UNIVERSIDADE ESTADUAL DO NORTE FLUMINENSE DARCY RIBEIRO – UENF

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ENVOLVIMENTO DE AUXINA, PROTEÍNAS E POLIAMINAS LIVRES NO ENRAIZAMENTO *ex vitro* DE BROTOS MICROPROPAGADOS DE *Cedrela fissilis* VELLOZO (MELIACEAE)

CAMPOS DOS GOYTACAZES- RJ
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“Tese apresentada ao Centro de Biociências e Biotecnologia da Universidade Estadual do Norte Fluminense Darcy Ribeiro, como parte das exigências para obtenção do título de Doutora em Biociências e Biotecnologia”.

Orientadora: Profa. Dra. Claudete Santa-Catarina

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Sumário

Resumo i

Abstract iii

1- Introdução...1

2- Revisão de Literatura...3

  2.1- *Cedrela fissilis,* uma espécie arbórea nativa da Mata Atlântica 3

  2.2- Propagação *in vitro*...4

  2.3- Enraizamento das brotações 6

  2.4- Alteração hormonal durante enraizamento: auxina como fator chave para indução de raízes adventícias 8

  2.5- Alterações bioquímicas e moleculares envolvidas no enraizamento 9

    2.5.1- Perfil proteômico...9

    2.5.2- Poliaminas 10

3- Objetivos..12

  3.1- Objetivo geral 12

  3.2- Objetivos específicos 12

4- Trabalhos...13

  4.1- Involvement of differentially accumulated proteins and endogenous auxin in adventitious root formation in micropropagated shoot cuttings of *Cedrela fissilis* Vellozo (Meliaceae) *..13

  4.2- Polyamines roles on adventitious root formation in micropropagated shoot cuttings of *Cedrela fissilis* Vellozo (Meliaceae) 47

5- Considerações finais 63

6- Referências Bibliográficas 65

Apêndice...70

Resumo

O enraizamento é uma etapa fundamental para a produção de mudas micropropagadas e a investigação das mudanças bioquímicas e moleculares durante este processo morfológico em espécies arbóreas pode revelar como moléculas específicas estão envolvidas na indução de raízes adventícias (RA). O presente estudo teve como objetivo investigar o envolvimento da auxina, proteínas diferencialmente acumuladas e poliaminas (PAs) no enraizamento *ex vitro* de brotações micropropagadas em *Cedrela fissilis*. Foram investigados os efeitos do ácido indol butírico (AIB) e dos inibidores da sinalização de auxina, o ácido p-clorofenoxiisobutírico (PCIB) e do transporte polar de auxina, o ácido triiodobenzóico (TIBA), no enraizamento *ex vitro* de brotos micropropagados de *C. fissilis* e foi avaliado o perfil proteômico e conteúdo endógeno de ácido indol acético (AIA) durante o início de RA. Foi a avaliado também o efeito da putrescina (Put) no metabolismo de poliaminas (PAs) e sua combinação com inibidores de auxina no enraizamento *ex vitro* na espécie de estudo. Observou-se que a adição de AIB não é necessária para o enraizamento *ex vitro* e a indução de RA foi significativamente reduzida pelos inibidores PCIB e TIBA. A presença de células meristemáticas e a formação de centros meristemáticos na base das brotações aos três dias de enraizamento foram observadas e promovem a formação de RAs. O acúmulo diferencial de proteínas relacionadas à divisão celular e auxina e a presença de proteínas únicas relacionadas à modificação da parede celular em brotações aos três dias de enraizamento foram associadas a maiores teores de AIA e iniciação de RAs. Além disso, o acúmulo de proteínas relacionadas à desfosforilação, as vias do ciclo do ácido glicolítico e tricarboxílico e a redução do acúmulo de proteínas do metabolismo dos isoflavonóides foram associados à promoção da iniciação de RAs. Observou-se que a Put exógena aumenta o comprimento da raiz, mas não o seu conteúdo endógeno comparativamente aos inibidores de auxina, combinados ou não com Put. A porcentagem e o número de brotos enraizados foram significativamente reduzidos nos tratamentos com Put associados com PCIB e TIBA, sugerindo que os inibidores de auxina e, não a Put, são os responsáveis pela diminuição do enraizamento. Este é o primeiro estudo mostrando o envolvimento do acúmulo de proteína e conteúdo de AIA endógeno na iniciação de RAs e o envolvimento de PAs durante o enraizamento em *C. fissilis*, uma espécie arbórea da Mata Atlântica ameaçada de extinção e considerada de fácil enraizamento.

Palavras-chave: Enraizamento adventício, Inibidor de auxina, Proteômica comparativa, Ácido indol acético, Propagação de brotos *in vitro*, Poliaminas, Putrescina.

Abstract

Rooting is a fundamental step to propagation micropropagated plantlet and the investigation of the biochemical and molecular changes during this morphological process in tree species can reveal how specific molecules are involved in the induction of adventitious roots (AR). The present study aimed to investigate the involvement of auxin, differentially accumulated proteins and polyamines (PAs) in the ex vitro rooting of micropropagated shoots in *Cedrela fissilis*. We investigated the effects of indole butyric acid (IBA) and the auxin signaling inhibitors, p-chlorophenoxyisobutyric acid (PCIB) and the polar transport of auxin, triiodobenzoic acid (TIBA), on ex vitro rooting of micropropagated *C fissilis* and the proteomic profile and endogenous indole acetic acid (IAA) content during the onset of AR were evaluated. The effect of putrescine (Put) on the metabolism of polyamines (PAs) and its combination with auxin inhibitors on ex vitro rooting in the study species was also evaluated. It was observed that the addition of IBA is not necessary for ex vitro rooting and the induction of AR was significantly reduced by the PCIB and TIBA inhibitors. The presence of meristematic cells and the formation of meristematic centers at the base of shoots at 3 days of rooting were observed and promote the formation of ARs. Differential accumulation of proteins related to cell division and auxin and the presence of unique proteins related to cell wall modification in shoots at 3 days of rooting were associated with higher levels of IAA and initiation of ARs. In addition, accumulation of proteins related to dephosphorylation, glycolytic and tricarboxylic acid cycle pathways and reduced accumulation of proteins from isoflavonoid metabolism were associated with promoting the initiation of ARs. It was observed that exogenous Put increases root length, but not its endogenous content compared to auxin inhibitors, combined or not with Put. The percentage and number of rooted shoots were significantly reduced in the treatments with Put associated with PCIB and TIBA, suggesting that auxin inhibitors and not Put are responsible for the decrease in rooting. This is the first study showing the involvement of protein accumulation and endogenous IAA content in the initiation of ARs and the involvement of PAs during rooting in *C. fissilis*, an easily rooted endangered woody species from the Brazilian rainforest.

Keywords: Adventitious rooting, Auxin inhibitor, Comparative proteomics, Indole-acid acetic, In vitro shoot propagation, Polyamines, Putrescine.

1- Introdução

Espécies arbóreas nativas da Mata Atlântica, como a *Cedrela fissilis* Vellozo (Meliaceae), popularmente conhecida como cedro rosa, vem sendo exploradas ao longo de décadas, principalmente pelo contínuo processo de extração madeireira. Em decorrência, muitas espécies encontram-se ameçadas de extinção, como é o caso de *C. fissilis*, a qual se encontra ameaçada de extinção na categoria vulnerável (Barstow 2018).

Alternativamente às técnicas convencionais, como a estaquia, a propagação dessa espécie pode ser realizada por técnicas biotecnológicas, como a micropropagação, a qual apresenta aplicação em programas de conservação, reflorestamento e recuperação de áreas degradadas, pois possibilita a produção de mudas em escala e independente da época do ano (Giri et al. 2004, Shukla et al. 2009). Devido à importância econômica e ecológica de *C. fissilis*, estudos com a propagação *in vitro* foram realizados para esta espécie (Nunes et al. 2002, Aragão et al. 2016, Aragão et al. 2017, Oliveira et al. 2020a, Bonfá et al. 2021, dos Reis de Oliveira et al. 2022). Apesar de estudos associados ao desenvolvimento de brotações *in vitro* e enraizamento *in vitro*, não há estudos referentes ao enraizamento *ex vitro* de brotos propagados *in vitro*, e o envolvimento de auxinas, proteínas diferencialmente reguladas e poliaminas durante a indução de raízes adventícias (RA) para esta espécie.

O estabelecimento de um protocolo de enraizamento é essencial para a produção de mudas (Kasthurirengan et al. 2013). Em geral, para espécies arbóreas é necessário o uso de regulador de crescimento vegetal, em especial auxinas, como o ácido-indolbutírico (AIB), para promover o enraizamento (Phulwaria et al. 2013). Este enraizamento pode ser promovido *in vitro* com adição de auxinas ao meio de cultura, ou *ex vitro*, com a imersão da base da brotação em solução de AIB, uma auxina sintética (Pop et al. 2011), com posterior transferência para o substrato (Yan et al. 2010).

A produção de auxina ocorre naturalmente nas brotações, e cada espécie possui níveis endógenos diferentes, o que irá influenciar o enraizamento (Da Costa et al. 2013). Havendo conteúdo endógeno de auxina em um nível ótimo requerido na promoção do enraizamento, a aplicação deste regulador é desnecessária, podendo ser inibitório em algumas espécies (Yin et al. 2011). Nunes et al. (2002) mostraram a necessidade de 2,5 µM de AIB para a indução do enraizamento *in vitro* em brotações de *C. fissilis*.

A utilização do inibidor de transporte de auxina, o ácido 2,3,5-triiodo benzoico (TIBA) e do inibidor de sinalização de auxina, o ácido 2-clorofenoxi-2-metil propiônico (PCIB) pode ser uma ferramenta eficaz para estudar as respostas de auxina. O TIBA é um inibidor do transporte de efluxo de auxina e está envolvido com a inibição do tráfego de auxina na membrana (Kleine-Vehn et al. 2006). O PCIB é um inibidor da sinalização da auxina, o qual regula a estabilidade da proteína auxin/indole acetic acid (Aux/AIA) (Di et al. 2015) e no acúmulo de transcritos de Aux/AIA (Oono et al. 2003), inibindo a formação de RAs em *Arabdopsis*. Assim, a auxina está envolvida com a ativação de células para a divisão celular durante o início do enraizamento adventício (Druege et al. 2019).

Proteínas e enzimas são sintetizadas e reguladas por uma cascata de eventos desencadeados pela auxina e podem estar relacionadas ao início do enraizamento adventício. A identificação dessas proteínas pode ser realizada por meio de análise proteômica, podendo assim revelar o envolvimento dessas proteínas diferencialmente acumuladas em vários processos no desenvolvimento da planta. Estudos permitiram identificar proteínas expressas em plântulas de *Arabidopsis* na presença e ausência de auxina (Xing e Xue 2012) e na investigação de desdiferenciação celular na mesma espécie (Chitteti et al. 2008). Algumas proteínas relacionadas com o ciclo celular são diferencialmente reguladas em resposta a auxina (Martínez-de la Cruz et al. 2015) e também durante o processo de enraizamento, estando associadas na regulação ou formação das RAs (Sukumar et al. 2013).

Além do envolvimento da auxina e proteínas, estudos tem mostrado o envolvimento de PAs na formação de RAs (Tang e Newton 2005). As PAs putrescina (Put), espermidina (Spd) e espermina (Spm), estão associadas a vários processos, como a divisão celular (Kusano et al. 2007), podendo apresentar papel fundamental durante a formação das RAs. Estudos tem mostrado o envolvimento de PAs na formação de raízes em algumas espécies, como em *Quercus suber* e *Vitis vinifera*, demonstrando que a Put pode ser considerada um marcador para o enraizamento (Neves et al. 2002). Entretanto, as PAs também podem ser consideradas mensageiras de sinais de estresse nas plantas (Liu et al. 2007). Em *Pyrus communis* cultivar Doyenne d'Hiver foi observado que o aumento do nível de Put promoveu a inibição do enraizamento (Baraldi et al. 1995).

Neste sentido, a investigação do envolvimento da auxina, a identificação de proteínas diferencialmente acumuladas e de PAs durante a indução do enraizamento é importante para elucidar o papel dessas biomoléculas neste processo morfogenético, auxiliando na compreensão dos sinais envolvidos no processo de enraizamento em uma espécie arbórea de interesse econômico e ecológico.

2- Revisão de Literatura

2.1- *Cedrela fissilis,* uma espécie arbórea nativa da Mata Atlântica

A Mata Atlântica brasileira tem sido considerada como um dos mais importantes *hotspots* mundiais, possuindo uma das mais importantes biodiversidades do mundo, mas, com significativa degradação, fragmentação de habitat e espécies endêmicas ameaçadas (Myers et al. 2000). Como resultado desse processo, atualmente, restam apenas 13% da área original de florestas (Fundação SOS Mata Atlântica e INPE 2021). Em decorrência desse cenário, alguns procedimentos são necessários para a conservação desse bioma e de sua biodiversidade, bem como a conservação dos remanescentes e a restauração das áreas degradadas (Ribeiro et al. 2009).

A *Cedrela fissilis* Vellozo (Meliaceae), popularmente conhecida como “cedro rosa”, é uma espécie arbórea nativa da Mata Atlântica, possuindo ampla distribuição no território brasileiro. A madeira desta espécie é utilizada para a fabricação de móveis e na construção civil (Carvalho 2003b), e por esses motivos tem sido explorada de modo não sustentável (Judd et al. 1999). Devido à intensa exploração ao longo dos anos, esta espécie está atualmente incluída na lista de espécies ameaçadas, na categoria vulnerável (Barstow 2018).

C. fissilis é uma árvore caducifólia com altura que varia entre 10 a 40 m de altura e 40 a 200 cm de diâmetro à altura do peito (DAP). Possui frutos em forma de cápsula piriforme deiscente, lenhosa, espessa, marrom-escura, abrindo-se até mais da metade por cinco valvas longitudinais contendo em média 45 sementes distribuídas em cinco lóculos (Carvalho 2003a) (Figura 1). As sementes desta espécie são classificadas como ortodoxas (Carvalho et al. 2006), porém quando armazenadas em condições não controladas perdem sua viabilidade, devido principalmente a condições de umidade, temperatura e ataque de patógenos (Cherobini et al. 2008). Estudos mostram que a mesma pode ser armazenada por 12 meses a 4ºC sem redução na percentagem de emergência das plântulas (Sousa et al. 2016). Desta forma, a progressiva perda de viabilidade de suas sementes em condições não controladas pode ser um obstáculo para produção contínua de mudas em viveiro, afetando ainda mais a disponibilidade de mudas para programas de reflorestamento comprometendo a regeneração da espécie em seu habitat.

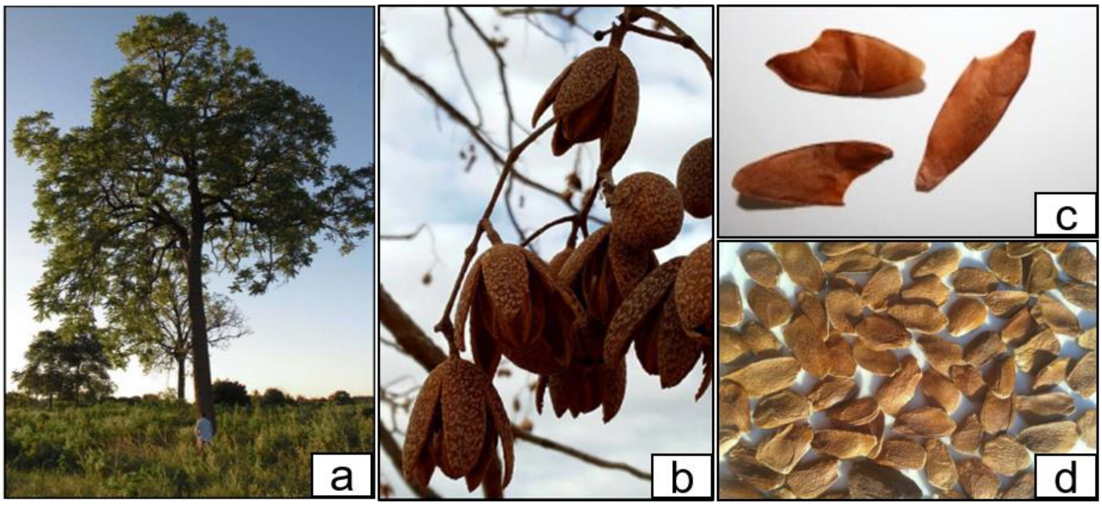

Figura 1- Aspectos morfológicos de árvore adulta (a), cápsulas com a infrutescência (b), e sementes com (c) e sem ala (d) de *Cedrela fissilis*. Fonte imagens a e b: Diaz-Soto et al. (2018). Fonte imagens c e d: da autora Yrexam.

Desta forma, a aplicação de metodologias alternativas às convencionais, como estaquia e via seminífera, de propagação para espécies florestais que se encontram ameaçadas de extinção, incluindo a *C. fissilis,* são indispensáveis para o estabelecimento de futuros programas de preservação e recuperação de áreas impactadas.

2.2- Propagação *in vitro*

A biotecnologia vegetal tem sido importante na geração de produtos e processos biotecnológicos para a agricultura, indústria alimentar, e meio ambiente. A propagação de plantas é possível a partir de metodologias que permitem respostas morfogenéticas *in vitro* utilizando células ou tecidos vegetais. Esta técnica biotecnológica é possível devido a totipotencialidade celular, demonstrada inicialmente por Haberlandt em 1902, ou seja, o potencial genético que cada célula possui para reconstituir um organismo inteiro. A cultura de células e tecidos vegetais é um método que permite o crescimento de células, tecidos e órgãos vegetais em condições assépticas. O explante, que é a parte do vegetal que será utilizada para estabelecer um cultivo in vitro, exibe um alto grau de plasticidade *in vitro* sob sinalizadores específicos e condições controladas, permitindo assim que o mesmo se desenvolva em uma rota morfogenética e, desta forma, uma planta inteira pode ser regenerada (Scragg 1992).

Dentre as técnicas biotecnológicas, a micropropagação tem sido utilizada para a pesquisa em diversas áreas, possibilitando a produção de mudas de interesse econômico e ecológico, se tornado cada vez mais importante para aplicações científicas e comerciais (Kumar e Reddy 2011). O processo de micropropagação se divide em várias fases, que se inicia pela seleção do explante adequado, indução e multiplicação de brotações, o enraizamento e por último, a aclimatização das mudas enraizadas, que consiste adaptar as mudas às condições do ambiente externo (George et al. 2008).

A micropropagação possui várias vantagens em relação a métodos tradicionais como a estaquia, dentre as quais se destaca a obtenção de plantas livres de doenças, a rápida propagação de genótipos, a produção de mudas independente da época do ano e espaço reduzido para a obtenção de mudas. Este processo pode ser realizado por meio de dois métodos: regeneração direta ou indireta. A regeneração indireta envolve a fase de calo antes do desenvolvimento de brotações, podendo se tornar uma estratégia indesejável para a propagação em larga escala pela possibilidade de induzir variação somaclonal. Por outro lado, a organogênese via regeneração direta é vantajosa para a propagação clonal evitando a formação de calos (Giri et al. 2004). Tradicionalmente, na micropropagação de espécies arbóreas utiliza-se a organogênese direta, usando-se como explantes segmentos nodais apicais e cotiledonares para a indução de brotações *in vitro* (Pijut et al. 2012). Assim, a micropropagação pode ser uma alternativa para propagação de espécies florestais que se encontram ameaçadas de extinção, com potencial de aplicação para a propagação destas espécies possibilitando a sua aplicação em programas de conservação, reflorestamento e recuperação de áreas degradadas (Giri et al. 2004, Shukla et al. 2009).

Devido à importância econômica e ecológica da espécie de estudo, a *C. fissilis*, estudos iniciais de propagação *in vitro* foram realizados. Para a propagação *in vitro*, foram testados efeitos de citocininas (Nunes et al. 2002, Aragão et al. 2016), PAs (Aragão et al. 2017), diferentes espectros de luz (Oliveira et al. 2020b) e o efeito de sucessivas subculturas no desenvolvimento de brotações *in vitro*. Nunes et al. (2002) e Bonfá et al. (2021) realizaram estudos com efeito de auxinas no enraizamento *in vitro* e aclimatização. No entanto, nenhum estudo foi realizado usando enraizamento *ex vitro* de brotos propagados *in vitro* nesta espécie.

2.3- Enraizamento das brotações

O enraizamento das brotações é uma etapa fundamental para a produção de mudas micropropagadas (Kasthurirengan et al. 2013). Este processo pode ser realizado *ex vitro* ou *in vitro*. A formação das raízes no enraizamento *ex vitro* é induzida a partir da imersão da base das brotações em regulador de crescimento vegetal, usualmente auxina, de forma geral por um curto período de tempo (min ou h) e em seguida, a transferência destas brotações para o substrato. Por outro lado, no enraizamento *in vitro*, as brotações são transferidas para meios de cultura suplementados com auxinas, permanecendo por um período maior (dias). Após o enraizamento *in vitro*, as mudas precisam ser aclimatizadas, ou seja, adaptadas as condições *ex vitro* (De Klerk et al. 1997, Yan et al. 2010).

O enraizamento *ex vitro* proporciona várias vantagens em relação ao *in vitro*, destacando-se a estimativa de redução de custos em até 71% (Yan et al. 2010, Ranaweera et al. 2013), redução de tempo e etapas durante o processo de micropropagação, sendo esse método altamente eficiente e econômico (Yan et al. 2010, Ranaweera et al. 2013). Adicionalmente, mudas enraizadas *ex vitro* apresentam, comparativamente às enraizadas *in vitro*, melhores qualidade das raízes desenvolvidas (Yan et al. 2010), além de conferir maior tolerância das mudas ao estresse provocado pelo ambiente externo durante a aclimatização (Phulwaria et al. 2013).

Aliada à fase de enraizamento das brotações micropropagadas é necessário a aclimatização, a qual é uma adaptação das novas mudas às condições ex vitro. A transferência com sucesso das brotações das condições *in vitro* para a *ex vitro* é uma das maiores dificuldades na micropropagação, pois diversos fatores como genótipo, estresse hídrico, alteração do metabolismo heterotrófico para autotrófico, infecção por patógenos, estresse pela luz, além das mudanças de temperatura interferem na sobrevivência das plantas (Ribas et al. 2003, Barboza et al. 2006). Uma das principais causas da baixa sobrevivência das plantas é a perda excessiva de água (Brainerd e Fuchigami 1982). As brotações obtidas *in vitro* normalmente apresentam deficiência de cera epicuticular, cuja função é limitar a perda de água através da transpiração durante a aclimatização (Grout e Aston 1978, Sutter e Langhans 1979). Desta forma, a reduzida capacidade de controlar a perda de água por transpiração a partir da superfície foliar, bem como o reduzido funcionamento dos estômatos de plantas cultivadas *in vitro* afetam a capacidade do ajuste das brotações ao ambiente externo, sendo necessária a aclimatização (Hazarika 2006). Adicionalmente, o enraizamento *ex vitro* associado à aclimatização é uma etapa essencial para a sobrevivência das mudas, pois quando estas duas etapas ocorrem de forma simultânea, as brotações geralmente apresentam melhor enraizamento e com redução de custos (Yan et al. 2010).

Durante a etapa de enraizamento, ocorre a formação de RAs, um processo organogênico pós-embrionário responsável pela indução de raízes. Este processo ocorre a partir de células diferenciadas que não foram especificadas para desenvolver uma raiz em posições onde normalmente não ocorrem durante o desenvolvimento normal da brotação (Díaz-Sala 2014). Elas podem ser originadas a partir de diferentes tipos celulares presentes no caule, como células do parênquima do floema ou do xilema, células secundárias do floema, ou células interfasciculares do câmbio vascular próximas às células do floema (Bellini et al. 2014).

A formação das RAs ocorre em dependência do genótipo e da condição fisiológica em resposta a estímulos (Druege et al. 2016). Células próximas aos feixes vasculares do tecido caulinar dos brotos são induzidas a divisão, e desdiferenciadas, adquirindo competência para responder a um sinal indutor do enraizamento, que promove a proliferação e diferenciação em células do tipo meristemático que permitirá a diferenciação de uma RA (Druege et al. 2019). A formação de RA ocorre por meio de fases conhecidas como indução, iniciação e emergência da raiz. A fase de indução é caracterizada pelo período de sinalização para induzir a formação de raiz, e ocorre anterior a qualquer evento histológico. Em seguida, na fase de iniciação ocorrem divisões celulares que levam à formação de meristemas radiculares, caracterizados pela presença de pequenas células, isodiamétricas, com núcleo evidente e citoplasma denso. Por fim, a fase de expressão é caracterizada pela formação do primórdio radicular a partir das células internas formadas na fase de iniciação e culminando na emergência da raiz (Li et al. 2009, Pacurar et al. 2014).

Interações regulatórias em níveis hormonais, bioquímicos e moleculares, estão envolvidas com a mudança na dinâmica do destino celular durante a formação de RAs (Pizarro e Díaz-Sala 2019). Neste sentido, investigação de processos hormonais e bioquímicos, podem fornecer informações relevantes para a formação do enraizamento adventício em espécies arbóreas.

2.4- Alteração hormonal durante enraizamento: auxina como fator chave para indução de raízes adventícias

O controle e o desenvolvimento da raiz são promovidos principalmente pela auxina (Woodward e Bartel 2005, Luijten e Heidstra 2009), conhecida como regulador chave no processo de enraizamento. É bem conhecido o papel da auxina atua no estabelecimento e manutenção da polaridade do embrião, na dominância apical (Woodward e Bartel 2005), além do seu envolvimento em processos fisiológicos associados a indução do meristema radicular (Luijten e Heidstra 2009, Weijers et al. 2018). A produção de auxina AIA ocorre naturalmente nas plantas, e cada espécie possui níveis endógenos que influenciará o enraizamento (Da Costa et al. 2013). Quando o conteúdo endógeno de auxina ocorre em um nível ótimo para promover a indução de raízes, a aplicação de auxina é desnecessária, e/ou ainda pode ser inibitória em algumas espécies (Yin et al. 2011). Sendo necessário o uso exógeno de auxina, geralmente é utilizado o ácido indol butírico (AIB) para promover o enraizamento das brotações, sendo a concentração dependente para cada espécie (Fermino Júnior et al. 2011, Phulwaria et al. 2013). Em geral, as plantas com facilidade de induzir RA contêm níveis mais altos de auxina livre, enquanto as que exibem recalcitrância ao enraizamento podem apresentar menor nível de auxina endógena (Blakesley 1994).

A utilização do inibidor de transporte de auxina, o ácido 2,3,5-trioodo benzoico (TIBA) e do inibidor de sinalização de auxina, o ácido 2-clorofenoxi-2-metil propiônico (PCIB) pode ser uma importante ferramenta para avaliar o papel do transporte e sinalização de auxina durante o enraizamento. O TIBA é um inibidor do transporte de efluxo de auxina e está envolvido com a inibição do tráfego de auxina na membrana, interferindo na organização do citoesqueleto de actina para a endocitose de proteínas PIN-FORMED (PIN), importantes para o efluxo de auxina (Geldner et al. 2001). O PCIB é um inibidor de auxina que regula a estabilidade da proteína *auxin/indole acetic acid* (Aux/AIA) (Di et al. 2015) e por redução na acumulação de transcritos de Aux/AIA (Oono et al. 2003).

A formação de padrões dependentes de auxina pode ser identificada por meio de metodologias que permitam a visualização direta da distribuição de auxina nos tecidos, por microscopia, ou quantificação, como a cromatografia líquida de alta eficiência. A expressão e transporte de auxina dentro dos órgãos e tecidos da planta são importantes, pois criam os gradientes de concentração de auxina que regulam o desenvolvimento das plantas e o enraizamento (Kharshiing et al. 2010). O uso de marcadores altamente específicos para AIA fornecem meios para detectar e localizar o AIA livre na planta durante a diferenciação de tecidos e desenvolvimento de órgãos (Forestan e Varotto 2013). Assim, a imunolocalização pode ser uma ferramenta eficiente para entender a translocação de AIA durante o desenvolvimento de RAs em *C. fissilis*.

Embora o envolvimento da auxina no desenvolvimento radicular seja conhecido, este não é o único fator envolvido na formação de raízes adventícias. Assim, estudos necessitam ser realizados para elucidar os mecanismos bioquímicos e moleculares envolvidos durante o enraizamento na espécie de estudo.

2.5- Alterações bioquímicas e moleculares envolvidas no enraizamento

2.5.1- Perfil proteômico

As proteínas estão presentes em todos tecidos de origem animal e vegetal, desempenhando uma diversidade de papéis, sendo essenciais para a vida (Arsul 2014). Elas são responsáveis por funções celulares básicas, como transcrição, tradução, metabolismo e transdução de sinal, e por características estruturais

(Bontinck et al. 2018), estando relacionadas a diferentes processos de desenvolvimento ou evento fisiológico.

A identificação de proteínas associadas a processos de desenvolvimento em plantas é possível pela análise de proteoma, que se tornou uma abordagem importante para caracterização funcional nestes processos (Cánovas et al. 2004). A análise proteômica comparativa permite identificar proteínas diferencialmente abundantes em uma amostra, podendo assim revelar o envolvimento dessas proteínas no crescimento e desenvolvimento da planta, incluindo a formação de raízes (Mitprasat et al. 2011, Sukumar et al. 2013).

Proteínas e enzimas além de estarem relacionadas ao início e formação da RA, elas são sintetizadas e reguladas por uma cascata de eventos desencadeados pela auxina. Proteínas relacionadas ao metabolismo de carboidratos e energia, fotossíntese, estrutura celular e degradação foram encontradas para desempenhar um papel fundamental na formação de novas raízes (Liu et al. 2013). Em *Arabdopsis,* proteínas sintetizadas durante a formação de RAs em diferentes genótipos mutantes se correlacionaram positiva ou negativamente durante esse processo (Sorin et al. 2006). Em *Pinus radiata*, a presença de proteínas relacionadas à organização da parede celular foi fundamental no processo de formação de novos meristemas durante o enraizamento adventício (Álvarez et al. 2016). Outras proteínas, como as relacionadas ao metabolismo de carboidratos e energia, foram correlacionadas com a indução do enraizamento em *Chrysanthemum morifolium* (Liu et al. 2013). Ademais, é possível caracterizar proteínas marcadoras moleculares, identificando proteínas relacionadas diretamente com a capacidade de enraizamento da planta (Han et al. 2009). Entretanto, poucos são os estudos que mostram proteínas correlacionadas com os mecanismos celulares durante o processo de enraizamento de brotações em espécies arbóreas. Dessa forma, salienta-se a importância de caracterizar as proteínas marcadoras do enraizamento para a *C. fissilis*.

2.5.2- Poliaminas

Além do envolvimento da auxina e proteínas, estudos tem mostrado o envolvimento de PAs na formação de RAs (Tang e Newton 2005). As PAs são moléculas policatiônicas alifáticas de baixa massa molecular contendo dois ou mais grupos aminas e estão presentes em todos os organismos vivos (Chen et al. 2019). Nos vegetais participam de vários processos de desenvolvimento, como germinação, organogênese e embriogênese (Minocha et al. 2004, Silveira et al. 2006, Pieruzzi et al. 2011, Aragão et al. 2016).

As principais PAs são a Put, Spd e Spm. Em algumas famílias ou gêneros de plantas, outras PAs são descritas, como a termoespermina, homoespermidina, norespermidina e canavalmina (Todorova et al. 2014). Na biossíntese de PAs, a Put pode ser produzida a partir da ornitina pela ação da ornitina descarboxilase (ODC) e da arginina, pela ação da arginina descarboxilase (ADC). A conversão de Put à Spd e Spm ocorre pela adição sucessiva de grupos aminopropil originados da metionina a partir da S-adenosilmetionina (SAM), pela ação da SAM descarboxilase (SAMDC) (Kusano et al. 2008). Desta forma, a Spd é formada a partir da Put pela ação da Spd sintase, e a Spm é formada a partir da Spd pela ação da Spm sintase (Kusano et al., 2008).

As PAs podem ser reguladas direta ou indiretamente por meio da interação com metabólitos de sinalização, como o ácido gama-aminobutírico, e hormônios de crescimento, como a auxina (Kamiab et al. 2020). O aumento de Put causada pela superexpressão da ADC1, gene que codifica a ADC, pode regular alguns genes relacionados à biossíntese de AIA como NIT2, GH3.3, GH3.5, YDK1, IAR3, ILL6, os quais são fatores de transcrição, relacionados a auxina em plantas transgênicas de *Arabidopsis thaliana* (Marco et al. 2011).

Estudos usando PAs exógenas e transgenia têm investigado o papel das PAs no desenvolvimento das plantas e seu mecanismo de ação. Tais estudos mostraram que os PAs estão intimamente associados ao crescimento da planta, à estabilidade dos ácidos nucléicos e estrutura da membrana, e resistência ao estresse, bem como proteínas de transporte de íons (Pottosin e Shabala 2014, Pál et al. 2015, Chen et al. 2019). Dados mostram que a poliamina oxidase (PAO) tem sua expressão ajustada pelo TIBA e o ácido naftilftalâmico (NPA) após o tratamento com luz, estando relacionada com a diferenciação da parede celular (Cona et al. 2003). Além disso, as PAs funcionam como reguladoras da interação da proteína 14-3-3 com a membrana plasmática via H + -ATPase. Inibidores da síntese de PAs causam uma pequena diminuição da atividade fosfohidrolítica da H^+ -ATPase, demonstrando um papel fisiológico das PAs na regulação da atividade enzimática (Garufi et al. 2007). PAs também induzem o efluxo de Ca^{2+}

através da membrana plasmática (Bose et al. 2011) e ativam ou suprimem o bombeamento de Ca^{2+} da membrana plasmática. Dependendo da espécie e conteúdo de PAs, o fenótipo da planta pode ser alterado.

Dessa forma, estudos que venham explicar a relação entre a sinalização da auxina e PAs durante o processo de enraizamento são importantes, pois possibilitam o entendimento destas rotas de sinalização durante esse processo morfogenético em uma espécie arbórea, como a *C. fissilis*.

3- Objetivos

3.1- Objetivo geral

O objetivo geral foi investigar o envolvimento da auxina, proteínas diferencialmente acumuladas e alterações de PAs durante o enraizamento *ex vitro* de brotações micropropagadas em *C. fissilis*.

3.2- Objetivos específicos

- Avaliar os efeitos do AIB e dos inibidores da auxina, TIBA e PCIB no enraizamento *ex vitro* de brotações micropropagadas de *C. fissilis*.
- Estabelecer as fases de desenvolvimento de raízes adventícias durante o enraizamento *ex vitro* em *C. fissilis*.
- Quantificar e localizar o conteúdo endógeno de AIA livre na ausência e na presença de TIBA e PCIB em brotações micropropagadas de *C. fissilis* durante o enraizamento;
- Identificar e comparar proteínas diferencialmente abundantes associadas com o desenvolvimento das raízes em brotações, na presença e ausência de TIBA e PCIB;
- Avaliar o efeito de Put no metabolismo de PAs sobre o desenvolvimento de raízes *ex vitro* em *C. fissilis*;
- Avaliar o efeito da Put combinada com inibidores de auxina, no conteúdo endógeno de PAs durante o enraizamento em *C. fissilis*.

4- Trabalhos

4.1- Involvement of differentially accumulated proteins and endogenous auxin in adventitious root formation in micropropagated shoot cuttings of *Cedrela fissilis* Vellozo (Meliaceae) *

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Resumo

A investigação das mudanças bioquímicas e moleculares durante o enraizamento em espécies arbóreas pode revelar como moléculas específicas estão envolvidas na indução de raízes adventícias (RAs). Foram investigados os efeitos do ácido indol butírico (AIB) e inibidores do transporte polar de auxina e sinalização de auxina no enraizamento *ex vitro* de brotos micropropagados de *Cedrela fissilis* e foi avaliado o perfil proteômico e conteúdo endógeno de ácido indol acético (AIA) durante o início de RAs. Observou-se que o AIB exógeno não foi necessário para o enraizamento *ex vitro* e a indução radicular foi significativamente reduzida pelos inibidores da sinalização de auxina (ácido p-clorofenoxisobutírico - PCIB) e do transporte polar de auxina (ácido triiodobenzóico - TIBA). A presença de células meristemáticas e a formação de centros meristemáticos na base das brotações aos três dias de enraizamento são necessárias para a formação de RA. O acúmulo de proteínas relacionadas à divisão celular e auxina e a presença de proteínas únicas relacionadas à modificação da parede celular em brotações aos três dias de enraizamento foram associadas a maiores teores de AIA e à iniciação de RAs. Além disso, o acúmulo de proteínas relacionadas à desfosforilação, as vias do ciclo do ácido glicolítico e tricarboxílico e a redução do acúmulo de proteínas do metabolismo dos isoflavonóides foram associados à promoção da iniciação de RA. Esses resultados mostram a relevância dessas proteínas para a iniciação de RA nesta espécie. Este é o primeiro estudo mostrando o envolvimento do acúmulo de proteína e conteúdo de AIA endógeno na iniciação do enraizamento adventício em *C. fissilis*, uma espécie arbórea ameaçada de extinção de fácil enraizamento da Mata Atlântica.

Palavras-chave: Enraizamento adventício, Inibidor de sinalização de auxina, Proteômica comparativa, Ácido indol-acético, Propagação de brotos in vitro, Auxina polar.

Abstract

Investigation of the biochemical and molecular changes during rooting in woody species can reveal how specific molecules are involved in adventitious root (AR) induction. We investigated the effects of indole butyric acid (IBA) and inhibitors of polar auxin transport and auxin signaling on ex vitro rooting of micropropagated shoots of *Cedrela fissilis* and evaluated the proteomic profile and endogenous contents of indole acetic acid (IAA) during AR initiation. We observed that exogenous IBA was not necessary for ex vitro rooting, and root induction was significantly reduced by auxin signaling (p-chlorophenoxyisobutyric acid - PCIB) and polar auxin transport (triiodobenzoic acid - TIBA) inhibitors. The presence of meristematic cells and the formation of meristematic centers in the base of shoot cuttings at 3 days of rooting are necessary for AR formation. The accumulation of cell division- and auxin-related proteins and the presence of unique proteins related to cell wall modification in shoot cuttings at 3 days of rooting were associated with higher IAA contents and AR initiation. In addition, an accumulation of proteins related to dephosphorylation, glycolytic and tricarboxylic acid cycle pathways and a reduction in the accumulation of proteins from isoflavonoid metabolism were associated with the promotion of AR initiation. These results show the relevance of these proteins for AR initiation in this species. This is the first study showing the involvement of protein accumulation and endogenous IAA contents in adventitious rooting initiation in *C. fissilis*, an easily rooted endangered woody species from the Brazilian rainforest.

Keywords: Adventitious rooting, Auxin signaling inhibitor, Comparative proteomics, Indole-acid acetic, *In vitro* shoot propagation, Polar auxin

Introduction

Native woody species from the Brazilian Atlantic Forest, including *Cedrela fissilis* Vellozo (Meliaceae), popularly known as “cedro rosa”, have been explored for decades. Due to intense exploitation over the years, this species is currently included on the list of threatened species and is placed in the vulnerable category (Barstow 2018). Due to the economic and ecological importance of *C. fissilis*, initial studies on in vitro propagation have been performed for this species (Aragão et al. 2017; Aragão et al. 2016; Nunes et al. 2002). However, no studies have been performed using ex vitro rooting of in vitro propagated shoots in this species.

The establishment of rooting is essential for plantlet production in a micropropagation system (Kasthurirengan et al. 2013). The process of adventitious root (AR) development can be divided into three successive phases: a) induction, the period prior to any histological event; b) initiation, with the occurrence of cell divisions leading to the formation of root meristems, characterized by the presence of small cells with large nuclei and dense cytoplasm; and c) expression, characterized by root primordium formation from the internal cells formed at the initiation phase and culminating in root emergence (Li et al. 2009; Pacurar et al. 2014). According to Pijut et al. (2011), an additional step before the induction phase, called dedifferentiation, is necessary for adventitious rooting. In this phase, cells such as parenchymal cells close to the vascular bundles of the stem shoots are dedifferentiated, acquiring competence to respond to an AR-inducing signal that evokes proliferation and differentiation into meristematic type cells followed by differentiation into the complete root body through the stages described (Druege et al. 2019).

Ex vitro rooting provides several advantages in relation to in vitro rooting, with a cost reduction of up to 70% (Ranaweera et al. 2013). Thus, the ex vitro rooting method can be highly efficient, and the rooted plantlets showed a better quality of developed roots than those established in vitro (Yan et al. 2010), conferring greater tolerance of plantlets to the stress caused by the external environment (Phulwaria et al. 2013). Ex vitro rooting has been applied for some woody species, and it is often necessary to use exogenous auxin to promote rooting (Husain and Anis 2009; Phulwaria et al. 2013), as observed for *Tecomella* *undulata* (Varshney and Anis 2012) and *Albizia lebbeck* (Perveen et al. 2013), both of which were treated with 200 µM IBA for 30 min. The use of exogenous auxin is necessary if the endogenous IAA content is insufficient to promote rooting. However, in *Tectonia grandis*, ex vitro rooting also occurred in the absence of IBA (Fermino Júnior et al. 2011). Thus, in some species, the content of endogenous auxin, which occurs naturally in the shoots, is sufficient to promote rooting (Da Costa et al. 2013). If endogenous auxin contents are optimal to promote rooting, the exogenous application of this regulator is unnecessary and may be inhibitory (Yin et al. 2011).

The use of chemical inhibitors has been an effective tool for studying auxin responses (Ma et al. 2018), both in signaling (Oono et al. 2003) and polar auxin transport (Ahkami et al. 2013) during rooting. p-Chlorophenoxyisobutyric acid (PCIB) has been widely used to impair the auxin signaling pathway, regulating the stability of the auxin/IAA repressor protein (Aux/IAA) and inhibiting root formation in *Arabidopsis* (Oono et al. 2003). Triiodobenzoic acid (TIBA) is an inhibitor of auxin efflux transport involved in the inhibition of auxin trafficking across membranes (Kleine-Vehn et al. 2006) as well as in blocking the recycling of the PIN-FORMED (PIN) protein between endosomes and plasmatic membranes (Geldner et al. 2001). Thus, it is suggested that auxin is needed to stimulate the founder cells involved in root formation during the induction and initiation phases of AR (Druege et al. 2016; Druege et al. 2019; Guan et al. 2019).

Proteins and enzymes are synthesized and regulated by a cascade of events triggered by auxin and may also be related to the initiation of AR, which allows root primordia formation. Proteins related to carbohydrate and energy metabolism, photosynthesis, cell structure, and degradation were found to play a key role in the formation of new roots (Liu et al. 2013). Similarly, proteins involved in glucose metabolism, flavonoid biosynthesis, cell wall modification, hormone regulation, cellular cytoskeleton formation, and protein degradation/folding and import showed potential contributions to adventitious rooting (Tang et al. 2016; Zhang et al. 2015). Thus, these studies illustrate that proteomic analyses are an effective tool for identifying relevant proteins involved in the regulation of biological processes associated with rooting.

In this sense, we investigated the effects of IBA and inhibitors of polar auxin transport and auxin signaling on ex vitro rooting of micropropagated shoots of *C.*

fissilis and evaluated the proteomic profile and endogenous contents of IAA during AR initiation.

Materials and methods

Plant material

Mature seeds of *C. fissilis* obtained from the Caiçara Comércio de Sementes LTDA located in Brejo Alegre, SP, Brazil (21°10'S and 50°10'W) were germinated in vitro, and 60-day-old seedlings were used as a source of explants (apical and cotyledonary nodal segments) for shoot development. Micropropagated shoots at 45 days of in vitro culture were used for ex vitro rooting experiments.

In vitro seed germination and shoot propagation

For germination, seeds were submitted to a disinfection process according to Aragão et al. (2016), with modifications. Disinfection of 250 seeds was performed with 250 mL of distilled water containing 60 µL of neutral commercial detergent (Limpol; São Paulo, Brazil) and rinsed in 100 mL of water 5 times. Then, seeds were immersed in 250 mL of 70% ethanol (Tupi; São Paulo, Brazil) for 1 min. Subsequently, seeds were immersed in 100% bleach (QBoa®; São Paulo, Brazil) containing 1.8 to 2.5% active chlorine, supplemented with 7 g L^{-1} fungicide (Cercobin® 700 wp; São Paulo, Brazil) for 90 min. Subsequently, seeds were submitted to five washes with autoclaved distilled water (200 mL each) in a laminar flow chamber. The seeds were sown in MS culture medium (Murashige and Skoog 1962) (PhytoTechnology Laboratories®; Overland Park, USA) supplemented with 20 g L^{-1} sucrose (Synth; São Paulo, Brazil) and 2.0 g L^{-1} Phytagel® (Sigma-Aldrich; St. Louis, USA). The pH of the culture medium was adjusted to 5.8, and then the medium was autoclaved at 121 °C at 1.5 atm for 15 min. In vitro sowed seeds were maintained in a growth room at 25 ± 2 °C under a 16 h photoperiod, with a light intensity of 55 µmol m^{-2} s^{-1} provided by light-emitting diodes (LED) lamps (Koninklijke Philips Electronics NV; Amsterdam, Netherlands).

Sixty-day-old seedlings were used as a source of explants (apical and cotyledonary nodal segments) for the induction of shoots. The explants were isolated in a flow chamber and transferred to MS culture medium supplemented with 20 g L^{-1} sucrose, 2 g L^{-1} Phytagel and 2.5 μM BA (Sigma-Aldrich) according to Nunes et al. (2002). The pH of the culture medium was adjusted to 5.8 and autoclaved at 121 °C at 1.5 atm for 15 min. After being transferred into the culture medium, the explants were maintained in a growth room at 25 ± 2 °C under a 16 h photoperiod, with a light intensity of 55 μmol m^{-2} s^{-1} provided by LED lamps (Koninklijke Philips Electronics NV). After 45 days, shoots from apical and cotyledonary nodal segments were used for ex vitro rooting.

Effect of IBA on ex vitro rooting of micropropagated shoots

Forty-five-day-old shoots obtained by in vitro culture from apical and cotyledonary nodal segments were separated into cuttings (1.5 to 2.0 cm), retaining the apical meristem of the shoots and four main leaves. The bases of the shoot cuttings were immersed in solutions containing different concentrations (0 [distilled water], 50, 100, 250 and 500 μM) of IBA (Sigma-Aldrich) for 30 s. The shoot cuttings were then transferred to plastic cups (50 mL; TotalPlast, Santa Catarina, Brazil) containing the substrate Basaplant® (São Paulo, Brazil) and vermiculite (Basil Minérios; Goiás, Brazil) (1:1; v/v) and maintained in plastic trays (39.4 x 31.9 x 15.4 cm) (Pleion; São Paulo, Brazil) covered with PVC-type plastic film (Lumipam; São Paulo, Brazil) to maintain high relative humidity. The trays were maintained in a growth room at 25 ± 2 °C under a photoperiod of 16 h, with a light intensity of 55 μmol m^{-2} s-^{1} provided by LED lamps (Koninklijke Philips Electronics NV).

After fifteen days, aiming to reduce the moisture inside trays and stimulate the start of an acclimatization process simultaneously with rooting induction, the PVC parafilm plastic was perforated. This procedure was carried out until the complete removal of the PVC at 24 days after the start of perforation.

The experiment followed a completely randomized design in a 2 x 5 factorial arrangement, with shoot cuttings originating from two types of explants (cotyledonary and apical nodal segments) under five concentrations of IBA. Each treatment consisted of eight replicates, with each replicate containing four shoot cuttings, with a total of thirty-two shoot cuttings per treatment. After 30 days, the percentage of rooted shoot cuttings and the number and length (cm) of roots per shoot cuttings were evaluated.

Effect of the auxin inhibitors PCIB and TIBA on ex vitro rooting of micropropagated shoots

The effects of the auxin signaling inhibitor PCIB (Sigma-Aldrich) and polar auxin transport inhibitor TIBA (Sigma-Aldrich) on the rooting of shoot cuttings from cotyledonary nodal segments were evaluated. Forty-five-day-old in vitro shoot cuttings (1.5 to 2.0 cm) with the apical meristem of the shoots and four main leaves were used. The bases of the shoot cuttings were immersed in different concentrations of PCIB (0, 400 and 800 μM) and TIBA (0, 100 and 200 μM) for 90 min. For the control, i.e., without PCIB or TIBA, the bases of the shoot cuttings were immersed in distilled water for 90 min. PCIB and TIBA inhibitors were dissolved in 1 N NaOH (Sigma-Aldrich) and diluted in distilled water, and the pH was adjusted to 7.0.

After the treatment, the shoot cuttings were transferred to plastic cups (50 mL) containing substrate Basaplant® and vermiculite (1:1; v/v), maintained in plastic trays (39.4 x 31.9 x 15.4 cm) (Pleion) covered with PVC-type plastic film (Lumipam) to maintain high relative humidity, and kept in a growth room at 25±2 °C under a 16 h photoperiod, with a light intensity of 55 μmol m^{-2} s^{-1} provided by LED lamps (Koninklijke Philips Electronics NV). After seven days, to simultaneously achieve the rooting of shoots and acclimatization, the PVC parafilm plastic was perforated until complete removal at 10 days of incubation, as described before.

The experiment followed a completely randomized design, with three concentrations of each inhibitor (TIBA or PCIB). Each treatment was composed of eight replicates, with five shoot cuttings per replicate, for a total of forty shoot cuttings per treatment. After 13 days, the percentage of rooted shoot cuttings and the number and length (cm) of roots per shoot cuttings were evaluated. In addition, samples containing the base (0.5 cm) of shoot cuttings were fixed for histomorphological analysis to establish the phases of rooting, as well as for IAA immunolocalization analysis. Moreover, samples containing the bases (0.5 cm) of shoot cuttings were collected for proteomic profile and endogenous IAA quantification analysis and maintained at -80°C until the analyses were performed.

Determination of adventitious root development phases by histomorphological analysis

To determine the phases of rooting, the bases (0.5 cm) of shoot cuttings originating from cotyledonary nodal segments incubated in the treatments without inhibitors (control treatment) and with 800 µM PCIB and 200 µM TIBA were collected each day during 10 days of incubation. These samples were fixed in fixative solution containing 2.5% glutaraldehyde (Sigma-Aldrich) and 4% paraformaldehyde (Sigma-Aldrich) in 0.1 M phosphate buffer (Sigma-Aldrich), pH 7.2, at room temperature for 24 h. The samples were then dehydrated with an increasing ethanol series (30, 50, 70, 90 and 100%) twice for 1 h each. Subsequently, the samples were infiltrated in 1:1 (v/v) Historesin (Leica, Heidelberger, Germany) and 100% ethanol (Merck; Darmstadt, Germany) for 12 h, followed by 100% Historesin for 24 h and hardened in 100% Historesin. Sections (5 µm) were obtained on a microtome (Leica), mounted on slides (Sail Brand; Zhejiang, China) and then stained with 1% aqueous toluidine blue (Synth) solution (Silveira et al. 2013). The sections were observed under an AxioImager M2 microscope (Carl Zeiss; Oberkochen, Germany) with the AxioVision 4.8 program (Carl Zeiss) and photographed with the aid of an AxioCam MR3 camera (Carl Zeiss) coupled to the equipment.

Proteomics analysis

For proteomic analysis, samples in biological triplicates (300 mg fresh matter – FM – each, in triplicate) containing the bases (0.5 cm) of shoot cuttings originating from cotyledonary nodal segments before (0 day) and after 3 days of treatment without and with 800 µM PCIB and 200 µM TIBA were used. Proteins were extracted using the trichloroacetic acid (TCA)/acetone method according to Damerval et al. (1986), with modifications. Initially, the samples were pulverized in liquid nitrogen using a ceramic mortar and pestle. The resulting powder was resuspended in 1 mL of chilled solution containing 10% (w/v) TCA (Sigma) in acetone with 20 mM dithiothreitol (DTT; GE Healthcare; Piscataway, USA) and vortexed for 5 min at 8 °C. Next, the samples were kept at −20 °C for 1 h before centrifugation at 16,000 x g for 30 min at 4 °C. The resulting pellets were washed three times with cold acetone plus 20 mM DTT and centrifuged for 5 min each time. The pellets were air dried and resuspended in buffer containing 7 M urea (GE Healthcare), 2 M thiourea (GE Healthcare), 2% Triton X-100 (GE Healthcare), 1% DTT, 1 mM phenylmethylsulfonyl fluoride (PMSF; Sigma-Aldrich), and a complete protease inhibitor cocktail (Roche Diagnostics; Mannheim, Germany), vortexed for 30 min at 8 °C, and centrifuged for 20 min at 16,000 x g at 4 °C. The supernatants were collected, and the protein concentrations were determined using a 2-D Quant Kit (GE Healthcare).

Aliquots of 100 µg of protein were subjected to tryptic digestion using the filter-aided sample preparation (FASP) methodology (Reis et al. 2021). Next, the peptides were resuspended in 100 µL solution containing 95% 50 mM ammonium bicarbonate, 5% acetonitrile and 0.1% formic acid and quantified by A205 nm protein and peptide methodology using a NanoDrop 2000c spectrophotometer (Thermo Fisher Scientific). The samples were transferred to Total Recovery Vials (Waters) for mass spectrometry analysis.

