsis thaliana GN=rps15 PE=3 SV=1
AT4G34620	O65686	-0,393	0,014	plastid	30S ribosomal protein S16-1, chloroplastic OS=Arabidopsis thaliana GN=RPS16-1 PE=2 SV=1
AT1G06430	Q8W585	-0,39	0,015	plastid	ATP-dependent zinc metalloprotease FTS8, chloroplastic OS=Arabidopsis thaliana GN=FTSH8 PE=1 SV=1
AT2G18190	F4IQG2	-0,381	0,029	plasma membrane	A-ATPase At2g18190 OS=Arabidopsis thaliana GN=At2g18190 PE=2 SV=1
AT4G12120	Q9SZ77	-0,372	0,035	cytosol	Protein transport Sec1b OS=Arabidopsis thaliana GN=SEC1B PE=2 SV=3
ATCG00820	P56808	-0,355	0,032	plastid	30S ribosomal protein S19, chloroplastic OS=Arabidopsis thaliana GN=rps19 PE=3 SV=1
AT4G25890	Q9SVZ6	0,352	0,036	cytosol	60S acidic ribosomal protein P3-1 OS=Arabidopsis thaliana GN=RPP3A PE=3 SV=1
AT2G40660	Q93VB0	0,357	0,014	cytosol	Nucleic acid-binding, OB-fold-like protein OS=Arabidopsis thaliana GN=At2g40660 PE=2 SV=1
AT3G53740	Q9M352	0,357	0,037	cytosol	60S ribosomal protein L36-2 OS=Arabidopsis thaliana GN=RPL36B PE=3 SV=1
AT4G01610	Q94K85	0,365	0,021	extracellular	Cathepsin B-like protease 3 OS=Arabidopsis thaliana GN=CATHB3 PE=1 SV=1
AT4G31180	Q9M084	0,366	0,013	cytosol	Aspartate--tRNA ligase 2, cytoplasmic OS=Arabidopsis thaliana GN=IBI1 PE=1 SV=1
AT5G14470	Q9LY82	0,366	0,036	cytosol	Probable glucuronokinase 2 OS=Arabidopsis thaliana GN=GLCAK2 PE=2 SV=1
AT3G13470	Q9LJE4	0,377	0,015	plastid	Chaperonin 60 subunit beta 2, chloroplastic OS=Arabidopsis thaliana GN=CPN60B2 PE=1 SV=1
AT4G16720	O23515	0,378	0,02	cytosol	60S ribosomal protein L15-1 OS=Arabidopsis thaliana GN=RPL15A PE=2 SV=1
AT3G54360	Q9M2V1	0,381	0,016	nucleus	Protein NCA1 OS=Arabidopsis thaliana GN=NCA1 PE=1 SV=1
AT2G39460	Q8LD46	0,384	0,014	cytosol	60S ribosomal protein L23a-1 OS=Arabidopsis thaliana GN=RPL23AA PE=2 SV=2
AT4G11260	Q9SUT5	0,387	0,02	cytosol	Protein SGT1 homolog B OS=Arabidopsis thaliana GN=SGT1B PE=1 SV=1
AT2G28900	Q9ZV24	0,394	0,013	plastid	Outer envelope pore protein 16-1, chloroplastic OS=Arabidopsis thaliana GN=OEP161 PE=1 SV=1
AT2G47110	P59232	0,401	0,026	cytosol	Ubiquitin-40S ribosomal protein S27a-2 OS=Arabidopsis thaliana GN=RPS27AB PE=2 SV=2
AT1G25350	Q8W4F3	0,455	0,03	cytosol	Glutamine--tRNA ligase, cytoplasmic OS=Arabidopsis thaliana GN=OVA9 PE=2 SV=1
AT5G12110	Q84WM9	0,465	0,016	cytosol	Elongation factor 1-beta 1 OS=Arabidopsis thaliana GN=At5g12110 PE=2 SV=2
AT2G32850	Q8H0Z0	0,488	0,025	nucleus	Protein kinase superfamily protein OS=Arabidopsis thaliana GN=At2g32850 PE=2 SV=1
AT2G31610	Q9SIP7	0,512	0,022	cytosol	40S ribosomal protein S3-1 OS=Arabidopsis thaliana GN=RPS3A PE=1 SV=1
AT5G23740	P42733	0,567	0,019	cytosol	40S ribosomal protein S11-3 OS=Arabidopsis thaliana GN=RPS11C PE=2 SV=2
AT2G04160	Q9ZSP5	0,583	0,019	extracellular	Subtilisin-like protease SBT5.3 OS=Arabidopsis thaliana GN=AIR3 PE=2 SV=1
AT3G27080	P82874	0,656	0,018	mitochondrion	Mitochondrial import receptor subunit TOM20-3 OS=Arabidopsis thaliana GN=TOM20-3 PE=1 SV=1
AT4G17510	Q8GWE1	0,699	0,016	cytosol	Ubiquitin carboxyl-terminal hydrolase 3 OS=Arabidopsis thaliana GN=UCH3 PE=2 SV=1
Redox metabolism					
AT2G28190	O78310	-0,537	0,039	plastid	Superoxide dismutase [Cu-Zn] 2, chloroplastic OS=Arabidopsis thaliana GN=CSD2 PE=1 SV=2
AT4G35090	P25819	-0,487	0,013	peroxisome	Catalase-2 OS=Arabidopsis thaliana GN=CAT2 PE=1 SV=3
AT1G76760	Q6NPF9	-0,37	0,031	plastid	Thioredoxin Y1, chloroplastic OS=Arabidopsis thaliana GN=At1g76760 PE=2 SV=1
AT2G16060	O24520	1,54	0,024	cytosol	Non-symbiotic hemoglobin 1 OS=Arabidopsis thaliana GN=AHB1 PE=1 SV=1
RNA					
AT5G04290	F4JW79	-1,269	0,049	nucleus	Protein RNA-directed DNA methylation 3 OS=Arabidopsis thaliana GN=RDM3 PE=1 SV=1
AT4G38890	Q9T0J6	-1,249	0,021	nucleus, cytosol	tRNA-dihydrouridine(47) synthase [NAD(P)(+)]-like OS=Arabidopsis thaliana GN=At4g38890 PE=1 SV=2
AT3G07670	Q9S7D2	-0,943	0,016	plastid	Putative ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I OS=Arabidopsis thaliana GN=F17A17.1 PE=1 SV=1
AT3G61260	Q9M2D8	-0,629	0,014	plasma membrane	Uncharacterized protein At3g61260 OS=Arabidopsis thaliana GN=At3g61260 PE=1 SV=1
AT5G26210	O81488	-0,56	0,019	nucleus	PHD finger protein ALFIN-LIKE 4 OS=Arabidopsis thaliana GN=AL4 PE=1 SV=2
AT2G23930	O82221	-0,503	0,021	cytosol	Probable small nuclear ribonucleoprotein G OS=Arabidopsis thaliana GN=At2g23930 PE=3 SV=1
AT1G73530	Q9FX45	-0,373	0,03	plastid	Organelle RRM domain-containing protein 6, chloroplastic OS=Arabidopsis thaliana GN=ORRM6 PE=1 SV=1
AT1G09750	O04496	-0,36	0,019	extracellular	Aspartyl protease AED3 OS=Arabidopsis thaliana GN=AED3 PE=1 SV=1
AT5G54900	Q9FPJ8	0,394	0,016	nucleus	Polyadenylate-binding protein RBP45A OS=Arabidopsis thaliana GN=RBP45A PE=2 SV=1

AT3G05060	Q9MAB3	0,398	0,018	nucleus	Probable nucleolar protein 5-2 OS=Arabidopsis thaliana GN=NOP5-2 PE=1 SV=1
AT1G73230	Q9CAT7	0,445	0,022	nucleus	Nascent polypeptide-associated complex subunit beta OS=Arabidopsis thaliana GN=At1g73230 PE=2 SV=1
ATCG00170	P56764	0,477	0,025	plastid	DNA-directed RNA polymerase subunit beta'' OS=Arabidopsis thaliana GN=rpoC2 PE=3 SV=1
AT3G03920	Q8VZT0	0,517	0,021	nucleus	Putative H/ACA ribonucleoprotein complex subunit 1-like protein 1 OS=Arabidopsis thaliana GN=At3g03920 PE=2 SV=1
AT4G34110	P42731	0,561	0,019	nucleus	Polyadenylate-binding protein 2 OS=Arabidopsis thaliana GN=PAB2 PE=1 SV=1
AT1G02080	F4HVV6	0,585	0,026	Golgi	Transcription regulator OS=Arabidopsis thaliana GN=At1g02080 PE=4 SV=1
AT5G46420	Q9FHG3	0,835	0,015	plastid	16S rRNA processing protein RimM family OS=Arabidopsis thaliana GN=At5g46420 PE=3 SV=1
S-assimilation					
AT2G14750	Q43295	0,378	0,043	plastid	Adenylyl-sulfate kinase 1, chloroplastic OS=Arabidopsis thaliana GN=APK1 PE=1 SV=1
Secondary metabolism					
AT2G37040	P35510	0,351	0,022	cytosol	Phenylalanine ammonia-lyase 1 OS=Arabidopsis thaliana GN=PAL1 PE=1 SV=3
AT5G16440	Q38929	0,354	0,026	plastid	Isopentenyl-diphosphate Delta-isomerase I, chloroplastic OS=Arabidopsis thaliana GN=IPP1 PE=2 SV=3
AT5G23010	Q9FG67	0,383	0,021	plastid	Methylthioalkylmalate synthase 1, chloroplastic OS=Arabidopsis thaliana GN=MAM1 PE=1 SV=1
AT4G13430	Q94AR8	0,422	0,014	plastid	3-isopropylmalate dehydratase large subunit, chloroplastic OS=Arabidopsis thaliana GN=IIL1 PE=1 SV=1
AT1G80560	P93832	0,425	0,027	plastid	3-isopropylmalate dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=IMDH2 PE=1 SV=1
AT5G58490	Q9FGH3	0,455	0,028	cytosol	Cinnamoyl-CoA reductase-like protein OS=Arabidopsis thaliana GN=MQJ2.6 PE=2 SV=1
AT4G34350	Q94B35	0,473	0,019	plastid	4-hydroxy-3-methylbut-2-enyl diphosphate reductase, chloroplastic OS=Arabidopsis thaliana GN=ISPPE=2 SV=1
AT2G20610	Q9SIV0	0,486	0,014	cytosol	S-alkyl-thiohydroximate lyase SUR1 OS=Arabidopsis thaliana GN=SUR1 PE=1 SV=1
AT3G51240	Q9S818	0,568	0,014	cytosol	Naringenin,2-oxoglutarate 3-dioxygenase OS=Arabidopsis thaliana GN=F3PE=1 SV=1
AT5G08640	Q96330	0,603	0,013	peroxisome	Flavonol synthase/flavanone 3-hydroxylase OS=Arabidopsis thaliana GN=FLS1 PE=1 SV=1
AT4G23600	Q9SUR6	0,638	0,017	peroxisome	Cystine lyase CORI3 OS=Arabidopsis thaliana GN=CORI3 PE=1 SV=1
AT5G13930	P13114	0,744	0,014	ER	Chalcone synthase OS=Arabidopsis thaliana GN=CHS PE=1 SV=1
AT2G43100	Q9ZW84	0,778	0,014	plastid	3-isopropylmalate dehydratase small subunit 1 OS=Arabidopsis thaliana GN=IPMI2 PE=1 SV=1
AT3G58990	Q9LYT7	0,984	0,014	plastid	3-isopropylmalate dehydratase small subunit 2 OS=Arabidopsis thaliana GN=IPMI1 PE=1 SV=1
AT3G19710	Q9LE06	1,175	0,013	cytosol	Methionine aminotransferase BCAT4 OS=Arabidopsis thaliana GN=BCAT4 PE=1 SV=1
AT1G74100	Q9C9D0	0,57	0,019	cytosol	Cytosolic sulfotransferase 16 OS=Arabidopsis thaliana GN=SOT16 PE=1 SV=1
AT3G14210	Q9LJG3	0,444	0,017	vacuole	GDSL esterase/lipase ESM1 OS=Arabidopsis thaliana GN=ESM1 PE=1 SV=1
AT5G25980	Q9C5C2	-0,415	0,018	extracellular	Myrosinase 2 OS=Arabidopsis thaliana GN=TGG2 PE=1 SV=1
Signalling					
AT3G19300	Q9LT87	-0,788	0,015	plasma membrane	At3g19300 OS=Arabidopsis thaliana GN=At3g19300 PE=2 SV=1
AT4G21940	O49717	-0,695	0,019	plasma membrane	Calcium-dependent protein kinase 15 OS=Arabidopsis thaliana GN=CPK15 PE=2 SV=1
AT5G46070	F4KG14	-0,37	0,036	nucleus, cytosol	Guanylate-binding family protein OS=Arabidopsis thaliana GN=MCL19.12 PE=4 SV=1
AT5G09440	Q9FY71	-0,364	0,021	extracellular	Protein EXORDIUM-like 4 OS=Arabidopsis thaliana GN=EXL4 PE=2 SV=1
AT4G09000	P42643	0,35	0,039	cytosol	14-3-3-like protein GF14 chi OS=Arabidopsis thaliana GN=GRF1 PE=1 SV=3
AT2G41110	P0DH97	0,376	0,03	cytosol	Calmodulin-2 OS=Arabidopsis thaliana GN=CAM2 PE=1 SV=1
AT5G37780	P0DH95	0,391	0,019	nucleus	Calmodulin-1 OS=Arabidopsis thaliana GN=CAM1 PE=1 SV=1
AT2G33380	O22788	0,548	0,021	cytosol	Probable peroxygenase 3 OS=Arabidopsis thaliana GN=PXG3 PE=1 SV=1
Stress					
AT2G42540	Q42512	-1,737	0,015	plastid	Protein COLD-REGULATED 15A, chloroplastic OS=Arabidopsis thaliana GN=COR15A PE=1 SV=1
AT4G02100	Q84VX5	-0,649	0,017	nucleus	reversed At4g02100 OS=Arabidopsis thaliana GN=At4g02100 PE=2 SV=1
AT2G42530	Q9SIN5	-0,511	0,013	plastid	Protein COLD-REGULATED 15B, chloroplastic OS=Arabidopsis thaliana GN=COR15B PE=1 SV=1
AT1G72610	P94040	-0,468	0,015	extracellular	Germin-like protein subfamily 3 member 1 OS=Arabidopsis thaliana GN=GLP1 PE=1 SV=1
AT1G23130	O49304	-0,395	0,015	cytosol	At1g23130/T26J12_10 OS=Arabidopsis thaliana GN=At1g23130 PE=2 SV=1
AT5G56010	P51818	0,362	0,025	cytosol	Heat shock protein 90-3 OS=Arabidopsis thaliana GN=HSP90-3 PE=1 SV=2
AT3G51780	Q8RX71	0,383	0,034	cytosol	BAG family molecular chaperone regulator 4 OS=Arabidopsis thaliana GN=BAG4 PE=1 SV=1
AT3G12580	Q9LHA8	0,397	0,013	cytosol	Probable mediator of RNA polymerase II transcription subunit 37c OS=Arabidopsis thaliana GN=MED37C PE=1 SV=1
AT1G20450	P42759	0,415	0,015	ytosol, plasma membran	Dehydrin ERD10 OS=Arabidopsis thaliana GN=ERD10 PE=1 SV=1
AT2G25140	Q8VYJ7	0,415	0,027	mitochondrion	Chaperone protein ClpB4, mitochondrial OS=Arabidopsis thaliana GN=CLPB4 PE=2 SV=1
AT5G56030	P55737	0,446	0,019	nucleus, cytosol	Heat shock protein 90-2 OS=Arabidopsis thaliana GN=HSP90-2 PE=1 SV=1
AT3G15700	Q9LW09	0,453	0,03	cytosol	Putative disease resistance protein At3g15700 OS=Arabidopsis thaliana GN=At3g15700 PE=3 SV=1
AT1G76180	P42763	0,455	0,014	peroxisome	Dehydrin ERD14 OS=Arabidopsis thaliana GN=ERD14 PE=1 SV=1
AT5G51700	Q9SE33	0,48	0,025	nucleus	Cysteine and histidine-ricdomain-containing protein RAR1 OS=Arabidopsis thaliana GN=RAR1 PE=1 SV=1
AT4G23680	Q9SUQ9	0,553	0,019	cytosol	AT4g23680/F9D16_150 OS=Arabidopsis thaliana GN=At4g23680 PE=2 SV=1
AT1G75310	A0A1P8AND3	0,767	0,016	nucleus	reversed Auxin-like 1 protein OS=Arabidopsis thaliana GN=AUL1 PE=4 SV=1

TCA/org transformation					
AT3G01500	A0A1I9LQB3	-0,402	0,02	plastid	Carbonic anhydrase OS=Arabidopsis thaliana GN=CA1 PE=1 SV=1
AT5G40650	Q8LB02	0,36	0,021	mitochondrion	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit 2, mitochondrial OS=Arabidopsis thaliana GN=SDH2-2 PE=1 SV=2
AT5G43330	P57106	0,452	0,019	cytosol	Malate dehydrogenase 2, cytoplasmic OS=Arabidopsis thaliana GN=MDH2 PE=1 SV=1
Tetrapyrrole synthesis					
AT1G58290	P42804	0,364	0,033	plastid	Glutamyl-tRNA reductase 1, chloroplastic OS=Arabidopsis thaliana GN=HEMA1 PE=1 SV=2
AT1G09940	P49294	0,478	0,024	plastid	Glutamyl-tRNA reductase 2, chloroplastic OS=Arabidopsis thaliana GN=HEMA2 PE=2 SV=2
AT1G03630	O48741	0,743	0,048	plastid	Protochlorophyllide reductase C, chloroplastic OS=Arabidopsis thaliana GN=PORC PE=1 SV=1
Transport					
AT1G72150	Q56WK6	-0,552	0,015	plasma membrane	Patellin-1 OS=Arabidopsis thaliana GN=PATL1 PE=1 SV=2
AT5G22830	Q058N4	-0,445	0,024	plastid	Magnesium transporter MRS2-11, chloroplastic OS=Arabidopsis thaliana GN=MRS2-11 PE=1 SV=1
AT4G33520	Q9SZC9	-0,398	0,018	plastid	Isoform 2 of Copper-transporting ATPase PAA1, chloroplastic OS=Arabidopsis thaliana GN=PAA1
AT4G00430	Q39196	0,379	0,039	plasma membrane	Probable aquaporin PIP1-4 OS=Arabidopsis thaliana GN=PIP1.4 PE=1 SV=1
AT3G54540	Q9M1H3	0,38	0,039	nucleus	ABC transporter F family member 4 OS=Arabidopsis thaliana GN=ABCF4 PE=2 SV=1
AT3G16240	Q41951	0,441	0,014	vacuole	Aquaporin TIP2-1 OS=Arabidopsis thaliana GN=TIP2-1 PE=1 SV=2
AT2G45960	Q06611	0,444	0,023	plasma membrane	Aquaporin PIP1-2 OS=Arabidopsis thaliana GN=PIP1-2 PE=1 SV=1
AT3G53420	P43286	0,452	0,017	plasma membrane	Aquaporin PIP2-1 OS=Arabidopsis thaliana GN=PIP2-1 PE=1 SV=1
AT4G30190	P19456	0,503	0,022	plasma membrane	ATPase 2, plasma membrane-type OS=Arabidopsis thaliana GN=AHA2 PE=1 SV=2
AT5G20650	Q93VM8	0,515	0,021	vacuole	Copper transporter 5 OS=Arabidopsis thaliana GN=COPT5 PE=1 SV=1
AT2G36830	P25818	0,669	0,013	vacuole	Aquaporin TIP1-1 OS=Arabidopsis thaliana GN=TIP1-1 PE=1 SV=1
AT1G49410	Q9XIA7	0,757	0,016	mitochondrion	Mitochondrial import receptor subunit TOM6 homolog OS=Arabidopsis thaliana GN=TOM6 PE=1 SV=1
Not assigned					
AT4G36630	Q8L5Y0	-0,893	0,041	cytosol	Uncharacterized protein At4g36630 OS=Arabidopsis thaliana GN=EMB2754 PE=2 SV=1
AT1G12150	Q9FWW5	-0,707	0,016	nucleus	reversed WEB family protein At1g12150 OS=Arabidopsis thaliana GN=At1g12150 PE=2 SV=1
AT1G03900	Q681Q7	-0,655	0,018	nucleus	Uncharacterized protein At1g03900 OS=Arabidopsis thaliana GN=At1g03900 PE=2 SV=1
AT3G24506	Q9LV56	-0,608	0,024	plastid	Uncharacterized protein At3g24506 OS=Arabidopsis thaliana GN=At3g24506 PE=2 SV=1
AT1G48790	Q8VYB5	-0,564	0,044	nucleus	AMSH-like ubiquitin thioesterase 1 OS=Arabidopsis thaliana GN=AMSH1 PE=2 SV=1
AT5G47690	B3H5K3	-0,562	0,019	nucleus	Binding protein OS=Arabidopsis thaliana GN=At5g47690 PE=1 SV=1
AT1G60420	O80763	-0,553	0,02	cytosol	Probable nucleoredoxin 1 OS=Arabidopsis thaliana GN=At1g60420 PE=1 SV=1
AT3G18790	Q9LS97	-0,52	0,021	nucleus	AT3G18790 protein OS=Arabidopsis thaliana GN=At3g18790 PE=2 SV=1
AT4G34260	Q8L7W8	-0,517	0,022	extracellular	Alpha-L-fucosidase 2 OS=Arabidopsis thaliana GN=FUC95A PE=1 SV=1
AT1G42480	F4I9G7	-0,489	0,034	extracellular	TLR4 regulator/MIR-interacting MSAP protein OS=Arabidopsis thaliana GN=At1g42480 PE=4 SV=1
AT5G16730	Q9LFE4	-0,488	0,018	cytosol	WEB family protein At5g16730, chloroplastic OS=Arabidopsis thaliana GN=At5g16730 PE=1 SV=1
AT5G53490	P81760	-0,488	0,021	plastid	Thylakoid lumenal 17.4 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=TL17 PE=1 SV=2
AT5G21160	Q940X9	-0,483	0,024	nucleus	La-related protein 1A OS=Arabidopsis thaliana GN=LARP1A PE=1 SV=1
AT4G10930	Q8L7I1	-0,482	0,023	nucleus	reversed Uncharacterized protein At4g10930 OS=Arabidopsis thaliana GN=At4g10930 PE=2 SV=1
AT3G21965	Q9LRL2	-0,461	0,024	extracellular	Putative cysteine-ricrepeat secretory protein 25 OS=Arabidopsis thaliana GN=CRRSP25 PE=5 SV=2
AT1G54520	Q8RWI0	-0,441	0,027	plastid	Myelin-associated oligodendrocyte basic protein OS=Arabidopsis thaliana GN=At1g54520 PE=1 SV=1
AT1G49750	Q9FXA1	-0,422	0,016	extracellular	AT1G49750 protein OS=Arabidopsis thaliana GN=At1g49750 PE=2 SV=1
AT3G47070	Q9SD66	-0,386	0,013	plastid	Thylakoid soluble phosphoprotein OS=Arabidopsis thaliana GN=F13I12.120 PE=1 SV=1
AT4g01870	A0A1P8B8B4	-0,384	0,013	cytosol	TolB protein-like protein OS=Arabidopsis thaliana GN=At4g01870 PE=4 SV=1
AT4G02530	O22773	-0,369	0,014	plastid	Thylakoid lumenal 16.5 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=At4g02530 PE=1 SV=3
AT2G32240	F4ISU2	-0,365	0,021	ER	reversed Early endosome antigen OS=Arabidopsis thaliana GN=At2g32240 PE=1 SV=1
AT1G15980	Q9S9N6	-0,364	0,022	plastid	Photosynthetic NDsubunit of subcomplex B 1, chloroplastic OS=Arabidopsis thaliana GN=PNSB1 PE=2 SV=1
AT1G21670	Q9XI11	-0,36	0,013	extracellular	DPP6 amino-terminal domain protein OS=Arabidopsis thaliana GN=At1g21670 PE=2 SV=1
AT1G50900	Q8VY88	-0,359	0,018	plastid	Protein LHCP TRANSLOCATION DEFECT OS=Arabidopsis thaliana GN=LTD PE=1 SV=1
AT3G57320	A8MQN7	0,359	0,041	nucleus	Threonine-tRNA ligase 2 OS=Arabidopsis thaliana GN=At3g57320 PE=4 SV=2
AT3G07090	Q9SFT9	0,364	0,017	cytosol	PPPDE putative thiol peptidase family protein OS=Arabidopsis thaliana GN=T1B9.26 PE=2 SV=1
AT5G08040	Q9SD80	0,396	0,035	mitochondrion	Mitochondrial import receptor subunit TOM5 homolog OS=Arabidopsis thaliana GN=TOM5 PE=1 SV=3
AT3G12050	Q9LHL7	0,405	0,024	cytosol	Aha1 domain-containing protein OS=Arabidopsis thaliana GN=T21B14.13 PE=1 SV=1
AT3G44330	Q9M292	0,417	0,033	ER	Nicalin OS=Arabidopsis thaliana GN=T22K7_10 PE=2 SV=1
AT1G56580	Q9FXB0	0,429	0,029	cytosol	At1g56580/F25P12_18 OS=Arabidopsis thaliana GN=SMALLER WIVARIABLE BRANCHES PE=2 SV=1
AT5G53620	Q93XY1	0,436	0,028	nucleus	At5g53620 OS=Arabidopsis thaliana GN=MNC6.16 PE=1 SV=1
AT2G38740	Q9ZVJ5	0,464	0,026	cytosol	Haloacid dehalogenase-like hydrolase domain-containing protein Sgpp OS=Arabidopsis thaliana GN=SGPP PE=1 SV=2
AT1G53280	Q9MAH3	0,497	0,019	plastid	Protein DJ-1 homolog B OS=Arabidopsis thaliana GN=DJ1B PE=1 SV=1
AT5G10840	F4KIB2	0,514	0,021	golgi	Transmembrane 9 superfamily member 8 OS=Arabidopsis thaliana GN=TMN8 PE=2 SV=1
AT5G51040	Q9FI44	0,527	0,021	mitochondrion	Succinate dehydrogenase assembly factor 2, mitochondrial OS=Arabidopsis thaliana GN=SDHAF2 PE=1 SV=1
AT3G49140	Q0WMN5	0,756	0,032	plastid	Uncharacterized protein At3g49140 OS=Arabidopsis thaliana GN=At3g49140 PE=1 SV=2

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Table S6: list of proteins that are differentially expressed in leaves by knocking down cFBP1 with a “confident” statistical significance level. DEPs are classified by functional categories. DEPs that are discussed in the ms. are highlighted in yellow.

