ASPECTOS MORFOLÓGICOS, FISIOLÓGICOS E BIOQUÍMICOS NA PROPAGAÇÃO *in vitro* DE *Dalbergia nigra* (VELL.) ALLEMÃO EX BENTH. (FABACEAE)

LÍDIA DOS SANTOS PESSANHA

UNIVERSIDADE ESTADUAL DO NORTE FLUMINENSE DARCY RIBEIRO - UENF

CAMPOS DOS GOYTACAZES - RJ
Agosto – 2021

ASPECTOS MORFOLÓGICOS, FISIOLÓGICOS E BIOQUÍMICOS NA PROPAGAÇÃO *in vitro* DE *Dalbergia nigra* (VELL.) ALLEMÃO EX BENTH. (FABACEAE)

LÍDIA DOS SANTOS PESSANHA

"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 Doutor em Biotecnologia Vegetal"

Orientadora: Profª. Drª. Claudete Santa Catarina

CAMPOS DOS GOYTACAZES - RJ
Agosto – 2021

FICHA CATALOGRÁFICA
UENF - Bibliotecas
Elaborada com os dados fornecidos pela autora.

P475 Pessanha, Lídia dos Santos.

Aspectos morfológicos, fisiológicos e bioquímicos na propagação *in vitro* de *Dalbergia nigra* (Vell.) Allemão ex Benth. (Fabaceae) / Lídia dos Santos Pessanha. - Campos dos Goytacazes, RJ, 2021.

100 f. : il.
Inclui bibliografia.

Tese (Doutorado em Biotecnologia Vegetal) - Universidade Estadual do Norte Fluminense Darcy Ribeiro, Centro de Biociências e Biotecnologia, 2021.
Orientadora: Claudete Santa Catarina.

1. Jacarandá-da-Bahia. 2. benziladenina. 3. poliaminas. 4. proteômica. 5. enraizamento *ex-vitro*. I. Universidade Estadual do Norte Fluminense Darcy Ribeiro. II. Título.

CDD - 660.6

ASPECTOS MORFOLÓGICOS, FISIOLÓGICOS E BIOQUÍMICOS NA PROPAGAÇÃO *in vitro* DE *Dalbergia nigra* (VELL.) ALLEMÃO EX BENTH. (FABACEAE)

LÍDIA DOS SANTOS PESSANHA

"Tese apresentada ao Centro de Biociências e Biotecnologia da Universidade Estadual do Norte Fluminense Darcy Ribeiro, comoparte das exigências para obtenção do título de Doutor em Biotecnologia Vegetal."

Aprovada em 09 de Agosto de 2021.

Dr.ª Virginia Silva Carvalho - UENF

Prof. Eliemar Campostrini
Fisiologia Vegetal
UENF/CCTA
Matr. 664-3

Dr. Eliemar Campostrini – UENF

Dr.ª Claudete Santa Catarina – UENF (Orientadora)

DEDICATÓRIA

Dedico esse trabalho com amor e carinho ao meu Pai Celício, à minha Mãe Eleonora e ao meu irmão Lício que tanto Amo, por todo apoio e incentivo durante minha jornada.

AGRADECIMENTOS

A Deus por todas as oportunidades dadas em minha vida, que possibilitam continuar construindo meu caminho;

Aos meus pais, Eleonora Cristina Pereira dos Santos Pessanha e Celício da Costa Pessanha por todos os valores ensinados durante a formação do meu ser, assim como por todo carinho e amor dedicados a mim;

Ao meu irmão, Lício dos Santos Pessanha, que sempre me apoia, me ouve e me ajuda quando necessário;

Ao meu namorado e amigo, Éricky Ferreira Rangel Gomes, por toda ajuda e incentivo para continuar a minha caminhada. Além de toda sua família que me apoiou ao longo da minha jornada.

À minha orientadora Professora Dr.ª Claudete Santa Catarina pela oportunidade de voltarmos a trabalhar no doutorado, agradeço a paciência ao orientar e instruir nos momentos fundamentais do trabalho;

Aos meus amigos e colegas do Laboratório de Biologia Celular e Tecidual (LBCT), Yrexam Ribeiro, por toda ajuda e parceria ao longo deste trabalho e pela amizade que me acompanha desde a graduação. Laíse Trugilio por toda sintonia, ajuda, disponibilidade e companheirismo que possibilitaram a construção de uma grande amizade. Tadeu Oliveira por toda disponibilidade, companheirismo e profissionalismo ao longo do trabalho, e pela amizade sincera. Victor Aragão e Kariane Sousa por todos os conhecimentos passados, toda paciência, dedicação e disponibilidade para me ajudar com o trabalho. Renan Carrari, Rosana Vettorazzi, Joviana Lerin e Jéssica Abreu por todos os momentos compartilhados. Jackellinne Douétts, Lorran Guizzi e Luísa Rodrigues pelos momentos compartilhados durante o projeto de extensão;

À equipe de limpeza que além de fazer seu trabalho ainda proporcionou vários momentos de alegria e descontração. Em especial Regiane Alvarenga e Maria Aparecida, carinhosamente chamada de Dona Cida, por todos os bons momentos e pelas palavras de apoio e incentivo;

Aos meus amigos do teatro, Luciano Martins, Ruan Trindade, Laís Rocha e Leonardo Ribeiro, que fizeram parte de um momento importante da minha vida e que permanecem nela com sua amizade;

À minha amiga Lívia Lontra, pelas palavras de incentivo e por reavivarmos nossa amizade em um momento importante;

Ao professor Dr. Vanildo Silveira e aos colegas do Laboratório de Biotecnologia Vegetal pela parceria construída;

Aos meus colegas do curso de pós-graduação em Biotecnologia Vegetal, com quem pude compartilhar diversos momentos marcantes nas disciplinas cursadas, principalmente nas que possibilitaram o trabalho em grupo;

A toda equipe de profissionais que compõe o curso de Biotecnologia Vegetal, que apesar de ser um curso recente, traz consigo uma grande proposta que proporciona o diferencial na formação;

À secretária da Biotecnologia Vegetal, Margareth de Vasconcelos Paes, por fazer além das suas atividades obrigatórias com muita eficiência e simpatia, me auxiliando em todo momento que precisei, sempre me orientando e fazendo de tudo para ajudar a todos nós alunos;

A todos os meus familiares, tios e primos, que me apoiaram e me incentivaram na minha caminhada;

À minha avó Nilce Rangel Pereira dos Santos, por sempre rezar e torcer por mim, por me ensinar que mesmo que não estejamos bem, devemos levar nossa vida com muita alegria e bom humor, que devemos agregar na vida do próximo;

À minha amiga, Rayanne Guedes Gomes, que sempre esteve comigo me ouvindo e me alegrando em todos os momentos, mesmo de longe sei que torce por mim e fica feliz por minhas conquistas, assim como toda sua família. Muito grata pelos quinze anos de nossa amizade. Ao meu amigo Arthur Rangel, por tantos anos de amizade, que vem resistindo até hoje;

A UENF pela formação, ao CNPq e FAPERJ, pelo apoio financeiro e pela concessão de bolsa FAPERJ.

O meu sincero agradecimento a todos!

MUITO OBRIGADA!