Mass spectrometry was performed using a nanoAcquity UPLC connected to a Q-TOF SYNAPT G2-Si instrument (Waters, Manchester, UK) according to Passamani et al. (2018). Runs consisted of three biological replicates of 1 µg of digested peptides. During separation, samples were loaded onto the nanoAcquity UPLC M-Class Symmetry C18 5 µm trap column (180 µm × 20 mm) at 5 µL min-1 for 3 min and then onto the nanoAcquity M-Class HSS T3 1.8 µm analytical reversed-phase column (75 µm × 150 mm) at 400 nL min-1, with a column temperature of 45 °C. For peptide elution, a binary gradient was used, with mobile phase A consisting of water (Tedia; Fairfield, Ohio, USA) and 0.1% formic acid (Sigma-Aldrich) and mobile phase B consisting of acetonitrile (Sigma-Aldrich) and 0.1% formic acid. The gradient elution started at 7% B, then ramped from 7 B to 40% B until 91.12 min, then ramped again from 40 B to 99.9% B until 92.72 min, then remained at 99.9% until 106.00 min, then decreased to 7% B until 106.1 min, and finally remained at 7% B until the end of run at 120 min. Mass spectrometry was performed in positive and resolution mode (V mode), at 35,000 FWHM, with ion mobility, and in data-independent acquisition mode (HDMSE). Human [Glu1]-

fibrinopeptide B at 100 fmol µL^{-1} was used as an external calibrant, and lock mass acquisition was performed every 30 s. Mass spectra were acquired by MassLynx v 4.0 software.

Spectral processing and comparative analysis were performed according to Passamani et al. (2020). Spectra processing and database searching were performed using ProteinLynx Global Server (PLGS) software v. 3.0.2 (Waters), and comparative label-free quantification was performed using ISOQuant software v. 1.7 (Distler et al. 2014; Distler et al. 2016). Briefly, for ISOQuant, the following parameters were used to identify proteins: a 1% FDR, a peptide score greater than six, a minimum peptide length of six amino acids, and at least two peptides per protein were required for label-free quantitation using the TOP3 approach, followed by the multidimensional normalized process within ISOQuant. For protein identification, the obtained data were processed against the nonredundant Cedrela fissilis databank (Oliveira et al. 2020). The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE (Perez-Riverol et al. 2019) partner repository with the dataset identifier PXD021070.

To ensure the quality of the results after data processing, only the proteins present or absent (for unique proteins) in all three of the biological replicates were considered for differential accumulation analysis using Student’s t-test (two-tailed; $P < 0.05$). Proteins with a significant t-test result were considered up-accumulated if the log2 value of the fold change (FC) was greater than 0.60 and down-accumulated if the log2 value of the FC was less than -0.60. Finally, proteins were used in BLAST searches against the Nonredundant (nr) Green Plants/Viridiplantae Protein Sequences database using OmicsBox software (https://www.biobam.com/omicsbox) for the description of high-throughput functional annotation (Götz et al. 2008).

Quantification of IAA

The quantification of endogenous IAA contents in the bases of shoot cuttings from cotyledonary nodal segments was performed according to Álvarez-Flórez et al. (2017) and Silveira et al. (2004), with modifications. For this analysis, the bases (0.5 cm) of shoot cuttings originating from cotyledonary nodal segments before (0 days) and after 3 days of treatment without and with 800 µM PCIB and 200 µM TIBA were used. The samples (500 mg FM each, in triplicate) were lyophilized, and IAA was extracted with chilled extraction solution containing 2.5 mL of methanol (Merck):isopropanol (Merck) (20:80; v/v) with 1% glacial acetic acid (Merck). IAA[3H] was added as an internal standard. Then, the samples were vortexed for 5 min and centrifuged at 11,000 x g for 20 min at 4 °C. The supernatants containing the IAA were collected, and the pellets were re-extracted with 2.5 mL of extraction solution and centrifuged again. Then, the supernatants were combined and dried completely in a speed vac at 45 °C. Each sample was then resuspended in 150 µL of solution containing 10% methanol (Merck) plus 0.5% glacial acetic acid (Merck). Next, samples were filtered through a 0.2 µm Minisart filter (Sartorius Stedim Biotech, Goettingen, Germany). Finally, 10 µL of each sample was used for high-performance liquid chromatography (HPLC) using a 5-µm reversed-phase column (Shim-pack CLC ODS, Shimadzu, Kyoto, Japan). The gradient was developed by a mixture of increasing proportions of absolute methanol with a water solution containing 10% methanol plus 0.5% glacial acetic acid. The absolute methanol gradient was set to 10% in the first 5 min, from 10 to 20% between 5 and 7 min, from 20 to 30% between 7 and 15 min, from 30 to 45% between 15 and 21 min and 100% from 21 to 35 min, with a flow rate of 1 mL min^{-1} at 40°C. The IAA concentration was determined using a fluorescence detector at 280 nm (excitation) and 350 nm (emission). The fraction containing the IAA peak was collected and analyzed by a Tri-Carb Liquid Scintillation counter (Packard Instrument Co., Meriden, USA) to estimate the losses. The IAA retention areas and times were evaluated by comparison with known concentrations of this hormone.

Immunolocalization of IAA

IAA immunolocalization analysis was performed according to Pence and Caruso (1987) and De Diego et al. (2013), with modifications. For this analysis, samples containing the bases (0.5 cm) of shoot cuttings originating from cotyledonary nodal segments before (0 days) and after 3 days of treatment without and with 800 µM PCIB and 200 µM TIBA were used, with the times selected from the histomorphological analysis. The samples were prefixed for 2 h in 4% 1-ethyl-3-(3-dimethylaminopropyl) carbodiimide (Sigma-Aldrich) at 4°C in a vacuum. The samples were then fixed in formalin-acetic acid-alcohol (FAA-50) solution containing 4% formaldehyde (Merck), 5% acetic acid (Merck) and 50% ethanol (Merck) in aqueous solution at 4°C in a vacuum. Afterwards, samples were dehydrated by an increasing ethanol series (50, 70, 90 and 100%) twice for 12 h each. Subsequently, the samples were infiltrated in LR White resin (Sigma-Aldrich) and polymerized at 57°C for 24 h. Seven-micrometer-thick sections were cut using a rotary microtome (Leica). The sections were also hydrated for 5 min in 10 mM phosphate-buffered saline (PBS) containing 138 mM NaCl, 2 mM KH2PO4, and 10 mM Na2HPO47.H2O. Next, the sections were incubated in blocking solution containing 10 mM PBS, 0.1% Triton-X 100, 1.5% glycine and 5% bovine serum albumin (BSA) for 1 h. Sections were further incubated in 10 mM PBS for 1 h. To determine the localization of endogenous IAA, sections were incubated for 6 h in anti-IAA rabbit polyclonal antibody (Agrisera AB; Vännäs, Sweden) and diluted 1:100 in a 10 mM PBS solution containing 10% BSA and 1% sodium azide. The sections were washed once for 5 min in PBS I solution containing 10 mM PBS, 0.1% Triton-X 100, and 0.8% BSA and twice for 5 min each in PBS II solution containing 10 mM PBS and 0.8% BSA. Next, for IAA signal verification, sections were incubated for 1 h in Alexa Fluor 488-labeled anti–rabbit immunoglobulin G antibody (Agrisera AB) diluted 1:300 in 10 mM PBS solution containing 10% BSA and 1% sodium azide. Sections were washed in Milli-Q-type water for 15 min once and assembled on slides with gold antifade reagent (Invitrogen - Molecular probes; Eugene, USA). The slides were covered and sealed with nail varnish. Sections were viewed with a confocal laser scanning microscope (Carl Zeiss).

Statistical analysis

Rooting and IAA content data were submitted to analysis of variance ($P < 0.05$), and the means were compared using a Student-Newman-Keuls (SNK) test (Sokal and Rohlf 1995) in the R program (R Core 2018) (R Foundation for Statistical Computing, version 3.4.4, 2018, Vienna, Austria).

Results

Effect of IBA on ex vitro rooting of micropropagated shoots

No significant effects of the different IBA concentrations tested were observed on the percentage of rooted shoot cuttings from both types of explants, cotyledonary and apical nodal segments (Fig. 1a). However, the different IBA concentrations significantly affected the number (Fig. 1b) and length (Fig. 1c) of roots per shoot cuttings from apical and cotyledonary nodal segments. Shoots from cotyledonary nodal segments showed a higher number of roots with 50 µM IBA, while in shoots from apical nodal segments, the number of roots was significantly reduced with 500 µM IBA when compared to that under other treatments (Fig. 1b). When the two types of explants (i.e., shoots from cotyledonary and apical nodal segments) were compared at the same concentration, no significant differences were observed for the number of roots (Fig. 1b). The highest length of roots was observed at concentrations of 50 and 250 µM IBA in shoots from apical and cotyledonary nodal segments, respectively, whereas the shortest roots were formed at the highest IBA concentration of 500 µM in the shoot cuttings from both segments (Fig. 1c).

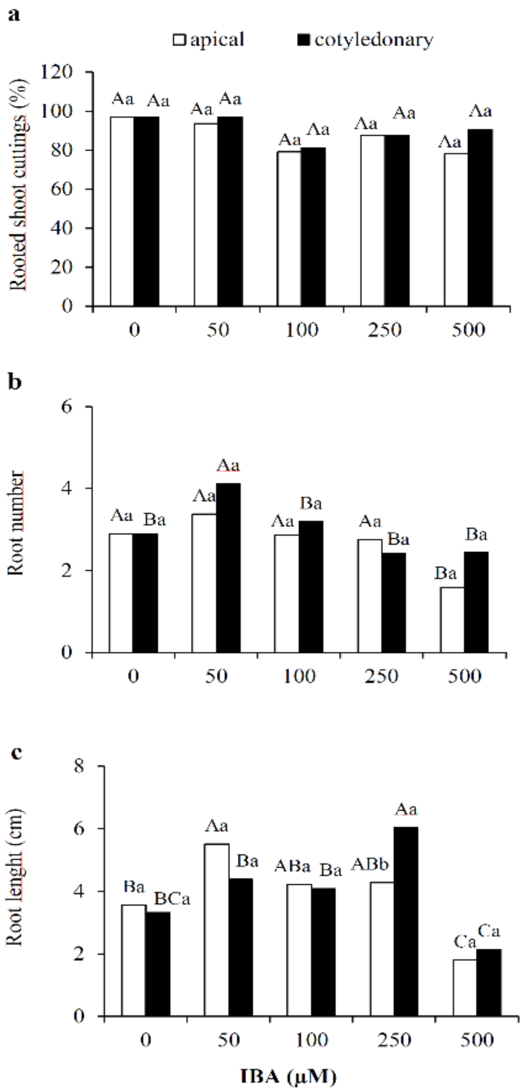

Fig. 1 - Percentage of rooted shoot cuttings (a), number (b) and length (c) of roots per shoot cuttings from apical and cotyledonary nodal segments of *Cedrela fissilis* at 30 days of rooting. Means followed by the same letter do not differ statistically according to the SNK test ($P < 0.05$). Different capital letters show significant differences comparing the different IBA concentrations in each type of shoot (apical or cotyledonary). Different lowercase letters show significant differences comparing the two types of shoots (apical and cotyledonary) under each IBA concentration. CV = coefficient of variation (n = 8; CV a = 17.5%, CV b = 31.8%, CV c = 33.5%).

Effect of PCIB and TIBA inhibitors on ex vitro rooting of micropropagated shoots

Shoot cuttings of *C. fissilis* can be rooted without IBA treatment, without significant differences among the types of explants used, i.e., cotyledonary and apical nodal segments (Fig. 1a). In this sense, the effects of the auxin signaling inhibitor PCIB and the auxin transport inhibitor TIBA on rooting were evaluated using shoot cuttings from cotyledonary nodal segments. The percentage of rooted shoot cuttings was significantly reduced by 800 µM PCIB (Fig. 2a). The number (Fig. 2b) and length (Fig. 2c) of roots were significantly reduced by 400 and 800 µM PCIB. In addition, the percentage of rooted shoot cuttings (Fig. 2d), number (Fig. 2e) and length (Fig. 2f) of roots per shoot cuttings were significantly reduced by 100 and 200 µM TIBA.

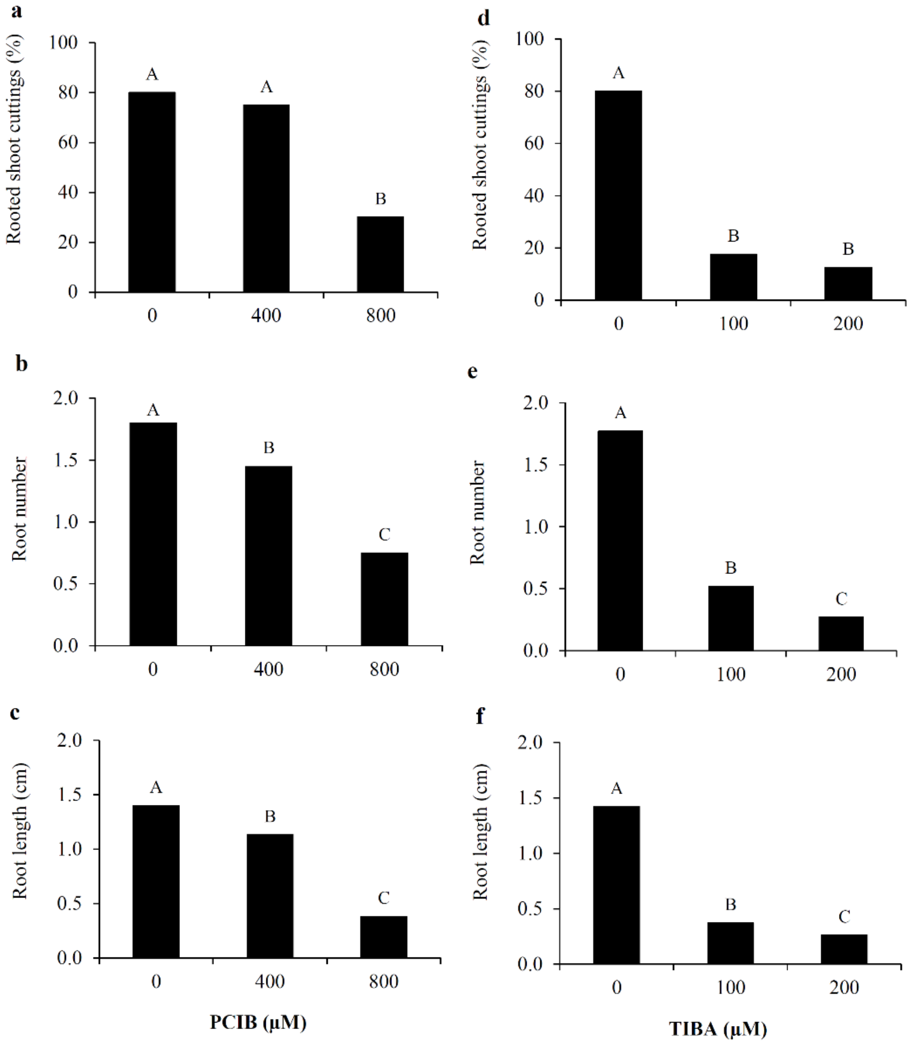

Fig. 2 - Percentage of rooted shoot cuttings (%), number and length (cm) of roots in shoot cuttings from cotyledonary nodal segments of *Cedrela fissilis* as affected by exposure to different concentrations (0, 400 and 800 µM) of PCIB (a, b, c) and different concentrations (0, 100 and 200 µM) of TIBA (d, e, f) after 13 days of ex vitro rooting. Means followed by the same letter do not differ statistically according to the SNK test ($P < 0.05$). CV = coefficient of variation. (n = 8, CV a = 13.2%, CV b = 18.0%; CV c = 16.3%, CV d = 19.7%; CV e = 16.6%, CV f = 13.8%).

Establishment of adventitious root development phases by histomorphological analysis

Histomorphological analysis was performed on shoot cuttings from cotyledonary nodal segments without (control) and with 800 µM PCIB and 200 µM TIBA during 10 days of incubation. In this analysis, samples at the beginning (i.e., day 0) and after 3, 6 and 10 days of incubation (Fig. 3) were used to describe the phases of AR development in *C. fissilis*. Several cells dividing at the bases of shoot cuttings not treated with the inhibitors PCIB and TIBA were observed at 3 days of rooting. These cells were induced from parenchymal cells close to vascular bundles, forming regions called meristematic centers (Fig. 3b, arrow), allowing the development of the root primordium observed at 6 days of rooting (Fig. 3c) and the elongation of the root observed at 10 days of rooting (Fig. 3d). In contrast, the shoots treated with PCIB and TIBA (Fig. 3f, g, h, j, k, l) did not present the histological events observed in the shoots that were not treated with auxin inhibitors.

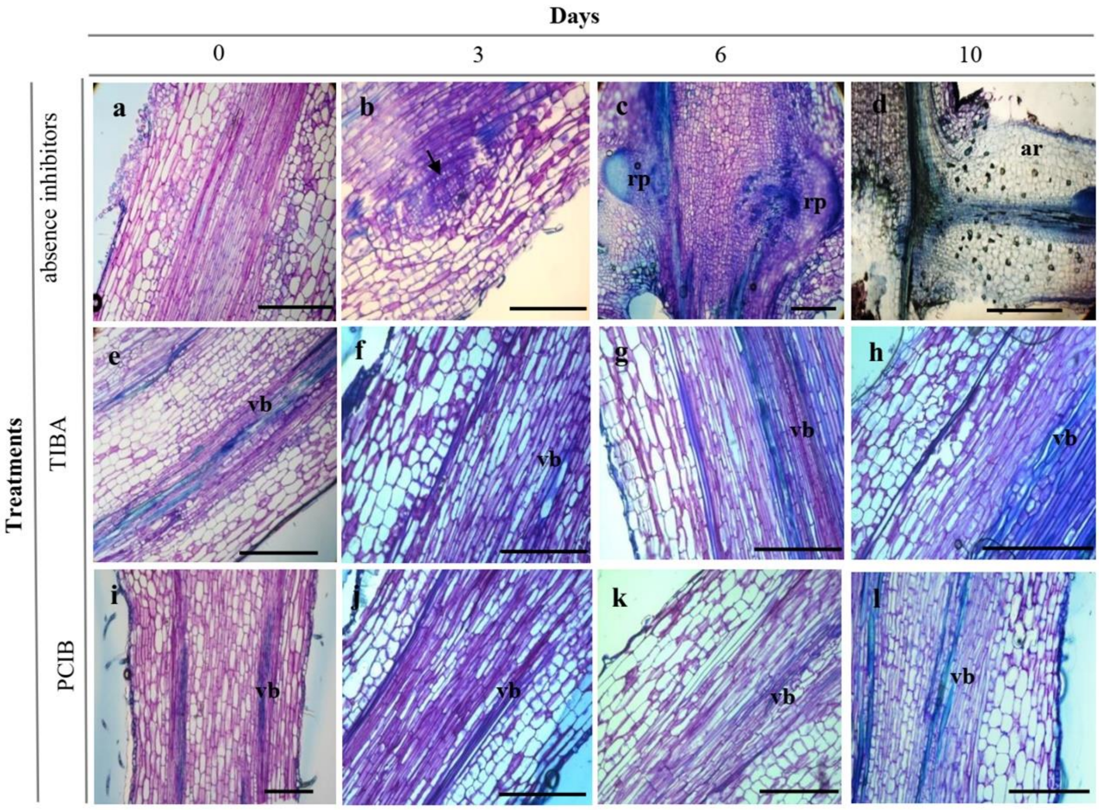

Fig. 3 - Histomorphological aspects during ex vitro rooting of *Cedrela fissilis* shoot cuttings from cotyledonary nodal segments before (0 days) and after 3, 6 and 10 days of root induction in the absence (control) and presence of TIBA (200 µM) and PCIB (800 µM). Arrows indicate cell divisions. rp = root primordium, vb = vascular bundle, ar = adventitious root. Bars = 200 µm.

Proteomic analysis

Proteomic analysis was performed comparing the bases of shoot cuttings from cotyledonary nodal segments at the beginning (0 days, initial time) and shoots at 3 days of rooting (3 days) (3-day/0-day comparison) to analyze the alterations in protein accumulation during the rooting initiation phase. In addition, we can analyze the alterations in protein accumulation induced by the PCIB and TIBA treatments in shoot cuttings at 3 days of rooting, with the goal of verifying proteins related to the inhibition of the root development process in this species.

From the proteomic analysis, a total of 1096 proteins were identified in at least one treatment (Table S1). Among these proteins, 528 were differentially accumulated proteins (DAPs) in the 3-day/0-day comparison, with 374 up- and 112 down-accumulated, 36 unique at 3 days and 6 unique at 0 days (Fig. 4). Comparing shoot cuttings at 3 days PCIB/3 days, 82 were DAPs, with 51 up- and 26 down-accumulated, 3 unique at 3 days of PCIB treatment and 2 unique at 3 days of shoot cutting rooting (Fig. 4). In addition, 159 were DAPs, with 80 up- and 72 down-accumulated, 5 unique at 3 days of TIBA treatment and 2 unique in shoots at 3 days of rooting compared with 3-days shoot cuttings treated with TIBA (3-days TIBA/3-days) (Fig. 4). Among the accumulated proteins, some were highlighted and discussed in this work according to their relevance in shoot rooting, mainly due to their relationship with auxin, cell division and cell wall organization (Table 1).

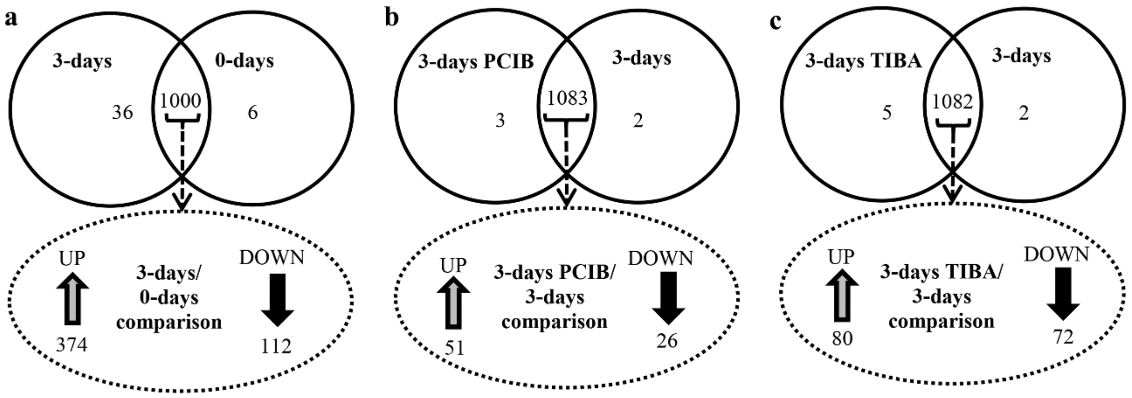

Fig. 4 - Venn diagram of proteins identified in *Cedrela fissilis* shoots during root initiation comparing cotyledonary nodal segments before (0 days) and after 3 days of rooting (3-day/0-day comparison) (a) and in shoot 3 at days of rooting without and with PCIB (3-day PCIB/3-day comparison) (b) and TIBA (3-day TIBA/3-day comparison) (c).

Considering the DAPs during the root initiation phase, in the 3-days/0-days comparison, some proteins were up-accumulated, such as Chorismate synthase, chloroplastic (Ce_fissilis.015065.1), Peroxidase 12 (Ce_fissilis.017405.2), Peroxidase 4 (Ce_fissilis.019038.1), Auxin-induced in root culture protein 12 (AIR12) (Ce_fissilis.015339.1), Patellin-3-like (Ce_fissilis.016593.1), Cell division cycle protein 48 homolog (CDC48) (Ce_fissilis.012572.1), Xylose isomerase (Ce_fissilis.014702.1), and Serine/threonine-protein phosphatase PP2A-4 catalytic subunit (Ce_fissilis.014280.1). On the other hand, the Vestitone reductase (Ce_fissilis.002557.2) protein was down-accumulated in this comparison. In addition, expansin-like B1 (EXPB1) (Ce_fissilis.010254.1) and probable xyloglucan endotransglucosylase/hydrolase protein 5 (XTH5) (Ce_fissilis.012480.1) were unique in shoot cuttings at 3 days of rooting (Table 1).

Considering the DAPs during root inhibition under the use of PCIB and TIBA inhibitors, some were DAPs in the 3-day PCIB/3-day comparison and 3-day TIBA/3-day comparison. Among the proteins, Vestitone reductase (Ce_fissilis.002557.2) was up-accumulated in both comparisons of shoots treated with PCIB and with TIBA, showing that both inhibitors affect the accumulation of this protein in addition to reducing rooting. Similarly, the protein serine/threonine-protein phosphatase PP2A-4 catalytic subunit (Ce_fissilis.014280.1) was down-accumulated in shoot cuttings treated with inhibitors (3-day PCIB/3-day and 3-day TIBA/3-day comparisons), showing that PCIB and TIBA decreased the accumulation of this protein and decreased rooting (Table 1). However, as this protein was up-accumulated in shoot cuttings during root initiation, i.e., in the 3-day/0-day comparison, the relevance of this protein for rooting promotion in this species seems likely. In addition, the phosphoglycerate kinase cytosolic (Ce_fissilis.016667.1) and pyruvate kinase 1 cytosolic (Ce_fissilis.011754.1) proteins were down-accumulated in shoot cuttings treated with both inhibitors (3-day PCIB/3-day and 3-day TIBA/3-day comparisons) (Table 1; Fig. S1).

In shoot cuttings at 3 days treated with TIBA (TIBA/3-day comparison), the xylose isomerase (Ce_fissilis.014702.1), glyceraldehyde-3-phosphate dehydrogenase, cytosolic (Ce_fissilis.011648.1), and succinate dehydrogenase subunit 6 mitochondrial (Ce_fissilis.015355.1) proteins were down-accumulated (Fig. S1). In addition, the cell division cycle protein 48 homolog (CDC48) (Ce_fissilis.012572.1) and chorismate synthase and chloroplastic

(Ce_fissilis.015065.1) proteins were down-accumulated in the shoot cuttings at 3-day TIBA/3-day comparison, showing that IAA efflux by the TIBA inhibitor reduced the accumulation of this protein and root initiation. However, these proteins were up-accumulated in shoot cuttings at 3 days of rooting compared with shoot cuttings before the start of the experiment (3-day/0-day comparison), suggesting their relevance to the initiation of roots in *C. fissilis*.

Table 1 - Highlighted differentially accumulated proteins related to rooting of *Cedrela fissilis* shoot cuttings. 3-days/0-days comparison = shoot cuttings at 3 days of rooting compared to shoot cuttings at the beginning of rooting (0 days). 3-days PCIB/3-days comparison = shoot cuttings at 3 days of rooting treated with PCIB compared to shoot cuttings at 3 days of rooting without PCIB. 3-days TIBA/3-days comparison = shoot cuttings at 3 days of rooting treated with TIBA compared to shoot cuttings at 3 days of rooting without TIBA.

Accession	Reported Peptide	Description	Biological Process	Accumulation 3-days/ 0-days	Accumulation 3-daysPCIB/ 3-days	Accumulation 3-daysTIBA/ 3-days
Ce_fissilis.019038.1	18	Peroxidase 4	Hydrogen peroxide catabolic process, oxidation-reduction process	UP	UNCHANGED	UNCHANGED
Ce_fissilis.017405.2	15	Peroxidase 12	Hydrogen peroxide catabolic process, oxidation-reduction process	UP	UNCHANGED	UNCHANGED
Ce_fissilis.015065.1	7	Chorismate synthase, chloroplastic	Aromatic amino acid family biosynthetic process	UP	UNCHANGED	DOWN
Ce_fissilis.010254.1	3	Expansin-like B1	Cell wall organization	Unique 3-days	UNCHANGED	UNCHANGED
Ce_fissilis.016593.1	16	Patellin-3-like	Cell cycle, cell division	UP	UNCHANGED	UNCHANGED
Ce_fissilis.012572.1	8	Cell division cycle protein 48 homolog	Mitotic spindle disassembly, cell cycle	UP	UNCHANGED	DOWN
Ce_fissilis.014280.1	12	Serine/threonine-protein phosphatase PP2A-4 catalytic subunit	Protein dephosphorylation, cellular protein modification process	UP	DOWN	DOWN
Ce_fissilis.011648.1	14	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	Glycolytic process, carbohydrate metabolic process	UP	UNCHANGED	DOWN
Ce_fissilis.016667.1	18	Phosphoglycerate kinase,	Glycolytic process, carbohydrate	UP	DOWN	DOWN

		cytosolic	metabolic process			
Ce_fissilis. 011754.1	11	Pyruvate kinase 1, cytosolic	Carbohydrate metabolic process	UP	DOWN	DOWN
Ce_fissilis. 015355.1	3	Succinate dehydrogenase subunit 6, mitochondrial	Tricarboxylic acid cycle	UP	UNCHANGED	DOWN
Ce_fissilis. 014702.1	8	Xylose isomerase	Carbohydrate metabolic process	UP	UNCHANGED	DOWN
Ce_fissilis. 015339.1	4	Auxin-induced in root cultures protein 12	Auxin-activated signaling pathway, metabolic process	UP	UNCHANGED	UNCHANGED
Ce_fissilis. 012480.1	5	Probable xyloglucan endotransglucosylase/hydrolase protein 5	Cell wall biogenesis	Unique 3-days	UNCHANGED	UNCHANGED
Ce_fissilis. 002557.2	7	Vestitone reductase	Flavonoid biosynthesis, biosynthetic process	DOWN	UP	UP

Endogenous IAA quantification and immunolocalization

As many proteins identified were related to auxin and rooting in plants (Table 1), the endogenous contents and immunolocalization of IAA were evaluated in the base of shoot cuttings from cotyledonary nodal segments before (0 days) and after 3 days of rooting without and with PCIB and TIBA treatments (Fig. 5).

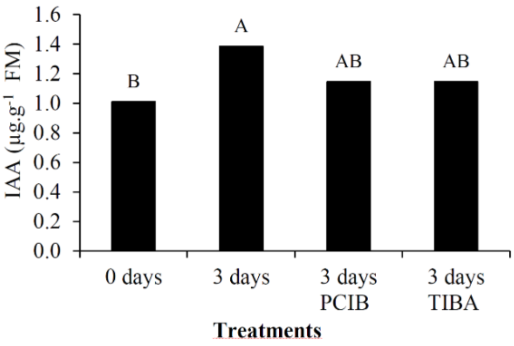

Fig. 5 - Quantification of IAA at the bases of *Cedrela fissilis* shoot cuttings from cotyledonary nodal segments before (0 days) and after 3 days of rooting without and with 800 µM PCIB and 200 µM

TIBA. Means followed by the same letter do not differ statistically according to the SNK test ($P < 0.05$). CV = coefficient of variation. (n = 3, CV = 11.7%).

The endogenous contents of IAA accumulated in the base of shoot cuttings at 3 days of rooting compared with shoot cuttings at day 0, whereas this increase was prevented in shoot cuttings at 3 days of rooting when auxin transport TIBA or auxin signaling PCIB were used (Figs. 5 and 6). The base of shoot cuttings at 3 days of rooting showed a more intense signal fluorescence around the cell (Fig. 6d), and some cells accumulated IAA on the intracellular cortex parenchyma (inset in Fig. 6d), suggesting IAA transport between cells. Some small cells from the meristematic center of shoot cuttings at 3 days of rooting showed an especially intense IAA fluorescence signal (Fig. 7, arrow), showing that the endogenous levels of IAA on the 3rd day of root initiation are important for AR initiation in this species.

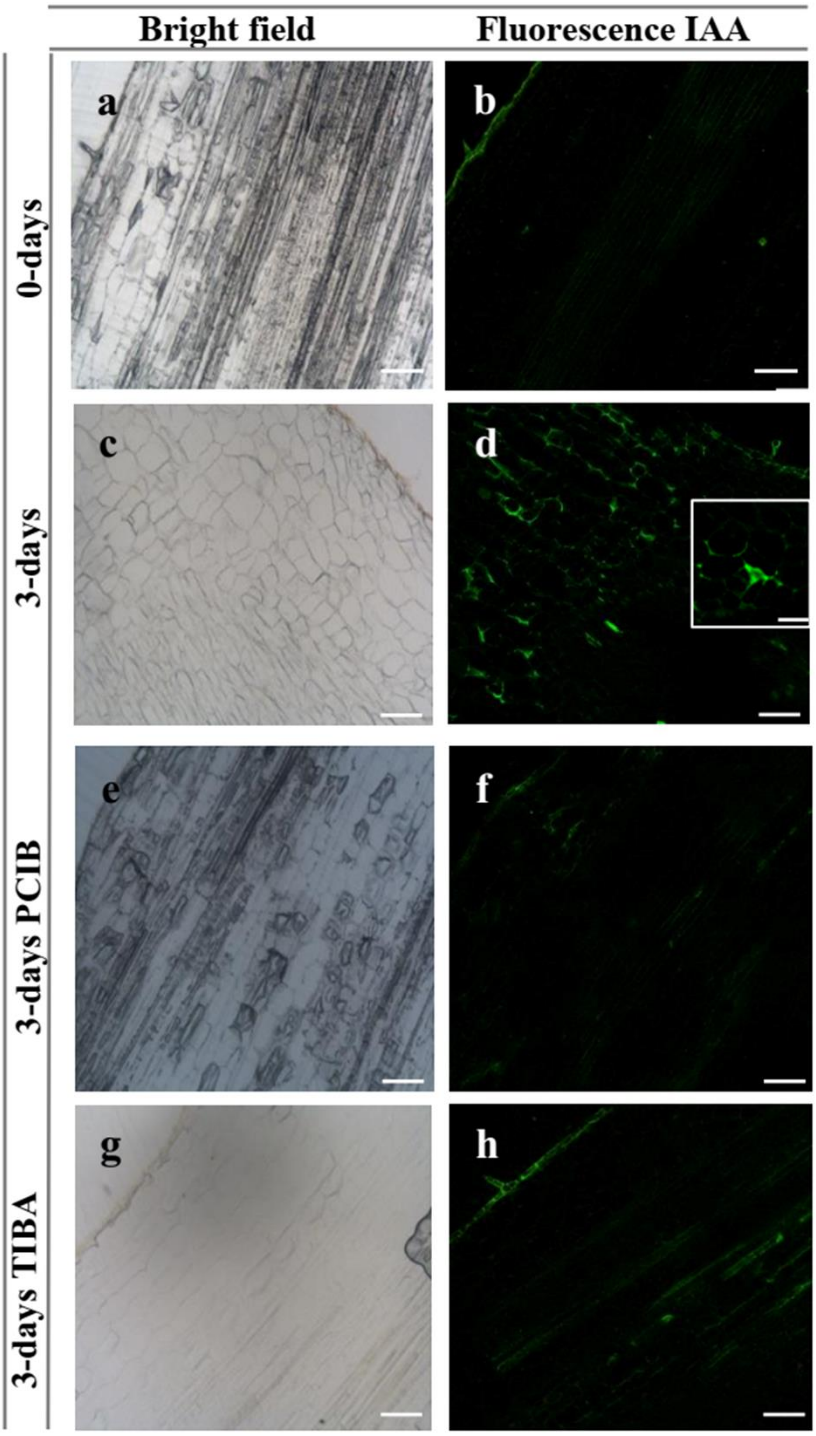

Fig. 6 - Immunolocalization of IAA in the bases of *Cedrela fissilis* stem shoots obtained from cotyledonary nodal segments before root initiation (0 days) (a, b), after 3 days of rooting (c, d), and at 3 days of rooting with 800 μM PCIB (e, f) and 200 μM TIBA (g, h). Inset in d: details of intracellular IAA presence. Bars a-h = 100 μm; Bar inset d = 50 μm.

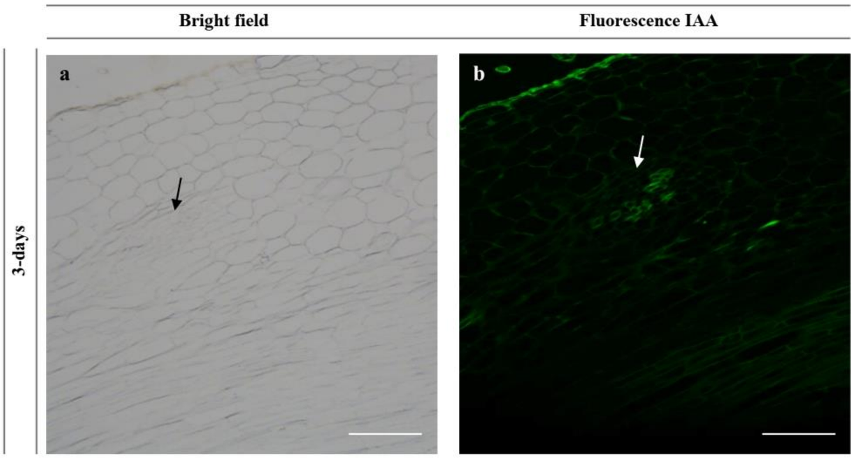

Fig. 7 - Immunolocalization of IAA in the bases of *Cedrela fissilis* stem shoots obtained from cotyledonary nodal segments at 3 days of root initiation showing the cells of the meristematic center in bright field (a) and IAA fluorescence microscopy (b). Arrow indicate meristematic center. Bars = 100 µm.

Discussion

Tree species often require the use of plant growth regulators, especially auxins, such as IBA, to promote adventitious rooting (Husain and Anis 2009; Phulwaria et al. 2013). However, our results showed that exogenous auxin is not necessary for adventitious rooting in micropropagated shoots of *C. fissilis*, since the IBA concentrations used did not present a significant effect on root induction (Fig. 1a). This ability to promote rooting without exogenous auxin can be explained by the existence of endogenous IAA metabolism and signaling, which can trigger root induction (Wilson 1994), and this hypothesis was confirmed in AR development of *C. fissilis* shoots by the IAA analyses performed (Fig. 5). Auxin has long been considered a key factor in root development (Da Costa et al. 2013; Pacurar et al. 2014), and auxin activity may be related to the cell cycle during AR formation, as auxin-dependent transcription factors regulate the control of G1/S and G2/M progression (Magyar et al. 2005). Any interference with endogenous auxin movement may alter cell cycle progression and influence AR formation (Wang and Ruan 2013). In our study, shoot cuttings of *C. fissilis* at 3 days of rooting were found to well represent the initiation phase, presenting regions with cell divisions characterized as meristematic centers, followed by the formation of root primordia at 6 days and root elongation at 10 days of rooting (Fig. 3), and the finding that those events were inhibited by the PCIB and TIBA treatments highlights the functional role of auxin in this process. There are increasing experimental data supporting the stimulating function of auxin during AR induction and early processes of AR initiation in root competent cells (Druege et al. 2019; Hu and Xu 2016; Sheng et al. 2017). During the phase of root initiation in shoots of *C. fissilis*, at 3 days, a higher content of IAA (Figs. 5 and 6) was critical to trigger adventitious rooting, as also demonstrated by Li et al. (Li et al. 2009). The finding that IAA accumulation in shoot cuttings at 3 days of rooting was prevented by the application of TIBA and by PCIB demonstrates the important role of auxin transport and auxin signaling in the auxin balance (Druege et al. 2019). The inhibition of polar auxin transport eliminated the IAA peak and root formation in *Petunia hybrida* shoots, showing the contribution of auxin in the stem base as dependent on polar auxin transport essential for subsequent AR formation (Ahkami et al. 2013). Thus, the endogenous auxin produced at the apex is conveyed basipetally to the cut surface of the stem shoot, acting as a stimulus for rooting (Da Costa et al. 2013). The use of chemical tools, such as the inhibitors TIBA and PCIB, can improve the identification of biochemical alterations modulating polar auxin transport and signaling involved in the rooting of micropropagated shoots of *C. fissilis*.

Proteomic analysis showed that the treatments significantly affected the accumulation of some DAPs during rooting of shoot cuttings in *C. fissilis*. Chorismate synthase is an important protein in the final step of the chiquimate pathway that gives rise to the main precursor of IAA, tryptophan (Tzin and Galili 2010). The increase in accumulation of chorismate synthase and chloroplastic (Ce_fissilis.015065.1) protein in the *C. fissilis* shoot cuttings at 3 days of rooting compared to 0-day shoot cuttings can be related to the increase in endogenous IAA content, which was observed at this time (Figs. 5 and 6), thus promoting root initiation. In addition, the higher accumulation of AIR12 (Ce_fissilis.015339.1) in shoot cuttings at 3 days of rooting compared to 0 days could be related to AR initiation in *C. fissilis*. This protein is a b-type cytochrome that can facilitate a redox link between the cytoplasm and apoplast, interacting with other redox partners within the plasmatic membrane (Preger et al. 2009). Redox regulation affects hormonal signaling pathways controlling meristem maintenance and organogenesis, such as renewal and differentiation of stem cells (Beveridge et al. 2007).

Endogenous auxin accumulation at the bases of stem shoots can also lead to cell division and expansion (Da Costa et al. 2013). An auxin-induced acidic pH is required to activate expansins, which are responsible for the disintegration and loosening of the connections between cellulose microfibrils (Cosgrove 2005; Majda and Robert 2018), while XTH cleaves and reconnects xyloglucan polymers, promoting cell wall loosening and extensibility (Cosgrove 2005). This process may be important for cell division since these cell wall proteins are necessary for normal cell expansion during the growth of various plant organs. In our work, the higher accumulation of the EXPB1 (Ce_fissilis.010254.1) and XTH5 (Ce_fissilis.012480.1) proteins in shoot cuttings of C. fissilis at 3 days of rooting (Table 1) and the simultaneous increase in endogenous IAA (Fig. 5) could be related to the loosening and extensibility of cell walls necessary for cell division and elongation, which are essential for AR development in *C. fissilis*.

The higher accumulation of the Patellin-3-like (Ce_fissilis.016593.1) and CDC48 (Ce_fissilis.012572.1) proteins in shoot cuttings at 3 days rooting, which also occurred with higher endogenous IAA contents (Fig. 5), can be related to cell divisions during the formation of meristematic centers (Figs. 3b and 7), promoting the formation of ARs in *C. fissilis* shoots. Patellin is a plasma membrane-localized protein required for auxin-induced PIN1 localization and multiple developmental processes, and patellin has been verified in different tissues going through mitosis or initiating differentiation (Tejos et al. 2018). The CDC48 protein may regulate endoplasmic reticulum assembly during cytokinesis and may also be involved in cell expansion and differentiation (Park et al. 2008). Thus, we propose that the accumulation of these proteins is related to the accumulation of endogenous IAA and induces the promotion of root initiation in *C. fissilis*.

Moreover, some peroxidases (Ce_fissilis.017405.2 and Ce_fissilis.019038.1) were highly accumulated in shoot cuttings at 3 days of rooting compared to 0 days. It is thought that the oxidative decarboxylation of IAA by plant peroxidases may be involved in controlling the content of endogenous IAA (Savitsky et al. 1999) and thus could be important for AR initiation in *C. fissilis* via the regulation of endogenous auxin contents. In this sense, the higher accumulation of auxin-related proteins (such as chorismate synthase chloroplastic, AIR12, peroxidase 4 and 12), cell division proteins (CDC48 and patellin-3-like) and cell wall modification proteins (EXPB1 and XTH5) can be markers for the initiation of AR in *C. fissilis*.

In addition, inhibition of rooting promoted by inhibitors of polar auxin transport (TIBA) and auxin signaling (PCIB) modulated the accumulation of some proteins that could be related to shoot rooting in *C. fissilis*. Among them, the reduction in the accumulation of the protein serine/threonine-protein phosphatase PP2A-4 catalytic subunit (Ce_fissilis.014280.1) in shoot cuttings at 3 days of treatment with PCIB and TIBA compared to untreated shoot cuttings suggests that this protein is relevant for rooting promotion in this species. PP2A may interact with plasma membrane components and can also interact with PIN proteins (Blakeslee et al. 2008). PINs are transporters acting in the efflux of auxin from cells at the plasma membrane, and their polarity determines the directionality of polarized intercellular auxin flow (Křeček et al. 2009). The polarization of PINs can be regulated by PP2A proteins by dephosphorylation (Li et al. 2011) and hence alter auxin flow and plant patterning (Ballesteros et al. 2013). In addition, the activity of PP2A is reduced in the presence of the N-1-naphthylphthalamic acid auxin transport inhibitor in *Arabidopsis* (Deruere et al. 1999), suggesting that PP2A may play a role in the regulation of auxin transport (Ludwig-Müller et al. 2005). In addition, it was shown that PP2A also acted by dephosphorylating other components of the plasma membrane by regulating their location and possibly their activity, such as that of *Arabidopsis* Crinkly 4 (ACR4). The ACR4 protein is part of a mechanism that controls cell division during the formation of roots in *Arabidopsis* (Yue et al. 2016). In this sense, our results suggest that the inhibition of rooting by the TIBA and PCIB treatments may be related to changes in the dynamics of membrane-associated protein dephosphorylation, which is essential for signal transduction during root development and can affect rooting in *C. fissilis*, dependent on auxin flow. Moreover, the TIBA and PCIB inhibitors affected the accumulation of Vestitone reductase (Ce_fissilis.002557.2) protein related to isoflavonoid metabolism (Table 1). This protein is involved in the biosynthesis of medicarpin, a type of natural isoflavonoid (Guo and Paiva 1995). Some authors have suggested that flavonoids may act as nonessential auxin transport inhibitors (Brown et al. 2001; Peer and Murphy 2007), affecting the localization of PIN proteins (Santelia et al. 2008). In this sense, this protein (Fig. 8) could be related to rooting inhibition in *C. fissilis* via the inhibition of auxin transport and efflux.

In addition to proteins related to auxin, proteins related to carbohydrates are important to provide the energy during cell divisions necessary for AR formation. The reduction in the accumulation of some proteins from the glycolysis and tricarboxylic acid cycle pathways, such as phosphoglycerate kinase cytosolic (Ce_fissilis.016667.1), pyruvate kinase 1 cytosolic (Ce_fissilis.011754.1), xylose isomerase (Ce_fissilis.014702.1) and glyceraldehyde-3-phosphate dehydrogenase cytosolic (Ce_fissilis.011648.1) (Fig. S1), promoted by chemical inhibitors, was related to the inhibition of AR formation and is relevant for energy supplies during AR initiation. These proteins act on the glycolysis pathway and are important for energy production in plant cells (Muñoz-Bertomeu et al. 2009), and during the phase of AR initiation, high levels of energy and carbon skeletons are required to promote cell division and growth (Ahkami et al. 2009; Kromer and Gamian 2000). In addition, the down-accumulation of succinate dehydrogenase subunit 6 mitochondria (Ce_fissilis.015355.1) was observed in shoot cuttings treated with TIBA at 3 days of rooting compared to shoot cuttings at 3 days without TIBA, while the up-accumulation in shoot cuttings at 3 days of rooting compared to shoot cuttings at 0 days of rooting was observed (Table 1). Succinate dehydrogenase, a protein of the tricarboxylic acid cycle pathway (Fig. S1), catalyzes the oxidation of succinate to fumarate (Hagerhall 1997) in the tricarboxylic acid cycle pathway, which, like glycolysis, is involved in the production of energy. In this sense, the reduction in the accumulation of these proteins induced by polar auxin transport and auxin signaling inhibitors, which leads to the inhibition of rooting, suggests the relevance of these proteins to the energy production needed for cell division and differentiation during AR initiation in *C. fissilis* (Fig. 8).

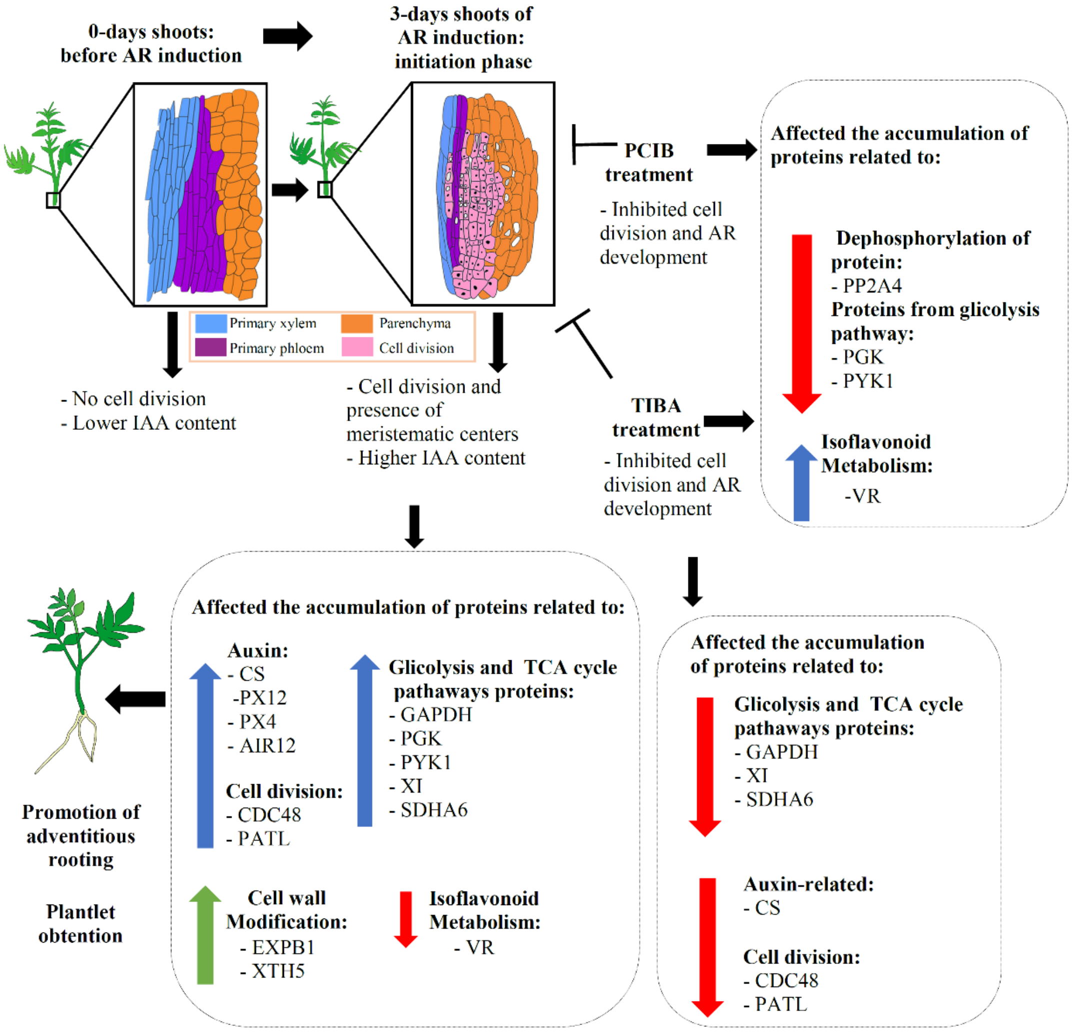

Fig. 8 - Overview of biochemical and proteomic alterations during adventitious root initiation in shoots of *Cedrela fissilis*. The arrow in red indicates down-accumulated proteins. The arrow in blue indicates the up-accumulated proteins. The arrow in green indicates the unique proteins. AIR12, Auxin-induced root culture protein 12 PP2A-4; Protein serine/threonine-protein phosphatase catalytic subunit; CDC48, Cell division cycle protein 48 homolog; EXPB1, Expansin-like B1; CS, Chorismate synthase, chloroplastic; GAPDH, Glyceraldehyde-3-phosphate dehydrogenase, cytosolic; PATL, Patellin-3-like; PGK, Phosphoglycerate kinase; PX12, Peroxidase 12; PX4, Peroxidase 4; PYK1, Pyruvate kinase 1, cytosolic; SDHA6, Succinate dehydrogenase subunit 6, mitochondrial; VR, Vestitone reductase; XI, Xylose isomerase; XTH5, Probable xyloglucan endotransglucosylase/hydrolase protein 5.

Conclusion

The use of IBA is not necessary for ex vitro rooting of in vitro propagated shoot cuttings. The proliferation of meristematic-type cells was observed on the 3rd day of rooting, leading to AR initiation. At this time, the up-accumulation of auxin-related proteins, cell division and unique proteins of cell wall modification was observed and can be markers of AR initiations. The higher accumulation of auxin-related proteins could increase the endogenous IAA content and AR initiation on shoot cuttings on the 3rd day of rooting than on day 0. Proteins related to dephosphorylation and the glycolytic and tricarboxylic acid cycle pathways were up-accumulated and down-accumulated, respectively, in shoot cuttings at 3 days of rooting and were relevant for AR development in this species. These findings reveal that there was a dynamic relationship between auxin-related proteins and IAA contents controlling AR initiation. Our results are the first to show the involvement of highlighted auxin-responsive proteins and endogenous auxin that contribute to the activation of meristematic-type cells, leading to meristematic center formation and AR initiation in micropropagated shoots of *C. fissilis*, an easy-to-root woody species.

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4.2- Polyamines roles on adventitious root formation in micropropagated shoot cuttings of *Cedrela fissilis* Vellozo (Meliaceae)

Resumo

Níveis endógenos de algumas moléculas como auxinas e as poliaminas (PAs), podem estar associados ao controle do enraizamento. No entanto, pouco se sabe sobre como as PAs modulam o enraizamento e se estas interagem com o metabolismo da auxina neste processo morfogenético. Nesse sentido, a elucidação do envolvimento das PAs durante o enraizamento é importante para entender a sua regulação nesse processo em brotações micropropagadas de espécies arbóreas nativas. Desta forma foi investigado o efeito da putrescina (Put) no metabolismo de PAs e sua combinação com inibidores de auxina, o ácido p-clorofenoxiisobutírico (PCIB) e ácido triiodobenzóico (TIBA) no enraizamento *ex vitro* em *C. fissilis*. Observou-se que a aplicação de Put aumenta o comprimento da raiz, mas não o seu conteúdo endógeno, comparativamente ao uso de inibidores de auxina combinados ou não com Put. A porcentagem e o número de brotos enraizados foram significativamente reduzidos pelo tratamento com Put combinado com PCIB ou com TIBA, mostrando que os inibidores de auxina e, não a Put, são os responsáveis pela diminuição do enraizamento. Dessa forma, verificou-se que a Put não está relacionada à indução de enraizamento em *C. fissilis*. Futuras pesquisas devem ser realizadas tentando entender se a formação de aminoácidos, como o ácido γ-aminobutírico (GABA), podem ser desencadeados pela alteração do conteúdo de PAs, e modular o enraizamento nesta espécie.