Accesion number	Protein ID	Fold change (log2)	qvalue (FDR)	Subcellular location	Description
Aminoacids metabolism					
AT4G33150	F4JVY8	-0,758	0,002	cytosol	reversed Lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme OS=Arabidopsis thaliana GN=LKR PE=4 SV=1
AT1G11860	O65396	-0,685	0,01	mitochondrion	Aminomethyltransferase, mitochondrial OS=Arabidopsis thaliana GN=GDCST PE=2 SV=1
AT1G68010	Q9C9W5	-0,659	0,001	peroxisome	Glycerate dehydrogenase HPR, peroxisomal OS=Arabidopsis thaliana GN=HPR PE=1 SV=1
AT2G13360	Q56YA5	-0,643	0,001	peroxisome	Serine--glyoxylate aminotransferase OS=Arabidopsis thaliana GN=AGT1 PE=1 SV=2
AT5G08100	P50287	-0,448	0,009	cytosol	Isoaspartyl peptidase/L-asparaginase 1 OS=Arabidopsis thaliana GN=At5g08100 PE=1 SV=2
AT3G26900	Q9LW20	-0,426	0,002	plastid	Probable inactive shikimate kinase like 1, chloroplastic OS=Arabidopsis thaliana GN=SKL1 PE=2 SV=1
AT2G36230	O82782	-0,413	0,009	plastid	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase, chloroplastic OS=Arabidopsis thaliana GN=HISN3 PE=2 SV=1
AT2G34470	O64700	-0,324	0,009	cytosol	Urease accessory protein G OS=Arabidopsis thaliana GN=UREG PE=2 SV=1
AT3G61440	Q9S757	0,301	0,001	mitochondrion	Bifunctional L-3-cyanoalanine synthase/cysteine synthase C1, mitochondrial OS=Arabidopsis thaliana GN=CYSC1 PE=1 SV=1
AT1G79230	O64530	0,317	0,004	mitochondrion,plastid	Thiosulfate/3-mercaptopyruvate sulfurtransferase 1, mitochondrial OS=Arabidopsis thaliana GN=STR1 PE=1 SV=1
AT3G06350	Q9SQT8	0,323	0,001	plastid	Bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase, chloroplastic OS=Arabidopsis thaliana GN=EMB3004 PE=1 SV=1
AT2G04400	P49572	0,337	0,002	plastid	Indole-3-glycerol phosphate synthase, chloroplastic OS=Arabidopsis thaliana GN=IGPS PE=1 SV=2
AT5G17920	O50008	0,337	0,001	cytosol	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1 OS=Arabidopsis thaliana GN=MS1 PE=1 SV=1
AT1G58080	Q9S762	0,347	0,008	plastid	ATP phosphoribosyltransferase 1, chloroplastic OS=Arabidopsis thaliana GN=HISN1A PE=1 SV=1
AT1G75330	O50039	0,358	0,004	plastid	rnithine carbamoyltransferase, chloroplastic OS=Arabidopsis thaliana GN=OTC PE=1 SV=2
AT3G60880	Q9LZX6	0,359	0,005	plastid	4-hydroxy-tetrahydrodipicolinate synthase 1, chloroplastic OS=Arabidopsis thaliana GN=DHDPS1 PE=2 SV=2
AT5G48880	Q570C8	0,361	0,006	peroxisome	3-ketoacyl-CoA thiolase 5, peroxisomal OS=Arabidopsis thaliana GN=KAT5 PE=1 SV=2
AT5G19550	P46645	0,363	0,002	cytosol	Aspartate aminotransferase, cytoplasmic isozyme 1 OS=Arabidopsis thaliana GN=ASP2 PE=1 SV=2
AT5G11520	P46644	0,364	0,003	peroxisome	Aspartate aminotransferase 3, chloroplastic OS=Arabidopsis thaliana GN=ASP3 PE=1 SV=1
AT3G58610	Q05758	0,369	0,001	plastid	Ketol-acid reductoisomerase, chloroplastic OS=Arabidopsis thaliana GN=At3g58610 PE=1 SV=2
AT5G17990	Q02166	0,376	0,002	plastid	Anthranilate phosphoribosyltransferase, chloroplastic OS=Arabidopsis thaliana GN=PAT1 PE=2 SV=1
AT2G17630	Q9SHP0	0,377	0,006	plastid	Phosphoserine aminotransferase 2, chloroplastic OS=Arabidopsis thaliana GN=PSAT2 PE=1 SV=1
AT5G65780	Q9FYA6	0,384	0,004	plastid	Branched-chain-amino-acid aminotransferase 5, chloroplastic OS=Arabidopsis thaliana GN=BCAT5 PE=1 SV=1
AT1G17290	F4I7I0	0,41	0,001	mitochondrion	Alanine aminotransferase 1, mitochondrial OS=Arabidopsis thaliana GN=ALAAT1 PE=1 SV=1
AT3G57050	P53780	0,417	0,004	plastid	Cystathionine beta-lyase, chloroplastic OS=Arabidopsis thaliana GN=At3g57050 PE=1 SV=1
AT4G35630	Q96255	0,426	0,003	plastid	Phosphoserine aminotransferase 1, chloroplastic OS=Arabidopsis thaliana GN=PSAT1 PE=1 SV=1
AT4G34200	O49485	0,434	0,001	plastid	D-3-phosphoglycerate dehydrogenase 1, chloroplastic OS=Arabidopsis thaliana GN=PGDH1 PE=1 SV=1
AT2G45300	P05466	0,439	0,002	plastid	3-phosphoshikimate 1-carboxyvinyltransferase, chloroplastic OS=Arabidopsis thaliana GN=At2g45300 PE=2 SV=3
AT5G13780	Q9FKI4	0,455	0,003	cytosol	N-terminal acetyltransferase A complex catalytic subunit NAA10 OS=Arabidopsis thaliana GN=NAA10 PE=1 SV=1
AT3G22200	Q94CE5	0,46	0,001	mitochondrion	Gamma-aminobutyrate transaminase POP2, mitochondrial OS=Arabidopsis thaliana GN=POP2 PE=1 SV=1
AT5G49810	Q9LTB2	0,468	0,002	cytosol	Methionine S-methyltransferase OS=Arabidopsis thaliana GN=MMT1 PE=1 SV=1
AT1G09795	Q8GSJ1	0,474	0,006	plastid	ATP phosphoribosyltransferase 2, chloroplastic OS=Arabidopsis thaliana GN=HISN1B PE=1 SV=1
AT3G54640	Q42529	0,489	0,001	plastid	Tryptophan synthase alpha chain, chloroplastic OS=Arabidopsis thaliana GN=TSA1 PE=1 SV=1
AT4G13940	O23255	0,497	0,001	cytosol	Adenosylhomocysteinase 1 OS=Arabidopsis thaliana GN=SAHH1 PE=1 SV=1
AT2G31810	Q93YZ7	0,501	0,001	plastid	Acetolactate synthase small subunit 2, chloroplastic OS=Arabidopsis thaliana GN=At2g31810 PE=1 SV=1
AT4G01850	P17562	0,523	0,002	nucleus,cytosol	S-adenosylmethionine synthase 2 OS=Arabidopsis thaliana GN=SAM2 PE=1 SV=1
AT5G54810	P14671	0,531	0,002	plastid	Tryptophan synthase beta chain 1, chloroplastic OS=Arabidopsis thaliana GN=TSB1 PE=2 SV=1
AT1G74040	Q9C550	0,533	0,005	plastid	2-isopropylmalate synthase 2, chloroplastic OS=Arabidopsis thaliana GN=IPMS2 PE=1 SV=1
AT3G45300	Q9SWG0	0,547	0,002	mitochondrion	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Arabidopsis thaliana GN=IVD PE=1 SV=2
AT1G02500	P23686	0,565	0,004	cytosol	S-adenosylmethionine synthase 1 OS=Arabidopsis thaliana GN=SAM1 PE=1 SV=2
AT5G62530	Q8VZC3	0,57	0,001	mitochondrion	Delta-1-pyrroline-5-carboxylate dehydrogenase 12A1, mitochondrial OS=Arabidopsis thaliana GN=ALDH12A1 PE=2 SV=1
AT3G49680	Q9M401	0,594	0,001	plastid	Branched-chain-amino-acid aminotransferase 3, chloroplastic OS=Arabidopsis thaliana GN=BCAT3 PE=1 SV=1
AT3G59760	Q43725	0,595	0,001	mitochondrion	Cysteine synthase, mitochondrial OS=Arabidopsis thaliana GN=OASC PE=1 SV=3
AT5G38530	Q9FFW8	0,599	0,001	plastid	Tryptophan synthase beta chain OS=Arabidopsis thaliana GN=TSBtype2 PE=2 SV=1
AT2G39800	P54887	0,648	0,001	peroxisome	Delta-1-pyrroline-5-carboxylate synthase A OS=Arabidopsis thaliana GN=P5CSA PE=1 SV=1
AT3G01120	P55217	0,649	0,001	plastid	Cystathionine gamma-synthase 1, chloroplastic OS=Arabidopsis thaliana GN=CGS1 PE=1 SV=3
AT2G36880	Q9SJL8	0,658	0,001	cytosol	S-adenosylmethionine synthase 3 OS=Arabidopsis thaliana GN=METK3 PE=1 SV=1

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AT5G46180	Q9FNK4	0,663	0,008	mitochondrion	Ornithine aminotransferase, mitochondrial OS=Arabidopsis thaliana GN=DELTA-OAT PE=1 SV=1
AT3G03780	Q9SRV5	0,668	0,001	cytosol	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 2 OS=Arabidopsis thaliana GN=MS2 PE=1 SV=1
AT5G65010	Q9LV77	0,682	0,001	golgi	Asparagine synthetase [glutamine-hydrolyzing] 2 OS=Arabidopsis thaliana GN=ASN2 PE=2 SV=1
AT1G80360	Q9C969	0,691	0,002	cytosol	Aromatic aminotransferase ISS1 OS=Arabidopsis thaliana GN=ISS1 PE=1 SV=1
AT5G05730	P32068	0,752	0,001	plastid	Anthranilate synthase alpha subunit 1, chloroplastic OS=Arabidopsis thaliana GN=ASA1 PE=1 SV=1
AT3G23810	Q9LK36	0,845	0,001	cytosol	Adenosylhomocysteinase 2 OS=Arabidopsis thaliana GN=SAHH2 PE=2 SV=1
AT3G47340	P49078	0,888	0,002	cytosol	Asparagine synthetase [glutamine-hydrolyzing] 1 OS=Arabidopsis thaliana GN=ASN1 PE=2 SV=2
AT5G16290	Q9FFF4	0,913	0,003	plastid	Acetolactate synthase small subunit 1, chloroplastic OS=Arabidopsis thaliana GN=VAT1 PE=1 SV=1
AT3G06850	Q9M7Z1	0,958	0,002	mitochondrion	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=Arabidopsis thaliana GN=BCE2 PE=1 SV=1
AT4G39980	P29976	0,972	0,001	plastid	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic OS=Arabidopsis thaliana GN=DHS1 PE=2 SV=2
AT3G55610	P54888	1,046	0,001	cytosol	Delta-1-pyrroline-5-carboxylate synthase B OS=Arabidopsis thaliana GN=P5CSB PE=2 SV=1
AT1G22410	Q9SK84	1,072	0,002	plastid	Phospho-2-dehydro-3-deoxyheptonate aldolase OS=Arabidopsis thaliana GN=At1g22410 PE=3 SV=1
AT5G14200	Q9FMT1	1,124	0,001	plastid	3-isopropylmalate dehydrogenase 3, chloroplastic OS=Arabidopsis thaliana GN=IMDH3 PE=1 SV=1
AT3G19710	Q9LE06	1,259	0,001	cytosol	Methionine aminotransferase BCAT4 OS=Arabidopsis thaliana GN=BCAT4 PE=1 SV=1
AT4G33510	Q00218	1,268	0,001	plastid	Phospho-2-dehydro-3-deoxyheptonate aldolase 2, chloroplastic OS=Arabidopsis thaliana GN=DHS2 PE=2 SV=2
Biodegradation of Xenobiotics					
AT1G67280	Q8W593	-0,331	0,002	plastid	Probable lactoylglutathione lyase, chloroplastic OS=Arabidopsis thaliana GN=At1g67280 PE=1 SV=1
AT5G57040	Q9LTR8	-0,313	0,008	plastid	At5g57040 OS=Arabidopsis thaliana GN=MHM17.18 PE=2 SV=1
AT1G11840	O65398	0,366	0,001	peroxisome	Lactoylglutathione lyase GLX1 OS=Arabidopsis thaliana GN=GLX1 PE=1 SV=1
C1- metabolism					
AT2G26080	O80988	-0,568	0,001	mitochondrion	Glycine dehydrogenase (decarboxylating) 2, mitochondrial OS=Arabidopsis thaliana GN=GLDP2 PE=1 SV=1
AT4G33010	Q94B78	-0,517	0,001	mitochondrion	Glycine dehydrogenase (decarboxylating) 1, mitochondrial OS=Arabidopsis thaliana GN=GLDP1 PE=1 SV=2
AT4G37930	Q9SZJ5	-0,443	0,001	mitochondrion	Serine hydroxymethyltransferase 1, mitochondrial OS=Arabidopsis thaliana GN=SHM1 PE=1 SV=1
AT5G26780	Q94C74	-0,364	0,001	mitochondrion	Serine hydroxymethyltransferase 2, mitochondrial OS=Arabidopsis thaliana GN=SHM2 PE=1 SV=2
AT1G50480	Q9SPK5	0,309	0,001	cytosol	Formate--tetrahydrofolate ligase OS=Arabidopsis thaliana GN=THFS PE=2 SV=1
AT2G44160	O80585	0,326	0,002	cytosol	Methylenetetrahydrofolate reductase 2 OS=Arabidopsis thaliana GN=MTHFR2 PE=1 SV=2
AT5G14780	Q9S7E4	0,404	0,001	mitochondrion	Formate dehydrogenase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=FDH1 PE=1 SV=1
AT4G13930	O23254	0,471	0,001	cytosol	Serine hydroxymethyltransferase 4 OS=Arabidopsis thaliana GN=SHM4 PE=1 SV=1
Cell					
AT4G15930	Q84VW0	-1,311	0,004	cytosol	At4g15930 OS=Arabidopsis thaliana GN=At4g15930 PE=1 SV=1
AT5G13850	Q6ICZ8	-0,881	0,001	cytosol	Nascent polypeptide-associated complex subunit alpha-like protein 3 OS=Arabidopsis thaliana GN=At5g13850 PE=1 SV=1
AT3G15520	P82869	-0,828	0,001	plastid	Peptidyl-prolyl cis-trans isomerase CYP37, chloroplastic OS=Arabidopsis thaliana GN=CYP37 PE=1 SV=3
AT4G04020	O81439	-0,822	0,001	plastid	Probable plastid-lipid-associated protein 1, chloroplastic OS=Arabidopsis thaliana GN=PAP1 PE=1 SV=1
AT4G22240	O49629	-0,667	0,003	plastid	Probable plastid-lipid-associated protein 2, chloroplastic OS=Arabidopsis thaliana GN=PAP2 PE=1 SV=1
AT1G78770	B3DNN5	-0,656	0,003	nucleus	Anaphase-promoting complex subunit 6 OS=Arabidopsis thaliana GN=APC6 PE=2 SV=1
AT1G51110	Q8LAP6	-0,521	0,001	plastid	Probable plastid-lipid-associated protein 12, chloroplastic OS=Arabidopsis thaliana GN=PAP12 PE=1 SV=1
AT3G62030	P34791	-0,486	0,002	plastid	Peptidyl-prolyl cis-trans isomerase CYP20-3, chloroplastic OS=Arabidopsis thaliana GN=CYP20-3 PE=1 SV=1
AT3G63190	Q9M1X0	-0,427	0,001	plastid	Ribosome-recycling factor, chloroplastic OS=Arabidopsis thaliana GN=RRF PE=2 SV=2
AT1G74070	F4HTT6	-0,408	0,003	plastid	Peptidyl-prolyl cis-trans isomerase CYP26-2, chloroplastic OS=Arabidopsis thaliana GN=CYP26-2 PE=2 SV=1
AT2G35490	O82291	-0,389	0,001	plastid	Probable plastid-lipid-associated protein 3, chloroplastic OS=Arabidopsis thaliana GN=PAP3 PE=1 SV=1
AT2G26210	Q8VZ34	-0,383	0,009	cytosol	Ankyrin repeat family protein OS=Arabidopsis thaliana GN=At2g26210 PE=2 SV=1
AT4G35450	Q9SAR5	-0,346	0,001	cytosol	Ankyrin repeat domain-containing protein 2A OS=Arabidopsis thaliana GN=AKR2A PE=1 SV=2
AT5G35100	O65220	-0,344	0,003	plastid	Peptidyl-prolyl cis-trans isomerase CYP28, chloroplastic OS=Arabidopsis thaliana GN=CYP28 PE=1 SV=1
AT1G80480	Q9M8L6	-0,339	0,002	plastid	At1g80480 OS=Arabidopsis thaliana GN=PTAC17 PE=2 SV=1
AT5G13120	Q9ASS6	-0,332	0,003	plastid	Photosynthetic NDsubunit of lumenal location 5, chloroplastic OS=Arabidopsis thaliana GN=PNSL5 PE=1 SV=1
AT3G09840	P54609	0,306	0,001	cytosol	Cell division control protein 48 homolog A OS=Arabidopsis thaliana GN=CDC48A PE=1 SV=1
AT1G21380	Q9LPL6	0,374	0,003	nucleus	TOM1-like protein 3 OS=Arabidopsis thaliana GN=TOL3 PE=1 SV=1
AT2G21390	Q9SJT9	0,378	0,001	cytosol	Coatomer subunit alpha-2 OS=Arabidopsis thaliana GN=At2g21390 PE=2 SV=1
AT2G21280	Q9SJU9	0,39	0,01	plastid	Epimerase family protein SDR39U1 homolog, chloroplastic OS=Arabidopsis thaliana GN=GC1 PE=2 SV=2
AT5G65020	Q9XEE2	0,392	0,002	asma membrane,cytos	Annexin D2 OS=Arabidopsis thaliana GN=ANN2 PE=1 SV=1
AT3G56070	Q38867	0,392	0,002	mitochondrion	Peptidyl-prolyl cis-trans isomerase CYP19-3 OS=Arabidopsis thaliana GN=CYP19-3 PE=2 SV=2
AT4G30160	O65570	0,398	0,01	cytosol	Villin-4 OS=Arabidopsis thaliana GN=VLN4 PE=1 SV=1

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AT5G44340	P24636	0,407	0,004	cytosol	Tubulin beta-4 chain OS=Arabidopsis thaliana GN=TUBB4 PE=2 SV=2
AT5G05010	Q93Y22	0,435	0,001	golgi	Coatomer subunit delta OS=Arabidopsis thaliana GN=At5g05010 PE=1 SV=2
AT3G57890	F4J4K6	0,445	0,009	golgi	Tubulin binding cofactor C domain-containing protein OS=Arabidopsis thaliana GN=At3g57890 PE=4 SV=1
AT5G40770	O04331	0,524	0,002	mitochondrion	Prohibitin-3, mitochondrial OS=Arabidopsis thaliana GN=PHB3 PE=1 SV=1
AT1G07660	P59259	0,535	0,002	nucleus	Histone H4 OS=Arabidopsis thaliana GN=At1g07660 PE=1 SV=2
AT1G35720	Q9SYT0	0,538	0,001	peroxisome	Annexin D1 OS=Arabidopsis thaliana GN=ANN1 PE=1 SV=1
AT1G03860	Q9ZNT7	0,539	0,002	mitochondrion	Prohibitin-2, mitochondrial OS=Arabidopsis thaliana GN=PHB2 PE=1 SV=1
AT4G23460	O81742	0,587	0,002	plasma membrane	Beta-adaptin-like protein C OS=Arabidopsis thaliana GN=BETAC-AD PE=1 SV=2
AT5G15970	P31169	0,717	0,001	cytosol	Stress-induced protein KIN2 OS=Arabidopsis thaliana GN=KIN2 PE=2 SV=1
AT2G29550	P29515	0,851	0,002	cytosol	Tubulin beta-7 chain OS=Arabidopsis thaliana GN=TUBB7 PE=2 SV=1
AT1G74790	Q9SSG3	1,068	0,002	plasma membrane	HIPL1 protein OS=Arabidopsis thaliana GN=HIPL1 PE=1 SV=2
Cell wall					
AT3G48530	Q8LBB2	-0,812	0,006	cytosol	SNF1-related protein kinase regulatory subunit gamma-1 OS=Arabidopsis thaliana GN=KING1 PE=1 SV=2
AT1G78060	Q9SGZ5	0,308	0,004	extracellular	Probable beta-D-xylosidase 7 OS=Arabidopsis thaliana GN=BXL7 PE=2 SV=2
AT1G63000	Q9LQ04	0,382	0,01	cytosol	Bifunctional dTDP-4-dehydrorhamnose 3,5-epimerase/dTDP-4-dehydrorhamnose reductase OS=Arabidopsis thaliana GN=NRS/ER PE=1 SV=1
AT4G19410	Q940J8	0,4	0,001	extracellular	Pectin acetylesterase 7 OS=Arabidopsis thaliana GN=PAE7 PE=2 SV=1
AT5G64570	Q9FLG1	0,41	0,001	extracellular	Beta-D-xylosidase 4 OS=Arabidopsis thaliana GN=BXL4 PE=1 SV=1
AT5G20950	A0A1P8BG25	0,41	0,004	extracellular	Glycosyl hydrolase family protein OS=Arabidopsis thaliana GN=At5g20950 PE=1 SV=1
AT2G45790	O80840	0,421	0,003	mitochondrion,cytosol	Phosphomannomutase OS=Arabidopsis thaliana GN=PMM PE=1 SV=1
AT2G27860	Q9ZUY6	0,432	0,008	cytosol	UDP-D-apiose/UDP-D-xylose synthase 1 OS=Arabidopsis thaliana GN=AXS1 PE=1 SV=1
AT5G15490	Q9LF33	0,441	0,007	extracellular	UDP-glucose 6-dehydrogenase 3 OS=Arabidopsis thaliana GN=UGD3 PE=1 SV=1
AT1G41830	F4I7X1	0,452	0,002	extracellular	SKU5-similar 6 OS=Arabidopsis thaliana GN=SKS6 PE=4 SV=1
AT4G24010	Q570S7	0,463	0,006	plasma membrane	Cellulose synthase-like protein G1 OS=Arabidopsis thaliana GN=CSLG1 PE=2 SV=1
AT2G39770	O22287	0,469	0,002	cytosol	Mannose-1-phosphate guanylyltransferase 1 OS=Arabidopsis thaliana GN=CYT1 PE=1 SV=1
AT4G12730	Q9SU13	0,48	0,005	plasma membrane	Fasciclin-like arabinogalactan protein 2 OS=Arabidopsis thaliana GN=FLA2 PE=1 SV=1
AT5G59290	Q9FIE8	0,491	0,001	cytosol	UDP-glucuronic acid decarboxylase 3 OS=Arabidopsis thaliana GN=UXS3 PE=1 SV=1
AT5G39320	Q9FM01	0,492	0,007	extracellular	UDP-glucose 6-dehydrogenase 4 OS=Arabidopsis thaliana GN=UGD4 PE=1 SV=1
AT5G57560	Q38857	0,563	0,005	extracellular	Xyloglucan endotransglucosylase/hydrolase protein 22 OS=Arabidopsis thaliana GN=XTH22 PE=1 SV=1
AT1G08200	Q9SGE0	0,568	0,001	cytosol	UDP-D-apiose/UDP-D-xylose synthase 2 OS=Arabidopsis thaliana GN=AXS2 PE=2 SV=1
AT5G06860	Q9M5J9	0,574	0,004	extracellular	Polygalacturonase inhibitor 1 OS=Arabidopsis thaliana GN=PGIP1 PE=1 SV=1
AT3G02230	Q9SRT9	0,645	0,001	cytosol	UDP-arabinopyranose mutase 1 OS=Arabidopsis thaliana GN=RGP1 PE=1 SV=1
AT3G51160	P93031	0,669	0,003	cytosol	GDP-mannose 4,6 dehydratase 2 OS=Arabidopsis thaliana GN=MUR1 PE=1 SV=3
AT3G44990	P93046	0,673	0,006	ıcellular,plasma memb	Xyloglucan endotransglucosylase/hydrolase protein 31 OS=Arabidopsis thaliana GN=XTH31 PE=1 SV=2
AT3G29360	Q9LIA8	0,682	0,002	extracellular	UDP-glucose 6-dehydrogenase 2 OS=Arabidopsis thaliana GN=UGD2 PE=1 SV=1
AT5G15650	Q9LFW1	0,684	0,001	golgi	UDP-arabinopyranose mutase 2 OS=Arabidopsis thaliana GN=RGP2 PE=1 SV=1
AT2G06850	Q39099	0,722	0,003	extracellular	Xyloglucan endotransglucosylase/hydrolase protein 4 OS=Arabidopsis thaliana GN=XTH4 PE=1 SV=1
AT5G49360	Q9FGY1	0,757	0,001	extracellular	Beta-D-xylosidase 1 OS=Arabidopsis thaliana GN=BXL1 PE=1 SV=1
AT5G16510	Q9FFD2	0,9	0,001	extracellular,cytosol	Probable UDP-arabinopyranose mutase 5 OS=Arabidopsis thaliana GN=RGP5 PE=1 SV=1
AT4G30270	P24806	0,946	0,001	extracellular	Xyloglucan endotransglucosylase/hydrolase protein 24 OS=Arabidopsis thaliana GN=XTH24 PE=1 SV=2
AT1G69530	Q9C554	1,133	0,005	extracellular	Expansin-A1 OS=Arabidopsis thaliana GN=EXPA1 PE=2 SV=1
AT1G65310	O80803	1,524	0,001	extracellular	Probable xyloglucan endotransglucosylase/hydrolase protein 17 OS=Arabidopsis thaliana GN=XTH17 PE=1 SV=1
Co-factor and vitamin metabolism					
AT2G38230	O80448	-0,36	0,001	cytosol	Pyridoxal 5'-phosphate synthase subunit PDX1.1 OS=Arabidopsis thaliana GN=PDX11 PE=1 SV=1
AT5G44720	O48588	0,321	0,007	cytosol	Molybdenum cofactor sulfurase family protein OS=Arabidopsis thaliana GN=T19K24.17 PE=2 SV=1
AT5G66120	Q8VYV7	0,434	0,001	peroxisome	3-dehydroquinate synthase, chloroplastic OS=Arabidopsis thaliana GN=DHQS PE=1 SV=1
AT5G59750	Q9FN89	0,435	0,009	plastid	Monofunctional riboflavin biosynthesis protein RIBA 3, chloroplastic OS=Arabidopsis thaliana GN=RIBA3 PE=1 SV=1
AT4G35360	Q8W4Q1	0,521	0,005	cytosol	At4g35360/F23E12_80 OS=Arabidopsis thaliana GN=At4g35360 PE=1 SV=1
AT5G64300	P47924	0,574	0,002	plastid	Bifunctional riboflavin biosynthesis protein RIBA 1, chloroplastic OS=Arabidopsis thaliana GN=RIBA1 PE=1 SV=2
AT5G20990	Q39054	0,865	0,001	cytosol	Molybdopterin biosynthesis protein CNX1 OS=Arabidopsis thaliana GN=CNX1 PE=1 SV=2
AT3G14990	Q9FPF0	0,881	0,001	golgi	Protein DJ-1 homolog A OS=Arabidopsis thaliana GN=DJ1A PE=1 SV=1

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Development					
AT2G03440	Q9ZQ80	-0,629	0,001	nucleus	Nodulin-related protein 1 OS=Arabidopsis thaliana GN=NRP1 PE=1 SV=1
AT3G02180	Q9S7P8	-0,417	0,003	plasma membrane	Protein SPIRAL1-like 3 OS=Arabidopsis thaliana GN=SP1L3 PE=1 SV=1
AT4G24220	Q9STX2	0,351	0,008	cytosol	3-oxo-Delta(4,5)-steroid 5-beta-reductase OS=Arabidopsis thaliana GN=VEP1 PE=1 SV=1
AT5G63420	Q84W56	0,357	0,004	plastid	RNA-metabolising metallo-beta-lactamase family protein OS=Arabidopsis thaliana GN=emb2746 PE=1 SV=1
AT3G18060	Q9LV35	0,383	0,009	cytosol	Actin-interacting protein 1-2 OS=Arabidopsis thaliana GN=AIP1-2 PE=2 SV=1
AT1G10510	Q93ZV8	0,407	0,004	plastid	RNI-like superfamily protein OS=Arabidopsis thaliana GN=emb2004 PE=2 SV=1
AT1G02140	O23676	0,432	0,004	nucleus	Protein mago nashi homolog OS=Arabidopsis thaliana GN=MAGO PE=1 SV=1
AT2G34040	O22957	0,446	0,001	cytosol	Apoptosis inhibitory protein 5 (API5) OS=Arabidopsis thaliana GN=At2g34040 PE=1 SV=2
AT3G51280	Q9SD20	0,456	0,009	nucleus	reversed Protein POLLENLESS 3-LIKE 2 OS=Arabidopsis thaliana GN=At3g51280 PE=2 SV=1
AT5G25940	Q9XGZ3	0,731	0,002	mitochondrion	Early nodulin-like protein OS=Arabidopsis thaliana GN=At5g25940 PE=2 SV=1
AT1G55450	F4I0B5	0,744	0,003	golgi	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein OS=Arabidopsis thaliana GN=At1g55450 PE=4 SV=1
AT2G38860	Q9ZV19	0,852	0,001	extracellular	DJ-1 protein homolog E OS=Arabidopsis thaliana GN=DJ1E PE=1 SV=1
AT2G42840	Q9S728	0,951	0,002	extracellular	Protodermal factor 1 OS=Arabidopsis thaliana GN=PDF1 PE=2 SV=1
AT2G26560	O48723	1,052	0,009	cytosol	Patatin-like protein 2 OS=Arabidopsis thaliana GN=PLP2 PE=1 SV=1
AT1G52690	Q96270	1,274	0,003	nucleus	Late embryogenesis abundant protein 7 OS=Arabidopsis thaliana GN=LEA7 PE=2 SV=1
AT5G06760	Q9FG31	1,345	0,001	peroxisome	Late embryogenesis abundant protein 46 OS=Arabidopsis thaliana GN=LEA46 PE=2 SV=1
DNA					
AT3G20475	F4JEP5	-1,403	0,001	nucleus	reversed DNA mismatcrepair protein MSH5 OS=Arabidopsis thaliana GN=MSH5 PE=2 SV=1
AT5G56950	Q94K07	-1,008	0,002	nucleus	Nucleosome assembly protein 1;3 OS=Arabidopsis thaliana GN=NAP1;3 PE=1 SV=1
AT1G18800	Q8LC68	-0,829	0,001	nucleus	NAP1-related protein 2 OS=Arabidopsis thaliana GN=NRP2 PE=1 SV=2
AT1G74560	Q9CA59	-0,803	0,002	nucleus,cytosol	NAP1-related protein 1 OS=Arabidopsis thaliana GN=NRP1 PE=1 SV=1
AT2G19480	Q9ZUP3	-0,746	0,001	nucleus	Nucleosome assembly protein 1;2 OS=Arabidopsis thaliana GN=NAP1;2 PE=1 SV=1
AT4G26110	Q9SZI2	-0,678	0,001	nucleus	Nucleosome assembly protein 1;1 OS=Arabidopsis thaliana GN=NAP1;1 PE=1 SV=1
AT4G09730	Q56X76	-0,454	0,007	plastid	DEAD-box ATP-dependent RNA helicase 39 OS=Arabidopsis thaliana GN=RH39 PE=2 SV=2
AT2G28560	Q9SK02	-0,423	0,008	nucleus	DNA repair protein RAD51 homolog 2 OS=Arabidopsis thaliana GN=RAD51B PE=2 SV=2
AT4G28440	O49453	0,335	0,003	cytosol	Uncharacterized protein At4g28440 OS=Arabidopsis thaliana GN=At4g28440 PE=1 SV=1
AT2G06500	Q9SKI5	0,417	0,008	nucleus	Ac-like transposase OS=Arabidopsis thaliana GN=At2g06500 PE=4 SV=1
AT1G08880	O04848	0,443	0,008	nucleus	Probable histone H2AXa OS=Arabidopsis thaliana GN=At1g08880 PE=1 SV=1
AT3G54560	O23628	0,497	0,005	nucleus	Histone H2A variant 1 OS=Arabidopsis thaliana GN=H2AV PE=1 SV=1
AT4G34180	Q93V74	0,538	0,002	extracellular	AT4g34180/F28A23_60 OS=Arabidopsis thaliana GN=At4g34180 PE=2 SV=1
AT3G15950	Q9LSB4	0,544	0,001	endoplasmic reticulum	TSA1-like protein OS=Arabidopsis thaliana GN=NAI2 PE=1 SV=1
AT5G22880	Q9FFC0	0,578	0,001	nucleus	Histone H2B.10 OS=Arabidopsis thaliana GN=At5g22880 PE=1 SV=3
AT5G59870	Q9FJE8	0,672	0,006	nucleus	Probable histone H2A.7 OS=Arabidopsis thaliana GN=At5g59870 PE=1 SV=1
AT1G06670	F4IDQ6	0,952	0,002	nucleus	reversed DExH-box ATP-dependent RNA helicase DExH2 OS=Arabidopsis thaliana GN=NIPE=1 SV=1
AT1G51060	Q9C681	1,022	0,002	nucleus	Probable histone H2A.1 OS=Arabidopsis thaliana GN=At1g51060 PE=1 SV=1
AT1G20960	Q9SYP1	1,199	0,004	nucleus	reversed DExH-box ATP-dependent RNA helicase DExH12 OS=Arabidopsis thaliana GN=BRR2A PE=1 SV=1
Fermentation					
AT5G54960	Q9FFT4	0,41	0,002	cytosol	Pyruvate decarboxylase 2 OS=Arabidopsis thaliana GN=PDC2 PE=2 SV=1
AT3G48000	Q9SU63	0,528	0,001	mitochondrion	Aldehyde dehydrogenase family 2 member B4, mitochondrial OS=Arabidopsis thaliana GN=ALDH2B4 PE=1 SV=1
AT3G24503	Q56YU0	0,57	0,001	cytosol	Aldehyde dehydrogenase family 2 member C4 OS=Arabidopsis thaliana GN=ALDH2C4 PE=1 SV=2
AT1G54100	Q9SYG7	0,585	0,001	cytosol	Aldehyde dehydrogenase family 7 member B4 OS=Arabidopsis thaliana GN=ALDH7B4 PE=2 SV=3
AT5G17380	Q9LF46	0,598	0,001	peroxisome	2-hydroxyacyl-CoA lyase OS=Arabidopsis thaliana GN=HACL PE=1 SV=1
AT4G36250	Q70E96	0,752	0,003	cytosol	Aldehyde dehydrogenase family 3 member F1 OS=Arabidopsis thaliana GN=ALDH3F1 PE=2 SV=2
Gluconeogenesis					
AT2G22780	O82399	-0,597	0,004	peroxisome	Malate dehydrogenase 1, peroxisomal OS=Arabidopsis thaliana GN=PMDH1 PE=1 SV=1
AT5G09660	Q9ZP05	-0,483	0,001	peroxisome	Malate dehydrogenase 2, peroxisomal OS=Arabidopsis thaliana GN=PMDH2 PE=1 SV=1
AT2G42790	Q9SJH7	0,485	0,007	peroxisome	Citrate synthase 3, peroxisomal OS=Arabidopsis thaliana GN=CSY3 PE=2 SV=1
AT3G58750	Q9LXS6	0,524	0,006	peroxisome	Citrate synthase 2, peroxisomal OS=Arabidopsis thaliana GN=CSY2 PE=2 SV=1
AT4G15530	O23404	0,555	0,001	plastid,cytosol	Pyruvate, phosphate dikinase 1, chloroplastic OS=Arabidopsis thaliana GN=PPDK PE=1 SV=2