Sumário

RESUMO

Dalbergia nigra é uma espécie arbórea da Mata Atlântica ameaçada de extinção devido à intensa exploração de madeira. A propagação *in vitro* pode ser aplicada como metodologia alternativa para a conservação desta espécie. O objetivo deste estudo foi estabelecer a propagação *in vitro* e o enraizamento *ex vitro* para *D. nigra*, e avaliar alterações no conteúdo de poliaminas (PAs) e perfil proteômico durante o desenvolvimento das brotações. Para a germinação das sementes *in vitro* foi testado o efeito dos meios de cultura MS e WPM, e após 45 dias foi avaliada a germinação (%). Para a indução de brotações, explantes de segmentos nodais apicais e cotiledonares foram inoculados em meio de cultura WPM suplementado com diferentes concentrações (0; 2,5 e 5 µM) de 6-benziladenina (BA). Após 45 dias foi analisada a indução, número e comprimento das brotações e foram coletadas amostras para as análises de PAs e proteômica. Brotações obtidas *in vitro* na ausência e com 2,5 µM de BA foram enraizadas *ex vitro* com diferentes concentrações (0, 100 e 500 µM) de ácido indol-3-butírico (AIB). Não houve diferença significativa entre os dois meios de cultura na percentagem de germinação, porém, o meio WPM proporcionou melhor desenvolvimento das plântulas. O tratamento com 2,5 µM de BA proporcionou maior comprimento das brotações em comparação ao controle, não diferindo estatisticamente das brotações obtidas com 5 µM BA. A adição de 2,5 µM de BA induziu um aumento significativo no conteúdo de PAs livres totais e putrescina em relação às brotações do controle, e este aumento foi relacionado ao maior alongamento das brotações. A adição de BA induziu o acúmulo diferencial de proteínas nas brotações, de ambos os tipos de explante (apical e cotiledonar) relacionadas ao metabolismo e divisão celular, desenvolvimento embrionário e vascular, assim como estrutura e permeabilidade das membranas celulares, podendo ser importante para o maior alongamento das brotações. Proteínas envolvidas no metabolismo central, na homeostase redox, na manutenção das taxas fotossintéticas e no fluxo de carbono durante as condições de fotorrespiração foram up-acumuladas em brotações oriundas de segmentos nodais cotiledonares com 2,5 µM de BA. Essas proteínas podem ser importantes para proporcionar maior crescimento a essas brotações. O enraizamento *ex vitro* foi obtido sem a necessidade do uso de AIB em brotações oriundas dos dois tipos de explantes. Embora BA tenha sido essencial para promover o alongamento das brotações, sua presença reduziu o número de raízes.

Os resultados obtidos neste trabalho são os primeiros que mostram a relevância das citocininas, PAs e perfil proteômico no desenvolvimento *in vitro* de brotações, bem como, a influência do balanço de auxina e citocinina no enraizamento *ex vitro* em *D. nigra*.

ABSTRACT

Dalbergia nigra is an endangered species from the Atlantic Forest due to the intensive exploitation of woody. *In vitro* propagation can be applied as an alterantive method for conservation of this species. The aim of this study was to establish *in vitro* propagation and *ex vitro* rooting in *D. nigra*, and evaluate the alterations on content of polyamines (PAs) and the proteomic profile during shoot development. The effect of MS and WPM culture media was tested on *in vitro* germination, and germination (%) was evaluated at 45 days. For shoot induction, explants from apical and cotyledonary nodal segments were inoculated in WPM culture medium supplemented with different concentrations (0, 2.5 and 5 µM) of 6-benzyladenine (BA). The induction, number and length of shoots were analyzed after 45 days, and samples were collected for PAs and proteomics analyses. Shoots obtained *in vitro* without and with 2.5 µM of BA were rooted *ex vitro* with different concentrations (0, 100 and 500 µM) of indole-3-butyric acid (IBA). No significant differences were observed for two culture mediums on percentage of germination. However, the WPM medium provided the best development of seedlings in germination. The addition of 2.5 µM BA provided greater shoot length compared to the control, without statistic differences from shoots at 5 µM BA. Addition of 2.5 µM BA induced a significant increase in the endogenous content of total free PAs and putrescine compared to shoots from the control treatment, and was related to the higher shoot elongation. The addition of 2.5 µM BA induced an accumulation of proteins in shoots from both types of explants (apical and cotyledonary) related to metabolism and cell division, embryonic and vascular development as well as structure and permeability of cell membranes, which may be important for the greater elongation of shoots. Proteins involved in central metabolism, redox homeostasis, maintenance of photosynthetic rates and carbon flux during photorespiration conditions were up-accumulated in shoots from cotyledonary nodal segments with 2.5 µM of BA. These proteins can be important to provide greater growth to these shoots. Ex vitro rooting was obtained not needing to use IBA in shoots from both types of explants. Although BA was essential to promote shoot elongation, its presence negatively affected the number of roots. The results obtained in this work are the first to show the relevance of cytokinins, PAs and proteomic profile in the *in vitro* development of shoots, as well as the influence of auxin and cytokinin balance in *ex vitro* rooting in *D. nigra.*

ÍNDICE DE FIGURAS

1. Capítulo 1 - Introdução geral

1.1. Mata Atlântica

A Mata Atlântica está localizada na Costa Atlântica brasileira entre as latitudes 6°S e 30°S e longitudes 30°W e 50°W, com altitudes variando do nível do mar até 2700 metros, ocorrendo desde o Rio Grande do Norte até o Rio Grande do Sul (Fundação SOS Mata Atlântica and INPE, 2018). O domínio da Mata Atlântica é um complexo de ecossistemas de grande importância, pois contém uma significativa parcela da diversidade biológica do Brasil e do mundo (Myers et al., 2000). Os altos níveis de riqueza e endemismo, associados à devastação sofrida no passado, incluíram a Mata Atlântica na lista dos 34 *hotspots* mundiais, ou seja, uma das áreas prioritárias para a conservação da biodiversidade em todo o mundo (Myers et al., 2000).

A Mata Atlântica sempre é considerada uma fonte importante de produtos agrícolas, com as maiores concentrações industriais, silviculturais e canavieiras, além dos destaques de áreas urbanizadas no Brasil. Desta forma, a maioria de seus ecossistemas naturais foi eliminada ao longo de diversos ciclos de exploração, resultando na destruição de habitats extremamente ricos em recursos biológicos (Pinto *et al.*, 2003). Entretanto, a Mata Atlântica ainda abriga cerca de 15.000 espécies de plantas, das quais 45% são endêmicas (Stehmann *et al.*, 2009). Alguns fatores, como os processos de devastação causados pela ocupação territorial e exploração desordenada dos recursos naturais contribuíram para que a Mata Atlântica se tornasse um dos ecossistemas com maiores riscos de extinção do mundo (Colombo e Joly, 2010).

A cobertura da mata está distribuída em fragmentos florestais de tamanho reduzido (<100 ha) e biologicamente empobrecida devido à exploração sem controle (Liebsch *et al.*, 2008). Devido ao grande desmatamento ao longo dos anos (Tabela 1), a Mata Atlântica foi reduzida a 12,4% da área original, somados os remanescentes florestais preservados e os fragmentos naturais acima de 3 ha (Fundação SOS Mata Atlântica and INPE, 2018). O Estado do Rio de Janeiro era integralmente coberto pela Mata Atlântica, estando atualmente restrito a menos de 20% (Fundação SOS Mata

Atlântica and INPE, 2018). Na região Norte Fluminense, este bioma sofreu grandes perturbações em seu domínio natural, principalmente causada pela extração madeireira e pela substituição de suas florestas por áreas agrícolas (Colombo e Joly, 2010).