Palavras-chave: Enraizamento, Inibidor de auxina, Poliaminas, Putrescina.

Abstract

Endogenous levels of some molecules, as polyamines (PAs), can be associated in rooting control. However, little is known about how PAs modulate rooting, and whether they interact with auxin metabolism during this morphogenetic process. In this sense, the elucidation of the involvement of PAs during rooting is essential to understand the regulation of PAs in this process in micropropagated shoots of native tree species. We investigated the effect of putrescine (Put) on PAs metabolism and its combination with auxin of inhibitors p-Chlorophenoxyisobutyric acid (PCIB) and Triiodobenzoic acid (TIBA) on ex vitro root development in *C. fissilis*. We observed that exogeneous Put increases the length of root, but not its endogenous content in relation to auxin inhibitors treatments, and these inhibitors combined with Put. The percentage and number of rooted shoots were significantly reduced by Put plus PCIB or TIBA, showing that auxin inhibitors and not Put are responsible for the decreasing on rooting. Thus, we can infer that Put is not related to rooting induction in *C. fissilis*. Future researches can be carried out trying to understand whether the formation of amino acids, such as γ-aminobutyric acid (GABA), can be triggered by the alteration of PAs content during rooting in this species.

Keywords: Rooting, Auxin inhibitor, Polyamines, Putrescine.

Introduction

Cedrela fissilis Vellozo (Meliaceae), popularly known as “cedro rosa” is native woody species from the Brazilian Atlantic Forest and have been explored for decades. Due to intense exploitation over the years, this species is currently included on the list of threatened species and is placed in the vulnerable category (Barstow 2018). This species has economic and ecological importance and initial studies in vitro propagation have been performed (Nunes et al. 2002, Aragão et al. 2016, Aragão et al. 2017).

The propagation in vitro of forest trees provides a large number of superior clonal plantlet in a short time throughout the year (Shahzad et al. 2017). Among the steps of in vitro propagation, rooting is essential for plantlet production

(Kasthurirengan et al. 2013). In general, to promote the rooting of tree species it is necessary to use a plant growth regulator, especially auxins (Phulwaria et al. 2013). Previous studies has been showed that the use of the exogenous auxin, indole butyric acid (IBA) is not necessary for ex vitro rooting of in vitro propagated shoot cuttings in *C. fissilis* (Ribeiro et al. 2022). In addition, the endogenous contents of indole acid acetic (IAA) accumulated in the base of shoot cuttings during rooting is related to root induction, while the auxin transport or auxin signaling were prevented whit p-Chlorophenoxyisobutyric acid (PCIB) and Triiodobenzoic acid (TIBA) (Ribeiro et al. 2022). The auxin signaling pathway can be impair for PCIB, regulating the stability of the auxin/IAA repressor protein (Aux/IAA) (Oono et al. 2003), while the TIBA is an inhibitor of auxin efflux transport involved in the inhibition of auxin trafficking across membranes (Kleine-Vehn et al. 2006) as well as in blocking the recycling of the PIN-FORMED (PIN) protein between endosomes and plasmatic membranes (Geldner et al. 2001).

In addition to the auxins, endogenous levels of some molecules, such as polyamines (PAs), can be associated to rooting control, and can be used as marker molecules for this process (Couée et al. 2004, Naija et al. 2009). The putrescine (Put), spermidine (Spd) and spermine (Spm) are the most common PAs in plants. In some families or genus of plants, other PAs, as thermospermine, homospermidine, norspermidine, and canavalmine were described (Todorova et al. 2014). It has been showed the involvement of the PAs in the root formation in some species, such as *Quercus suber* and *Vitis vinifera*, demonstrating that Put can be considerated a marker of root development (Neves et al. 2002).

PAs are also involved in various other physiological processes in plants, including organogenesis, senescence, embryogenesis, and stress response (Chen et al. 2018). Due to the cationic nature of PAs, they can interact with negatively charged macromolecules (Kuznetsov and Shevyakova 2007), helping to stabilize protein, nucleic acid, and the plasma membrane (Spormann et al. 2021), including transcription factors, protein kinases and phospholipases (Miller-Fleming et al. 2015), as well as ion transport proteins (Pottosin and Shabala 2014). Other than that, alterations in PA metabolism can impact aminoacids levels in living cells (Majumdar et al., 2016).

Synergistic or antagonistic interactions between plant hormones and PAs are described. Studies have shown that an increase in Put contents may regulate some genes related to IAA biosynthesis, auxin-related transcription factors and other genes related to signal transduction during abiotic stress in transgenic plants of *Arabidopsis thaliana* (Marco et al. 2011). In addition, it was showed that Put modulated the expression of PIN1 and PIN2 auxin transporters in *Arabidopsis* (Hashem et al. 2021). On the other hand, spermine action was related to the regulation of auxin and cytokinins signaling genes (Anwar et al. 2015). Thus, the use of auxin inhibitors, such as TIBA and PCIB, can be an interesting tool in the investigation of the involvement of auxin in PA metabolism.

Although studies show the involvement of PAs in rooting, little is known about how PAs modulate this morphological process, and whether they interact with auxin metabolism. In this sense, the elucidation of the involvement of PAs during rooting is essential to understand the regulation of PAs in this process in micropropagated shoots of native tree species.

Materials and methods

Plant material

Mature seeds of *C. fissilis* obtained from the Caiçara Comércio de Sementes LTDA located in the city of Brejo Alegre, SP, Brazil (21°10’S and 50°10’W).

In vitro seed germination and shoot obtention

For germination, seeds were submitted to a disinfection process according to Ribeiro et al. (2022). Subsequently, seeds were inoculated in MS culture medium (Murashige and Skoog 1962) (PhytoTechnology Laboratories, Overland Park, USA), supplemented with 20 g L^{-1} sucrose (Synth, São Paulo, Brazil) and 2.0 g L^{-1} Phytagel (Sigma-Aldrich, St. Louis, USA). The pH of the culture medium was adjusted to 5.8, and then the medium was autoclaved at 121 °C, at 1.5 atm for 15 min. After inoculation, seeds were maintained in a growth room at 25±2°C under a photoperiod of 16 h, with a light intensity of 55 µmol m^{-2} s^{-1} provided by LED lamps (Koninklijke Philips Electronics NV; Amsterdam, Netherlands).

Sixty-day-old seedlings were used as a source of explants (apical and cotyledonary nodal segments) for the induction of shoots. The explants were inoculated in MS medium supplemented with 20 g L^{-1} sucrose, 2 g L^{-1} Phytagel and 2.5 μM BA (Sigma-Aldrich) according to Nunes et al. 2002). The pH of the culture medium was adjusted to 5.8 and autoclaved at 121 °C, at 1.5 atm for 15 min. After being transferred into the culture medium, the explants were maintained in a growth room at 25±2 °C under a photoperiod of 16 h, with a light intensity of 55 μmol m^{-2} s^{-1} provided by LED lamps (Koninklijke Philips Electronics NV). After 45 days, shoots from apical and cotyledonary nodal segments were used for ex vitro rooting.

Effect of the auxin inhibitors PCIB and TIBA in PAs endogenous contents during ex vitro rooting of micropropagated shoots

The contents of endogenous PA after treatment without and with 800 μM PCIB e 200 μM TIBA, which inhibited rooting according to results previously showed by Ribeiro et al. (2022), were evaluated. Forty-five-day-old in vitro shoot cuttings (1.5 to 2.0 cm) with the apical meristem of the shoots and four main leaves were used. The bases of the shoot cuttings were immersed in 800 μM PCIB and 200 μM TIBA for 90 min according to Ribeiro et al. (2022). After the treatment, the shoot cuttings were transferred to plastic cups (50 ml) containing substrate Basaplant and vermiculite (1:1; v/v), maintained in plastic trays (39.4 x 31.9 x 15.4 cm) (Pleion) covered with PVC-type plastic film (Lumipam) to maintain high relative humidity, and kept in a growth room at 25±2 °C under a photoperiod of 16 h, with a light intensity of 55 μmol m^{-2} s^{-1} provided by LED lamps (Koninklijke Philips Electronics NV). After seven days, to simultaneously achieve the rooting of shoots and acclimatization, the PVC parafilm plastic was perforated until complete removal at 10 days of incubation, according to Ribeiro et al. (2022).

For PA analysis, three biological samples (100 mg fresh matter—FM – each sample) containing the bases (0.5 cm) of shoot incubated in the treatments without inhibitors (control treatment) and with 800 μM PCIB and 200 μM TIBA before (day 0) and after 3, 6, 10 days during rooting were collected and stored at −20 °C until free-PA evaluation.

Free-PA determination

The determination of free PAs was performed according to Santa-Catarina et al. (2006). The samples were initially macerated with liquid nitrogen, and then with 0.6 mL of 5% (v/v) perchloric acid (Merck), incubated at ice for 1 h and centrifuged at 16,000 x g for 20 min at 4 °C. Then, the free PAs were derived by dansyl chloride (Merk). The PAs were partitioned with 200 µL of toluene (Merk), and 175 µL of the apolar (organic) phase, containing the PAs, was collected, dried under a nitrogen jet, and resuspended in 175 µL of absolute acetonitrile (Merk). Identification and quantification was performed by high-performance liquid chromatography (HPLC) (Shimadzu, Kyoto, Japan) with reverse phase C18 column (Shimadzu Shim-pack CLC ODS) of 5 µm. As solvent, 10% acetonitrile in water, pH 3.5 adjusted with 1N HCl (Merk) and absolute acetonitrile (Merk) were used. The absolute acetonitrile gradient was programmed to 65% for the first 10 min, increased from 65 to 100% between 10 and 13 min and 100% to 21 min with 1 mL min^{-1} flow at 40 °C. The PA concentration was determined using the fluorescence detector was set for excitation at 340 nm and emission at 510 nm. Peak areas and retention times of each sample were evaluated by comparison with standard PAs Put, Spd and Spm (Sigma-Aldrich).

Effect of the Put on ex vitro rooting of micropropagated shoots

Forty-five-day-old in vitro shoot cuttings (1.5 to 2.0 cm) containing the apical meristem and four main leaves were used. The bases of the shoot cuttings were immersed in different concentrations of Put (1 and 5 mM) for 90 min. After, the shoot cuttings were transferred to substrate and incubated under the same conditions previously described by Ribeiro et al (2022).

Each treatment was composed of eight replicates, with five shoot cuttings per replicate, in a total of forty shoot cuttings per treatment. After 13 days, the percentage of rooted shoot cuttings, the number and length (cm) of roots per shoot cutting were evaluated.

Effect of the auxin inhibitors PCIB and TIBA combined with exogenous Put on ex vitro rooting and endogenous PAs contents in micropropagated shoots

In vitro shoot cuttings (1.5 to 2.0 cm) with the apical meristem of the shoots and four main leaves from forty-five-day-old were used. The bases of the shoot cuttings were immersed in 800 µM PCIB, 200 µM TIBA, 5 mM Put, 5 mM Put combined with 800 µM PCIB or 200 µM TIBA for 90 min.

After, the shoot cuttings were transferred substrate and incubated under the same conditions previously described by Ribeiro et al (2022).

Three biological samples (100 mg FM each sample) containing the bases (0.5 cm) of shoot incubated in the treatments described before (day 0) and after 3, 6, 10 days during rooting were collected and stored at −20°C until free-PA analysis.

Statistical analysis

The data were presented by analysis of variance (ANOVA) ($P < 0.05$), and the means were compared using a Student–Newman–Keuls (SNK) test (Sokal and Rohlf 1995) with program R Foundation for Statistical ComPuting, version 3.1.1, 2014, Vienna, Austria (R Core 2018).

Results

Effect of the auxin inhibitors PCIB and TIBA on endogenous free-PAs contents during ex vitro rooting

As the treatment with 800 µM PCIB e 200 µM TIBA induced a reduction on rooting in *C. fissilis* cuttings, the endogenous contents of free PAs Put, Spd and Spm were analyzed in shoots cuttings from cotyledonary nodal segments treatment without and with 800 µM PCIB and 200 µM TIBA (Fig 1). Among the analyzed PAs, the endogenous free-Put contents were increased in the shoot cuttings treated with 800 µM PCIB or 200 µM TIBA in 3rd, 6rd and 10th of rooting (Fig 1a). Free-Spd content was not affected by the TIBA and PCIB treatments (Fig 1b), while lower Spm contents was verified in shoots on the 3rd and 6th day of rooting treated with PCIB and TIBA (Fig 1c).

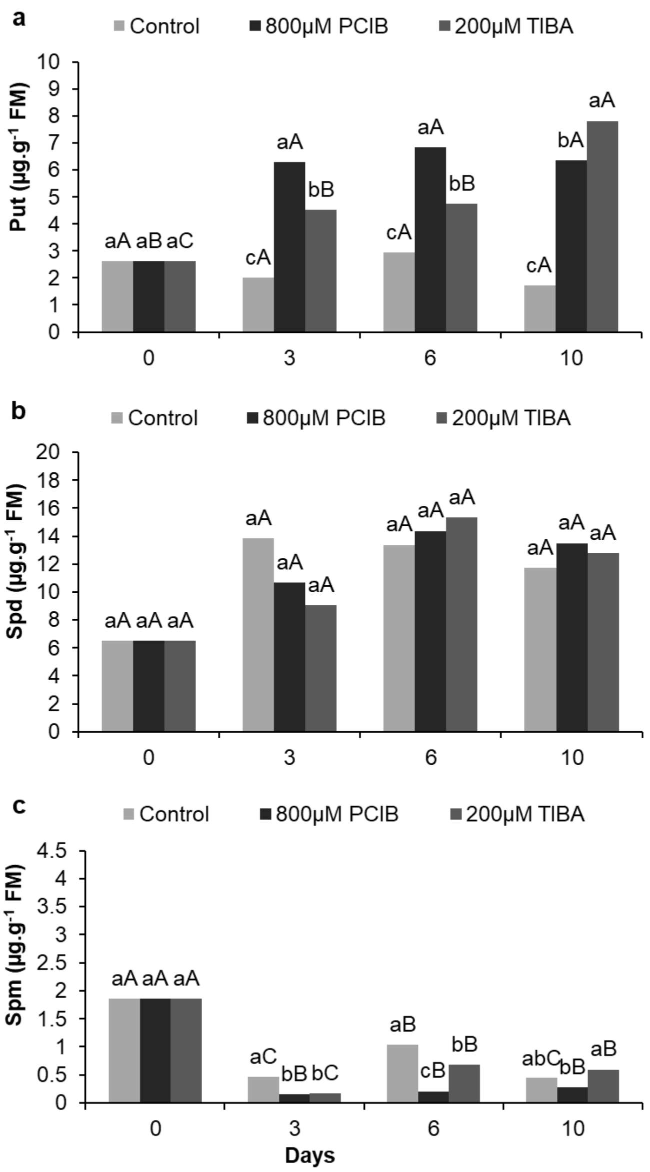

Fig. 1 – Free contents (µg.g^{-1} FM) of putrescine (a), spermidine (b) and spermine (c) in *C. fissilis* shoots before (time 0) and after 3, 6 and 10 days of rooting in the control, 200 µM of TIBA and 800 µM of PCIB treatments. Means followed by the same letter do not differ statistically from each other according to the SNK test (P<0.05). Different capital letters show significant differences comparing the days of rooting in each treatment. Different lowercase letters show significant differences comparing treatments on each rooting day. CV = coefficient of variation. FM = fresch matter; Put = putrescine; Spd = spermidine; Spm = spermine. (n = 3, CV a = 17.5%, CV b = 15.6%, CV c = 16.4%).

Effect of the Put on ex vitro rooting

As the free-Put contents were increased in the shoots cutting treatment with PCIB and TIBA during rooting (Fig 1a), we evaluated the effect of Put on rooting of shoot cuttings from cotiledonary nodal segments. The treatment of Put did not affected significantly the root induction (Fig 2a), root number (Fig 2b) and root length (Fig 3c), while the shoot cuttings treated with 5mM Put showed a significant increase in the length of the roots (Fig 2c).

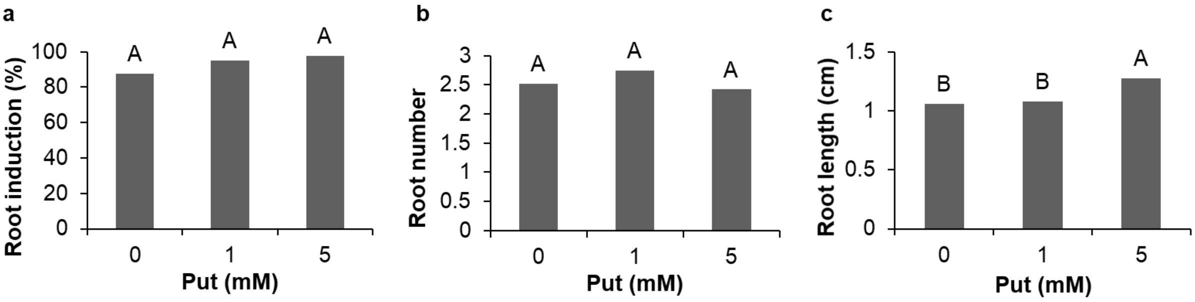

Fig. 2- Percentage of rooted shoot cuttings (a), number (b) and length (c) of roots per shoot cuttings of *Cedrela fissilis* at 13 days of rooting. Means followed by the same letter do not differ statistically according to the SNK test (P<0.05). CV = coefficient of variation. Put = putrescine. (n = 8; CV a = 9.64%, CV b = 16.11%, CV c = 12.93%).

Effect of the Put, combined or not with PCIB and TIBA auxin inhibitors, on ex vitro rooting

Shoot cuttings of *C. fissilis* in 5mM of Put showed a significant increase in the length of the roots (Fig 2c). In this sense, the effects of the Put and your combination auxin signaling inhibitor PCIB and the auxin transport inhibitor TIBA on rooting were evaluated using shoot cuttings from cotyledonary nodal segments. The percentage of rooted shoot cuttings (Fig 3a) and number of roots per shoot cutting (Fig 3b) were significantly reduced by Put treatment combined with PCIB or TIBA, while the length of roots was significantly increased by Put treatment (Fig 3c).

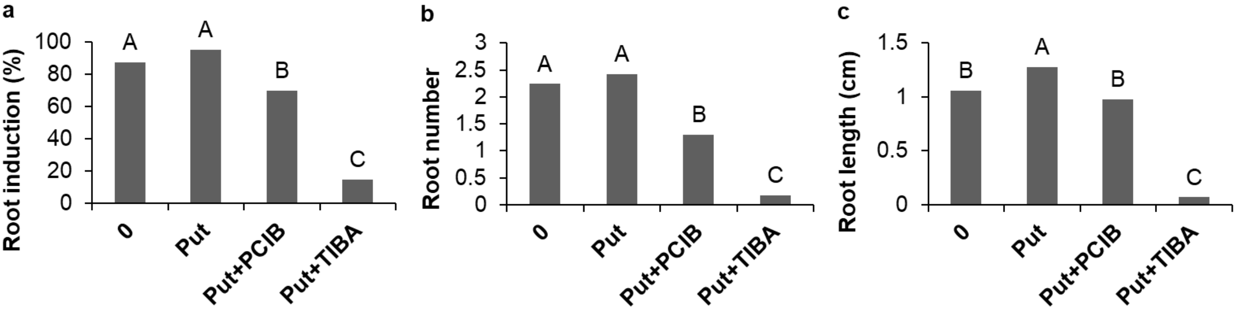

Fig. 3- Percentage of rooted shoot cuttings (a), number (b) and length (c) of roots per shoot cuttings of *Cedrela fissilis* at 13 days of rooting. Means followed by the same letter do not differ statistically according to the SNK test ($P < 0.05$). CV = coefficient of variation. Put = putrescine. PCIB = p-

Chlorophenoxyisobutyric acid. TIBA = Triiodobenzoic acid. (n = 8; CV a = 15.80%, CV b = 24.49%, CV c = 18.83%).

Effect of Put, combined or not with auxin inhibitors, on endogenous PAs contents

The endogenous contents of free PAs Put, Spd and Spm were analyzed in shoot cuttings from cotyledonary nodal segments treatment without and with 5mM Put, combined or not with PCIB or TIBA (Fig 4). Among the analyzed PAs, the endogenous free-Put contents increased at 3rd day of rooting in shoot cuttings under 800 µM PCIB treatment, but it does not differ statistically from TIBA. In 6rd of rooting, the shoots cuttings treated with Put+PCIB showed higher put content, while in 10th of rooting this result was observed in the treatment of TIBA or PCIB (Fig 4a).

Higher content of free-Spd was observed in shoot cuttings treated with Put+TIBA on the 3rd and 6th day of rooting, while on the 10th day the highest Spd content was observed in the PCIB or TIBA treatment (Fig 4b). The treatment of Put combined with PCIB or TIBA reduced the endogenous contents of free-Spm compared to shoot cuttings before root induction (Fig 4c).

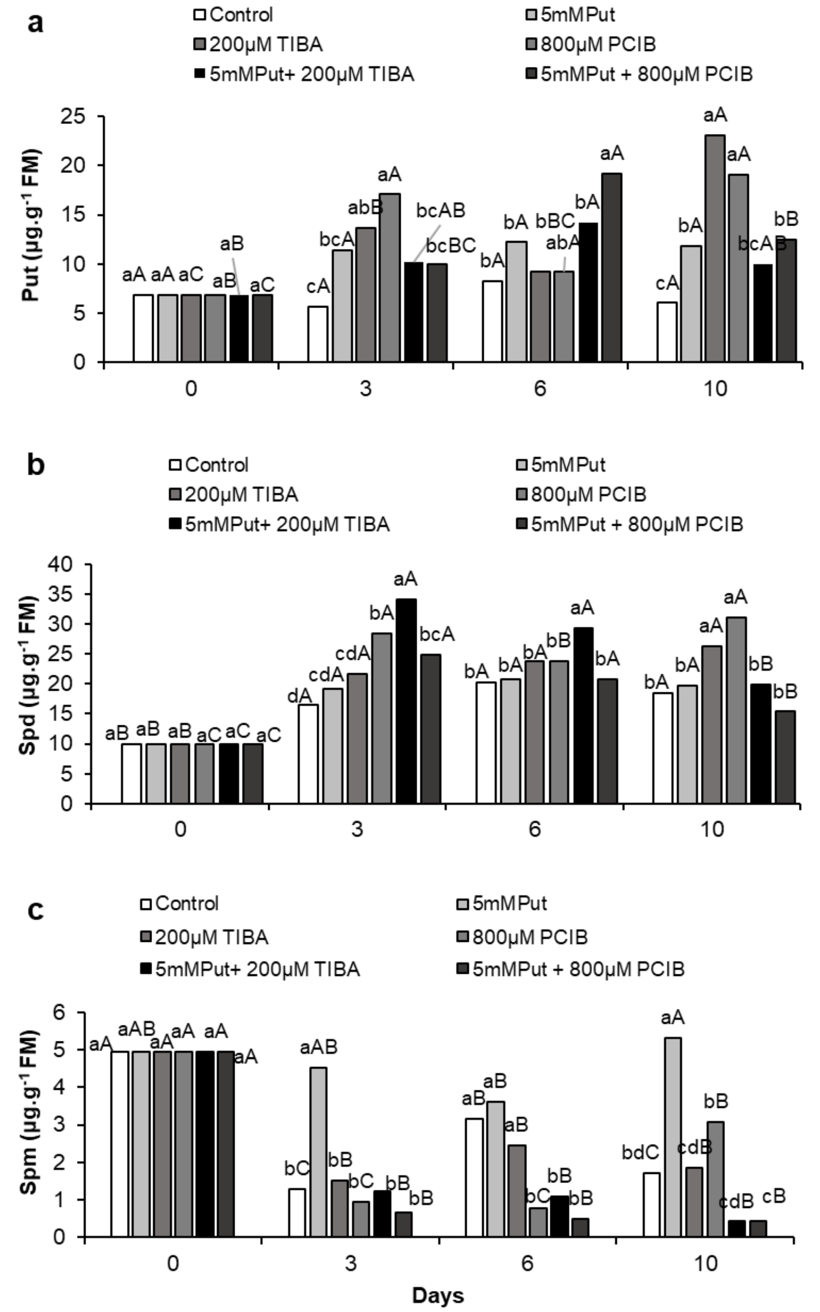

Fig. 4 – Endogeous content (μg.g^{-1} MF) of putrescine (a), spermidine (b) and spermine (c) in *C. fissilis* shoot cuttings before (time 0) and after 3, 6 and 10 days of rooting in the control, 200 μM TIBA, 800 μM PCIB, 5mM Put, 5mM Put combined 200 μM TIBA or 800 μM PCIB treatments. Means followed by the same letter do not differ statistically from each other according to the SNK test (P<0.05). Different capital letters show significant differences comparing the days of rooting in each treatment. Different lowercase letters show significant differences comparing treatments on each rooting day. CV = coefficient of variation. FM = fresh matter; Put = putrescine; Spd = spermidine; Spm = spermine. (n = 3, CV a = 25%, CV b = 15.38%, CV c = 27.16%).

Discussion

The rooting of shoot cuttings is an important step in micropropagation process, fundamental for production of plantlets. In *C. fissilis*, the rooting of shoots can be achieved in absence of exogenous auxin treatment, such as the indole-3-butyric acid (IBA), being endogenous levels of auxin enough to promote this morphological process (Ribeiro et al. 2022). PAs also play an important role on rooting, and studies show a possible interaction with auxin (Tonon et al. 2001). Our work showed an increase on endogenous contents of free-Put in shoot cuttings treated with 800 µM PCIB and 200 µM TIBA in 3rd, 6rd and 10th days of rooting. On the other hand, shoots of *C. fissilis* maintained in the control treatment, where the greater rooting was observed, there was a lower content of this PA (Fig 1a). Similarly, in *Pyrus communis* cv Doyenne d´Hiver an increase of Put level was associate to rooting reduction (Baraldi et al. 1995). In contrast, studies show that Put accumulation is associated with rooting promotion in some species, such as *Pinus strobus* (Fei et al. 2016), *Quercus suber*, *Vitis vinifera* (Neves et al. 2002) and *Fraxinus angustifolia* (Tonon et al. 2001). Although studies suggest that the accumulation of PAs may be associated with the promotion of rooting and Put with cell division during this process (Couée et al. 2004), in *C. fissilis* the relationship of this PA with rooting was not direct related, once there was a higher Put content in shoot cuttings treated with TIBA and PCIB inhibitors (Fig. 1a), in which a significant reduction in rooting was observed, compared to the control, according to results previously showed by Ribeiro et al. (2022).

However, we do not know whether the endogenous content of Put is related to auxin and whether it is associated with inhibition of rooting. Thus, we analyzed the effect of Put, combined or not with auxin inhibitors TIBA and PCIB, on rooting of shoot cuttings, and its effects on endogenous content of PAs in these treatments. The percentage of rooted shoots (Fig 3a) and number of roots per shoot cuttings (Fig 3b) were significantly reduced in shoots under Put combined with auxin inhibitos (Put + PCIB and Put +TIBA) treatments, while the length of roots was significantly increased by Put treatment (Fig 3c). Thus, we observed that auxin inhibitors and not Put are responsible for decreasing rooting. These results also corroborate with the endogenous Put content data (Fig 4a). The endogenous free-Put contents increased in the shoot cuttings treated with 800 µM PCIB in 3rd and 6rd days of rooting he shoots cuttings treatment with Put+PCIB had higher Put content, while in 10th of rooting this result was observed in the treatment of TIBA or PCIB. Thus, we suggest that the increase in endogenous Put content may be the result of the auxin inhibitors effect and not the cause of the root inhibition, being Put not related to inhibition of rooting in *C. fissilis*.

Alterations in PA metabolism can impact aminoacids levels in living cells (Majumdar et al. 2016). Homeostasis of PAs, which adjusts the levels of Put, Spd and Spm, is regulated by reprogramming the anabolic and catabolic pathways of this molecule's metabolism. A substantial part of the effects of PA can be attributed to its catabolites, such as γ-aminobutyric acid (GABA), which in plants is produced via decarboxylation of glutamate or by a two-step catabolization of Put. According to Shelp et al. (2012), an increase on expression of diamine oxidase (DAO) can lead to an increase on GABA production. GABA inhibits malate efflux from roots by a direct binding to the anion transporter aluminium-activated malate transporters (ALMT1) (Ramesh et al. 2015), causing hyperpolarization in *Hordeum vulgare* roots (Shabala et al. 2014). In addition, data show that GABA negatively regulates development of adventitious roots in *Populus* (Xie et al. 2019). In *Brassica napus* endogenous GABA content contributed to the decrease the primary root growth (Deleu et al., 2013). In this sence, a higher content of Put can inhibit the rooting by increase on GABA from its catabolism, and further studies can be developed during AR induction in *C. fissilis*. Interestingly, in maize mesocotyl epidermal tissues, it has been showed that the auxina inhibitors TIBA and naphthylphtalamic acid (NPA) increased the expression of polyamine oxidase (PAO), an enzyme of PAs catabolism, after treatment with light and reverted by exogenously supplied auxin, showing like this that both light and auxin adjust PAO expression in cell wall differentiation (Cona et al. 2003). Moreover, Put depletion affects root phenotype through the antagonistic actions of hormonal signaling, with auxin and reactive oxygen species accumulation (Hashem et al. 2021). In this sence, as our data shows more Put content in the presence of auxin inhibitors treatments during shoot rooting in *C. In fissilis*, we can suggest that it can affect the metabolism of some amino acids, such as GABA, trigged by the alteration of PAs content, especially Put. Therefore, it is likely that the perturbation of any PAs will result in the rebalancing of its biosynthesis and affect phenotype outcomes by multiple direct and indirect pathways. Future research can be carried out trying to understand whether intracellular the formation of amino acids, such as GABA, can be triggered by the alteration of PAs content during rooting in *C. fissilis*, and its involviment with rooting.

Conclusion

The percentage and number of roots in shoot cuttings was significantly reduced by Put + PCIB and Put +TIBA treatments, and not affected by Put treatments. The endogenous free-Put contents increased in the shoot cuttings treated with TIBA or PCIB at 10th of rooting. Thus, we can infer that Put is not related to rooting induction, but can affect the length of roots, in *C. fissilis*.

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5- Considerações finais

A formação de raízes adventícias é essencial para a obtenção de mudas pela micropropagação, uma ferramenta biotecnológica que pode ser aplicada para a propagação de plantas, incluindo espécies arbóreas de importância econômica e ecológica, como *C. fissilis*. Neste sentido, foram realizados estudos visando estabelecer o enraizamento *ex vitro* e entender o envolvimento da auxina, proteínas diferencialmente acumuladas e PAs em brotações micropropagadas na espécie de estudo.

No primeiro capítulo foi mostrado que o uso de AIB não é necessário para o enraizamento *ex vitro* de brotações propagadas *in vitro*, podendo ser obtidas mudas com alta percentagem de enraizamento sem adição de auxina exógena. Por meio de análise histológica observamos a proliferação de células com características meristemáticas no 3º dia de enraizamento, que caracterizam o início do da formação de RAs. Neste momento, o acúmulo de proteínas relacionadas à auxina, divisão celular e à modificação da parede celular foram observadas e podem ser proteínas marcadoras de iniciação de RA. O maior acúmulo de proteínas relacionadas à auxina poderia aumentar o conteúdo de ácido indol acético (AIA) endógeno e a iniciação de RA nos brotos no 3º dia de enraizamento em relação às brotações antes de indução do enraizamento (tempo 0). Além disso, o acúmulo de proteínas relacionadas à desfosforilação e as vias do ciclo dos ácidos glicolítico e tricarboxílico foram relevantes para o desenvolvimento de RA nesta espécie. Os resultados obtidos mostram que houve uma relação dinâmica entre as proteínas relacionadas à auxina e os conteúdos de AIA controlando a iniciação do RA. Estes resultados são os primeiros a mostrar o envolvimento de proteínas responsivas a auxina endógena que contribuem para a ativação de células do tipo meristemática, levando à formação de centros meristemáticos e iniciação de RA em brotos micropropagados de *C. fissilis*. Ademais, este capítulo mostrou resultados inéditos para a espécie alvo de estudo ao mostrar que o enraizamento *ex vitro* é uma possibilidade viável para a produção de mudas, permitindo assim a redução nos custos de produção de mudas ao aplicar a metodologia estabelecida devido a realização simultânea do enraizamento das brotações e a aclimatização das mudas. Desta forma, este estudo contribui significativamente aos estudos em andamento com a espécie alvo no grupo de pesquisa. Além do conhecimento científico gerado, é importante ressaltar que mudas obtidas durante estes estudos foram doadas para a reserva ecológica da União (dados não apresentados) visando contribuir com o estabelecimento de corredores ecológicos entre remanescentes florestais da Mata Atlântica, contribuindo assim com a recuperação ambiental.

No segundo capítulo foi mostrado que as brotações tratadas com 5mM de Put apresentaram aumento significativo no comprimento das raízes, enquanto a porcentagem e número de brotos enraizados foi significativamente reduzida quando a Put foi combinada com os inibidors PCIB ou TIBA. Estes resultados mostram que os inibidores de auxina, e não a Put, são responsáveis pela diminuição do enraizamento nesta espécie. Pode-se inferir que o acúmulo de Put endógena induzido pelo TIBA e PCIB, não está relacionado à inibição do enraizamento, assim como o tratamento com Put exógena não promoveu aumento na indução de enraizamento. Estudos futuros devem ser realizados buscando entender se a formação de aminoácidos, como o ácido γ-aminobutírico (GABA), um produto do catabalismo de PAs, pode ser desencadeada pela alteração do conteúdo de PAs durante o enraizamento em *C. fissilis*.

Os estudos realizados nos dois capítulos abrem novas perspectivas sobre a relação de biomoléculas relacionadas ao complexo processo de enraizamento. Além das ferramentas descritas no presente trabalho, outras podem ser sugeridas, como análises moleculares, visando desvendar processos desconhecidos, agregando maior conhecimento científico, além de possibilitar mais caminhos para a conservação e propagação de espécies ameaçadas de extinção.

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Apêndice

Apêndice – Capítulo 1: Involvement of differentially accumulated proteins and endogenous auxin in adventitious root formation in micropropagated shoot cuttings of *Cedrela fissilis* Vellozo (Meliaceae)

Supplementary table. Complete list of all identified proteins during rooting of *Cedrela fissilis* shoot cuttings from cotyledonary nodal segments before (0 days) and after 3 days of rooting (3-days/0-days comparison) and in shoot cuttings at 3 days of rooting treated with PCIB (3-days PCIB/3-days comparison) and with TIBA (3-days TIBA/3-days comparison) compared to nontreated shoots at 3 days of rooting.

Accession	Reported peptides	Max score	Description	Average				t-Test	Log2 of Fold Change	Differential accumulation	t-Test	Log2 of Fold Change	Differential accumulation	t-Test	Log2 of Fold Change	Differential accumulation
				0-days	3-days	3-days PCIB	3-days TIBA	3-days/0-days	3-days/0-days	3-days/0-days	3-days PCIB/3-days	3-days PCIB/3-days	3-days PCIB/3-days	3-days TIBA/3-days	3- days TIBA/3-days	3-daysTIBA/3-days
Ce_fissilis.012078.2	31	57818.93	Actin-97	44075	182755	314854	318145	0.002747985	2.051865761	UP	0.011259808	0.784773667	UP	0.002978358	0.799778667	UP
Ce_fissilis.000575.1	15	5832.30	NADPH-dependent aldo-keto reductase, chloroplastic	39802	87052	184202	142379	0.021199194	1.129029321	UP	0.009908658	1.081342509	UP	0.030478807	0.709792395	UP
Ce_fissilis.013428.1	18	11918.07	Probable aldehyde dehydrogenase	74715	130575	220078	200311	0.026112045	0.805402034	UP	0.009404534	0.753136829	UP	0.005101687	0.617366813	UP
Ce_fissilis.014837.1	10	2373.00	Protochlorophyllide reductase, chloroplastic	15967	66428	114802	102122	0.000225601	2.056699169	UP	0.007484497	0.789289032	UP	0.037257701	0.620441432	UP
Ce_fissilis.005901.1	10	15634.33	Putative methyltransferase DDB_G0268948	23935	253043	588190	416538	0.004115822	3.402168762	UP	0.002107178	1.216899964	UP	0.025373656	0.71906632	UP
Ce_fissilis.016610.2	8	2739.10	12-oxophytodienoate reductase 2	27253	96464	192805	136587	0.000218406	1.823568937	UP	0.000965511	0.99908491	UP	0.066249596	0.501763112	UNCHANGED
Ce_fissilis.013428.3	21	12047.43	Delta-1-pyrroline-5-carboxylate dehydrogenase 12A1, mitochondrial	51750	98708	149917	135817	0.016498537	0.931608778	UP	0.004586216	0.60292552	UP	0.016089726	0.460428491	UNCHANGED
Ce_fissilis.013186.1	7	4945.05	Heat shock cognate 70 kDa protein	12676	47238	0	22502	0.002167541	1.897807174	UP	0.000611941	-	Unique 3-days	0.01121697	-1.069886829	DOWN
Ce_fissilis.015354.1	9	4755.53	1-aminocyclopropane-1-carboxylate oxidase	20906	89564	91993	210232	0.000273366	2.099003449	UP	0.869228109	0.038606504	UNCHANGED	0.004267702	1.230990875	UP
Ce_fissilis.008918.1	9	11047.23	Calmodulin	9062	18883	27196	31651	0.006709595	1.059178985	UP	0.000396351	0.526249867	UNCHANGED	0.000709171	0.745134716	UP
Ce_fissilis.015771.1	10	4971.17	Peroxidase 21	12439	152255	197878	290031	0.000669718	3.613564291	UP	0.438532789	0.378119025	UNCHANGED	0.023867863	0.929712188	UP
Ce_fissilis.017791.1	15	21490.91	Uncharacterized isomerase BH0283	146613	488511	634142	747170	3.87797E-05	1.736381405	UP	0.069314094	0.376413096	UNCHANGED	0.009348187	0.613045499	UP
Ce_fissilis.018860.1	12	8392.27	14-3-3 protein 7	15300	91844	111813	86435	0.0272502	2.585617223	UP	0.613370157	0.283830544	UNCHANGED	0.839999825	-0.08757953	UNCHANGED
Ce_fissilis.013260.1	5	1221.27	1-aminocyclopropane-1-carboxylate oxidase	2451	26368	30429	18162	4.71479E-06	3.427323925	UP	0.271461286	0.206676151	UNCHANGED	0.012483692	-0.537862132	UNCHANGED
Ce_fissilis.012656.1	5	1838.32	26S proteasome non-ATPase regulatory subunit 14 homolog	15424	96719	95607	83891	9.14745E-06	2.64864459	UP	0.916502869	-0.01669306	UNCHANGED	0.088621316	-0.205282271	UNCHANGED
Ce_fissilis.012358.1	7	4269.01	26S proteasome non-ATPase regulatory subunit 4 homolog	104949	231599	234477	234882	0.000241739	1.141945878	UP	0.7927993	0.017815331	UNCHANGED	0.835167413	0.020305077	UNCHANGED
Ce_fissilis.015976.1	2	537.52	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, chloroplastic	13479	20593	30320	28580	0.022719645	0.611417198	UP	0.066006865	0.558115297	UNCHANGED	0.142368154	0.472858425	UNCHANGED
Ce_fissilis.0	12	4077.	2-dehydro-3-deoxyphosphooctonate aldolase	37595	65868	59774	62422	0.00473	0.8090101	UP	0.17341	-0.140055285	UNCHANGED	0.64738	-	UNCHANGED

04678.1		78	1					4626	54		3053			8107	0.077505725	
Ce_fissilis.004200.1	10	3276.27	2-keto-3-deoxy-L-rhamnonate aldolase	38379	100667	130236	148529	0.000148062	1.39120415	UP	0.06988347	0.371535576	UNCHANGED	0.001970317	0.561148323	UNCHANGED
Ce_fissilis.017839.2	15	8671.73	2-keto-3-deoxy-L-rhamnonate aldolase	83002	198639	309611	296258	0.00648214	1.258933606	UP	0.052532406	0.640307585	UNCHANGED	0.050880268	0.576703106	UNCHANGED
Ce_fissilis.004682.1	6	560.94	2-oxoisovalerate dehydrogenase subunit alpha 2, mitochondrial	23635	69659	67338	65499	0.000427196	1.559404276	UP	0.399922779	-0.048905236	UNCHANGED	0.51761163	-0.088850981	UNCHANGED
Ce_fissilis.011358.1	5	801.31	3-dehydroquinate synthase, chloroplastic	10938	36671	38794	47679	0.002052295	1.745308126	UP	0.710929449	0.081176445	UNCHANGED	0.034189605	0.37869016	UNCHANGED
Ce_fissilis.015244.1	4	1821.64	3-deoxy-manno-octulosonate cytidylyltransferase, mitochondrial	9751	56868	62669	58557	1.29559E-06	2.544041482	UP	0.185403969	0.140135167	UNCHANGED	0.673663794	0.042227395	UNCHANGED
Ce_fissilis.005743.2	3	764.14	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	40760	73821	64951	75643	0.015481182	0.856894054	UP	0.252998492	-0.184680931	UNCHANGED	0.827139189	0.035171048	UNCHANGED
Ce_fissilis.010435.1	14	2465.75	3-isopropylmalate dehydratase large subunit, chloroplastic	40322	88600	96126	94014	0.002447953	1.135736238	UP	0.442829661	0.117630575	UNCHANGED	0.554242081	0.085569328	UNCHANGED
Ce_fissilis.009079.1	26	14940.47	3-ketoacyl-CoA thiolase 2, peroxisomal	92888	578380	695219	710908	0.00062043	2.638450079	UP	0.079100971	0.265450306	UNCHANGED	0.061241874	0.297644302	UNCHANGED
Ce_fissilis.000736.1	5	775.68	3-phosphoshikimate 1-carboxyvinyltransferase, chloroplastic	32450	58599	57069	67961	0.009039849	0.852665242	UP	0.848759556	-0.038177115	UNCHANGED	0.332068779	0.213835376	UNCHANGED
Ce_fissilis.011006.1	6	15340.14	40S ribosomal protein S12	341852	577490	623079	622943	0.001667153	0.756424463	UP	0.209971617	0.109617525	UNCHANGED	0.172403607	0.109302592	UNCHANGED
Ce_fissilis.001412.1	3	1139.95	4-coumarate--CoA ligase 1	9686	88684	91683	117175	0.001313572	3.194679906	UP	0.905748027	0.047983249	UNCHANGED	0.046900545	0.401913199	UNCHANGED
Ce_fissilis.001903.1	46	21018.22	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1	94148	1370720	1185466	1057392	2.73208E-05	3.863853039	UP	0.398583467	-0.209479053	UNCHANGED	0.046550189	-0.374423229	UNCHANGED
Ce_fissilis.007799.1	9	8617.27	60S ribosomal protein L12	10818	400794	384849	286012	0.000339482	5.211391449	UP	0.837004709	-0.058568862	UNCHANGED	0.089638579	-0.486782191	UNCHANGED
Ce_fissilis.003688.1	7	11635.94	6-phosphogluconate dehydrogenase, decarboxylating 1	14014	244119	181923	190179	0.002340392	4.122653668	UP	0.137844271	-0.424260498	UNCHANGED	0.224747738	-0.360223494	UNCHANGED
Ce_fissilis.000080.1	25	19488.88	6-phosphogluconate dehydrogenase, decarboxylating 2	31802	418728	350906	377067	0.002959633	3.718825508	UP	0.321844692	-0.254927098	UNCHANGED	0.56536764	-0.151191527	UNCHANGED
Ce_fissilis.000080.2	22	16001.39	6-phosphogluconate dehydrogenase, decarboxylating 2	14734	221442	202197	206106	0.000993194	3.909714229	UP	0.512802585	-0.13116979	UNCHANGED	0.628791755	-0.103545086	UNCHANGED
Ce_fissilis.018223.1	17	2498.03	6-phosphogluconate dehydrogenase, decarboxylating 3, chloroplastic	72620	134528	125945	123043	0.00193149	0.889454399	UP	0.305224035	-0.095110112	UNCHANGED	0.33295285	-0.128742834	UNCHANGED
Ce_fissilis.007385.1	5	601.06	Acetyl-coenzyme A synthetase, chloroplastic/glyoxysomal	13986	46902	46541	59848	0.001443321	1.745645424	UP	0.960859635	-0.011154149	UNCHANGED	0.039366093	0.351663706	UNCHANGED
Ce_fissilis.013329.1	31	17375.40	Aconitate hydratase 1	117156	234285	236504	193400	0.004472651	0.999835062	UP	0.966326599	0.013598309	UNCHANGED	0.062211424	-0.276672243	UNCHANGED
Ce_fissilis.006429.1	10	15881.50	Aconitate hydratase 2, mitochondrial	4732	58776	43418	45338	3.7105E-05	3.634793348	UP	0.233744924	-0.436924591	UNCHANGED	0.035074675	-0.374513537	UNCHANGED
Ce_fissilis.013330.1	32	17451.35	Aconitate hydratase, cytoplasmic	102037	316194	343670	298056	0.000412706	1.631714693	UP	0.686744723	0.120212873	UNCHANGED	0.254077056	-0.085230191	UNCHANGED
Ce_fissilis.014659.1	20	7442.82	Aconitate hydratase, cytoplasmic	9574	269068	260728	197593	6.58583E-06	4.812689655	UP	0.891281727	-0.045428205	UNCHANGED	0.013587233	-0.445437742	UNCHANGED
Ce_fissilis.0	19	36677	Actin	12211	28190	184964	352615	0.01904	1.2070005	UP	0.08181	-0.607978162	UNCHANGED	0.14671	0.32286	UNCHANGED

14799.1		.60		4	8			6518	76		6303			5507	645	
Ce_fissilis.011695.1	7	2096.08	Acyl-coenzyme A oxidase 4, peroxisomal	12725	61928	71735	69073	0.001255301	2.282913601	UP	0.308329694	0.212078634	UNCHANGED	0.358663771	0.157520748	UNCHANGED
Ce_fissilis.014541.1	16	18020.24	Adenosine kinase 2	406627	690467	713183	688641	0.006748196	0.763865219	UP	0.694873595	0.046700636	UNCHANGED	0.972967613	-0.003819274	UNCHANGED
Ce_fissilis.014748.1	15	31206.21	ADP-ribosylation factor 2	407127	831212	672798	833957	0.008590508	1.029738148	UP	0.058901596	-0.305042766	UNCHANGED	0.962562687	0.004756461	UNCHANGED
Ce_fissilis.005239.1	23	7607.49	Alanine aminotransferase 2, mitochondrial	80054	243184	266659	257003	0.000519633	1.603010241	UP	0.420230113	0.132948796	UNCHANGED	0.378997329	0.079733075	UNCHANGED
Ce_fissilis.007668.1	9	1409.79	Alanine--glyoxylate aminotransferase 2 homolog 1, mitochondrial	7739	74096	104247	75901	0.000187637	3.259147231	UP	0.103034076	0.492548491	UNCHANGED	0.849409332	0.034723437	UNCHANGED
Ce_fissilis.002415.1	19	18761.49	Alcohol dehydrogenase	20018	313649	256140	170664	0.005323696	3.969810595	UP	0.357290325	-0.292216506	UNCHANGED	0.062674064	-0.877995162	UNCHANGED
Ce_fissilis.002414.1	13	14938.77	Alcohol dehydrogenase 2	91526	581100	617982	558986	5.93039E-05	2.666534746	UP	0.550381757	0.088778545	UNCHANGED	0.65799145	-0.055974667	UNCHANGED
Ce_fissilis.002416.1	12	5735.61	Alcohol dehydrogenase class-3	98768	250365	285389	300136	0.005932284	1.341913063	UP	0.216735942	0.188897318	UNCHANGED	0.146046521	0.26158284	UNCHANGED
Ce_fissilis.019019.1	9	25291.08	Alcohol dehydrogenase class-P	201315	408150	482743	362562	0.030073915	1.019644977	UP	0.267364593	0.24215579	UNCHANGED	0.429920308	-0.1708711	UNCHANGED
Ce_fissilis.004732.1	23	18159.67	Aldehyde dehydrogenase family 2 member B7, mitochondrial	395684	829593	940037	939327	0.006253216	1.0680564	UP	0.069675294	0.180313799	UNCHANGED	0.131788152	0.179223223	UNCHANGED
Ce_fissilis.012511.1	3	1460.05	Arginase 1, mitochondrial	7685	60296	80883	49914	0.014296162	2.971934499	UP	0.316098598	0.423776918	UNCHANGED	0.527938898	-0.272594295	UNCHANGED
Ce_fissilis.015643.1	5	646.20	Aspartate aminotransferase, chloroplastic	14757	27243	25221	25322	0.010326495	0.884426406	UP	0.662755245	-0.111211143	UNCHANGED	0.515926923	-0.105477019	UNCHANGED
Ce_fissilis.018656.1	12	2461.95	Aspartate aminotransferase, cytoplasmic	41610	89338	105902	97833	0.004117534	1.102362229	UP	0.083549978	0.245372308	UNCHANGED	0.307351505	0.131043366	UNCHANGED
Ce_fissilis.009153.1	10	2132.68	Aspartate-semialdehyde dehydrogenase	58023	93118	86770	108962	0.029587203	0.682445872	UP	0.579085347	-0.101868907	UNCHANGED	0.238575957	0.22669089	UNCHANGED
Ce_fissilis.013077.2	13	2654.11	Aspartic proteinase A1	83776	138938	115657	109405	0.034208593	0.729824837	UP	0.038307382	-0.26458776	UNCHANGED	0.012029278	-0.344759613	UNCHANGED
Ce_fissilis.010053.1	8	1296.69	Aspartic proteinase nepenthesin-1	30636	87804	86017	102413	0.015546347	1.51905507	UP	0.903539424	-0.029663061	UNCHANGED	0.397097757	0.222037679	UNCHANGED
Ce_fissilis.013426.1	11	2043.95	Aspartyl protease family protein 2	38846	165376	114545	149119	0.008293612	2.089912174	UP	0.095314151	-0.529835716	UNCHANGED	0.528612577	-0.149281913	UNCHANGED
Ce_fissilis.005482.1	7	5925.81	ATP synthase subunit delta', mitochondrial	100560	220650	215393	237164	0.000801995	1.133707248	UP	0.548010102	-0.034790633	UNCHANGED	0.544003152	0.104124662	UNCHANGED
Ce_fissilis.008972.1	3	575.24	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	24256	42826	46298	51476	0.004270443	0.82016785	UP	0.278421499	0.112439732	UNCHANGED	0.309934899	0.265395875	UNCHANGED
Ce_fissilis.010661.1	14	1090.24	ATP-dependent zinc metalloprotease FTSH, chloroplastic	20177	69550	68247	78578	0.010178786	1.785361634	UP	0.925941737	-0.027296497	UNCHANGED	0.465225225	0.176059859	UNCHANGED
Ce_fissilis.015339.1	4	1438.12	Auxin-induced in root cultures protein 12	38044	133999	112710	116397	5.13438E-05	1.816481143	UP	0.107026286	-0.249606796	UNCHANGED	0.001601822	-0.203163096	UNCHANGED
Ce_fissilis.015306.1	25	39725.23	Basic 7S globulin	461874	929480	737238	767139	0.002262109	1.008923103	UP	0.057777812	-0.334292263	UNCHANGED	0.284128555	-0.276935334	UNCHANGED
Ce_fissilis.018100.1	16	14963.72	Basic 7S globulin	626940	1179340	1052586	850396	0.008932983	0.911581217	UP	0.377669837	-0.16404244	UNCHANGED	0.025215161	-0.471772776	UNCHANGED