Glycolisis					
AT1G70820	Q9SSL0	-0,738	0,001	plastid	At1g70820 OS=Arabidopsis thaliana GN=At1g70820 PE=2 SV=1
AT5G22620	Q9FNJ9	-0,387	0,005	plastid	Probable 2-carboxy-D-arabinitol-1-phosphatase OS=Arabidopsis thaliana GN=At5g22620 PE=1 SV=1
AT1G79550	Q9SAJ4	0,319	0,001	cytosol	Phosphoglycerate kinase 3, cytosolic OS=Arabidopsis thaliana GN=PGK3 PE=1 SV=1
AT3G03250	Q9M9P3	0,33	0,002	cytosol	UTP--glucose-1-phosphate uridylyltransferase 2 OS=Arabidopsis thaliana GN=UGP2 PE=1 SV=1
AT1G09780	O04499	0,37	0,001	cytosol	2,3-bisphosphoglycerate-independent phosphoglycerate mutase 1 OS=Arabidopsis thaliana GN=PGM1 PE=2 SV=3
AT1G53310	Q9MAH0	0,385	0,001	cytosol	Phosphoenolpyruvate carboxylase 1 OS=Arabidopsis thaliana GN=PPC1 PE=1 SV=1
AT1G76550	Q9C9K3	0,421	0,003	cytosol	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha 2 OS=Arabidopsis thaliana GN=PFP-ALPHA2 PE=2 SV=1
AT1G20950	Q9SYP2	0,44	0,002	cytosol	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha 1 OS=Arabidopsis thaliana GN=PFP-ALPHA1 PE=2 SV=1
AT1G23190	O49299	0,451	0,001	cytosol	Probable phosphoglucomutase, cytoplasmic 1 OS=Arabidopsis thaliana GN=At1g23190 PE=2 SV=2
AT1G12000	Q8W4M5	0,474	0,002	golgi	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta 1 OS=Arabidopsis thaliana GN=PFP-BETA1 PE=1 SV=1
AT2G36530	P25696	0,478	0,001	cytosol	Bifunctional enolase 2/transcriptional activator OS=Arabidopsis thaliana GN=ENO2 PE=1 SV=1
AT3G52990	Q94KE3	0,479	0,002	cytosol	Pyruvate kinase OS=Arabidopsis thaliana GN=At3g52990 PE=2 SV=1
AT5G56350	Q9FM97	0,481	0,004	cytosol	Pyruvate kinase OS=Arabidopsis thaliana GN=MCD7.8 PE=2 SV=1
AT2G42600	Q5GM68	0,507	0,001	cytosol	Phosphoenolpyruvate carboxylase 2 OS=Arabidopsis thaliana GN=PPC2 PE=1 SV=2
AT4G04040	F4JGR5	0,543	0,002	cytosol	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta 2 OS=Arabidopsis thaliana GN=PFP-BETA2 PE=3 SV=1
AT3G04120	P25858	0,636	0,002	nucleus,cytosol	Glyceraldehyde-3-phosphate dehydrogenase GAPC1, cytosolic OS=Arabidopsis thaliana GN=GAPC1 PE=1 SV=2
AT1G13440	Q9FX54	0,666	0,001	nucleus,cytosol	Glyceraldehyde-3-phosphate dehydrogenase GAPC2, cytosolic OS=Arabidopsis thaliana GN=GAPC2 PE=1 SV=1
Hormone metabolism					
AT4G19170	O49675	-0,943	0,001	plastid	Probable carotenoid cleavage dioxygenase 4, chloroplastic OS=Arabidopsis thaliana GN=CCD4 PE=1 SV=1
AT3G45140	P38418	-0,869	0,003	plastid	Lipoxygenase 2, chloroplastic OS=Arabidopsis thaliana GN=LOX2 PE=1 SV=1
AT1G30100	Q9C6Z1	-0,82	0,002	plastid	reversed Probable 9-cis-epoxycarotenoid dioxygenase NCED5, chloroplastic OS=Arabidopsis thaliana GN=NCED5 PE=1 SV=1
AT5G42650	Q96242	-0,614	0,001	plastid	Allene oxide synthase, chloroplastic OS=Arabidopsis thaliana GN=CYP74A PE=1 SV=3
AT2G33830	P93017	-0,345	0,006	peroxisome	Dormancy-associated protein homolog 1 OS=Arabidopsis thaliana GN=DRMH1 PE=1 SV=1
AT1G05010	Q06588	-0,331	0,004	golgi	1-aminocyclopropane-1-carboxylate oxidase 4 OS=Arabidopsis thaliana GN=ACO4 PE=1 SV=2
AT3G11930	B9DG73	0,442	0,003	nucleus	AT3G11930 protein OS=Arabidopsis thaliana GN=At3g11930 PE=1 SV=1
AT5G13370	Q8GZ29	0,456	0,002	cytosol	At5g13370 OS=Arabidopsis thaliana GN=At5g13370 PE=2 SV=1
AT3G16460	O04310	0,552	0,001	cytosol	Jacalin-related lectin 34 OS=Arabidopsis thaliana GN=JAL34 PE=1 SV=1
AT3G44310	P32961	0,596	0,001	cytosol	Nitrilase 1 OS=Arabidopsis thaliana GN=NIT1 PE=1 SV=2
AT1G52100	Q5XF82	0,976	0,001	cytosol	Jacalin-related lectin 11 OS=Arabidopsis thaliana GN=JAL11 PE=2 SV=1
AT1G22400	Q9SK82	1,203	0,001	cytosol	UDP-glycosyltransferase 85A1 OS=Arabidopsis thaliana GN=UGT85A1 PE=2 SV=1
AT3G02480	Q9M892	2,093	0,001	cytosol	AT3g02480/F16B3_11 OS=Arabidopsis thaliana GN=At3g02480 PE=2 SV=1
AT3G44300	P32962	2,239	0,001	cytosol	Nitrilase 2 OS=Arabidopsis thaliana GN=NIT2 PE=1 SV=1
Lipid metabolism					
AT4G16155	F4JLP5	-0,61	0,001	plastid	Dihydrolipoyl dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=LPD2 PE=2 SV=2
AT3G56130	Q93W03	-0,581	0,004	plastid	AT3g56130/F18O21_90 OS=Arabidopsis thaliana GN=At3g56130 PE=2 SV=1
AT4G36480	Q94IB8	-0,501	0,006	endoplasmic reticulum	Long chain base biosynthesis protein 1 OS=Arabidopsis thaliana GN=LCB1 PE=1 SV=1
AT4G25970	A4GNA8	-0,427	0,007	endoplasmic reticulum	Phosphatidylserine decarboxylase proenzyme 3 OS=Arabidopsis thaliana GN=PSD3 PE=1 SV=1
AT1G45201	A0A1P8AVY3	-0,414	0,001	golgi	Triacylglycerol lipase-like 1 OS=Arabidopsis thaliana GN=TLL1 PE=4 SV=1
AT1G32200	Q43307	-0,395	0,001	plastid	Glycerol-3-phosphate acyltransferase, chloroplastic OS=Arabidopsis thaliana GN=ATS1 PE=2 SV=2
AT2G42690	Q9SJI7	-0,371	0,005	cytosol	Phospholipase A1-IIdelta OS=Arabidopsis thaliana GN=At2g42690 PE=1 SV=1
AT3G15690	Q8GRT9	-0,342	0,006	plastid	Putative acetyl-CoA carboxylase biotin-containing subunit OS=Arabidopsis thaliana GN=At3g15690 PE=2 SV=1
AT5G16390	Q42533	-0,325	0,004	plastid	Biotin carboxyl carrier protein of acetyl-CoA carboxylase 1, chloroplastic OS=Arabidopsis thaliana GN=BCCP1 PE=1 SV=2
AT3G05020	P11829	0,303	0,008	plastid	Acyl carrier protein 1, chloroplastic OS=Arabidopsis thaliana GN=ACP1 PE=1 SV=1
AT5G36880	B9DGD6	0,318	0,005	plastid	cetyl-coenzyme A synthetase, chloroplastic/glyoxysomal OS=Arabidopsis thaliana GN=ACS PE=1 SV=1
AT2G34590	O64688	0,379	0,003	plastid	Pyruvate dehydrogenase E1 component subunit beta-3, chloroplastic OS=Arabidopsis thaliana GN=E1-BETA-2 PE=2 SV=1
AT2G43710	O22832	0,394	0,01	plastid	Stearoyl-[acyl-carrier-protein] 9-desaturase 7, chloroplastic OS=Arabidopsis thaliana GN=FAB2 PE=1 SV=1
AT1G80460	Q9M8L4	0,419	0,005	cytosol	Glycerol kinase OS=Arabidopsis thaliana GN=GLPK PE=1 SV=1
AT4G16760	O65202	0,485	0,001	peroxisome	Peroxisomal acyl-coenzyme A oxidase 1 OS=Arabidopsis thaliana GN=ACX1 PE=1 SV=1
AT4G26690	Q9SZ11	0,487	0,002	plasma membrane	Glycerophosphodiester phosphodiesterase GDPDL3 OS=Arabidopsis thaliana GN=GDPDL3 PE=1 SV=3
AT1G54580	P25701	0,489	0,006	plastid	Acyl carrier protein 2, chloroplastic OS=Arabidopsis thaliana GN=ACP2 PE=1 SV=2
AT4G33030	O48917	0,541	0,001	plastid	UDP-sulfoquinovose synthase, chloroplastic OS=Arabidopsis thaliana GN=SQD1 PE=1 SV=1
AT3G48990	Q9SMT7	0,542	0,001	peroxisome	Oxalate--CoA ligase OS=Arabidopsis thaliana GN=AAE3 PE=1 SV=1

AT5G55480	Q9FJ62	0,583	0,004	plasma membrane	Glycerophosphodiester phosphodiesterase GDPDL4 OS=Arabidopsis thaliana GN=GDPDL4 PE=1 SV=1
AT1G77590	Q9CAP8	0,598	0,004	plastid	Long chain acyl-CoA synthetase 9, chloroplastic OS=Arabidopsis thaliana GN=LACS9 PE=1 SV=1
AT5G54500	Q9LSQ5	0,61	0,001	plasma membrane	NAD(P)dehydrogenase (quinone) FQR1 OS=Arabidopsis thaliana GN=FQR1 PE=1 SV=1
AT2G38540	Q42589	0,613	0,002	extracellular	Non-specific lipid-transfer protein 1 OS=Arabidopsis thaliana GN=LTP1 PE=2 SV=1
AT3G08770	Q9LDB4	0,778	0,001	extracellular	Non-specific lipid-transfer protein 6 OS=Arabidopsis thaliana GN=LTP6 PE=3 SV=1
AT1G48600	Q944H0	0,841	0,002	cytosol	Phosphomethylethanolamine N-methyltransferase OS=Arabidopsis thaliana GN=NMT2 PE=2 SV=2
AT1G52760	Q9C942	0,887	0,002	mitochondrion	Caffeoylshikimate esterase OS=Arabidopsis thaliana GN=CSE PE=1 SV=1
AT5G20060	Q8L9X1	1,092	0,002	mitochondrion	Alpha/beta-Hydrolases superfamily protein OS=Arabidopsis thaliana GN=At5g20060 PE=1 SV=1
AT2G38530	Q9S7I3	1,199	0,001	extracellular	Non-specific lipid-transfer protein 2 OS=Arabidopsis thaliana GN=LTP2 PE=3 SV=1
AT3G51600	Q9XFS7	1,392	0,001	extracellular	Non-specific lipid-transfer protein 5 OS=Arabidopsis thaliana GN=LTP5 PE=1 SV=1
AT5G59320	Q9LLR7	1,473	0,001	extracellular	Non-specific lipid-transfer protein 3 OS=Arabidopsis thaliana GN=LTP3 PE=3 SV=1
AT1G73600	Q9C6B9	2,558	0,001	cytosol	Phosphoethanolamine N-methyltransferase 3 OS=Arabidopsis thaliana GN=NMT3 PE=2 SV=2
AT5G59310	Q9LLR6	2,619	0,001	extracellular	Non-specific lipid-transfer protein 4 OS=Arabidopsis thaliana GN=LTP4 PE=3 SV=1
Major CHO metabolism					
AT2G36390	O23647	-0,332	0,007	plastid	1,4-alpha-glucan-branching enzyme 2-1, chloroplastic/amyloplastic OS=Arabidopsis thaliana GN=SBE2.1 PE=1 SV=1
AT2G31390	Q9SID0	0,391	0,002	cytosol	Probable fructokinase-1 OS=Arabidopsis thaliana GN=At2g31390 PE=2 SV=1
AT4G09020	Q9M0S5	0,424	0,006	plastid	Isoamylase 3, chloroplastic OS=Arabidopsis thaliana GN=ISA3 PE=1 SV=2
AT3G23920	Q9LIR6	0,437	0,008	plastid	Beta-amylase 1, chloroplastic OS=Arabidopsis thaliana GN=BAM1 PE=1 SV=1
AT1G62660	Q43348	0,491	0,002	vacuole	Acid beta-fructofuranosidase 3, vacuolar OS=Arabidopsis thaliana GN=BFRUCT3 PE=2 SV=1
AT3G52180	Q9FEB5	0,67	0,001	plastid	Phosphoglucan phosphatase DSP4, chloroplastic OS=Arabidopsis thaliana GN=DSP4 PE=1 SV=1
AT3G13790	Q43866	1,022	0,002	extracellular	Beta-fructofuranosidase, insoluble isoenzyme CWINV1 OS=Arabidopsis thaliana GN=CWINV1 PE=1 SV=1
AT1G35580	Q9LQF2	1,08	0,002	cytosol	Alkaline/neutral invertase CINV1 OS=Arabidopsis thaliana GN=CINV1 PE=1 SV=1
AT5G64860	Q9LV91	6,046	0,001	plastid	4-alpha-glucanotransferase DPE1, chloroplastic/amyloplastic OS=Arabidopsis thaliana GN=DPE1 PE=1 SV=1
Metal handling					
AT2G40300	Q9S756	-0,687	0,002	plastid	Ferritin-4, chloroplastic OS=Arabidopsis thaliana GN=FER4 PE=2 SV=1
AT5G01600	Q39101	-0,627	0,001	plastid	Ferritin-1, chloroplastic OS=Arabidopsis thaliana GN=FER1 PE=2 SV=1
AT3G56090	Q9LYN2	-0,619	0,004	plastid	Ferritin-3, chloroplastic OS=Arabidopsis thaliana GN=FER3 PE=2 SV=1
AT5G19140	Q94BR2	-0,377	0,003	plasma membrane	Aluminum induced protein witYGL and LRDR motifs OS=Arabidopsis thaliana GN=AILP1 PE=2 SV=1
AT1G30470	F4I6B2	0,37	0,01	golgi	SIT4 phosphatase-associated family protein OS=Arabidopsis thaliana GN=At1g30470 PE=1 SV=1
AT4G14710	Q8W108	0,374	0,005	cytosol	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase 3 OS=Arabidopsis thaliana GN=ARD3 PE=2 SV=1
AT4G14030	O23264	0,387	0,002	cytosol	Selenium-binding protein 1 OS=Arabidopsis thaliana GN=SBP1 PE=1 SV=1
AT4G14040	Q93WN0	0,451	0,001	cytosol	Selenium-binding protein 2 OS=Arabidopsis thaliana GN=SBP2 PE=1 SV=1
AT3G17390	Q9LUT2	0,491	0,003	ıcleus,plasma membra	S-adenosylmethionine synthase 4 OS=Arabidopsis thaliana GN=METK4 PE=1 SV=1
Minor CHO metabolism					
AT1G31190	Q94F00	-0,356	0,003	plastid	Phosphatase IMPL1, chloroplastic OS=Arabidopsis thaliana GN=IMPL1 PE=1 SV=2
AT2G37760	O80944	0,305	0,008	cytosol	Aldo-keto reductase family 4 member C8 OS=Arabidopsis thaliana GN=AKR4C8 PE=1 SV=2
AT5G57655	Q9FKK7	0,328	0,002	endoplasmic reticulum	Xylose isomerase OS=Arabidopsis thaliana GN=XYLA PE=2 SV=2
AT4G30310	F4JQ90	0,496	0,006	cytosol	FGGY family of carbohydrate kinase OS=Arabidopsis thaliana GN=At4g30310 PE=1 SV=1
AT3G47800	Q9STT3	0,503	0,002	extracellular	Aldose 1-epimerase OS=Arabidopsis thaliana GN=T23J7.130 PE=2 SV=1
AT3G17770	Q494P3	0,771	0,003	cytosol	At3g17770 OS=Arabidopsis thaliana GN=At3g17770 PE=2 SV=1
AT4G28706	F4JM15	2,572	0,001	plastid	PfkB-like carbohydrate kinase family protein OS=Arabidopsis thaliana GN=At4g28706 PE=3 SV=1
Miscelaneous					
AT1G28580	Q9FXJ2	-1,057	0,002	extracellular	GDSL esterase/lipase At1g28580 OS=Arabidopsis thaliana GN=At1g28580 PE=2 SV=1
AT4G32320	Q8GY91	-0,734	0,003	cytosol	Putative L-ascorbate peroxidase 6 OS=Arabidopsis thaliana GN=APX6 PE=2 SV=1
AT3G32980	Q9LHB9	-0,649	0,001	extracellular	Peroxidase 32 OS=Arabidopsis thaliana GN=PER32 PE=1 SV=3
AT1G09010	Q75W54	-0,63	0,004	vacuole	Mannosylglycoprotein endo-beta-mannosidase OS=Arabidopsis thaliana GN=EBM PE=1 SV=3
AT1G07440	P0DKI3	-0,441	0,008	peroxisome	Tropinone reductase homolog At1g07440 OS=Arabidopsis thaliana GN=At1g07440 PE=1 SV=1
AT4G18970	Q93YW8	-0,422	0,004	extracellular	GDSL esterase/lipase At4g18970 OS=Arabidopsis thaliana GN=At4g18970 PE=2 SV=1
AT1G23740	Q9ZUC1	-0,406	0,001	plastid	ADPH-dependent alkenal/one oxidoreductase, chloroplastic OS=Arabidopsis thaliana GN=AOR PE=1 SV=2
AT2G45180	Q42044	-0,377	0,005	vacuole	At2g45180 OS=Arabidopsis thaliana GN=At2g45180 PE=2 SV=2
AT2G26740	Q42566	-0,365	0,002	cytosol	TsEOS=Arabidopsis thaliana GN=ATsEPE=2 SV=1

AT4G27700	Q94A65	-0,322	0,002	plastid	Rhodanese-like domain-containing protein 14, chloroplastic OS=Arabidopsis thaliana GN=At4g27700 PE=2 SV=1
AT2G39020	Q9ZV06	0,316	0,008	plastid	Probable acetyltransferase NATA1-like OS=Arabidopsis thaliana GN=At2g39020 PE=2 SV=1
AT4G27520	Q9T076	0,326	0,001	plasma membrane	Early nodulin-like protein 2 OS=Arabidopsis thaliana GN=At4g27520 PE=1 SV=1
AT4G31840	Q9SZ51	0,349	0,006	extracellular	Early nodulin-like protein 15 OS=Arabidopsis thaliana GN=ENODL15 PE=2 SV=1
AT4G21580	O65423	0,354	0,002	cytosol	AT4g21580/F18E5_200 OS=Arabidopsis thaliana GN=F18E5.200 PE=2 SV=1
AT4G30140	Q9SZW7	0,358	0,003	extracellular	GDSL esterase/lipase At4g30140 OS=Arabidopsis thaliana GN=At4g30140 PE=2 SV=1
AT1G71695	Q96520	0,361	0,002	extracellular	Peroxidase 12 OS=Arabidopsis thaliana GN=PER12 PE=1 SV=1
AT1G80410	Q8VZM1	0,364	0,002	cytosol	N-terminal acetyltransferase A complex auxiliary subunit NAA15 OS=Arabidopsis thaliana GN=NAA15 PE=1 SV=1
AT1G31800	Q93VK5	0,383	0,005	plastid	Protein LUTEIN DEFICIENT 5, chloroplastic OS=Arabidopsis thaliana GN=CYP97A3 PE=1 SV=1
AT2G10940	Q9SKI0	0,405	0,002	vacuole	At2g10940/F15K19.1 OS=Arabidopsis thaliana GN=At2g10940 PE=2 SV=1
AT4G38990	Q9SVJ4	0,423	0,01	extracellular	Endoglucanase 22 OS=Arabidopsis thaliana GN=GH9B16 PE=3 SV=1
AT3G16420	O04314	0,426	0,001	cytosol	PYK10-binding protein 1 OS=Arabidopsis thaliana GN=PBP1 PE=1 SV=1
AT4G15550	O23406	0,432	0,008	plastid	UDP-glycosyltransferase 75D1 OS=Arabidopsis thaliana GN=UGT75D1 PE=2 SV=2
AT3G16520	Q9LK73	0,432	0,002	cytosol	UDP-glycosyltransferase 88A1 OS=Arabidopsis thaliana GN=UGT88A1 PE=2 SV=1
AT5G16980	F4KFK3	0,484	0,006	cytosol	Zinc-binding dehydrogenase family protein OS=Arabidopsis thaliana GN=At5g16980 PE=4 SV=1
AT2G16430	Q9SIV9	0,485	0,007	extracellular	Purple acid phosphatase 10 OS=Arabidopsis thaliana GN=PAP10 PE=2 SV=1
AT3G09260	Q9SR37	0,494	0,001	endoplasmic reticulum	Beta-glucosidase 23 OS=Arabidopsis thaliana GN=BGLU23 PE=1 SV=1
AT3G04000	Q9SQR2	0,528	0,005	plastid	NADPH-dependent aldehyde reductase 2, chloroplastic OS=Arabidopsis thaliana GN=ChlADR2 PE=1 SV=1
AT3G15356	Q9LJR2	0,531	0,003	extracellular	Lectin-like protein LEC OS=Arabidopsis thaliana GN=LEC PE=1 SV=1
AT3G45190	F4J5I0	0,551	0,005	plasma membrane	SIT4 phosphatase-associated family protein OS=Arabidopsis thaliana GN=At3g45190 PE=1 SV=1
AT3G16530	Q9LK72	0,555	0,001	extracellular	Lectin-like protein At3g16530 OS=Arabidopsis thaliana GN=At3g16530 PE=1 SV=1
AT4G02520	P46422	0,561	0,001	cytosol	Glutathione S-transferase F2 OS=Arabidopsis thaliana GN=GSTF2 PE=1 SV=3
AT3G49110	P24101	0,581	0,002	extracellular	Peroxidase 33 OS=Arabidopsis thaliana GN=PER33 PE=1 SV=1
AT5G04900	Q8LEU3	0,592	0,004	plastid	Chlorophyll(ide) b reductase NOL, chloroplastic OS=Arabidopsis thaliana GN=NOL PE=1 SV=1
AT4G20860	Q9SUC6	0,594	0,002	extracellular	Berberine bridge enzyme-like 22 OS=Arabidopsis thaliana GN=FAD-OXR PE=2 SV=1
AT5G63840	Q9FN05	0,61	0,004	endoplasmic reticulum	Probable glucan 1,3-alpha-glucosidase OS=Arabidopsis thaliana GN=PSL5 PE=1 SV=1
AT1G59700	Q9XIF8	0,617	0,004	cytosol	Glutathione S-transferase U16 OS=Arabidopsis thaliana GN=GSTU16 PE=2 SV=1
AT4G33650	Q8S944	0,628	0,002	mitochondrion	Dynamin-related protein 3A OS=Arabidopsis thaliana GN=DRP3A PE=1 SV=2
AT1G02930	P42760	0,654	0,003	cytosol	Glutathione S-transferase F6 OS=Arabidopsis thaliana GN=GSTF6 PE=2 SV=2
AT3G18080	Q9LV33	0,669	0,001	extracellular	Beta-glucosidase 44 OS=Arabidopsis thaliana GN=BGLU44 PE=2 SV=1
AT4G22513	A8MQX6	0,677	0,002	extracellular	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein OS=Arabidopsis thaliana GN=At4g22513 PE=4 SV=1
AT2G30860	O80852	0,755	0,001	cytosol	Glutathione S-transferase F9 OS=Arabidopsis thaliana GN=GSTF9 PE=1 SV=1
AT3G48460	Q9STM6	0,756	0,003	extracellular	GDSL esterase/lipase At3g48460 OS=Arabidopsis thaliana GN=At3g48460 PE=2 SV=1
AT1G78850	Q9ZVA4	0,768	0,001	extracellular	EP1-like glycoprotein 3 OS=Arabidopsis thaliana GN=At1g78850 PE=1 SV=1
AT2G30870	P42761	0,783	0,001	cytosol	Glutathione S-transferase F10 OS=Arabidopsis thaliana GN=GSTF10 PE=1 SV=3
AT3G28200	Q9LHA7	0,784	0,002	extracellular	Peroxidase 31 OS=Arabidopsis thaliana GN=PER31 PE=2 SV=1
AT1G64710	Q8VZ49	0,787	0,001	golgi	Alcohol dehydrogenase-like 4 OS=Arabidopsis thaliana GN=At1g64710 PE=2 SV=1
AT1G78370	Q8L7C9	0,799	0,001	peroxisome	Glutathione S-transferase U20 OS=Arabidopsis thaliana GN=GSTU20 PE=1 SV=1
AT5G19440	Q29Q34	0,815	0,001	cytosol	At5g19440 OS=Arabidopsis thaliana GN=At5g19440 PE=2 SV=1
AT4G19880	F4JU03	0,849	0,001	plastid	Glutathione S-transferase family protein OS=Arabidopsis thaliana GN=At4g19880 PE=1 SV=1
AT1G59610	Q9LQ55	0,874	0,001	plasma membrane	Dynamin-2B OS=Arabidopsis thaliana GN=DRP2B PE=1 SV=2
AT1G29670	Q9C7N4	0,919	0,001	extracellular	GDSL esterase/lipase At1g29670 OS=Arabidopsis thaliana GN=At1g29670 PE=2 SV=1
AT4G21960	Q9SB81	0,922	0,002	extracellular	Peroxidase 42 OS=Arabidopsis thaliana GN=PER42 PE=1 SV=2
AT4G34135	Q94C57	0,924	0,002	plasma membrane	UDP-glucosyl transferase 73B2 OS=Arabidopsis thaliana GN=UGT73B2 PE=1 SV=1
AT5G42100	Q9FHX5	0,929	0,002	extracellular	Glucan endo-1,3-beta-glucosidase 10 OS=Arabidopsis thaliana GN=At5g42100 PE=1 SV=1
AT1G22360	Q9ZWJ3	0,933	0,002	plasma membrane	UDP-glycosyltransferase 85A2 OS=Arabidopsis thaliana GN=UGT85A2 PE=2 SV=1
AT1G28600	Q94F40	1,055	0,002	extracellular	GDSL esterase/lipase At1g28600 OS=Arabidopsis thaliana GN=At1g28600 PE=2 SV=1
AT1G48750	Q94AQ3	1,066	0,002	extracellular	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein OS=Arabidopsis thaliana GN=At1g48750 PE=2 SV=1
AT4G20830	Q9SVG4	1,214	0,001	extracellular	Berberine bridge enzyme-like 19 OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2
AT4G13180	Q9SVQ9	1,431	0,001	plastid	AT4g13180/F17N18_70 OS=Arabidopsis thaliana GN=At4g13180 PE=1 SV=1
AT5G64120	Q43387	1,845	0,001	extracellular	Peroxidase 71 OS=Arabidopsis thaliana GN=PER71 PE=1 SV=1
AT4G12480	Q39176	2,495	0,001	extracellular	Lipid transfer protein EARLI 1 OS=Arabidopsis thaliana GN=EARLI1 PE=1 SV=1
AT4G12470	Q9SU35	2,587	0,001	golgi	pEARLI1-like lipid transfer protein 1 OS=Arabidopsis thaliana GN=AZI1 PE=1 SV=1