Tabela 1. Histórico de desmatamento desde o início do monitoramento do Atlas (Fundação SOS Mata Atlântica and INPE, 2018)

Desmatamento Observado	Total Desmatado (ha)	Intervalo (anos)	Taxa anual (ha)
Período de 2017 a 2018	11.399	1	11.399
Período de 2016 a 2017	12.562	1	12.562
Período de 2015 a 2016	29.075	1	29.075
Período de 2014 a 2015	18.433	1	18.433
Período de 2013 a 2014	18.267	1	18.267
Período de 2012 a 2013	23.948	1	23.948
Período de 2011 a 2012	21.977	1	21.977
Período de 2010 a 2011	14.090	1	14.090
Período de 2008 a 2010	30.366	2	15.183
Período de 2005 a 2008	102.938	3	34.313
Período de 2000 a 2005	174.828	5	34.966
Período de 1995 a 2000	445.952	5	89.190
Período de 1990 a 1995	500.317	5	100.063

Algumas ações têm sido realizadas visando à conservação e recuperação da biodiversidade desse bioma na região norte fluminense. Uma das estratégias implementadas foram os corredores ecológicos ou também denominados como corredores de conservação da biodiversidade (Carneiro e Bernini, 2013). Esses corredores referem-se às faixas de vegetação que ligam blocos de remanescentes naturais, compreendidos como unidades de planejamento regional, contemplam grandes unidades de paisagem e envolvem áreas protegidas e outras áreas sujeitas aos diversos tipos de manejo que devem fazer parte das estratégias de conservação. Por finalidade, é esperado que esses corredores possam diminuir o isolamento de áreas naturais da mata. Para possibilitar o sucesso da sua implementação, um

planejamento baseado em informações biológicas, sociais e econômicas da área é essencial (Carneiro e Bernini, 2013; Pinto et al., 2003).

Desta forma, a produção de mudas de espécies ameaçadas torna-se de grande importância para preservação desse bioma e reposição da mata em áreas impactadas. Para tanto, torna-se essencial o estudo de métodos alternativos de propagação que possibilitem maior produção de mudas. Contudo, técnicas biotecnológicas possuem grande potencial de aplicação para a propagação de espécies ameaçadas de extinção, principalmente as arbóreas de alto valor econômico e ecológico.

1.2. Espécie de estudo

Dentre as diversas espécies presentes nas extensões da Mata Atlântica, a *Dalbergia nigra* (Fabaceae - Papilionoideae), conhecida popularmente como jacarandá-da-bahia, jacarandá-preto ou caviúna, é uma espécie exclusiva da Floresta Ombrófila Densa Submontana deste bioma. Sua distribuição possui ocorrência restrita aos Estados da Bahia, Espírito Santo, Minas Gerais, Rio de Janeiro e São Paulo (Fig. 2) (Carvalho, 2003). É uma árvore semicaducifólia que pode ser encontrada com 15 a 25 m de altura. Essa planta é adaptada a locais secos e indicada para o plantio misto em áreas degradadas de preservação permanente, possuindo caráter pioneiro. Possui tronco tortuoso e irregular, folhas compostas e alternadas, podendo ser classificada como uma espécie secundária com características pioneiras (Lorenzi, 1992). Sua madeira é considerada de alta qualidade e com características decorativas, podendo ser utilizada na fabricação de móveis de luxo, decorações, na construção civil, no paisagismo em geral e fabricação de instrumentos musicais (Martinelli e Moraes, 2013).

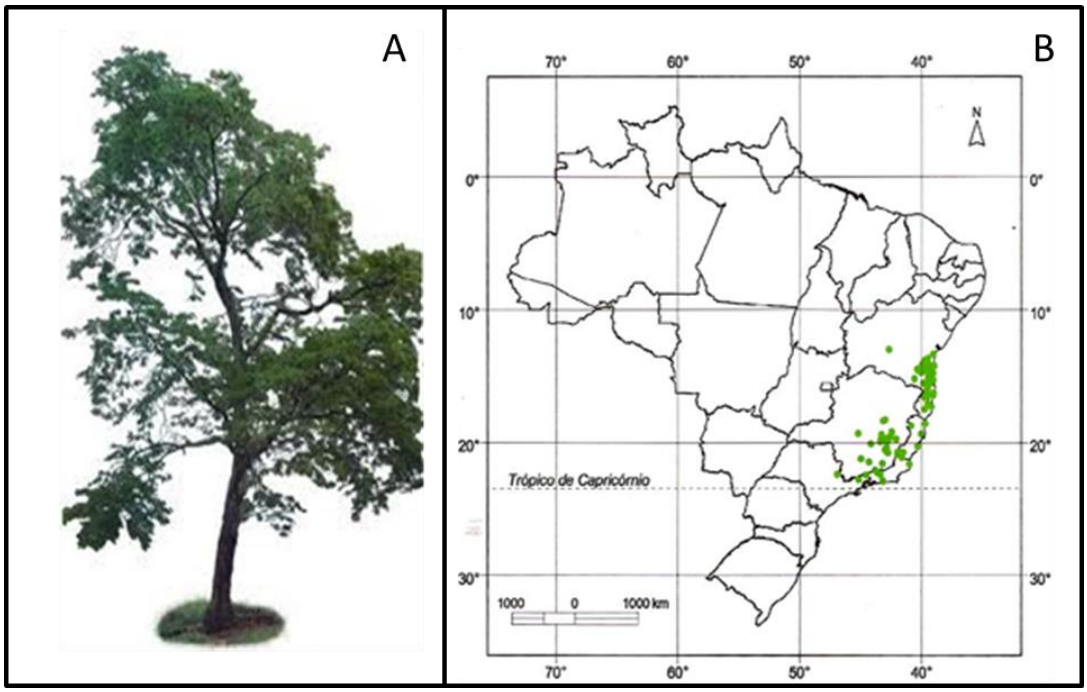

Fig. 1: Aspectos morfológicos de um exemplar da espécie em fase adulta (A), e mapa da distribuição de *Dalbergia nigra* no Brasil (B). Os pontos verdes indicam os locais de ocorrência natural da espécie. Fonte figuras: (A): Árvores nativas (www.vivaterra.org.br); (B): (Carvalho, 2003).

Essa espécie produz sementes que possuem comportamento ortodoxo, possibilitando o armazenamento por um período de até dois anos em sacos plásticos em baixa temperatura, com redução de cerca de 50% de sua capacidade germinativa (Aguiar *et al.*, 2010). Sua germinação ocorre em menos de 10 dias após a semeadura, a partir da qual ocorre o crescimento da raiz e o desenvolvimento rápido do hipocótilo (Aguiar *et al.*, 2010). Sua floração ocorre entre os meses de setembro e janeiro, possuindo flores com característica hermafrodita. A polinização ocorre com o auxílio de abelhas e outros pequenos insetos (Carvalho, 2003). Os frutos resultantes são legumes secos, glabros, não segmentados e planos. As sementes são estenopérmicas, oblongo-ovaladas, planas, com ápice e base arredondada e superfície glabra (Donadio e Demattê, 2000).

A *D. nigra* era utilizada para a produção de carvão e lenha, mas possui aplicações diversas, em geral, indicada para arborização de praças, parques e avenidas, com grande potencial para recuperação de solo, pois apresenta queda nas folhas proporcionando ganho de matéria orgânica no ambiente, além de demonstrar grande amplitude de tolerância ambiental (Carvalho, 2003). Devido principalmente à exploração da madeira, esta espécie encontra-se atualmente ameaçada de extinção

na categoria vulnerável, caracterizada por espécies que sofreram redução de 30% nos últimos dez anos ou que esta redução está projetada para os próximos dez anos com probabilidade de redução de pelo menos 10% neste período (IUCN, 2021).