Ce_fissilis.018100.2	18	39045.05	Basic 7S globulin	849651	1747477	1512305	1180548	0.006472691	1.04033139	UP	0.408371067	-0.20852426	UNCHANGED	0.022673511	-0.565817125	UNCHANGED
Ce_fissilis.010199.1	13	16431.21	Basic secretory protease	121512	319468	302911	241184	0.006563775	1.394566669	UP	0.785618481	-0.076773864	UNCHANGED	0.068135059	-0.405533889	UNCHANGED
Ce_fissilis.007024.1	3	469.71	Basic transcription factor 3	53778	90190	97289	102203	0.004208157	0.745942436	UP	0.618695228	0.109301801	UNCHANGED	0.084101779	0.180395806	UNCHANGED
Ce_fissilis.017209.1	2	1711.02	Berberine bridge enzyme-like 13	8298	62040	46061	55010	0.000663426	2.902294701	UP	0.044313087	-0.429659092	UNCHANGED	0.450855987	-0.173513348	UNCHANGED
Ce_fissilis.005602.1	10	5251.27	Beta carbonic anhydrase 4	25307	110669	121025	126233	0.000928118	2.128622308	UP	0.529356871	0.129056418	UNCHANGED	0.287087129	0.189837602	UNCHANGED
Ce_fissilis.017232.1	20	7481.74	Beta-D-xylosidase 1	30934	135658	184041	272845	0.006900313	2.132706907	UP	0.098134066	0.44004981	UNCHANGED	0.193873092	1.008104803	UNCHANGED
Ce_fissilis.015677.1	16	2605.58	Beta-galactosidase 10	66014	120090	111148	117102	0.013952211	0.863282294	UP	0.550923968	-0.111640814	UNCHANGED	0.789337744	-0.036350169	UNCHANGED
Ce_fissilis.002805.1	2	357.58	Beta-hexosaminidase 3	6857	18777	16312	16539	0.009013394	1.45322141 3	UP	0.386087762	-0.203051513	UNCHANGED	0.48093772	-0.183054425	UNCHANGED
Ce_fissilis.008783.2	4	2221.92	Bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase	35446	73173	54624	60379	0.005224993	1.045691533	UP	0.017042834	-0.421762747	UNCHANGED	0.033161471	-0.27725495	UNCHANGED
Ce_fissilis.012355.1	10	3632.73	Bifunctional dTDP-4-dehydrorhamnose 3,5-epimerase/dTDP-4-dehydrorhamnose reductase	42821	79443	72992	81314	0.001993068	0.891592112	UP	0.243205764	-0.122184127	UNCHANGED	0.895911514	0.033583708	UNCHANGED
Ce_fissilis.017834.2	12	2903.88	Bifunctional epoxide hydrolase 2	106048	181483	211305	195468	0.001839194	0.775120907	UP	0.043096682	0.219490091	UNCHANGED	0.32436016	0.107100427	UNCHANGED
Ce_fissilis.005300.1	2	427.39	Bifunctional purple acid phosphatase 26	11545	38459	31500	31786	0.001168389	1.736121812	UP	0.00444531	-0.287998574	UNCHANGED	0.174150011	-0.27494359	UNCHANGED
Ce_fissilis.007375.1	10	2645.69	Branched-chain amino acid aminotransferase 2, chloroplastic	74714	219016	229367	243269	0.000506426	1.551580006	UP	0.466799478	0.066621637	UNCHANGED	0.139554359	0.151519001	UNCHANGED
Ce_fissilis.006261.1	19	20383.94	Caffeoyl-CoA O-methyltransferase 1	181957	791427	793399	731931	0.026729139	2.120855683	UP	0.99268809	0.003590094	UNCHANGED	0.753509078	-0.11274801	UNCHANGED
Ce_fissilis.013083.1	3	752.76	Caffeoylshikimate esterase	12693	66525	68939	72732	0.019174651	2.389862018	UP	0.876903717	0.051425923	UNCHANGED	0.722183026	0.128689926	UNCHANGED
Ce_fissilis.015546.1	28	19693.39	Calreticulin-1	138849	1004455	908766	1004605	0.000202988	2.854823602	UP	0.348256916	-0.144431529	UNCHANGED	0.998444275	0.000215428	UNCHANGED
Ce_fissilis.003225.1	4	1141.79	Carbonic anhydrase, chloroplastic	449207	753996	504720	583407	0.001416448	0.747175631	UP	0.003511231	-0.579073693	UNCHANGED	0.007770865	-0.370052616	UNCHANGED
Ce_fissilis.003900.1	4	1748.41	Cationic peroxidase 1	4248	41491	31822	38948	0.007670083	3.288075734	UP	0.377175967	-0.382757856	UNCHANGED	0.759439992	-0.091232913	UNCHANGED
Ce_fissilis.014596.1	10	1297.02	Cell division protein FtsZ homolog 2-1, chloroplastic	41852	183447	214576	148961	0.012202249	2.13199867	UP	0.566750894	0.226124663	UNCHANGED	0.486459119	-0.300428649	UNCHANGED
Ce_fissilis.001833.1	37	11573.38	Chaperonin 60 subunit beta 1, chloroplastic	213618	531584	583283	585458	0.00198358	1.315263862	UP	0.386638666	0.133898948	UNCHANGED	0.246303122	0.139268872	UNCHANGED
Ce_fissilis.009699.1	28	10147.81	Chaperonin CPN60-2, mitochondrial	82859	485494	505194	504546	0.002214266	2.550716734	UP	0.819924863	0.057383035	UNCHANGED	0.775882261	0.05552975	UNCHANGED
Ce_fissilis.009802.1	12	36002.63	Chlorophyll a-b binding protein 151, chloroplastic	830287	1423845	1384143	1481730	0.004049825	0.778110018	UP	0.849178947	-0.040798932	UNCHANGED	0.422078705	0.057490854	UNCHANGED
Ce_fissilis.000008.1	6	11796.66	Chlorophyll a-b binding protein 3, chloroplastic	83919	213718	288510	276631	0.001751503	1.348645045	UP	0.239338876	0.432910813	UNCHANGED	0.017447719	0.372252297	UNCHANGED

Ce_fissilis.015248.1	12	7220.97	Chlorophyll a-b binding protein CP29.2, chloroplastic	197484	579642	550242	690457	0.000834263	1.553424204	UP	0.589533327	-0.075097311	UNCHANGED	0.107331613	0.252388695	UNCHANGED
Ce_fissilis.008189.1	2	571.92	Chlorophyll a-b binding protein CP29.3, chloroplastic	27512	46490	42082	46983	0.047396234	0.756853208	UP	0.526886563	-0.143710298	UNCHANGED	0.930854237	0.015225797	UNCHANGED
Ce_fissilis.015214.1	21	4851.36	Citrate synthase, mitochondrial	26195	188467	197328	130093	0.014904427	2.846940746	UP	0.871129555	0.0662822	UNCHANGED	0.259435953	-0.534770593	UNCHANGED
Ce_fissilis.011391.1	20	735.57	Clathrin heavy chain 1	65155	127636	101779	94510	0.034119648	0.970099905	UP	0.048873289	-0.326595679	UNCHANGED	0.025891826	-0.433506521	UNCHANGED
Ce_fissilis.000579.1	14	1000.79	Coatomer subunit gamma	16012	62777	47184	58259	0.000460575	1.971120058	UP	0.144868422	-0.411945998	UNCHANGED	0.406329971	-0.107763601	UNCHANGED
Ce_fissilis.009657.1	11	1735.48	Cyclase-associated protein 1	34813	79400	88625	100247	0.029353468	1.189518602	UP	0.496862956	0.158582791	UNCHANGED	0.163398824	0.33634983	UNCHANGED
Ce_fissilis.006103.1	13	18069.61	Cysteine-rich repeat secretory protein 38	16296	521062	661540	604622	3.97727E-05	4.998875092	UP	0.008774698	0.344374073	UNCHANGED	0.058267045	0.214579489	UNCHANGED
Ce_fissilis.014551.1	10	5445.04	Cysteine-rich repeat secretory protein 38	7590	159186	145306	114527	2.84613E-06	4.390444617	UP	0.503460217	-0.131610743	UNCHANGED	0.018245551	-0.475020023	UNCHANGED
Ce_fissilis.015110.1	6	11757.18	Cytochrome b5 isoform E	66540	243477	196057	218703	0.000453381	1.871492157	UP	0.040230609	-0.31251282	UNCHANGED	0.293445377	-0.154811975	UNCHANGED
Ce_fissilis.014909.1	9	958.95	Delta-aminolevulinic acid dehydratase 1, chloroplastic	34605	66438	71443	69496	0.011353002	0.941002372	UP	0.398271275	0.104789013	UNCHANGED	0.713689719	0.064928537	UNCHANGED
Ce_fissilis.001068.1	18	1812.37	Dihydrolipoyllysine-residue acetyltransferase component 2 of pyruvate dehydrogenase complex, mitochondrial	41795	157294	137617	140840	0.002007051	1.912072102	UP	0.371567134	-0.192806834	UNCHANGED	0.218565122	-0.159414118	UNCHANGED
Ce_fissilis.017020.1	12	1917.79	Dihydrolipoyllysine-residue acetyltransferase component 5 of pyruvate dehydrogenase complex, chloroplastic	37243	72298	73555	75988	0.006389661	0.956966411	UP	0.732341504	0.024867827	UNCHANGED	0.529536535	0.071831066	UNCHANGED
Ce_fissilis.010676.1	5	637.14	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 2, mitochondrial	47600	92512	95191	95293	0.014511755	0.958660223	UP	0.773873978	0.041193279	UNCHANGED	0.732880161	0.042733294	UNCHANGED
Ce_fissilis.018441.1	23	2226.47	Dipeptidyl aminopeptidase BIII	47362	115161	118837	123863	0.00632359	1.281838166	UP	0.555393732	0.045333175	UNCHANGED	0.123236144	0.10509168	UNCHANGED
Ce_fissilis.001053.1	2	353.14	Early nodulin-like protein 2	23988	57609	53858	66043	0.010740209	1.263962966	UP	0.648508372	-0.09713414	UNCHANGED	0.34375489	0.197112507	UNCHANGED
Ce_fissilis.017696.1	8	4063.25	Endo-1,3	37356	175290	112198	141228	0.004817203	2.230331174	UP	0.075792332	-0.643698965	UNCHANGED	0.24221762	-0.311724611	UNCHANGED
Ce_fissilis.003482.2	8	8182.27	Endochitinase	51854	205405	184443	192283	0.024448492	1.9859379	UP	0.683689208	-0.155290535	UNCHANGED	0.813842311	-0.095240296	UNCHANGED
Ce_fissilis.009203.1	2	428.66	Endoglucanase 9	9234	32109	29743	25187	0.001282019	1.797950097	UP	0.542648905	-0.110451817	UNCHANGED	0.180600103	-0.350288894	UNCHANGED
Ce_fissilis.014854.1	34	50254.76	Enolase	370438	1420017	1511275	1495221	8.74613E-06	1.938605043	UP	0.258574799	0.0898588	UNCHANGED	0.146043287	0.074451199	UNCHANGED
Ce_fissilis.013782.2	14	23870.10	Epidermis-specific secreted glycoprotein EP1	675346	1046812	878125	773855	0.037863733	0.632304649	UP	0.230988938	-0.253504702	UNCHANGED	0.018811953	-0.435868496	UNCHANGED
Ce_fissilis.001894.1	3	1270.03	Erlin-2-B	14090	76894	66165	69520	0.001216676	2.448241888	UP	0.236179015	-0.216811107	UNCHANGED	0.365367809	-0.145458204	UNCHANGED
Ce_fissilis.008811.1	13	13695.77	Esterase	225565	629478	800633	480754	0.001012889	1.480609123	UP	0.14307436	0.346985688	UNCHANGED	0.123194503	-0.38885	UNCHANGED

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Ce_fissilis.002759.1	21	15663.68	Eukaryotic initiation factor 4A-8	36047	229256	188448	251594	2.27828E-05	2.668999837	UP	0.145364926	-0.282794589	UNCHANGED	0.352100409	0.134140726	UNCHANGED
Ce_fissilis.012548.1	11	4719.61	Eukaryotic translation initiation factor 3 subunit F	79410	145150	158654	171468	0.024652298	0.870148124	UP	0.302853378	0.128334083	UNCHANGED	0.166767482	0.240394449	UNCHANGED
Ce_fissilis.003115.1	5	2065.20	Eukaryotic translation initiation factor 5A	13444	38475	40200	28343	0.000147341	1.516909095	UP	0.693622124	0.063284366	UNCHANGED	0.034212794	-0.440901545	UNCHANGED
Ce_fissilis.017165.1	9	1684.05	Flowering locus K homology domain	42380	81815	75678	91639	0.005763001	0.948989621	UP	0.294910425	-0.112503483	UNCHANGED	0.225423936	0.163590256	UNCHANGED
Ce_fissilis.000714.1	4	943.00	FMN binding	9493	33413	32665	34240	0.002505143	1.815512103	UP	0.819826696	-0.032653957	UNCHANGED	0.838439322	0.035277746	UNCHANGED
Ce_fissilis.002280.1	24	12799.81	Formate dehydrogenase, mitochondrial	78936	1252389	1242983	997927	0.000160953	3.987863257	UP	0.973419576	-0.010876051	UNCHANGED	0.138398841	-0.32767649	UNCHANGED
Ce_fissilis.003264.1	6	1315.89	Formate--tetrahydrofolate ligase	20199	66645	64856	73767	0.004450609	1.722219022	UP	0.818394451	-0.039254388	UNCHANGED	0.561293221	0.14649289	UNCHANGED
Ce_fissilis.013557.1	24	30291.03	Fructose-bisphosphate aldolase 6, cytosolic	841344	1863962	1973851	1407469	0.001512571	1.147604633	UP	0.613513019	0.08264054	UNCHANGED	0.030142552	-0.405269882	UNCHANGED
Ce_fissilis.013775.1	9	809.88	Galactokinase	6682	67174	73265	65709	2.29349E-05	3.329666168	UP	0.4542609	0.125220627	UNCHANGED	0.731597704	-0.031823991	UNCHANGED
Ce_fissilis.019066.2	18	4142.23	Gamma aminobutyrate transaminase 1, mitochondrial	30235	164267	188602	173171	9.46368E-06	2.441770032	UP	0.175954133	0.199298515	UNCHANGED	0.484998362	0.076148037	UNCHANGED
Ce_fissilis.000227.1	4	1172.97	Gamma-glutamyl hydrolase 2	24155	57910	68992	52881	0.01128708	1.261507785	UP	0.453007608	0.252610061	UNCHANGED	0.587716617	-0.13106027	UNCHANGED
Ce_fissilis.001213.1	8	7572.74	GDSL esterase/lipase 2	88997	463916	522777	449618	4.72649E-06	2.382033193	UP	0.311643227	0.172333292	UNCHANGED	0.880400271	-0.045162385	UNCHANGED
Ce_fissilis.015257.1	2	1744.14	GDSL esterase/lipase At5g33370	36935	67877	37769	46446	0.042634537	0.877921205	UP	0.081346695	-0.845732949	UNCHANGED	0.142419767	-0.547358094	UNCHANGED
Ce_fissilis.013494.1	2	535.92	Glucose-1-phosphate adenylyltransferase small subunit 2, chloroplastic	8390	36932	44000	40485	0.000215013	2.138109144	UP	0.296064426	0.25263527	UNCHANGED	0.652436893	0.132523739	UNCHANGED
Ce_fissilis.016601.1	18	1489.00	Glucose-6-phosphate isomerase 1, chloroplastic	50205	91572	101056	110827	0.006249885	0.86706621	UP	0.316783877	0.14216987	UNCHANGED	0.118232135	0.275327459	UNCHANGED
Ce_fissilis.016775.1	12	3074.16	Glucose-6-phosphate isomerase, cytosolic	36236	280088	259155	214239	0.01687315	2.950365149	UP	0.781165311	-0.112060755	UNCHANGED	0.421437938	-0.386655829	UNCHANGED
Ce_fissilis.011344.1	5	657.16	Glutamate decarboxylase 4	5727	40799	30621	27235	0.00455569	2.832666567	UP	0.324421468	-0.413996677	UNCHANGED	0.156027716	-0.583044437	UNCHANGED
Ce_fissilis.009844.1	15	3383.51	Glutamate dehydrogenase 1	14676	190565	173054	166355	1.83557E-06	3.698761015	UP	0.427372818	-0.139058275	UNCHANGED	0.027894571	-0.196020115	UNCHANGED
Ce_fissilis.009843.1	11	3488.81	Glutamate dehydrogenase 2	27195	396338	310594	251524	0.001290534	3.865299391	UP	0.313116622	-0.351700461	UNCHANGED	0.056159385	-0.656031783	UNCHANGED
Ce_fissilis.012369.1	13	1943.09	Glutamate--glyoxylate aminotransferase 2	25276	60406	64665	62570	0.026799993	1.256925305	UP	0.709721925	0.098287725	UNCHANGED	0.859746495	0.050771286	UNCHANGED
Ce_fissilis.008404.1	13	8749.75	Glutamine synthetase cytosolic isozyme 2	48534	281777	207254	195069	0.000103109	2.537496632	UP	0.00522272	-0.443158719	UNCHANGED	0.007344351	-0.53056927	UNCHANGED
Ce_fissilis.013307.1	18	7173.69	Glutamine synthetase nodule isozyme	83432	314708	259052	270705	9.35143E-05	1.915337259	UP	0.012000685	-0.280773982	UNCHANGED	0.095209306	-0.217292987	UNCHANGED

Ce_fissilis.002001.1	16	5220.12	Glutathione reductase, cytosolic	30477	183516	213438	189257	0.000104137	2.590118307	UP	0.018588817	0.217912704	UNCHANGED	0.330710409	0.044440811	UNCHANGED
Ce_fissilis.017339.1	11	17552.07	Glutathione S-transferase F6	57298	373573	605117	404499	0.038671627	2.704823168	UP	0.184084036	0.69582307	UNCHANGED	0.800687064	0.11474509	UNCHANGED
Ce_fissilis.009977.1	18	6754.34	Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic	212527	389900	365055	330280	0.036821677	0.875455001	UP	0.704955353	-0.094990315	UNCHANGED	0.269040757	-0.239415515	UNCHANGED
Ce_fissilis.011648.2	23	31925.04	Glyceraldehyde-3-phosphate dehydrogenase GAPC1, cytosolic	111941	748645	642685	487016	0.001520757	2.741538494	UP	0.518565837	-0.220168853	UNCHANGED	0.065360257	-0.620312263	UNCHANGED
Ce_fissilis.016375.2	8	8857.17	Glycine-rich RNA-binding protein	174190	351242	424839	386906	0.000575226	1.011802845	UP	0.009064937	0.27445119	UNCHANGED	0.072215773	0.139516779	UNCHANGED
Ce_fissilis.015021.1	7	9503.07	Glycine-rich RNA-binding protein 3, mitochondrial	254359	657547	734509	740152	0.002619452	1.37022749	UP	0.063092333	0.159686779	UNCHANGED	0.109438999	0.170727532	UNCHANGED
Ce_fissilis.002030.1	11	13574.65	GTP-binding nuclear protein Ran-3	47601	331784	392542	288876	1.25512E-05	2.801175243	UP	0.44912982	0.242602484	UNCHANGED	0.398111472	-0.199794306	UNCHANGED
Ce_fissilis.004112.2	18	16820.54	Guanine nucleotide-binding protein subunit beta-like protein	106550	466105	465571	472761	6.82248E-05	2.129125772	UP	0.989670401	-0.001655512	UNCHANGED	0.800148031	0.020455679	UNCHANGED
Ce_fissilis.006142.1	5	1874.70	Haloacid dehalogenase-like hydrolase domain-containing protein Sgpp	7848	51494	41289	36083	0.045171103	2.714010508	UP	0.536552683	-0.318646095	UNCHANGED	0.424401834	-0.513097048	UNCHANGED
Ce_fissilis.007536.1	28	6043.16	Heat shock 70 kDa protein, mitochondrial	44136	387444	386856	389773	6.84173E-06	3.13397454	UP	0.990171488	-0.00218991	UNCHANGED	0.938044406	0.008647177	UNCHANGED
Ce_fissilis.013185.1	27	30967.36	Heat shock cognate 70 kDa protein	74995	117187	113295	101250	0.0111724	0.643944381	UP	0.583612525	-0.048735873	UNCHANGED	0.038086332	-0.210892924	UNCHANGED
Ce_fissilis.000754.1	8	1556.94	Heparanase-like protein 1	42946	265928	286147	283094	0.001018023	2.630456155	UP	0.518536248	0.105720147	UNCHANGED	0.604191084	0.090245411	UNCHANGED
Ce_fissilis.008751.1	12	2667.98	Importin subunit alpha-4	76320	265609	298470	254656	0.000564983	1.799163473	UP	0.143726368	0.168281941	UNCHANGED	0.601650207	-0.060750961	UNCHANGED
Ce_fissilis.013984.1	5	480.99	Importin-5	19885	45210	51435	49957	0.006215755	1.184965871	UP	0.319304068	0.1861058	UNCHANGED	0.503342654	0.144035636	UNCHANGED
Ce_fissilis.016925.1	12	1977.57	Inosine-5'-monophosphate dehydrogenase 2	74005	128095	153750	162947	0.001807188	0.791515853	UP	0.013643256	0.263367242	UNCHANGED	0.007695126	0.347186573	UNCHANGED
Ce_fissilis.014602.1	10	2500.51	Isocitrate dehydrogenase [NAD] catalytic subunit 5, mitochondrial	12567	146234	165800	146115	0.00021184	3.540593195	UP	0.142762642	0.181165095	UNCHANGED	0.993832504	-0.001171199	UNCHANGED
Ce_fissilis.014757.2	11	4448.32	Isocitrate dehydrogenase [NAD] regulatory subunit 1, mitochondrial	43690	180102	179468	185692	0.000313548	2.043447745	UP	0.944449126	-0.00508271	UNCHANGED	0.520525393	0.044101814	UNCHANGED
Ce_fissilis.004558.1	4	1257.99	Isoflavone reductase homolog	17380	49299	43326	44561	0.000349056	1.504111267	UP	0.281652674	-0.186342489	UNCHANGED	0.504895125	-0.145772139	UNCHANGED
Ce_fissilis.003226.1	21	6881.91	Ketol-acid reductoisomerase, chloroplastic	157755	356395	340822	400332	0.0043747	1.175793882	UP	0.703020274	-0.064456549	UNCHANGED	0.208765027	0.167721858	UNCHANGED
Ce_fissilis.008225.2	9	4176.44	Ketol-acid reductoisomerase, chloroplastic	6856	24570	17924	32372	0.000857479	1.841471932	UP	0.022811943	-0.45503273	UNCHANGED	0.009754969	0.397807686	UNCHANGED
Ce_fissilis.000925.1	5	974.29	KH domain-containing protein At4g18375	12050	52303	57973	64471	0.000313979	2.117843663	UP	0.285617227	0.14847885	UNCHANGED	0.123739247	0.301748624	UNCHANGED
Ce_fissilis.015083.1	6	1493.79	L-ascorbate oxidase homolog	2343	8491	8127	8599	0.000584383	1.857612021	UP	0.36890564	-0.063194889	UNCHANGED	0.886931991	0.018272891	UNCHANGED
Ce_fissilis.010163.1	15	3002.11	L-ascorbate peroxidase T, chloroplastic	74191	222741	267325	199573	0.002059818	1.586053929	UP	0.519504317	0.263226904	UNCHANGED	0.437959863	-0.1584497	UNCHANGED
Ce_fissilis.017763.1	13	20907.73	L-ascorbate peroxidase, cytosolic	233945	1100766	1075176	942922	6.91801E-05	2.234268964	UP	0.829285908	-0.033934683	UNCHANGED	0.06500749	-0.223297014	UNCHANGED

Ce_fissilis.008921.1	11	12160.87	Late embryogenesis abundant protein Lea14-A	348936	763064	666054	831396	0.015188815	1.128843164	UP	0.343922424	-0.196166509	UNCHANGED	0.491068287	0.123730727	UNCHANGED
Ce_fissilis.008924.1	5	6513.37	Late embryogenesis abundant protein, group 2	58919	130740	122919	139366	0.016338426	1.149888817	UP	0.718790182	-0.088989981	UNCHANGED	0.687356048	0.092180264	UNCHANGED
Ce_fissilis.001602.1	3	431.35	Leucine aminopeptidase	9680	21693	19297	22709	0.047646299	1.164231649	UP	0.583484488	-0.168884398	UNCHANGED	0.821298142	0.066048052	UNCHANGED
Ce_fissilis.013176.1	3	2106.85	L-lactate dehydrogenase A	31510	68709	46439	55415	0.003583354	1.124699506	UP	0.012718634	-0.565151824	UNCHANGED	0.035822108	-0.310219649	UNCHANGED
Ce_fissilis.009026.1	8	889.26	Long chain acyl-CoA synthetase 7, peroxisomal	5584	79184	68386	65810	0.000540168	3.825967288	UP	0.22361089	-0.211514973	UNCHANGED	0.218369094	-0.266894818	UNCHANGED
Ce_fissilis.003786.1	11	67509.35	Major allergen Pru ar 1	480241	3740359	3494678	3482004	3.00053E-05	2.961346427	UP	0.206628479	-0.098016906	UNCHANGED	0.167877666	-0.103258623	UNCHANGED
Ce_fissilis.003787.1	12	84390.27	Major allergen Pru av 1	213319	1997403	2008968	1904510	0.001317178	3.227041309	UP	0.96602342	0.00832882	UNCHANGED	0.703328197	-0.068706158	UNCHANGED
Ce_fissilis.005206.1	13	32540.33	Membrane steroid-binding protein 1	349105	694221	646974	699819	0.007290079	0.991734441	UP	0.341562493	-0.1016861	UNCHANGED	0.777892918	0.011587751	UNCHANGED
Ce_fissilis.016828.1	9	2134.75	Metacaspase-4	56281	289356	309157	260192	3.33094E-05	2.362115961	UP	0.336712396	0.095491932	UNCHANGED	0.170545823	-0.153268769	UNCHANGED
Ce_fissilis.013981.1	7	2463.91	Mitochondrial outer membrane protein porin 2	70558	120924	121481	131265	0.01763671	0.777227555	UP	0.900333569	0.006631384	UNCHANGED	0.520873343	0.118376488	UNCHANGED
Ce_fissilis.017338.1	12	2106.22	Mitochondrial outer membrane protein porin 4	42315	119303	133961	117830	0.000156465	1.495374097	UP	0.277707516	0.167182729	UNCHANGED	0.855553115	-0.017919338	UNCHANGED
Ce_fissilis.014689.1	22	5022.39	Monodehydroascorbate reductase, chloroplastic/mitochondrial	50803	196329	204629	213622	0.001326393	1.950278933	UP	0.682063693	0.059736643	UNCHANGED	0.47974581	0.12178864	UNCHANGED
Ce_fissilis.010928.1	12	1352.50	Monothiol glutaredoxin-S17	19479	40384	59320	45541	0.002606809	1.051835833	UP	0.015195297	0.554746691	UNCHANGED	0.550643057	0.173390544	UNCHANGED
Ce_fissilis.000871.1	2	357.60	G2/mitotic-specific cyclin-B	4901	11619	19918	13058	0.00037938	1.245296466	UP	0.129913012	0.777640345	UNCHANGED	0.471357847	0.168526256	UNCHANGED
Ce_fissilis.004229.1	18	972.81	titin isoform X2	15539	45730	59467	64739	0.000990425	1.557244627	UP	0.177094681	0.37894733	UNCHANGED	0.045773619	0.501512543	UNCHANGED
Ce_fissilis.004229.2	14	720.67	titin isoform X2	7807	23081	29601	23855	0.001504689	1.563775448	UP	0.063680693	0.358941498	UNCHANGED	0.803517799	0.047595893	UNCHANGED
Ce_fissilis.009066.1	3	5727.88	putative cupredoxin	8960	157142	132911	147878	0.000739627	4.132426285	UP	0.214984303	-0.241605905	UNCHANGED	0.678975467	-0.087658139	UNCHANGED
Ce_fissilis.012372.1	15	553.37	titin isoform X3	17223	38888	53971	58501	0.006967717	1.17502993	UP	0.252760493	0.472867138	UNCHANGED	0.007901436	0.589121164	UNCHANGED
Ce_fissilis.014316.2	10	40452.29	Unknown	228455	855478	830302	815632	0.003221189	1.904820082	UP	0.785281721	-0.043095909	UNCHANGED	0.799991431	-0.068813518	UNCHANGED
Ce_fissilis.015057.1	2	653.23	Butirosin biosynthesis	16959	35404	36412	25497	0.011036786	1.06186186	UP	0.740318266	0.040515202	UNCHANGED	0.036847755	-0.473552415	UNCHANGED
Ce_fissilis.010335.1	18	1594.27	NAD-dependent malic enzyme 59 kDa isoform, mitochondrial	14914	98458	89929	93803	8.92465E-05	2.722805687	UP	0.411948766	-0.130725882	UNCHANGED	0.255660045	-0.069864279	UNCHANGED
Ce_fissilis.001984.1	22	2327.25	NADH dehydrogenase [ubiquinone] iron-sulfur protein 1, mitochondrial	34868	137822	126278	144740	0.00057287	1.982827189	UP	0.424747997	-0.126194315	UNCHANGED	0.698837	0.070656538	UNCHANGED
Ce_fissilis.010680.1	8	2739.57	NADH--cytochrome b5 reductase 1	19931	86123	86994	78866	3.99213E-05	2.111350447	UP	0.919388488	0.01452103	UNCHANGED	0.266583329	-0.126987144	UNCHANGED
Ce_fissilis.0	19	10966	NADP-dependent malic enzyme	23209	47095	338504	422719	8.04072	4.3428064	UP	0.00105	-0.476416094	UNCHANGED	0.10729	-	UNCHANGED

12161.1		.55			6			E-06	98		1563			6502	0.155892936	
Ce_fissilis.013135.1	29	18285.35	NADP-dependent malic enzyme	47574	462220	455445	484945	4.65759E-05	3.28032554	UP	0.842545301	-0.021303401	UNCHANGED	0.326656809	0.069240605	UNCHANGED
Ce_fissilis.008054.1	11	8937.69	NADP-dependent malic enzyme 4, chloroplastic	8091	84560	127100	81495	1.67757E-05	3.385515825	UP	0.00483072	0.587911015	UNCHANGED	0.434747558	-0.053275507	UNCHANGED
Ce_fissilis.002901.3	5	4860.46	Non-classical arabinogalactan protein 30	97004	167739	222668	163256	0.001017822	0.790107492	UP	0.240985331	0.408670818	UNCHANGED	0.900828488	-0.039087932	UNCHANGED
Ce_fissilis.008707.1	2	667.95	NPL4-like protein 1	12732	45318	35654	41759	0.000155121	1.831662902	UP	0.034445162	-0.346040484	UNCHANGED	0.518560874	-0.117997029	UNCHANGED
Ce_fissilis.007988.1	5	1268.52	Nucleosome assembly protein 1	4668	77373	83398	44383	4.43037E-06	4.050812249	UP	0.706613779	0.108188639	UNCHANGED	0.177918828	-0.801833329	UNCHANGED
Ce_fissilis.018158.1	7	2327.75	Omega-amidase, chloroplastic	29253	55341	64325	65834	0.009400777	0.919768981	UP	0.148789905	0.217049901	UNCHANGED	0.061181499	0.250493295	UNCHANGED
Ce_fissilis.013672.1	9	2079.34	Ornithine carbamoyltransferase, chloroplastic	13892	60941	68998	86259	4.83077E-05	2.133157841	UP	0.315180314	0.179128525	UNCHANGED	0.031586039	0.501255012	UNCHANGED
Ce_fissilis.016593.1	16	1896.60	Patellin-5	13494	101869	92500	61330	0.005408081	2.916283894	UP	0.780783334	-0.139197845	UNCHANGED	0.088358037	-0.732046072	UNCHANGED
Ce_fissilis.018619.1	4	739.82	Pectin acetylesterase 6	5944	20125	24967	22526	0.002859006	1.759377964	UP	0.216444153	0.311070433	UNCHANGED	0.569969613	0.16265473	UNCHANGED
Ce_fissilis.018055.1	28	14117.37	Pectinesterase 3	462472	712565	626006	672231	0.009383349	0.623656866	UP	0.18474344	-0.186844338	UNCHANGED	0.50889973	-0.08406525	UNCHANGED
Ce_fissilis.018837.2	12	20030.66	Peptidyl-prolyl cis-trans isomerase	639348	1050778	1148065	1165374	0.003438825	0.716783931	UP	0.415496062	0.127746996	UNCHANGED	0.211003535	0.149335006	UNCHANGED
Ce_fissilis.001041.1	8	4082.26	Peptidyl-prolyl cis-trans isomerase CYP19-3	40023	75031	92777	94749	0.000279741	0.906639318	UP	0.000221248	0.306280819	UNCHANGED	0.015853206	0.336627759	UNCHANGED
Ce_fissilis.018743.1	4	9040.64	Peptidyl-prolyl cis-trans isomerase FKBP12	63237	129283	156587	162580	0.001571908	1.031693099	UP	0.060758776	0.276438653	UNCHANGED	0.142853915	0.330621918	UNCHANGED
Ce_fissilis.002071.1	31	65692.46	Perakine reductase	1094250	3423548	3520033	3216315	0.000261596	1.645549803	UP	0.788286485	0.040096712	UNCHANGED	0.459650213	-0.090083725	UNCHANGED
Ce_fissilis.008153.1	12	4960.73	Perakine reductase	29129	139341	220381	115145	0.006179783	2.258093072	UP	0.202408792	0.661382157	UNCHANGED	0.288696633	-0.275172031	UNCHANGED
Ce_fissilis.017405.2	15	23419.58	Peroxidase 12	543049	893920	885610	963543	0.000422088	0.719061523	UP	0.827518014	-0.013473028	UNCHANGED	0.128847546	0.108203217	UNCHANGED
Ce_fissilis.015096.1	6	9958.52	Peroxidase 15	98581	358999	276057	197253	0.027501215	1.864605782	UP	0.229790181	-0.379014847	UNCHANGED	0.071626472	-0.86393762	UNCHANGED
Ce_fissilis.008801.1	15	10374.60	Peroxidase 4	219788	536095	615689	589528	0.011089033	1.286373572	UP	0.327564709	0.199713673	UNCHANGED	0.523865465	0.137072772	UNCHANGED
Ce_fissilis.015659.1	16	12788.55	Peroxidase 4	78183	666865	792259	701941	0.00245	3.092470895	UP	0.257271774	0.248575843	UNCHANGED	0.720611407	0.073954993	UNCHANGED
Ce_fissilis.019038.1	18	15644.53	Peroxidase 4	105146	597058	840450	683379	0.001628159	2.505478643	UP	0.032978108	0.493290335	UNCHANGED	0.454779591	0.194815767	UNCHANGED
Ce_fissilis.007285.1	7	4861.80	Peroxiredoxin Q, chloroplastic	13401	161818	133898	88352	0.000317536	3.593946579	UP	0.362794104	-0.273236694	UNCHANGED	0.057971277	-0.873038222	UNCHANGED
Ce_fissilis.012710.1	7	7474.17	Peroxiredoxin-2	198916	361596	388262	416484	0.01871427	0.862220843	UP	0.260227671	0.102653569	UNCHANGED	0.067485486	0.203884512	UNCHANGED
Ce_fissilis.006689.1	11	1212.76	Phenylalanine ammonia-lyase	43311	90064	76409	79760	0.010853125	1.056217889	UP	0.243190841	-0.2371967	UNCHANGED	0.397553315	-0.17528	UNCHANGED

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Ce_fissilis.009200.1	31	7466.47	Phosphoglucomutase, cytoplasmic	61686	363141	351102	388606	0.000110972	2.557511782	UP	0.67019857	-0.048638256	UNCHANGED	0.41979028	0.097779205	UNCHANGED
Ce_fissilis.012795.1	3	993.19	Phosphomannomutase	6661	37676	26555	31282	4.17179E-05	2.499854197	UP	0.004668762	-0.50462111	UNCHANGED	0.167550089	-0.268278097	UNCHANGED
Ce_fissilis.001790.1	15	43897.80	Photosystem I reaction center subunit II, chloroplastic	369382	933621	1136916	1095613	0.009043954	1.337723365	UP	0.247598171	0.284217123	UNCHANGED	0.257988791	0.23083018	UNCHANGED
Ce_fissilis.003800.3	9	11261.87	Photosystem I reaction center subunit III, chloroplastic	62050	207995	256312	208396	0.000831027	1.745040294	UP	0.064746749	0.301349864	UNCHANGED	0.989526217	0.002778734	UNCHANGED
Ce_fissilis.000738.1	7	4745.34	Plasma membrane-associated cation-binding protein 1	98478	203162	212252	185700	0.001601895	1.044756699	UP	0.701618935	0.063150655	UNCHANGED	0.656633833	-0.129657778	UNCHANGED
Ce_fissilis.000738.2	4	1301.79	Plasma membrane-associated cation-binding protein 1	16174	30227	35584	30188	0.008691935	0.902131238	UP	0.069438003	0.235411308	UNCHANGED	0.996117572	-0.001852021	UNCHANGED
Ce_fissilis.013227.1	22	3543.46	Polyadenylate-binding protein 2	60937	148423	151114	158133	0.00033371	1.284323821	UP	0.715126389	0.025916249	UNCHANGED	0.500366994	0.091419608	UNCHANGED
Ce_fissilis.014181.1	5	1072.30	Polyadenylate-binding protein 8	26098	56652	69301	65948	0.001531574	1.118210872	UP	0.006888931	0.290732322	UNCHANGED	0.073802857	0.219185292	UNCHANGED
Ce_fissilis.014612.1	5	1211.70	Polyadenylate-binding protein RBP45B	22801	41388	54531	53405	0.005331257	0.860128688	UP	0.00610989	0.397887326	UNCHANGED	0.01553641	0.367771404	UNCHANGED
Ce_fissilis.014293.1	17	3962.61	Probable acetyl-CoA acetyltransferase, cytosolic 2	56801	148739	143105	156103	0.000715495	1.388797339	UP	0.760354398	-0.055704626	UNCHANGED	0.465645941	0.069719133	UNCHANGED
Ce_fissilis.013797.1	8	11855.30	Probable aldo-keto reductase 1	13974	538333	375520	363598	0.000507412	5.267715138	UP	0.051559122	-0.519607074	UNCHANGED	0.058167525	-0.56615297	UNCHANGED
Ce_fissilis.014865.2	11	3207.12	Probable aldo-keto reductase 1	20417	148411	161993	149529	0.000616965	2.861755806	UP	0.593390793	0.126339619	UNCHANGED	0.959173985	0.010829197	UNCHANGED
Ce_fissilis.010992.1	10	4640.35	Probable aldo-keto reductase 2	9185	167466	186132	123820	2.14994E-05	4.188523226	UP	0.672449854	0.152459608	UNCHANGED	0.028270836	-0.435625151	UNCHANGED
Ce_fissilis.012275.1	4	2080.90	Probable aquaporin PIP1-2	72271	136557	173464	166585	0.018628905	0.918023509	UP	0.116720593	0.345132514	UNCHANGED	0.187022838	0.286750959	UNCHANGED
Ce_fissilis.005036.1	12	1082.05	Probable beta-D-xylosidase 7	7316	52572	46664	48029	0.003196685	2.845223659	UP	0.487297151	-0.171989967	UNCHANGED	0.59743077	-0.130414396	UNCHANGED
Ce_fissilis.017925.1	4	1055.58	Probable carbohydrate esterase At4g34215	15855	42785	54184	49122	0.000202885	1.432172447	UP	0.084143624	0.340779755	UNCHANGED	0.131926971	0.19929225	UNCHANGED
Ce_fissilis.017736.1	4	1311.11	Probable cinnamyl alcohol dehydrogenase	4181	29031	28191	21523	0.001794528	2.795615781	UP	0.853138508	-0.042386986	UNCHANGED	0.341177557	-0.431759549	UNCHANGED
Ce_fissilis.014432.1	8	1454.89	Probable cinnamyl alcohol dehydrogenase 1	13227	45151	43668	43904	6.36348E-05	1.771269976	UP	0.504482018	-0.048181966	UNCHANGED	0.516821415	-0.040398655	UNCHANGED
Ce_fissilis.003620.1	5	3096.63	Probable glutathione S-transferase parC	6040	72417	93108	69394	0.006833447	3.583672575	UP	0.415337236	0.36257918	UNCHANGED	0.852467603	-0.06152422	UNCHANGED
Ce_fissilis.016304.2	13	3989.78	Probable lactoylglutathione lyase, chloroplastic	30748	47813	61869	55165	0.045963123	0.636889714	UP	0.248686976	0.371817872	UNCHANGED	0.266049783	0.206354574	UNCHANGED
Ce_fissilis.019092.1	21	6024.77	Probable mitochondrial-processing peptidase subunit beta, mitochondrial	9192	265982	239051	178762	0.001256331	4.854860737	UP	0.68145661	-0.154011916	UNCHANGED	0.088383825	-0.573293626	UNCHANGED
Ce_fissilis.009947.2	11	32262.05	Probable NAD(P)H dehydrogenase (quinone) FQR1-like 1	393064	1026708	778822	826476	0.00113121	1.38519045	UP	0.084218608	-0.398659821	UNCHANGED	0.112725093	-0.312981332	UNCHANGED
Ce_fissilis.014710.1	15	5630.07	Probable nitronate monooxygenase	68221	114400	160378	143567	0.009196626	0.745802047	UP	0.033038004	0.487387397	UNCHANGED	0.219234488	0.327636551	UNCHANGED

Ce_fissilis.002047.1	18	3825.36	Probable nucleoredoxin 1	32062	359721	336537	284413	2.29066E-05	3.48795476	UP	0.606510595	-0.096112664	UNCHANGED	0.296981111	-0.338891364	UNCHANGED
Ce_fissilis.002047.2	2	1496.36	Probable nucleoredoxin 1	6258	26830	27118	16680	0.002351745	2.100101174	UP	0.94523007	0.015405885	UNCHANGED	0.134476807	-0.685779088	UNCHANGED
Ce_fissilis.018507.1	5	1942.97	Probable pectinesterase/pectinesterase inhibitor 41	3939	104502	108217	101542	0.000688745	4.729550442	UP	0.815045749	0.050397308	UNCHANGED	0.806792126	-0.041448653	UNCHANGED
Ce_fissilis.001324.1	8	34805.71	Probable phospholipid hydroperoxide glutathione peroxidase	465979	876286	1074290	1064352	0.002818709	0.911138268	UP	0.03560796	0.293910011	UNCHANGED	0.037031747	0.280501424	UNCHANGED
Ce_fissilis.018290.1	6	661.39	Probable pyridoxal 5'-phosphate synthase subunit PDX1	25583	56315	59583	49483	0.002322801	1.138329804	UP	0.539299659	0.081383739	UNCHANGED	0.163466223	-0.186581861	UNCHANGED
Ce_fissilis.016675.1	10	26280.95	Probable UDP-arabinopyranose mutase 2	208362	360150	398001	376172	0.01024915	0.78950236	UP	0.390943852	0.144176274	UNCHANGED	0.649440195	0.062793844	UNCHANGED
Ce_fissilis.016893.2	23	26010.43	Probable UDP-arabinopyranose mutase 2	301855	574406	576453	573547	0.012850131	0.928216221	UP	0.982287246	0.005132442	UNCHANGED	0.988637937	-0.002160443	UNCHANGED
Ce_fissilis.003737.1	12	3904.76	Probable voltage-gated potassium channel subunit beta	30937	251144	236887	266897	1.49627E-05	3.021114781	UP	0.510466979	-0.084316457	UNCHANGED	0.209155714	0.087768281	UNCHANGED
Ce_fissilis.016278.1	6	1462.99	Prohibitin-2, mitochondrial	24464	95001	104252	97573	0.002157083	1.957290726	UP	0.560715961	0.134052319	UNCHANGED	0.796034097	0.038540796	UNCHANGED
Ce_fissilis.018922.1	10	1709.02	Proline iminopeptidase	29631	69614	59006	59958	0.01152277	1.232296403	UP	0.432814372	-0.238528568	UNCHANGED	0.4476645	-0.215435166	UNCHANGED
Ce_fissilis.016289.1	12	3662.92	Proteasome subunit alpha type-3	37306	314340	277655	258662	0.000115249	3.074839218	UP	0.173103585	-0.179033444	UNCHANGED	0.07540118	-0.281260514	UNCHANGED
Ce_fissilis.018172.1	11	5003.43	Proteasome subunit alpha type-6	73425	178201	195087	189194	0.001152234	1.279156392	UP	0.15120317	0.13060865	UNCHANGED	0.324920539	0.086358215	UNCHANGED
Ce_fissilis.006965.2	6	4566.38	Proteasome subunit alpha type-7	5552	59135	63896	49366	0.016484779	3.413048339	UP	0.758430625	0.111708513	UNCHANGED	0.562075463	-0.260507972	UNCHANGED
Ce_fissilis.006965.1	7	5350.44	Proteasome subunit alpha type-7-B	24690	92452	101829	65944	0.024369224	1.904788935	UP	0.684786948	0.139365981	UNCHANGED	0.281873994	-0.487461711	UNCHANGED
Ce_fissilis.012486.1	9	12525.85	Proteasome subunit beta type-1	123808	376406	382385	432122	0.000811174	1.604191117	UP	0.837534688	0.022735454	UNCHANGED	0.237771455	0.199146722	UNCHANGED
Ce_fissilis.012347.1	10	2098.00	Proteasome subunit beta type-4	36770	78231	86691	82638	0.010944352	1.089220472	UP	0.583201971	0.148148166	UNCHANGED	0.730701068	0.079073128	UNCHANGED
Ce_fissilis.017980.1	16	7216.71	Proteasome subunit beta type-5-B	77461	160903	184205	198507	0.000651501	1.054652259	UP	0.099338869	0.19511652	UNCHANGED	0.084879456	0.302994431	UNCHANGED
Ce_fissilis.017755.1	3	2231.64	Proteasome subunit beta type-7-B	25117	81523	103252	102886	0.000633175	1.698515974	UP	0.038946671	0.340892334	UNCHANGED	0.111864328	0.335772385	UNCHANGED
Ce_fissilis.017454.1	14	2210.74	Protein disulfide isomerase-like 1-4	67007	109319	103972	115751	0.001378631	0.706171481	UP	0.4491683	-0.072350576	UNCHANGED	0.447306603	0.082483178	UNCHANGED
Ce_fissilis.017828.1	10	1380.59	Protein disulfide isomerase-like 1-6	20965	45978	45500	52329	0.011068517	1.13297336	UP	0.935280715	-0.015052615	UNCHANGED	0.313607892	0.186683564	UNCHANGED
Ce_fissilis.015113.1	5	844.37	Protein disulfide isomerase-like 2-3	9454	58915	54361	50921	1.64917E-05	2.639652462	UP	0.417735542	-0.116072076	UNCHANGED	0.190511012	-0.210368376	UNCHANGED
Ce_fissilis.012685.1	30	8731.97	Protein disulfide-isomerase	138756	363343	370256	383027	0.000147626	1.388782124	UP	0.599332133	0.027189679	UNCHANGED	0.086190957	0.076114331	UNCHANGED
Ce_fissilis.017536.1	9	3954.62	Protein DJ-1 homolog D	152115	294688	321335	389414	0.002635294	0.954020043	UP	0.256596662	0.124889451	UNCHANGED	0.060471481	0.402117659	UNCHANGED
Ce_fissilis.010805.1	11	1620.85	Protein DNA-DAMAGE INDUCIBLE 1	60979	191040	188167	203358	7.48419E-05	1.647488444	UP	0.895936138	-0.021866166	UNCHANGED	0.487494277	0.090143649	UNCHANGED

Ce_fissilis.013019.1	12	23948.05	Protein of unknown function, DUF642	458960	998036	604673	755672	0.043142534	1.120723782	UP	0.116771964	-0.722937755	UNCHANGED	0.248205645	-0.40133084	UNCHANGED
Ce_fissilis.011139.1	5	1084.30	Protein PLASTID TRANSCRIPTIONALLY ACTIVE 16, chloroplastic	35034	87830	76177	85749	0.02696294	1.325942998	UP	0.480511625	-0.205363098	UNCHANGED	0.89465746	-0.034594046	UNCHANGED
Ce_fissilis.017138.1	6	1643.69	Protein STRICTOSIDINE SYNTHASE-LIKE 4	55983	111251	105023	101964	0.007572393	0.990749018	UP	0.486426954	-0.083112906	UNCHANGED	0.627445527	-0.125759869	UNCHANGED
Ce_fissilis.014130.1	13	1650.12	Protein transport protein SEC23	48160	110854	104613	124327	0.000618235	1.202745428	UP	0.48831429	-0.083598772	UNCHANGED	0.126005667	0.165480257	UNCHANGED
Ce_fissilis.007256.1	14	801.31	Protein transport protein SEC31 homolog B	63964	99539	99762	112499	0.013459268	0.638005315	UP	0.979700193	0.003241364	UNCHANGED	0.176754185	0.176583396	UNCHANGED
Ce_fissilis.016958.1	2	1838.94	Protein-L-isoaspartate O-methyltransferase 1	45407	74470	86229	95748	0.023295669	0.713740502	UP	0.426077483	0.211498968	UNCHANGED	0.285215339	0.362576537	UNCHANGED
Ce_fissilis.010261.1	24	2029.10	Puromycin-sensitive aminopeptidase	7481	103407	78273	70721	2.1115E-05	3.788958909	UP	0.34148385	-0.4017513	UNCHANGED	0.041609903	-0.548121004	UNCHANGED
Ce_fissilis.000472.1	4	6948.28	Putative ATP synthase protein YMF19	59736	97620	71529	93712	0.00105303	0.7085794	UP	0.045897128	-0.448658487	UNCHANGED	0.499068975	-0.058951368	UNCHANGED
Ce_fissilis.019068.1	3	466.48	Putative G3BP-like protein	32095	69234	63158	52352	0.000354606	1.10914741	UP	0.683724786	-0.132516678	UNCHANGED	0.044913979	-0.403233719	UNCHANGED
Ce_fissilis.019068.2	4	532.79	Putative G3BP-like protein	12522	23800	23945	25355	0.016183241	0.92651702	UP	0.971409768	0.008747159	UNCHANGED	0.770040583	0.091282974	UNCHANGED
Ce_fissilis.014532.1	28	7937.44	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha	46564	409455	372178	328106	7.76605E-06	3.136426064	UP	0.451432089	-0.137714594	UNCHANGED	0.05017316	-0.319546058	UNCHANGED
Ce_fissilis.001873.1	21	5538.47	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta	45334	233304	226089	223956	4.5106E-06	2.363551374	UP	0.730491829	-0.045318158	UNCHANGED	0.696170255	-0.058992919	UNCHANGED
Ce_fissilis.009238.1	8	1814.11	Pyruvate decarboxylase 1	11883	94433	135365	108342	0.000486068	2.990429938	UP	0.007107207	0.519485478	UNCHANGED	0.284550432	0.198230446	UNCHANGED
Ce_fissilis.017860.1	4	551.72	Pyruvate decarboxylase 1	15036	39348	35390	38302	0.000215614	1.387896317	UP	0.191556084	-0.152923743	UNCHANGED	0.675032883	-0.038851766	UNCHANGED
Ce_fissilis.005166.1	7	1664.59	Pyruvate kinase, cytosolic isozyme	13337	245771	215935	188806	0.000353936	4.203760933	UP	0.300127616	-0.186715333	UNCHANGED	0.057639878	-0.380406323	UNCHANGED
Ce_fissilis.012678.1	17	4752.14	Pyruvate kinase, cytosolic isozyme	85247	233298	283589	291238	0.002343652	1.452458106	UP	0.039130428	0.281625129	UNCHANGED	0.052643203	0.320022192	UNCHANGED
Ce_fissilis.007310.1	2	612.15	RAN GTPase-activating protein 2	31322	60965	52782	63861	0.004762688	0.960813803	UP	0.191436812	-0.207944259	UNCHANGED	0.568784072	0.066953654	UNCHANGED
Ce_fissilis.002776.1	7	1450.65	Ribose-phosphate pyrophosphokinase 4	14366	46672	50666	48975	6.83331E-05	1.699912609	UP	0.152069829	0.118453233	UNCHANGED	0.526204157	0.06947119	UNCHANGED
Ce_fissilis.010144.1	2	1177.11	Ricin B-like lectin EULS3	25740	83229	97552	72486	0.000854287	1.693099385	UP	0.486247034	0.229080642	UNCHANGED	0.173900546	-0.199377718	UNCHANGED
Ce_fissilis.007983.1	20	7394.64	S-adenosylmethionine synthase	18080	202790	177865	171342	0.00056559	3.487530868	UP	0.320530541	-0.189203987	UNCHANGED	0.177624473	-0.243100477	UNCHANGED
Ce_fissilis.004789.1	23	17542.96	S-adenosylmethionine synthase 1	49800	893673	702696	738511	2.30441E-05	4.165533104	UP	0.056418697	-0.346844966	UNCHANGED	0.064303682	-0.275127788	UNCHANGED
Ce_fissilis.001878.1	15	3919.06	Serine carboxypeptidase-like 45	28135	146438	193472	178111	0.002279046	2.379847504	UP	0.130069253	0.401831234	UNCHANGED	0.278552482	0.282483749	UNCHANGED
Ce_fissilis.0	9	2210.	Serine/threonine-protein phosphatase PP2A	41200	62862	60672	69207	0.00803	0.6095519	UP	0.56682	-0.051168087	UNCHANGED	0.12467	0.13872	UNCHANGED