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Mitochondrial electron transport					
AT3G15640	Q9LW15	-0,432	0,008	mitochondrion	Cytochrome c oxidase subunit 5b-1, mitochondrial OS=Arabidopsis thaliana GN=COX5B-1 PE=1 SV=1
AT3G52730	Q9LXJ2	0,392	0,01	mitochondrion	Ubiquinol--cytochrome-c reductase-like protein OS=Arabidopsis thaliana GN=F3C22_130 PE=2 SV=1
AT5G05370	Q9FLB7	0,43	0,009	mitochondrion	At5g05370 OS=Arabidopsis thaliana GN=At5g05370 PE=2 SV=1
AT5G11770	Q42577	0,435	0,008	mitochondrion	NADdehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=Arabidopsis thaliana GN=At5g11770 PE=1 SV=1
ATMG00160	P93285	0,451	0,008	mitochondrion	Cytochrome c oxidase subunit 2 OS=Arabidopsis thaliana GN=COX2 PE=1 SV=2
AT2G20360	Q9SK66	0,454	0,001	mitochondrion	NADdehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Arabidopsis thaliana GN=At2g20360 PE=1 SV=2
AT5G40810	Q9FKS5	0,471	0,002	mitochondrion	Cytochrome c1 2, heme protein, mitochondrial OS=Arabidopsis thaliana GN=CYC12 PE=1 SV=1
AT4G32470	Q9SUU5	0,533	0,002	mitochondrion	Cytochrome b-c1 complex subunit 7-1 OS=Arabidopsis thaliana GN=QCR7-1 PE=1 SV=1
AT3G54110	O81845	0,604	0,002	mitochondrion	Mitochondrial uncoupling protein 1 OS=Arabidopsis thaliana GN=PUMP1 PE=1 SV=1
AT4G28510	O49460	0,74	0,003	mitochondrion	Prohibitin-1, mitochondrial OS=Arabidopsis thaliana GN=PHB1 PE=1 SV=1
AT4G37830	Q9T070	0,813	0,003	mitochondrion	Cytochrome c oxidase subunit 6a, mitochondrial OS=Arabidopsis thaliana GN=COX6A PE=3 SV=1
N- metabolism					
AT5G57440	Q8VZP1	-0,899	0,002	mitochondrion	(DL)-glycerol-3-phosphatase 2 OS=Arabidopsis thaliana GN=GPP2 PE=1 SV=1
AT5G35630	Q43127	-0,501	0,001	plastid	Glutamine synthetase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=GLN2 PE=1 SV=1
AT5G04140	Q9ZNZ7	-0,416	0,002	plastid	Ferredoxin-dependent glutamate synthase 1, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=GLU1 PE=1 SV=3
AT1G66200	Q8LCE1	0,322	0,004	cytosol	Glutamine synthetase cytosolic isozyme 1-2 OS=Arabidopsis thaliana GN=GLN1-2 PE=1 SV=2
AT1G77760	P11832	0,482	0,008	cytosol	Nitrate reductase [NADH] 1 OS=Arabidopsis thaliana GN=NIA1 PE=1 SV=3
AT5G18170	Q43314	0,568	0,002	mitochondrion	Glutamate dehydrogenase 1 OS=Arabidopsis thaliana GN=GDH1 PE=2 SV=1
AT5G53460	Q9LV03	1,173	0,003	plastid	Glutamate synthase 1 [NADH], chloroplastic OS=Arabidopsis thaliana GN=GLT1 PE=1 SV=2
AT5G07440	Q38946	1,509	0,001	mitochondrion	Glutamate dehydrogenase 2 OS=Arabidopsis thaliana GN=GDH2 PE=1 SV=1
Nucleotide metabolism					
AT5G09650	Q9LXC9	-0,436	0,001	plastid	Soluble inorganic pyrophosphatase 6, chloroplastic OS=Arabidopsis thaliana GN=PPA6 PE=1 SV=1
AT5G47840	Q9FIJ7	-0,411	0,001	plastid	Adenylate kinase 2, chloroplastic OS=Arabidopsis thaliana GN=At5g47840 PE=1 SV=1
AT5G35170	Q8VYL1	-0,361	0,001	plastid	Adenylate kinase 5, chloroplastic OS=Arabidopsis thaliana GN=At5g35170 PE=1 SV=1
AT3G54470	Q42586	0,331	0,002	golgi	Uridine 5'-monophosphate synthase OS=Arabidopsis thaliana GN=PYRE-F PE=2 SV=2
AT5G26667	O04905	0,35	0,002	cytosol	UMP-CMP kinase 3 OS=Arabidopsis thaliana GN=UMK3 PE=1 SV=1
AT1G27450	P31166	0,358	0,003	cytosol	Isoform 2 of Adenine phosphoribosyltransferase 1, chloroplastic OS=Arabidopsis thaliana GN=APT1
AT4G12720	Q9SU14	0,483	0,007	cytosol	Nudix hydrolase 7 OS=Arabidopsis thaliana GN=NUDT7 PE=1 SV=1
AT4G11010	O49203	0,521	0,002	mitochondrion	Nucleoside diphosphate kinase III, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=NDPK3 PE=1 SV=1
AT2G37690	Q84TI2	0,666	0,001	plastid	Phosphoribosylaminoimidazole carboxylase like protein OS=Arabidopsis thaliana GN=At2g37690 PE=2 SV=1
AT5G03300	Q9LZG0	0,834	0,006	cytosol	Adenosine kinase 2 OS=Arabidopsis thaliana GN=ADK2 PE=1 SV=1
AT4G30530	Q9M0A7	0,893	0,001	cytosol	Gamma-glutamyl peptidase 1 OS=Arabidopsis thaliana GN=GGP1 PE=1 SV=1
OPP					
AT2G45290	F4IW47	-0,344	0,002	plastid	Transketolase-2, chloroplastic OS=Arabidopsis thaliana GN=TKL-2 PE=1 SV=1
AT4G05390	Q9M0V6	0,344	0,003	plastid	Ferredoxin--NADP reductase, root isozyme 1, chloroplastic OS=Arabidopsis thaliana GN=RFNR1 PE=2 SV=2
AT3G02360	Q9FWA3	0,412	0,002	peroxisome	6-phosphogluconate dehydrogenase, decarboxylating 3 OS=Arabidopsis thaliana GN=At3g02360 PE=2 SV=1
AT1G64190	Q9SH69	0,441	0,002	plastid	6-phosphogluconate dehydrogenase, decarboxylating 1, chloroplastic OS=Arabidopsis thaliana GN=At1g64190 PE=1 SV=1
AT5G41670	Q9FFR3	0,509	0,006	mitochondrion	6-phosphogluconate dehydrogenase, decarboxylating 2, chloroplastic OS=Arabidopsis thaliana GN=At5g41670 PE=1 SV=1
AT5G13420	Q9LYR4	0,867	0,001	plastid	Aldolase-type TIM barrel family protein OS=Arabidopsis thaliana GN=TRA2 PE=2 SV=1
Photosyntesis					
AT3G54050	P25851	-4,489	0,001	plastid	Fructose-1,6-bisphosphatase 1, chloroplastic OS=Arabidopsis thaliana GN=CFBP1 PE=1 SV=2
AT1G51400	Q9SYE2	-1,97	0,001	plastid	At1g51400/F5D21_10 OS=Arabidopsis thaliana GN=F11M15.26 PE=2 SV=1
AT4G05180	Q41932	-1,558	0,001	plastid	Oxygen-evolving enhancer protein 3-2, chloroplastic OS=Arabidopsis thaliana GN=PSBQ2 PE=1 SV=2
AT3G16250	Q9LU21	-1,463	0,001	plastid	Photosynthetic NDsubunit of subcomplex B 3, chloroplastic OS=Arabidopsis thaliana GN=PNSB3 PE=2 SV=1
AT5G64040	P49107	-1,427	0,001	plastid	Photosystem I reaction center subunit N, chloroplastic OS=Arabidopsis thaliana GN=PSAN PE=1 SV=2
AT3G15840	F4J036	-1,269	0,001	plastid	Post-illumination chlorophyll fluorescence increase OS=Arabidopsis thaliana GN=PIFI PE=4 SV=1
AT3G62410	Q9LZP9	-1,228	0,001	plastid	Calvin cycle protein CP12-2, chloroplastic OS=Arabidopsis thaliana GN=CP12-2 PE=1 SV=1
AT5G58260	Q9LVM2	-1,169	0,001	plastid	NAD(P)H-quinone oxidoreductase subunit N, chloroplastic OS=Arabidopsis thaliana GN=ndhN PE=2 SV=1
AT3G21055	Q39195	-1,15	0,001	plastid	Photosystem II 5 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=PSBT PE=3 SV=2
AT1G74880	Q9S829	-1,136	0,001	plastid	NAD(P)H-quinone oxidoreductase subunit O, chloroplastic OS=Arabidopsis thaliana GN=ndhO PE=2 SV=1

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AT4G03280	Q9ZR03	-1,13	0,001	plastid	Cytochrome b6-f complex iron-sulfur subunit, chloroplastic OS=Arabidopsis thaliana GN=petC PE=1 SV=1
AT4G37925	Q2V2S7	-1,123	0,001	plastid	NAD(P)H-quinone oxidoreductase subunit M, chloroplastic OS=Arabidopsis thaliana GN=ndhM PE=2 SV=1
ATCG01060	P62090	-1,084	0,001	plastid	Photosystem I iron-sulfur center OS=Arabidopsis thaliana GN=psaC PE=3 SV=2
AT5G66570	P23321	-1,069	0,001	plastid	Oxygen-evolving enhancer protein 1-1, chloroplastic OS=Arabidopsis thaliana GN=PSBO1 PE=1 SV=2
AT4G28750	Q9S831	-1,032	0,001	plastid	Photosystem I reaction center subunit IV A, chloroplastic OS=Arabidopsis thaliana GN=PSAE1 PE=1 SV=1
AT2G30790	O49344	-1,027	0,001	plastid	Putative oxygen-evolving enhancer protein 2-2 OS=Arabidopsis thaliana GN=PSBP2 PE=5 SV=3
AT1G52230	Q9SUI6	-0,975	0,001	plastid	Photosystem I reaction center subunit VI-2, chloroplastic OS=Arabidopsis thaliana GN=PSAH2 PE=2 SV=1
AT4G26530	O65581	-0,968	0,001	plastid	Fructose-bisphosphate aldolase 5, cytosolic OS=Arabidopsis thaliana GN=FBA5 PE=1 SV=1
AT1G06680	Q42029	-0,964	0,001	plastid	Oxygen-evolving enhancer protein 2-1, chloroplastic OS=Arabidopsis thaliana GN=PSBP1 PE=1 SV=2
AT1G60950	P16972	-0,954	0,002	plastid	Ferredoxin-2, chloroplastic OS=Arabidopsis thaliana GN=FD2 PE=1 SV=1
AT4G21280	Q9XFT3	-0,947	0,001	plastid	Isoform 2 of Oxygen-evolving enhancer protein 3-1, chloroplastic OS=Arabidopsis thaliana GN=PSBQ1
AT4G02770	Q9S7H1	-0,939	0,001	plastid	Photosystem I reaction center subunit II-1, chloroplastic OS=Arabidopsis thaliana GN=psaD1 PE=1 SV=1
AT3G50820	Q9S841	-0,922	0,001	plastid	Oxygen-evolving enhancer protein 1-2, chloroplastic OS=Arabidopsis thaliana GN=PSBO2 PE=1 SV=1
AT2G20260	Q9S714	-0,905	0,001	plastid	Photosystem I reaction center subunit IV B, chloroplastic OS=Arabidopsis thaliana GN=PSAE2 PE=2 SV=1
ATCG00540	P56771	-0,902	0,001	plastid	Cytochrome f OS=Arabidopsis thaliana GN=petA PE=3 SV=1
AT3G61470	Q9SYW8	-0,889	0,001	plastid	Photosystem I chlorophyll a/b-binding protein 2, chloroplastic OS=Arabidopsis thaliana GN=LHCA2 PE=1 SV=1
AT3G54890	Q01667	-0,882	0,001	plastid	Chlorophyll a-b binding protein 6, chloroplastic OS=Arabidopsis thaliana GN=LHCA1 PE=1 SV=1
ATCG00430	P56756	-0,868	0,001	plastid	NAD(P)H-quinone oxidoreductase subunit K, chloroplastic OS=Arabidopsis thaliana GN=ndhK PE=3 SV=1
AT2G26500	O48717	-0,866	0,001	plastid	At2g26500 OS=Arabidopsis thaliana GN=At2g26500 PE=2 SV=1
ATCG01090	P56755	-0,864	0,001	plastid	NAD(P)H-quinone oxidoreductase subunit I, chloroplastic OS=Arabidopsis thaliana GN=ndhI PE=3 SV=1
ATCG01110	P56753	-0,844	0,001	plastid	NAD(P)H-quinone oxidoreductase subunit H, chloroplastic OS=Arabidopsis thaliana GN=ndhPE=1 SV=1
AT1G32470	Q9LQL0	-0,835	0,001	mitochondrion	Glycine cleavage system protein 3, mitochondrial OS=Arabidopsis thaliana GN=GDH3 PE=1 SV=1
AT1G03600	Q9LR64	-0,834	0,001	plastid	Photosystem II repair protein PSB27-H1, chloroplastic OS=Arabidopsis thaliana GN=PSB27-1 PE=1 SV=1
AT3G01440	Q9SGH4	-0,823	0,002	plastid	Photosynthetic NDsubunit of lumenal location 3, chloroplastic OS=Arabidopsis thaliana GN=PNSL3 PE=1 SV=1
ATCG00420	P56754	-0,812	0,003	plastid	NAD(P)H-quinone oxidoreductase subunit J, chloroplastic OS=Arabidopsis thaliana GN=ndhJ PE=3 SV=1
AT5G01530	Q07473	-0,785	0,002	plastid	Chlorophyll a-b binding protein CP29.1, chloroplastic OS=Arabidopsis thaliana GN=LHCB4.1 PE=1 SV=1
AT3G47470	P27521	-0,748	0,001	plastid	Chlorophyll a-b binding protein 4, chloroplastic OS=Arabidopsis thaliana GN=LHCA4 PE=1 SV=1
AT1G55670	Q9S7N7	-0,734	0,002	plastid	Photosystem I reaction center subunit V, chloroplastic OS=Arabidopsis thaliana GN=PSAG PE=1 SV=1
AT2G35370	P25855	-0,722	0,001	mitochondrion	Glycine cleavage system protein 1, mitochondrial OS=Arabidopsis thaliana GN=GDH1 PE=1 SV=1
AT2G21170	Q9SKP6	-0,699	0,001	plastid	Triosephosphate isomerase, chloroplastic OS=Arabidopsis thaliana GN=TIM PE=1 SV=1
AT2G47400	O22914	-0,686	0,001	plastid	Calvin cycle protein CP12-1, chloroplastic OS=Arabidopsis thaliana GN=CP12-1 PE=1 SV=1
AT1G30380	Q9SUI5	-0,661	0,002	plastid	Photosystem I reaction center subunit psaK, chloroplastic OS=Arabidopsis thaliana GN=PSAK PE=2 SV=2
ATCG00120	P56757	-0,646	0,001	plastid	ATP synthase subunit alpha, chloroplastic OS=Arabidopsis thaliana GN=atpA PE=1 SV=1
AT4G04640	Q01908	-0,639	0,002	plastid	ATP synthase gamma chain 1, chloroplastic OS=Arabidopsis thaliana GN=ATPC1 PE=1 SV=1
AT4G09650	Q9SSS9	-0,636	0,001	plastid	ATP synthase subunit delta, chloroplastic OS=Arabidopsis thaliana GN=ATPD PE=1 SV=1
AT3G16140	Q9SUI7	-0,621	0,004	plastid	Photosystem I reaction center subunit VI-1, chloroplastic OS=Arabidopsis thaliana GN=PSAH1 PE=2 SV=1
ATCG00470	P09468	-0,612	0,001	plastid	ATP synthase epsilon chain, chloroplastic OS=Arabidopsis thaliana GN=atpE PE=1 SV=2
AT2G06520	Q9SKI3	-0,608	0,004	plastid	Expressed protein OS=Arabidopsis thaliana GN=PSBX PE=1 SV=1
AT1G61520	Q9SY97	-0,587	0,001	plastid	Photosystem I chlorophyll a/b-binding protein 3-1, chloroplastic OS=Arabidopsis thaliana GN=LHCA3 PE=1 SV=1
AT5G44520	Q9FI13	-0,583	0,004	plastid	Probable ribose-5-phosphate isomerase 4, chloroplastic OS=Arabidopsis thaliana GN=RPI4 PE=2 SV=1
AT1G15820	Q9LMQ2	-0,577	0,001	plastid	Chlorophyll a-b binding protein, chloroplastic OS=Arabidopsis thaliana GN=CHLOROPHYLL PROTEIN 24 PE=1 SV=1
AT2G39470	O80634	-0,573	0,001	plastid	Photosynthetic NDsubunit of lumenal location 1, chloroplastic OS=Arabidopsis thaliana GN=PNSL1 PE=1 SV=2
AT5G54270	Q9S7M0	-0,57	0,001	plastid	Chlorophyll a-b binding protein 3, chloroplastic OS=Arabidopsis thaliana GN=LHCB3 PE=1 SV=1
ATCG00480	P19366	-0,57	0,002	plastid	ATP synthase subunit beta, chloroplastic OS=Arabidopsis thaliana GN=atpB PE=1 SV=2
AT1G20020	Q8W493	-0,569	0,002	plastid	Ferredoxin--NADP reductase, leaf isozyme 2, chloroplastic OS=Arabidopsis thaliana GN=LFNR2 PE=1 SV=1
AT4G15510	O23403	-0,565	0,002	plastid	PsbP domain-containing protein 1, chloroplastic OS=Arabidopsis thaliana GN=PPD1 PE=1 SV=1
AT1G29930	P04778	-0,559	0,002	plastid	Chlorophyll a-b binding protein 1, chloroplastic OS=Arabidopsis thaliana GN=LHCB1.3 PE=1 SV=1
AT1G31330	Q9SHE8	-0,558	0,001	plastid	Photosystem I reaction center subunit III, chloroplastic OS=Arabidopsis thaliana GN=PSAF PE=1 SV=1
AT3G14420	Q9LRR9	-0,549	0,001	peroxisome	(S)-2-hydroxy-acid oxidase GLO1 OS=Arabidopsis thaliana GN=GLO1 PE=1 SV=1
AT5G36700	P0DKC3	-0,541	0,001	plastid	Phosphoglycolate phosphatase 1A, chloroplastic OS=Arabidopsis thaliana GN=PGLP1A PE=1 SV=1
AT4G32590	F4JUE0	-0,527	0,006	plastid	2Fe-2S ferredoxin-like superfamily protein OS=Arabidopsis thaliana GN=At4g32590 PE=4 SV=1
AT3G56650	Q9LXX5	-0,516	0,001	plastid	PsbP domain-containing protein 6, chloroplastic OS=Arabidopsis thaliana GN=PPD6 PE=1 SV=1
AT5G11450	P82715	-0,516	0,002	plastid	PsbP domain-containing protein 5, chloroplastic OS=Arabidopsis thaliana GN=PPD5 PE=1 SV=3
ATCG00150	P56758	-0,499	0,002	plastid	ATP synthase subunit a, chloroplastic OS=Arabidopsis thaliana GN=atpI PE=3 SV=1
AT5G38410	B3H5S2	-0,488	0,001	plastid	Ribulose bisphosphate carboxylase small chain OS=Arabidopsis thaliana GN=RBCS3B PE=3 SV=1

AT2G40100	Q9S7W1	-0,481	0,003	plastid	Chlorophyll a-b binding protein CP29.3, chloroplastic OS=Arabidopsis thaliana GN=LHCB4.3 PE=2 SV=1
AT4G32260	Q42139	-0,461	0,001	plastid	AT4g32260/F10M6_100 OS=Arabidopsis thaliana GN=PDE334 PE=1 SV=2
AT1G76100	P11490	-0,456	0,006	plastid	Plastocyanin minor isoform, chloroplastic OS=Arabidopsis thaliana GN=PETE PE=1 SV=2
AT3G55330	P82538	-0,445	0,001	plastid	PsbP-like protein 1, chloroplastic OS=Arabidopsis thaliana GN=PPL1 PE=1 SV=1
AT1G32060	P25697	-0,443	0,001	plastid	Phosphoribulokinase, chloroplastic OS=Arabidopsis thaliana GN=At1g32060 PE=2 SV=1
ATCG00730	P56774	-0,427	0,003	plastid	Cytochrome b6-f complex subunit 4 OS=Arabidopsis thaliana GN=petD PE=3 SV=1
ATCG00350	P56766	-0,414	0,003	plastid	Photosystem I P700 chlorophyll a apoprotein A1 OS=Arabidopsis thaliana GN=psaA PE=2 SV=1
ATCG00340	P56767	-0,411	0,002	plastid	Photosystem I P700 chlorophyll a apoprotein A2 OS=Arabidopsis thaliana GN=psaB PE=3 SV=1
AT2G05100	Q9SHR7	-0,404	0,009	plastid	Chlorophyll a-b binding protein 2.1, chloroplastic OS=Arabidopsis thaliana GN=LHCB2.1 PE=1 SV=1
AT1G77090	O49292	-0,401	0,003	plastid	PsbP domain-containing protein 4, chloroplastic OS=Arabidopsis thaliana GN=PPD4 PE=1 SV=2
AT1G56190	P50318	-0,394	0,001	plastid	Phosphoglycerate kinase 2, chloroplastic OS=Arabidopsis thaliana GN=At1g56190 PE=1 SV=3
AT4G28660	Q8W0Y8	-0,39	0,005	plastid	Photosystem II reaction center PSB28 protein, chloroplastic OS=Arabidopsis thaliana GN=PSB28 PE=2 SV=1
AT2G46820	Q8LCA1	-0,388	0,002	plastid	Protein CURVATURE THYLAKOID 1B, chloroplastic OS=Arabidopsis thaliana GN=CURT1B PE=1 SV=2
AT2G39730	P10896	-0,386	0,001	plastid	Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic OS=Arabidopsis thaliana GN=RCA PE=1 SV=2
AT1G55490	P21240	-0,379	0,002	plastid	Chaperonin 60 subunit beta 1, chloroplastic OS=Arabidopsis thaliana GN=CPN60B1 PE=1 SV=3
AT1G80380	Q944I4	-0,369	0,001	plastid	D-glycerate 3-kinase, chloroplastic OS=Arabidopsis thaliana GN=GLYK PE=1 SV=2
AT5G38430	P10796	-0,355	0,003	plastid	Ribulose bisphosphate carboxylase small chain 1B, chloroplastic OS=Arabidopsis thaliana GN=RBCS-1B PE=1 SV=1
AT1G76450	Q9S720	-0,351	0,007	plastid	PsbP domain-containing protein 3, chloroplastic OS=Arabidopsis thaliana GN=PPD3 PE=1 SV=2
ATCG00580	P56779	-0,35	0,004	plastid	Cytochrome b559 subunit alpha OS=Arabidopsis thaliana GN=psbE PE=1 SV=4
AT3G55800	P46283	-0,337	0,001	plastid	Sedoheptulose-1,7-bisphosphatase, chloroplastic OS=Arabidopsis thaliana GN=At3g55800 PE=2 SV=1
ATCG00130	P56759	-0,333	0,001	plastid	ATP synthase subunit b, chloroplastic OS=Arabidopsis thaliana GN=atpF PE=3 SV=1
ATCG00720	P56773	-0,332	0,003	plastid	Cytochrome b6 OS=Arabidopsis thaliana GN=petB PE=1 SV=1
AT1G15140	Q9XI55	-0,32	0,001	plastid	F9L1.8 protein OS=Arabidopsis thaliana GN=At1g15140 PE=2 SV=1
AT2G34430	Q39142	-0,315	0,004	plastid	Chlorophyll a-b binding protein, chloroplastic OS=Arabidopsis thaliana GN=Lhb1B1 PE=1 SV=1
AT5G66190	Q9FKW6	-0,305	0,001	plastid	Ferredoxin--NADP reductase, leaf isozyme 1, chloroplastic OS=Arabidopsis thaliana GN=LFNR1 PE=1 SV=1
AT3G12780	Q9LD57	-0,303	0,001	plastid	Phosphoglycerate kinase 1, chloroplastic OS=Arabidopsis thaliana GN=PGK1 PE=1 SV=1
AT3G26650	P25856	0,326	0,001	plastid	Glyceraldehyde-3-phosphate dehydrogenase GAPA1, chloroplastic OS=Arabidopsis thaliana GN=GAPA1 PE=1 SV=3
AT1G79530	Q9SAJ6	0,383	0,009	plastid	Glyceraldehyde-3-phosphate dehydrogenase GAPCP1, chloroplastic OS=Arabidopsis thaliana GN=GAPCP1 PE=1 SV=1
AT2G01140	Q9ZU52	0,42	0,001	plastid	Fructose-bisphosphate aldolase 3, chloroplastic OS=Arabidopsis thaliana GN=FBA3 PE=1 SV=1
AT1G67740	O49347	0,701	0,002	plastid	Photosystem II core complex proteins psbY, chloroplastic OS=Arabidopsis thaliana GN=PSBY PE=2 SV=1
Protein					
AT1G03740	Q9LR53	-1,544	0,001	nucleus	F21B7.34 OS=Arabidopsis thaliana GN=At1g03740 PE=2 SV=1
AT4G39710	Q9SCY3	-1,537	0,001	plastid	Photosynthetic NDsubunit of lumenal location 4, chloroplastic OS=Arabidopsis thaliana GN=PNSL4 PE=1 SV=1
AT3G15120	Q9LIM2	-1,301	0,001	nucleus	reversed P-loop containing nucleoside triphosphate hydrolases superfamily protein OS=Arabidopsis thaliana GN=At3g15120 PE=4 SV=1
AT5G59300	Q42540	-1,213	0,001	nucleus	Ubiquitin-conjugating enzyme E2 7 OS=Arabidopsis thaliana GN=UBC7 PE=1 SV=1
AT3G27160	A0A1I9LRJ3	-0,992	0,002	plastid	Ribosomal protein S21 family protein OS=Arabidopsis thaliana GN=GHS1 PE=3 SV=1
AT5G27700	Q3E902	-0,957	0,005	cytosol	40S ribosomal protein S21-2 OS=Arabidopsis thaliana GN=RPS21C PE=1 SV=2
AT5G13410	Q9LYR5	-0,922	0,001	plastid	Peptidyl-prolyl cis-trans isomerase FKBP19, chloroplastic OS=Arabidopsis thaliana GN=FKBP19 PE=1 SV=1
AT1G20810	Q9LM71	-0,921	0,001	plastid	Peptidyl-prolyl cis-trans isomerase FKBP18, chloroplastic OS=Arabidopsis thaliana GN=FKBP18 PE=1 SV=2
AT4G12120	Q9SZ77	-0,904	0,002	cytosol	Protein transport Sec1b OS=Arabidopsis thaliana GN=SEC1B PE=2 SV=3
AT1G18670	A0A1P8AQ94	-0,9	0,002	plasma membrane	reversed Protein kinase superfamily protein OS=Arabidopsis thaliana GN=IBS1 PE=4 SV=1
AT4G26555	Q944B0	-0,889	0,002	plastid	Peptidyl-prolyl cis-trans isomerase FKBP16-1, chloroplastic OS=Arabidopsis thaliana GN=FKBP16-1 PE=2 SV=1
AT5G24490	Q94K97	-0,817	0,001	plastid	30S ribosomal protein OS=Arabidopsis thaliana GN=At5g24490 PE=1 SV=1
AT3G56910	Q9LER7	-0,81	0,002	plastid	50S ribosomal protein 5, chloroplastic OS=Arabidopsis thaliana GN=PSRP5 PE=1 SV=1
AT3G44620	F4J355	-0,796	0,002	plastid	Protein-tyrosine phosphatase OS=Arabidopsis thaliana GN=At3g44620 PE=4 SV=1
AT4G30690	Q94B52	-0,751	0,001	plastid	Translation initiation factor IF3-4, chloroplastic OS=Arabidopsis thaliana GN=IF3-4 PE=2 SV=1
AT3G01480	Q9SSA5	-0,729	0,001	plastid	Peptidyl-prolyl cis-trans isomerase CYP38, chloroplastic OS=Arabidopsis thaliana GN=CYP38 PE=1 SV=1
AT3G12390	Q9LHG9	-0,727	0,002	nucleus	Nascent polypeptide-associated complex subunit alpha-like protein 1 OS=Arabidopsis thaliana GN=At3g12390 PE=1 SV=1
AT2G33450	O22795	-0,702	0,005	plastid	50S ribosomal protein L28, chloroplastic OS=Arabidopsis thaliana GN=RPL28 PE=2 SV=2
AT2G43560	O22870	-0,673	0,001	plastid	Peptidyl-prolyl cis-trans isomerase FKBP16-3, chloroplastic OS=Arabidopsis thaliana GN=FKBP16-3 PE=1 SV=2
AT3G27830	P36210	-0,661	0,001	plastid	50S ribosomal protein L12-1, chloroplastic OS=Arabidopsis thaliana GN=RPL12A PE=2 SV=1
AT5G37680	Q8W4C8	-0,648	0,004	plasma membrane	reversed ADP-ribosylation factor-like protein 8c OS=Arabidopsis thaliana GN=ARL8C PE=2 SV=1
AT3G17250	Q9LUU7	-0,616	0,003	mitochondrion	Probable protein phosphatase 2C 43 OS=Arabidopsis thaliana GN=At3g17250 PE=2 SV=1
AT1G75690	Q8GSJ6	-0,605	0,004	plastid	Protein disulfide-isomerase LQY1, chloroplastic OS=Arabidopsis thaliana GN=LQY1 PE=1 SV=1