Neste sentido, trabalhos envolvendo a micropropagação *in vitro*, o envolvimento de poliaminas (PAs) e proteínas diferencialmente abundantes com suas respectivas respostas morfogênicas são fundamentais para o estabelecimento de metodologias alternativas de propagação e conservação de *D. nigra*.

1.3. Micropropagação

O uso de técnicas biotecnológicas, como a cultura *in vitro* de tecidos vegetais, representa uma ferramenta relevante para a regeneração de plantas em larga escala, conservação de germoplasma, e reflorestamento de áreas ambientais degradadas (Perveen *et al.*, 2013). A micropropagação oferece vantagens sobre os métodos convencionais de propagação vegetativa como a estaquia, devido ao controle das condições de crescimento e a obtenção de plantas livres de doenças (Fermino e Scherwinski-Pereira, 2012). A cultura *in vitro* permite também a realização de estudos básicos para a compreensão das bases bioquímicas e moleculares, como os mecanismos celulares envolvidos no crescimento e desenvolvimento de espécies arbóreas (Pijut *et al.*, 2007).

A obtenção de explantes utilizando a micropropagação pode ser realizada por meio da proliferação de gemas; a organogênese, que pode ser denominada como adventícia direta e indireta; e a embriogênese somática também classificada como direta ou indireta (Ferreira *et al.*, 2015). A organogênese se trata do desenvolvimento de órgãos a partir de tecidos não meristemáticos, como partes de folhas, raízes e segmentos internodais. A organogênese pode ocorrer de forma direta com a formação de órgãos adventícios diretamente do explante, ou ocorrer de forma indireta, onde novas gemas e outros eixos caulinares são induzidos para formação a partir de tecidos não organizados, que são denominados calos (Tang e Newton, 2005). A proliferação de gemas se refere ao crescimento de meristemas que já estão presentes na planta, para tanto são utilizados como fonte de explantes, tais como ápices meristemáticos e gemas axilares presentes em segmentos nodais (Ferreira *et al.*, 2015). A obtenção de

brotações *in vitro* via desenvolvimento de gemas axilares é comumente utilizada para a micropropagação de arbóreas como *Acacia mangium* e *Eucalyptus camaldlensis* (Kozai e Kubota, 2001), *Cedrela fissilis* (Nunes *et al.*, 2002; Aragão *et al.*, 2017a; 2016) *Cariniana legalis* (Aragão *et al.*, 2017b; Lerin *et al.*, 2019).

A micropropagação é dividida em várias etapas, tais como a obtenção do explante, estabelecimento *in vitro* das brotações, enraizamento e aclimatização das mudas (Hussain *et al.*, 2018). É necessário estabelecer as melhores condições para cada etapa do processo de micropropagação, para cada espécie em estudo.

Na micropropagação de espécies arbóreas, vários são os fatores que afetam o processo de indução e desenvolvimento de brotações *in vitro*. Dentre os fatores, a escolha do tipo de explante é importante para a regeneração de brotações. Nesse sentido, o tipo de explante, a sua posição na planta matriz e sua juvenilidade, devem ser levados em consideração, pois estes fatores refletem o nível endógeno hormonal desse tecido e influenciam os processos de divisão celular e desenvolvimento das brotações (Mujib, 2005; Silva *et al.*, 2019).

Além do tipo de explante, outros fatores, como meio de cultura e reguladores de crescimento vegetal, também controlam a resposta morfogênica *in vitro*. Os reguladores de crescimento são utilizados em diferentes etapas do processo de micropropagação, tanto para indução de brotações quanto para formação de raízes (González-Rodríguez *et al.*, 2015; Hassan *et al.*, 2011; Golle *et al.*, 2012). Neste sentido, o estabelecimento das melhores condições de cultivo *in vitro*, tais como meio de cultura, tipo de explante, concentração de reguladores de crescimento e eficientes métodos de aclimatização são importantes passos para a produção de mudas micropropagadas. Adicionalmente, fatores físicos como temperatura, umidade, intensidade luminosa e fotoperíodo também afetam a morfogênese *in vitro*.

1.3.1. A escolha do explante e o estabelecimento das culturas assépticas *in vitro*

A escolha do explante e a desinfestação deste são fatores importantes para o estabelecimento *in vitro* e o sucesso no processo de micropropagação da espécie alvo (Fick et al., 2007). De acordo com Lédo et al. (2007), a germinação *in vitro* é a forma mais comum de estabelecimento de material em condições assépticas, fornecendo explantes para as etapas da micropropagação. O uso de sementes para germinação *in vitro* e obtenção de explantes assépticos tem sido utilizado para várias

espécies arbóreas, como *Amburana acreana* (Fermino e Scherwinski-Pereira, 2012), *Cedrela fissilis* (Aragão et al., 2016; 2017) e *Cariniana legalis* (Aragão et al., 2019; Lerin et al., 2019).

Estudos relacionando o tipo do meio de cultura e a taxa de germinação in vitro são fundamentais para identificar a melhor condição nesta etapa, visando à obtenção de plântulas com qualidade genética e fitossanitária adequada (Perveen et al., 2013). A obtenção dos explantes a partir de plântulas germinadas *in vitro* apresenta vantagens sobre a obtenção de explantes diretamente de indivíduos adultos, evitando a contaminação do material vegetal e o aumento no potencial de resposta morfogênica *in vitro* (Prudente et al., 2016).

Durante a cultura in vitro, as soluções de sais e açúcares que compõem os meios de cultura não exercem efeito puramente nutritivo, mas também influenciam o crescimento celular e a morfogênese por meio de propriedades osmóticas (Nogueira et al., 2004). Diversas formulações de meios básicos têm sido utilizadas. Apesar de não haver uma formulação padrão, o meio de cultura MS (Murashige e Skoog, 1962), com suas modificações e diluições, tem sido utilizado com sucesso para diferentes espécies (Koene et al., 2019; Saiprasad et al., 2004). Entretanto, o meio MS não se mostra satisfatório em alguns casos, se fazendo necessário o uso de outros meios nutritivos como o Wood Plant Medium (WPM) (Lloyd e McCown, 1980), amplamente utilizado para a propagação de espécies arbóreas (Stein et al., 2017; Golle et al., 2012; Zhou et al., 2010).

1.3.2. Multiplicação das brotações *in vitro*

Para a indução das brotações são necessárias algumas etapas que envolvem o isolamento de órgãos meristemáticos pré-formados, a quebra da dominância apical e a multiplicação das partes aéreas, geralmente com a aplicação de citocinina exógena. As gemas axilares preexistentes nas inserções das folhas com o caule recebem o estímulo para o crescimento, possibilitando a origem de brotações que podem ser utilizadas para repetir o processo (Ferreira *et al.*, 2015).

O sucesso da propagação por via da cultura de tecidos é influenciado pelas características nutricionais do meio de cultura. Os meios de cultura para plantas não

só fornecem macro e micronutrientes, mas também carboidratos, geralmente a sacarose, como fonte de carbono. A adição de compostos orgânicos como vitaminas, aminoácidos, e reguladores de crescimento permite um aumento na resposta morfogenética (Silva *et al.*, 2019). Para se obter as brotações, o meio de cultura é suplementado com citocininas que atuam estimulando a divisão celular, podendo ser combinadas ou não com outros compostos, como auxinas (Nicioli *et al.*, 2008). Dentre as citocininas, a 6-benziladenina (BA) é uma das mais utilizadas para o desenvolvimento de gemas axilares, principalmente em espécies arbóreas (Aragão et al., 2016; Giri et al., 2004). Este regulador de crescimento vegetal tem como função superar a dominância apical exercida pelas auxinas endógenas presentes nos explantes de segmentos nodais e assim, gemas presentes abaixo do nó apical, recebem estímulo para o desenvolvimento (Röck-Okuyucu *et al.*, 2016).