11707.1		57	catalytic subunit					4614	36		6877			0731	1281	
Ce_fissilis.014280.2	11	3959.04	Serine/threonine-protein phosphatase PP2A-3 catalytic subunit	52675	100363	99194	116005	0.003676818	0.930036441	UP	0.888438922	-0.016892173	UNCHANGED	0.103435423	0.208971252	UNCHANGED
Ce_fissilis.014984.2	7	4869.79	S-formylglutathione hydrolase	83010	146902	179755	193635	0.040926068	0.823503621	UP	0.20187725	0.291180738	UNCHANGED	0.159604099	0.398485145	UNCHANGED
Ce_fissilis.008734.1	10	3030.23	Shikimate O-hydroxycinnamoyltransferase	35366	165584	124880	191028	0.003155455	2.227142881	UP	0.208825309	-0.40701795	UNCHANGED	0.303882068	0.206223231	UNCHANGED
Ce_fissilis.014363.1	16	10497.38	Short-chain dehydrogenase TIC 32, chloroplastic	178705	500838	374043	353351	0.012367703	1.486762554	UP	0.225318693	-0.421140216	UNCHANGED	0.113120467	-0.503243717	UNCHANGED
Ce_fissilis.016896.1	2	379.87	Spermidine coumaroyl-CoA acyltransferase	19048	59428	37372	45105	0.011290152	1.641465919	UP	0.075471244	-0.669185786	UNCHANGED	0.189201107	-0.397859315	UNCHANGED
Ce_fissilis.004268.1	7	4137.83	Stem-specific protein TSJT1	94445	196481	205245	195965	0.016837612	1.056840022	UP	0.403848981	0.06295798	UNCHANGED	0.96619379	-0.003793797	UNCHANGED
Ce_fissilis.014222.2	30	4664.46	Stromal 70 kDa heat shock-related protein, chloroplastic	97813	201944	261636	215262	0.013963316	1.045850857	UP	0.020415941	0.373610487	UNCHANGED	0.329236167	0.092142884	UNCHANGED
Ce_fissilis.002306.1	24	2826.45	Subtilisin-like protease SBT1.6	70729	185979	247728	234163	0.002452844	1.394770172	UP	0.011659587	0.413621741	UNCHANGED	0.047970396	0.332374624	UNCHANGED
Ce_fissilis.016194.1	6	1170.84	Succinate-semialdehyde dehydrogenase (acetylating)	5297	104612	98486	89257	2.65343E-06	4.30360186	UP	0.757031309	-0.087053288	UNCHANGED	0.233894888	-0.229006796	UNCHANGED
Ce_fissilis.008442.1	13	1958.72	T-complex protein 1 subunit delta	7438	117005	95457	90602	0.000136496	3.975556097	UP	0.277383628	-0.293648651	UNCHANGED	0.034287088	-0.368958519	UNCHANGED
Ce_fissilis.005519.1	14	2337.56	T-complex protein 1 subunit eta	14936	171447	160435	156247	2.95485E-05	3.520903915	UP	0.598041458	-0.095768012	UNCHANGED	0.348545468	-0.133926327	UNCHANGED
Ce_fissilis.012740.1	21	3326.65	T-complex protein 1 subunit theta	70952	185244	172304	184707	3.3032E-05	1.384501319	UP	0.517198806	-0.10446716	UNCHANGED	0.907955797	-0.004182207	UNCHANGED
Ce_fissilis.003780.1	3	1631.82	Temperature-induced lipocalin-1	25322	55033	72897	63622	0.000481501	1.119921698	UP	0.080614997	0.405567579	UNCHANGED	0.02896926	0.209221583	UNCHANGED
Ce_fissilis.018735.1	7	1230.02	Thioredoxin reductase 2	37649	138482	155027	152363	0.000505196	1.879028946	UP	0.029128203	0.162824014	UNCHANGED	0.389002596	0.137816133	UNCHANGED
Ce_fissilis.009832.1	8	3665.05	Thiosulfate/3-mercaptopyruvate sulfurtransferase 1, mitochondrial	62113	127850	136193	146827	0.003230455	1.041495255	UP	0.415204285	0.091197886	UNCHANGED	0.131215274	0.199663713	UNCHANGED
Ce_fissilis.017526.1	5	712.81	Threonine dehydratase biosynthetic, chloroplastic	11126	27791	33303	29628	0.003074806	1.320653922	UP	0.161002068	0.261029583	UNCHANGED	0.575502211	0.092354315	UNCHANGED
Ce_fissilis.018478.1	3	609.68	Threonine synthase 1, chloroplastic	3820	47382	47984	44613	2.31795E-06	3.632828906	UP	0.934496175	0.018209214	UNCHANGED	0.677838433	-0.086897761	UNCHANGED
Ce_fissilis.002433.1	19	1948.84	Tol-Pal system protein TolB	21626	124745	145689	172393	0.000473985	2.528139385	UP	0.109279793	0.223911617	UNCHANGED	0.052323841	0.46671934	UNCHANGED
Ce_fissilis.004237.1	20	6575.19	Transaldolase	89790	250831	259356	269633	0.024680667	1.482084127	UP	0.862576227	0.048219981	UNCHANGED	0.691165378	0.104282694	UNCHANGED
Ce_fissilis.014396.1	2	428.47	Trans-resveratrol di-O-methyltransferase	22169	37175	41093	36041	0.045473474	0.745786958	UP	0.553473773	0.144555298	UNCHANGED	0.866071396	-0.04470078	UNCHANGED
Ce_fissilis.002549.1	6	2751.59	Tropinone reductase homolog	10365	197647	219093	150972	0.001612116	4.253150133	UP	0.648692208	0.148616682	UNCHANGED	0.168256959	-0.388644241	UNCHANGED
Ce_fissilis.016182.1	13	11347.22	Tropinone reductase homolog At2g29360	84289	356086	412083	381145	0.000273168	2.078808093	UP	0.221137683	0.210710972	UNCHANGED	0.696958897	0.098116427	UNCHANGED
Ce_fissilis.004152.1	6	2569.86	Tropinone reductase-like 3	32932	212179	188301	184536	0.001459362	2.687723196	UP	0.402446138	-0.172242257	UNCHANGED	0.398646945	-0.201377205	UNCHANGED

Ce_fissilis.014031.1	9	33521.23	Tubulin beta-2 chain	2314	8379	9175	6935	0.00045293	1.856377146	UP	0.420811256	0.130924671	UNCHANGED	0.080335006	-0.272759429	UNCHANGED
Ce_fissilis.007359.1	7	994.98	Ubiquitin carboxyl-terminal hydrolase 14	22404	65009	74071	81374	0.004195212	1.53687844	UP	0.17761337	0.188275543	UNCHANGED	0.01674716	0.323920072	UNCHANGED
Ce_fissilis.018551.1	11	3168.16	Ubiquitin receptor RAD23c	91615	190694	174383	176508	0.002680308	1.057612289	UP	0.039994557	-0.129001864	UNCHANGED	0.272833517	-0.111527092	UNCHANGED
Ce_fissilis.005115.2	7	7695.03	Ubiquitin-60S ribosomal protein L40	372685	682749	698752	621992	0.000322395	0.873397432	UP	0.571352429	0.03342643	UNCHANGED	0.137091053	-0.1344593	UNCHANGED
Ce_fissilis.016105.1	10	6051.14	Ubiquitin-conjugating enzyme E2 36	66698	152371	238929	202921	0.038794924	1.191867835	UP	0.05006845	0.648993532	UNCHANGED	0.13729959	0.413328513	UNCHANGED
Ce_fissilis.016106.1	7	3069.80	Ubiquitin-conjugating enzyme E2 36	23608	60955	88610	74609	0.02140166	1.368477284	UP	0.080198661	0.539723067	UNCHANGED	0.228649283	0.291601673	UNCHANGED
Ce_fissilis.003231.1	4	2011.07	Ubiquitin-conjugating enzyme E2 variant 1D	35962	126599	123278	104527	1.53053E-05	1.815706208	UP	0.765431518	-0.038348081	UNCHANGED	0.088131543	-0.276384494	UNCHANGED
Ce_fissilis.009678.1	4	28215.73	Ubiquitin-conjugating enzyme E2-17 kDa	187906	385236	525698	462047	0.000149962	1.035731436	UP	0.000514963	0.448494602	UNCHANGED	0.015796251	0.262299095	UNCHANGED
Ce_fissilis.003776.1	10	1940.29	UDP-D-apiose/UDP-D-xylose synthase 2	67941	108724	127118	126165	0.002288646	0.678320505	UP	0.049855251	0.225492208	UNCHANGED	0.104321829	0.214634338	UNCHANGED
Ce_fissilis.000235.1	22	8388.14	UDP-glucose 6-dehydrogenase 1	33838	71957	68297	57031	0.009965294	1.088479295	UP	0.743868832	-0.075319486	UNCHANGED	0.19883003	-0.335384273	UNCHANGED
Ce_fissilis.008064.1	9	3534.63	UDP-glucose 6-dehydrogenase 1	8878	97700	92761	119512	0.00151021	3.460054333	UP	0.707187284	-0.074846286	UNCHANGED	0.267047597	0.290718008	UNCHANGED
Ce_fissilis.011362.1	27	12233.17	UDP-glucose 6-dehydrogenase 1	162397	402000	421136	352889	0.000796435	1.307666828	UP	0.76141164	0.06709076	UNCHANGED	0.09452611	-0.187979521	UNCHANGED
Ce_fissilis.000234.1	7	5550.81	UDP-glucose 6-dehydrogenase 5	4772	82172	72583	65737	0.000183349	4.105941935	UP	0.496558978	-0.179024463	UNCHANGED	0.056147486	-0.321954798	UNCHANGED
Ce_fissilis.012521.1	13	3467.35	UDP-glucuronic acid decarboxylase 3	8005	62613	57655	44960	0.010775417	2.967452156	UP	0.775453777	-0.119003308	UNCHANGED	0.293789474	-0.477817641	UNCHANGED
Ce_fissilis.014035.1	10	5990.32	UDP-glucuronic acid decarboxylase 5	11395	259573	233770	229564	0.000992162	4.5097223	UP	0.450010825	-0.151047348	UNCHANGED	0.481454712	-0.177244913	UNCHANGED
Ce_fissilis.000114.1	6	1411.11	Ultraviolet-B receptor UVR8	17779	65060	69831	83722	0.047653504	1.871604034	UP	0.79000093	0.10209401	UNCHANGED	0.335949031	0.363826647	UNCHANGED
Ce_fissilis.015402.1	2	2540.10	UMP-CMP kinase 3	10872	40339	46044	34017	0.013145291	1.891590271	UP	0.636984851	0.190849772	UNCHANGED	0.482689195	-0.245907485	UNCHANGED
Ce_fissilis.017791.2	4	9802.57	Phenazine biosynthesis PhzF protein	6093	96874	100449	138540	8.92188E-05	3.9909942	UP	0.834483432	0.052281286	UNCHANGED	0.003893039	0.516121096	UNCHANGED
Ce_fissilis.003758.1	5	1412.80	Uncharacterized oxidoreductase At4g09670	19823	43092	41622	50577	0.017999441	1.12028825	UP	0.773272706	-0.050100334	UNCHANGED	0.3164816	0.231037569	UNCHANGED
Ce_fissilis.009068.1	3	3707.32	Nucleic acid-binding, OB-fold containing protein	72162	143996	142307	129451	0.017717464	0.996728617	UP	0.874653807	-0.017024347	UNCHANGED	0.260792766	-0.153621263	UNCHANGED
Ce_fissilis.010324.1	2	2227.47	DNA-binding family protein-like 2	16803	36902	41989	45376	0.000740861	1.135015311	UP	0.259242217	0.186288725	UNCHANGED	0.043052094	0.298213315	UNCHANGED
Ce_fissilis.015728.1	6	678.50	Stomatin-like protein 2, mitochondrial	14397	36662	37766	35299	0.002503946	1.348475125	UP	0.207501034	0.042794264	UNCHANGED	0.544958006	-0.054635809	UNCHANGED
Ce_fissilis.000639.1	6	808.10	NAD(P)-binding Rossmann-fold superfamily protein	20676	37779	28098	32360	0.029549832	0.869628874	UP	0.108403578	-0.427139748	UNCHANGED	0.556854074	-0.22339	UNCHANGED

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Ce_fissilis.009906.2	31	21826.78	UTP--glucose-1-phosphate uridylyltransferase	273536	441661	538100	540197	0.015983706	0.691208642	UP	0.180954317	0.284933476	UNCHANGED	0.063894595	0.290544502	UNCHANGED
Ce_fissilis.009974.1	10	1604.43	V-type proton ATPase subunit C	25853	91703	84341	91756	0.000221358	1.826635482	UP	0.367101862	-0.120727354	UNCHANGED	0.980593718	0.000835317	UNCHANGED
Ce_fissilis.015657.1	15	2970.10	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	5519	117739	115628	31281	0.001637331	4.414959897	UP	0.97598678	-0.026101383	UNCHANGED	0.007842574	-1.91225456	DOWN
Ce_fissilis.012853.1	24	7552.38	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	25359	453653	324263	258057	0.00017995	4.161013155	UP	0.175038519	-0.484426333	UNCHANGED	0.012557352	-0.813901498	DOWN
Ce_fissilis.005135.1	5	546.95	Aldehyde dehydrogenase family 2 member C4	9195	61847	56361	40140	0.001938787	2.74978732	UP	0.546986017	-0.134005903	UNCHANGED	0.040499524	-0.623684158	DOWN
Ce_fissilis.014672.1	3	595.66	ATP-citrate synthase beta chain protein 1	12251	27633	19140	13191	0.011015175	1.173417141	UP	0.170582316	-0.529778164	UNCHANGED	0.017005783	-1.066802903	DOWN
Ce_fissilis.010325.2	13	23796.62	Berberine bridge enzyme-like 24	32670	467768	308324	265911	0.002124009	3.839765652	UP	0.072340504	-0.601349085	UNCHANGED	0.040876605	-0.814852548	DOWN
Ce_fissilis.015486.1	12	1913.05	Biotin carboxylase 1, chloroplastic	17554	78643	50716	34311	0.000512789	2.163550017	UP	0.198678628	-0.632871988	UNCHANGED	0.001953725	-1.196637244	DOWN
Ce_fissilis.007320.1	18	7473.51	Catalase isozyme 3	144299	394180	313106	195560	0.001632582	1.449796093	UP	0.14953619	-0.332201285	UNCHANGED	0.007459876	-1.011239182	DOWN
Ce_fissilis.012572.1	8	715.47	Cell division cycle protein 48 homolog	6796	56670	41131	26014	0.001502391	3.059792543	UP	0.204913677	-0.462336048	UNCHANGED	0.02906022	-1.123297962	DOWN
Ce_fissilis.015065.1	7	1603.69	Chorismate synthase, chloroplastic	7260	91148	70032	51688	0.00011072	3.650141704	UP	0.285079271	-0.380208854	UNCHANGED	0.009242545	-0.818399302	DOWN
Ce_fissilis.009289.1	10	3970.94	Elongation factor 1-alpha	41084	193731	168752	105489	0.000458902	2.237397614	UP	0.613494646	-0.199152447	UNCHANGED	0.016764639	-0.876967147	DOWN
Ce_fissilis.009290.1	10	2903.79	Elongation factor 1-alpha	59071	155550	99402	45801	0.002852279	1.396867274	UP	0.125738158	-0.646033579	UNCHANGED	0.000634108	-1.763929758	DOWN
Ce_fissilis.015174.1	17	8237.38	Elongation factor 1-gamma	22595	360823	285204	198250	0.000332646	3.997215397	UP	0.440304324	-0.339297205	UNCHANGED	0.022437213	-0.863969993	DOWN
Ce_fissilis.017563.2	32	8724.31	Elongation factor 2	51729	376007	319647	211446	0.000809209	2.861701918	UP	0.613271531	-0.23428097	UNCHANGED	0.023788298	-0.830470252	DOWN
Ce_fissilis.000055.1	20	14920.56	Eukaryotic initiation factor 4A-14	21464	243495	190932	149611	1.5928E-05	3.503903738	UP	0.084860122	-0.350831133	UNCHANGED	0.002962244	-0.702676446	DOWN
Ce_fissilis.015281.1	12	1431.36	Eukaryotic translation initiation factor 2 subunit 3, Y-linked	5357	80227	80165	46118	7.965E-05	3.904688414	UP	0.998493986	-0.00111535	UNCHANGED	0.024106502	-0.798769369	DOWN
Ce_fissilis.011648.1	14	20749.29	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	18751	530644	441486	193145	0.000886306	4.822710544	UP	0.680594668	-0.26537654	UNCHANGED	0.012233975	-1.458057184	DOWN
Ce_fissilis.016012.1	13	52667.29	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	70063	1045530	820196	474331	0.000318127	3.899428904	UP	0.372715115	-0.350194667	UNCHANGED	0.008863236	-1.140269122	DOWN
Ce_fissilis.015758.1	16	4359.06	Guanosine nucleotide diphosphate dissociation inhibitor 1	5457	203297	167009	89798	2.29682E-07	5.219281477	UP	0.40198213	-0.283669109	UNCHANGED	0.006050478	-1.17883	DOWN

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Ce_fissilis.012696.1	6	674.96	Heat shock cognate 70 kDa protein	2491	30894	23253	13437	0.000308355	3.632391476	UP	0.164056821	-0.409892971	UNCHANGED	0.003498971	-1.201120579	DOWN
Ce_fissilis.006480.1	11	1437.89	Heat shock cognate protein 80	55333	155435	120924	89382	0.012100189	1.490108874	UP	0.179468583	-0.362204752	UNCHANGED	0.031413934	-0.798258484	DOWN
Ce_fissilis.018095.1	6	1649.89	Isocitrate dehydrogenase [NADP]	13218	80490	54579	28307	0.004829253	2.606311807	UP	0.212430817	-0.560463493	UNCHANGED	0.01462373	-1.507627733	DOWN
Ce_fissilis.013936.1	10	3661.45	Luminal-binding protein 5	13046	66976	43884	35038	0.002926819	2.360080237	UP	0.063322595	-0.609949008	UNCHANGED	0.021843981	-0.934727433	DOWN
Ce_fissilis.015325.1	8	8156.41	MLP-like protein 34	57225	237944	262022	70975	0.014648875	2.055906713	UP	0.757062811	0.13906573	UNCHANGED	0.020955816	-1.745239603	DOWN
Ce_fissilis.001325.1	3	1869.87	Osmotin-like protein	4113	45534	52211	28823	0.000460831	3.468759173	UP	0.764767512	0.19740345	UNCHANGED	0.019710156	-0.659712573	DOWN
Ce_fissilis.000045.1	15	7552.83	Pectin acetylesterase 8	13978	191638	205023	86764	1.23499E-05	3.777203024	UP	0.818151733	0.09739641	UNCHANGED	0.001033671	-1.143220385	DOWN
Ce_fissilis.010182.1	3	441.24	Phospholipase D alpha 1	8702	26644	22834	15198	0.000316126	1.614385935	UP	0.325474365	-0.222633098	UNCHANGED	0.022835059	-0.809903616	DOWN
Ce_fissilis.016574.1	14	6136.60	Probable carboxylesterase 17	7818	185204	154376	106170	0.000123368	4.566255612	UP	0.408869063	-0.26267266	UNCHANGED	0.003175686	-0.802740821	DOWN
Ce_fissilis.016597.2	34	19892.12	Probable L-gulonolactone oxidase 6	104655	1215229	996607	594397	0.000272736	3.537511468	UP	0.299913566	-0.286131707	UNCHANGED	0.006797361	-1.031728936	DOWN
Ce_fissilis.002646.1	8	6523.65	Ras-related protein RABA1f	10501	39729	31798	8172	5.4967E-05	1.919681838	UP	0.002152811	-0.321286055	UNCHANGED	2.24468E-06	-2.281383214	DOWN
Ce_fissilis.010376.1	21	9242.80	Serine hydroxymethyltransferase 4	14369	535430	342156	236529	0.000868983	5.219666109	UP	0.163685155	-0.646042961	UNCHANGED	0.018766122	-1.178681953	DOWN
Ce_fissilis.011024.1	13	3940.90	Succinate dehydrogenase [ubiquinone] flavoprotein subunit 1, mitochondrial	31597	226279	179554	122256	4.44807E-05	2.840246042	UP	0.412890845	-0.333689527	UNCHANGED	0.009173892	-0.88819633	DOWN
Ce_fissilis.015355.1	3	4019.44	Succinate dehydrogenase subunit 6, mitochondrial	50099	124594	91130	71853	0.00120557	1.314388222	UP	0.097701373	-0.451231004	UNCHANGED	0.014424576	-0.79411713	DOWN
Ce_fissilis.005337.1	28	4887.10	Transketolase-2, chloroplastic	45557	486589	376759	277281	1.89877E-05	3.416965763	UP	0.26770113	-0.369061827	UNCHANGED	0.005753835	-0.811354615	DOWN
Ce_fissilis.002714.1	16	1055.12	Ubiquitin-activating enzyme E1 1	12443	93324	76072	52585	2.4792E-05	2.906972187	UP	0.5330944	-0.294893694	UNCHANGED	0.002010154	-0.827600641	DOWN
Ce_fissilis.005128.1	11	693.30	Villin-2	40888	77779	60157	51157	0.013049071	0.92771289	UP	0.152621327	-0.370648668	UNCHANGED	0.014782682	-0.604459497	DOWN
Ce_fissilis.014702.1	8	1180.87	Xylose isomerase	3798	59966	56734	30636	0.001440264	3.980708991	UP	0.890465795	-0.079925355	UNCHANGED	0.031757098	-0.968909007	DOWN
Ce_fissilis.001412.2	9	1886.67	4-coumarate--CoA ligase 1	11810	148071	92647	155103	0.000239423	3.648244634	UP	0.019766712	-0.676470347	DOWN	0.604026335	0.066945942	UNCHANGED

Ce_fissilis.001130.1	7	10516.98	Fructose-bisphosphate aldolase, cytoplasmic isozyme 1	27317	49351	28094	45088	0.003820242	0.853256031	UP	0.005646181	-0.812830813	DOWN	0.360958608	-0.13033977	UNCHANGED
Ce_fissilis.018148.1	2	459.36	Pyrophosphate-energized vacuolar membrane proton pump	24337	48971	31964	23642	0.021721029	1.008771407	UP	0.018133835	-0.615459742	DOWN	0.065402769	-1.050580831	UNCHANGED
Ce_fissilis.007984.1	19	10115.58	S-adenosylmethionine synthase 1	11363	341883	214845	241541	8.02613E-06	4.911111926	UP	0.008530198	-0.670205548	DOWN	0.021934737	-0.501235229	UNCHANGED
Ce_fissilis.014760.3	7	2921.00	S-adenosylmethionine synthase 2	16073	67582	44521	78863	8.13382E-06	2.072005047	UP	0.006725515	-0.602155071	DOWN	0.066790903	0.222717128	UNCHANGED
Ce_fissilis.014222.1	25	4276.90	Stromal 70 kDa heat shock-related protein, chloroplastic	23450	110897	53805	137359	0.000280111	2.241560176	UP	0.00046931	-1.043395602	DOWN	0.02070517	0.308732992	UNCHANGED
Ce_fissilis.012207.1	3	1244.57	Transcription factor Pur-alpha 1	14517	22198	14194	20949	0.001387645	0.612677011	UP	0.049649202	-0.645155708	DOWN	0.431263616	-0.083589975	UNCHANGED
Ce_fissilis.011838.1	3	881.57	Tropinone reductase homolog At5g06060	3227	20456	6366	9348	0.005709893	2.664070211	UP	0.019561285	-1.684082325	DOWN	0.058248782	-1.129815078	UNCHANGED
Ce_fissilis.017820.1	22	16827.20	Adenosylhomocysteinase 1	24809	583570	214917	169416	0.001042035	4.555976142	UP	0.007963274	-1.441124819	DOWN	0.006391383	-1.784335038	DOWN
Ce_fissilis.010325.1	11	3252.20	Berberine bridge enzyme-like 26	12188	212585	119294	106264	0.002021609	4.124562364	UP	0.032450572	-0.833516185	DOWN	0.025439298	-1.000396588	DOWN
Ce_fissilis.013185.2	15	25813.12	Heat shock cognate 70 kDa protein	22498	115333	73569	33693	9.95144E-07	2.357905196	UP	0.038701071	-0.648643707	DOWN	3.16292E-05	-1.775301565	DOWN
Ce_fissilis.010551.1	24	4692.69	Methylenetetrahydrofolate reductase 2	16514	230615	139908	135834	0.000180498	3.803766447	UP	0.021423693	-0.721006093	DOWN	0.009483577	-0.763639775	DOWN
Ce_fissilis.004527.1	11	7803.48	Monodehydroascorbate reductase	24855	510221	293711	274993	1.99937E-05	4.359502001	UP	0.004428389	-0.796727793	DOWN	0.00382252	-0.891725681	DOWN
Ce_fissilis.000421.1	6	1166.86	Pectinesterase 2	7808	79065	15382	14948	0.011965059	3.340005997	UP	0.016692342	-2.361818965	DOWN	0.016675119	-2.403078028	DOWN
Ce_fissilis.016667.1	18	21594.44	Phosphoglycerate kinase, cytosolic	54387	630672	415325	358591	3.64221E-05	3.535565865	UP	0.045121506	-0.602649593	DOWN	0.006859024	-0.814550279	DOWN
Ce_fissilis.009009.1	3	1930.05	Probable pectate lyase 5	5634	47058	22570	20689	0.005621988	3.062278567	UP	0.039282059	-1.060007605	DOWN	0.043155824	-1.185584007	DOWN
Ce_fissilis.011754.1	11	1361.08	Pyruvate kinase 1, cytosolic	4589	120914	50976	38134	0.000172428	4.719552889	UP	0.015954971	-1.246100653	DOWN	0.001994694	-1.664814709	DOWN
Ce_fissilis.014280.1	12	3496.76	Serine/threonine-protein phosphatase PP2A-4 catalytic subunit	2113	8820	4229	5624	1.3731E-05	2.061250462	UP	7.716E-05	-1.060562438	DOWN	0.00018122	-0.649232558	DOWN
Ce_fissilis.009080.1	2	956.29	3-ketoacyl-CoA thiolase 2, peroxisomal	14810	0	40131	39140	0.000847265	-	Unique 0-days	0.00013617	-	Unique 3-days PCIB	0.000940805	-	Unique 3-days TIBA
Ce_fissilis.015876.1	4	1572.70	Legumin B	4003	0	0	11833	0.007200156	-	Unique 0-days	-	-	-	0.000571906	-	Unique 3-days TIBA
Ce_fissilis.010582.1	8	7229.08	Ras-related protein RABA1f	61151	0	0	50129	0.005615249	-	Unique 0-days	-	-	-	7.03143E-06	-	Unique 3-days TIBA
Ce_fissilis.013555.1	15	31206.21	ADP-ribosylation factor	70564	0	0	0	0.005904399	-	Unique 0-days	-	-	-	-	-	-
Ce_fissilis.0	2	3263.	Chlorophyll a-b binding protein 16,	4789	0	0	0	0.00088	-	Unique 0-days	-	-	-	-	-	-

05035.1		68	chloroplastic					7476								
Ce_fissilis.015416.1	2	3412.03	Ras-related protein RABA5d	2548	0	0	0	0.00642072	-	Unique 0-days	-	-	-	-	-	-
Ce_fissilis.004794.1	2	2361.02	2-hydroxyacyl-CoA lyase	0	23901	39458	38275	-	-	Unique 3-days	0.019292236	0.72325992	UP	0.026330559	0.679342912	UP
Ce_fissilis.000091.1	5	2852.95	Probable 2-oxoglutarate-dependent dioxygenase At5g05600	0	68927	122214	90557	-	-	Unique 3-days	0.034790723	0.826269444	UP	0.115047181	0.393752186	UNCHANGED
Ce_fissilis.000431.1	2	1036.82	Universal stress protein PHOS32	0	152732	0	0	-	-	Unique 3-days	0.033932432	-	Unique 3-days	0.033932432	-	Unique 3-days
Ce_fissilis.006691.2	4	1383.07	Isocitrate dehydrogenase [NADP]	0	3329	4409	0	-	-	Unique 3-days	0.422608577	0.405259384	UNCHANGED	0.015313076	-	Unique 3-days
Ce_fissilis.000729.1	4	806.76	1-aminocyclopropane-1-carboxylate oxidase 1	0	46948	33561	20804	-	-	Unique 3-days	0.378651193	-0.484280394	UNCHANGED	0.083872912	-1.174207002	UNCHANGED
Ce_fissilis.000335.1	3	355.19	26S proteasome non-ATPase regulatory subunit 2 homolog A	0	18894	14248	12278	-	-	Unique 3-days	0.247468745	-0.407163209	UNCHANGED	0.08588052	-0.621836917	UNCHANGED
Ce_fissilis.018656.2	2	747.22	Aspartate aminotransferase, cytoplasmic	0	94554	111028	89809	-	-	Unique 3-days	0.17846531	0.231712347	UNCHANGED	0.58426464	-0.074279083	UNCHANGED
Ce_fissilis.004464.1	2	496.04	Beta-ureidopropionase	0	20028	22140	15027	-	-	Unique 3-days	0.610695054	0.14459113	UNCHANGED	0.172091278	-0.414469353	UNCHANGED
Ce_fissilis.008823.1	2	495.00	Dihydropyrimidinase	0	36224	32405	33156	-	-	Unique 3-days	0.509942975	-0.160738414	UNCHANGED	0.486179862	-0.127648116	UNCHANGED
Ce_fissilis.010254.1	3	1347.35	Expansin-like B1	0	41191	27747	29264	-	-	Unique 3-days	0.072066831	-0.570016572	UNCHANGED	0.188046573	-0.493203757	UNCHANGED
Ce_fissilis.016383.3	2	989.06	Flavanone 3-dioxygenase	0	47794	76214	54557	-	-	Unique 3-days	0.136106464	0.673229675	UNCHANGED	0.599708881	0.190921578	UNCHANGED
Ce_fissilis.001890.1	2	876.66	Lignin-forming anionic peroxidase	0	19800	7328	6307	-	-	Unique 3-days	0.065812394	-1.433906966	UNCHANGED	0.053299739	-1.650361913	UNCHANGED
Ce_fissilis.008577.1	5	926.81	Phenylalanine ammonia-lyase	0	28548	18639	20089	-	-	Unique 3-days	0.085763528	-0.615088482	UNCHANGED	0.138840542	-0.506983336	UNCHANGED
Ce_fissilis.000001.1	2	372.96	Presequence protease 2, chloroplastic/mitochondrial	0	22170	21518	15838	-	-	Unique 3-days	0.809739329	-0.043054261	UNCHANGED	0.112279566	-0.485212095	UNCHANGED
Ce_fissilis.014865.1	10	2891.83	Probable aldo-keto reductase 1	0	12278	28432	8827	-	-	Unique 3-days	0.180298352	1.211435266	UNCHANGED	0.251010172	-0.476068827	UNCHANGED
Ce_fissilis.009216.1	3	402.68	Probable glutamyl endopeptidase, chloroplastic	0	24225	20396	18558	-	-	Unique 3-days	0.256238385	-0.248236891	UNCHANGED	0.055217495	-0.384507808	UNCHANGED
Ce_fissilis.016304.1	8	1091.02	Probable lactoylglutathione lyase, chloroplastic	0	33560	48406	43228	-	-	Unique 3-days	0.024399497	0.528440557	UNCHANGED	0.09919991	0.365195511	UNCHANGED
Ce_fissilis.010515.1	2	565.84	Probable prolyl 4-hydroxylase 10	0	61869	35574	33728	-	-	Unique 3-days	0.152092712	-0.798406018	UNCHANGED	0.122508775	-0.875283558	UNCHANGED
Ce_fissilis.012480.1	5	4040.81	Probable xyloglucan endotransglucosylase/hydrolase protein 5	0	15395	15655	15875	-	-	Unique 3-days	0.950541163	0.024104451	UNCHANGED	0.886908025	0.04425128	UNCHANGED
Ce_fissilis.006269.1	7	2790.18	Protein of unknown function, DUF642	0	65427	69845	75638	-	-	Unique 3-days	0.788676523	0.094262409	UNCHANGED	0.292769857	0.209211492	UNCHANGED
Ce_fissilis.013173.1	3	681.70	Pyruvate kinase isozyme A, chloroplastic	0	48862	38528	33782	-	-	Unique 3-days	0.068751022	-0.342806499	UNCHANGED	0.056744567	-0.532440658	UNCHANGED

Ce_fissilis.011761.1	7	4911.36	Ras-related protein RABH1e	0	21440	16807	17112	-	-	Unique 3-days	0.015373591	-0.351260155	UNCHANGED	0.012661258	-0.325264019	UNCHANGED
Ce_fissilis.013418.1	4	643.34	Subtilisin-like protease SBT1.8	0	27136	25996	21633	-	-	Unique 3-days	0.890107742	-0.061925106	UNCHANGED	0.065313144	-0.326992153	UNCHANGED
Ce_fissilis.018184.1	2	398.37	T-complex protein 1 subunit zeta 1	0	28216	23972	13074	-	-	Unique 3-days	0.630941254	-0.235200306	UNCHANGED	0.074103427	-1.109866705	UNCHANGED
Ce_fissilis.000573.1	2	1148.20	Wound-induced protein WIN2	0	33468	21794	23947	-	-	Unique 3-days	0.171412168	-0.618817418	UNCHANGED	0.022866769	-0.482955375	UNCHANGED
Ce_fissilis.009003.1	7	1780.17	Argininosuccinate synthase, chloroplastic	0	101794	79810	62223	-	-	Unique 3-days	0.366744827	-0.351015389	UNCHANGED	0.029260856	-0.710146696	DOWN
Ce_fissilis.018656.3	9	1815.69	Aspartate aminotransferase 3, chloroplastic	0	38517	37079	18483	-	-	Unique 3-days	0.797925064	-0.054888635	UNCHANGED	0.004149997	-1.05930857	DOWN
Ce_fissilis.006559.1	3	1263.89	Guanosine nucleotide diphosphate dissociation inhibitor At5g09550	0	29288	25619	13190	-	-	Unique 3-days	0.481954124	-0.193089354	UNCHANGED	0.001648504	-1.150810824	DOWN
Ce_fissilis.018094.1	8	752.68	Heat shock protein 90-6, mitochondrial	0	23383	27364	8669	-	-	Unique 3-days	0.724467058	0.226840662	UNCHANGED	0.011417738	-1.431421165	DOWN
Ce_fissilis.002946.1	3	534.55	Organellar oligopeptidase A, chloroplastic/mitochondrial	0	17919	15553	4969	-	-	Unique 3-days	0.823307651	-0.204361513	UNCHANGED	0.044742844	-1.850593486	DOWN
Ce_fissilis.015473.1	9	938.90	Peroxisomal acyl-coenzyme A oxidase 1	0	57320	39745	17312	-	-	Unique 3-days	0.412206072	-0.528264318	UNCHANGED	0.007068115	-1.727240354	DOWN
Ce_fissilis.007528.1	6	1281.71	Plastidial pyruvate kinase 2	0	30221	24868	9391	-	-	Unique 3-days	0.723978858	-0.281279112	UNCHANGED	0.009719771	-1.686223077	DOWN
Ce_fissilis.006571.1	3	728.81	T-complex protein 1 subunit gamma	0	90885	79619	46833	-	-	Unique 3-days	0.784518164	-0.190922782	UNCHANGED	0.032999252	-0.956507259	DOWN
Ce_fissilis.014244.1	2	1317.64	40S ribosomal protein S3-3	0	22954	36204	9494	-	-	Unique 3-days	0.600691983	0.65738257	UNCHANGED	-	-	-
Ce_fissilis.009700.1	2	446.66	Chaperonin CPN60-like 2, mitochondrial	0	15451	9036	9261	-	-	Unique 3-days	0.040601181	-0.773923351	DOWN	0.04361836	-0.73843602	DOWN
Ce_fissilis.010259.1	2	403.43	Dihydrolipoyl dehydrogenase 1, chloroplastic	0	56616	44332	31458	-	-	Unique 3-days	-	-	-	0.003290459	-0.847771833	DOWN
Ce_fissilis.003154.2	8	1675.54	4-hydroxy-tetrahydrodipicolinate reductase 2, chloroplastic	45339	28269	47333	57441	0.057885694	-0.681543797	UNCHANGED	0.015251461	0.743648197	UP	0.010350871	1.022893861	UP
Ce_fissilis.000745.1	17	8222.27	Alpha-galactosidase 1	125526	117059	183379	204427	0.528911614	-0.10074746	UNCHANGED	0.004441018	0.647593075	UP	0.012463928	0.804347816	UP
Ce_fissilis.011698.1	5	5611.82	Alpha-galactosidase 1	509937	17511	43364	54784	0.077415925	-4.863995655	UNCHANGED	0.027471327	1.308235056	UP	0.029672635	1.645509711	UP
Ce_fissilis.005032.1	17	12841.51	DNA damage-repair/toleration protein DRT102	240032	212690	329582	355216	0.230768502	-0.174478813	UNCHANGED	0.003281391	0.631887023	UP	0.024919428	0.739945721	UP
Ce_fissilis.006770.1	24	11064.62	Enolase	69943	45160	102338	143253	0.268171655	-0.6311280	UNCHANGED	0.01116813	1.180210546	UP	0.00110874	1.665437748	UP

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Ce_fissilis.008930.1	2	748.18	Formamidase	12247	19579	38669	41257	0.07067072	0.67681486	UNCHANGED	0.00028791	0.981901155	UP	0.000202709	1.075356401	UP
Ce_fissilis.018872.1	2	855.94	Glutathione S-transferase L2, chloroplastic	9895	8490	19208	18428	0.339276141	-0.220935671	UNCHANGED	0.002345742	1.177898089	UP	0.020286872	1.118133616	UP
Ce_fissilis.007676.1	7	2718.32	Importin subunit alpha-1	5173	7045	14426	13855	0.254148833	0.445530321	UNCHANGED	0.002361841	1.034028308	UP	0.003360949	0.975768317	UP
Ce_fissilis.014897.1	7	1961.69	L-idonate 5-dehydrogenase	25095	30670	56527	66080	0.3300287	0.289412367	UNCHANGED	0.004067158	0.882089698	UP	0.012140635	1.107378154	UP
Ce_fissilis.012542.2	5	2574.34	Non-functional NADPH-dependent codeinone reductase 2	20674	34241	125970	93355	0.248369104	0.727944594	UNCHANGED	0.019675959	1.879265591	UP	0.020682361	1.446981545	UP
Ce_fissilis.015481.1	8	3110.97	Probable mannitol dehydrogenase	5737	6446	33051	83622	0.574642251	0.16825828	UNCHANGED	0.022479989	2.358183261	UP	0.000489752	3.697375837	UP
Ce_fissilis.000071.1	5	4943.57	Ribulose bisphosphate carboxylase small chain, chloroplastic	37920	37437	125362	61301	0.940666628	-0.018498253	UNCHANGED	0.003648066	1.743552246	UP	0.005435609	0.71142937	UP
Ce_fissilis.000495.1	4	2563.39	Tryptophan synthase alpha chain, chloroplastic	22209	17012	28794	32866	0.34084787	-0.384586661	UNCHANGED	0.042698853	0.759213747	UP	0.009126447	0.950057422	UP
Ce_fissilis.000430.1	4	3654.66	Universal stress protein PHOS32	29942	39146	78662	77269	0.1447328	0.386695737	UNCHANGED	0.008978927	1.006794548	UP	0.000386511	0.981013295	UP
Ce_fissilis.016967.1	12	9684.08	Beta carbonic anhydrase 1, chloroplastic	100343	123183	257017	198806	0.414374028	0.295870025	UNCHANGED	0.029969085	1.06105511	UP	0.099851923	0.690551177	UNCHANGED
Ce_fissilis.002621.1	11	17312.67	Glutathione S-transferase F9	163043	216001	432760	340858	0.642201907	0.405787696	UNCHANGED	0.031302121	1.002529537	UP	0.082909552	0.658135475	UNCHANGED
Ce_fissilis.009612.1	15	1373.75	Probable alpha-mannosidase At5g13980	68219	46217	80930	65148	0.050727947	-0.561728167	UNCHANGED	0.012741314	0.808238748	UP	0.096462284	0.495285231	UNCHANGED
Ce_fissilis.012774.2	13	3588.66	Probable polygalacturonase	73595	108135	214631	99467	0.121992811	0.555158252	UNCHANGED	0.004234198	0.989024163	UP	0.656588913	-0.12054852	UNCHANGED
Ce_fissilis.009689.2	11	3801.01	Ras-related protein RABB1b	38014	25398	39846	34333	0.056205702	-0.581772599	UNCHANGED	0.000188364	0.649695414	UP	0.008624959	0.434865129	UNCHANGED
Ce_fissilis.017963.1	12	2065.77	Selenium-binding protein 2	67520	71225	107988	70345	0.715292744	0.077077938	UNCHANGED	0.009779251	0.600413084	UP	0.905178169	-0.017938028	UNCHANGED
Ce_fissilis.007803.1	14	3592.03	Sorbitol dehydrogenase	44011	59847	96578	87858	0.085186381	0.443413237	UNCHANGED	0.007659198	0.690403992	UP	0.001345573	0.553882596	UNCHANGED
Ce_fissilis.000919.1	5	8603.12	2S seed storage protein 5	148985	18021	5428	47936	0.059955428	-3.047403844	UNCHANGED	0.22566124	-1.731303152	UNCHANGED	0.036523011	1.411418789	UP
Ce_fissilis.000840.1	7	2106.30	Acetylornithine deacetylase	81831	61736	91130	94756	0.121634679	-0.406531554	UNCHANGED	0.024450021	0.561812298	UNCHANGED	0.035970874	0.618110363	UP
Ce_fissilis.014749.1	13	18144.39	ADP-ribosylation factor 1	133284	204663	261166	327497	0.052006129	0.618751988	UNCHANGED	0.039072491	0.351713839	UNCHANGED	0.004070881	0.678230386	UP
Ce_fissilis.004204.1	7	1061.93	Alcohol dehydrogenase-like 7	62407	79019	105641	122399	0.062616772	0.340475368	UNCHANGED	0.045766999	0.41890749	UNCHANGED	0.001113475	0.631330292	UP
Ce_fissilis.007214.1	21	1896.71	Beta-galactosidase 9	141183	102054	133990	157480	0.086750747	-0.468235659	UNCHANGED	0.060699142	0.392799334	UNCHANGED	0.007689665	0.625842083	UP
Ce_fissilis.005821.1	13	2557.87	Cysteine synthase	80272	56299	74608	92289	0.177517492	-0.511796758	UNCHANGED	0.164767961	0.406217012	UNCHANGED	0.035272346	0.713042056	UP
Ce_fissilis.014101.1	5	784.23	Dihydropyrimidine dehydrogenase (NADP(+)), chloroplastic	20227	37263	43917	60482	0.069801758	0.881425467	UNCHANGED	0.508441272	0.23705093	UNCHANGED	0.034280993	0.698761019	UP

Ce_fissilis.003571.1	6	6240.66	MLP-like protein 43	63771	113405	189089	200863	0.146244514	0.830507913	UNCHANGED	0.102784739	0.737581755	UNCHANGED	0.030450454	0.824726606	UP
Ce_fissilis.002226.1	9	4541.37	Peroxidase 3	299935	142969	228437	244459	0.055322833	-1.068950833	UNCHANGED	0.208573051	0.676099032	UNCHANGED	0.039822417	0.773891746	UP
Ce_fissilis.013768.1	5	2923.93	Peroxidase 4	107705	72505	106602	113375	0.049674468	-0.570927142	UNCHANGED	0.079585831	0.556076728	UNCHANGED	0.02388531	0.644936823	UP
Ce_fissilis.008583.1	4	2358.90	Peroxidase 53	89089	136196	310512	221501	0.055838134	0.612361275	UNCHANGED	0.060816695	1.188966085	UNCHANGED	0.007125209	0.701629651	UP
Ce_fissilis.003326.2	11	8390.75	Polygalacturonase inhibitor	56761	89326	188174	197005	0.129485875	0.65417424	UNCHANGED	0.07282247	1.074909856	UNCHANGED	0.003333468	1.141073984	UP
Ce_fissilis.015933.1	12	2409.94	Probable acetyl-CoA acetyltransferase, cytosolic 2	41314	45654	78884	85196	0.404693084	0.144096365	UNCHANGED	0.110509794	0.789003661	UNCHANGED	0.00693518	0.900058119	UP
Ce_fissilis.009745.2	20	9247.79	Probable cinnamyl alcohol dehydrogenase 1	224455	252493	285172	383712	0.118112067	0.169817102	UNCHANGED	0.169344085	0.175589919	UNCHANGED	0.011658045	0.603782615	UP
Ce_fissilis.016894.1	20	10559.77	Probable UDP-arabinopyranose mutase 2	50597	51325	75786	94292	0.852007048	0.020634746	UNCHANGED	0.121942659	0.562249045	UNCHANGED	4.75016E-06	0.877458901	UP
Ce_fissilis.008692.1	4	1133.83	Rhodanese-like domain-containing protein 9, chloroplastic	43509	24977	31231	38391	0.142988385	-0.800707236	UNCHANGED	0.551046428	0.322367009	UNCHANGED	0.016358578	0.620178219	UP
Ce_fissilis.008197.1	3	1722.64	Ubiquitin thioesterase OTU1	15996	22628	31440	35933	0.172063511	0.500400827	UNCHANGED	0.025881688	0.474489028	UNCHANGED	0.006004308	0.667211858	UP
Ce_fissilis.007298.1	3	1151.09	NAD(P)-binding domain containing protein	38821	27513	29600	44869	0.192760726	-0.49672286	UNCHANGED	0.466417676	0.105460823	UNCHANGED	0.012576393	0.705595238	UP
Ce_fissilis.013669.1	8	5033.56	Zeaxanthin epoxidase, chloroplastic	126762	80924	107732	172410	0.142426706	-0.647479924	UNCHANGED	0.471609192	0.412793429	UNCHANGED	0.03576613	1.091193204	UP
Ce_fissilis.004298.1	17	10935.53	(+)-neomenthol dehydrogenase	164706	189006	201522	220165	0.716699754	0.198540368	UNCHANGED	0.709500761	0.092500328	UNCHANGED	0.643891973	0.220152626	UNCHANGED
Ce_fissilis.016765.1	20	15060.47	(R,S)-reticuline 7-O-methyltransferase	378752	356571	395821	407350	0.699889224	-0.087064928	UNCHANGED	0.505278822	0.150658693	UNCHANGED	0.423389974	0.192079817	UNCHANGED
Ce_fissilis.015713.1	14	2273.14	(S)-2-hydroxy-acid oxidase GLO1	141716	176600	209457	227767	0.056022126	0.31747938	UNCHANGED	0.07851632	0.246170603	UNCHANGED	0.02068008	0.367076533	UNCHANGED
Ce_fissilis.001212.2	2	3764.49	14 kDa proline-rich protein DC2.15	420644	460291	537075	520088	0.340905156	0.129946044	UNCHANGED	0.002349377	0.222578453	UNCHANGED	0.237178615	0.176209697	UNCHANGED
Ce_fissilis.010535.1	18	22039.53	14-3-3 protein 4	273993	269903	416396	304804	0.979411012	-0.021697616	UNCHANGED	0.330852803	0.625515439	UNCHANGED	0.656844426	0.175442605	UNCHANGED
Ce_fissilis.004765.1	12	5307.34	14-3-3 protein 6	17308	27022	46280	29847	0.364150203	0.642717758	UNCHANGED	0.302872862	0.776255893	UNCHANGED	0.768070249	0.143435779	UNCHANGED
Ce_fissilis.017019.1	18	15038.67	14-3-3-like protein	212159	133766	250995	181268	0.470179849	-0.665437351	UNCHANGED	0.297974905	0.907950819	UNCHANGED	0.293260153	0.438411714	UNCHANGED
Ce_fissilis.013638.1	9	8508.52	14-3-3-like protein B	85505	34509	24946	25782	0.344239168	-1.309014825	UNCHANGED	0.068552981	-0.468194737	UNCHANGED	0.056634885	-0.42063436	UNCHANGED
Ce_fissilis.018774.1	15	10388.91	14-3-3-like protein D	196951	334948	402225	321677	0.232997625	0.766100109	UNCHANGED	0.592591511	0.264068328	UNCHANGED	0.85292275	-0.058320443	UNCHANGED
Ce_fissilis.018517.1	2	681.40	1-deoxy-D-xylulose 5-phosphate reductoisomerase, chloroplastic	27647	48047	43718	45971	0.130206954	0.797330798	UNCHANGED	0.702444752	-0.136203442	UNCHANGED	0.861725428	-0.063727987	UNCHANGED
Ce_fissilis.005977.1	25	13054.48	2,3-dimethylmalate lyase	386174	580945	629166	655515	0.032232038	0.589150133	UNCHANGED	0.149694382	0.115037532	UNCHANGED	0.058389036	0.174227114	UNCHANGED
Ce_fissilis.0	18	8534.	20 kDa chaperonin, chloroplastic	54820	66299	781913	802373	0.24079	0.2743005	UNCHANGED	0.02311	0.238002441	UNCHANGED	0.01055	0.27526	UNCHANGED

10974.1		94		1	8			9077	76		9641			4285	7816	
Ce_fissilis.007644.1	6	3615.04	26S proteasome non-ATPase regulatory subunit 8 homolog A	54893	20689	25609	26672	0.437399534	-1.407789265	UNCHANGED	0.299853898	0.307843034	UNCHANGED	0.133921424	0.366481067	UNCHANGED
Ce_fissilis.007313.1	2	965.34	26S proteasome regulatory subunit 8 homolog B	17101	21042	17737	27330	0.289444978	0.299189643	UNCHANGED	0.084491493	-0.246509729	UNCHANGED	0.452243258	0.377193	UNCHANGED
Ce_fissilis.018219.1	17	7089.19	2-alkenal reductase (NADP(+)-dependent)	82278	58312	46750	48055	0.024407999	-0.496702574	UNCHANGED	0.021308596	-0.318824689	UNCHANGED	0.029871609	-0.279103052	UNCHANGED
Ce_fissilis.018219.2	23	7668.43	2-alkenal reductase (NADP(+)-dependent)	82667	88223	131134	127791	0.316892507	0.093844846	UNCHANGED	0.004956001	0.571813661	UNCHANGED	0.003110687	0.53456461	UNCHANGED
Ce_fissilis.018219.3	19	12275.03	2-alkenal reductase (NADP(+)-dependent)	295309	376573	398993	466286	0.067424988	0.350705947	UNCHANGED	0.387359855	0.083434465	UNCHANGED	0.04532349	0.308284616	UNCHANGED
Ce_fissilis.018333.1	6	3026.62	2-alkenal reductase (NADP(+)-dependent)	124448	140839	178961	203180	0.290596706	0.178498003	UNCHANGED	0.125409346	0.34560647	UNCHANGED	0.012151727	0.528717639	UNCHANGED
Ce_fissilis.010608.1	16	15758.44	2-Cys peroxiredoxin BAS1-like, chloroplastic	757595	971909	1038643	1189499	0.027432999	0.359393796	UNCHANGED	0.436480451	0.095806251	UNCHANGED	0.00742532	0.291461183	UNCHANGED
Ce_fissilis.006652.1	12	1135.68	2-hydroxyacyl-CoA lyase	92594	84141	70726	119020	0.698385205	-0.138113035	UNCHANGED	0.418237896	-0.250567933	UNCHANGED	0.324698214	0.500321248	UNCHANGED
Ce_fissilis.000498.1	10	2078.87	2-methylacyl-CoA dehydrogenase, mitochondrial	64010	63819	72203	80538	0.989471119	-0.004303771	UNCHANGED	0.179458281	0.178056363	UNCHANGED	0.156342032	0.335676108	UNCHANGED
Ce_fissilis.014783.1	2	625.23	2-oxoisovalerate dehydrogenase subunit beta 1, mitochondrial	42228	42657	52218	51716	0.939632099	0.014576893	UNCHANGED	0.068441875	0.291760091	UNCHANGED	0.067073746	0.277823537	UNCHANGED
Ce_fissilis.006734.1	10	9625.71	31 kDa ribonucleoprotein, chloroplastic	307504	210316	217776	246407	0.037909019	-0.548048362	UNCHANGED	0.886116081	0.050286645	UNCHANGED	0.455519853	0.228487157	UNCHANGED
Ce_fissilis.005744.1	4	4956.35	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	174225	122858	110263	116673	0.058483201	-0.503955214	UNCHANGED	0.251696106	-0.156040926	UNCHANGED	0.603428398	-0.074525888	UNCHANGED
Ce_fissilis.015290.1	3	1096.70	3-hydroxyisobutyryl-CoA hydrolase-like protein 3, mitochondrial	75303	69964	86347	95488	0.711711145	-0.106092972	UNCHANGED	0.286463247	0.303527661	UNCHANGED	0.016323009	0.44870049	UNCHANGED
Ce_fissilis.015290.2	8	3925.08	3-hydroxyisobutyryl-CoA hydrolase-like protein 3, mitochondrial	85472	74597	85860	97290	0.394397648	-0.196324071	UNCHANGED	0.46610747	0.20285838	UNCHANGED	0.262818522	0.383167466	UNCHANGED
Ce_fissilis.001679.1	8	3343.95	3-isopropylmalate dehydratase small subunit 3	95928	145171	149088	158098	0.033357411	0.597737725	UNCHANGED	0.546720706	0.03840647	UNCHANGED	0.357634673	0.123066577	UNCHANGED
Ce_fissilis.017631.1	10	3416.07	3-isopropylmalate dehydrogenase, chloroplastic	169027	122465	136981	151573	0.103282588	-0.464880299	UNCHANGED	0.352134565	0.16160706	UNCHANGED	0.03815065	0.307635137	UNCHANGED
Ce_fissilis.000393.1	9	2220.31	3-oxoacyl-[acyl-carrier-protein] reductase, chloroplastic	103954	110957	120532	140823	0.411228739	0.094064375	UNCHANGED	0.042133547	0.119408538	UNCHANGED	0.110901209	0.3438791	UNCHANGED
Ce_fissilis.016174.1	13	5328.90	3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplastic	140853	199375	228744	251064	0.09405607	0.501291951	UNCHANGED	0.221968804	0.198250784	UNCHANGED	0.109462809	0.332571934	UNCHANGED
Ce_fissilis.011254.2	7	1299.44	3-oxoacyl-[acyl-carrier-protein] synthase II, chloroplastic	50487	57026	63651	70333	0.232498119	0.175710334	UNCHANGED	0.1409065	0.158560236	UNCHANGED	0.017910125	0.30258541	UNCHANGED
Ce_fissilis.018749.1	6	1114.99	3-oxoacyl-[acyl-carrier-protein] synthase III, chloroplastic	35008	46633	42671	48522	0.088525623	0.413670039	UNCHANGED	0.4712741	-0.128098761	UNCHANGED	0.773390223	0.057274425	UNCHANGED
Ce_fissilis.002720.1	14	21774.23	40S ribosomal protein SA	565722	707226	863372	874388	0.07229474	0.322077925	UNCHANGED	0.089800304	0.287810929	UNCHANGED	0.00258452	0.306102784	UNCHANGED
Ce_fissilis.015165.1	4	659.41	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase, chloroplastic/chromoplastic	23878	13310	17967	18878	0.079831831	-0.843239746	UNCHANGED	0.242755739	0.432869298	UNCHANGED	0.143029443	0.504235041	UNCHANGED
Ce_fissilis.003122.1	3	493.93	4-hydroxy-tetrahydrodipicolinate synthase, chloroplastic	35439	37118	32938	37344	0.794003388	0.066816449	UNCHANGED	0.505586805	-0.172383294	UNCHANGED	0.970184864	0.008727337	UNCHANGED