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AT3G27080	P82874	-0,596	0,008	mitochondrion	Mitochondrial import receptor subunit TOM20-3 OS=Arabidopsis thaliana GN=TOM20-3 PE=1 SV=1
AT3G10060	Q9SR70	-0,576	0,002	plastid	Peptidyl-prolyl cis-trans isomerase FKBP16-4, chloroplastic OS=Arabidopsis thaliana GN=FKBP16-4 PE=1 SV=1
AT2G36060	Q9SJ44	-0,56	0,006	cytosol	Ubiquitin-conjugating enzyme E2 variant 1C OS=Arabidopsis thaliana GN=UEV1C PE=1 SV=1
AT2G41620	O22224	-0,557	0,005	nucleus	Nuclear pore complex protein NUP93A OS=Arabidopsis thaliana GN=NUP93A PE=1 SV=2
AT2G25840	Q8RXE9	-0,556	0,005	plastid	Tryptophan--tRNA ligase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=OVA4 PE=1 SV=1
AT3G27925	O22609	-0,555	0,001	plastid	Protease Do-like 1, chloroplastic OS=Arabidopsis thaliana GN=DEGP1 PE=1 SV=2
AT5G30510	Q93VC7	-0,554	0,001	plastid	30S ribosomal protein S1, chloroplastic OS=Arabidopsis thaliana GN=RPS1 PE=1 SV=1
AT5G45680	Q9SCY2	-0,553	0,001	plastid	Peptidyl-prolyl cis-trans isomerase FKBP13, chloroplastic OS=Arabidopsis thaliana GN=FKBP13 PE=1 SV=2
AT3G60370	Q0WRJ7	-0,519	0,003	plastid	Peptidyl-prolyl cis-trans isomerase FKBP20-2, chloroplastic OS=Arabidopsis thaliana GN=FKBP20-2 PE=1 SV=1
AT1G07320	O50061	-0,514	0,001	plastid	50S ribosomal protein L4, chloroplastic OS=Arabidopsis thaliana GN=RPL4 PE=2 SV=2
AT2G38140	O80439	-0,513	0,003	plastid	30S ribosomal protein S31, chloroplastic OS=Arabidopsis thaliana GN=RPS31 PE=1 SV=1
AT1G06380	Q9LMI1	-0,501	0,006	plastid	Ribosomal protein L1p/L10e family OS=Arabidopsis thaliana GN=At1g06380 PE=1 SV=1
AT5G40950	Q9FLN4	-0,5	0,002	plastid	50S ribosomal protein L27, chloroplastic OS=Arabidopsis thaliana GN=RPL27 PE=2 SV=1
AT3G56150	O49160	-0,489	0,002	nucleus,cytosol	Eukaryotic translation initiation factor 3 subunit C OS=Arabidopsis thaliana GN=TIF3C1 PE=1 SV=2
AT4G17740	O23614	-0,475	0,002	plastid	Carboxyl-terminal-processing peptidase 2, chloroplastic OS=Arabidopsis thaliana GN=CTPA2 PE=1 SV=1
AT4G20360	P17745	-0,469	0,006	plastid	Elongation factor Tu, chloroplastic OS=Arabidopsis thaliana GN=TUFA PE=1 SV=1
AT3G15190	Q9ASV6	-0,45	0,003	plastid	30S ribosomal protein S20, chloroplastic OS=Arabidopsis thaliana GN=RPS20 PE=2 SV=1
AT2G44650	O80504	-0,441	0,002	plastid	10 kDa chaperonin 2, chloroplastic OS=Arabidopsis thaliana GN=CPN10-2 PE=2 SV=1
AT3G54360	Q9M2V1	-0,436	0,003	nucleus	Protein NCA1 OS=Arabidopsis thaliana GN=NCA1 PE=1 SV=1
AT3G13120	Q9LK61	-0,421	0,008	plastid	30S ribosomal protein S10, chloroplastic OS=Arabidopsis thaliana GN=RPS10 PE=2 SV=1
AT1G64510	Q8VY91	-0,414	0,002	plastid	30S ribosomal protein S6 alpha, chloroplastic OS=Arabidopsis thaliana GN=RPS6 PE=2 SV=1
AT4G29060	Q9SZD6	-0,409	0,001	plastid	Elongation factor Ts, mitochondrial OS=Arabidopsis thaliana GN=emb2726 PE=2 SV=1
AT1G62750	Q9SI75	-0,408	0,001	plastid	Elongation factor G, chloroplastic OS=Arabidopsis thaliana GN=CPEFG PE=1 SV=1
AT5G12110	Q84WM9	-0,402	0,004	cytosol	Elongation factor 1-beta 1 OS=Arabidopsis thaliana GN=At5g12110 PE=2 SV=2
AT5G20720	O65282	-0,399	0,001	plastid	20 kDa chaperonin, chloroplastic OS=Arabidopsis thaliana GN=CPN20 PE=1 SV=2
AT2G45740	O80845	-0,398	0,003	peroxisome	Peroxisomal membrane protein 11D OS=Arabidopsis thaliana GN=PEX11D PE=1 SV=2
AT5G47190	Q8RXX5	-0,395	0,005	plastid	50S ribosomal protein L19-2, chloroplastic OS=Arabidopsis thaliana GN=At5g47190 PE=2 SV=1
AT1G75350	Q9FWS4	-0,384	0,002	plastid	50S ribosomal protein L31, chloroplastic OS=Arabidopsis thaliana GN=RPL31 PE=2 SV=1
AT1G48350	Q9SX68	-0,375	0,003	plastid	50S ribosomal protein L18, chloroplastic OS=Arabidopsis thaliana GN=RPL18 PE=2 SV=1
AT2G24060	O82234	-0,352	0,003	plastid	Translation initiation factor IF3-2, chloroplastic OS=Arabidopsis thaliana GN=IF3-2 PE=2 SV=1
AT1G79850	P16180	-0,345	0,003	plastid	30S ribosomal protein S17, chloroplastic OS=Arabidopsis thaliana GN=RPS17 PE=1 SV=1
AT4G25130	P54150	-0,338	0,002	plastid	Peptide methionine sulfoxide reductase A4, chloroplastic OS=Arabidopsis thaliana GN=MSR4 PE=1 SV=2
AT3G13470	Q9LJE4	-0,331	0,003	plastid	Chaperonin 60 subunit beta 2, chloroplastic OS=Arabidopsis thaliana GN=CPN60B2 PE=1 SV=1
ATCG00800	P56798	-0,331	0,002	plastid	30S ribosomal protein S3, chloroplastic OS=Arabidopsis thaliana GN=rps3 PE=3 SV=1
AT5G17710	Q9XQC7	-0,329	0,001	plastid	GrpE protein homolog OS=Arabidopsis thaliana GN=grpE PE=2 SV=1
AT5G23120	O82660	-0,324	0,001	plastid	Photosystem II stability/assembly factor HCF136, chloroplastic OS=Arabidopsis thaliana GN=HCF136 PE=1 SV=1
AT2G33800	P93014	-0,302	0,001	plastid	30S ribosomal protein S5, chloroplastic OS=Arabidopsis thaliana GN=rps5 PE=2 SV=1
AT3G46560	Q9XGX9	0,302	0,01	mitochondrion	Mitochondrial import inner membrane translocase subunit TIM9 OS=Arabidopsis thaliana GN=TIM9 PE=1 SV=2
AT3G14290	Q42134	0,303	0,009	nucleus,cytosol	Proteasome subunit alpha type-5-B OS=Arabidopsis thaliana GN=PAE2 PE=1 SV=2
AT4G16720	O23515	0,305	0,008	cytosol	60S ribosomal protein L15-1 OS=Arabidopsis thaliana GN=RPL15A PE=2 SV=1
AT3G23990	P29197	0,307	0,001	mitochondrion	Chaperonin CPN60, mitochondrial OS=Arabidopsis thaliana GN=CPN60 PE=1 SV=2
AT3G03960	Q94K05	0,308	0,002	cytosol	T-complex protein 1 subunit theta OS=Arabidopsis thaliana GN=CCT8 PE=1 SV=1
AT5G56680	Q9SW96	0,309	0,004	cytosol	Asparagine--tRNA ligase, cytoplasmic 1 OS=Arabidopsis thaliana GN=SYNC1 PE=1 SV=1
AT1G20200	Q9LNU4	0,31	0,004	nucleus,cytosol	26S proteasome non-ATPase regulatory subunit 3 homolog A OS=Arabidopsis thaliana GN=RPN3A PE=1 SV=3
AT4G24820	Q93Y35	0,31	0,002	nucleus,cytosol	26S proteasome non-ATPase regulatory subunit 6 homolog OS=Arabidopsis thaliana GN=RPN7 PE=1 SV=1
AT3G11830	Q9SF16	0,311	0,001	cytosol	T-complex protein 1 subunit eta OS=Arabidopsis thaliana GN=CCT7 PE=1 SV=1
AT5G26710	O82462	0,312	0,008	cytosol	Glutamate--tRNA ligase, cytoplasmic OS=Arabidopsis thaliana GN=At5g26710 PE=1 SV=1
AT2G33210	Q8L7B5	0,314	0,002	mitochondrion	Chaperonin CPN60-like 1, mitochondrial OS=Arabidopsis thaliana GN=At2g33210 PE=1 SV=1
AT5G52650	Q9LTF2	0,315	0,004	cytosol	40S ribosomal protein S10-3 OS=Arabidopsis thaliana GN=RPS10C PE=2 SV=2
AT2G30110	P93028	0,322	0,001	cytosol	Ubiquitin-activating enzyme E1 1 OS=Arabidopsis thaliana GN=UBA1 PE=1 SV=1
AT3G20000	Q9LHE5	0,322	0,009	mitochondrion	Mitochondrial import receptor subunit TOM40-1 OS=Arabidopsis thaliana GN=TOM40-1 PE=1 SV=3
AT1G25490	Q38845	0,323	0,003	plasma membrane	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Arabidopsis thaliana GN=PP2AA1 PE=1 SV=1
AT5G64050	Q9FEA2	0,323	0,003	mitochondrion,plastid	Glutamate--tRNA ligase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=OVA3 PE=1 SV=1
AT5G02500	P22953	0,324	0,009	cytosol	Probable mediator of RNA polymerase II transcription subunit 37e OS=Arabidopsis thaliana GN=MED37E PE=1 SV=3
AT5G26830	O04630	0,326	0,002	mitochondrion,plastid	Threonine--tRNA ligase, mitochondrial 1 OS=Arabidopsis thaliana GN=THRRS PE=1 SV=3

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AT3G25520	Q8LBI1	0,328	0,003	cytosol	60S ribosomal protein L5-1 OS=Arabidopsis thaliana GN=ATL5 PE=1 SV=2
AT5G66140	O24616	0,33	0,004	nucleus,cytosol	Proteasome subunit alpha type-7-B OS=Arabidopsis thaliana GN=PAD2 PE=1 SV=2
AT2G18110	Q9SI20	0,332	0,008	cytosol	Elongation factor 1-delta 2 OS=Arabidopsis thaliana GN=At2g18110 PE=1 SV=1
AT1G57720	Q9FVT2	0,333	0,001	cytosol	Probable elongation factor 1-gamma 2 OS=Arabidopsis thaliana GN=At1g57720 PE=1 SV=1
AT3G57290	Q9C5Z3	0,333	0,002	cytosol	Eukaryotic translation initiation factor 3 subunit E OS=Arabidopsis thaliana GN=TIF3E1 PE=1 SV=1
AT1G64520	Q9SGW3	0,337	0,002	nucleus,cytosol	26S proteasome non-ATPase regulatory subunit 8 homolog A OS=Arabidopsis thaliana GN=RPN12A PE=1 SV=1
AT5G17020	Q9SMV6	0,338	0,008	nucleus	Protein EXPORTIN 1A OS=Arabidopsis thaliana GN=XPO1 PE=1 SV=1
AT2G20140	Q9SL67	0,343	0,002	nucleus,cytosol	26S proteasome regulatory subunit 4 homolog B OS=Arabidopsis thaliana GN=RPT2B PE=1 SV=1
AT3G45030	P49200	0,346	0,006	cytosol	40S ribosomal protein S20-1 OS=Arabidopsis thaliana GN=RPS20A PE=2 SV=2
AT5G20890	Q940P8	0,346	0,002	cytosol	T-complex protein 1 subunit beta OS=Arabidopsis thaliana GN=CCT2 PE=1 SV=1
AT3G13490	Q9LJE2	0,348	0,006	mitochondrion,plastid	Lysine--tRNA ligase, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=OVA5 PE=2 SV=1
AT5G20000	Q94BQ2	0,349	0,004	nucleus,cytosol	26S proteasome regulatory subunit 8 homolog B OS=Arabidopsis thaliana GN=RPT6B PE=1 SV=1
AT3G18190	Q9LV21	0,35	0,001	cytosol	T-complex protein 1 subunit delta OS=Arabidopsis thaliana GN=CCT4 PE=1 SV=1
AT1G54270	P41377	0,351	0,002	cytosol	Eukaryotic initiation factor 4A-2 OS=Arabidopsis thaliana GN=TIF4A-2 PE=1 SV=1
AT1G09620	F4I116	0,353	0,001	cytosol	Leucine--tRNA ligase, cytoplasmic OS=Arabidopsis thaliana GN=At1g09620 PE=1 SV=1
AT2G27020	O23715	0,357	0,002	nucleus,cytosol	Proteasome subunit alpha type-3 OS=Arabidopsis thaliana GN=PAG1 PE=1 SV=2
AT3G52500	Q9SVD1	0,357	0,002	extracellular	At3g52500 OS=Arabidopsis thaliana GN=F22O6_120 PE=2 SV=1
AT1G61570	Q9XH48	0,359	0,01	mitochondrion	Mitochondrial import inner membrane translocase subunit TIM13 OS=Arabidopsis thaliana GN=TIM13 PE=1 SV=2
AT1G43170	P17094	0,361	0,002	cytosol	60S ribosomal protein L3-1 OS=Arabidopsis thaliana GN=ARP1 PE=1 SV=5
AT5G26360	Q84WV1	0,362	0,002	cytosol	T-complex protein 1 subunit gamma OS=Arabidopsis thaliana GN=CCT3 PE=1 SV=1
AT3G61110	Q9M2F1	0,365	0,005	cytosol	40S ribosomal protein S27-2 OS=Arabidopsis thaliana GN=RPS27B PE=2 SV=2
AT3G18740	Q9LSA3	0,366	0,006	cytosol	60S ribosomal protein L30-3 OS=Arabidopsis thaliana GN=RPL30C PE=3 SV=1
AT2G20580	Q9SIV2	0,368	0,001	nucleus,cytosol	26S proteasome non-ATPase regulatory subunit 2 homolog A OS=Arabidopsis thaliana GN=RPN1A PE=1 SV=2
AT3G24830	Q9LRX8	0,372	0,003	cytosol	60S ribosomal protein L13a-2 OS=Arabidopsis thaliana GN=RPL13AB PE=2 SV=1
AT1G56070	Q9ASR1	0,383	0,001	cytosol	longation factor 2 OS=Arabidopsis thaliana GN=LOS1 PE=1 SV=1
AT5G20290	Q93VG5	0,384	0,002	nucleus,cytosol	40S ribosomal protein S8-1 OS=Arabidopsis thaliana GN=RPS8A PE=1 SV=1
AT2G41790	O22941	0,386	0,002	peroxisome	Insulin-degrading enzyme-like 1, peroxisomal OS=Arabidopsis thaliana GN=PXM16 PE=2 SV=1
AT4G17100	F4JNE0	0,386	0,001	cytosol	Poly(U)-specific endoribonuclease-B protein OS=Arabidopsis thaliana GN=At4g17100 PE=4 SV=1
AT5G45620	Q8RWF0	0,388	0,006	nucleus,cytosol	26S proteasome non-ATPase regulatory subunit 13 homolog A OS=Arabidopsis thaliana GN=RPN9A PE=1 SV=1
AT2G27600	Q9ZNT0	0,389	0,005	cytosol	Protein SUPPRESSOR OF K(+) TRANSPORT GROWTDEFECT 1 OS=Arabidopsis thaliana GN=SKD1 PE=1 SV=1
AT4G05420	Q9M0V3	0,394	0,01	nucleus	DNA damage-binding protein 1a OS=Arabidopsis thaliana GN=DDB1A PE=1 SV=1
AT2G47110	P59232	0,395	0,008	cytosol	Ubiquitin-40S ribosomal protein S27a-2 OS=Arabidopsis thaliana GN=RPS27AB PE=2 SV=2
AT5G27470	Q39230	0,396	0,001	cytosol	Serine--tRNA ligase, cytoplasmic OS=Arabidopsis thaliana GN=At5g27470 PE=2 SV=1
AT3G47370	Q9STY6	0,397	0,005	cytosol	40S ribosomal protein S20-2 OS=Arabidopsis thaliana GN=RPS20B PE=2 SV=1
AT1G58380	Q8L8Y0	0,399	0,003	cytosol	40S ribosomal protein S2-1 OS=Arabidopsis thaliana GN=RPS2A PE=2 SV=2
AT3G11710	Q9ZPI1	0,401	0,001	cytosol	Lysine--tRNA ligase, cytoplasmic OS=Arabidopsis thaliana GN=At3g11710 PE=1 SV=1
AT2G46520	Q9ZPY7	0,405	0,003	nucleus,cytosol	Exportin-2 OS=Arabidopsis thaliana GN=CAS PE=2 SV=1
AT4G36760	A0A1P8B667	0,405	0,002	cytosol	Aminopeptidase P1 OS=Arabidopsis thaliana GN=APP1 PE=1 SV=1
AT1G10940	P43291	0,407	0,004	cytosol	Serine/threonine-protein kinase SRK2A OS=Arabidopsis thaliana GN=SRK2A PE=1 SV=1
AT5G09900	Q9FIB6	0,407	0,001	nucleus,cytosol	26S proteasome non-ATPase regulatory subunit 12 homolog A OS=Arabidopsis thaliana GN=RPN5A PE=1 SV=1
AT2G41840	P49688	0,411	0,003	cytosol	40S ribosomal protein S2-3 OS=Arabidopsis thaliana GN=RPS2C PE=1 SV=2
AT3G08943	F4IYK3	0,415	0,01	nucleus,cytosol	ARM repeat superfamily protein OS=Arabidopsis thaliana GN=At3g08943 PE=1 SV=2
AT3G09630	Q9SF40	0,416	0,002	cytosol	60S ribosomal protein L4-1 OS=Arabidopsis thaliana GN=RPL4A PE=1 SV=1
AT1G03230	Q9ZVS5	0,416	0,003	extracellular	Eukaryotic aspartyl protease family protein OS=Arabidopsis thaliana GN=At1g03230 PE=2 SV=1
AT1G70600	P49637	0,416	0,004	cytosol	60S ribosomal protein L27a-3 OS=Arabidopsis thaliana GN=RPL27AC PE=2 SV=2
AT4G13780	Q9SVN5	0,417	0,002	cytosol	Methionine--tRNA ligase, cytoplasmic OS=Arabidopsis thaliana GN=At4g13780 PE=2 SV=1
AT3G58700	P42794	0,42	0,002	cytosol	60S ribosomal protein L11-2 OS=Arabidopsis thaliana GN=RPL11B PE=2 SV=2
AT1G09640	O04487	0,422	0,001	cytosol	Probable elongation factor 1-gamma 1 OS=Arabidopsis thaliana GN=At1g09640 PE=1 SV=1
AT4G31180	Q9M084	0,422	0,001	cytosol	Aspartate--tRNA ligase 2, cytoplasmic OS=Arabidopsis thaliana GN=IBI1 PE=1 SV=1
AT1G69410	Q9C505	0,423	0,003	cytosol	Eukaryotic translation initiation factor 5A-3 OS=Arabidopsis thaliana GN=ELF5A-3 PE=2 SV=1
AT2G26140	O80983	0,424	0,007	mitochondrion	ATP-dependent zinc metalloprotease FTS4, mitochondrial OS=Arabidopsis thaliana GN=FTSH4 PE=1 SV=2
AT4G00100	P59224	0,426	0,008	cytosol	40S ribosomal protein S13-2 OS=Arabidopsis thaliana GN=RPS13B PE=2 SV=1
AT3G53740	Q9M352	0,427	0,009	cytosol	60S ribosomal protein L36-2 OS=Arabidopsis thaliana GN=RPL36B PE=3 SV=1
AT5G46210	Q8LGH4	0,43	0,007	cytosol	Cullin-4 OS=Arabidopsis thaliana GN=CUL4 PE=1 SV=1
AT5G41520	Q9FFS8	0,43	0,003	cytosol	40S ribosomal protein S10-2 OS=Arabidopsis thaliana GN=RPS10B PE=2 SV=1

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AT1G27970	Q9C7F5	0,432	0,002	nucleus	Nuclear transport factor 2B OS=Arabidopsis thaliana GN=NTF2B PE=1 SV=1
AT3G02530	Q9M888	0,436	0,009	cytosol	T-complex protein 1 subunit zeta 1 OS=Arabidopsis thaliana GN=CCT6A PE=1 SV=1
AT1G24510	O04450	0,437	0,001	cytosol	T-complex protein 1 subunit epsilon OS=Arabidopsis thaliana GN=CCT5 PE=1 SV=1
AT1G07770	P42798	0,442	0,002	cytosol	40S ribosomal protein S15a-1 OS=Arabidopsis thaliana GN=RPS15AA PE=2 SV=2
AT5G02870	P49691	0,442	0,003	cytosol	60S ribosomal protein L4-2 OS=Arabidopsis thaliana GN=RPL4D PE=1 SV=2
AT5G06460	P92974	0,444	0,008	nucleus	Ubiquitin-activating enzyme E1 2 OS=Arabidopsis thaliana GN=UBA2 PE=1 SV=1
AT4G14800	O24633	0,445	0,007	cytosol,vacuole	Proteasome subunit beta type-2-B OS=Arabidopsis thaliana GN=PBD2 PE=1 SV=1
AT3G60240	Q76E23	0,446	0,01	cytosol	Eukaryotic translation initiation factor 4G OS=Arabidopsis thaliana GN=EIF4G PE=1 SV=2
AT5G15200	Q9LXG1	0,448	0,001	cytosol	40S ribosomal protein S9-1 OS=Arabidopsis thaliana GN=RPS9B PE=1 SV=1
AT5G10540	Q949P2	0,459	0,006	cytosol	Probable cytosolic oligopeptidase A OS=Arabidopsis thaliana GN=CYOP PE=1 SV=1
AT2G34480	P51418	0,465	0,004	cytosol	60S ribosomal protein L18a-2 OS=Arabidopsis thaliana GN=RPL18AB PE=1 SV=2
AT1G11910	O65390	0,465	0,001	vacuole	Aspartic proteinase A1 OS=Arabidopsis thaliana GN=APA1 PE=1 SV=1
AT5G57870	Q93ZT6	0,471	0,001	nucleus,cytosol	Eukaryotic translation initiation factor isoform 4G-1 OS=Arabidopsis thaliana GN=EIF(ISO)4G1 PE=1 SV=1
AT1G29150	Q9LP45	0,472	0,006	nucleus,cytosol	26S proteasome non-ATPase regulatory subunit 11 homolog OS=Arabidopsis thaliana GN=RPN6 PE=1 SV=1
AT1G56450	Q7DLR9	0,475	0,004	nucleus,cytosol	Proteasome subunit beta type-4 OS=Arabidopsis thaliana GN=PBG1 PE=1 SV=2
AT3G53870	Q9M339	0,475	0,006	cytosol	40S ribosomal protein S3-2 OS=Arabidopsis thaliana GN=RPS3B PE=1 SV=1
AT3G62870	Q9LZH9	0,475	0,002	cytosol	60S ribosomal protein L7a-2 OS=Arabidopsis thaliana GN=RPL7AB PE=2 SV=1
AT4G10320	F4JLM5	0,481	0,001	cytosol	Isoleucine--tRNA ligase, cytoplasmic OS=Arabidopsis thaliana GN=At4g10320 PE=2 SV=1
AT5G16620	Q9FMD5	0,482	0,002	plastid	Protein TIC 40, chloroplastic OS=Arabidopsis thaliana GN=TIC40 PE=1 SV=1
AT5G17170	Q9FFJ2	0,485	0,003	plastid	Rubredoxin family protein OS=Arabidopsis thaliana GN=ENH1 PE=2 SV=1
AT1G50250	Q39102	0,487	0,007	plastid	ATP-dependent zinc metalloprotease FTS1, chloroplastic OS=Arabidopsis thaliana GN=FTSH1 PE=1 SV=2
AT1G53750	Q9SSB5	0,487	0,002	nucleus,cytosol	26S proteasome regulatory subunit 7 homolog A OS=Arabidopsis thaliana GN=RPT1A PE=1 SV=1
AT2G32850	Q8H0Z0	0,488	0,007	nucleus	Protein kinase superfamily protein OS=Arabidopsis thaliana GN=At2g32850 PE=2 SV=1
AT1G51710	Q949Y0	0,488	0,007	cytosol	Ubiquitin carboxyl-terminal hydrolase 6 OS=Arabidopsis thaliana GN=UBP6 PE=1 SV=1
AT1G45000	Q9MAK9	0,493	0,002	nucleus,cytosol	26S proteasome regulatory subunit S10B homolog B OS=Arabidopsis thaliana GN=RPT4B PE=1 SV=1
AT2G29530	Q9ZW33	0,494	0,006	mitochondrion	Mitochondrial import inner membrane translocase subunit TIM10 OS=Arabidopsis thaliana GN=TIM10 PE=1 SV=1
AT3G02560	Q9M885	0,503	0,004	cytosol	40S ribosomal protein S7-2 OS=Arabidopsis thaliana GN=RPS7B PE=2 SV=1
ATCG00065	P62126	0,508	0,005	plastid	30S ribosomal protein S12, chloroplastic OS=Arabidopsis thaliana GN=rps12-A PE=2 SV=2
AT2G24200	P30184	0,525	0,001	cytosol	Leucine aminopeptidase 1 OS=Arabidopsis thaliana GN=LAP1 PE=1 SV=1
AT3G25800	Q38950	0,533	0,003	cytosol	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Arabidopsis thaliana GN=PP2AA2 PE=1 SV=2
AT5G43970	Q9FNC9	0,534	0,006	mitochondrion	Mitochondrial import receptor subunit TOM9-2 OS=Arabidopsis thaliana GN=TOM9-2 PE=1 SV=3
AT3G05560	Q9M9W1	0,534	0,005	cytosol	60S ribosomal protein L22-2 OS=Arabidopsis thaliana GN=RPL22B PE=2 SV=1
AT4G20980	P56820	0,535	0,002	cytosol	Eukaryotic translation initiation factor 3 subunit D OS=Arabidopsis thaliana GN=TIF3D1 PE=1 SV=1
AT5G08260	Q9LEY1	0,536	0,002	extracellular	Serine carboxypeptidase-like 35 OS=Arabidopsis thaliana GN=SCPL35 PE=2 SV=1
AT4G27090	Q9T043	0,536	0,002	cytosol	60S ribosomal protein L14-2 OS=Arabidopsis thaliana GN=RPL14B PE=1 SV=1
AT3G62120	Q9M1R2	0,537	0,002	cytosol	Proline--tRNA ligase, cytoplasmic OS=Arabidopsis thaliana GN=At3g62120 PE=1 SV=1
AT5G27770	Q9FE58	0,541	0,002	cytosol	60S ribosomal protein L22-3 OS=Arabidopsis thaliana GN=RPL22C PE=2 SV=1
AT1G48830	Q9C514	0,543	0,001	cytosol	40S ribosomal protein S7-1 OS=Arabidopsis thaliana GN=RPS7A PE=2 SV=1
AT3G13920	P41376	0,549	0,002	cytosol	Eukaryotic initiation factor 4A-1 OS=Arabidopsis thaliana GN=TIF4A-1 PE=1 SV=1
AT1G14610	P93736	0,55	0,001	mitochondrion	Valine--tRNA ligase, mitochondrial 1 OS=Arabidopsis thaliana GN=TWN2 PE=1 SV=2
AT1G16890	Q9FZ48	0,563	0,004	golgi	Ubiquitin-conjugating enzyme E2 36 OS=Arabidopsis thaliana GN=UBC36 PE=1 SV=1
AT3G52580	P42036	0,563	0,002	cytosol	40S ribosomal protein S14-3 OS=Arabidopsis thaliana GN=RPS14C PE=2 SV=2
AT5G67360	O65351	0,569	0,001	extracellular	Subtilisin-like protease SBT1.7 OS=Arabidopsis thaliana GN=SBT1.7 PE=1 SV=1
AT3G07100	Q9SFU0	0,572	0,005	endoplasmic reticulum	Protein transport protein Sec24-like At3g07100 OS=Arabidopsis thaliana GN=At3g07100 PE=2 SV=2
AT3G60770	P59223	0,575	0,002	cytosol	40S ribosomal protein S13-1 OS=Arabidopsis thaliana GN=RPS13A PE=2 SV=1
AT2G21270	A8MQW3	0,576	0,004	cytosol	AT2G21270 protein OS=Arabidopsis thaliana GN=UFD1 PE=2 SV=1
AT3G20050	P28769	0,576	0,001	cytosol	T-complex protein 1 subunit alpha OS=Arabidopsis thaliana GN=CCT1 PE=1 SV=1
AT1G65590	Q8L7S6	0,579	0,005	cellular,plasma memb	Beta-hexosaminidase 3 OS=Arabidopsis thaliana GN=HEXO3 PE=1 SV=1
AT1G13060	O23717	0,579	0,003	nucleus,cytosol	Proteasome subunit beta type-5-A OS=Arabidopsis thaliana GN=PBE1 PE=1 SV=1
AT3G04840	Q9CAV0	0,587	0,001	cytosol	40S ribosomal protein S3a-1 OS=Arabidopsis thaliana GN=RPS3AA PE=1 SV=3
AT2G04390	P49205	0,592	0,001	cytosol	40S ribosomal protein S17-1 OS=Arabidopsis thaliana GN=RPS17A PE=2 SV=3
AT1G60780	O22715	0,593	0,002	golgi	AP-1 complex subunit mu-2 OS=Arabidopsis thaliana GN=AP1M2 PE=1 SV=1
AT2G40510	Q8LPJ7	0,593	0,002	cytosol	40S ribosomal protein S26-2 OS=Arabidopsis thaliana GN=RPS26B PE=2 SV=2
AT3G05590	P42791	0,596	0,001	cytosol	60S ribosomal protein L18-2 OS=Arabidopsis thaliana GN=RPL18B PE=1 SV=2
AT1G17720	Q39247	0,602	0,004	cytosol	Serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B beta isoform OS=Arabidopsis thaliana GN=PP2AB2 PE=1 SV=1