Em *C. fissilis,* o uso da citocinina BA foi fundamental para a formação de novas brotações a partir do desenvolvimento de gemas axilares (Nunes et al., 2002; Aragão et al., 2016). Segundo Tanaka et al. (2006), a auxina produzida no meristema apical controla negativamente a biossíntese de citocinina em gemas axilares. Quando efetuada a retirada do meristema apical, a biossíntesede citocinina é aumentada nas gemas laterais, alterando o balanço de auxina e citocinina e, consequentemente, promovendo o desenvolvimento das brotações.

1.3.3. Enraizamento *ex vitro* e aclimatização das mudas

Durante a micropropagação, algumas etapas como o enraizamento e a aclimatização das mudas são críticas, pois a mudança de ambiente pode provocar danos às mudas, principalmente relacionados à perda de água, pois a umidade nos dois ambientes, *in vitro* e *ex vitro* é diferente, influenciando no desenvolvimento das plantas (Bortolotti *et al.*, 2003) . O enraizamento é uma etapa crucial no processo de micropropagação, é um processo considerado crítico para a produção de mudas, pois diversos fatores, como espécie, genótipos, fatores ambientais, influenciam a taxa de enraizamento (de Carvalho *et al.*, 2011; Prudente *et al.*, 2016).

As raízes originadas desta etapa são chamadas de adventícias pois não se originam da radícula do embrião ou da raiz principal, e sim, por qualquer tecido que não seja radicular (Hussain *et al.*, 2019). Levando em consideração a técnica de

enraizamento *in vitro,* as brotações são transferidas para meios de cultura que podem ser suplementados ou não com auxinas, utilizando com mais frequência concentrações baixas, já que a exposição é prolongada (dias ou meses) (Hussain *et al.*, 2019). Por outro lado, no enraizamento *ex vitro*, a base das brotações é imersa em solução de auxina mais concentrada, e geralmente por um curto período de tempo (min ou h), e posteriormente estas são transferidas diretamente para o substrato (Yan *et al.*, 2010).

O enraizamento *ex vitro* é um método que apresenta bons resultados na produção de mudas micropropagadas, pois permite o desenvolvimento de raízes simultaneamente à aclimatização. Em adição, ele também reduz mão de obra e custo na produção de mudas, pois não necessita de todo material utilizado *in vitro* para o enraizamento, além de economizar tempo (Phulwaria *et al.*, 2013). Brotações de várias espécies foram enraizadas com sucesso utilizando o enraizamento *ex vitro*, exibindo alta taxa de sobrevivência quando transferidas para o campo (Benmahioul et al., 2012; Phulwaria et al., 2013), incluindo arbóreas nativas como *C. fissilis* (Ribeiro, 2018). Mudas produzidas através do enraizamento *ex vitro* têm diversas vantagens em relação àquelas desenvolvidas a partir de enraizamento *in vitro*. Dentre estas vantagens destaca-se a formação de um sistema radicular mais desenvolvido, apresentando maior número de raízes, melhor potencial para aclimatização e maior percentual de sobrevivência de plantas (Yan *et al.*, 2010; Benmahioul *et al.*, 2012).

Durante a aclimatização, as mudas podem sofrer alguns estresses, tais como, estresse devido a alteração do metabolismo heterotrófico para autotrófico, infecção por patógenos, estresse pela luz e temperatura, o que pode interferir diretamente na transferência das plantas para o ambiente a campo (Bortolotti *et al.*, 2003). O enraizamento *ex vitro* associado à aclimatização é uma etapa efetiva para a sobrevivência das mudas, pois quando estas duas etapas ocorrem de forma simultânea, as brotações comumente apresentam melhor enraizamento, e consequentemente, diminuição de custos de produção, quando comparado ao enraizamento *in vitro* (Yan *et al.*, 2010), possibilitando assim a produção de mudas que poderão ser direcionadas para o reflorestamento de áreas degradadas. Portanto, para que essa etapa ocorra com sucesso é fundamental o desenvolvimento adequado de raízes para auxiliar na hidratação e nutrição das plantas, além da necessidade do aperfeiçoamento dos mecanismos de controle da transpiração.

1.4. Estudos bioquímicos durante a morfogênese *in vitro*

A melhor compreensão dos fatores bioquímicos e moleculares durante a morfogênese *in vitro* é importante para otimização da produção em larga escala de plantas, principalmente para espécies arbóreas (Moura et al., 2012). Alterações no conteúdo de poliaminas (PAs) e proteínas têm sido descritas para várias espécies, incluindo arbóreas (Aragão *et al.*, 2016; Aragão, Reis, *et al.*, 2017; Lerin *et al.*, 2019; Oliveira *et al.*, 2020; Tang and Newton, 2005).

1.4.1. As poliaminas (PAs) e as respostas morfogênicas *in vitro*

As PAs são aminas alifáticas com cargas positivas, o que possibilita sua ligação às moléculas com cargas negativas, como DNA, RNA e proteínas, podendo influenciar diretamente os processos de replicação, transcrição, tradução, divisão e expansão celular (Tiburcio et al., 2014). As PAs são relevantes para o desenvolvimento da planta, pois estão envolvidas com processos celulares como divisão celular, desenvolvimento, síntese de proteínas e respostas ao estresse abiótico (Kakkar e Sawhney, 2002; Aragão et al., 2016; Silveira et al., 2006).

As principais PAs presentes em plantas são a putrescina (Put), espermidina (Spd) e espermina (Spm), as quais podem ocorrer na forma livre, conjugada solúvel e conjugada ligada (Kusano *et al.*, 2008). Na via biossintética, as enzimas arginina descarboxilase (ADC) e ornitina descarboxilase (ODC) são responsáveis pela síntese da Put a partir dos aminoácidos arginina e ornitina, respectivamente. Para a produção de Spd e Spm são necessários a adição de grupos aminopropil provenientes do aminoácido metionina, a partir da rota da S-adenosil-metionina (SAM), pela ação da enzima SAM descarboxilase (SAMDC). Com adição de um grupo aminopropil à Put é formada a Spd pela ação da enzima Spd sintase (SPDS), a adição de outro grupo aminopropil à Spd resulta na formação da Spm pela ação da Spm sintase (SPMS). O catabolismo de Put, Spd e Spm é feito pela ação das enzimas diamina oxidase (DAO) e PA oxidase (PAO), respectivamente (Kusano *et al.*, 2008).

As PAs estão envolvidas com os processos de desenvolvimento e germinação de sementes (Santa-Catarina *et al.*, 2006; Lerin *et al.*, 2019), bem como na

morfogênese *in vitro*, como a embriogênese somática e desenvolvimento de brotações (Dutra *et al.*, 2013; Aragão, *et al.*, 2017; Oliveira *et al.*, 2020; Lerin *et al.*, 2019). Estudos mostram que a proliferação celular e a regeneração de tecidos estão relacionadas com a presença da Put, enquanto a combinação de Put, Spd e Spm é importante para o desenvolvimento de brotações (DebiasiI *et al*., 2007). Desta forma, a Put tem sido associada à promoção de divisões celulares envolvidas com o crescimento e desenvolvimento vegetal, portanto essa substância pode ser considerada um marcador bioquímico durante a diferenciação celular e a organogênese *in vitro* (Viu *et al*., 2009).