Ce_fissilis.016614.1	3	22752.92	60S acidic ribosomal protein P1-1	399978	533602	550438	628194	0.045859982	0.415845628	UNCHANGED	0.687009092	0.044815979	UNCHANGED	0.103151544	0.235444468	UNCHANGED
Ce_fissilis.006173.1	5	3432.62	60S acidic ribosomal protein P2B	107297	146903	163148	169561	0.007133148	0.453257569	UNCHANGED	0.307121372	0.151324647	UNCHANGED	0.018280711	0.206944741	UNCHANGED
Ce_fissilis.014568.1	5	11612.15	60S acidic ribosomal protein P2B	167054	202050	204683	235479	0.18007483	0.274397529	UNCHANGED	0.916215776	0.018682889	UNCHANGED	0.107739113	0.220886505	UNCHANGED
Ce_fissilis.017422.1	4	593.95	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic	32584	39058	41646	44765	0.420482541	0.261458461	UNCHANGED	0.06312506	0.092548056	UNCHANGED	0.060000437	0.196741844	UNCHANGED
Ce_fissilis.005099.1	3	462.34	Acetylglutamate kinase, chloroplastic	33082	30570	28741	32854	0.615392131	-0.113931929	UNCHANGED	0.290911272	-0.089019903	UNCHANGED	0.540272886	0.103939916	UNCHANGED
Ce_fissilis.011946.2	8	6998.09	Acidic endochitinase	267883	282291	339779	336796	0.830156523	0.075581929	UNCHANGED	0.182281528	0.26741318	UNCHANGED	0.242837569	0.254691011	UNCHANGED
Ce_fissilis.002366.1	2	678.94	ACT domain-containing protein ACR12	52372	38159	40932	38897	0.37984874	-0.456785508	UNCHANGED	0.654523723	0.101218541	UNCHANGED	0.918209185	0.02766053	UNCHANGED
Ce_fissilis.012078.1	12	21929.31	Actin	24837	32423	46184	35304	0.012396308	0.384521009	UNCHANGED	0.007468988	0.510346112	UNCHANGED	0.137596827	0.122795717	UNCHANGED
Ce_fissilis.014428.1	33	60158.35	Actin-7	1911082	2109965	2776059	2703435	0.579578837	0.142829836	UNCHANGED	0.078139785	0.395819091	UNCHANGED	0.064246968	0.357574224	UNCHANGED
Ce_fissilis.000363.1	4	3194.69	Actin-depolymerizing factor 1	39443	74961	83230	58689	0.154532342	0.926354444	UNCHANGED	0.544657003	0.150973493	UNCHANGED	0.463828066	-0.353037602	UNCHANGED
Ce_fissilis.018120.1	4	2994.34	Actin-depolymerizing factor 2	39824	47994	57005	43410	0.570954553	0.269217207	UNCHANGED	0.177116454	0.248212612	UNCHANGED	0.7752254	-0.144825224	UNCHANGED
Ce_fissilis.007894.1	4	959.76	Actin-related protein 4	10236	14501	16855	20030	0.231358763	0.502441241	UNCHANGED	0.471452874	0.217062294	UNCHANGED	0.161475397	0.466024064	UNCHANGED
Ce_fissilis.011305.1	3	1045.01	Actin-related protein 7	390536	414422	301896	335871	0.749150283	0.085645857	UNCHANGED	0.10841572	-0.457048082	UNCHANGED	0.359946513	-0.303192596	UNCHANGED
Ce_fissilis.016159.1	2	342.99	Acylamino-acid-releasing enzyme	18249	30492	26170	25905	0.074934327	0.740613371	UNCHANGED	0.367811445	-0.220526045	UNCHANGED	0.342203064	-0.235228044	UNCHANGED
Ce_fissilis.007583.1	8	2130.78	Adenine phosphoribosyltransferase 1, chloroplastic	78292	123511	126610	126121	0.110544208	0.657693446	UNCHANGED	0.82815329	0.035755747	UNCHANGED	0.877713295	0.030175441	UNCHANGED
Ce_fissilis.016186.1	15	10002.48	Adenosine kinase 2	106718	139992	156404	168626	0.059785287	0.391534817	UNCHANGED	0.026544406	0.15993073	UNCHANGED	0.004376183	0.268483988	UNCHANGED
Ce_fissilis.018746.1	13	2856.18	Adenylosuccinate synthetase 2, chloroplastic	57911	90940	99087	117599	0.05106036	0.651088667	UNCHANGED	0.458655524	0.123780787	UNCHANGED	0.201576272	0.370883431	UNCHANGED
Ce_fissilis.008343.1	3	3056.66	Adenylylsulfatase HINT1	112094	121221	118476	132840	0.303426176	0.112937526	UNCHANGED	0.774999092	-0.033048809	UNCHANGED	0.045194142	0.132043714	UNCHANGED
Ce_fissilis.014746.1	14	25544.54	ADP-ribosylation factor 2	37884	28659	27035	36867	0.288525459	-0.402595512	UNCHANGED	0.576020931	-0.084177107	UNCHANGED	0.018654438	0.363328089	UNCHANGED
Ce_fissilis.018575.1	25	16083.11	Aldehyde dehydrogenase family 2 member B4, mitochondrial	767864	826761	912215	984251	0.552010599	0.106619092	UNCHANGED	0.047279053	0.141903891	UNCHANGED	0.013850554	0.251556232	UNCHANGED
Ce_fissilis.001312.1	15	2797.55	Aldehyde dehydrogenase family 7 member B4	99071	95023	127054	136593	0.863436394	-0.060179311	UNCHANGED	0.019337872	0.419091435	UNCHANGED	0.012592651	0.52352697	UNCHANGED
Ce_fissilis.004271.1	7	757.38	Aldehyde oxidase GLOX1	76517	45743	60236	47787	0.071379061	-0.742213936	UNCHANGED	0.121813529	0.397057331	UNCHANGED	0.738471591	0.063056851	UNCHANGED
Ce_fissilis.014152.1	6	1553.48	Aldose 1-epimerase	43337	62834	76364	73979	0.171580658	0.535940144	UNCHANGED	0.136869546	0.281337949	UNCHANGED	0.358586411	0.235573939	UNCHANGED
Ce_fissilis.001385.1	2	353.97	Allene oxide cyclase, chloroplastic	154145	132317	132274	157330	0.416455361	-0.220291995	UNCHANGED	0.998599022	-0.000468921	UNCHANGED	0.33419219	0.249802343	UNCHANGED

Ce_fissilis.018295.1	7	5611.30	Allene oxide cyclase, chloroplastic	400552	570303	610857	698148	0.019732191	0.509739756	UNCHANGED	0.338178419	0.099106048	UNCHANGED	0.00655538	0.29180492	UNCHANGED
Ce_fissilis.015584.1	2	397.57	Alpha-amylase	20448	17891	20531	23968	0.319847573	-0.192749232	UNCHANGED	0.493789208	0.198581582	UNCHANGED	0.128560434	0.421875501	UNCHANGED
Ce_fissilis.008304.1	12	1997.12	Alpha-galactosidase 3	546539	523143	571774	621740	0.608706671	-0.063120902	UNCHANGED	0.473230813	0.128240606	UNCHANGED	0.062055859	0.249107266	UNCHANGED
Ce_fissilis.013568.1	21	1938.27	Alpha-glucosidase	219150	153436	194548	223034	0.004196838	-0.514285529	UNCHANGED	0.052585753	0.342489796	UNCHANGED	0.003706549	0.539631212	UNCHANGED
Ce_fissilis.015371.1	2	811.45	Alpha-L-fucosidase 3	11654	23588	30617	18501	0.307570221	1.017238077	UNCHANGED	0.546392712	0.376285341	UNCHANGED	0.681500745	-0.350473037	UNCHANGED
Ce_fissilis.017944.1	37	5850.83	Alpha-xylosidase 1	319549	317936	322131	395371	0.978375816	-0.007304813	UNCHANGED	0.935310706	0.018911645	UNCHANGED	0.183428582	0.314473095	UNCHANGED
Ce_fissilis.006567.1	3	460.36	Aminoacylase-1	12102	19894	19306	21313	0.061449593	0.717139441	UNCHANGED	0.674794329	-0.04327604	UNCHANGED	0.428620787	0.099408356	UNCHANGED
Ce_fissilis.017280.1	12	3623.57	Ankyrin repeat domain-containing protein 2B	183611	221472	305650	309201	0.139436995	0.270468778	UNCHANGED	0.01205537	0.464759997	UNCHANGED	0.002114634	0.481424397	UNCHANGED
Ce_fissilis.012274.1	2	2537.22	Aquaporin PIP2-7	239828	163640	186213	178193	0.337438284	-0.551472656	UNCHANGED	0.368190722	0.186427061	UNCHANGED	0.369421121	0.122916571	UNCHANGED
Ce_fissilis.017121.1	2	4324.09	Aquaporin TIP1-1	476260	490506	320041	318907	0.88056687	0.042521918	UNCHANGED	0.118164163	-0.616015308	UNCHANGED	0.140984486	-0.621134529	UNCHANGED
Ce_fissilis.004804.1	6	1787.31	Aromatic aminotransferase ISS1	44286	59184	61729	65302	0.07011701	0.418349295	UNCHANGED	0.697884143	0.060741661	UNCHANGED	0.419575211	0.141935716	UNCHANGED
Ce_fissilis.013077.1	17	2673.58	Aspartic proteinase A1	79461	67738	63093	63011	0.237818048	-0.230275753	UNCHANGED	0.267593128	-0.102496047	UNCHANGED	0.273845884	-0.104360728	UNCHANGED
Ce_fissilis.010338.1	17	12738.20	Aspartyl protease AED3	713642	601593	554735	689627	0.22506659	-0.24641311	UNCHANGED	0.566298677	-0.116990427	UNCHANGED	0.379923172	0.197027946	UNCHANGED
Ce_fissilis.016683.1	14	24340.50	Aspartyl protease AED3	648411	815341	1034229	1087736	0.310600056	0.330493813	UNCHANGED	0.165768594	0.343080237	UNCHANGED	0.189786583	0.415853766	UNCHANGED
Ce_fissilis.014515.1	28	14992.15	ATP synthase subunit alpha, mitochondrial	771281	1033151	987905	1064247	0.006926894	0.421721353	UNCHANGED	0.138483181	-0.064606117	UNCHANGED	0.402419179	0.042782664	UNCHANGED
Ce_fissilis.011041.1	39	39944.33	ATP synthase subunit beta, chloroplastic	1384246	1268378	1380338	1706310	0.62963536	-0.126115246	UNCHANGED	0.559373522	0.122036472	UNCHANGED	0.070147071	0.427894736	UNCHANGED
Ce_fissilis.016865.1	32	44389.43	ATP synthase subunit beta, mitochondrial	1251783	1829732	1703557	1894115	0.004192213	0.547648064	UNCHANGED	0.354759163	-0.103082525	UNCHANGED	0.687425916	0.049891181	UNCHANGED
Ce_fissilis.016594.1	2	487.25	ATPase ARSA1	22403	17737	25228	26958	0.374871478	-0.3369785	UNCHANGED	0.197343003	0.508281404	UNCHANGED	0.10507732	0.603951806	UNCHANGED
Ce_fissilis.004189.1	2	428.02	ATPase ARSA2	31727	33266	36196	40494	0.793229609	0.068337642	UNCHANGED	0.603497001	0.121802386	UNCHANGED	0.00921995	0.283672923	UNCHANGED
Ce_fissilis.002370.1	18	3527.51	ATP-dependent zinc metalloprotease FTSH 2, chloroplastic	130831	238225	301729	327934	0.082732898	0.864617707	UNCHANGED	0.222429123	0.340930703	UNCHANGED	0.100926329	0.461081891	UNCHANGED
Ce_fissilis.009048.1	5	786.81	ATP-dependent zinc metalloprotease FTSH 2, chloroplastic	54900	55639	66110	89030	0.973384799	0.019286919	UNCHANGED	0.40003304	0.248775124	UNCHANGED	0.057545516	0.67818521	UNCHANGED
Ce_fissilis.015339.2	2	997.82	Auxin-induced in root cultures protein 12	69992	49162	50400	60664	0.11984141	-0.509652215	UNCHANGED	0.635111294	0.035884688	UNCHANGED	0.002426662	0.303301613	UNCHANGED
Ce_fissilis.014150.1	17	3731.02	Berberine bridge enzyme-like 13	263157	172990	150852	214570	0.060152365	-0.605239366	UNCHANGED	0.284568999	-0.197554215	UNCHANGED	0.115495951	0.310763218	UNCHANGED

Ce_fissilis.005619.1	19	7024.84	Beta-glucosidase BoGH3B	376304	309987	296575	336038	0.330578623	-0.279688933	UNCHANGED	0.765325547	-0.063813897	UNCHANGED	0.521374649	0.116415597	UNCHANGED
Ce_fissilis.005621.1	3	755.09	Beta-glucosidase BoGH3B	26298	23187	14449	17909	0.732484442	-0.181665271	UNCHANGED	0.346114152	-0.682372661	UNCHANGED	0.544839739	-0.372569348	UNCHANGED
Ce_fissilis.000204.1	4	733.24	Beta-hexosaminidase 1	84700	62377	66614	84640	0.140395121	-0.441350232	UNCHANGED	0.651614116	0.094806106	UNCHANGED	0.061143241	0.440314638	UNCHANGED
Ce_fissilis.006783.1	19	3914.87	Betaine aldehyde dehydrogenase 1, chloroplastic	95202	146227	169697	208641	0.071980397	0.619143584	UNCHANGED	0.269995064	0.214746954	UNCHANGED	0.005400123	0.51280551	UNCHANGED
Ce_fissilis.011879.1	5	560.16	Bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase, chloroplastic	38685	51145	49867	55119	0.003428835	0.402826211	UNCHANGED	0.609582431	-0.036504499	UNCHANGED	0.241339344	0.107959189	UNCHANGED
Ce_fissilis.008783.1	4	1890.05	Bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase	28235	23732	18455	21936	0.464874946	-0.250649075	UNCHANGED	0.045679344	-0.362850807	UNCHANGED	0.377003073	-0.11353188	UNCHANGED
Ce_fissilis.018908.1	5	2768.33	Bifunctional L-3-cyanoalanine synthase/cysteine synthase D1	16591	20130	27132	20291	0.162023129	0.278915341	UNCHANGED	0.090669877	0.430656376	UNCHANGED	0.935929913	0.011505185	UNCHANGED
Ce_fissilis.006939.1	2	709.75	Bifunctional nitrilase/nitrile hydratase NIT4A	12304	15157	15471	14745	0.418953645	0.300927636	UNCHANGED	0.840279612	0.02953495	UNCHANGED	0.499296745	-0.039822751	UNCHANGED
Ce_fissilis.013920.1	4	1496.76	Bifunctional protein FolD 2	13587	27298	24478	21346	0.050297529	1.0065153	UNCHANGED	0.51136921	-0.157298501	UNCHANGED	0.207159547	-0.35478185	UNCHANGED
Ce_fissilis.003393.1	3	832.31	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	29240	26705	28939	33416	0.577953683	-0.130837209	UNCHANGED	0.63914502	0.115933808	UNCHANGED	0.207206534	0.32344117	UNCHANGED
Ce_fissilis.002282.1	18	10371.58	Caffeic acid 3-O-methyltransferase	123110	133797	134726	165324	0.518279549	0.120097369	UNCHANGED	0.950551881	0.009980036	UNCHANGED	0.059710811	0.305250324	UNCHANGED
Ce_fissilis.002282.2	22	12061.67	Caffeic acid 3-O-methyltransferase	524662	439235	466058	554021	0.3684565	-0.256393977	UNCHANGED	0.671970529	0.085516217	UNCHANGED	0.124983	0.334947633	UNCHANGED
Ce_fissilis.013403.1	6	1122.65	Calcium sensing receptor, chloroplastic	74167	67520	82894	93696	0.605437216	-0.135466833	UNCHANGED	0.288219481	0.295954711	UNCHANGED	0.041785773	0.472672555	UNCHANGED
Ce_fissilis.008123.1	3	606.53	calcium-binding EF hand family protein	32223	32546	34740	37612	0.930785895	0.014409325	UNCHANGED	0.435295832	0.094112897	UNCHANGED	0.007923567	0.208725566	UNCHANGED
Ce_fissilis.019088.1	2	878.54	Calcium-binding EF-hand family protein	102704	57283	58298	75914	0.072038794	-0.842302679	UNCHANGED	0.726780921	0.025318571	UNCHANGED	0.091828289	0.406253692	UNCHANGED
Ce_fissilis.002927.1	11	36430.94	Calmodulin-related protein	708628	815921	703978	722054	0.620501058	0.203400618	UNCHANGED	0.369079097	-0.212898713	UNCHANGED	0.368833811	-0.176322089	UNCHANGED
Ce_fissilis.017444.1	3	948.18	Carbamoyl-phosphate synthase small chain, chloroplastic	29028	29697	24632	28159	0.90373161	0.032883315	UNCHANGED	0.399750076	-0.269756359	UNCHANGED	0.802027208	-0.076713147	UNCHANGED
Ce_fissilis.011918.1	7	1300.53	Cathepsin B-like protease 2	64519	49491	63738	40138	0.249735007	-0.382567602	UNCHANGED	0.363314824	0.364992244	UNCHANGED	0.252212757	-0.302195732	UNCHANGED
Ce_fissilis.018166.1	13	11101.99	CBS domain-containing protein CBSX3, mitochondrial	229802	333012	411484	390765	0.03996366	0.535179756	UNCHANGED	0.00292984	0.305262353	UNCHANGED	0.155781323	0.230726821	UNCHANGED
Ce_fissilis.013029.1	8	6585.77	Chitinase 4	217559	22584	34697	37497	0.05313588	-3.268068649	UNCHANGED	0.317840594	0.619537216	UNCHANGED	0.404774864	0.731488982	UNCHANGED
Ce_fissilis.000974.1	9	13341.64	Chlorophyll a-b binding protein 13, chloroplastic	252708	254673	293110	342528	0.980609291	0.011172161	UNCHANGED	0.576777988	0.202798691	UNCHANGED	0.080135232	0.4275803	UNCHANGED
Ce_fissilis.0	14	55681	Chlorophyll a-b binding protein 21,	18294	27391	2672999	2666399	0.03049	0.5822796	UNCHANGED	0.84586	-0.035244574	UNCHANGED	0.37066	-	UNCHANGED

15704.1		.54	chloroplastic	68	03			8543	3		0979			4278	0.038811152	
Ce_fissilis.012313.1	4	8824.41	Chlorophyll a-b binding protein 4, chloroplastic	257724	161478	219984	216795	0.259268046	-0.674491313	UNCHANGED	0.481687752	0.446061401	UNCHANGED	0.192004863	0.424995729	UNCHANGED
Ce_fissilis.000008.2	7	30931.86	Chlorophyll a-b binding protein 8, chloroplastic	771650	478203	651679	647605	0.071783669	-0.690321605	UNCHANGED	0.220464297	0.446537085	UNCHANGED	0.030919621	0.437489443	UNCHANGED
Ce_fissilis.003105.1	16	13570.67	Chlorophyll a-b binding protein CP24 10A, chloroplastic	247690	243404	238019	251572	0.974161639	-0.025184053	UNCHANGED	0.927350742	-0.03227817	UNCHANGED	0.764789667	0.047617229	UNCHANGED
Ce_fissilis.011301.1	17	22874.33	Chlorophyll a-b binding protein CP26, chloroplastic	623860	561889	774756	619109	0.735055827	-0.150937953	UNCHANGED	0.44036732	0.463457771	UNCHANGED	0.54738609	0.139907783	UNCHANGED
Ce_fissilis.000798.1	5	2239.86	Cinnamoyl-CoA reductase 1	41247	60125	80136	84611	0.001285466	0.543649587	UNCHANGED	0.074040084	0.414502176	UNCHANGED	0.022461027	0.492889017	UNCHANGED
Ce_fissilis.006579.1	5	968.75	Coatomer subunit delta	56555	83823	68418	80555	0.116922509	0.567696325	UNCHANGED	0.221264874	-0.292965108	UNCHANGED	0.72965333	-0.057381889	UNCHANGED
Ce_fissilis.008367.1	4	654.95	Cocosin 1	29103	22389	23878	26338	0.530004668	-0.378374758	UNCHANGED	0.883130667	0.092886992	UNCHANGED	0.774631078	0.234348905	UNCHANGED
Ce_fissilis.001535.1	5	26774.89	Cold shock domain-containing protein 4	297789	359079	407793	407018	0.073344398	0.270007957	UNCHANGED	0.107550471	0.183537514	UNCHANGED	0.107656792	0.180794283	UNCHANGED
Ce_fissilis.003687.1	4	2001.95	Cyanate hydratase	43752	43943	47627	50656	0.962897953	0.006280719	UNCHANGED	0.561483262	0.116139297	UNCHANGED	0.128523596	0.205092982	UNCHANGED
Ce_fissilis.018164.1	4	5759.76	Cyclase-like protein 2	86596	109730	109644	122807	0.110745604	0.341583332	UNCHANGED	0.986333314	-0.001134069	UNCHANGED	0.227199736	0.162437553	UNCHANGED
Ce_fissilis.006369.1	2	647.13	Cysteine protease RD19A	34952	28880	24796	28089	0.351853254	-0.275288563	UNCHANGED	0.227071748	-0.220002074	UNCHANGED	0.773789164	-0.040110374	UNCHANGED
Ce_fissilis.006370.1	4	749.63	Cysteine proteinase 15A	41299	46118	60353	38932	0.445870118	0.159217289	UNCHANGED	0.107483565	0.388097373	UNCHANGED	0.215177533	-0.244389317	UNCHANGED
Ce_fissilis.018028.1	4	8627.60	Cysteine proteinase inhibitor	91207	41124	62117	42874	0.414469589	-1.149160441	UNCHANGED	0.179433833	0.595002396	UNCHANGED	0.810583954	0.060126163	UNCHANGED
Ce_fissilis.009261.1	21	24888.86	Cysteine synthase	447528	443927	453686	521933	0.912761839	-0.011654778	UNCHANGED	0.848585505	0.031371338	UNCHANGED	0.001586182	0.233543754	UNCHANGED
Ce_fissilis.009651.2	8	1546.49	Cysteine synthase, chloroplastic/chromoplastic	54431	49813	56049	57798	0.326065197	-0.127893882	UNCHANGED	0.082419226	0.170163952	UNCHANGED	0.118267592	0.214486415	UNCHANGED
Ce_fissilis.009651.3	16	4673.73	Cysteine synthase, chloroplastic/chromoplastic	138992	76793	98422	84569	0.079440567	-0.855951673	UNCHANGED	0.057704777	0.358013131	UNCHANGED	0.33377418	0.139152215	UNCHANGED
Ce_fissilis.004379.1	2	2070.74	Cysteine-rich repeat secretory protein 38	48489	43150	39926	53533	0.719144109	-0.168318004	UNCHANGED	0.653215416	-0.11201485	UNCHANGED	0.464973086	0.311070106	UNCHANGED
Ce_fissilis.017423.1	3	11681.89	Cytochrome b559 subunit alpha	504552	537930	447045	478175	0.760822598	0.092416201	UNCHANGED	0.391703156	-0.266998683	UNCHANGED	0.626727412	-0.16988211	UNCHANGED
Ce_fissilis.015424.1	11	16293.00	Cytochrome b6-f complex iron-sulfur subunit, chloroplastic	372153	376169	362856	418913	0.95512314	0.015483799	UNCHANGED	0.790942484	-0.051983378	UNCHANGED	0.468366192	0.155267737	UNCHANGED
Ce_fissilis.014513.1	6	3494.37	Cytochrome c oxidase subunit 2	214093	220856	211132	208482	0.630082179	0.044869875	UNCHANGED	0.295309282	-0.064963015	UNCHANGED	0.564451142	-0.083186999	UNCHANGED
Ce_fissilis.0	3	1863.	Cytochrome c oxidase subunit 6b-1	46239	61331	57296	59019	0.25825	0.4075053	UNCHANGED	0.50504	-0.098165816	UNCHANGED	0.41751	-	UNCHANGED

03017.1		64						3312	69		4868			4052	0.055423725	
Ce_fissilis.011778.1	8	2601.08	Cytochrome c1-1, heme protein, mitochondrial	54440	53127	68622	51825	0.96272065	-0.035212985	UNCHANGED	0.444554511	0.36923527	UNCHANGED	0.922260647	-0.035787758	UNCHANGED
Ce_fissilis.013598.1	24	8111.79	D-3-phosphoglycerate dehydrogenase 1, chloroplastic	216500	318502	313088	348730	0.001761796	0.55693527	UNCHANGED	0.507087672	-0.024731566	UNCHANGED	0.130253798	0.130808533	UNCHANGED
Ce_fissilis.001617.1	19	3222.68	D-3-phosphoglycerate dehydrogenase 2, chloroplastic	139635	161192	156151	184553	0.338934259	0.20712482	UNCHANGED	0.585613449	-0.045837213	UNCHANGED	0.26271932	0.195251193	UNCHANGED
Ce_fissilis.001088.1	6	2308.34	D-3-phosphoglycerate dehydrogenase 3, chloroplastic	13869	14815	13708	16718	0.636013994	0.095193817	UNCHANGED	0.384212258	-0.112027844	UNCHANGED	0.067163548	0.174279116	UNCHANGED
Ce_fissilis.011572.1	8	1212.41	Dihydrolipoyllysine-residue acetyltransferase component 4 of pyruvate dehydrogenase complex, chloroplastic	78918	94652	101243	113158	0.482193123	0.262278948	UNCHANGED	0.477734916	0.097117279	UNCHANGED	0.25050805	0.257638266	UNCHANGED
Ce_fissilis.000685.1	14	1552.60	Dihydroxy-acid dehydratase, chloroplastic	61398	120017	152702	174240	0.118917383	0.966977696	UNCHANGED	0.31587928	0.347484477	UNCHANGED	0.156963607	0.537845189	UNCHANGED
Ce_fissilis.013717.1	7	1179.01	DNA damage-repair/toleration protein DRT100	27569	32780	22929	29674	0.667799879	0.249753963	UNCHANGED	0.418363911	-0.515662007	UNCHANGED	0.798602936	-0.143607917	UNCHANGED
Ce_fissilis.015700.1	17	7643.32	DNA damage-repair/toleration protein DRT100	258015	344703	271174	360785	0.238286681	0.417898293	UNCHANGED	0.409746629	-0.346135586	UNCHANGED	0.806129404	0.065787281	UNCHANGED
Ce_fissilis.012496.1	4	2674.45	DNA repair RAD52-like protein 2, chloroplastic	62895	80449	87917	94938	0.039666281	0.35513203	UNCHANGED	0.429526876	0.128052406	UNCHANGED	0.06332729	0.238906576	UNCHANGED
Ce_fissilis.006549.1	4	7443.21	Elicitor-responsive protein 3	116849	93659	77978	85336	0.319769474	-0.319146258	UNCHANGED	0.34191799	-0.264361439	UNCHANGED	0.655056445	-0.134264357	UNCHANGED
Ce_fissilis.013983.1	13	16776.65	Elongation factor 1-beta 1	337655	504558	602118	525018	0.000138083	0.579467698	UNCHANGED	0.139195913	0.255027224	UNCHANGED	0.061678673	0.057348103	UNCHANGED
Ce_fissilis.010970.1	14	17135.92	Elongation factor 1-delta	465943	513556	538532	606842	0.545722731	0.140369177	UNCHANGED	0.58787581	0.068509088	UNCHANGED	0.158694253	0.240797736	UNCHANGED
Ce_fissilis.010970.2	10	6862.67	Elongation factor 1-delta	65007	58400	69247	57645	0.511413604	-0.154631327	UNCHANGED	0.006400166	0.245788873	UNCHANGED	0.820429162	-0.018765264	UNCHANGED
Ce_fissilis.001259.1	19	6156.47	Elongation factor Tu, chloroplastic	243555	261760	273453	303766	0.747388909	0.10399846	UNCHANGED	0.792432834	0.063048289	UNCHANGED	0.37948369	0.2147175	UNCHANGED
Ce_fissilis.001261.1	17	7399.98	Elongation factor Tu, mitochondrial	340520	179437	175646	174094	0.053175302	-0.924267587	UNCHANGED	0.878723415	-0.030804022	UNCHANGED	0.625858874	-0.043610112	UNCHANGED
Ce_fissilis.016025.1	11	6560.75	Endo-1,3	259257	235246	272467	261446	0.477990783	-0.140208914	UNCHANGED	0.078327393	0.211907599	UNCHANGED	0.018123768	0.15234083	UNCHANGED
Ce_fissilis.016026.1	7	2304.92	Endo-1,3	49263	67166	69424	79830	0.121784168	0.447225759	UNCHANGED	0.791360557	0.0477033	UNCHANGED	0.210100477	0.249199519	UNCHANGED
Ce_fissilis.003482.1	9	7953.78	Endochitinase	336524	202566	272891	310457	0.233985839	-0.732320681	UNCHANGED	0.429112667	0.429932796	UNCHANGED	0.064064837	0.616003276	UNCHANGED
Ce_fissilis.011457.1	7	435.92	Enhancer of mRNA-decapping protein 4	27363	42038	45177	48236	0.232159232	0.619455628	UNCHANGED	0.828366738	0.103893643	UNCHANGED	0.573593015	0.198398157	UNCHANGED
Ce_fissilis.002488.1	11	1914.42	Enolase 1, chloroplastic	79937	93924	94790	115677	0.38412115	0.232630421	UNCHANGED	0.820826825	0.0132444	UNCHANGED	0.076760837	0.300533515	UNCHANGED
Ce_fissilis.007245.1	15	4207.34	Enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic	324704	258528	307970	352179	0.06679615	-0.328803135	UNCHANGED	0.006332354	0.252470843	UNCHANGED	0.000927446	0.4459888	UNCHANGED
Ce_fissilis.003449.2	3	609.39	Enoyl-[acyl-carrier-protein] reductase, mitochondrial	10759	14079	20217	17466	0.101906625	0.388079729	UNCHANGED	0.026510514	0.522005767	UNCHANGED	0.208422141	0.310933511	UNCHANGED
Ce_fissilis.005917.1	12	31457.13	Epidermis-specific secreted glycoprotein EP1	654368	798999	719240	889152	0.027910736	0.288091058	UNCHANGED	0.365303246	-0.151720761	UNCHANGED	0.055427287	0.154236045	UNCHANGED
Ce_fissilis.0	6	5201.	Epidermis-specific secreted glycoprotein EP1	20346	41206	308183	351430	0.05395	1.0180638	UNCHANGED	0.26573	-0.419071945	UNCHANGED	0.42230	-	UNCHANGED

12362.1		33		7	1			8836	97		8589			9739	0.229617969	
Ce_fissilis.013782.1	30	36942.88	Epidermis-specific secreted glycoprotein EP1	1553596	2291935	1903188	2497990	0.001497736	0.560954554	UNCHANGED	0.055194501	-0.268148241	UNCHANGED	0.063004439	0.124201414	UNCHANGED
Ce_fissilis.005981.1	9	1464.33	Epoxide hydrolase A	30821	55631	71620	54532	0.055790515	0.851956321	UNCHANGED	0.147613588	0.364488839	UNCHANGED	0.917958136	-0.028768508	UNCHANGED
Ce_fissilis.002760.1	15	13115.74	Eukaryotic initiation factor 4A-15	25859	31122	34496	27733	0.024840753	0.267282002	UNCHANGED	0.447152322	0.148480584	UNCHANGED	0.236182541	-0.166343666	UNCHANGED
Ce_fissilis.017291.1	8	787.19	Eukaryotic translation initiation factor 3 subunit H	32588	42473	47119	66036	0.300632376	0.382201427	UNCHANGED	0.544554601	0.149759877	UNCHANGED	0.09300539	0.636705639	UNCHANGED
Ce_fissilis.000239.3	4	1131.56	Eukaryotic translation initiation factor 3 subunit K	52366	63301	73228	64760	0.447373274	0.273602947	UNCHANGED	0.33466059	0.21015766	UNCHANGED	0.875822882	0.03286468	UNCHANGED
Ce_fissilis.000562.1	7	1294.38	Eukaryotic translation initiation factor 5A	127672	189080	185579	182403	0.086223429	0.566560381	UNCHANGED	0.833108395	-0.026968799	UNCHANGED	0.719880328	-0.051867398	UNCHANGED
Ce_fissilis.007184.1	6	3683.99	Eukaryotic translation initiation factor 6-2	63533	67346	77857	85942	0.710273125	0.084085544	UNCHANGED	0.058723374	0.209227034	UNCHANGED	0.026365796	0.351755975	UNCHANGED
Ce_fissilis.016155.1	5	809.06	Expansin-A4	51342	70498	62894	71414	0.052788019	0.457438285	UNCHANGED	0.327237783	-0.164663035	UNCHANGED	0.91867133	0.018633635	UNCHANGED
Ce_fissilis.013745.1	7	1292.34	Far upstream element-binding protein 2	68368	80057	79065	94615	0.509568481	0.227714341	UNCHANGED	0.907032948	-0.017996371	UNCHANGED	0.210163132	0.241026582	UNCHANGED
Ce_fissilis.019104.1	2	379.44	Farnesylcysteine lyase	36488	43618	43197	42621	0.287592862	0.257521314	UNCHANGED	0.937544955	-0.014003631	UNCHANGED	0.888625687	-0.033347894	UNCHANGED
Ce_fissilis.006144.1	7	5352.26	Fasciclin-like arabinogalactan protein 1	166685	129453	153483	173039	0.326363444	-0.364692853	UNCHANGED	0.458286024	0.245646561	UNCHANGED	0.148347656	0.418664807	UNCHANGED
Ce_fissilis.015796.1	8	3925.03	Fasciclin-like arabinogalactan protein 10	192034	177783	141144	191896	0.736373746	-0.111240081	UNCHANGED	0.430007026	-0.332954786	UNCHANGED	0.740444884	0.110206294	UNCHANGED
Ce_fissilis.007862.1	7	8547.33	Fasciclin-like arabinogalactan protein 6	595550	592075	557341	655969	0.963454356	-0.008443238	UNCHANGED	0.706434863	-0.087219955	UNCHANGED	0.353939538	0.147846992	UNCHANGED
Ce_fissilis.015846.1	6	5393.78	Fasciclin-like arabinogalactan protein 7	294799	257554	244583	286241	0.394689591	-0.194855361	UNCHANGED	0.697355404	-0.074550716	UNCHANGED	0.326563239	0.152352959	UNCHANGED
Ce_fissilis.001428.1	5	27940.84	Ferredoxin-1, chloroplastic	748804	627588	690988	782369	0.258554321	-0.254770671	UNCHANGED	0.481643417	0.138844096	UNCHANGED	0.10667568	0.318031541	UNCHANGED
Ce_fissilis.011506.1	3	2136.00	ferredoxin-related	51634	40551	41664	46804	0.236266665	-0.348598558	UNCHANGED	0.827359875	0.039064337	UNCHANGED	0.543789534	0.206901854	UNCHANGED
Ce_fissilis.017877.1	4	520.86	Flagellar radial spoke protein 5	26272	32247	32974	31758	0.30179439	0.295634396	UNCHANGED	0.872480109	0.032124628	UNCHANGED	0.932126662	-0.022064774	UNCHANGED
Ce_fissilis.018977.1	4	738.57	Fructose-1,6-bisphosphatase, chloroplastic	13540	17637	22059	26208	0.238705893	0.38141655	UNCHANGED	0.226976899	0.322705873	UNCHANGED	0.075837062	0.571387045	UNCHANGED
Ce_fissilis.005604.1	2	983.18	Fructose-1,6-bisphosphatase, cytosolic	30265	39853	58443	57295	0.186705913	0.397045923	UNCHANGED	0.039017291	0.552333678	UNCHANGED	0.008343649	0.523716718	UNCHANGED
Ce_fissilis.007079.1	17	29521.40	Fructose-bisphosphate aldolase 2, chloroplastic	920502	651520	776724	901481	0.108656012	-0.498611072	UNCHANGED	0.302174084	0.253592499	UNCHANGED	0.054810151	0.468486771	UNCHANGED
Ce_fissilis.013763.1	16	13618.26	Fructose-bisphosphate aldolase 3, chloroplastic	398447	586979	603459	644358	0.016287486	0.55892094	UNCHANGED	0.397466634	0.03994657	UNCHANGED	0.008757819	0.134552976	UNCHANGED
Ce_fissilis.001130.2	9	11287.27	Fructose-bisphosphate aldolase, cytoplasmic isozyme 1	11871	20512	29776	28778	0.077198495	0.789014595	UNCHANGED	0.056110627	0.537691036	UNCHANGED	0.098314023	0.488530278	UNCHANGED

Ce_fissilis.009542.1	10	4349.12	Gamma carbonic anhydrase 1, mitochondrial	136391	143913	144381	151357	0.810825557	0.07745473	UNCHANGED	0.968685986	0.004674877	UNCHANGED	0.634710322	0.072757336	UNCHANGED
Ce_fissilis.016813.1	10	2659.59	Gamma carbonic anhydrase 1, mitochondrial	50325	57074	58592	59285	0.506947595	0.181562055	UNCHANGED	0.789521683	0.037856167	UNCHANGED	0.745577894	0.054828758	UNCHANGED
Ce_fissilis.015954.1	6	1878.92	Gamma carbonic anhydrase-like 1, mitochondrial	93537	103728	94036	91692	0.469777048	0.149200596	UNCHANGED	0.015349759	-0.141518149	UNCHANGED	0.107106718	-0.177945139	UNCHANGED
Ce_fissilis.015954.2	6	1264.60	Gamma carbonic anhydrase-like 1, mitochondrial	59603	44074	46246	52553	0.035841359	-0.435445992	UNCHANGED	0.299337708	0.069381055	UNCHANGED	0.049523186	0.253845797	UNCHANGED
Ce_fissilis.018049.1	4	1114.18	GDSL esterase/lipase APG	25662	62768	25062	25863	0.061276121	1.290366672	UNCHANGED	0.056063184	-1.32451108	UNCHANGED	0.057343749	-1.279154186	UNCHANGED
Ce_fissilis.006015.1	6	38785.80	Germin-like protein subfamily 1 member 14	732961	773200	842231	944641	0.811347815	0.077105443	UNCHANGED	0.499785491	0.123375326	UNCHANGED	0.076418264	0.288924422	UNCHANGED
Ce_fissilis.007193.1	14	4582.63	Glucan endo-1,3-beta-glucosidase	159650	67449	78098	91867	0.145984881	-1.243038841	UNCHANGED	0.65438962	0.211487901	UNCHANGED	0.291851958	0.445746655	UNCHANGED
Ce_fissilis.017003.1	12	5340.76	Glucan endo-1,3-beta-glucosidase	211749	126380	143957	133208	0.139724755	-0.744588499	UNCHANGED	0.485924525	0.187873112	UNCHANGED	0.840356799	0.075908947	UNCHANGED
Ce_fissilis.018867.1	2	380.14	Glucan endo-1,3-beta-glucosidase	59170	44488	51325	59511	0.15757895	-0.411452335	UNCHANGED	0.400239541	0.206251605	UNCHANGED	0.037954178	0.419742847	UNCHANGED
Ce_fissilis.011909.1	9	1233.36	Glutamate-1-semialdehyde 2,1-aminomutase, chloroplastic	85960	52145	67975	43145	0.064292085	-0.721122775	UNCHANGED	0.096861062	0.382452544	UNCHANGED	0.218159571	-0.273361359	UNCHANGED
Ce_fissilis.008156.1	13	12808.52	Glutamine synthetase leaf isozyme, chloroplastic	166797	355334	414125	480013	0.084797871	1.091084889	UNCHANGED	0.489194017	0.220892687	UNCHANGED	0.183671656	0.433898759	UNCHANGED
Ce_fissilis.005087.1	6	27258.14	Glutaredoxin	313049	278204	347638	350034	0.228037602	-0.170247122	UNCHANGED	0.032286281	0.321446777	UNCHANGED	0.032996848	0.331352831	UNCHANGED
Ce_fissilis.013635.2	2	953.22	Glutathione hydrolase 1	174890	168303	122879	190275	0.94094847	-0.05538405	UNCHANGED	0.568545519	-0.453821456	UNCHANGED	0.819997358	0.17702227	UNCHANGED
Ce_fissilis.012967.2	12	7962.94	Glutathione S-transferase L3	143517	119681	229202	207236	0.491057572	-0.262020691	UNCHANGED	0.065162166	0.937420046	UNCHANGED	0.066428831	0.792074571	UNCHANGED
Ce_fissilis.018702.2	3	1756.23	Glutathione transferase GST 23	38878	17034	23459	27966	0.383719836	-1.190496149	UNCHANGED	0.023717775	0.461716529	UNCHANGED	0.06630382	0.715211236	UNCHANGED
Ce_fissilis.008229.1	13	2883.21	Glyceraldehyde-3-phosphate dehydrogenase GAPCP1, chloroplastic	64500	88020	92401	77175	0.025569746	0.448524353	UNCHANGED	0.475085935	0.070086027	UNCHANGED	0.475901161	-0.18969233	UNCHANGED
Ce_fissilis.006148.1	7	25598.27	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	19993	22001	19716	22750	0.370661713	0.13809787	UNCHANGED	0.58331805	-0.15824317	UNCHANGED	0.815984954	0.048241463	UNCHANGED
Ce_fissilis.001633.1	6	851.31	Glycerol kinase	44973	65508	67245	67614	0.013189719	0.542612191	UNCHANGED	0.791037195	0.037753324	UNCHANGED	0.716569145	0.045645925	UNCHANGED
Ce_fissilis.007235.1	5	602.02	Glycerophosphodiester phosphodiesterase GDPD6	11238	63106	40427	35982	0.055061126	2.489370968	UNCHANGED	0.356891294	-0.642457722	UNCHANGED	0.313199352	-0.810518332	UNCHANGED
Ce_fissilis.005415.1	15	3579.38	Glycerophosphodiester phosphodiesterase GDPDL3	357210	306926	346118	391781	0.246890038	-0.218878693	UNCHANGED	0.409408735	0.173369689	UNCHANGED	0.101739161	0.352153367	UNCHANGED
Ce_fissilis.016050.2	5	10252.97	Glycine cleavage system H protein, mitochondrial	496225	413300	524563	572961	0.289023899	-0.263803377	UNCHANGED	0.19643	0.343927522	UNCHANGED	0.059537317	0.47124747	UNCHANGED
Ce_fissilis.0	14	1274.	Glycine dehydrogenase (decarboxylating),	33637	36717	365605	358960	0.45304	0.1263946	UNCHANGED	0.94121	-0.006164569	UNCHANGED	0.76473	-	UNCHANGED

07577.1		14	mitochondrial	2	1			5564	57		9126			8401	0.032627727	
Ce_fissilis.016317.1	14	3562.74	Glyoxylate/succinic semialdehyde reductase 1	122911	119366	109203	110719	0.861969493	-0.042223303	UNCHANGED	0.606938454	-0.128377752	UNCHANGED	0.570007377	-0.10849762	UNCHANGED
Ce_fissilis.001060.1	7	4596.89	GTP-binding protein SAR1A	52326	55134	52317	54461	0.939422138	0.075423425	UNCHANGED	0.678342436	-0.075673157	UNCHANGED	0.92828273	-0.017719504	UNCHANGED
Ce_fissilis.003060.1	5	3375.79	GTP-binding protein SAR1A	16384	20850	18603	14609	0.705386468	0.347801248	UNCHANGED	0.57569783	-0.164506297	UNCHANGED	0.176090237	-0.513203496	UNCHANGED
Ce_fissilis.015261.1	24	17862.09	Heat shock 70 kDa protein	783519	528748	449998	501634	0.296609573	-0.567387274	UNCHANGED	0.769634701	-0.23266253	UNCHANGED	0.906697986	-0.075945505	UNCHANGED
Ce_fissilis.007567.1	24	2155.13	Heat shock 70 kDa protein 15	121125	141371	131426	129429	0.198578141	0.222981033	UNCHANGED	0.493468053	-0.105233396	UNCHANGED	0.085341657	-0.127319525	UNCHANGED
Ce_fissilis.012012.2	8	1657.95	Hexokinase-2	33564	47852	37737	28116	0.201421268	0.51163633	UNCHANGED	0.475356463	-0.342595557	UNCHANGED	0.104745811	-0.767155231	UNCHANGED
Ce_fissilis.002664.1	11	1650.44	Hexokinase-2, chloroplastic	48106	32718	35008	43330	0.103976063	-0.556159232	UNCHANGED	0.631198361	0.097609758	UNCHANGED	0.096947851	0.405298995	UNCHANGED
Ce_fissilis.017817.1	5	713.73	Histidinol dehydrogenase, chloroplastic	32737	30841	35873	41881	0.791521594	-0.086056682	UNCHANGED	0.428072402	0.218028066	UNCHANGED	0.073724954	0.4414179	UNCHANGED
Ce_fissilis.010986.2	9	1512.96	Histone deacetylase 5	81693	77100	70476	79485	0.683591453	-0.083483449	UNCHANGED	0.497579006	-0.129594072	UNCHANGED	0.849662169	0.043957756	UNCHANGED
Ce_fissilis.008728.1	2	510.88	Homogentisate 1,2-dioxygenase	10103	12235	16969	17725	0.517992238	0.276230349	UNCHANGED	0.18910064	0.471844936	UNCHANGED	0.138476057	0.53475796	UNCHANGED
Ce_fissilis.015744.1	4	764.27	Homoserine kinase	13214	18480	19828	24405	0.233205795	0.483968597	UNCHANGED	0.715983579	0.101572048	UNCHANGED	0.275786268	0.401190435	UNCHANGED
Ce_fissilis.003137.2	6	2425.53	Hydroxyacylglutathione hydrolase cytoplasmic	51431	53850	60925	71415	0.81427004	0.066316072	UNCHANGED	0.456293055	0.178088347	UNCHANGED	0.131544987	0.407279272	UNCHANGED
Ce_fissilis.015062.2	15	8207.58	Hypersensitive-induced response protein 1	244859	320648	286864	344237	0.100901323	0.389040029	UNCHANGED	0.200929516	-0.160623862	UNCHANGED	0.473841308	0.102408401	UNCHANGED
Ce_fissilis.004365.1	5	1803.84	Hypersensitive-induced response protein-like protein 1	36733	25021	15093	18626	0.265401467	-0.553915961	UNCHANGED	0.051593618	-0.729305568	UNCHANGED	0.171460968	-0.425835004	UNCHANGED
Ce_fissilis.004928.1	10	3196.20	Importin subunit alpha-1	18582	19470	27600	28903	0.773404822	0.067322314	UNCHANGED	0.059047945	0.503447632	UNCHANGED	0.028101227	0.57000255	UNCHANGED
Ce_fissilis.018173.1	16	5205.98	Importin subunit alpha-2	75316	105375	127197	131176	0.020324338	0.484503654	UNCHANGED	0.025742431	0.27152745	UNCHANGED	0.013590246	0.315971502	UNCHANGED
Ce_fissilis.010265.1	7	633.64	Importin subunit beta-1	24544	45880	38237	45437	0.268221066	0.902521128	UNCHANGED	0.622655065	-0.262891862	UNCHANGED	0.976246498	-0.013987224	UNCHANGED
Ce_fissilis.014757.1	7	2286.18	Isocitrate dehydrogenase [NAD] regulatory subunit 1, mitochondrial	57680	41221	42040	41410	0.108234036	-0.484685221	UNCHANGED	0.751437148	0.028391327	UNCHANGED	0.938898566	0.006590551	UNCHANGED
Ce_fissilis.009131.1	4	3603.57	Isoflavone reductase homolog PCBER	306532	370708	265358	366144	0.083547633	0.274246705	UNCHANGED	0.02622003	-0.482342042	UNCHANGED	0.926423418	-0.017872739	UNCHANGED
Ce_fissilis.002902.1	9	16388.91	Kunitz trypsin inhibitor 2	535278	870317	920988	834656	0.103262704	0.701253332	UNCHANGED	0.678623075	0.081641914	UNCHANGED	0.805013103	-0.06035965	UNCHANGED
Ce_fissilis.017223.1	8	1619.36	L-3-cyanoalanine synthase 1, mitochondrial	70516	71680	66563	61630	0.924407371	0.023601959	UNCHANGED	0.495122292	-0.106843643	UNCHANGED	0.211827701	-0.21793	UNCHANGED

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Ce_fissilis.010244.1	7	1931.43	Lactoylglutathione lyase	87428	119242	143921	149088	0.005017945	0.447723467	UNCHANGED	0.00611321	0.271391129	UNCHANGED	0.008640626	0.322272739	UNCHANGED
Ce_fissilis.002699.1	10	3887.58	L-ascorbate oxidase homolog	65136	59454	48068	64829	0.599946087	-0.131701561	UNCHANGED	0.246937322	-0.30668304	UNCHANGED	0.651429858	0.124869307	UNCHANGED
Ce_fissilis.002700.1	5	1261.89	L-ascorbate oxidase homolog	8180	8427	5811	10319	0.922913866	0.042968882	UNCHANGED	0.286113956	-0.536286449	UNCHANGED	0.471398889	0.292304279	UNCHANGED
Ce_fissilis.015082.1	18	18609.28	L-ascorbate oxidase homolog	613348	820314	646976	785910	0.080966904	0.419470259	UNCHANGED	0.125272714	-0.342464941	UNCHANGED	0.701022248	-0.06181294	UNCHANGED
Ce_fissilis.003317.1	4	2194.96	L-ascorbate peroxidase 2, cytosolic	47493	45901	42406	46647	0.793561288	-0.049206898	UNCHANGED	0.585193954	-0.114232625	UNCHANGED	0.916838511	0.023274405	UNCHANGED
Ce_fissilis.008713.1	28	11889.51	Leucine aminopeptidase 2, chloroplastic	339465	397866	472714	477274	0.221470669	0.229022338	UNCHANGED	0.028543589	0.248683703	UNCHANGED	0.017923502	0.26253251	UNCHANGED
Ce_fissilis.001215.1	5	18450.86	Leucine-rich repeat protein 1	491221	581333	603232	491401	0.467836783	0.242992394	UNCHANGED	0.879849023	0.053348185	UNCHANGED	0.333792875	-0.242461881	UNCHANGED
Ce_fissilis.006001.1	12	1803.19	Leucine-rich repeat receptor-like protein kinase PXC2	94054	59968	77100	85518	0.105688414	-0.649307871	UNCHANGED	0.31994028	0.362552259	UNCHANGED	0.151297653	0.512048898	UNCHANGED
Ce_fissilis.002887.1	5	1111.41	L-galactose dehydrogenase	77035	64499	82121	82505	0.424302813	-0.256236002	UNCHANGED	0.147250798	0.348471565	UNCHANGED	0.032318703	0.355213616	UNCHANGED
Ce_fissilis.005689.1	18	1878.01	LL-diaminopimelate aminotransferase, chloroplastic	50237	74753	94594	99450	0.006544978	0.573385454	UNCHANGED	0.010678666	0.339611215	UNCHANGED	0.000563315	0.411830768	UNCHANGED
Ce_fissilis.009374.1	4	1227.89	LysM domain-containing GPI-anchored protein 2	84508	83474	76904	95450	0.927307866	-0.01775919	UNCHANGED	0.445078652	-0.11826459	UNCHANGED	0.165687292	0.193430771	UNCHANGED
Ce_fissilis.012884.1	3	1286.20	Macro domain-containing protein XCC3184	33047	31814	38434	46495	0.773857207	-0.054840088	UNCHANGED	0.243779995	0.272689992	UNCHANGED	0.017462029	0.547411551	UNCHANGED
Ce_fissilis.004767.2	12	55433.82	Major allergen Pru av 1	871542	919805	1008668	605212	0.798913695	0.077757811	UNCHANGED	0.617953207	0.133050593	UNCHANGED	0.076588318	-0.603888674	UNCHANGED
Ce_fissilis.009112.1	21	32022.34	Malate dehydrogenase	1239407	1503981	1635568	1738548	0.10671693	0.279135877	UNCHANGED	0.227283003	0.121005364	UNCHANGED	0.072104723	0.209097267	UNCHANGED
Ce_fissilis.002539.1	9	3181.30	Malate dehydrogenase [NADP], chloroplastic	169383	180803	195444	213485	0.79227602	0.094129529	UNCHANGED	0.716096955	0.112335039	UNCHANGED	0.39063167	0.239718343	UNCHANGED
Ce_fissilis.012930.1	19	7513.45	Malate dehydrogenase, chloroplastic	153168	172539	210886	189949	0.353791847	0.171805839	UNCHANGED	0.0658867	0.28954361	UNCHANGED	0.491398825	0.138694092	UNCHANGED
Ce_fissilis.004061.1	15	7138.87	Malate dehydrogenase, glyoxysomal	102913	73375	87991	94254	0.023279663	-0.488051011	UNCHANGED	0.198853616	0.262062656	UNCHANGED	0.077339261	0.361254766	UNCHANGED
Ce_fissilis.015536.1	18	34637.73	Malate dehydrogenase, mitochondrial	1126669	1221694	1292141	1432544	0.038850213	0.116818527	UNCHANGED	0.18739316	0.080880964	UNCHANGED	0.091558999	0.229696575	UNCHANGED
Ce_fissilis.014973.1	8	1223.08	Methionine gamma-lyase	30477	78967	82057	90345	0.069583179	1.373526124	UNCHANGED	0.878176328	0.055376833	UNCHANGED	0.607493462	0.194197674	UNCHANGED
Ce_fissilis.007698.1	8	2408.48	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	132765	143765	185550	206634	0.652721721	0.114832977	UNCHANGED	0.150100137	0.368095149	UNCHANGED	0.03857315	0.523369725	UNCHANGED
Ce_fissilis.013292.1	2	588.74	Methylthioribose-1-phosphate isomerase	15765	21648	22211	20626	0.004532408	0.45748636	UNCHANGED	0.856017367	0.037051993	UNCHANGED	0.667660955	-0.069735806	UNCHANGED
Ce_fissilis.010718.1	2	737.22	MFP1 attachment factor 1	20475	12029	8984	9165	0.111617988	-0.767303263	UNCHANGED	0.535160263	-0.421160398	UNCHANGED	0.514538276	-0.392382388	UNCHANGED