AT1G14320	Q93VT9	0,615	0,002	cytosol	60S ribosomal protein L10-1 OS=Arabidopsis thaliana GN=RPL10A PE=1 SV=1
AT2G03640	F4IT98	0,618	0,006	nucleus	Nuclear transport factor 2 (NTF2) family protein witRNA binding (RRM-RBD-RNP motifs) domain-containing protein OS=Arabidopsis thaliana GN=At2g03640 PE=4 SV=1
AT3G04920	Q9SS17	0,618	0,004	cytosol	40S ribosomal protein S24-1 OS=Arabidopsis thaliana GN=RPS24A PE=2 SV=1
AT5G61170	Q9FNP8	0,62	0,003	cytosol	40S ribosomal protein S19-3 OS=Arabidopsis thaliana GN=RPS19C PE=2 SV=1
AT2G39390	O80626	0,623	0,004	cytosol	60S ribosomal protein L35-2 OS=Arabidopsis thaliana GN=RPL35B PE=2 SV=1
AT5G20920	Q41969	0,643	0,004	cytosol	Eukaryotic translation initiation factor 2 subunit beta OS=Arabidopsis thaliana GN=EIF2B PE=1 SV=3
AT5G20160	F4K455	0,654	0,003	nucleus	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein OS=Arabidopsis thaliana GN=At5g20160 PE=4 SV=1
AT3G11940	P51427	0,659	0,002	cytosol	40S ribosomal protein S5-2 OS=Arabidopsis thaliana GN=RPS5B PE=1 SV=2
AT2G09990	Q9SK22	0,66	0,003	cytosol	40S ribosomal protein S16-1 OS=Arabidopsis thaliana GN=RPS16A PE=2 SV=1
AT1G70490	P0DH91	0,666	0,001	endoplasmic reticulum	ADP-ribosylation factor 2-B OS=Arabidopsis thaliana GN=ARF2-B PE=2 SV=1
AT1G26880	Q42351	0,667	0,002	nucleus,cytosol	60S ribosomal protein L34-1 OS=Arabidopsis thaliana GN=RPL34A PE=2 SV=1
AT1G74050	Q9C9C5	0,68	0,001	cytosol	60S ribosomal protein L6-3 OS=Arabidopsis thaliana GN=RPL6C PE=2 SV=1
AT4G16190	Q9SUL1	0,684	0,003	vacuole	Probable cysteine protease RD19C OS=Arabidopsis thaliana GN=RD19C PE=2 SV=1
AT1G74270	Q9C912	0,685	0,002	cytosol	60S ribosomal protein L35a-3 OS=Arabidopsis thaliana GN=RPL35AC PE=3 SV=1
AT3G02080	Q9SGA6	0,685	0,003	cytosol	40S ribosomal protein S19-1 OS=Arabidopsis thaliana GN=RPS19A PE=2 SV=1
AT3G49910	P51414	0,687	0,001	cytosol	60S ribosomal protein L26-1 OS=Arabidopsis thaliana GN=RPL26A PE=2 SV=2
AT5G07090	P49204	0,689	0,001	cytosol	40S ribosomal protein S4-2 OS=Arabidopsis thaliana GN=RPS4B PE=2 SV=4
AT4G34670	Q42262	0,69	0,001	cytosol	40S ribosomal protein S3a-2 OS=Arabidopsis thaliana GN=RPS3AB PE=2 SV=3
AT1G18540	Q9FZ76	0,691	0,002	cytosol	60S ribosomal protein L6-1 OS=Arabidopsis thaliana GN=RPL6A PE=2 SV=1
AT3G11510	Q9CAX6	0,696	0,003	cytosol	40S ribosomal protein S14-2 OS=Arabidopsis thaliana GN=RPS14B PE=1 SV=1
AT5G56710	P51420	0,712	0,003	cytosol	60S ribosomal protein L31-3 OS=Arabidopsis thaliana GN=RPL31C PE=3 SV=2
AT2G36160	Q9SIH0	0,724	0,003	cytosol	40S ribosomal protein S14-1 OS=Arabidopsis thaliana GN=RPS14A PE=1 SV=1
AT2G18020	P46286	0,73	0,001	cytosol	60S ribosomal protein L8-1 OS=Arabidopsis thaliana GN=RPL8A PE=1 SV=2
AT2G13540	Q9SIU2	0,734	0,003	cytosol	Nuclear cap-binding protein subunit 1 OS=Arabidopsis thaliana GN=ABH1 PE=1 SV=2
AT5G54990	Q9FFT1	0,734	0,003	nucleus	RING/U-box superfamily protein OS=Arabidopsis thaliana GN=MBG8.26 PE=4 SV=1
AT5G09510	Q9FY64	0,743	0,003	cytosol	40S ribosomal protein S15-4 OS=Arabidopsis thaliana GN=RPS15D PE=2 SV=1
AT5G27850	Q940B0	0,746	0,003	cytosol	60S ribosomal protein L18-3 OS=Arabidopsis thaliana GN=RPL18C PE=2 SV=1
AT3G48930	P16181	0,757	0,002	cytosol	40S ribosomal protein S11-1 OS=Arabidopsis thaliana GN=RPS11A PE=2 SV=1
AT3G09500	Q9SF53	0,768	0,002	cytosol	60S ribosomal protein L35-1 OS=Arabidopsis thaliana GN=RPL35A PE=2 SV=1
AT3G07110	Q9SFU1	0,774	0,001	cytosol	60S ribosomal protein L13a-1 OS=Arabidopsis thaliana GN=RPL13AA PE=2 SV=1
AT5G48760	Q9FKC0	0,777	0,002	cytosol	60S ribosomal protein L13a-4 OS=Arabidopsis thaliana GN=RPL13AD PE=2 SV=1
AT2G20450	Q9SIM4	0,781	0,001	cytosol	60S ribosomal protein L14-1 OS=Arabidopsis thaliana GN=RPL14A PE=2 SV=1
AT1G03220	Q9ZVS4	0,787	0,002	extracellular	Eukaryotic aspartyl protease family protein OS=Arabidopsis thaliana GN=At1g03220 PE=2 SV=1
AT4G15000	P51419	0,787	0,001	cytosol	60S ribosomal protein L27-3 OS=Arabidopsis thaliana GN=RPL27C PE=2 SV=2
AT2G01250	P60040	0,799	0,001	cytosol	60S ribosomal protein L7-2 OS=Arabidopsis thaliana GN=RPL7B PE=1 SV=1
AT4G39200	Q9T029	0,803	0,002	nucleus,cytosol	40S ribosomal protein S25-4 OS=Arabidopsis thaliana GN=RPS25E PE=3 SV=1
AT2G44120	P60039	0,806	0,001	cytosol	60S ribosomal protein L7-3 OS=Arabidopsis thaliana GN=RPL7C PE=2 SV=1
AT5G02960	P49201	0,809	0,002	cytosol	40S ribosomal protein S23-2 OS=Arabidopsis thaliana GN=RPS23B PE=2 SV=2
AT1G27400	Q93VI3	0,842	0,001	nucleus,plastid,cytosol	60S ribosomal protein L17-1 OS=Arabidopsis thaliana GN=RPL17A PE=2 SV=1
AT1G04480	P49690	0,845	0,001	nucleus,cytosol	60S ribosomal protein L23 OS=Arabidopsis thaliana GN=RPL23A PE=2 SV=3
AT2G27530	P59230	0,853	0,002	cytosol	60S ribosomal protein L10a-2 OS=Arabidopsis thaliana GN=RPL10AB PE=1 SV=1
AT1G22780	P34788	0,895	0,001	cytosol	40S ribosomal protein S18 OS=Arabidopsis thaliana GN=RPS18A PE=1 SV=1
AT2G05920	Q9ZUF6	0,902	0,001	extracellular	Subtilisin-like protease SBT1.8 OS=Arabidopsis thaliana GN=SBT1.8 PE=1 SV=1
AT1G09590	Q43291	0,93	0,001	cytosol	60S ribosomal protein L21-1 OS=Arabidopsis thaliana GN=RPL21A PE=2 SV=2
AT2G19730	O82204	1,057	0,002	cytosol	60S ribosomal protein L28-1 OS=Arabidopsis thaliana GN=RPL28A PE=1 SV=1
AT5G28060	Q8LC83	1,093	0,002	cytosol	40S ribosomal protein S24-2 OS=Arabidopsis thaliana GN=RPS24B PE=2 SV=2
AT1G04270	Q08112	1,18	0,001	cytosol	40S ribosomal protein S15-1 OS=Arabidopsis thaliana GN=RPS15A PE=2 SV=1
AT5G16130	Q8LD03	1,475	0,001	cytosol	40S ribosomal protein S7-3 OS=Arabidopsis thaliana GN=RPS7C PE=1 SV=2
AT5G23740	P42733	1,53	0,002	cytosol	40S ribosomal protein S11-3 OS=Arabidopsis thaliana GN=RPS11C PE=2 SV=2
AT2G37190	P50883	1,539	0,001	cytosol	60S ribosomal protein L12-1 OS=Arabidopsis thaliana GN=RPL12A PE=2 SV=2
AT5G15250	Q1PDW5	3,244	0,001	plastid	ATP-dependent zinc metalloprotease FTS6, chloroplastic OS=Arabidopsis thaliana GN=FTSH6 PE=2 SV=1
Redox metabolism					
AT2G04700	Q9SJ89	-0,805	0,001	plastid	Ferredoxin-thioredoxin reductase catalytic chain, chloroplastic OS=Arabidopsis thaliana GN=FTRC PE=2 SV=1
AT4G35090	P25819	-0,756	0,001	peroxisome	Catalase-2 OS=Arabidopsis thaliana GN=CAT2 PE=1 SV=3

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AT5G16400	Q9XFH9	-0,715	0,001	plastid	Thioredoxin F2, chloroplastic OS=Arabidopsis thaliana GN=At5g16400/TRXF2 PE=2 SV=1
AT1G03680	O48737	-0,697	0,001	plastid	Thioredoxin M1, chloroplastic OS=Arabidopsis thaliana GN=At1g03680/TRXM1 PE=2 SV=1
AT3G26060	Q9LU86	-0,675	0,001	plastid	Peroxiredoxin Q, chloroplastic OS=Arabidopsis thaliana GN=PRXQ PE=1 SV=1
AT1G50320	Q8LD49	-0,63	0,001	plastid	Thioredoxin X, chloroplastic OS=Arabidopsis thaliana GN=ATHX PE=2 SV=2
AT1G76760	Q6NPF9	-0,572	0,004	plastid	Thioredoxin Y1, chloroplastic OS=Arabidopsis thaliana GN=At1g76760 PE=2 SV=1
AT5G06290	Q9C5R8	-0,571	0,002	plastid	2-Cys peroxiredoxin BAS1-like, chloroplastic OS=Arabidopsis thaliana GN=At5g06290 PE=2 SV=3
AT5G23440	Q9FHL4	-0,559	0,002	plastid	At5g23440 OS=Arabidopsis thaliana GN=FTRA1 PE=2 SV=1
AT5G16710	Q8LE52	-0,557	0,001	plastid	Glutathione S-transferase DHAR3, chloroplastic OS=Arabidopsis thaliana GN=DHAR3 PE=1 SV=1
AT5G08410	A0A1P8BDN6	-0,556	0,002	plastid	Ferredoxin/thioredoxin reductase subunit A (Variable subunit) 2 OS=Arabidopsis thaliana GN=FTRA2 PE=4 SV=1
AT3G02730	Q9XFH8	-0,543	0,001	plastid	Thioredoxin F1, chloroplastic OS=Arabidopsis thaliana GN=At3g02730 PE=1 SV=2
AT1G07890	Q05431	-0,542	0,001	cytosol	L-ascorbate peroxidase 1, cytosolic OS=Arabidopsis thaliana GN=APX1 PE=1 SV=2
AT4G03520	Q9SEU8	-0,54	0,001	plastid	Thioredoxin M2, chloroplastic OS=Arabidopsis thaliana GN=At4g03520 PE=1 SV=2
AT2G24940	Q9SK39	-0,487	0,009	nucleus	Probable steroid-binding protein 3 OS=Arabidopsis thaliana GN=MP3 PE=1 SV=1
AT1G76080	Q9SGS4	-0,487	0,001	plastid	Thioredoxin-like protein CDSP32, chloroplastic OS=Arabidopsis thaliana GN=CDSP32 PE=1 SV=1
AT3G52960	Q949U7	-0,472	0,001	plastid	Peroxiredoxin-2E, chloroplastic OS=Arabidopsis thaliana GN=PRXIIE PE=1 SV=2
AT3G15360	Q9SEU6	-0,468	0,001	plastid	Thioredoxin M4, chloroplastic OS=Arabidopsis thaliana GN=At3g15360 PE=2 SV=2
AT3G11630	Q96291	-0,382	0,002	plastid	2-Cys peroxiredoxin BAS1, chloroplastic OS=Arabidopsis thaliana GN=BAS1 PE=1 SV=2
AT1G43560	Q8L7S9	-0,365	0,002	plastid	Thioredoxin Y2, chloroplastic OS=Arabidopsis thaliana GN=At1g43560 PE=2 SV=1
AT4G09010	P82281	-0,357	0,001	plastid	Thylakoid lumenal 29 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=TL29 PE=1 SV=2
AT3G48890	Q9M2Z4	0,37	0,007	endoplasmic reticulum	Membrane steroid-binding protein 2 OS=Arabidopsis thaliana GN=MSBP2 PE=1 SV=1
AT1G77510	Q9SRG3	0,37	0,003	endoplasmic reticulum	Protein disulfide isomerase-like 1-2 OS=Arabidopsis thaliana GN=PDIL1-2 PE=2 SV=1
AT1G21750	Q9XI01	0,397	0,001	endoplasmic reticulum	Protein disulfide isomerase-like 1-1 OS=Arabidopsis thaliana GN=PDIL1-1 PE=1 SV=1
AT1G08830	P24704	0,438	0,008	cytosol	Superoxide dismutase [Cu-Zn] 1 OS=Arabidopsis thaliana GN=CSD1 PE=1 SV=2
AT4G23100	P46309	0,447	0,001	plastid	Glutamate--cysteine ligase, chloroplastic OS=Arabidopsis thaliana GN=GSH1 PE=1 SV=2
AT2G32920	O48773	0,496	0,003	endoplasmic reticulum	Protein disulfide-isomerase 2-3 OS=Arabidopsis thaliana GN=PDIL2-3 PE=2 SV=1
AT3G54960	Q8VX13	0,634	0,004	endoplasmic reticulum	Protein disulfide isomerase-like 1-3 OS=Arabidopsis thaliana GN=PDIL1-3 PE=2 SV=1
AT3G24170	P48641	0,734	0,001	peroxisome	Glutathione reductase, cytosolic OS=Arabidopsis thaliana GN=At3g24170 PE=1 SV=1
AT2G16060	O24520	0,932	0,007	cytosol	Non-symbiotic hemoglobin 1 OS=Arabidopsis thaliana GN=AHB1 PE=1 SV=1
AT2G28190	O78310	0,994	0,004	plastid	Superoxide dismutase [Cu-Zn] 2, chloroplastic OS=Arabidopsis thaliana GN=CSD2 PE=1 SV=2
RNA					
AT4G00830	Q9ASP6	-1,133	0,001	nucleus	Heterogeneous nuclear ribonucleoprotein Q OS=Arabidopsis thaliana GN=LIF2 PE=1 SV=1
AT1G34410	Q9C8N9	-0,906	0,002	nucleus	reversed Putative auxin response factor 21 OS=Arabidopsis thaliana GN=ARF21 PE=3 SV=2
AT1G77640	Q9CAP4	-0,857	0,002	plastid	Ethylene-responsive transcription factor ERF013 OS=Arabidopsis thaliana GN=ERF013 PE=2 SV=1
AT3G52150	Q8VYM4	-0,686	0,001	plastid	30S ribosomal protein 2, chloroplastic OS=Arabidopsis thaliana GN=PSRP2 PE=2 SV=1
AT2G24590	Q9SJA6	-0,677	0,002	nucleus	Serine/arginine-ricsplicing factor RSZ22A OS=Arabidopsis thaliana GN=RSZ22A PE=1 SV=1
AT4G24770	Q04836	-0,674	0,001	plastid	31 kDa ribonucleoprotein, chloroplastic OS=Arabidopsis thaliana GN=CP31A PE=1 SV=1
AT5G26210	O81488	-0,608	0,004	nucleus	PHD finger protein ALFIN-LIKE 4 OS=Arabidopsis thaliana GN=AL4 PE=1 SV=2
AT5G47640	Q9FGJ3	-0,584	0,004	nucleus	Nuclear transcription factor Y subunit B-2 OS=Arabidopsis thaliana GN=NFYB2 PE=1 SV=1
AT3G63140	Q9LYA9	-0,569	0,001	plastid	Chloroplast stem-loop binding protein of 41 kDa a, chloroplastic OS=Arabidopsis thaliana GN=CSP41A PE=1 SV=1
AT2G29540	Q42483	-0,546	0,005	nucleus	DNA-directed RNA polymerase 14 kDa subunit (AtRPAC14) OS=Arabidopsis thaliana GN=AtRPAC14 PE=2 SV=1
AT1G65260	O80796	-0,49	0,001	plastid	Membrane-associated protein VIPP1, chloroplastic OS=Arabidopsis thaliana GN=VIPP1 PE=1 SV=1
AT1G17680	Q8GUP0	-0,481	0,006	nucleus	Tetratricopeptide repeat (TPR)-containing protein OS=Arabidopsis thaliana GN=At1g17680 PE=2 SV=1
AT2G35410	O82299	-0,473	0,001	plastid	Putative chloroplast RNA binding protein OS=Arabidopsis thaliana GN=At2g35410 PE=1 SV=1
AT1G15340	Q9XI36	-0,451	0,002	nucleus	Methyl-CpG-binding domain-containing protein 10 OS=Arabidopsis thaliana GN=MBD10 PE=1 SV=1
AT5G14610	Q9LYJ9	-0,435	0,009	nucleus	DEAD-box ATP-dependent RNA helicase 46 OS=Arabidopsis thaliana GN=RH46 PE=2 SV=2
AT3G52380	Q39061	-0,399	0,001	plastid	RNA-binding protein CP33, chloroplastic OS=Arabidopsis thaliana GN=CP33 PE=2 SV=1
AT2G17390	Q29Q26	-0,339	0,008	nucleus	Ankyrin repeat domain-containing protein 2B OS=Arabidopsis thaliana GN=AKR2B PE=1 SV=1
AT3G59980	Q9M1X8	-0,309	0,006	plastid	Nucleic acid-binding, OB-fold-like protein OS=Arabidopsis thaliana GN=F24G16.250 PE=2 SV=1
AT1G60000	Q9ZUJ3	-0,308	0,008	plastid	AT1G60000 protein OS=Arabidopsis thaliana GN=At1g60000 PE=2 SV=1
AT3G53460	Q43349	0,303	0,004	plastid	29 kDa ribonucleoprotein, chloroplastic OS=Arabidopsis thaliana GN=CP29A PE=2 SV=2
AT1G76010	Q93VA8	0,334	0,006	nucleus	Alba DNA/RNA-binding protein OS=Arabidopsis thaliana GN=At1g76010 PE=2 SV=1
AT4G25630	Q94AH9	0,344	0,006	nucleus	Mediator of RNA polymerase II transcription subunit 36a OS=Arabidopsis thaliana GN=MED36A PE=1 SV=2
AT2G21660	Q03250	0,39	0,001	nucleus	Glycine-ricRNA-binding protein 7 OS=Arabidopsis thaliana GN=RBG7 PE=1 SV=1
AT4G20440	Q9SUN5	0,397	0,006	nucleus	Small nuclear ribonucleoprotein-associated protein OS=Arabidopsis thaliana GN=smB PE=2 SV=1

AT2G20490	Q93XX8	0,403	0,004	nucleus	H/ACA ribonucleoprotein complex subunit 3-like protein OS=Arabidopsis thaliana GN=At2g20490 PE=3 SV=2
AT4G13850	Q9SVM8	0,416	0,002	mitochondrion	Glycine-ricRNA-binding protein 2, mitochondrial OS=Arabidopsis thaliana GN=RBG2 PE=1 SV=1
AT2G03870	Q9SI54	0,417	0,009	cytosol	Sm-like protein LSM7 OS=Arabidopsis thaliana GN=LSM7 PE=1 SV=1
AT3G18490	Q9LS40	0,421	0,002	extracellular	Protein ASPARTIC PROTEASE IN GUARD CELL 1 OS=Arabidopsis thaliana GN=ASPG1 PE=1 SV=1
AT4G17600	Q9SYX1	0,439	0,008	plastid	Light-harvesting complex-like protein 3 isotype 1, chloroplastic OS=Arabidopsis thaliana GN=LIL3.1 PE=1 SV=1
AT5G07350	Q8VZG7	0,445	0,001	nucleus	Ribonuclease TUDOR 1 OS=Arabidopsis thaliana GN=TSN1 PE=1 SV=1
AT1G73230	Q9CAT7	0,458	0,006	nucleus	Nascent polypeptide-associated complex subunit beta OS=Arabidopsis thaliana GN=At1g73230 PE=2 SV=1
AT2G20280	Q9SK74	0,477	0,005	nucleus	Zinc finger CCCdomain-containing protein 21 OS=Arabidopsis thaliana GN=At2g20280 PE=4 SV=1
AT3G07810	F4JFN7	0,519	0,006	nucleus	RNA-binding (RRM/RBD/RNP motifs) family protein OS=Arabidopsis thaliana GN=At3g07810 PE=1 SV=1
AT3G10640	Q9LPN5	0,528	0,006	nucleus	Vacuolar protein sorting-associated protein 60.1 OS=Arabidopsis thaliana GN=VPS60-1 PE=1 SV=1
AT5G61780	Q9FLT0	0,529	0,001	nucleus	Ribonuclease TUDOR 2 OS=Arabidopsis thaliana GN=TSN2 PE=1 SV=1
AT2G47640	Q8RUH0	0,547	0,005	nucleus	Putative small nuclear ribonucleoprotein D2 OS=Arabidopsis thaliana GN=At2g47640 PE=4 SV=1
AT3G03920	Q8VZT0	0,566	0,004	nucleus	Putative H/ACA ribonucleoprotein complex subunit 1-like protein 1 OS=Arabidopsis thaliana GN=At3g03920 PE=2 SV=1
AT2G42520	Q84W89	0,568	0,005	nucleus	DEAD-box ATP-dependent RNA helicase 37 OS=Arabidopsis thaliana GN=RH37 PE=2 SV=2
AT5G54310	Q9FL69	0,578	0,004	nucleus	Probable ADP-ribosylation factor GTPase-activating protein AGD5 OS=Arabidopsis thaliana GN=AGD5 PE=1 SV=1
AT3G54400	Q9M2U7	0,671	0,001	extracellular	AT3g54400/T12E18_90 OS=Arabidopsis thaliana GN=T12E18_90 PE=2 SV=1
AT1G09760	P43333	0,673	0,002	nucleus	U2 small nuclear ribonucleoprotein A' OS=Arabidopsis thaliana GN=At1g09760 PE=2 SV=2
AT4G30330	Q8LAK5	0,677	0,003	cytosol	At4g30330 OS=Arabidopsis thaliana GN=At4g30330 PE=2 SV=1
AT3G22320	O81098	0,699	0,005	nucleus	DNA-directed RNA polymerases II and IV subunit 5A OS=Arabidopsis thaliana GN=NRPB5A PE=1 SV=1
AT2G47250	O22899	0,766	0,002	nucleus	Probable pre-mRNA-splicing factor ATP-dependent RNA helicase DEAH3 OS=Arabidopsis thaliana GN=At2g47250 PE=2 SV=1
AT1G26761	Q93ZE3	0,863	0,003	plastid	Arabinanase/levansucrase/invertase OS=Arabidopsis thaliana GN=At1g26761 PE=2 SV=1
AT5G46420	Q9FHG3	0,989	0,002	plastid	16S rRNA processing protein RimM family OS=Arabidopsis thaliana GN=At5g46420 PE=3 SV=1
AT4G38890	Q9T0J6	3,192	0,002	nucleus,cytosol	tRNA-dihydrouridine(47) synthase [NAD(P)(+)]-like OS=Arabidopsis thaliana GN=At4g38890 PE=1 SV=2
S-assimilation					
AT1G19920	Q43870	-0,303	0,002	plastid	ATP sulfurylase 2 OS=Arabidopsis thaliana GN=APS2 PE=1 SV=1
AT5G04590	Q9LZ66	0,413	0,001	plastid	Assimilatory sulfite reductase (ferredoxin), chloroplastic OS=Arabidopsis thaliana GN=SIR PE=1 SV=1
AT2G14750	Q43295	0,658	0,006	plastid	Adenylyl-sulfate kinase 1, chloroplastic OS=Arabidopsis thaliana GN=APK1 PE=1 SV=1
Secondary metabolism					
AT1G08550	Q39249	-0,976	0,001	plastid	Violaxanthin de-epoxidase, chloroplastic OS=Arabidopsis thaliana GN=VDE1 PE=1 SV=1
AT5G25980	Q9C5C2	-0,872	0,001	extracellular	Myrosinase 2 OS=Arabidopsis thaliana GN=TGG2 PE=1 SV=1
AT5G26000	P37702	-0,567	0,004	peroxisome	Myrosinase 1 OS=Arabidopsis thaliana GN=TGG1 PE=1 SV=1
AT5G22300	P46011	-0,514	0,005	plasma membrane	Bifunctional nitrilase/nitrile hydratase NIT4 OS=Arabidopsis thaliana GN=NIT4 PE=1 SV=1
AT2G29290	Q9ZW13	-0,469	0,008	lasma membrane,golg	Tropinone reductase homolog At2g29290 OS=Arabidopsis thaliana GN=At2g29290 PE=2 SV=1
AT2G02500	P69834	-0,386	0,005	plastid	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase, chloroplastic OS=Arabidopsis thaliana GN=ISPD PE=1 SV=1
AT3G51240	Q9S818	-0,384	0,003	cytosol	Naringenin,2-oxoglutarate 3-dioxygenase OS=Arabidopsis thaliana GN=F3PE=1 SV=1
AT1G74470	Q9CA67	-0,355	0,001	plastid	Geranylgeranyl diphosphate reductase, chloroplastic OS=Arabidopsis thaliana GN=CHLP PE=1 SV=1
AT1G75280	P52577	-0,309	0,002	cytosol	Isoflavone reductase homolog P3 OS=Arabidopsis thaliana GN=At1g75280 PE=2 SV=1
AT1G63970	Q9CAK8	-0,304	0,002	plastid	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, chloroplastic OS=Arabidopsis thaliana GN=ISPF PE=1 SV=1
AT5G48230	Q8S4Y1	0,334	0,002	peroxisome	Acetyl-CoA acetyltransferase, cytosolic 1 OS=Arabidopsis thaliana GN=AAT1 PE=1 SV=1
AT4G34230	O49482	0,372	0,006	plasma membrane	Cinnamyl alcohol dehydrogenase 5 OS=Arabidopsis thaliana GN=CAD5 PE=1 SV=1
AT1G30530	Q9S9P6	0,394	0,003	golgi	UDP-glycosyltransferase 78D1 OS=Arabidopsis thaliana GN=UGT78D1 PE=1 SV=1
AT3G14210	Q9LJG3	0,395	0,001	vacuole	GDSL esterase/lipase ESM1 OS=Arabidopsis thaliana GN=ESM1 PE=1 SV=1
AT3G55120	P41088	0,395	0,002	endoplasmic reticulum	Chalcone--flavonone isomerase 1 OS=Arabidopsis thaliana GN=CHI1 PE=1 SV=2
AT5G36160	Q9LVY1	0,432	0,009	cytosol	Tyrosine aminotransferase OS=Arabidopsis thaliana GN=TAT PE=2 SV=1
AT3G44320	P46010	0,472	0,006	cytosol	Nitrilase 3 OS=Arabidopsis thaliana GN=NIT3 PE=1 SV=1
AT4G34050	O49499	0,576	0,001	cytosol	Caffeoyl-CoA O-methyltransferase 1 OS=Arabidopsis thaliana GN=CCOAOMT1 PE=1 SV=1
AT4G39330	P42734	0,583	0,001	cytosol	Probable cinnamyl alcohol dehydrogenase 9 OS=Arabidopsis thaliana GN=CAD9 PE=2 SV=2
AT1G74090	Q9C9C9	0,587	0,004	cytosol	Cytosolic sulfotransferase 18 OS=Arabidopsis thaliana GN=SOT18 PE=1 SV=1
AT2G33590	O22809	0,612	0,002	golgi,cytosol	NAD(P)-binding Rossmann-fold superfamily protein OS=Arabidopsis thaliana GN=CRL1 PE=2 SV=1
AT2G29340	F4IKM1	0,64	0,001	cytosol	Tropinone reductase homolog At2g29340 OS=Arabidopsis thaliana GN=At2g29340 PE=2 SV=1
AT5G54160	Q9FK25	0,72	0,001	cytosol	Flavone 3'-O-methyltransferase 1 OS=Arabidopsis thaliana GN=OMT1 PE=1 SV=1
AT2G25450	Q9SKK4	0,742	0,001	golgi	Probable 2-oxoacid dependent dioxygenase OS=Arabidopsis thaliana GN=GSL-OPE=2 SV=1
AT1G74100	Q9C9D0	0,792	0,002	cytosol	Cytosolic sulfotransferase 16 OS=Arabidopsis thaliana GN=SOT16 PE=1 SV=1