Em arbóreas, o papel das PAs foi relatado durante o desenvolvimento de brotações *in vitro* em *C. fissilis*, nesse estudo a adição da citocinina BA proporcionou aumento na concentração de Put endógena e este foi relacionado com o aumento do número de brotações (Aragão *et al.*, 2016). Além disso, a adição de Put no meio de cultura proporcionou maior alongamento das brotações de *C. fissilis* (Aragão et al., 2017). O maior alongamento das brotações em *C. legalis* sob incubação com lâmpadas do tipo LED também foi relacionado com acúmulo no conteúdo de Put (Lerin et al., 2019). Em *C. fisslis*, o melhor alongamento das brotações foi obtido com o uso de lâmpada LED com a combinação de azul e vermelho (LED WmBdR), que propiciou maior acúmulo de putrescina que pode estar relacionada com a divisão celular (Oliveira *et al.*, 2020). Embora alguns estudos relacionando as PAs durante o desenvolvimento de brotações tenham sido concretizados para algumas arbóreas, estes ainda não foram realizados durante o desenvolvimento de brotações *in vitro* para *D. nigra*.

1.4.2. A abordagem proteômica no cultivo *in vitro*

Para o estudo do padrão de proteínas diferencialmente abundantes é utilizada a análise proteômica nas amostras biológicas, podendo ser aplicada em diversos tecidos e diferentes células em qualquer período do desenvolvimento (Takáč et al., 2011; Deng et al., 2014). A abordagem proteômica possibilita obter informações sobre as proteínas diferencialmente abundantes durante mudanças no crescimento e desenvolvimento de uma planta (Hochholdinger *et al.*, 2006). Essa análise permite comparar a influência de sinais exógenos que promovam mudanças no acúmulo

diferencial de proteínas, podendo desempenhar papel chave no desenvolvimento da planta (Takáč *et al.*, 2011).

Nos processos morfogênicos *in vitro*, a proteômica comparativa vem sendo utilizada para identificar proteínas diferencialmente acumuladas durante o desenvolvimento de brotações em *C. fissilis* (Aragão *et al.*, 2017; Aragão *et al.*, 2016; Oliveira *et al.*, 2020) , e em *Cariniana legalis* (Lerin *et al.*, 2019). Na propagação *in vitro* de espécies florestais, a alteração do perfil proteômico em brotações da espécie *C. fissilis* cultivadas com e sem Put mostrou que a adição desta PA pode alterar o acúmulo de proteínas associadas com respostas a estresse e divisão celular das brotações em desenvolvimento ™.

Diante do exposto, destaca-se a importância da abordagem proteômica durante a morfogênese *in vitro* em espécies arbóreas, como *D. nigra*. Estes estudos representam uma alternativa promissora para a obtenção de dados comparativos e identificação de proteínas diferencialmente abundantes que podem ser utilizadas como marcadores bioquímicos de determinados processos de crescimento e desenvolvimento, bem como a otimização para as técnicas de micropropagação destas espécies.

1.5. Referência Bibliográfica

Aguiar, F., Tavares, A.R., Kanashiro, S., Baptista, P., Augusto, N. (2010) Germinação de sementes de *Dalbergia nigra* (Vell.) Allemao. Ciência e Agrotecnologia. 34(1), 1624–1629.

Aragão, V.P.M., Navarro, B.V., Silva, A.T. da, Silveira, V., Santa-Catarina, C. (2017) Micropropagation of *Cariniana legalis* (Martius) O. Kuntze, an endangered hardwood tree from the Brazilian Atlantic Forest. Plant Cell Culture & Micropropagation. 13(2), 41–50.

Aragão, V.P.M., Reis, R.S., Silveira, V., Santa-Catarina, C. (2017) Putrescine promotes changes in the endogenous polyamine levels and proteomic profiles to regulate organogenesis in *Cedrela fissilis* Vellozo (Meliaceae). Plant Cell, Tissue and Organ Culture. 130(3), 495–505.

Aragão, V.P.M., de Souza Ribeiro, Y.R., Reis, R.S., Macedo, A.F., Floh, E.I.S., Silveira, V., Santa-Catarina, C. (2016) *In vitro* organogenesis of *Cedrela fissilis* Vell. (Meliaceae): the involvement of endogenous polyamines and carbohydrates on shoot development. Plant Cell, Tissue and Organ Culture.

124(3), 611–620.

Aragão, V.P.M., Trindade, B.M.C., Reis, R.S., Silveira, V., Santa-Catarina, C. (2019) Storage time affects the germination and proteomic profile of seeds of *Cariniana legalis* (Mart.) O. Kuntze (Lecythidaceae), an endangered tree species native to the Brazilian Atlantic Forest. Revista Brasileira de Botanica. 42(3), 407–419.

Benmahioul, B., Dorion, N., Kaid-Harche, M., Daguin, F. (2012) Micropropagation and *ex vitro* rooting of pistachio (Pistacia vera L.). Plant Cell, Tissue and Organ Culture. 108(2), 353–358.

Bortolotti, A., Pasqual, M., De Rezende Maciel, A.L., Dutra Ferreira, L. (2003) BAP e Substratos na aclimatização de plântulas de (Sinningia speciosa Lood . Hiern .) provenientes de cultura de tecidos. Ciencias agrotec.. 27, 255–260.

Carneiro, B.M., Bernini, H. (2013) Perspectivas de conexão entre fragmentos florestais do Corredor Ecológico Burarama-Pacotuba- Cafundó ,na Mata Atlântica do Espírito Santo, através de recomposição de Áreas de Proteção Permanente de cursos d'água. Natureza on line. 11(1), 20–28.

Carvalho, P. E. R. (2003) Espécies arbóreas brasileiras. Colombo: Empresa Brasileira de Pesquisa Agropecuária, p.1039.

Colombo, A.F., Joly, C.A. (2010) Brazilian Atlantic Forest lato sensu: the most ancient Brazilian forest, and a biodiversity hotspot, is highly threatened by climate change. Revista Brasleira de Biologia. 70(3), 697–708.

Debiasi C., B.C.F.G.P.P.L.I. (2007) Study of polyamines in the morphogenesis i*n vitro* of *Hemerocallis* sp. Ciência Rural. 37(4), 1014–1020.

de Carvalho, D.C., da Silva, A.L.L., Tanno, G.N., Purcino, M., Biasi, L.A. (2011) Organogênese a partir de segmentos foliares e internodais de videira cv. merlot. Ciencia e Agrotecnologia. 35(1), 108–114.

Deng, Z., Oses-Prieto, J.A., Kutschera, U., Tseng, T.S., Hao, L., Burlingame, A.L., Wang, Z.Y., Briggs, W.R. (2014) Blue light-induced proteomic changes in etiolated *Arabidopsis* seedlings. Journal of Proteome Research. 13(5), 2524–2533.

Dutra, N.T., Silveira, V., de Azevedo, I.G., Gomes-Neto, L.R., Façanha, A.R., Steiner, N., Guerra, M.P., Floh, E.I.S., Santa-Catarina, C. (2013) Polyamines affect the cellular growth and structure of pro-embryogenic masses in *Araucaria angustifolia* embryogenic cultures through the modulation of proton pump activities and endogenous levels of polyamines. Physiologia Plantarum. 148(1), 121–132.

Fermino, P.C.P., Scherwinski-Pereira, J.E. (2012) Germinação e propagação *in vitro* de cerejeira (*Amburana acreana* (Ducke) A.C.Smith - Fabaceae). Ciência Florestal. 22(1), 1–9.

Ferreira, D.A.T., Sattler, M.C., Carvalho, C.R., Clarindo, W.R. (2015) Embryogenic potential of immature zygotic embryos of *Passiflora*: a new a'dvance for *in vitro*

propagation without plant growth regulators. Plant Cell, Tissue and Organ Culture. 122(3), 629–638.