Ce_fissilis.001601.1	12	7364.90	Mitochondrial dicarboxylate/tricarboxylate transporter DTC	254490	271720	292466	315681	0.5738568	0.094511752	UNCHANGED	0.457537087	0.10614976	UNCHANGED	0.017524158	0.216345066	UNCHANGED
Ce_fissilis.001378.1	11	4077.50	Mitochondrial import receptor subunit TOM40-1	155398	213132	219955	199014	0.165199743	0.455784912	UNCHANGED	0.889654972	0.045456759	UNCHANGED	0.726494359	-0.098876383	UNCHANGED
Ce_fissilis.009300.1	13	15757.47	Mitochondrial outer membrane protein porin of 34 kDa	670846	712859	738464	797948	0.601171466	0.087635606	UNCHANGED	0.242932835	0.050909689	UNCHANGED	0.188450861	0.162677069	UNCHANGED
Ce_fissilis.003446.1	11	8042.53	Mitochondrial outer membrane protein porin of 36 kDa	422399	305205	289292	297598	0.00124672	-0.468828297	UNCHANGED	0.415693653	-0.077250284	UNCHANGED	0.622658693	-0.036412432	UNCHANGED
Ce_fissilis.000462.1	8	3048.15	Mitochondrial phosphate carrier protein 3, mitochondrial	130166	125916	114490	113602	0.68942788	-0.04788476	UNCHANGED	0.173765802	-0.137237555	UNCHANGED	0.378357396	-0.148482935	UNCHANGED
Ce_fissilis.000463.1	12	3258.74	Mitochondrial phosphate carrier protein 3, mitochondrial	275377	335907	318507	338805	0.086973111	0.286650719	UNCHANGED	0.439214771	-0.076733865	UNCHANGED	0.835383007	0.012396634	UNCHANGED
Ce_fissilis.009638.1	4	1600.07	Mitochondrial pyruvate carrier 4	80579	71388	90171	81008	0.411293392	-0.174718851	UNCHANGED	0.039171115	0.336982873	UNCHANGED	0.507570169	0.182379381	UNCHANGED
Ce_fissilis.018467.1	7	1634.88	Mitochondrial uncoupling protein 1	60340	62507	57933	77876	0.732973222	0.050895004	UNCHANGED	0.570178429	-0.109637719	UNCHANGED	0.280856032	0.317152282	UNCHANGED
Ce_fissilis.012383.1	23	6001.75	Mitochondrial-processing peptidase subunit alpha	182482	256441	262154	302173	0.119433752	0.490877287	UNCHANGED	0.854016862	0.031785133	UNCHANGED	0.1159794	0.236747534	UNCHANGED
Ce_fissilis.000342.1	5	10152.10	MLP-like protein 31	263554	77662	174840	67708	0.069590714	-1.762810174	UNCHANGED	0.100010174	1.170749928	UNCHANGED	0.702513776	-0.197888445	UNCHANGED
Ce_fissilis.012396.1	2	748.21	MLP-like protein 31	112507	70002	122224	132493	0.327802546	-0.684535576	UNCHANGED	0.132548924	0.804052685	UNCHANGED	0.092114213	0.920441224	UNCHANGED
Ce_fissilis.015325.2	11	35935.86	MLP-like protein 31	968014	592942	935662	850948	0.075658016	-0.707138475	UNCHANGED	0.141510626	0.65809813	UNCHANGED	0.076588857	0.52118069	UNCHANGED
Ce_fissilis.006334.1	3	3263.27	MLP-like protein 423	48627	94697	29173	50639	0.334721605	0.961548571	UNCHANGED	0.198473734	-1.698693836	UNCHANGED	0.359537047	-0.903062189	UNCHANGED
Ce_fissilis.013512.1	2	798.82	Multiple organellar RNA editing factor 9, chloroplastic	17025	20014	24109	25787	0.536889826	0.23340701	UNCHANGED	0.516067792	0.268548224	UNCHANGED	0.143822516	0.365629031	UNCHANGED
Ce_fissilis.000218.1	3	5359.36	Unknown	88162	98040	100738	103554	0.456601856	0.15321917	UNCHANGED	0.721652943	0.03916724	UNCHANGED	0.616485694	0.078939432	UNCHANGED
Ce_fissilis.001224.1	2	3393.08	Unknown	31897	29643	30937	26235	0.615223038	-0.105729279	UNCHANGED	0.745578064	0.061618525	UNCHANGED	0.49374538	-0.176189507	UNCHANGED
Ce_fissilis.002231.1	7	3820.56	Unknown	42242	59016	86707	76474	0.149659811	0.48241226	UNCHANGED	0.03093244	0.555056023	UNCHANGED	0.269668711	0.373873441	UNCHANGED
Ce_fissilis.006593.1	8	18342.81	Unknown	256225	332954	422143	500334	0.405663715	0.377910662	UNCHANGED	0.250803442	0.342408363	UNCHANGED	0.106225275	0.587568943	UNCHANGED
Ce_fissilis.011841.1	3	2214.79	Unknown	121328	198097	166352	124649	0.283039463	0.707295052	UNCHANGED	0.63046315	-0.251965662	UNCHANGED	0.324224462	-0.668333079	UNCHANGED
Ce_fissilis.013432.1	4	1663.18	Unknown	65751	66172	72621	69526	0.98259975	0.009211728	UNCHANGED	0.771163462	0.134171753	UNCHANGED	0.817046794	0.071338798	UNCHANGED
Ce_fissilis.014316.1	8	17534.29	Unknown	891478	856247	727513	758923	0.91790737	-0.058173081	UNCHANGED	0.651363108	-0.235054507	UNCHANGED	0.762803461	-0.174073981	UNCHANGED
Ce_fissilis.018593.1	3	4460.10	Unknown	150565	69136	112395	113174	0.087138141	-1.122872386	UNCHANGED	0.090345476	0.701055263	UNCHANGED	0.191060828	0.711024243	UNCHANGED
Ce_fissilis.018632.1	4	1394.37	Unknown	21266	25830	19611	19402	0.225047371	0.280530203	UNCHANGED	0.146697972	-0.397380604	UNCHANGED	0.068188468	-0.41287	UNCHANGED

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Ce_fissilis.018886.1	24	2894.72	NAD-dependent malic enzyme 62 kDa isoform, mitochondrial	176238	176459	144518	159427	0.996645873	0.001811622	UNCHANGED	0.387987958	-0.2880812	UNCHANGED	0.625626237	-0.14643684	UNCHANGED
Ce_fissilis.012940.1	7	1284.26	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	45728	75648	76123	86585	0.053303024	0.726229744	UNCHANGED	0.958244355	0.009019936	UNCHANGED	0.294912589	0.194816757	UNCHANGED
Ce_fissilis.002481.1	2	1243.51	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	91319	103169	97779	104311	0.609601293	0.17602581	UNCHANGED	0.498026696	-0.077415698	UNCHANGED	0.918923257	0.015888732	UNCHANGED
Ce_fissilis.011805.1	12	2760.00	NADH-cytochrome b5 reductase-like protein	135223	182856	192988	199806	0.090636824	0.435368542	UNCHANGED	0.56558022	0.07779884	UNCHANGED	0.337144562	0.127886027	UNCHANGED
Ce_fissilis.001377.2	6	896.31	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	16515	24686	29490	28572	0.297195896	0.579964718	UNCHANGED	0.282135663	0.256529561	UNCHANGED	0.343189812	0.210872627	UNCHANGED
Ce_fissilis.012598.1	14	4031.61	NADPH-dependent alkenal/one oxidoreductase, chloroplastic	114648	104730	127465	145828	0.645804635	-0.130531833	UNCHANGED	0.247752245	0.283426835	UNCHANGED	0.053496801	0.477589499	UNCHANGED
Ce_fissilis.016008.2	3	1157.07	NAP1-related protein 2	47053	49816	52678	59045	0.741579029	0.082322097	UNCHANGED	0.652698463	0.080584953	UNCHANGED	0.239048889	0.245199276	UNCHANGED
Ce_fissilis.002464.1	7	6781.46	Nascent polypeptide-associated complex subunit alpha-like protein	240066	338420	371996	405247	0.046726234	0.495386216	UNCHANGED	0.375725826	0.13647051	UNCHANGED	0.094434783	0.259985805	UNCHANGED
Ce_fissilis.016917.1	5	29768.57	Non-specific lipid-transfer protein	531149	496965	687402	693601	0.700287594	-0.095972035	UNCHANGED	0.082641972	0.468009854	UNCHANGED	0.108410149	0.480961546	UNCHANGED
Ce_fissilis.016916.1	11	1298.65	Non-specific phospholipase C3	65064	77008	62208	89764	0.472399455	0.243164909	UNCHANGED	0.400002507	-0.307904142	UNCHANGED	0.482285565	0.221124178	UNCHANGED
Ce_fissilis.003162.1	4	903.45	Non-symbiotic hemoglobin 1	33726	62272	84060	61316	0.221246969	0.884717246	UNCHANGED	0.220780989	0.432839083	UNCHANGED	0.943586412	-0.022309654	UNCHANGED
Ce_fissilis.012147.1	3	11135.74	Nuclear transport factor 2B	109409	132649	134846	141572	0.070016358	0.277887508	UNCHANGED	0.5863397	0.02369655	UNCHANGED	0.193759593	0.093926688	UNCHANGED
Ce_fissilis.012880.1	8	19725.03	Nucleoside diphosphate kinase 1	575321	693327	654688	652121	0.171222801	0.269167356	UNCHANGED	0.273437605	-0.082727443	UNCHANGED	0.435640551	-0.088395755	UNCHANGED
Ce_fissilis.007805.1	5	4498.34	Nucleoside diphosphate kinase 2, chloroplastic	64035	80623	92545	100250	0.300320441	0.332313789	UNCHANGED	0.419646588	0.198967897	UNCHANGED	0.126147254	0.314350373	UNCHANGED
Ce_fissilis.017776.1	8	1285.09	Octicosapeptide/Phox/Bem1p family protein	60559	61881	68870	86608	0.776037091	0.031165603	UNCHANGED	0.310429603	0.154373985	UNCHANGED	0.010080396	0.485002303	UNCHANGED
Ce_fissilis.006379.1	8	9875.34	Osmotin-like protein OSML13	412590	212712	292030	251223	0.079590255	-0.955807042	UNCHANGED	0.209479407	0.457216806	UNCHANGED	0.53498477	0.240065852	UNCHANGED
Ce_fissilis.005614.1	21	62999.34	Oxygen-evolving enhancer protein 1, chloroplastic	1951264	1873045	1837905	2192050	0.804669269	-0.059023334	UNCHANGED	0.878721621	-0.027323884	UNCHANGED	0.218783822	0.226895267	UNCHANGED
Ce_fissilis.004609.1	15	30965.39	Oxygen-evolving enhancer protein 2, chloroplastic	1280238	1166761	1116199	1400589	0.578099759	-0.133903206	UNCHANGED	0.793254446	-0.063914947	UNCHANGED	0.23549282	0.26352457	UNCHANGED
Ce_fissilis.015459.1	13	27167.45	Oxygen-evolving enhancer protein 3-2, chloroplastic	843429	1095207	1214362	1328643	0.020734884	0.376864894	UNCHANGED	0.408594345	0.148995653	UNCHANGED	0.050880403	0.278750568	UNCHANGED
Ce_fissilis.013698.1	4	981.11	Peptidyl-prolyl cis-trans isomerase CYP20-3, chloroplastic	97137	100471	104123	129756	0.711567501	0.048686196	UNCHANGED	0.749186132	0.051500294	UNCHANGED	0.145273699	0.369016448	UNCHANGED
Ce_fissilis.009742.1	8	1395.33	Peptidyl-prolyl cis-trans isomerase CYP38, chloroplastic	68430	58327	64028	70598	0.489633962	-0.230468949	UNCHANGED	0.64041848	0.134538584	UNCHANGED	0.122690345	0.275453403	UNCHANGED
Ce_fissilis.017405.1	18	18972.42	Peroxidase 12	561639	771752	762843	854441	0.016307177	0.458493362	UNCHANGED	0.801246791	-0.016749624	UNCHANGED	0.017976222	0.146844632	UNCHANGED
Ce_fissilis.005535.1	11	18348.22	Peroxidase 15	717251	1010960	1125249	946615	0.10344686	0.49517603	UNCHANGED	0.56459696	0.154517622	UNCHANGED	0.668400812	-0.094876376	UNCHANGED

Ce_fissilis.013923.1	7	12622.37	Peroxidase 15	188487	649619	507615	343208	0.059599339	1.785126144	UNCHANGED	0.383146512	-0.355859552	UNCHANGED	0.107108064	-0.920510453	UNCHANGED
Ce_fissilis.015095.1	6	32941.38	Peroxidase 15	875167	959564	1042522	1066697	0.59237323	0.132821227	UNCHANGED	0.150656819	0.119626416	UNCHANGED	0.258010041	0.152699476	UNCHANGED
Ce_fissilis.015772.1	12	9459.72	Peroxiredoxin-2E, chloroplastic	603990	398834	393509	484330	0.01341396	-0.598735055	UNCHANGED	0.926918686	-0.019392161	UNCHANGED	0.15072723	0.280199436	UNCHANGED
Ce_fissilis.002293.1	10	3108.16	Peroxiredoxin-2F, mitochondrial	92664	95015	96416	120084	0.852780135	0.036137851	UNCHANGED	0.842934272	0.021119049	UNCHANGED	0.037758482	0.337827498	UNCHANGED
Ce_fissilis.015714.1	22	5750.29	Peroxisomal (S)-2-hydroxy-acid oxidase	188191	205338	232086	273614	0.677952265	0.125808188	UNCHANGED	0.230954632	0.176654689	UNCHANGED	0.117449949	0.414137346	UNCHANGED
Ce_fissilis.001297.1	2	485.36	Peroxisomal membrane protein PEX14	10772	12841	15010	13751	0.14171365	0.253437568	UNCHANGED	0.001753469	0.225206577	UNCHANGED	0.255958123	0.098782698	UNCHANGED
Ce_fissilis.007229.1	26	27252.09	Phosphoglycerate kinase 2, chloroplastic	520288	651724	741862	901190	0.212377426	0.324949258	UNCHANGED	0.238112963	0.186890319	UNCHANGED	0.00446919	0.467570741	UNCHANGED
Ce_fissilis.002774.1	18	4552.48	Phosphoribulokinase, chloroplastic	308132	247477	326336	368791	0.358086765	-0.316256795	UNCHANGED	0.218846208	0.399065328	UNCHANGED	0.068357477	0.575511385	UNCHANGED
Ce_fissilis.013697.2	8	3534.79	Photosynthetic NDH subunit of lumenal location 5, chloroplastic	111762	137829	154701	188920	0.145250669	0.302451976	UNCHANGED	0.12711175	0.166602396	UNCHANGED	0.052370809	0.45489861	UNCHANGED
Ce_fissilis.004692.1	3	2567.10	Photosystem I reaction center subunit V, chloroplastic	179298	98054	92193	99515	0.127095068	-0.870719486	UNCHANGED	0.760690196	-0.088910888	UNCHANGED	0.953195213	0.021339199	UNCHANGED
Ce_fissilis.018999.1	3	34266.17	Photosystem I reaction center subunit VI-2, chloroplastic	527708	424518	468543	485760	0.259509308	-0.313913898	UNCHANGED	0.504755379	0.142355764	UNCHANGED	0.325408032	0.194419667	UNCHANGED
Ce_fissilis.015428.1	4	4152.42	Photosystem I reaction center subunit XI, chloroplastic	218984	251623	256266	306180	0.361678776	0.20044098	UNCHANGED	0.874944829	0.026378248	UNCHANGED	0.073780956	0.28311643	UNCHANGED
Ce_fissilis.000704.1	15	9719.44	Photosystem II 22 kDa protein, chloroplastic	344662	377606	383638	426117	0.307607465	0.131699605	UNCHANGED	0.855730247	0.022864803	UNCHANGED	0.092909364	0.174371123	UNCHANGED
Ce_fissilis.006118.1	16	15606.64	Photosystem II CP43 reaction center protein	539960	588065	470139	522525	0.742771841	0.123125369	UNCHANGED	0.323914673	-0.322890037	UNCHANGED	0.602120344	-0.170476961	UNCHANGED
Ce_fissilis.001288.2	9	2704.46	Photosystem II CP47 reaction center protein	54708	181050	88007	85841	0.110391691	1.726569431	UNCHANGED	0.206312977	-1.040691643	UNCHANGED	0.196142222	-1.076646636	UNCHANGED
Ce_fissilis.012931.1	13	2579.14	Photosystem II stability/assembly factor HCF136, chloroplastic	100485	100671	100207	119969	0.987548921	0.002663216	UNCHANGED	0.971168535	-0.006653683	UNCHANGED	0.273472545	0.253012943	UNCHANGED
Ce_fissilis.015185.1	4	5321.21	PITH domain-containing protein At3g04780	25226	13286	24050	35325	0.146510311	-0.925034484	UNCHANGED	0.205435735	0.856192932	UNCHANGED	0.121708365	1.410818937	UNCHANGED
Ce_fissilis.019047.1	4	13936.43	PLAT domain-containing protein 2	397173	349492	365667	371663	0.373349578	-0.184507312	UNCHANGED	0.733975777	0.06527188	UNCHANGED	0.774677404	0.088736502	UNCHANGED
Ce_fissilis.018641.1	5	2342.09	Polyadenylate-binding protein RBP45	53761	79155	87070	94697	0.071474639	0.558118173	UNCHANGED	0.274732155	0.137494198	UNCHANGED	0.0680564	0.258642283	UNCHANGED
Ce_fissilis.011448.1	2	598.36	Polyadenylate-binding protein RBP45A	45520	30960	35900	37626	0.050432838	-0.556107821	UNCHANGED	0.192639927	0.21360837	UNCHANGED	0.158192242	0.281360534	UNCHANGED
Ce_fissilis.014143.1	6	688.42	Porphobilinogen deaminase, chloroplastic	57197	44038	35589	54389	0.320107184	-0.377175969	UNCHANGED	0.444749951	-0.30732761	UNCHANGED	0.421465231	0.304557285	UNCHANGED
Ce_fissilis.018195.1	4	2026.58	Probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial	48758	30720	35243	46787	0.286588314	-0.66645823	UNCHANGED	0.657098578	0.198147415	UNCHANGED	0.066701618	0.606900151	UNCHANGED
Ce_fissilis.013718.1	11	2537.40	Probable 3-hydroxyisobutyrate dehydrogenase-like 1, mitochondrial	113131	89508	100090	120474	0.166963433	-0.3379096	UNCHANGED	0.237906554	0.161201107	UNCHANGED	0.017821361	0.428635489	UNCHANGED

									48							
Ce_fissilis.012830.2	5	1073.52	Probable 3-hydroxyisobutyrate dehydrogenase-like 2, mitochondrial	24232	19363	20089	25198	0.287115728	-0.323630835	UNCHANGED	0.800313414	0.053087298	UNCHANGED	0.248312382	0.379987651	UNCHANGED
Ce_fissilis.001988.1	9	3766.32	Probable 6-phosphogluconolactonase 4, chloroplastic	128622	149930	162816	186332	0.118926392	0.221150058	UNCHANGED	0.562986864	0.118953226	UNCHANGED	0.015299122	0.313581654	UNCHANGED
Ce_fissilis.009611.1	11	791.56	Probable alpha-mannosidase At5g13980	53455	50010	65895	61636	0.730247163	-0.096114572	UNCHANGED	0.240758504	0.397941141	UNCHANGED	0.334178485	0.301558519	UNCHANGED
Ce_fissilis.013279.1	7	2548.02	Probable aquaporin PIP1-2	81028	118678	148795	141939	0.039627384	0.550566113	UNCHANGED	0.088073411	0.326269476	UNCHANGED	0.101675477	0.258213346	UNCHANGED
Ce_fissilis.018834.1	4	8126.81	Probable aquaporin PIP2-2	149423	93077	137872	120445	0.46654506	-0.682910133	UNCHANGED	0.077668997	0.566836322	UNCHANGED	0.023929738	0.371881333	UNCHANGED
Ce_fissilis.010249.1	7	4867.84	Probable calcium-binding protein CML13	93092	76143	94852	81765	0.597578134	-0.289939848	UNCHANGED	0.49106442	0.316965951	UNCHANGED	0.685895478	0.102761916	UNCHANGED
Ce_fissilis.017629.1	2	554.94	Probable calcium-binding protein CML49	39537	26304	28934	34614	0.063065021	-0.587909039	UNCHANGED	0.614655625	0.137483579	UNCHANGED	0.345728591	0.396080412	UNCHANGED
Ce_fissilis.003219.1	6	5568.07	Probable chalcone--flavonone isomerase 3	75397	42073	27494	28141	0.16906731	-0.84160605	UNCHANGED	0.133792793	-0.613789539	UNCHANGED	0.367095967	-0.580243882	UNCHANGED
Ce_fissilis.009303.1	4	1605.22	Probable cinnamyl alcohol dehydrogenase 9	15576	35365	18077	26630	0.29255533	1.183004457	UNCHANGED	0.326597255	-0.968117921	UNCHANGED	0.65635385	-0.409268274	UNCHANGED
Ce_fissilis.001741.1	19	17169.49	Probable cysteine protease RD21B	722387	594030	639958	675198	0.088755696	-0.282236504	UNCHANGED	0.413537171	0.107441491	UNCHANGED	0.130718982	0.184775885	UNCHANGED
Ce_fissilis.018301.1	2	985.09	Probable cysteine protease RD21C	23581	41746	63861	38205	0.079808075	0.824033462	UNCHANGED	0.166805022	0.61329341	UNCHANGED	0.60943183	-0.127876508	UNCHANGED
Ce_fissilis.017998.1	3	395.15	Probable endo-1,3(4)-beta-glucanase ARB_01444	25040	36726	28629	29110	0.009246537	0.552600385	UNCHANGED	0.074214979	-0.359306464	UNCHANGED	0.05604629	-0.335280286	UNCHANGED
Ce_fissilis.002712.1	18	27174.71	Probable fructokinase-4	547579	699766	705345	817339	0.041742962	0.353806099	UNCHANGED	0.90342961	0.011457426	UNCHANGED	0.086042054	0.224061647	UNCHANGED
Ce_fissilis.007403.1	11	2133.34	Probable fructokinase-6, chloroplastic	93139	75540	87432	102107	0.077814923	-0.30215519	UNCHANGED	0.185472336	0.210923043	UNCHANGED	0.00082259	0.434775396	UNCHANGED
Ce_fissilis.018544.1	6	1359.72	Probable fructokinase-7	29223	37496	33186	44086	0.40769443	0.359643123	UNCHANGED	0.229059205	-0.176142275	UNCHANGED	0.472249014	0.233586813	UNCHANGED
Ce_fissilis.002060.1	11	2783.29	Probable glucan endo-1,3-beta-glucosidase A6	182460	121080	149790	168537	0.018629892	-0.591624059	UNCHANGED	0.191128188	0.306988168	UNCHANGED	0.050620593	0.477110066	UNCHANGED
Ce_fissilis.005902.1	3	1013.30	Probable glutathione peroxidase 3, mitochondrial	30997	31858	48070	41530	0.924049951	0.039531702	UNCHANGED	0.085279388	0.593498267	UNCHANGED	0.167549651	0.382518029	UNCHANGED
Ce_fissilis.007814.1	8	1257.16	Probable N-acetyl-gamma-glutamyl-phosphate reductase, chloroplastic	58845	41588	48613	51256	0.089562011	-0.500756848	UNCHANGED	0.013396765	0.2251809	UNCHANGED	0.06787865	0.30155599	UNCHANGED
Ce_fissilis.006915.1	10	17745.33	Probable NAD(P)H dehydrogenase (quinone) FQR1-like 1	323775	462483	403127	381731	0.061613899	0.514409089	UNCHANGED	0.409210371	-0.198167065	UNCHANGED	0.146755664	-0.276846011	UNCHANGED
Ce_fissilis.000407.1	3	1613.45	Probable NAD(P)H dehydrogenase (quinone) FQR1-like 2	38991	29731	29456	35466	0.278511398	-0.391178828	UNCHANGED	0.95221118	-0.013428125	UNCHANGED	0.15542534	0.254448814	UNCHANGED
Ce_fissilis.014756.1	8	4946.33	Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5, mitochondrial	92016	69241	80430	84512	0.177707543	-0.4102610	UNCHANGED	0.274334362	0.216096872	UNCHANGED	0.075582848	0.287523537	UNCHANGED

									93							
Ce_fissilis.000459.1	5	558.33	Probable pectinesterase/pectinesterase inhibitor 40	60879	48255	52918	61340	0.24149566	-0.335263122	UNCHANGED	0.503615435	0.133088078	UNCHANGED	0.111860543	0.346148338	UNCHANGED
Ce_fissilis.001012.1	3	1154.95	Probable plastid-lipid-associated protein 4, chloroplastic	28753	22908	35864	34874	0.518342471	-0.327863712	UNCHANGED	0.268069991	0.64667984	UNCHANGED	0.087286153	0.606267959	UNCHANGED
Ce_fissilis.001160.1	3	582.13	Probable polygalacturonase	31824	31187	32361	31540	0.922096683	-0.029149841	UNCHANGED	0.882570354	0.053310663	UNCHANGED	0.942316631	0.016224943	UNCHANGED
Ce_fissilis.012091.1	2	550.00	Probable polygalacturonase	43026	26601	29914	25665	0.125602753	-0.693717065	UNCHANGED	0.423658683	0.169324278	UNCHANGED	0.807389763	-0.05168759	UNCHANGED
Ce_fissilis.015802.1	3	410.10	Probable serine protease EDA2	32556	49061	49228	54283	0.018458926	0.591653187	UNCHANGED	0.965416303	0.004889463	UNCHANGED	0.364440182	0.145923814	UNCHANGED
Ce_fissilis.013094.1	2	7504.29	Probable steroid-binding protein 3	142633	147749	152588	183634	0.818215669	0.050843775	UNCHANGED	0.80735954	0.046491429	UNCHANGED	0.137088206	0.31368224	UNCHANGED
Ce_fissilis.016893.1	21	15066.45	Probable UDP-arabinopyranose mutase 1	128431	202363	213933	211866	0.084888437	0.655947104	UNCHANGED	0.743773724	0.080214939	UNCHANGED	0.77484909	0.066203523	UNCHANGED
Ce_fissilis.002068.1	2	642.96	Probable xyloglucan endotransglucosylase/hydrolase protein 27	20857	29224	21753	28044	0.272304605	0.486633527	UNCHANGED	0.259779591	-0.425917172	UNCHANGED	0.873325123	-0.059444371	UNCHANGED
Ce_fissilis.015751.1	3	7357.29	Probable xyloglucan endotransglucosylase/hydrolase protein 6	12342	75386	24006	21506	0.136369473	2.610703069	UNCHANGED	0.206363573	-1.650933765	UNCHANGED	0.190933403	-1.809570715	UNCHANGED
Ce_fissilis.011671.2	6	8584.50	Profilin-4	351817	337001	395985	460460	0.775588989	-0.062072264	UNCHANGED	0.064170651	0.232692697	UNCHANGED	0.014212745	0.450321188	UNCHANGED
Ce_fissilis.002297.1	9	1623.78	Prohibitin-3, mitochondrial	52519	37839	46566	59948	0.680528295	-0.472964984	UNCHANGED	0.263074345	0.299397174	UNCHANGED	0.074224407	0.663827626	UNCHANGED
Ce_fissilis.000078.1	5	1339.55	Proline iminopeptidase	32881	49883	52590	63455	0.117702882	0.601299598	UNCHANGED	0.493725271	0.076224362	UNCHANGED	0.039307692	0.347182865	UNCHANGED
Ce_fissilis.008361.1	12	9703.99	Proteasome subunit alpha type-1-B	183341	270041	292492	321059	0.014688792	0.558654297	UNCHANGED	0.172070562	0.115218563	UNCHANGED	0.078762968	0.249659192	UNCHANGED
Ce_fissilis.012992.1	14	8376.53	Proteasome subunit alpha type-2-A	198126	300172	306311	328676	0.028623975	0.599372794	UNCHANGED	0.618841756	0.029205119	UNCHANGED	0.288611419	0.130876079	UNCHANGED
Ce_fissilis.009901.1	13	5222.23	Proteasome subunit alpha type-4	151652	212249	230230	245690	0.005604025	0.484997158	UNCHANGED	0.213413308	0.117318716	UNCHANGED	0.168534386	0.211081279	UNCHANGED
Ce_fissilis.014343.1	10	9185.20	Proteasome subunit alpha type-5	207949	251929	271212	289612	0.074382732	0.27678491	UNCHANGED	0.308944345	0.106408129	UNCHANGED	0.036599677	0.201107831	UNCHANGED
Ce_fissilis.018172.2	10	3232.81	Proteasome subunit alpha type-6	68278	91633	99009	102293	0.013862466	0.424457598	UNCHANGED	0.175151821	0.111695835	UNCHANGED	0.116721273	0.158761354	UNCHANGED
Ce_fissilis.015561.1	9	3606.22	Proteasome subunit beta type-2-A	232831	228298	214676	255309	0.896257989	-0.028366327	UNCHANGED	0.271094044	-0.088754367	UNCHANGED	0.177594014	0.161326877	UNCHANGED
Ce_fissilis.008309.1	8	5966.82	Proteasome subunit beta type-3-A	129551	75415	113585	127752	0.379393407	-0.780596394	UNCHANGED	0.101086188	0.590855277	UNCHANGED	0.065608416	0.760422085	UNCHANGED
Ce_fissilis.009086.1	16	6905.85	Proteasome subunit beta type-6	244179	250404	257745	293575	0.822191132	0.036321071	UNCHANGED	0.695985151	0.04168493	UNCHANGED	0.050407632	0.229472413	UNCHANGED
Ce_fissilis.012882.1	5	846.57	Protein ASPARTIC PROTEASE IN GUARD CELL 1	70491	62996	72113	74267	0.69512718	-0.162173431	UNCHANGED	0.529654434	0.195006126	UNCHANGED	0.540420051	0.237457145	UNCHANGED
Ce_fissilis.018079.3	4	1046.33	Protein DJ-1 homolog B	52519	36903	47054	54268	0.115372504	-0.50910827	UNCHANGED	0.171221508	0.350588891	UNCHANGED	0.057298155	0.556382576	UNCHANGED

Ce_fissilis.017086.1	2	606.41	Protein EXORDIUM	33418	45977	40706	47636	0.384095989	0.46031179	UNCHANGED	0.654198262	-0.175693146	UNCHANGED	0.881826744	0.051139578	UNCHANGED
Ce_fissilis.011090.1	4	3169.74	Protein FATTY ACID EXPORT 2, chloroplastic	137969	80966	87620	95087	0.192604771	-0.76895184	UNCHANGED	0.525253647	0.113943558	UNCHANGED	0.215772951	0.231919226	UNCHANGED
Ce_fissilis.011270.1	7	1225.03	Protein GrpE	85450	57646	69939	74544	0.061603691	-0.567857273	UNCHANGED	0.111276343	0.27886603	UNCHANGED	0.048079072	0.37086984	UNCHANGED
Ce_fissilis.011383.1	7	875.38	Protein HOTHEAD	56337	105994	51949	74128	0.113896295	0.911814881	UNCHANGED	0.083839864	-1.02881018	UNCHANGED	0.224567541	-0.515883246	UNCHANGED
Ce_fissilis.015745.1	13	12783.78	Protein of unknown function, DUF642	481816	418824	326324	360637	0.567486448	-0.202138624	UNCHANGED	0.375370411	-0.360040443	UNCHANGED	0.569837015	-0.215796807	UNCHANGED
Ce_fissilis.004604.1	7	1994.10	Protein SRC2	108021	82958	124989	113295	0.407180987	-0.380862068	UNCHANGED	0.278496985	0.591358408	UNCHANGED	0.376055769	0.449643148	UNCHANGED
Ce_fissilis.005782.1	7	1032.68	Protein TIC 40, chloroplastic	43691	29116	44357	40620	0.028546619	-0.585540474	UNCHANGED	0.071198785	0.607380597	UNCHANGED	0.11414646	0.480390641	UNCHANGED
Ce_fissilis.000726.1	2	512.50	Protein TIC 62, chloroplastic	21918	27898	28139	33416	0.460227347	0.34805651	UNCHANGED	0.974835059	0.01240936	UNCHANGED	0.483220298	0.260362958	UNCHANGED
Ce_fissilis.006288.1	7	3126.94	Protein transport protein SEC13 homolog B	72064	104813	99672	109465	0.034673114	0.540455767	UNCHANGED	0.555248155	-0.072546462	UNCHANGED	0.676128163	0.062658047	UNCHANGED
Ce_fissilis.011580.1	2	388.58	Protein TRIGALACTOSYLDIACYLGLYCEROL 2, chloroplastic	12040	21777	24835	26982	0.053276542	0.855000842	UNCHANGED	0.435008381	0.189529437	UNCHANGED	0.214364918	0.309154292	UNCHANGED
Ce_fissilis.015457.1	10	10931.23	Protein usf	244462	326133	357252	366159	0.067145267	0.415851678	UNCHANGED	0.033070282	0.131481531	UNCHANGED	0.108514647	0.16700704	UNCHANGED
Ce_fissilis.017575.1	5	3599.72	Protein YLS3	218127	207887	161299	170664	0.782321672	-0.069372563	UNCHANGED	0.17483094	-0.366056532	UNCHANGED	0.240376119	-0.284636416	UNCHANGED
Ce_fissilis.011997.1	4	1315.01	PsbP-like protein 1, chloroplastic	52938	43921	21624	20559	0.58331785	-0.269381218	UNCHANGED	0.202670831	-1.022277258	UNCHANGED	0.198588796	-1.095182698	UNCHANGED
Ce_fissilis.013031.1	3	797.23	Pto-interacting protein 1	36730	49412	38629	41155	0.222881652	0.427880232	UNCHANGED	0.012178033	-0.355159806	UNCHANGED	0.021681149	-0.263783026	UNCHANGED
Ce_fissilis.008066.1	3	460.68	Putative 3,4-dihydroxy-2-butanone kinase	18802	14890	15583	16267	0.021199012	-0.336539921	UNCHANGED	0.686183245	0.065586667	UNCHANGED	0.172137228	0.127591868	UNCHANGED
Ce_fissilis.001268.1	11	4549.35	Putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase 2	293456	258075	275552	301750	0.112851805	-0.185350311	UNCHANGED	0.436760855	0.094531179	UNCHANGED	0.044447825	0.225562577	UNCHANGED
Ce_fissilis.000392.1	5	1004.44	Putative glucose-6-phosphate 1-epimerase	75226	52445	49332	61723	0.106578536	-0.520434108	UNCHANGED	0.632090153	-0.088262733	UNCHANGED	0.08872992	0.235025563	UNCHANGED
Ce_fissilis.018187.1	13	2045.71	Putative glucose-6-phosphate 1-epimerase	201454	206160	228247	248984	0.779244087	0.033319506	UNCHANGED	0.307793883	0.14683123	UNCHANGED	0.087644478	0.272284973	UNCHANGED
Ce_fissilis.000696.1	7	558.71	Putative glycosyl hydrolase of unknown function (DUF1680)	38143	25340	27821	32193	0.047354371	-0.589980693	UNCHANGED	0.508522369	0.134709402	UNCHANGED	0.229243514	0.345290259	UNCHANGED
Ce_fissilis.016305.1	14	6735.63	Putative lactoylglutathione lyase	238622	245614	272975	344620	0.740704754	0.041667714	UNCHANGED	0.242194216	0.152376244	UNCHANGED	0.00660183	0.488613977	UNCHANGED
Ce_fissilis.009721.1	3	11175.34	Putative phosphatidylglycerol/phosphatidylinositol transfer protein DDB_G0282179	233942	199176	234486	244667	0.172724177	-0.232112008	UNCHANGED	0.071544192	0.235458456	UNCHANGED	0.03568672	0.296780894	UNCHANGED
Ce_fissilis.0	22	8694.	Pyruvate dehydrogenase E1 component	22581	28687	275336	318291	0.14408	0.3453176	UNCHANGED	0.49793	-0.059232348	UNCHANGED	0.23004	0.14991	UNCHANGED

16136.1		90	subunit beta-1, mitochondrial	0	6			5137	44		104			7824	8748	
Ce_fissilis.014676.1	3	361.38	Pyruvate dehydrogenase E1 component subunit beta-3, chloroplastic	41994	31854	38607	47132	0.061801297	-0.398705371	UNCHANGED	0.096955634	0.277389666	UNCHANGED	0.008657949	0.565256024	UNCHANGED
Ce_fissilis.012804.1	17	2727.37	Pyruvate kinase, cytosolic isozyme	39031	62236	48265	59536	0.075023422	0.673103658	UNCHANGED	0.24970382	-0.366761658	UNCHANGED	0.809147969	-0.063971356	UNCHANGED
Ce_fissilis.017826.2	17	21229.10	Quinone oxidoreductase	247703	331248	394066	394059	0.031641075	0.419299679	UNCHANGED	0.014878606	0.250525002	UNCHANGED	0.010113428	0.25049915	UNCHANGED
Ce_fissilis.003917.1	15	5598.56	Quinone oxidoreductase PIG3	226506	259949	244104	266193	0.063702652	0.198678358	UNCHANGED	0.243738376	-0.090731893	UNCHANGED	0.573582398	0.034241576	UNCHANGED
Ce_fissilis.001419.1	3	579.57	RAN GTPase-activating protein 1	26186	17963	18055	20145	0.14804837	-0.543752226	UNCHANGED	0.954161195	0.007381295	UNCHANGED	0.319783012	0.165393311	UNCHANGED
Ce_fissilis.016943.1	5	4895.38	Ras-related protein Rab11C	30837	36003	46819	33594	0.445412531	0.223479378	UNCHANGED	0.065460341	0.378978099	UNCHANGED	0.585640015	-0.099936804	UNCHANGED
Ce_fissilis.004017.1	6	4727.23	Ras-related protein Rab7	32352	19238	21789	23665	0.077382272	-0.749885568	UNCHANGED	0.331602453	0.179607774	UNCHANGED	0.015585199	0.298758933	UNCHANGED
Ce_fissilis.010874.4	7	6429.65	Ras-related protein RABA1c	26367	17616	14539	13083	0.301118722	-0.581834016	UNCHANGED	0.01617485	-0.277011923	UNCHANGED	0.018520845	-0.429202304	UNCHANGED
Ce_fissilis.015887.1	14	6901.85	Ras-related protein RABA2a	75336	91369	109333	108486	0.123804425	0.278356997	UNCHANGED	0.004163407	0.258953735	UNCHANGED	0.000611766	0.247735299	UNCHANGED
Ce_fissilis.000226.1	4	4107.81	Ras-related protein RABA5a	49909	74720	55451	81257	0.002880077	0.582183251	UNCHANGED	0.017822532	-0.430279757	UNCHANGED	0.569534402	0.121007877	UNCHANGED
Ce_fissilis.014540.1	14	4984.95	Ras-related protein RABB1c	137742	110375	99808	120131	0.187115038	-0.319558597	UNCHANGED	0.227302497	-0.145188027	UNCHANGED	0.205616035	0.122205239	UNCHANGED
Ce_fissilis.006301.1	2	1352.14	Ras-related protein RABC2a	30582	32988	21356	32546	0.839695741	0.109235036	UNCHANGED	0.153118004	-0.627284546	UNCHANGED	0.960040966	-0.019460109	UNCHANGED
Ce_fissilis.014380.1	7	12009.51	Ras-related protein RABD1	47570	39885	36966	42597	0.366517233	-0.254225264	UNCHANGED	0.543095973	-0.109622549	UNCHANGED	0.076126496	0.094915802	UNCHANGED
Ce_fissilis.006337.1	10	13118.03	Ras-related protein RABD2a	47550	64004	74325	78040	0.301011336	0.428721625	UNCHANGED	0.149979821	0.215678344	UNCHANGED	0.039730969	0.286052982	UNCHANGED
Ce_fissilis.011761.2	8	5156.52	Ras-related protein RABH1b	64732	47276	42396	51306	0.349971657	-0.453350864	UNCHANGED	0.503685849	-0.157180812	UNCHANGED	0.509502882	0.118010582	UNCHANGED
Ce_fissilis.004249.1	15	15345.03	Reactive Intermediate Deaminase A, chloroplastic	631953	887372	984955	1024938	0.002490408	0.489720029	UNCHANGED	0.109845355	0.150519667	UNCHANGED	0.020794728	0.207926897	UNCHANGED
Ce_fissilis.012520.1	3	411.89	Red chlorophyll catabolite reductase, chloroplastic	22842	30560	36360	36758	0.126828365	0.419941604	UNCHANGED	0.22231636	0.250719821	UNCHANGED	0.311821328	0.266421627	UNCHANGED
Ce_fissilis.016779.1	16	3062.30	Rhodanese-like domain-containing protein 4, chloroplastic	123570	89496	111616	133999	0.004998228	-0.465437267	UNCHANGED	0.185205814	0.318661107	UNCHANGED	0.016388879	0.58233302	UNCHANGED
Ce_fissilis.016779.2	8	1975.59	Rhodanese-like domain-containing protein 4, chloroplastic	47636	46294	59248	66018	0.87912266	-0.041242444	UNCHANGED	0.078859612	0.355947876	UNCHANGED	0.013039381	0.512034832	UNCHANGED
Ce_fissilis.000411.1	14	17665.75	Ribulose bisphosphate carboxylase small chain, chloroplastic	1021724	947538	983161	1054484	0.285678623	-0.108749944	UNCHANGED	0.658884108	0.053243704	UNCHANGED	0.06334044	0.154281446	UNCHANGED
Ce_fissilis.018684.1	31	30967.60	Ribulose bisphosphate carboxylase/oxygenase activase 1, chloroplastic	1446658	1139239	1356711	1532453	0.126991981	-0.344653708	UNCHANGED	0.307769586	0.252043327	UNCHANGED	0.018940119	0.427772447	UNCHANGED

Ce_fissilis.006726.1	9	5842.63	Ribulose-phosphate 3-epimerase, chloroplastic	253933	227929	274742	315187	0.522869826	-0.155862984	UNCHANGED	0.335611002	0.269496256	UNCHANGED	0.06039534	0.467626664	UNCHANGED
Ce_fissilis.006659.1	2	1389.84	Rieske (2Fe-2S) domain-containing protein	46884	28709	29287	41252	0.193570381	-0.707604205	UNCHANGED	0.950132503	0.028782301	UNCHANGED	0.25884234	0.522966081	UNCHANGED
Ce_fissilis.007253.1	32	7095.75	RuBisCO large subunit-binding protein subunit alpha, chloroplastic	243465	336789	406799	417275	0.001615477	0.468128473	UNCHANGED	0.091917183	0.272471032	UNCHANGED	0.004458094	0.309151456	UNCHANGED
Ce_fissilis.004356.1	10	5467.39	Secoisolariciresinol dehydrogenase	189915	168935	141479	146445	0.174385942	-0.168885391	UNCHANGED	0.054613093	-0.25588676	UNCHANGED	0.100899565	-0.20610684	UNCHANGED
Ce_fissilis.015866.1	13	4994.03	Secoisolariciresinol dehydrogenase	76012	116167	137573	122333	0.17429802	0.611906757	UNCHANGED	0.388830281	0.244002516	UNCHANGED	0.802491747	0.074617276	UNCHANGED
Ce_fissilis.015866.2	9	3939.97	Secoisolariciresinol dehydrogenase	6327	8351	7636	5289	0.207652581	0.400333967	UNCHANGED	0.578128111	-0.129124992	UNCHANGED	0.05694844	-0.658891224	UNCHANGED
Ce_fissilis.000319.1	7	1617.10	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	54006	43672	44834	54392	0.719746457	-0.30641655	UNCHANGED	0.510369458	0.037911813	UNCHANGED	0.277336028	0.316694204	UNCHANGED
Ce_fissilis.012734.1	6	1362.61	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	61178	51351	55720	74524	0.742493519	-0.252627858	UNCHANGED	0.20943918	0.117801178	UNCHANGED	0.094517048	0.537305582	UNCHANGED
Ce_fissilis.011703.1	14	2906.03	Serine--glyoxylate aminotransferase	146295	87458	110826	152381	0.124310195	-0.742222603	UNCHANGED	0.353864145	0.341636724	UNCHANGED	0.106592858	0.801025213	UNCHANGED
Ce_fissilis.012174.1	4	845.36	Single-stranded DNA-binding protein WHY2, mitochondrial	17869	20141	21787	23745	0.495020818	0.172648492	UNCHANGED	0.628540681	0.113324282	UNCHANGED	0.414980019	0.237500735	UNCHANGED
Ce_fissilis.000314.1	2	1245.64	SKP1-like protein 1B	13593	18752	44078	23919	0.475327746	0.464162889	UNCHANGED	0.193006263	1.23301429	UNCHANGED	0.266319627	0.3511126	UNCHANGED
Ce_fissilis.018570.1	3	408.88	Small nuclear ribonucleoprotein-associated protein B'	39906	49580	52199	56479	0.146790761	0.313166311	UNCHANGED	0.361741158	0.074244985	UNCHANGED	0.204292995	0.187933802	UNCHANGED
Ce_fissilis.016214.1	3	1014.22	Soluble inorganic pyrophosphatase 1	12112	18488	20880	13385	0.105133246	0.610202683	UNCHANGED	0.605551029	0.175527387	UNCHANGED	0.175721569	-0.465913641	UNCHANGED
Ce_fissilis.019182.1	2	1123.06	Soluble inorganic pyrophosphatase 2	25090	55597	65967	44050	0.078259868	1.147916025	UNCHANGED	0.516089233	0.246745502	UNCHANGED	0.245341813	-0.335881664	UNCHANGED
Ce_fissilis.002278.1	6	1192.44	Soluble inorganic pyrophosphatase 6, chloroplastic	89652	120014	131908	132459	0.102690371	0.420787885	UNCHANGED	0.485685388	0.136333	UNCHANGED	0.480651191	0.142345582	UNCHANGED
Ce_fissilis.015635.1	4	995.06	Spermidine synthase	55102	82646	96130	88681	0.00056541	0.584838858	UNCHANGED	0.002503685	0.218034252	UNCHANGED	0.214416761	0.101672416	UNCHANGED
Ce_fissilis.006747.1	7	6422.89	Stem-specific protein TSJT1	193375	159253	201511	215724	0.278227097	-0.280081748	UNCHANGED	0.086882573	0.339542233	UNCHANGED	0.054742607	0.437868633	UNCHANGED
Ce_fissilis.006853.1	2	2172.30	Stress-response A/B barrel domain-containing protein At5g22580	65103	60262	37280	43301	0.730558838	-0.111483154	UNCHANGED	0.160449868	-0.692862054	UNCHANGED	0.306455967	-0.476838668	UNCHANGED
Ce_fissilis.016815.1	10	4544.40	Stress-response A/B barrel domain-containing protein UP3	138557	135488	198600	192543	0.868269322	-0.032316885	UNCHANGED	0.026894608	0.551700488	UNCHANGED	0.031048108	0.507016296	UNCHANGED
Ce_fissilis.015839.1	11	3271.23	Subtilisin-like protease SBT1.4	190551	133275	145953	147253	0.08145784	-0.515770879	UNCHANGED	0.561759598	0.131103383	UNCHANGED	0.584625761	0.143892161	UNCHANGED
Ce_fissilis.016498.1	13	1195.11	Subtilisin-like protease SBT1.7	80158	84189	102297	89430	0.780999764	0.070785328	UNCHANGED	0.120855336	0.28106209	UNCHANGED	0.48539182	0.08713262	UNCHANGED
Ce_fissilis.017159.1	19	2843.76	Subtilisin-like protease SBT1.7	145044	145461	117235	142003	0.988490443	0.004141773	UNCHANGED	0.31705742	-0.311236463	UNCHANGED	0.911122334	-0.034713168	UNCHANGED

Ce_fissilis.014796.1	10	5969.23	Succinate dehydrogenase subunit 5, mitochondrial	158234	207293	187459	208078	0.115826164	0.389613504	UNCHANGED	0.182412267	-0.145090567	UNCHANGED	0.955990853	0.005455358	UNCHANGED
Ce_fissilis.014022.1	7	2914.72	Succinate--CoA ligase [ADP-forming] subunit alpha-1, mitochondrial	143825	218039	224926	259522	0.060589225	0.600269912	UNCHANGED	0.764026242	0.044865031	UNCHANGED	0.118278667	0.251272339	UNCHANGED
Ce_fissilis.011945.1	31	6591.75	Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial	232384	330824	338784	374506	0.009490987	0.509552601	UNCHANGED	0.744448734	0.034303779	UNCHANGED	0.173384964	0.178927726	UNCHANGED
Ce_fissilis.017714.1	10	1028.95	Succinate-semialdehyde dehydrogenase, mitochondrial	96286	113996	139980	146009	0.529292853	0.243580775	UNCHANGED	0.040501172	0.296238033	UNCHANGED	0.095524398	0.357080203	UNCHANGED
Ce_fissilis.003655.1	12	1104.51	Sucrose synthase	57883	137940	132919	82027	0.055831191	1.252839902	UNCHANGED	0.879735842	-0.05349344	UNCHANGED	0.115922426	-0.749878288	UNCHANGED
Ce_fissilis.001119.1	4	3756.11	Superoxide dismutase [Cu-Zn]	79909	97986	75514	71350	0.447410377	0.294217109	UNCHANGED	0.291477901	-0.375827075	UNCHANGED	0.173764113	-0.457664648	UNCHANGED
Ce_fissilis.010672.1	2	3626.06	Superoxide dismutase [Mn], mitochondrial	38482	45106	66399	47511	0.413244735	0.229140647	UNCHANGED	0.018613612	0.557851879	UNCHANGED	0.725896121	0.074933681	UNCHANGED
Ce_fissilis.010672.2	10	5603.13	Superoxide dismutase [Mn], mitochondrial	139219	134497	205457	186184	0.789279905	-0.049780821	UNCHANGED	0.112629886	0.611258838	UNCHANGED	0.133764609	0.469152434	UNCHANGED
Ce_fissilis.002854.1	10	25092.19	Thaumatin-like protein	387605	123786	224236	186531	0.254817019	-1.646733485	UNCHANGED	0.375210194	0.857163728	UNCHANGED	0.202218837	0.591559935	UNCHANGED
Ce_fissilis.003520.1	3	449.55	Thiamine thiazole synthase, chloroplastic	28298	20616	19089	29010	0.264551429	-0.456970306	UNCHANGED	0.72435712	-0.110999588	UNCHANGED	0.244107716	0.492792603	UNCHANGED
Ce_fissilis.018863.1	11	8551.58	Thiol protease aleurain	194462	242758	294651	295052	0.315821699	0.320025958	UNCHANGED	0.179396696	0.279488555	UNCHANGED	0.235935729	0.281451718	UNCHANGED
Ce_fissilis.004434.1	7	16370.90	Thioredoxin H-type	192856	144761	188287	196133	0.50914492	-0.413857144	UNCHANGED	0.177836396	0.379268251	UNCHANGED	0.277831242	0.438165379	UNCHANGED
Ce_fissilis.018888.1	4	2315.48	Thioredoxin M4, chloroplastic	121918	89749	105871	118956	0.066419877	-0.441933598	UNCHANGED	0.185886058	0.238332549	UNCHANGED	0.044719621	0.406454475	UNCHANGED
Ce_fissilis.001167.2	5	3395.71	Thylakoid lumenal 15 kDa protein 1, chloroplastic	73191	43643	48383	62647	0.109916609	-0.745927708	UNCHANGED	0.7191141	0.148753984	UNCHANGED	0.093644092	0.521507613	UNCHANGED
Ce_fissilis.003701.1	3	729.85	Thylakoid lumenal 19 kDa protein, chloroplastic	21373	22625	27181	28402	0.806402081	0.082133363	UNCHANGED	0.331939633	0.264678407	UNCHANGED	0.105524479	0.328107275	UNCHANGED
Ce_fissilis.004964.1	11	1178.97	Tol-Pal system protein TolB	65040	50648	70186	83023	0.219565139	-0.360818792	UNCHANGED	0.072217176	0.470681671	UNCHANGED	0.099409901	0.71300646	UNCHANGED
Ce_fissilis.000145.1	3	654.50	TOM1-like protein 1	44706	31827	36068	35331	0.001851856	-0.490210122	UNCHANGED	0.145181435	0.180463807	UNCHANGED	0.122556175	0.150701556	UNCHANGED
Ce_fissilis.010272.1	4	2221.91	Translationally-controlled tumor protein homolog	549478	688760	788037	741868	0.056005434	0.32593984	UNCHANGED	0.071574853	0.194261404	UNCHANGED	0.571957421	0.107159952	UNCHANGED
Ce_fissilis.014356.1	12	14062.59	Translationally-controlled tumor protein homolog	597919	823753	917402	869501	0.029335195	0.462261851	UNCHANGED	0.134154294	0.155341983	UNCHANGED	0.480462553	0.077975965	UNCHANGED
Ce_fissilis.005132.1	20	24750.32	Triosephosphate isomerase, chloroplastic	575804	448986	525809	590905	0.120255934	-0.35890628	UNCHANGED	0.183591934	0.227867914	UNCHANGED	0.02334391	0.396255217	UNCHANGED
Ce_fissilis.008983.1	12	25970.46	Triosephosphate isomerase, cytosolic	626837	541731	617658	690504	0.242940692	-0.210513334	UNCHANGED	0.422080796	0.189229375	UNCHANGED	0.106507234	0.350071554	UNCHANGED
Ce_fissilis.008984.1	12	25570.48	Triosephosphate isomerase, cytosolic	696061	903879	990360	889045	0.018218063	0.37691641	UNCHANGED	0.024228246	0.131823323	UNCHANGED	0.741708459	-0.023874377	UNCHANGED
Ce_fissilis.0	24	38517	Tubulin alpha chain	10611	95469	1019619	1150910	0.37201	-	UNCHANGED	0.48245	0.094922391	UNCHANGED	0.12068	0.26966	UNCHANGED