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AT2G31790	Q9SKC1	0,81	0,002	mitochondrion	UDP-glycosyltransferase 74C1 OS=Arabidopsis thaliana GN=UGT74C1 PE=2 SV=1
AT1G80560	P93832	0,818	0,002	plastid	3-isopropylmalate dehydrogenase 2, chloroplastic OS=Arabidopsis thaliana GN=IMDH2 PE=1 SV=1
AT4G11820	P54873	0,825	0,001	cytosol	Hydroxymethylglutaryl-CoA synthase OS=Arabidopsis thaliana GN=HMGS PE=1 SV=2
AT2G20610	Q9SIV0	0,859	0,001	cytosol	S-alkyl-thiohydroximate lyase SUR1 OS=Arabidopsis thaliana GN=SUR1 PE=1 SV=1
AT1G72680	Q9CAI3	1,133	0,001	cytosol	Probable cinnamyl alcohol dehydrogenase 1 OS=Arabidopsis thaliana GN=CAD1 PE=2 SV=1
AT2G37040	P35510	1,179	0,001	cytosol	Phenylalanine ammonia-lyase 1 OS=Arabidopsis thaliana GN=PAL1 PE=1 SV=3
AT2G43100	Q9ZW84	1,303	0,001	plastid	3-isopropylmalate dehydratase small subunit 1 OS=Arabidopsis thaliana GN=IPMI2 PE=1 SV=1
AT5G23010	Q9FG67	1,428	0,001	plastid	Methylthioalkylmalate synthase 1, chloroplastic OS=Arabidopsis thaliana GN=MAM1 PE=1 SV=1
AT5G13930	P13114	1,702	0,001	endoplasmic reticulum	Chalcone synthase OS=Arabidopsis thaliana GN=CHS PE=1 SV=1
Signalling					
AT4G09570	Q38869	-1,277	0,007	cytosol	Calcium-dependent protein kinase 4 OS=Arabidopsis thaliana GN=CPK4 PE=1 SV=1
AT1G49340	Q9SXA1	-0,728	0,003	plasma membrane	Phosphatidylinositol 4-kinase alpha 1 OS=Arabidopsis thaliana GN=PI4KA1 PE=1 SV=2
AT5G17790	Q8S9K3	-0,586	0,007	plastid	Zinc finger protein VAR3, chloroplastic OS=Arabidopsis thaliana GN=VAR3 PE=1 SV=2
AT3G45780	O48963	-0,519	0,005	plasma membrane	Phototropin-1 OS=Arabidopsis thaliana GN=PHOT1 PE=1 SV=1
AT5G37780	P0DH95	-0,422	0,004	nucleus	Calmodulin-1 OS=Arabidopsis thaliana GN=CAM1 PE=1 SV=1
AT4G01900	Q9ZST4	-0,405	0,002	plastid	Nitrogen regulatory protein P-II homolog OS=Arabidopsis thaliana GN=GLB1 PE=1 SV=1
AT1G08490	Q93WX6	0,303	0,007	plastid	Cysteine desulfurase 1, chloroplastic OS=Arabidopsis thaliana GN=NFS2 PE=1 SV=1
AT5G20010	P41916	0,311	0,002	cytosol	GTP-binding nuclear protein Ran-1 OS=Arabidopsis thaliana GN=RAN1 PE=1 SV=1
AT5G08650	Q9FNM5	0,325	0,006	plastid	Translation factor GUF1 homolog, chloroplastic OS=Arabidopsis thaliana GN=At5g08650 PE=1 SV=2
AT1G48630	Q9C4Z6	0,351	0,004	cytosol	Receptor for activated C kinase 1B OS=Arabidopsis thaliana GN=RACK1B PE=1 SV=1
AT4G02080	O04834	0,353	0,003	plasma membrane	GTP-binding protein SAR1A OS=Arabidopsis thaliana GN=SAR1A PE=2 SV=1
AT2G44100	Q96254	0,374	0,004	cytosol	Guanosine nucleotide diphosphate dissociation inhibitor 1 OS=Arabidopsis thaliana GN=GDI1 PE=1 SV=1
AT5G42080	P42697	0,382	0,002	plasma membrane	Dynamin-related protein 1A OS=Arabidopsis thaliana GN=DRP1A PE=1 SV=3
AT4G09000	P42643	0,436	0,01	cytosol	14-3-3-like protein GF14 chi OS=Arabidopsis thaliana GN=GRF1 PE=1 SV=3
AT1G52280	Q9C820	0,449	0,007	na membrane,golgi,va	Ras-related protein RABG3d OS=Arabidopsis thaliana GN=RABG3D PE=2 SV=1
AT5G56360	Q9FM96	0,543	0,01	endoplasmic reticulum	Glucosidase 2 subunit beta OS=Arabidopsis thaliana GN=PSL4 PE=2 SV=1
AT5G39620	Q948K6	0,604	0,003	vacuole	Ras-related protein RABG1 OS=Arabidopsis thaliana GN=RABG1 PE=2 SV=1
AT5G60860	Q9FJH0	0,66	0,002	golgi	Ras-related protein RABA1f OS=Arabidopsis thaliana GN=RABA1F PE=2 SV=1
AT5G42970	Q8L5U0	0,678	0,003	nucleus	COP9 signalosome complex subunit 4 OS=Arabidopsis thaliana GN=CSN4 PE=1 SV=2
AT4G17530	Q9SEH3	0,739	0,001	cytosol	Ras-related protein RABD2c OS=Arabidopsis thaliana GN=RABD2C PE=1 SV=1
AT3G46060	P28186	0,778	0,003	plasma membrane	Ras-related protein RABE1c OS=Arabidopsis thaliana GN=RABE1C PE=1 SV=1
AT5G47520	Q9FGK5	0,82	0,002	plasma membrane	Ras-related protein RABA5a OS=Arabidopsis thaliana GN=RABA5A PE=1 SV=1
AT3G22060	Q9LRJ9	0,935	0,001	extracellular	Cysteine-ricrepeat secretory protein 38 OS=Arabidopsis thaliana GN=CRRSP38 PE=2 SV=1
AT4G21940	O49717	0,969	0,006	plasma membrane	Calcium-dependent protein kinase 15 OS=Arabidopsis thaliana GN=CPK15 PE=2 SV=1
AT5G09440	Q9FY71	1,101	0,001	extracellular	Protein EXORDIUM-like 4 OS=Arabidopsis thaliana GN=EXL4 PE=2 SV=1
AT5G61790	P29402	1,101	0,001	endoplasmic reticulum	Calnexin homolog 1 OS=Arabidopsis thaliana GN=CNX1 PE=1 SV=1
AT5G07340	Q38798	1,118	0,001	endoplasmic reticulum	Calnexin homolog 2 OS=Arabidopsis thaliana GN=At5g07340 PE=2 SV=2
AT2G33380	O22788	1,323	0,001	cytosol	Probable peroxygenase 3 OS=Arabidopsis thaliana GN=PXG3 PE=1 SV=1
AT3G19300	Q9LT87	1,443	0,001	plasma membrane	At3g19300 OS=Arabidopsis thaliana GN=At3g19300 PE=2 SV=1
Stress					
AT2G18465	Q8L763	-1,17	0,001	mitochondrion	Chaperone DnaJ-domain superfamily protein OS=Arabidopsis thaliana GN=DJC72 PE=2 SV=1
AT5G21430	Q84VQ4	-1,062	0,001	plastid	NAD(P)H-quinone oxidoreductase subunit U, chloroplastic OS=Arabidopsis thaliana GN=ndhU PE=1 SV=1
AT3G15700	Q9LW09	-0,911	0,006	cytosol	Putative disease resistance protein At3g15700 OS=Arabidopsis thaliana GN=At3g15700 PE=3 SV=1
AT1G76180	P42763	-0,79	0,001	peroxisome	Dehydrin ERD14 OS=Arabidopsis thaliana GN=ERD14 PE=1 SV=1
AT1G20440	P31168	-0,662	0,003	nucleus	Dehydrin COR47 OS=Arabidopsis thaliana GN=COR47 PE=1 SV=2
AT4G39960	Q940V1	-0,615	0,004	plastid	AT4g39960/T5J17_130 OS=Arabidopsis thaliana GN=DJA5 PE=2 SV=1
AT4G02100	Q84VX5	-0,595	0,004	nucleus	reversed At4g02100 OS=Arabidopsis thaliana GN=At4g02100 PE=2 SV=1
AT1G80030	Q0WN54	-0,528	0,002	plastid	Molecular chaperone Hsp40/DnaJ family protein OS=Arabidopsis thaliana GN=DJA7 PE=2 SV=1
AT1G54410	Q9SLJ2	-0,513	0,005	cytosol	Dehydrin HIRD11 OS=Arabidopsis thaliana GN=HIRD11 PE=1 SV=1
AT3G12580	Q9LHA8	-0,506	0,001	cytosol	Probable mediator of RNA polymerase II transcription subunit 37c OS=Arabidopsis thaliana GN=MED37C PE=1 SV=1
AT3G62020	Q9M263	-0,471	0,006	extracellular	Germin-like protein subfamily 2 member 4 OS=Arabidopsis thaliana GN=GLP10 PE=2 SV=1
AT4G31310	A2RVS4	-0,457	0,007	cytosol	AIG2-like protein C OS=Arabidopsis thaliana GN=AIG2LC PE=1 SV=1
AT1G70890	Q9SSK5	-0,443	0,006	peroxisome	MLP-like protein 43 OS=Arabidopsis thaliana GN=MLP43 PE=1 SV=1

AT5G49910	Q9LTX9	-0,441	0,001	plastid	Heat shock 70 kDa protein 7, chloroplastic OS=Arabidopsis thaliana GN=HSP70-7 PE=2 SV=1
AT1G72610	P94040	-0,437	0,002	extracellular	Germin-like protein subfamily 3 member 1 OS=Arabidopsis thaliana GN=GLP1 PE=1 SV=1
AT2G41430	Q39096	-0,384	0,01	cytosol	Protein EARLY RESPONSIVE TO DEHYDRATION 15 OS=Arabidopsis thaliana GN=ERD15 PE=1 SV=1
AT3G25760	Q9LS03	-0,364	0,006	plastid	Allene oxide cyclase 1, chloroplastic OS=Arabidopsis thaliana GN=AOC1 PE=1 SV=1
AT4G24280	Q9STW6	-0,352	0,001	plastid	Heat shock 70 kDa protein 6, chloroplastic OS=Arabidopsis thaliana GN=HSP70-6 PE=1 SV=1
AT1G23130	O49304	-0,302	0,003	cytosol	At1g23130/T26J12_10 OS=Arabidopsis thaliana GN=At1g23130 PE=2 SV=1
AT4G37910	Q8GUM2	0,311	0,001	mitochondrion	Heat shock 70 kDa protein 9, mitochondrial OS=Arabidopsis thaliana GN=HSP70-9 PE=1 SV=1
AT2G21620	Q9SIJ8	0,337	0,005	plasma membrane	Adenine nucleotide alpha hydrolases-like superfamily protein OS=Arabidopsis thaliana GN=RD2 PE=1 SV=2
AT5G28540	Q9LKR3	0,365	0,005	endoplasmic reticulum	Mediator of RNA polymerase II transcription subunit 37a OS=Arabidopsis thaliana GN=MED37A PE=1 SV=1
AT1G28290	Q9FZA2	0,399	0,004	extracellular	Non-classical arabinogalactan protein 31 OS=Arabidopsis thaliana GN=AGP31 PE=1 SV=1
AT4G16660	F4JMJ1	0,408	0,002	endoplasmic reticulum	Heat shock 70 kDa protein 17 OS=Arabidopsis thaliana GN=HSP70-17 PE=2 SV=1
AT5G42020	Q39043	0,426	0,008	endoplasmic reticulum	Mediator of RNA polymerase II transcription subunit 37f OS=Arabidopsis thaliana GN=MED37F PE=1 SV=2
AT1G79930	Q9S7C0	0,438	0,007	cytosol	Heat shock 70 kDa protein 14 OS=Arabidopsis thaliana GN=HSP70-14 PE=1 SV=1
AT4G00860	Q38842	0,476	0,007	mitochondrion	protein OS=Arabidopsis thaliana GN=ATOZI1 PE=2 SV=1
AT3G62600	Q9LZK5	0,572	0,004	endoplasmic reticulum	DnaJ protein ERDJ3B OS=Arabidopsis thaliana GN=ERDJ3B PE=1 SV=1
AT2G43590	O24658	0,626	0,004	extracellular	Endochitinase At2g43590 OS=Arabidopsis thaliana GN=At2g43590 PE=2 SV=1
AT1g33590	A0A1P8AWX3	0,67	0,001	extracellular	Leucine-ricrepeat (LRR) family protein OS=Arabidopsis thaliana GN=At1g33590 PE=4 SV=1
AT5G52310	Q06738	0,718	0,003	nucleus	Low-temperature-induced 78 kDa protein OS=Arabidopsis thaliana GN=RD29A PE=1 SV=2
AT1G17860	Q9LMU2	0,723	0,001	extracellular	Kunitz trypsin inhibitor 2 OS=Arabidopsis thaliana GN=KTI2 PE=2 SV=1
AT5G55530	Q5HZ03	0,872	0,002	nucleus	At5g55530 OS=Arabidopsis thaliana GN=MTE17.25 PE=1 SV=1
AT2G42530	Q9SIN5	0,891	0,001	plastid	Protein COLD-REGULATED 15B, chloroplastic OS=Arabidopsis thaliana GN=COR15B PE=1 SV=1
AT1G33950	Q9C8V2	0,898	0,002	nucleus	reversed Immune-associated nucleotide-binding protein 7 OS=Arabidopsis thaliana GN=IAN7 PE=2 SV=1
AT2G38870	Q9ZV18	0,961	0,002	cytosol	Putative protease inhibitor OS=Arabidopsis thaliana GN=At2g38870 PE=2 SV=2
AT2G42540	Q42512	1,603	0,001	plastid	Protein COLD-REGULATED 15A, chloroplastic OS=Arabidopsis thaliana GN=COR15A PE=1 SV=1
AT2G43620	O22841	2,494	0,001	extracellular	Endochitinase At2g43620 OS=Arabidopsis thaliana GN=At2g43620 PE=3 SV=1
TCA/org transformation					
AT3G01500	P27140	-1,083	0,001	plastid	Beta carbonic anhydrase 1, chloroplastic OS=Arabidopsis thaliana GN=BCA1 PE=1 SV=2
AT3G17240	Q9M5K2	-0,559	0,001	mitochondrion	Dihydrolipoyl dehydrogenase 2, mitochondrial OS=Arabidopsis thaliana GN=LPD2 PE=1 SV=1
AT1G48030	Q9M5K3	-0,502	0,001	mitochondrion	Dihydrolipoyl dehydrogenase 1, mitochondrial OS=Arabidopsis thaliana GN=LPD1 PE=1 SV=2
AT3G16950	A8MS68	-0,41	0,001	plastid	Dihydrolipoyl dehydrogenase 1, chloroplastic OS=Arabidopsis thaliana GN=LPD1 PE=2 SV=1
AT5G40650	Q8LB02	0,333	0,007	mitochondrion	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit 2, mitochondrial OS=Arabidopsis thaliana GN=SDH2-2 PE=1 SV=2
AT5G08300	P68209	0,336	0,004	mitochondrion	Succinate--CoA ligase [ADP-forming] subunit alpha-1, mitochondrial OS=Arabidopsis thaliana GN=At5g08300 PE=1 SV=1
AT1G59900	P52901	0,341	0,006	mitochondrion	Pyruvate dehydrogenase E1 component subunit alpha-1, mitochondrial OS=Arabidopsis thaliana GN=E1 ALPHA PE=1 SV=2
AT1G53240	Q9ZP06	0,344	0,001	mitochondrion	Malate dehydrogenase 1, mitochondrial OS=Arabidopsis thaliana GN=At1g53240 PE=1 SV=1
AT5G14590	Q8LPJ5	0,352	0,003	mitochondrion	Isocitrate dehydrogenase [NADP], chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=At5g14590 PE=1 SV=1
AT1G04410	P93819	0,362	0,001	vacuole	Malate dehydrogenase 1, cytoplasmic OS=Arabidopsis thaliana GN=MDH1 PE=1 SV=2
AT4G35830	Q42560	0,372	0,01	mitochondrion,cytoso	Aconitate hydratase 1 OS=Arabidopsis thaliana GN=ACO1 PE=1 SV=2
AT5G43330	P57106	0,375	0,007	cytosol	Malate dehydrogenase 2, cytoplasmic OS=Arabidopsis thaliana GN=MDH2 PE=1 SV=1
AT5G50950	Q9FI53	0,378	0,01	mitochondrion,cytoso	Fumarate hydratase 2, chloroplastic OS=Arabidopsis thaliana GN=FUM2 PE=2 SV=1
AT2G47510	P93033	0,385	0,003	mitochondrion	Fumarate hydratase 1, mitochondrial OS=Arabidopsis thaliana GN=FUM1 PE=1 SV=2
AT3G55410	F4IWV2	0,406	0,001	mitochondrion	2-oxoglutarate dehydrogenase, E1 component OS=Arabidopsis thaliana GN=At3g55410 PE=1 SV=1
AT3G06650	Q9C522	0,455	0,001	cytosol	ATP-citrate synthase beta chain protein 1 OS=Arabidopsis thaliana GN=ACLB-1 PE=2 SV=1
AT1G24180	Q8H1Y0	0,47	0,004	mitochondrion	Pyruvate dehydrogenase E1 component subunit alpha-2, mitochondrial OS=Arabidopsis thaliana GN=IAR4 PE=1 SV=2
AT1G10670	Q9SGY2	0,48	0,003	cytosol	ATP-citrate synthase alpha chain protein 1 OS=Arabidopsis thaliana GN=ACLA-1 PE=1 SV=1
AT5G11670	Q9LYG3	0,513	0,001	cytosol	NADP-dependent malic enzyme 2 OS=Arabidopsis thaliana GN=NADP-ME2 PE=1 SV=1
AT5G66760	O82663	0,52	0,001	mitochondrion	Succinate dehydrogenase [ubiquinone] flavoprotein subunit 1, mitochondrial OS=Arabidopsis thaliana GN=SDH1-1 PE=1 SV=1
AT1G65930	Q9SRZ6	0,535	0,001	cytosol	Cytosolic isocitrate dehydrogenase [NADP] OS=Arabidopsis thaliana GN=CICDPE=2 SV=1
AT5G49460	Q9FGX1	0,572	0,003	cytosol	ATP-citrate synthase beta chain protein 2 OS=Arabidopsis thaliana GN=ACLB-2 PE=1 SV=1
AT2G44350	P20115	0,576	0,001	mitochondrion	Citrate synthase 4, mitochondrial OS=Arabidopsis thaliana GN=CSY4 PE=1 SV=3
AT4G35260	Q8LFC0	0,605	0,001	mitochondrion	Isocitrate dehydrogenase [NAD] regulatory subunit 1, mitochondrial OS=Arabidopsis thaliana GN=IDH1 PE=1 SV=2
AT4G26970	Q94A28	0,612	0,001	mitochondrion	Aconitate hydratase 2, mitochondrial OS=Arabidopsis thaliana GN=ACO2 PE=1 SV=3
AT1G09430	O80526	0,646	0,002	cytosol	ATP-citrate synthase alpha chain protein 3 OS=Arabidopsis thaliana GN=ACLA-3 PE=2 SV=1
Tetrapyrrole synthesis					

AT4G25080	Q9SW18	-0,518	0,001	plastid	Magnesium protoporphyrin IX methyltransferase, chloroplastic OS=Arabidopsis thaliana GN=CHLM PE=1 SV=1
AT4G01690	P55826	0,374	0,001	plastid	Protoporphyrinogen oxidase 1, chloroplastic OS=Arabidopsis thaliana GN=PPOX1 PE=1 SV=1
AT3G59400	Q9LX31	0,435	0,008	plastid	Tetrapyrrole-binding protein, chloroplastic OS=Arabidopsis thaliana GN=GUN4 PE=1 SV=1
AT1G69740	Q9SFH9	0,437	0,001	plastid	Delta-aminolevulinic acid dehydratase 1, chloroplastic OS=Arabidopsis thaliana GN=HEMB1 PE=2 SV=1
AT4G27440	P21218	0,561	0,001	plastid	Protochlorophyllide reductase B, chloroplastic OS=Arabidopsis thaliana GN=PORB PE=1 SV=3
AT5G13630	Q9FNB0	0,9	0,001	plastid	Magnesium-chelatase subunit ChlH, chloroplastic OS=Arabidopsis thaliana GN=CHLPE=1 SV=1
AT1G58290	P42804	1,042	0,002	plastid	Glutamyl-tRNA reductase 1, chloroplastic OS=Arabidopsis thaliana GN=HEMA1 PE=1 SV=2
Transport					
AT2G45960	Q06611	-0,833	0,002	plasma membrane	Aquaporin PIP1-2 OS=Arabidopsis thaliana GN=PIP1-2 PE=1 SV=1
AT2G25600	Q8GXE6	-0,816	0,002	cytosol	reversed Potassium channel AKT6 OS=Arabidopsis thaliana GN=AKT6 PE=1 SV=2
AT4G35100	P93004	-0,727	0,001	plasma membrane	Aquaporin PIP2-7 OS=Arabidopsis thaliana GN=PIP2-7 PE=1 SV=2
AT3G16240	Q41951	-0,609	0,001	vacuole	Aquaporin TIP2-1 OS=Arabidopsis thaliana GN=TIP2-1 PE=1 SV=2
AT3G26520	Q41963	-0,602	0,002	vacuole	Aquaporin TIP1-2 OS=Arabidopsis thaliana GN=TIP1-2 PE=1 SV=2
AT3G53420	P43286	-0,592	0,001	plasma membrane	Aquaporin PIP2-1 OS=Arabidopsis thaliana GN=PIP2-1 PE=1 SV=1
AT4G00430	Q39196	-0,589	0,007	plasma membrane	Probable aquaporin PIP1-4 OS=Arabidopsis thaliana GN=PIP1.4 PE=1 SV=1
AT5G22830	Q058N4	-0,546	0,005	plastid	Magnesium transporter MRS2-11, chloroplastic OS=Arabidopsis thaliana GN=MRS2-11 PE=1 SV=1
AT2G36830	P25818	-0,502	0,002	vacuole	Aquaporin TIP1-1 OS=Arabidopsis thaliana GN=TIP1-1 PE=1 SV=1
AT5G20650	Q93VM8	-0,43	0,009	vacuole	Copper transporter 5 OS=Arabidopsis thaliana GN=COPT5 PE=1 SV=1
AT1G30690	Q94C59	0,361	0,003	cytosol	Patellin-4 OS=Arabidopsis thaliana GN=PATL4 PE=1 SV=2
AT5G19760	Q9C5M0	0,381	0,001	mitochondrion	Mitochondrial dicarboxylate/tricarboxylate transporter DTC OS=Arabidopsis thaliana GN=DTC PE=1 SV=1
AT5G14040	Q9FMU6	0,45	0,001	mitochondrion	Mitochondrial phosphate carrier protein 3, mitochondrial OS=Arabidopsis thaliana GN=MPT3 PE=1 SV=1
AT1G72660	Q9CAI1	0,591	0,004	cytosol	Developmentally-regulated G-protein 2 OS=Arabidopsis thaliana GN=DRG2 PE=2 SV=1
AT3G08580	P31167	0,641	0,001	mitochondrion	ADP,ATP carrier protein 1, mitochondrial OS=Arabidopsis thaliana GN=AAC1 PE=1 SV=2
Not assigned					
AT3G47070	Q9SD66	-1,472	0,005	plastid	Thylakoid soluble phosphoprotein OS=Arabidopsis thaliana GN=F13I12.120 PE=1 SV=1
AT2G04039	Q93Z84	-1,195	0,001	plastid	At2g04039/At2g04039 OS=Arabidopsis thaliana GN=At2g04039 PE=2 SV=1
AT1G12250	Q8H1Q1	-1,188	0,001	plastid	Thylakoid lumenal protein TL20.3, chloroplastic OS=Arabidopsis thaliana GN=TL20.3 PE=1 SV=1
AT2G23670	O64835	-1,064	0,001	plastid	At2g23670/F26B6.32 OS=Arabidopsis thaliana GN=YCF37 PE=2 SV=1
AT4G23890	Q9T0A4	-1,016	0,001	plastid	NAD(P)H-quinone oxidoreductase subunit S, chloroplastic OS=Arabidopsis thaliana GN=ndhS PE=1 SV=1
AT1G15980	Q9S9N6	-0,995	0,001	plastid	Photosynthetic NDsubunit of subcomplex B 1, chloroplastic OS=Arabidopsis thaliana GN=PNSB1 PE=2 SV=1
AT1G42480	F4I9G7	-0,96	0,006	extracellular	TLR4 regulator/MIR-interacting MSAP protein OS=Arabidopsis thaliana GN=At1g42480 PE=4 SV=1
AT5G52970	Q9LVV5	-0,954	0,001	plastid	Thylakoid lumenal 15.0 kDa protein 2, chloroplastic OS=Arabidopsis thaliana GN=At5g52970 PE=1 SV=2
AT2G26340	F4IUJ0	-0,951	0,001	plastid	Uncharacterized protein OS=Arabidopsis thaliana GN=At2g26340 PE=4 SV=1
AT1G29240	Q9LP52	-0,936	0,002	nucleus	reversed F28N24.8 protein OS=Arabidopsis thaliana GN=At1g29240 PE=2 SV=1
AT5G48790	Q94F50	-0,906	0,002	plastid	AT5g48790/K24G6_12 OS=Arabidopsis thaliana GN=At5g48790 PE=2 SV=1
AT2G36145	Q8VXY0	-0,896	0,002	plastid	Expressed protein OS=Arabidopsis thaliana GN=At2g36145 PE=2 SV=1
AT3G03440	F4J139	-0,863	0,002	nucleus	reversed ARM repeat superfamily protein OS=Arabidopsis thaliana GN=At3g03440 PE=4 SV=1
AT4G37300	O23157	-0,854	0,001	nucleus	AT4g37300/C7A10_60 OS=Arabidopsis thaliana GN=C7A10.60 PE=1 SV=1
AT4G02530	O22773	-0,829	0,001	plastid	Thylakoid lumenal 16.5 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=At4g02530 PE=1 SV=3
AT1G49975	Q8LFL5	-0,824	0,002	plastid	At1g49975 OS=Arabidopsis thaliana GN=At1g49975 PE=2 SV=1
AT5G53490	P81760	-0,791	0,001	plastid	Thylakoid lumenal 17.4 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=TL17 PE=1 SV=2
AT4G24930	Q9SW33	-0,79	0,001	plastid	Thylakoid lumenal 17.9 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=At4g24930 PE=1 SV=1
AT2G44920	O22160	-0,766	0,001	plastid	Thylakoid lumenal 15 kDa protein 1, chloroplastic OS=Arabidopsis thaliana GN=At2g44920 PE=1 SV=2
AT1G55480	Q94BS2	-0,696	0,001	plastid	Protein MET1, chloroplastic OS=Arabidopsis thaliana GN=MET1 PE=1 SV=1
AT4G10930	Q8L7I1	-0,681	0,003	nucleus	reversed Uncharacterized protein At4g10930 OS=Arabidopsis thaliana GN=At4g10930 PE=2 SV=1
AT4G03150	Q944G6	-0,668	0,003	plastid	AT4g03150/F4C21_7 OS=Arabidopsis thaliana GN=At4g03150 PE=2 SV=1
AT5G08050	Q9SD79	-0,665	0,002	plastid	Uncharacterized protein F13G24.250 OS=Arabidopsis thaliana GN=F13G24.250 PE=1 SV=1
AT4G30720	F4JQE2	-0,662	0,005	plastid	reversed FAD/NAD(P)-binding oxidoreductase family protein OS=Arabidopsis thaliana GN=PDE327 PE=4 SV=1
AT4G13200	Q8LDV3	-0,661	0,001	plastid	Uncharacterized protein At4g13200, chloroplastic OS=Arabidopsis thaliana GN=At4g13200 PE=1 SV=2
AT4G22670	Q93YR3	-0,654	0,001	cytosol	FAM10 family protein At4g22670 OS=Arabidopsis thaliana GN=At4g22670 PE=1 SV=1
AT2G03420	Q9ZQ78	-0,653	0,004	plastid	Uncharacterized protein At2g03420 OS=Arabidopsis thaliana GN=At2g03420 PE=2 SV=2
AT2G40600	Q8H114	-0,652	0,003	plastid	Appr-1-p processing enzyme family protein OS=Arabidopsis thaliana GN=At2g40600 PE=1 SV=1
AT2G47960	O82263	-0,652	0,004	golgi	At2g47960/T9J23.10 OS=Arabidopsis thaliana GN=At2g47960 PE=2 SV=2