Fick, T.A., Bisognin, D.A., Quadros, K.M. de, Horbach, M., Reiniger, L.R.S. (2007) Estabelecimento e crescimento *in vitro* de plântulas de louro-pardo. Ciência Florestal. 17(4), 343.

Fonseca, C. eduardo, Sperândio, J.P., Corrêa, M.P.F., Bueno, D.M., Lima, R. (1991) Propagação Vegetativa do Jacarandá-da-Baía através da estaquia. Pesquisa Agropecuária Brasileira. 26(1), 31–37.

Fundação SOS Mata Atlântica, INPE (2018) Atlas dos Remanescentes Florestais da Mata Atlântica. Relatório Técnico, 65.

Ghosh, S., Pal, A. (2013). Proteomic analysis of cotyledonary explants during shoot organogenesis in *Vigna radiata*. Plant Cell, Tissue and Organ Culture, 115(1): 55- 68.

Giri, C.C., Shyamkumar, B., Anjaneyulu, C. (2004) Progress in tissue culture, genetic transformation and applications of biotechnology to trees: an overview. Trees - Structure and Function. 18(2), 115–135.

Golle, D.P., Reiniger, L.R.S., Curti, A.R., León, E.A.B. (2012) Estabelecimento e desenvolvimento *in vitro* de Eugenia involucrata DC.: influência do tipo de explante e do meio nutritivo. Ciência Florestal. 22(1), 207–214.

González-Rodríguez, J.A., Ramírez-Garduza, F., Robert, M.L., O'Connor-Sánchez, A., Peña-Ramírez, Y.J. (2015) Adventitious shoot induction from adult tissues of the tropical timber tree yellow Ipé primavera (*Tabebuia donnell-smithii* rose [bignoniaceae]). *In Vitro* Cellular & Developmental Biology. Plant. 46, 411–421.

Hassan, N., Ali, N., Zainudin, F., Ismail, H. (2011) Effect of 6-benzylaminopurine (BAP) in different basal media on shoot multiplication of *Aquilaria hirta* and detection of essential oils in the *in vitro* shoots. African Journal of Biotechnology. 10(51), 10500–10503.

Hochholdinger, F., Sauer, M., Dembinsky, D., Hoecker, N., Muthreich, N., Saleem, M., Liu, Y. (2006) Proteomic dissection of plant development. PROTEOMICS. 6(14), 4076–4083.

Hussain, S.A., Ahmad, N., Anis, M. (2018) Synergetic effect of TDZ and BA on minimizing the post-exposure effects on axillary shoot proliferation and assessment of genetic fidelity in *Rauvolfia tetraphylla* (L.). Rendiconti Lincei. 29(1), 109–115.

Hussain, S.A., Ahmad, N., Anis, M., Alatar, A.A. (2019) Influence of meta-topolin on in *vitro* organogenesis in *Tecoma stans* L., assessment of genetic fidelity and phytochemical profiling of wild and regenerated plants. Plant Cell, Tissue and Organ Culture. 138(2), 339–351.

International Union for Conservation of Nature and Natural Resources. (2017) The IUCN red list of threatened species. [online]. Available from:

http://www.iucnredlist.org/ [Accessed March 10, 2018].

Kakkar, R.K., Sawhney, V.K. (2002) Polyamine research in plants - a changing perspective. Physiologia Plantarum. 116(3), 281–292.

Koene, F.M., Amano, Ribas, L.L.F. (2019) Asymbiotic seed germination and in vitro seedling development of *Acianthera prolifera* (Orchidaceae). South African Journal of Botany. 121, 83–91.

Kozai, T., Kubota, C. (2001) Developing a photoautotrophic micropropagation system for woody plants. Journal of Plant Research. 114(4), 525–537.

Kusano, T., Berberich, T., Tateda, C., Takahashi, Y. (2008) Polyamines: essential factors for growth and survival. Planta. 228(3), 367–381.

Lédo, A. da S., Seca, G.S.V., Barboza, S.B.S.C., Silva Junior, J.F. da (2007) Crescimento inicial de mangabeira (Hancornia speciosa Gomes) em diferentes meios de germinação *in vitro*. Ciência e Agrotecnologia. 31(4), 989–993.

Lerin, J., Aragão, V.P.M., Reis, R.S., Silveira, V., Santa-Catarina, C. (2019) Proteomic profile and polyamine contents are modulated by light source to promote *in vitro* shoot development in *Cariniana legalis* (Martius) O. Kuntze (Lecythidaceae). Plant Cell, Tissue and Organ Culture. 137(2), 329–342.

Liebsch, D., Marques, M.C.M., Goldenberg, R. (2008) How long does the Atlantic Rain Forest take to recover after a disturbance? Changes in species composition and ecological features during secondary succession. Biological Conservation. 141(6), 1717–1725.

Martinelli, G. e, Moraes, M. (2013) Livro vermelho da flora do Brasil. 1a. Rio de Janeiro.

Mujib, A. (2005) In vitro regeneration of sandal (*Santalum album* L.) from leaves. Turkish Journal of Botany. 29(1), 63–67.

Murashige, T., Skoog, F. (1962) A Revised Medium for Rapid Growth and Bio Assays with *Tobacco* Tissue Cultures. Physiologia Plantarum. 15(3), 473–497.

Nicioli, P.M., Paiva, R., Nogueira, R.C., Santana, J.R.F. de, Silva, L.C., Silva, D.P.C. da, Porto, J.M.P. (2008) Ajuste do processo de micropropagação de barbatimão. Ciência Rural. 38(3), 685–689.

Nogueira, R.C., Paiva, R., Castro, A.H. de, Vieira, C.V., Abbade, L.C., Alvarenga, A.A. (2004) *In vitro* germination of (Byrsonima intermedia A. Juss.). Ciência e Agrotecnologia. 28(5), 1053–1059.

Nunes, E.D.C., de Castilho, C.V., Moreno, F.N., Viana, A.M. (2002) *In vitro* culture of *Cedrela fissilis* Vellozo (Meliaceae). Plant Cell, Tissue and Organ Culture. 70(3), 259–268.

Oliveira, T. dos R., Aragão, V.P.M., Moharana, K.C., Fedosejevs, E., do Amaral, F.P., Sousa, K.R., Thelen, J.J., Venâncio, T.M., Silveira, V., Santa-Catarina, C. (2020) Light spectra affect the *in vitro* shoot development of *Cedrela fissilis* Vell. (Meliaceae) by changing the protein profile and polyamine contents. Biochimica

et Biophysica Acta - Proteins and Proteomics. 1868(12), 140529.

Perveen, S., Anis, M., Aref, I.M. (2013) Resource communication. *In vitro* plant regeneration of *Albizia lebbeck* (L.) Benth. from seed explants. Forest Systems. 22(2), 241–248.

Phulwaria, M., Shekhawat, N.S., Rathore, J.S., Singh, R.P. (2013) An efficient *in vitro* regeneration and *ex vitro* rooting of *Ceropegia bulbosa* Roxb. A threatened and pharmaceutical important plant of Indian Thar Desert. Industrial Crops and Products. 42(1), 25–29.

Pijut, P.M., Beasley, R.R., Lawson, S.S., Palla, K.J., Stevens, M.E., Wang, Y. (2012) *In vitro* propagation of tropical hardwood tree species – A review (2001-2011). Propagation of Ornamental Plants. 12(1), 25–51.