06084.1		.41		45	2			4893	0.152514298		925			8879	7101	
Ce_fissilis.006085.1	37	71013.16	Tubulin alpha chain	1149509	1153008	1185722	1295371	0.985769335	0.004384478	UNCHANGED	0.855152247	0.040363758	UNCHANGED	0.460465797	0.167962728	UNCHANGED
Ce_fissilis.006083.1	21	28110.11	Tubulin alpha-3 chain	357552	422782	429774	492516	0.180192389	0.241761496	UNCHANGED	0.860103831	0.023666299	UNCHANGED	0.156215425	0.220257688	UNCHANGED
Ce_fissilis.008398.2	11	10466.08	Tubulin alpha-3 chain	100785	77910	92060	110416	0.175319715	-0.371394525	UNCHANGED	0.097486715	0.240769048	UNCHANGED	0.012040685	0.503069268	UNCHANGED
Ce_fissilis.006840.1	13	28093.15	Tubulin beta-1 chain	82582	83587	96009	110112	0.937725957	0.017456118	UNCHANGED	0.392313984	0.199888989	UNCHANGED	0.147120749	0.397629334	UNCHANGED
Ce_fissilis.006997.1	18	9387.90	Tubulin beta-1 chain	130138	84969	47946	83343	0.235492303	-0.615038092	UNCHANGED	0.283431003	-0.825526902	UNCHANGED	0.960804744	-0.027866767	UNCHANGED
Ce_fissilis.014997.1	8	29739.28	Tubulin beta-2 chain	101016	88935	39182	73507	0.54233396	-0.183763994	UNCHANGED	0.050865733	-1.182561341	UNCHANGED	0.454468134	-0.274867576	UNCHANGED
Ce_fissilis.013959.2	39	83914.30	Tubulin beta-4 chain	225154	287217	310719	366413	0.21198728	0.351229447	UNCHANGED	0.567864527	0.113471773	UNCHANGED	0.176040258	0.351333539	UNCHANGED
Ce_fissilis.017401.1	23	56895.41	Tubulin beta-6 chain	371643	375629	457120	493068	0.926326034	0.015393197	UNCHANGED	0.117307587	0.283264287	UNCHANGED	0.042377797	0.39247744	UNCHANGED
Ce_fissilis.014996.1	36	91270.13	Tubulin beta-8 chain	741464	733184	821320	924691	0.926057032	-0.016200278	UNCHANGED	0.263169303	0.163767454	UNCHANGED	0.078635342	0.334794493	UNCHANGED
Ce_fissilis.009396.1	8	761.22	Ubiquitin domain-containing protein DSK2b	45127	39215	48752	51053	0.393113651	-0.2025588	UNCHANGED	0.206591467	0.31404683	UNCHANGED	0.084969904	0.380565317	UNCHANGED
Ce_fissilis.004398.1	6	1116.16	Ubiquitin receptor RAD23c	19711	17977	18783	24882	0.563210658	-0.132887711	UNCHANGED	0.519004688	0.063302129	UNCHANGED	0.002480492	0.468933627	UNCHANGED
Ce_fissilis.004398.2	10	1907.71	Ubiquitin receptor RAD23c	73181	88380	89218	103880	0.328330588	0.272248023	UNCHANGED	0.853067246	0.013625457	UNCHANGED	0.018285447	0.233139889	UNCHANGED
Ce_fissilis.016477.1	4	1321.37	UBP1-associated protein 2C	38579	56111	64991	82728	0.237081247	0.540462423	UNCHANGED	0.57476699	0.211955932	UNCHANGED	0.093308706	0.560096974	UNCHANGED
Ce_fissilis.011004.1	13	1686.07	UDP-glucose 4-epimerase GEPI48	70959	80932	92662	99732	0.203361382	0.189727107	UNCHANGED	0.055689769	0.195267824	UNCHANGED	0.004784032	0.301349822	UNCHANGED
Ce_fissilis.019119.1	3	814.36	UDP-glycosyltransferase 88B1	31540	30246	34491	47649	0.840252663	-0.060438735	UNCHANGED	0.434496159	0.189472254	UNCHANGED	0.069914487	0.655718905	UNCHANGED
Ce_fissilis.005797.1	7	12631.73	Uncharacterized protein At2g37660, chloroplastic	250129	241752	296826	296542	0.662128882	-0.049143912	UNCHANGED	0.090300652	0.296092589	UNCHANGED	0.041837568	0.294710493	UNCHANGED
Ce_fissilis.016336.2	3	1612.97	Uncharacterized protein At2g39795, mitochondrial	82351	70223	70371	77466	0.458700527	-0.229848882	UNCHANGED	0.991725578	0.003031696	UNCHANGED	0.642372621	0.14162511	UNCHANGED
Ce_fissilis.015764.1	8	19485.63	Uncharacterized protein At5g01610	655872	496547	572933	628402	0.127840454	-0.401483281	UNCHANGED	0.030575694	0.206434069	UNCHANGED	0.000307336	0.339756778	UNCHANGED
Ce_fissilis.010160.1	5	2378.44	Uncharacterized protein OsI_027940	173093	188952	198336	213365	0.404342771	0.126471325	UNCHANGED	0.535424497	0.069926694	UNCHANGED	0.312418031	0.175303527	UNCHANGED
Ce_fissilis.010160.2	6	1984.29	Uncharacterized protein OsI_027940	121062	82325	102905	86653	0.055079149	-0.556351063	UNCHANGED	0.027058418	0.321916588	UNCHANGED	0.501345855	0.073919471	UNCHANGED
Ce_fissilis.009533.1	5	2680.38	Universal stress protein A-like protein	18945	44335	59166	58443	0.080902565	1.226607783	UNCHANGED	0.145957425	0.416316869	UNCHANGED	0.35585645	0.398575933	UNCHANGED
Ce_fissilis.004456.1	9	42534.25	Universal stress protein PHOS32	610967	531505	612804	751944	0.348351087	-0.201010388	UNCHANGED	0.309735803	0.205341905	UNCHANGED	0.01005917	0.50054021	UNCHANGED
Ce_fissilis.0	6	17477	Universal stress protein PHOS32	27395	24017	339064	317921	0.69671	-	UNCHANGED	0.23517	0.497501469	UNCHANGED	0.39164	0.40461	UNCHANGED

04456.2		.36		5	0			2897	0.18988437		5234			1101	3151	
Ce_fissilis.013656.1	5	2059.50	UPF0587 protein C1orf123 homolog	20591	26659	36934	36475	0.13057646	0.372622567	UNCHANGED	0.014535863	0.470333859	UNCHANGED	0.024322466	0.452266116	UNCHANGED
Ce_fissilis.015731.1	6	723.86	Ureidoglycolate hydrolase	28507	33756	37674	42045	0.261150657	0.243858852	UNCHANGED	0.238834861	0.158411013	UNCHANGED	0.072362597	0.316787478	UNCHANGED
Ce_fissilis.011699.1	40	14942.66	V-type proton ATPase catalytic subunit A	532113	740833	793394	822741	0.052747148	0.477414377	UNCHANGED	0.364955511	0.09888895	UNCHANGED	0.158643132	0.151289629	UNCHANGED
Ce_fissilis.010564.1	29	20747.50	V-type proton ATPase subunit B2	688131	645125	699624	791467	0.592310948	-0.093104994	UNCHANGED	0.272929673	0.117001533	UNCHANGED	0.015099127	0.294951532	UNCHANGED
Ce_fissilis.017972.1	4	937.61	V-type proton ATPase subunit d2	34347	17721	17574	25219	0.398245214	-0.954699273	UNCHANGED	0.918683417	-0.01207192	UNCHANGED	0.03734109	0.509036628	UNCHANGED
Ce_fissilis.018696.1	7	717.16	Xylulose kinase 2	32640	55878	60129	76130	0.073769506	0.775644238	UNCHANGED	0.440896126	0.105769917	UNCHANGED	0.099624032	0.446191011	UNCHANGED
Ce_fissilis.012697.1	22	26027.81	Heat shock cognate 70 kDa protein 2	148582	200345	148795	114361	0.087635753	0.431230776	UNCHANGED	0.059859817	-0.429159687	UNCHANGED	0.00831976	-0.808899158	DOWN
Ce_fissilis.008896.1	8	3441.14	Probable xyloglucan endotransglucosylase/hydrolase protein B	71718	122237	61540	46605	0.084647723	0.769279096	UNCHANGED	0.072312954	-0.990083155	UNCHANGED	0.031853513	-1.391132488	DOWN
Ce_fissilis.010839.1	7	12729.94	Superoxide dismutase [Cu-Zn], chloroplastic	307893	114215	50835	43979	0.061078094	-1.430674647	UNCHANGED	0.054914841	-1.167864052	UNCHANGED	0.025423289	-1.376864591	DOWN
Ce_fissilis.003483.1	2	649.93	Basic endochitinase A	42859	22993	11422	17036	0.183691155	-0.898397865	UNCHANGED	0.032016806	-1.009442579	DOWN	0.303602608	-0.432622192	UNCHANGED
Ce_fissilis.015956.1	7	1905.33	Chalcone--flavonone isomerase	54188	46812	25844	42426	0.551794471	-0.211095928	UNCHANGED	0.006967613	-0.857048378	DOWN	0.564906336	-0.141919112	UNCHANGED
Ce_fissilis.002546.1	2	1738.65	Ras-related protein RABC2a	18088	11886	7551	9810	0.078566099	-0.605763254	UNCHANGED	0.020952831	-0.654567122	DOWN	0.153311429	-0.276991548	UNCHANGED
Ce_fissilis.003679.1	6	10374.33	Ras-related protein RABE1c	14472	20647	11718	21498	0.16479236	0.512736284	UNCHANGED	0.032838137	-0.817274029	DOWN	0.783832657	0.058247398	UNCHANGED
Ce_fissilis.011357.1	5	10357.63	Ras-related protein RABE1c	17350	17896	9759	14317	0.904632826	0.044734283	UNCHANGED	0.034574253	-0.874784505	DOWN	0.243936918	-0.321884997	UNCHANGED
Ce_fissilis.007075.1	5	2717.21	Berberine bridge enzyme-like 8	16408	19522	10841	10428	0.320970958	0.250672157	UNCHANGED	0.007175793	-0.848662169	DOWN	0.027318879	-0.904592259	DOWN
Ce_fissilis.008553.1	6	1475.65	Aspartyl protease family protein At5g10770	129894	35544	111913	118324	0.002533246	-1.869641269	DOWN	0.000641319	1.654680209	UP	0.036179549	1.735052157	UP
Ce_fissilis.010887.1	16	8828.35	Aspartyl protease family protein At5g10770	341727	103531	180326	228776	0.005285072	-1.722781285	DOWN	0.049570592	0.800544839	UP	0.036639711	1.14387135	UP
Ce_fissilis.013030.1	9	36144.13	Chitinase 4	1086268	26842	81482	87668	0.000472918	-5.33874366	DOWN	0.01006818	1.601989221	UP	0.004902626	1.707550851	UP
Ce_fissilis.009745.1	21	5882.83	Cinnamyl alcohol dehydrogenase 1	241261	135178	220449	253359	0.000395027	-0.835732499	DOWN	0.003987471	0.705581399	UP	0.000491368	0.906319621	UP
Ce_fissilis.006732.1	7	1215.02	Glutathione S-transferase DHAR3, chloroplastic	94053	39338	63296	65327	0.038793178	-1.25754324	DOWN	0.02317907	0.686183561	UP	0.003920347	0.731736192	UP
Ce_fissilis.0	17	8849.	Glutelin type-D 1	29882	14630	284647	315683	0.00320	-	DOWN	0.00070	0.960247382	UP	0.00692	1.10955	UP

11776.1		72		3	0			3105	1.030366344		3221			8737	3216	
Ce_fissilis.015152.1	5	11697.71	GTP-binding protein YPTM2	62378	7456	68824	94499	0.030434207	-3.064630751	DOWN	0.046378801	3.20650105	UP	3.71583E-05	3.663892892	UP
Ce_fissilis.016231.1	3	2181.62	Importin subunit alpha-4	17580	5204	10554	10912	0.026038758	-1.756166971	DOWN	0.000254655	1.02003788	UP	0.001003645	1.06811753	UP
Ce_fissilis.017762.1	4	1459.23	Isoflavone reductase homolog TP7	61235	6335	14688	18838	0.002591433	-3.272903946	DOWN	0.005417405	1.213169586	UP	0.000190409	1.572189818	UP
Ce_fissilis.013923.2	4	21897.66	Peroxidase 15	566366	163361	277289	306318	0.015693491	-1.793667525	DOWN	0.037089236	0.763321806	UP	0.012756472	0.906963796	UP
Ce_fissilis.003179.1	10	2230.77	Serine carboxypeptidase II-3	64215	12416	23965	27562	0.004139279	-2.370699459	DOWN	0.00425405	0.948742322	UP	0.011397884	1.150484654	UP
Ce_fissilis.010976.1	3	1164.51	Tropinone reductase homolog At5g06060	50726	23890	49269	41241	0.018064037	-1.086315491	DOWN	0.007996709	1.044273505	UP	0.011650793	0.787660082	UP
Ce_fissilis.002557.2	7	3750.84	Vestitone reductase	139623	41216	92828	128528	0.000119463	-1.760261805	DOWN	0.006629723	1.171359426	UP	0.00473922	1.640810172	UP
Ce_fissilis.008441.2	4	6273.09	Fasciclin-like arabinogalactan protein 11	351445	37554	90550	87234	0.017879804	-3.226264711	DOWN	0.043491007	1.269755868	UP	0.072354717	1.21592088	UNCHANGED
Ce_fissilis.009318.1	3	7081.79	Germin-like protein subfamily 3 member 1	153665	30770	81829	35527	0.032647699	-2.320193297	DOWN	0.006069938	1.411085819	UP	0.559484193	0.207386913	UNCHANGED
Ce_fissilis.010530.1	8	6130.63	NADPH-dependent oxidoreductase 2-alkenal reductase	70807	34207	70948	46929	0.00036143	-1.049630253	DOWN	0.002731546	1.05249844	UP	0.029949806	0.456217382	UNCHANGED
Ce_fissilis.016383.1	6	1081.06	Probable 2-oxoglutarate-dependent dioxygenase At5g05600	209834	70228	109535	74835	0.008098403	-1.579127933	DOWN	0.028560283	0.641270575	UP	0.698863162	0.091657971	UNCHANGED
Ce_fissilis.017826.1	7	13339.17	2-haloacrylate reductase	164919	82995	97714	127883	0.002874508	-0.990660684	DOWN	0.116997808	0.235549025	UNCHANGED	0.000106059	0.623731403	UP
Ce_fissilis.013078.1	3	452.06	Aspartic proteinase A1	32939	3153	5386	5076	0.018856142	-3.384980733	DOWN	0.17193604	0.772378428	UNCHANGED	0.030071062	0.686829613	UP
Ce_fissilis.017302.2	2	569.94	Dormancy-associated protein 1	89633	50721	69157	77802	0.002109178	-0.821437313	DOWN	0.24396293	0.447272186	UNCHANGED	0.019275212	0.617211481	UP
Ce_fissilis.011103.1	4	2041.89	Expansin-like A1	105986	43877	63323	72841	0.001456428	-1.272346618	DOWN	0.033628049	0.529275966	UNCHANGED	0.010824548	0.731289494	UP
Ce_fissilis.003143.1	6	1819.06	Fasciclin-like arabinogalactan protein 2	346320	161916	244538	247235	0.017576711	-1.096863648	DOWN	0.030562954	0.594815109	UNCHANGED	0.045023846	0.610643992	UP
Ce_fissilis.002164.1	2	520.52	Germin-like protein subfamily 1 member 1	64025	14226	23599	28319	0.001081289	-2.170127817	DOWN	0.234418698	0.730249841	UNCHANGED	0.0027328	0.993274058	UP
Ce_fissilis.002863.1	2	13727.10	Germin-like protein subfamily 1 member 13	221556	21920	60042	66193	0.048906642	-3.33732867	DOWN	0.093188499	1.453706302	UNCHANGED	0.021495631	1.594416186	UP
Ce_fissilis.003443.1	4	1432.05	Heme-binding-like protein At3g10130, chloroplastic	25638	5897	8836	11526	0.00045103	-2.1201093	DOWN	0.117896298	0.583303496	UNCHANGED	0.007157412	0.966771819	UP

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Ce_fissilis.007218.1	3	2664.61	Kunitz trypsin inhibitor 2	73663	5762	9755	15762	9.90291E-05	-3.676384227	DOWN	0.118195741	0.759655675	UNCHANGED	0.003994405	1.451877248	UP
Ce_fissilis.015876.2	8	2684.08	Legumin B	167260	28730	8795	168600	0.000976084	-2.541445592	DOWN	0.16342152	-1.707873928	UNCHANGED	0.000379636	2.55295872	UP
Ce_fissilis.015325.3	6	14613.01	MLP-like protein 31	744369	185955	284504	357688	0.000638438	-2.001061266	DOWN	0.134169567	0.613493993	UNCHANGED	0.020927909	0.943744724	UP
Ce_fissilis.000198.1	5	702.21	Monocopper oxidase-like protein SKS1	56221	33043	48009	51207	0.016721474	-0.76677129	DOWN	0.026038994	0.538969912	UNCHANGED	0.019284912	0.632012327	UP
Ce_fissilis.001837.1	7	1567.69	Omega-hydroxypalmitate O-feruloyl transferase	56803	8822	11103	24293	0.023168897	-2.686841151	DOWN	0.169675465	0.331783075	UNCHANGED	0.047214	1.461437305	UP
Ce_fissilis.002939.2	4	7274.90	Peptide methionine sulfoxide reductase B2, chloroplastic	85222	38613	52169	85296	0.010141368	-1.142143831	DOWN	0.294632098	0.434115986	UNCHANGED	0.017418888	1.143385426	UP
Ce_fissilis.015542.1	7	2414.40	Phospholipid hydroperoxide glutathione peroxidase 1, chloroplastic	78299	32367	50563	56089	0.000183769	-1.274460502	DOWN	0.099372695	0.643545713	UNCHANGED	0.009714316	0.793183897	UP
Ce_fissilis.000097.1	8	6536.46	Polyubiquitin	42376	19786	23342	33094	0.001023618	-1.098770431	DOWN	0.024931847	0.238426238	UNCHANGED	0.005058014	0.742098632	UP
Ce_fissilis.018214.2	9	3522.98	Serine carboxypeptidase-like 46	111698	58943	74461	112490	0.027685081	-0.922213828	DOWN	0.327847764	0.337168806	UNCHANGED	0.018953153	0.93240436	UP
Ce_fissilis.000751.2	2	1441.66	Thioredoxin X, chloroplastic	51033	24074	37677	39846	0.045088914	-1.083949306	DOWN	0.155184298	0.646179091	UNCHANGED	0.000468603	0.726961114	UP
Ce_fissilis.018728.1	3	3068.76	Thioredoxin-like protein CXXS1	102005	42362	55615	68460	0.000961426	-1.267818684	DOWN	0.244166945	0.392715597	UNCHANGED	0.016782107	0.6924987	UP
Ce_fissilis.000916.1	7	870.25	Thylakoid lumenal 29 kDa protein, chloroplastic	101253	56440	84636	94950	0.003818433	-0.843175413	DOWN	0.154923761	0.584551565	UNCHANGED	0.020131604	0.750437579	UP
Ce_fissilis.016690.1	23	42056.71	Tubulin beta-8 chain	84116	26497	19738	54491	0.000922873	-1.666528059	DOWN	0.071933387	-0.424890214	UNCHANGED	0.001687873	1.040157613	UP
Ce_fissilis.018198.1	6	1105.75	2-isopropylmalate synthase 1, chloroplastic	376697	49933	73037	61578	0.001154273	-2.915353169	DOWN	0.246719074	0.548646762	UNCHANGED	0.713104038	0.302442074	UNCHANGED
Ce_fissilis.016326.1	4	840.62	5'-nucleotidase SurE	68839	41860	39736	46813	0.004637715	-0.717637683	DOWN	0.561783645	-0.07512908	UNCHANGED	0.269787259	0.161328847	UNCHANGED
Ce_fissilis.014429.1	20	35240.35	Actin	362736	218342	322887	237517	0.040033071	-0.732333756	DOWN	0.037890595	0.564443209	UNCHANGED	0.500733069	0.121444312	UNCHANGED
Ce_fissilis.006751.1	6	1382.41	Alpha-L-arabinofuranosidase 1	108120	46868	57240	68237	0.024738151	-1.205962155	DOWN	0.163791143	0.288438482	UNCHANGED	0.139706802	0.541948433	UNCHANGED
Ce_fissilis.009610.1	22	1481.09	Alpha-mannosidase At3g26720	261566	118036	126075	144772	0.000142215	-1.147954611	DOWN	0.311234612	0.09505682	UNCHANGED	0.064167532	0.294559739	UNCHANGED
Ce_fissilis.017136.1	2	425.03	Arginine biosynthesis bifunctional protein ArgJ, chloroplastic	22386	12490	15293	15588	0.042325834	-0.841891785	DOWN	0.222201936	0.292155724	UNCHANGED	0.095058322	0.31973554	UNCHANGED

Ce_fissilis.009377.1	19	26693.46	ATP synthase subunit beta, mitochondrial	56897	17387	13985	18375	2.8975E-05	-1.710349374	DOWN	0.048181271	-0.314143891	UNCHANGED	0.593494346	0.079728279	UNCHANGED
Ce_fissilis.014974.2	2	18240.83	Basic blue protein	111995	47421	36042	34645	0.019850304	-1.239840627	DOWN	0.418169535	-0.395853688	UNCHANGED	0.311381152	-0.45287893	UNCHANGED
Ce_fissilis.007025.1	9	4310.65	Basic transcription factor 3	1127450	52664	63787	48759	4.23862E-05	-4.420090793	DOWN	0.044857652	0.276430637	UNCHANGED	0.568682037	-0.111173891	UNCHANGED
Ce_fissilis.017395.1	6	497.95	Beta-D-xylosidase 4	57018	27734	42595	34452	0.024809498	-1.039764696	DOWN	0.131633845	0.619030399	UNCHANGED	0.016401816	0.312942462	UNCHANGED
Ce_fissilis.002924.1	14	3813.16	Beta-galactosidase 8	161015	82584	114349	120066	0.027524018	-0.963262883	DOWN	0.014256923	0.469515154	UNCHANGED	0.019051821	0.539896137	UNCHANGED
Ce_fissilis.009651.1	12	3224.94	Cysteine synthase, chloroplastic/chromoplastic	94156	41586	48502	57416	0.002246386	-1.178932541	DOWN	0.163714896	0.221918659	UNCHANGED	0.072683548	0.465344993	UNCHANGED
Ce_fissilis.017207.1	3	3118.63	Early nodulin-like protein 1	193298	87906	102903	76653	0.039262645	-1.136796483	DOWN	0.437924792	0.227252277	UNCHANGED	0.519474539	-0.197617292	UNCHANGED
Ce_fissilis.017918.1	5	3251.58	Early nodulin-like protein 1	181518	100481	97105	121583	0.02643733	-0.853191315	DOWN	0.864126238	-0.049295446	UNCHANGED	0.402576847	0.275016712	UNCHANGED
Ce_fissilis.000985.1	3	939.73	Expansin-A1	87650	50790	58259	71212	0.027346315	-0.78719832	DOWN	0.347744934	0.197929747	UNCHANGED	0.082073281	0.487564178	UNCHANGED
Ce_fissilis.008441.3	2	3908.88	Fasciclin-like arabinogalactan protein 11	318354	58768	53486	50116	0.010546373	-2.437527674	DOWN	0.801576056	-0.135869487	UNCHANGED	0.632495711	-0.229754733	UNCHANGED
Ce_fissilis.015795.1	4	1353.56	Fruit protein pKIWI502	58515	20698	22772	32904	0.00318017	-1.499299166	DOWN	0.666481011	0.137775969	UNCHANGED	0.077487922	0.66875899	UNCHANGED
Ce_fissilis.016930.1	10	3249.83	Fumarylacetoacetase	127377	83315	116213	114320	0.043513219	-0.612469363	DOWN	0.006725579	0.480130993	UNCHANGED	0.013903768	0.456433145	UNCHANGED
Ce_fissilis.002804.1	2	1665.49	Gamma-interferon-responsive lysosomal thiol protein	144422	80065	83116	121427	0.02740865	-0.851051249	DOWN	0.834897828	0.053966304	UNCHANGED	0.122698454	0.600845696	UNCHANGED
Ce_fissilis.015494.1	2	892.54	GEM-like protein 1	65128	42040	39731	51955	0.009028588	-0.631507871	DOWN	0.671664786	-0.081503616	UNCHANGED	0.037226574	0.305486043	UNCHANGED
Ce_fissilis.001958.1	2	330.97	Glucan endo-1,3-beta-glucosidase 5	46662	18269	19968	28885	0.00130998	-1.352868793	DOWN	0.65799749	0.128281251	UNCHANGED	0.150056777	0.660927665	UNCHANGED
Ce_fissilis.003975.1	7	2119.55	Glucan endo-1,3-beta-glucosidase, basic vacuolar isoform	61521	18543	33530	43262	0.017535434	-1.730235429	DOWN	0.057637457	0.854608527	UNCHANGED	0.1432838	1.222236805	UNCHANGED
Ce_fissilis.011909.2	12	1441.18	Glutamate-1-semialdehyde 2,1-aminomutase, chloroplastic	181372	66228	90703	75332	0.004860919	-1.453439222	DOWN	0.03863543	0.4537202	UNCHANGED	0.259019347	0.185826638	UNCHANGED
Ce_fissilis.012967.1	2	793.27	Glutathione S-transferase L3	23759	6227	8501	7359	0.012069695	-1.931916002	DOWN	0.254318089	0.449132939	UNCHANGED	0.514069	0.241083088	UNCHANGED
Ce_fissilis.015284.1	9	2862.80	Glutelin type-A 2	123177	22637	40502	39398	0.008527114	-2.443982694	DOWN	0.165073865	0.839321414	UNCHANGED	0.063035712	0.799434494	UNCHANGED
Ce_fissilis.0	3	575.2	Glycerate dehydrogenase HPR, peroxisomal	63239	30953	38467	37574	0.00100	-	DOWN	0.25928	0.313530141	UNCHANGED	0.30464	0.27964	UNCHANGED

01892.1		8						4821	1.030727542		6714			5144	7697	
Ce_fissilis.016375.3	6	6377.75	Glycine-rich RNA-binding protein GRP1A	158302	83445	103294	125041	0.003350837	-0.923779303	DOWN	0.010463833	0.307855837	UNCHANGED	0.000574686	0.583500484	UNCHANGED
Ce_fissilis.015598.1	20	15008.45	Heat shock 70 kDa protein	49911	25867	18028	27435	0.01804037	-0.948262686	DOWN	0.073084362	-0.520883302	UNCHANGED	0.751051992	0.084917402	UNCHANGED
Ce_fissilis.010897.1	4	2692.89	Heme-binding protein 2	115667	44157	38107	41784	0.029822935	-1.389254609	DOWN	0.68263579	-0.212580765	UNCHANGED	0.86419002	-0.079694975	UNCHANGED
Ce_fissilis.006645.1	2	342.42	Heparanase-like protein 3	19774	10873	13225	15719	0.001060782	-0.862842524	DOWN	0.077318554	0.282481306	UNCHANGED	0.033763199	0.531728793	UNCHANGED
Ce_fissilis.000870.2	4	835.12	HIPL1 protein	73485	31663	45008	42639	0.009091233	-1.214666676	DOWN	0.079247915	0.507381914	UNCHANGED	0.027935354	0.429377028	UNCHANGED
Ce_fissilis.009132.1	14	10139.52	Isoflavone reductase homolog PCBER	198751	114782	126531	131755	0.014606454	-0.792070324	DOWN	0.344949532	0.140595866	UNCHANGED	0.244401494	0.198957824	UNCHANGED
Ce_fissilis.017753.1	14	18977.63	Isoflavone reductase homolog TP7	681986	316515	342053	308549	0.002940668	-1.107468794	DOWN	0.395321893	0.111948899	UNCHANGED	0.750106837	-0.03677428	UNCHANGED
Ce_fissilis.017266.1	2	325.04	Leucine-rich repeat receptor-like protein kinase PXC2	33465	17277	15847	20590	0.047414929	-0.953750897	DOWN	0.601439986	-0.124640467	UNCHANGED	0.190534427	0.253028233	UNCHANGED
Ce_fissilis.018592.1	3	1307.95	LysM domain-containing GPI-anchored protein 1	108254	48912	49642	43336	0.029738352	-1.146152094	DOWN	0.966148856	0.021372711	UNCHANGED	0.759308838	-0.174632926	UNCHANGED
Ce_fissilis.004006.1	12	7735.19	Malate dehydrogenase 1, mitochondrial	236206	64617	65448	74993	0.006069812	-1.87005314	DOWN	0.914862216	0.018427924	UNCHANGED	0.294986111	0.21484148	UNCHANGED
Ce_fissilis.011438.1	8	14471.98	Malate dehydrogenase, cytoplasmic	24555	12762	11661	15294	0.005760845	-0.944128956	DOWN	0.065309881	-0.13013364	UNCHANGED	0.026639176	0.261066025	UNCHANGED
Ce_fissilis.014972.1	11	2082.14	Malate dehydrogenase, glyoxysomal	26993	15989	23536	19255	0.018467989	-0.755485711	DOWN	0.055684064	0.557792643	UNCHANGED	0.247123168	0.268179674	UNCHANGED
Ce_fissilis.008517.2	9	9896.94	Metalloendoproteinase 3-MMP	604744	88616	104367	111903	0.001442859	-2.770692409	DOWN	0.427389114	0.236029131	UNCHANGED	0.184350302	0.336615405	UNCHANGED
Ce_fissilis.005225.2	4	1027.60	Metallo-hydrolase/oxidoreductase superfamily protein	33431	18984	23256	26900	0.016625525	-0.816404902	DOWN	0.3937019	0.292825864	UNCHANGED	0.037777376	0.502822167	UNCHANGED
Ce_fissilis.012378.2	10	4500.53	Mitochondrial carnitine/acylcarnitine carrier-like protein	134862	70239	70185	83095	0.016518998	-0.941140686	DOWN	0.996095677	-0.001100443	UNCHANGED	0.360060446	0.242501645	UNCHANGED
Ce_fissilis.002033.1	11	2448.07	Monocopper oxidase-like protein SKU5	230416	147239	129316	168018	0.023409907	-0.646081347	DOWN	0.466202685	-0.187262637	UNCHANGED	0.456029319	0.190451992	UNCHANGED
Ce_fissilis.015066.1	3	1425.32	NADPH-dependent aldo-keto reductase, chloroplastic	18884	9071	9286	7216	0.023244484	-1.057731121	DOWN	0.888832118	0.033641471	UNCHANGED	0.036499162	-0.330220794	UNCHANGED
Ce_fissilis.002025.1	6	1153.40	NADPH-dependent alkenal/one oxidoreductase, chloroplastic	57499	15140	24446	15658	0.013445843	-1.925123734	DOWN	0.262421215	0.691171194	UNCHANGED	0.871830924	0.048482155	UNCHANGED
Ce_fissilis.000574.1	3	4325.50	Pathogenesis-related protein PR-4B	124654	42089	60190	60572	0.001341196	-1.5663937	DOWN	0.465932432	0.516074937	UNCHANGED	0.192946506	0.525191326	UNCHANGED

									73							
Ce_fissilis.014480.1	3	733.15	Peptide methionine sulfoxide reductase	46370	24340	32338	27611	0.006827228	-0.929825845	DOWN	0.031339596	0.409894772	UNCHANGED	0.233480616	0.181876017	UNCHANGED
Ce_fissilis.001171.1	6	7142.51	Peptide methionine sulfoxide reductase B5	77214	41864	48051	41489	0.020415114	-0.883141751	DOWN	0.574785754	0.198850575	UNCHANGED	0.970126664	-0.012985738	UNCHANGED
Ce_fissilis.002384.1	6	1962.13	Peptidyl-prolyl cis-trans isomerase FKBP16-3, chloroplastic	54991	23178	29936	42365	0.002075663	-1.246415776	DOWN	0.371608608	0.369088568	UNCHANGED	0.053642143	0.870107389	UNCHANGED
Ce_fissilis.001101.1	10	1872.89	Phosphoglycolate phosphatase 1B, chloroplastic	73816	44839	65256	62552	0.012594439	-0.719182265	DOWN	0.085131832	0.541370973	UNCHANGED	0.100518953	0.480303934	UNCHANGED
Ce_fissilis.007829.1	12	6983.16	Plastid-lipid-associated protein 6, chloroplastic	216852	126690	163199	175930	0.007612579	-0.775405878	DOWN	0.190783655	0.365326618	UNCHANGED	0.063503629	0.473697951	UNCHANGED
Ce_fissilis.015141.1	13	5414.81	Plastid-lipid-associated protein, chloroplastic	217318	119137	144295	163263	0.005199209	-0.867186269	DOWN	0.175994658	0.276396206	UNCHANGED	0.065586941	0.454575973	UNCHANGED
Ce_fissilis.018179.1	4	840.65	Probable plastid-lipid-associated protein 13, chloroplastic	95469	50321	63908	68597	0.021825057	-0.92386052	DOWN	0.332776788	0.344828898	UNCHANGED	0.094281339	0.446982345	UNCHANGED
Ce_fissilis.014524.1	3	1006.32	Proliferating cell nuclear antigen	39500	23063	21347	29326	0.01658858	-0.776282027	DOWN	0.60224704	-0.111565906	UNCHANGED	0.250933552	0.346587192	UNCHANGED
Ce_fissilis.005711.1	9	2143.55	Protease Do-like 1, chloroplastic	98021	55149	67235	82956	0.007460874	-0.829744148	DOWN	0.358586708	0.285868995	UNCHANGED	0.239070603	0.589010615	UNCHANGED
Ce_fissilis.009576.1	2	1183.66	Protein CURVATURE THYLAKOID 1D, chloroplastic	74822	41992	50922	61056	0.007490698	-0.833348728	DOWN	0.476465475	0.278168855	UNCHANGED	0.119932221	0.540012848	UNCHANGED
Ce_fissilis.009213.1	6	2127.50	Protein EXORDIUM-like 2	206001	72995	81161	101461	0.025887813	-1.496786822	DOWN	0.687162549	0.152993608	UNCHANGED	0.123509657	0.475059162	UNCHANGED
Ce_fissilis.010352.1	2	527.56	Protein of unknown function (DUF674)	87720	35482	35837	49125	0.040955751	-1.305810257	DOWN	0.915550187	0.014362539	UNCHANGED	0.045155026	0.469379865	UNCHANGED
Ce_fissilis.001196.1	14	13381.99	Ras-related protein Rab7	244114	146330	166255	174291	0.006244457	-0.738330885	DOWN	0.171315248	0.18417195	UNCHANGED	0.028481339	0.252274681	UNCHANGED
Ce_fissilis.001393.1	7	5883.84	Ras-related protein Rab7	41088	26920	26640	31957	0.002375253	-0.610018032	DOWN	0.924537873	-0.015081051	UNCHANGED	0.048733473	0.247420398	UNCHANGED
Ce_fissilis.018513.1	31	22160.15	Ribulose bisphosphate carboxylase/oxygenase activase 1, chloroplastic	179051	69044	121985	78454	0.00234315	-1.374770192	DOWN	0.112875254	0.821110983	UNCHANGED	0.22649196	0.184327822	UNCHANGED
Ce_fissilis.006733.1	4	4644.13	RNA-binding protein CP31B, chloroplastic	52144	24942	29317	25688	0.004618099	-1.063907013	DOWN	0.309184764	0.233124409	UNCHANGED	0.827001769	0.042478172	UNCHANGED
Ce_fissilis.007537.1	16	10782.52	Sedoheptulose-1,7-bisphosphatase, chloroplastic	325791	170624	242867	268815	0.018126722	-0.933124817	DOWN	0.061383323	0.509341085	UNCHANGED	0.052004572	0.655790234	UNCHANGED
Ce_fissilis.015941.1	3	2122.84	Single-stranded DNA-binding protein WHY1, chloroplastic	52052	31806	40854	46029	0.02485549	-0.710633372	DOWN	0.136834829	0.361178968	UNCHANGED	0.076760604	0.533239481	UNCHANGED
Ce_fissilis.011298.1	10	6219.60	Thioredoxin superfamily protein	168183	94006	131648	132279	0.002184028	-0.83920769	DOWN	0.015844471	0.485864269	UNCHANGED	0.016226541	0.492765132	UNCHANGED

Ce_fissilis.002283.1	2	1768.91	Tobamovirus multiplication protein 2A	80953	24843	40749	37215	0.009719686	-1.704231727	DOWN	0.091364376	0.713899996	UNCHANGED	0.270132886	0.583038399	UNCHANGED
Ce_fissilis.006082.1	11	18975.23	Tubulin alpha-3 chain	96579	50566	62846	40359	0.004424421	-0.933541945	DOWN	0.042773965	0.313647021	UNCHANGED	0.072726788	-0.325281145	UNCHANGED
Ce_fissilis.014995.2	28	39921.84	Tubulin beta-1 chain	51693	31686	35304	39129	1.13294E-05	-0.706148275	DOWN	0.140290099	0.155998409	UNCHANGED	0.022518121	0.304397528	UNCHANGED
Ce_fissilis.016689.1	31	64845.43	Tubulin beta-2 chain	91357	60043	72111	72166	0.034212883	-0.60552629	DOWN	0.123125762	0.264219452	UNCHANGED	0.137578151	0.265327434	UNCHANGED
Ce_fissilis.002484.1	13	26648.56	Tubulin beta-3 chain	90087	42543	54502	55416	0.01927222	-1.082382332	DOWN	0.270790636	0.357372263	UNCHANGED	0.142280837	0.381356388	UNCHANGED
Ce_fissilis.013959.1	18	38599.06	Tubulin beta-4 chain	94699	57723	69833	71597	0.011553973	-0.714203774	DOWN	0.136520708	0.274764119	UNCHANGED	0.110126284	0.310750894	UNCHANGED
Ce_fissilis.002002.1	6	1463.51	NAD(P)-binding Rossmann-fold superfamily protein isoform 1	156949	69242	82699	95907	0.010529703	-1.180580621	DOWN	0.234692857	0.25622055	UNCHANGED	0.029806881	0.46998705	UNCHANGED
Ce_fissilis.014484.1	2	2381.80	glycosyl transferase	145230	65969	84866	99417	0.015021145	-1.138486983	DOWN	0.096055085	0.363406546	UNCHANGED	0.016850586	0.591720105	UNCHANGED
Ce_fissilis.002787.1	4	610.82	Uracil phosphoribosyltransferase	35078	12198	17830	16030	0.000953876	-1.523988149	DOWN	0.175867878	0.547732629	UNCHANGED	0.046110476	0.394152371	UNCHANGED
Ce_fissilis.015852.1	2	830.91	ADP-ribosylation factor-like protein 8a	47789	20942	30630	33079	0.043982314	-1.190274319	DOWN	0.243298874	0.548522587	UNCHANGED	-	-	-
Ce_fissilis.014496.2	4	1976.15	Crocetin glucosyltransferase, chloroplastic	5544	27151	102364	94309	-	-	-	0.001933376	1.914638659	UP	0.00028642	1.796397724	UP
Ce_fissilis.018569.1	7	1345.58	Flavonol 3-O-glucosyltransferase UGT89B1	4840	37434	90140	72396	-	-	-	0.00034477	1.267819686	UP	0.006535991	0.95156048	UP
Ce_fissilis.008596.1	2	717.10	Uncharacterized protein At5g02240	2940	25141	40862	43007	-	-	-	0.026837198	0.700729553	UP	0.006733307	0.774535054	UP
Ce_fissilis.016610.3	4	3160.46	12-oxophytodienoate reductase 1	12749	53493	152869	91957	-	-	-	0.000649236	1.51486322	UP	0.11132288	0.781599644	UNCHANGED
Ce_fissilis.017402.1	2	950.12	Cysteine-rich repeat secretory protein 38	0	0	30686	39807	-	-	-	4.26781E-05	-	Unique 3-days PCIB	0.000331084	-	Unique 3-days TIBA
Ce_fissilis.012813.1	3	3530.58	Ras-related protein RABC1	0	0	1163	0	-	-	-	0.039561421	-	Unique 3-days PCIB	-	-	-
Ce_fissilis.018686.1	14	2601.70	26S proteasome regulatory subunit 6B homolog	3810	103658	104322	72478	-	-	-	0.970431396	0.009211065	UNCHANGED	0.143061026	-0.516214801	UNCHANGED
Ce_fissilis.018077.1	4	709.84	4-coumarate--CoA ligase-like 5	8387	78508	70588	81931	-	-	-	0.629917472	-0.153418998	UNCHANGED	0.735669328	0.061571707	UNCHANGED
Ce_fissilis.015103.1	2	421.46	Acetylornithine aminotransferase, mitochondrial	3601	22136	18864	18069	-	-	-	0.096379947	-0.230758926	UNCHANGED	0.186980079	-0.292917807	UNCHANGED
Ce_fissilis.011695.2	4	1193.88	Acyl-coenzyme A oxidase 4, peroxisomal	6262	32647	34935	34111	-	-	-	0.671150364	0.097726982	UNCHANGED	0.762681139	0.063277015	UNCHANGED
Ce_fissilis.001487.1	2	1143.18	Annexin D1	10732	27306	25019	9924	-	-	-	0.816872687	-0.126193865	UNCHANGED	0.058606507	-1.460175894	UNCHANGED
Ce_fissilis.008775.1	3	714.43	ATP synthase gamma chain, chloroplastic	59189	89194	77151	95758	-	-	-	0.528542864	-0.209255575	UNCHANGED	0.801703958	0.102438823	UNCHANGED
Ce_fissilis.0	2	535.6	Benzoate carboxyl methyltransferase	13040	29250	26329	25057	-	-	-	0.76890	-0.151782073	UNCHANGED	0.68845	-	UNCHANGED

16642.1		1									9794			5795	0.223258562	
Ce_fissilis.014642.1	2	435.63	Beta-amylase	4889	28435	30822	25326	-	-	-	0.626915442	0.116260161	UNCHANGED	0.707382433	-0.16708447	UNCHANGED
Ce_fissilis.013858.1	9	765.35	Bifunctional aspartokinase/homoserine dehydrogenase 2, chloroplastic	5939	46357	30590	32792	-	-	-	0.080618044	-0.599706244	UNCHANGED	0.079778766	-0.499413383	UNCHANGED
Ce_fissilis.018361.1	5	1760.36	Cinnamoyl-CoA reductase 1	5009	47381	66223	47888	-	-	-	0.127010939	0.483027571	UNCHANGED	0.953543498	0.015359027	UNCHANGED
Ce_fissilis.001262.1	3	334.45	Coatomer subunit alpha-1	14834	43511	35306	34696	-	-	-	0.236088904	-0.301462384	UNCHANGED	0.305363583	-0.326615416	UNCHANGED
Ce_fissilis.016924.1	5	910.94	Cytosolic enolase 3	3111	22136	19531	18231	-	-	-	0.157575073	-0.180663012	UNCHANGED	0.147653606	-0.280036303	UNCHANGED
Ce_fissilis.006036.1	3	1170.49	Epoxide hydrolase A	3830	20711	26805	17331	-	-	-	0.325757792	0.372122161	UNCHANGED	0.502105682	-0.256982097	UNCHANGED
Ce_fissilis.008180.1	4	663.86	Glucose-1-phosphate adenylyltransferase large subunit 1	7372	10258	23180	15202	-	-	-	0.170023521	1.17608421	UNCHANGED	0.579640044	0.567433149	UNCHANGED
Ce_fissilis.018261.2	5	769.03	Glutamate--cysteine ligase, chloroplastic	4514	38903	33429	19943	-	-	-	0.617339635	-0.218802491	UNCHANGED	0.070268289	-0.96403956	UNCHANGED
Ce_fissilis.006810.1	4	2081.69	Glutathionyl-hydroquinone reductase YqjG	44754	36189	69175	43515	-	-	-	0.064894574	0.934694656	UNCHANGED	0.57384149	0.265962299	UNCHANGED
Ce_fissilis.012304.1	3	567.88	Imidazole glycerol phosphate synthase hisHF, chloroplastic	3984	19382	19955	18881	-	-	-	0.852428198	0.042037916	UNCHANGED	0.874071911	-0.037757789	UNCHANGED
Ce_fissilis.015774.1	4	699.90	Isoflavone reductase homolog	1909	48907	54944	53396	-	-	-	0.712464434	0.167934115	UNCHANGED	0.783832515	0.126712847	UNCHANGED
Ce_fissilis.003997.1	6	3406.43	Luminal-binding protein 5	10012	17686	17073	23508	-	-	-	0.853596914	-0.050891765	UNCHANGED	0.095261334	0.41060512	UNCHANGED
Ce_fissilis.011010.1	8	1744.16	Peroxidase 72	10133	18573	54328	22340	-	-	-	0.196092939	1.548494753	UNCHANGED	0.689707005	0.266409425	UNCHANGED
Ce_fissilis.007109.1	2	603.19	Phosphoserine aminotransferase 1, chloroplastic	3883	42919	41885	30129	-	-	-	0.943358792	-0.035171446	UNCHANGED	0.173897795	-0.510482012	UNCHANGED
Ce_fissilis.013191.1	3	2329.88	Photosystem I reaction center subunit N, chloroplastic	18306	17694	36603	13752	-	-	-	0.418588963	1.048703859	UNCHANGED	0.539208515	-0.363653748	UNCHANGED
Ce_fissilis.002058.1	3	2044.21	Probable beta-D-xylosidase 2	2314	4443	4753	4109	-	-	-	0.497087571	0.09716292	UNCHANGED	0.761019019	-0.112862993	UNCHANGED
Ce_fissilis.007062.1	5	1183.32	Prostaglandin reductase-3	12757	47977	43173	36610	-	-	-	0.422250595	-0.152227711	UNCHANGED	0.020924652	-0.390107479	UNCHANGED
Ce_fissilis.000551.1	2	581.72	Protein RAE1	11721	8593	9702	11025	-	-	-	0.669808295	0.175197833	UNCHANGED	0.347605993	0.359507408	UNCHANGED
Ce_fissilis.005824.1	3	522.07	Protein transport protein Sec24-like At4g32640	8621	12830	12722	16397	-	-	-	0.975415886	-0.012107901	UNCHANGED	0.364180131	0.353931361	UNCHANGED
Ce_fissilis.000324.1	6	986.35	Protochlorophyllide reductase, chloroplastic	6689	32906	43879	35568	-	-	-	0.118069748	0.415162306	UNCHANGED	0.499573975	0.112221829	UNCHANGED
Ce_fissilis.001222.1	3	1486.62	Pyrrolidone-carboxylate peptidase	5428	19135	22834	23642	-	-	-	0.605255912	0.254968674	UNCHANGED	0.632161285	0.305102014	UNCHANGED
Ce_fissilis.003211.1	2	432.31	Pyrrolidone-carboxylate peptidase	20471	36435	40744	50702	-	-	-	0.485714285	0.161272164	UNCHANGED	0.107509772	0.476721544	UNCHANGED
Ce_fissilis.0	2	1127.	Transaldolase	44701	32377	25946	23124	-	-	-	0.38313	-0.319484976	UNCHANGED	0.30174	-	UNCHANGED

10318.1		06									1635			1989	0.48555754	
Ce_fissilis.013200.1	2	727.50	Ubiquitin recognition factor in ER-associated degradation protein 1	11236	24589	20056	20307	-	-	-	0.066104445	-0.29399872	UNCHANGED	0.084056547	-0.276031817	UNCHANGED
Ce_fissilis.018953.1	2	361.44	UDP-N-acetylglucosamine diphosphorylase 1	11351	22857	26286	26108	-	-	-	0.249401853	0.201676854	UNCHANGED	0.248651017	0.191837464	UNCHANGED
Ce_fissilis.010426.1	5	1309.46	Uridine 5'-monophosphate synthase	5326	51334	55785	34312	-	-	-	0.740455968	0.119980307	UNCHANGED	0.059602221	-0.581213902	UNCHANGED
Ce_fissilis.012564.1	7	538.33	Vesicle-fusing ATPase	7356	33845	29268	26338	-	-	-	0.130056001	-0.20959339	UNCHANGED	0.010447724	-0.361770538	UNCHANGED
Ce_fissilis.009319.1	5	922.33	26S proteasome regulatory subunit 7	5320	26448	19943	10387	-	-	-	0.556693876	-0.407300295	UNCHANGED	0.017412745	-1.348348733	DOWN
Ce_fissilis.002115.2	4	581.69	Beta-fructofuranosidase, insoluble isoenzyme CWINV1	2113	49995	53226	27335	-	-	-	0.531420404	0.090356367	UNCHANGED	0.01974537	-0.8710579	DOWN
Ce_fissilis.005188.1	2	3830.71	DEAD-box ATP-dependent RNA helicase 56	4909	71712	77109	43866	-	-	-	0.851899529	0.104697647	UNCHANGED	0.040821111	-0.709121135	DOWN
Ce_fissilis.005188.2	7	4120.25	DEAD-box ATP-dependent RNA helicase 56	1823	69214	56359	30961	-	-	-	0.679269088	-0.296412709	UNCHANGED	0.016662383	-1.160630208	DOWN
Ce_fissilis.012380.1	12	2252.55	Fumarate hydratase 1, mitochondrial	2858	62029	62159	25578	-	-	-	0.996955776	0.003025585	UNCHANGED	0.034858655	-1.278026871	DOWN
Ce_fissilis.010841.1	11	1667.02	Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform	2644	52188	36844	14827	-	-	-	0.436459629	-0.502277923	UNCHANGED	0.023062531	-1.815496061	DOWN
Ce_fissilis.006234.1	5	513.07	Heat shock protein 90-5, chloroplastic	8404	25610	27645	11602	-	-	-	0.790964532	0.110319424	UNCHANGED	0.027908797	-1.142296453	DOWN
Ce_fissilis.006692.1	6	3374.75	Isocitrate dehydrogenase [NADP]	2653	92616	46723	16619	-	-	-	0.21282169	-0.98713136	UNCHANGED	0.0161591	-2.478443509	DOWN
Ce_fissilis.002677.1	3	566.21	Ornithine aminotransferase, mitochondrial	1711	18477	22415	9512	-	-	-	0.693841162	0.278734493	UNCHANGED	0.035766664	-0.95796097	DOWN
Ce_fissilis.009196.1	2	500.52	Oxygen-dependent coproporphyrinogen-III oxidase, chloroplastic	3533	34999	28237	18745	-	-	-	0.426989869	-0.309738688	UNCHANGED	0.005811635	-0.900768481	DOWN
Ce_fissilis.007330.2	3	542.23	Serine hydroxymethyltransferase 2, mitochondrial	1565	9504	10350	3550	-	-	-	0.9065388	0.123033839	UNCHANGED	-	-	-
Ce_fissilis.018123.1	8	1961.18	ATP synthase subunit gamma, mitochondrial	4095	104534	43512	28336	-	-	-	0.002400193	-1.264493475	DOWN	0.001024711	-1.883265294	DOWN
Ce_fissilis.006085.3	36	65750.56	Tubulin alpha chain	0	0	0	80195	-	-	-	-	-	-	0.000137775	-	Unique 3-days TIBA
Ce_fissilis.008602.1	6	3190.72	Beta-D-xylosidase 1	0	0	0	881	-	-	-	-	-	-	0.05937038	-	UNCHANGED