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AT2G30170	O64730	-0,641	0,002	plastid	Probable protein phosphatase 2C 26 OS=Arabidopsis thaliana GN=At2g30170 PE=2 SV=2
AT5G39210	Q9FL87	-0,637	0,001	nucleus	Protein CHLORORESPIRATORY REDUCTION 7, chloroplastic OS=Arabidopsis thaliana GN=CRR7 PE=2 SV=1
AT5G05200	Q9ASX5	-0,636	0,002	plastid	Uncharacterized aarF domain-containing protein kinase At5g05200, chloroplastic OS=Arabidopsis thaliana GN=At5g05200 PE=1 SV=1
AT2G35810	Q8VZP3	-0,611	0,003	cytosol	Uncharacterized protein At2g35810 OS=Arabidopsis thaliana GN=At2g35810 PE=2 SV=1
AT5G07020	Q9FL44	-0,61	0,003	plastid	Protein MAINTENANCE OF PSII UNDER HIGLIGHT 1 OS=Arabidopsis thaliana GN=MPH1 PE=1 SV=1
AT5G42960	Q8H0Y1	-0,602	0,001	plastid	Outer envelope pore protein 24B, chloroplastic OS=Arabidopsis thaliana GN=OEP24B PE=2 SV=1
AT5G20935	F4K6X0	-0,6	0,002	mitochondrion	DUF3148 family protein OS=Arabidopsis thaliana GN=CRR42 PE=4 SV=2
AT1G11930	Q944L8	-0,582	0,002	cytosol	At1g11930/F12F1_20 OS=Arabidopsis thaliana GN=At1g11930 PE=1 SV=1
AT5G27390	A0A1P8BEU1	-0,577	0,004	plastid	Tagatose-6-phosphate ketose/aldose isomerase, putative (Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein) OS=Arabidopsis thaliana GN=At5g27390 PE=4 SV=1
AT1G32080	Q9FVQ4	-0,562	0,002	plastid	Plastidal glycolate/glycerate translocator 1, chloroplastic OS=Arabidopsis thaliana GN=PLGG1 PE=1 SV=1
AT4G10300	Q9SV91	-0,556	0,002	plastid	At4g10300 OS=Arabidopsis thaliana GN=F24G24.100 PE=2 SV=1
AT3G63540	P82658	-0,55	0,001	plastid	Thylakoid lumenal 19 kDa protein, chloroplastic OS=Arabidopsis thaliana GN=At3g63540 PE=1 SV=2
AT5G14910	Q93VK7	-0,545	0,001	plastid	AT5g14910/F2G14_30 OS=Arabidopsis thaliana GN=At5g14910 PE=2 SV=1
AT5G20090	Q949R9	-0,539	0,004	mitochondrion	Mitochondrial pyruvate carrier 1 OS=Arabidopsis thaliana GN=MPC1 PE=3 SV=1
AT1G16720	A0A1P8AWU9	-0,537	0,001	plastid	Higchlorophyll fluorescence phenotype 173 OS=Arabidopsis thaliana GN=HCF173 PE=4 SV=1
AT3G46780	Q9STF2	-0,529	0,001	plastid	Protein plastid transcriptionally active 16, chloroplastic OS=Arabidopsis thaliana GN=PTAC16 PE=1 SV=1
AT2G21530	Q8GWP4	-0,528	0,001	plastid	At2g21530 OS=Arabidopsis thaliana GN=At2g21530 PE=1 SV=1
AT5G39570	Q9FKA5	-0,526	0,001	nucleus	Uncharacterized protein At5g39570 OS=Arabidopsis thaliana GN=At5g39570 PE=1 SV=1
AT4G39970	Q680K2	-0,514	0,001	plastid	Haloacid dehalogenase-like hydrolase domain-containing protein At4g39970 OS=Arabidopsis thaliana GN=At4g39970 PE=2 SV=1
AT4G15545	Q93W28	-0,512	0,001	nucleus	Uncharacterized protein At4g15545 OS=Arabidopsis thaliana GN=At4g15545 PE=1 SV=1
AT3G58875	A0A1I9LQC5	-0,509	0,005	mitochondrion	Uncharacterized protein OS=Arabidopsis thaliana GN=At3g58875 PE=4 SV=1
AT2G15960	Q9XIM6	-0,508	0,009	nucleus	Expressed protein OS=Arabidopsis thaliana GN=At2g15960 PE=1 SV=1
AT1G16080	Q9S9M7	-0,505	0,001	plastid	Nuclear protein OS=Arabidopsis thaliana GN=At1g16080 PE=1 SV=1
AT3G28770	Q9LH98	-0,505	0,006	extracellular	reversed Transmembrane protein, putative (DUF1216) OS=Arabidopsis thaliana GN=At3g28770 PE=4 SV=1
AT3G48420	Q94K71	-0,493	0,001	plastid	CBBY-like protein OS=Arabidopsis thaliana GN=CBBY PE=1 SV=1
AT5G42765	F4K329	-0,491	0,002	plastid	Plasma membrane fusion protein OS=Arabidopsis thaliana GN=At5g42765 PE=4 SV=1
AT5G66550	A0A1P8BDL4	-0,489	0,007	plastid	Maf-like protein OS=Arabidopsis thaliana GN=At5g66550 PE=4 SV=1
AT5G24165	Q8LDQ8	-0,485	0,002	mitochondrion	At5g24165 OS=Arabidopsis thaliana GN=At5g24165 PE=2 SV=1
AT3G18790	Q9LS97	-0,48	0,006	nucleus	AT3G18790 protein OS=Arabidopsis thaliana GN=At3g18790 PE=2 SV=1
AT2G37660	O80934	-0,475	0,001	plastid	Uncharacterized protein At2g37660, chloroplastic OS=Arabidopsis thaliana GN=At2g37660 PE=1 SV=2
AT4G24750	Q0WWT7	-0,466	0,003	plastid	Rhodanese-like domain-containing protein 11, chloroplastic OS=Arabidopsis thaliana GN=STR11 PE=2 SV=1
AT5G38520	F4KBJ3	-0,463	0,008	plastid	Alpha/beta-Hydrolases superfamily protein OS=Arabidopsis thaliana GN=MBB18.5 PE=4 SV=1
AT5G42070	Q8RWR9	-0,456	0,002	plastid	Uncharacterized protein At5g42070 OS=Arabidopsis thaliana GN=MJC20.18 PE=2 SV=1
AT1G79790	Q84VZ1	-0,454	0,003	plastid	Flavin mononucleotide hydrolase 1, chloroplatic OS=Arabidopsis thaliana GN=FHY1 PE=1 SV=1
AT1G47470	Q3ECV8	-0,451	0,009	extracellular	ECA1 gametogenesis family protein (DUF784) OS=Arabidopsis thaliana GN=At1g47470 PE=4 SV=2
AT4G17870	O49686	-0,448	0,002	nucleus	Abscisic acid receptor PYR1 OS=Arabidopsis thaliana GN=PYR1 PE=1 SV=1
AT3G09350	Q84J81	-0,447	0,002	cytosol	Fes1A OS=Arabidopsis thaliana GN=Fes1A PE=2 SV=1
AT1G04530	Q8VZ31	-0,445	0,004	cytosol	Tetratricopeptide repeat (TPR)-like superfamily protein OS=Arabidopsis thaliana GN=TPR4 PE=1 SV=1
AT1G02475	Q94K52	-0,441	0,007	plastid	Polyketide cyclase/dehydrase and lipid transport superfamily protein OS=Arabidopsis thaliana GN=At1g02475 PE=2 SV=1
AT2G43945	F4IT21	-0,44	0,004	plastid	Uncharacterized protein OS=Arabidopsis thaliana GN=At2g43945 PE=4 SV=1
AT1G56500	Q8VZ10	-0,436	0,001	plastid	Protein SUPPRESSOR OF QUENCHING 1, chloroplastic OS=Arabidopsis thaliana GN=SOQ1 PE=1 SV=1
AT3G52920	Q9LF99	-0,434	0,009	nucleus	Transcriptional activator (DUF662) OS=Arabidopsis thaliana GN=F8J2_90 PE=2 SV=1
AT4G35760	Q8L540	-0,422	0,01	plastid	Thiol-disulfide oxidoreductase LTO1 OS=Arabidopsis thaliana GN=LTO1 PE=1 SV=1
AT3G62540	Q3EAF8	-0,42	0,01	mitochondrion	Pentatricopeptide repeat-containing protein At3g62540, mitochondrial OS=Arabidopsis thaliana GN=At3g62540 PE=2 SV=1
AT1G22630	Q9SKA5	-0,419	0,008	vacuole	At1g22630/F12K8_2 OS=Arabidopsis thaliana GN=At1g22630 PE=2 SV=1
AT4G34090	F4JJY7	-0,417	0,003	plastid	Cyclin delta-3 OS=Arabidopsis thaliana GN=At4g34090 PE=4 SV=1
AT1G14310	Q9M9T1	-0,399	0,01	mitochondrion	F14L17.7 protein OS=Arabidopsis thaliana GN=At1g14310 PE=4 SV=1
AT1G09340	Q9SA52	-0,397	0,001	plastid	Chloroplast stem-loop binding protein of 41 kDa b, chloroplastic OS=Arabidopsis thaliana GN=CSP41B PE=1 SV=1
AT1G29350	F4I1G1	-0,394	0,003	nucleus	RNA polymerase II degradation factor-like protein (DUF1296) OS=Arabidopsis thaliana GN=At1g29350 PE=4 SV=1
AT4G21860	Q9C5C8	-0,394	0,008	plastid	Peptide methionine sulfoxide reductase B2, chloroplastic OS=Arabidopsis thaliana GN=MSRB2 PE=1 SV=1
AT2G42130	Q8S9M1	-0,384	0,001	plastid	Isoform 3 of Probable plastid-lipid-associated protein 13, chloroplastic OS=Arabidopsis thaliana GN=PAP13
AT1G52670	Q8VZ68	-0,382	0,004	plastid	Is a member of the PF|00364 Biotin-requiring enzymes family OS=Arabidopsis thaliana GN=At1g52670 PE=2 SV=1
AT1G61090	B3H4X2	-0,379	0,01	nucleus	reversed Uncharacterized protein OS=Arabidopsis thaliana GN=At1g61090 PE=4 SV=1
AT4G01150	O04616	-0,376	0,001	plastid	Protein CURVATURE THYLAKOID 1A, chloroplastic OS=Arabidopsis thaliana GN=CURT1A PE=1 SV=1
AT1G21680	Q9XI10	-0,374	0,001	extracellular	DPP6 N-terminal domain-like protein OS=Arabidopsis thaliana GN=At1g21680 PE=2 SV=1

AT5G47690	B3H5K3	-0,374	0,01	nucleus	Binding protein OS=Arabidopsis thaliana GN=At5g47690 PE=1 SV=1
AT1G16880	Q9FZ47	-0,368	0,002	plastid	ACT domain-containing protein ACR11 OS=Arabidopsis thaliana GN=ACR11 PE=1 SV=1
AT5G03880	Q940I2	-0,36	0,003	plastid	Thioredoxin family protein OS=Arabidopsis thaliana GN=MED24.18 PE=2 SV=1
AT3G63160	Q9M1X3	-0,355	0,003	plastid	AT3g63160/F16M2_10 OS=Arabidopsis thaliana GN=F16M2_10 PE=1 SV=1
AT2G35830	Q9SJ67	-0,355	0,005	cytosol	At2g35830/F11F19.26 OS=Arabidopsis thaliana GN=At2g35830 PE=2 SV=2
AT5G01650	F4K9G5	-0,355	0,003	plastid	Tautomerase/MIF superfamily protein OS=Arabidopsis thaliana GN=At5g01650 PE=4 SV=1
AT3G58010	Q9M2P7	-0,345	0,002	plastid	Probable plastid-lipid-associated protein 9, chloroplastic OS=Arabidopsis thaliana GN=PAP9 PE=1 SV=1
AT1G55805	Q682I1	-0,333	0,007	plastid	Protein BOLA1, chloroplastic OS=Arabidopsis thaliana GN=BOLA1 PE=1 SV=1
AT4g15790	A0A1I9LNC0	-0,326	0,001	nucleus	Copper chaperone OS=Arabidopsis thaliana GN=CCPE=4 SV=1
AT2G33255	Q8RYE9	-0,317	0,005	mitochondrion	Haloacid dehalogenase-like hydrolase domain-containing protein At2g33255 OS=Arabidopsis thaliana GN=At2g33255 PE=1 SV=1
AT3G07470	Q94AG1	-0,309	0,009	extracellular	At3g07470/F21O3_18 OS=Arabidopsis thaliana GN=At3g07470 PE=2 SV=1
AT1G73060	Q8H0W0	-0,302	0,003	plastid	Protein LOW PSII ACCUMULATION 3, chloroplastic OS=Arabidopsis thaliana GN=LPA3 PE=1 SV=1
AT4G21445	Q8W1B3	-0,301	0,007	plastid	At4g21445 OS=Arabidopsis thaliana GN=PRIP PE=2 SV=1
AT2G27730	Q9ZUX4	0,307	0,004	mitochondrion	Uncharacterized protein At2g27730, mitochondrial OS=Arabidopsis thaliana GN=At2g27730 PE=1 SV=1
AT1G33120	P49209	0,321	0,001	cytosol	60S ribosomal protein L9-1 OS=Arabidopsis thaliana GN=RPL9B PE=1 SV=3
AT4G16390	Q8GWE0	0,324	0,008	plastid	Pentatricopeptide repeat-containing protein At4g16390, chloroplastic OS=Arabidopsis thaliana GN=P67 PE=1 SV=3
AT3G05540	Q9M9V9	0,342	0,008	cytosol	Translationally controlled tumor protein 2 OS=Arabidopsis thaliana GN=TCTP2 PE=1 SV=1
AT5G08540	Q93VT6	0,351	0,003	plastid	Ribosomal RNA small subunit methyltransferase J OS=Arabidopsis thaliana GN=MAH20.10 PE=1 SV=1
AT3G44100	Q9LXQ2	0,364	0,006	extracellular	At3g44100 OS=Arabidopsis thaliana GN=F26G5_50 PE=2 SV=1
AT2G35605	Q93W30	0,366	0,006	mitochondrion	Expressed protein OS=Arabidopsis thaliana GN=At2g35605 PE=2 SV=1
AT1G21440	Q501F7	0,371	0,003	plastid	At1g21440 OS=Arabidopsis thaliana GN=At1g21440 PE=2 SV=1
AT4G21210	O49562	0,38	0,002	plastid	Pyruvate, phosphate dikinase regulatory protein 1, chloroplastic OS=Arabidopsis thaliana GN=RP1 PE=1 SV=1
AT1G21670	Q9XI11	0,386	0,001	extracellular	ADPP6 amino-terminal domain protein OS=Arabidopsis thaliana GN=At1g21670 PE=2 SV=1
AT1G64980	Q9XIP8	0,422	0,002	cytosol	Protein CDI OS=Arabidopsis thaliana GN=CDI PE=2 SV=1
AT3G04550	Q9SR19	0,429	0,002	plastid	Rubisco accumulation factor 1.2, chloroplastic OS=Arabidopsis thaliana GN=RAF1.2 PE=1 SV=1
AT5G42850	Q9FMN4	0,436	0,004	cytosol	Thioredoxin-like protein Clot OS=Arabidopsis thaliana GN=At5g42850 PE=2 SV=1
AT2G46540	Q9ZPY5	0,442	0,01	mitochondrion	At2g46540/F11C10.23 OS=Arabidopsis thaliana GN=At2g46540 PE=2 SV=2
AT3G52140	F4J5S1	0,456	0,001	cytosol	Clustered mitochondria protein OS=Arabidopsis thaliana GN=FMT PE=2 SV=1
AT5G58160	Q9LVN1	0,48	0,007	cytosol	Formin-like protein 13 OS=Arabidopsis thaliana GN=FH13 PE=2 SV=3
AT1G76160	Q9SGR6	0,498	0,002	extracellular	AT1G76160 protein OS=Arabidopsis thaliana GN=sks5 PE=2 SV=1
AT1G55980	F4I3I1	0,499	0,006	cytosol	FAD/NAD(P)-binding oxidoreductase family protein OS=Arabidopsis thaliana GN=At1g55980 PE=4 SV=2
AT4G26910	Q8H107	0,507	0,002	mitochondrion	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 2, mitochondrial OS=Arabidopsis thaliana GN=At4g26910 PE=1 SV=2
AT2G40765	Q94K78	0,511	0,003	mitochondrion	Transmembrane protein OS=Arabidopsis thaliana GN=At2g40765 PE=2 SV=1
AT4G32915	F4JV80	0,512	0,006	plastid	Glutamyl-tRNA(Gln) amidotransferase subunit C, chloroplastic/mitochondrial OS=Arabidopsis thaliana GN=GATC PE=1 SV=1
AT5G64130	A8MS32	0,527	0,006	nucleus	AT5G64130 protein OS=Arabidopsis thaliana GN=MHJ24.11 PE=1 SV=1
AT4G27585	Q93VP9	0,528	0,006	mitochondrion	SPFH/Band 7/PHB domain-containing membrane-associated protein family OS=Arabidopsis thaliana GN=AtSLP1 PE=1 SV=1
AT1G56580	Q9FXB0	0,546	0,002	cytosol	At1g56580/F25P12_18 OS=Arabidopsis thaliana GN=SMALLER WITVARIABLE BRANCHES PE=2 SV=1
AT1G10522	Q9XIK0	0,546	0,002	plastid	Protein PLASTID REDOX INSENSITIVE 2, chloroplastic OS=Arabidopsis thaliana GN=PRIN2 PE=1 SV=1
AT5G10840	F4KIB2	0,549	0,005	golgi	Transmembrane 9 superfamily member 8 OS=Arabidopsis thaliana GN=TMN8 PE=2 SV=1
AT3G28270	Q9LHD9	0,554	0,001	plasma membrane	UPF0496 protein At3g28270 OS=Arabidopsis thaliana GN=At3g28270 PE=2 SV=1
AT3G62810	Q9LZI4	0,572	0,004	mitochondrion	At3g62810 OS=Arabidopsis thaliana GN=F26K9_240 PE=2 SV=1
AT5G41950	Q9FHY8	0,574	0,005	golgi	Protein HLB1 OS=Arabidopsis thaliana GN=HLB1 PE=1 SV=1
AT3G01310	F4J8C6	0,578	0,005	golgi	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase VIP1 OS=Arabidopsis thaliana GN=VIP1 PE=1 SV=1
AT1G30580	Q9SA73	0,607	0,001	cytosol	Obg-like ATPase 1 OS=Arabidopsis thaliana GN=YchF1 PE=1 SV=1
AT3G20370	Q9LTQ5	0,615	0,001	extracellular	AT3g20370/MQC12_13 OS=Arabidopsis thaliana GN=At3g20370 PE=2 SV=1
AT4G19003	Q8VZC9	0,617	0,004	nucleus,cytosol	Vacuolar protein sorting-associated protein 25 OS=Arabidopsis thaliana GN=VPS25 PE=1 SV=1
AT2G17120	O23006	0,633	0,002	plasma membrane	LysM domain-containing GPI-anchored protein 2 OS=Arabidopsis thaliana GN=LYM2 PE=1 SV=1
AT5G48540	Q9LV60	0,642	0,003	extracellular	Cysteine-ricrepeat secretory protein 55 OS=Arabidopsis thaliana GN=CRRSP55 PE=2 SV=1
AT1G33600	Q9FW48	0,652	0,001	extracellular	Leucine-ricrepeat (LRR) family protein OS=Arabidopsis thaliana GN=At1g33600 PE=4 SV=1
AT1G09310	Q9ZPZ4	0,66	0,001	cytosol	AT31J12.3 protein OS=Arabidopsis thaliana GN=At1g09310 PE=1 SV=1
AT2G32840	Q8GYK6	0,686	0,003	nucleus	reversed Proline-ricfamily protein OS=Arabidopsis thaliana GN=At2g32840 PE=2 SV=1
AT5G10730	Q93VH5	0,712	0,001	mitochondrion	AT5g10730/MAJ23_90 OS=Arabidopsis thaliana GN=MAJ23.90 PE=2 SV=1
AT2g16980	A0A1P8B0Q4	0,719	0,003	plasma membrane	reversed Major facilitator superfamily protein OS=Arabidopsis thaliana GN=At2g16980 PE=4 SV=1
AT4G27500	O23144	0,737	0,002	nic reticulum,plasma n	Proton pump-interactor 1 OS=Arabidopsis thaliana GN=PPI1 PE=1 SV=2
AT1G25420	Q9C6L2	0,776	0,002	mitochondrion	At1g25420/F2J7_16 OS=Arabidopsis thaliana GN=At1g25420 PE=2 SV=1

AT3G21200	Q9LU39	0,809	0,002	plastid	Glutamyl-tRNA reductase-binding protein, chloroplastic OS=Arabidopsis thaliana GN=GLUTRBP PE=1 SV=1
AT3G21965	Q9LRL2	0,815	0,002	extracellular	Putative cysteine-ricrepeat secretory protein 25 OS=Arabidopsis thaliana GN=CRRSP25 PE=5 SV=2
AT3G54600	Q9M1G8	0,823	0,002	plasma membrane	DJ-1 protein homolog F OS=Arabidopsis thaliana GN=DJ1F PE=1 SV=1
AT5G14030	Q94BY3	0,839	0,002	endoplasmic reticulum	Translocon-associated protein subunit beta OS=Arabidopsis thaliana GN=MUA22.2 PE=2 SV=1
AT2G05520	Q9SL15	0,882	0,002	extracellular	Glycine-ricprotein 3 OS=Arabidopsis thaliana GN=GRP3 PE=1 SV=1
AT4G15802	Q8GW48	0,945	0,001	nucleus	At4g15810 OS=Arabidopsis thaliana GN=HSBP PE=2 SV=1
AT5g26280	A0A1P8BA53	0,962	0,001	extracellular	TRAF-like family protein OS=Arabidopsis thaliana GN=At5g26280 PE=4 SV=1
AT1G02816	Q9SRX5	1,101	0,004	extracellular	F22D16.19 protein OS=Arabidopsis thaliana GN=F22D16.19 PE=2 SV=1
AT5G51040	Q9FI44	1,112	0,002	mitochondrion	Succinate dehydrogenase assembly factor 2, mitochondrial OS=Arabidopsis thaliana GN=SDHAF2 PE=1 SV=1
AT2G05380	Q9ZSJ6	1,22	0,001	extracellular	Glycine-ricprotein 3 short isoform OS=Arabidopsis thaliana GN=GRP3S PE=1 SV=2
AT2G21160	P45434	1,228	0,001	endoplasmic reticulum	Translocon-associated protein subunit alpha OS=Arabidopsis thaliana GN=At2g21160 PE=2 SV=3
AT5G66470	Q8VZ74	1,262	0,003	plastid	TPase ERA-like, chloroplastic OS=Arabidopsis thaliana GN=At5g66470 PE=2 SV=1
AT2G34070	O22960	1,367	0,001	extracellular	Protein trichome birefringence-like 37 OS=Arabidopsis thaliana GN=TBL37 PE=2 SV=2
AT1G16850	Q9FE54	2,089	0,001	endoplasmic reticulum	OS=Arabidopsis thaliana GN=F6I1.15 PE=2 SV=1

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CONCLUSIONES

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1. NTRC juega un papel fundamental en la respuesta de las plantas a VCs emitidos por hongos fitopatógenos a través de mecanismos que implican la regulación redox de la fotosíntesis y la señalización de ABA y CKs.

2. En plantas *wild-type*, los VCs emitidos por el hongo fitopatógeno *Alternaria alternata* provocan cambios en el estado redox de proteínas relacionadas con la fotosíntesis y el metabolismo primario que podrían explicar la respuesta fenotípica y metabólica de las plantas a los VCs.

3. La pobre respuesta de plantas *ntrc* a VCs no es debida a la sobreacumulación de ROS como consecuencia de la inactivación de la 2-Cys peroxiredoxina, sino probablemente a una oxidación e inactivación global de proteínas, especialmente proteínas relacionadas con la fotosíntesis, el metabolismo primario, la regulación redox, la señalización y la traducción.

4. La activación redox de las enzimas del CBC, particularmente la isoforma 1 de la fructosa bifosfatasa (cFBP1), es un determinante importante en la respuesta de las plantas a VCs microbianos.

5. Los VCs microbianos dan lugar a cambios en el proteoma que pueden explicar, al menos en parte, la respuesta de la planta a los VCs (particularmente los cambios en derivados de las rutas MEP y shikimato).

6. En plantas *wild-type*, la mayoría de las proteínas diferencialmente expresadas por los VCs microbianos están codificadas por genes que no responden a los VCs microbianos, concluyendo así que la respuesta de las plantas a VCs microbianos está regulada en gran medida a nivel no-transcripcional.

7. Los sistemas de control de calidad de las proteínas plastidiales están implicados en algunos cambios observados en el proteoma del cloroplasto de plantas expuestas a VCs microbianos.

8. La respuesta de la planta a VCs microbianos está mediada por mecanismos de señalización retrograda del cloroplasto al núcleo.

9. Globalmente, la respuesta de las plantas a los VCs fúngicos implica una activación redox de la fotosíntesis y una posterior señalización retrógrada del cloroplasto al núcleo para la regulación proteostática de las rutas MEP y del shikimato a través de mecanismos que implican la intervención del sistema de control de calidad de las proteínas plastidiales.

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APÉNDICE

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LISTA DE ABREVIATURAS

3-PGA	3-Fosfoglicerato
ABA	Acido abscísico
AGPasa	ADP-glucosa pirofosforilasa
A_n	Tasa neta de asimilación de CO_2
ATP	Adenosina trifosfato
ATPasa	ATP sintasa
CAM	Carbamidometilación
CBC	Ciclo de Calvin-Benson
CDP-ME	Difosfocitidil metileritriol
CDP-MEP	CDP-ME 2-fosfato
cFBP1	Fructosa-1,6-bisfosfatasa plastidial
Chl	Clorofila
CHL1	Magnesio quelatasa subunidad 1
C_i	Concentración intercelular de CO_2
CKs	Citoquininas
Clp	Proteasa caseinolitica
CMK	CDP-ME quinasa
Cyt	Citocromo
DAHP	3-deoxy-d-arabinoheptulosonato 7-fosfato
DHAP	Dihidroacetona fosfato
DMAPP	Dimetilalil difosfato
DTT	Ditiotreitol
DXS	1-deoxy-D-xylulosa 5 fosfato sintasa
ETR	Tasa de transporte electrónico
F6P	Fructosa 6-fosfato
FBP	Fructosa 1,6-bisfosfatasa
Fd	Ferredoxina
FNR	Fd-NADP reductasa
FTR	Fd-Trx reductasa
FW	Peso fresco
GAP	Gliceraldeido 3-fosfato

GAPDH	Gliceraldeido 3-fosfato deshidrogenasa
GGPP	Geranilgeranil difosfato
HDR	4-hidroxi-3-metilbut-2-enil difosfato reductasa
HDS	4-hidroxi-3-metilbut-2-enil difosfato sintasa
Hsp	Proteínas de choque térmico
IAM	Iodoactetamida
IPP	Isopentenil difosfato
J_{max}	Tasa máxima de transporte electrónico que contribuye a la regeneración de RuBP
LC	Cromatografía líquida
LHC	Complejo antena
LR	Raíces laterales
MCT	CDP-ME citidiltransferasa
MEP	2-C-metil-D-eritritol 4-fosfato
MS	Espectrometría de masas
NADPH	Nicotinamida adenina dinucleótido fosfato
NEM	N-etilmaleimida
NTRC	Trx reductasa C dependiente de NADPH
OPPP	Ruta de las pentosas fosfato oxidativa
PC	Plastocianina
PEP	Fosfoenolpiruvato
PET	Transporte de electrones fotosintéticos
PPT	Translocador PEP
PQ	Plastoquinona
PQH_2	Plastoquinol
PRK	Fosforibuloquinasa
PrxQ	Peroxirredoxina Q
PSI	Fotosistema I
PSII	Fotosistema II
qP	Extinción fotoquímica
ROS	Especies reactivas de oxigeno
RuBisCO	RuBP carboxilasa oxigenasa
RuBP	Ribulosa 1,5-bisfosfato

SBP	Sedoheptulosa 1,7-bisfosfatasa
TIC	Translocador de la membrana interna del cloroplasto
TOC	Translocador de la membrana externa del cloroplasto
TP	Triosas fosfato
TPU	Tasa de utilización de TP
Trx	Tiorredoxina
V_{cmax}	Velocidad máxima de carboxilación de la Rubisco
VCs	Compuestos volátiles
VICs	Compuestos inorgánicos volátiles
VOCs	Compuestos orgánicos volátiles
WT	Genotipo silvestre
Φ_{NPQ}	Extinción no fotoquímica de la fluorescencia de las clorofilas
Φ_{Po}	Máximo rendimiento cuántico del PSII en la fase oscura
Φ_{PSII}	Eficiencia máxima del PSII

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