Pijut, P.M., Woeste, K.E., Vengadesan, G., Michler, C.H. (2007) Technological advances in temperate hardwood tree improvement including breeding and molecular marker applications. *In Vitro* Cellular & Developmental Biology - Plant. 43(4), 283–303.

Pinto, L.P., Thomas, W.W., York, N., Garden, B., Estadual, U., Cruz, D.S. (2003) Caracterização dos registros de ocorrência de espécies de plantas e mamíferos no sul da Bahia, Brasil.

Prudente, D. de O., Nery, F.C., Paiva, R., Reis, M.V. dos, Paiva, P.D. de O., Nery, M.C. (2016) Cultivo *in vitro* de *Miconia ligustroides* (DC.) Naudim. Plant Cell Culture & Micropropagation. 12(1), 13–19.

Reis, R.S., Vale, E. de M., Heringer, A.S., Santa-Catarina, C., Silveira, V. (2016) Putrescine induces somatic embryo development and proteomic changes in embryogenic callus of sugarcane. Journal of Proteomics. 130(1), 170–179.

Ribeiro, Y.R. de S. (2018) Envolvimento da auxina e poliaminas no enraizamento *ex vitro* de brotações micropropagadas de Cedrela fissillis Vell. (Meliaceae). Campos dos Goytacazes.

Röck-Okuyucu, B., Bayraktar, M., Akgun, I.H., Gurel, A. (2016) Plant growth regulator effects on i*n vitro* propagation and stevioside production in *Stevia rebaudiana* bertoni. HortScience. 51(12), 1573–1580.

Saiprasad, G.V.S., Raghuveer, P., Khetarpal, S., Chandra, R. (2004) Effect of various polyamines on production of protocorm-like bodies in orchid—*Dendrobium* '*Sonia*.' Scientia Horticulturae. 100(1–4), 161–168.

Santa-Catarina, C., Maciel, S. da C., Pedrotti, E.L. (2001) Germinação *in vitro* e embriogênese somática a partir de embriões imaturos de canela sassafrás (*Ocotea odorifera* Mez). Revista Brasileira de Botânica. 24(4), 501–510.

Santa-Catarina, C., Silveira, V., Balbuena, T.S., Viana, A.M., Estelita, M.E.M., Handro, W., Floh, E.I.S. (2006) IAA, ABA, polyamines and free amino acids associated with zygotic embryo development of *Ocotea catharinensis*. Plant Growth Regulation. 49(2–3), 237–247.

Santa-Catarina, C., Silveira, V., Scherer, G.F.E., Floh, E.I.S. (2007) Polyamine and nitric oxide levels relate with morphogenetic evolution in somatic embryogenesis of *Ocotea catharinensis*. Plant Cell, Tissue and Organ Culture. 90(1), 93–101.

Silva, T.D., Chagas, K., Batista, D.S., Felipe, S.H.S., Louback, E., Machado, L.T., Fernandes, A.M., Buttrós, V.H.T., Koehler, A.D., Farias, L.M., Santos, A.F., Silva, P.O., Otoni, W.C. (2019) Morphophysiological *in vitro* performance of *Brazilian ginseng* (*Pfaffia glomerata* (Spreng.) Pedersen) based on culture medium formulations. *In Vitro* Cellular & Developmental Biology - Plant.

Sghaier-Hammami, B., Valledor, L., Drira, N., & Jorrin-Novo, J. V. (2009). Proteomic analysis of the development and germination of date palm (*Phoenix dactylifera* L.) zygotic embryos. Proteomics, 9(9), 2543-2554.

Silveira, V., Santa-Catarina, C., Tun, N.N., Scherer, G.F.E., Handro, W., Guerra, M.P., Floh, E.I.S. (2006) Polyamine effects on the endogenous polyamine contents, nitric oxide release, growth and differentiation of embryogenic suspension cultures of *Araucaria angustifolia* (Bert.) O. Ktze. Plant Science. 171(1), 91–98.

Stehmann, J.R., Forzza, R.C., Salino, A., Sobral, M., Pinheiro, D., Kamino, H.Y., Inácio, L., Da, L., Presidente, S. (2009) P lantas da F loresta A tlântica.

Stein, V.C., Ferreira, T.R., Rossato, M., Macedo, B.F., Da Silva, F.F., Paiva, R., Paiva, L. V. (2017) Establishment and i*n vitro* multiplication of *Calophyllum brasiliensis*. Acta Horticulturae. 1155, 149–156.

Takáč, T., Pechan, T., Šamaj, J. (2011) Differential proteomics of plant development. Journal of Proteomics. 74(5), 577–588.

Tanaka, M., Takei, K., Kojima, M., Sakakibara, H., Mori, H. (2006) Auxin controls local cytokinin biosynthesis in the nodal stem in apical dominance. Plant Journal. 45(6), 1028–1036.

Tang, W., Newton, R.J. (2005) Peroxidase and catalase activities are involved in direct adventitious shoot formation induced by thidiazuron in eastern white pine (*Pinus strobus* L.) zygotic embryos. Plant Physiology and Biochemistry. 43(8), 760–769.

Tiburcio, A.F., Altabella, T., Bitrián, M., Alcázar, R. (2014) The roles of polyamines during the lifespan of plants: from development to stress. Planta. 240(1), 1–18.

Viu, A.F.M., Viu, M.A.O., Tavares, A.R., Vianello, F., Lima, G.P.P. (2009) Endogenous and exogenous polyamines in the organogenesis in *Curcuma longa* L. Scientia Horticulturae. 121(4), 501–504.

Yan, H., Liang, C., Yang, L., Li, Y. (2010) *In vitro* and *ex vitro* rooting of Siratia grosvenorii , a traditional medicinal plant. Acta Physiologiae Plantarum. 32, 115–120.

Zhou, H., Li, M., Zhao, X., Fan, X., Guo, A. (2010) Plant regeneration from *in vitro* leaves of the peach rootstock “Nemaguard” (*Prunus persica* × *P. davidiana*). Plant Cell, Tissue and Organ Culture. 101(1), 79–87

2. Capítulo 2 – Benziladenine effects on polyamines contents and proteomic profile during *in vitro* shoot development and *ex vitro* rooting in *Dalbergia nigra* (Vell.) Allemão ex Benth. (Fabaceae)

Lídia dos Santos Pessanha[1] Victor Paulo Mesquita Aragão[1] Tadeu dos Reis de Oliveira[1] Kariane Rodrigues de Sousa[1] Vanildo Silveira[2,3] Claudete Santa-Catarina[1]

[1] Laboratório de Biologia Celular e Tecidual (LBCT), Centro de Biociências e Biotecnologia (CBB), Universidade Estadual do Norte Fluminense Darcy Ribeiro (UENF), Avenida Alberto Lamego, 2000, Parque Califórnia, Campos dos Goytacazes, RJ, 28013-602, Brazil

[2] Laboratório de Biotecnologia (LBT), CBB, UENF, Campos dos Goytacazes, RJ, Brazil

[3] Unidade de Biologia Integrativa, Setor de Genômica e Proteômica, UENF, Campos dos Goytacazes, RJ, Brazil.

Correspondence
*Corresponding author, e-mail: claudete@uenf.br, ORCID: 0000-0002-1669-660X
Vanildo Silveira ORCID: 0000-0001-5697-6932

2.1. Abstract

Dalbergia nigra is an endangered species due to the intense exploitation of woody. *In vitro* propagation can be applied for conservation of this species. The aim of this study was to establish the *in vitro* propagation and *ex vitro* rooting in D. *nigra*, and evaluate the alterations on polyamines (PAs) and protein profile during shoot development. The effect of MS and WPM culture media was tested on *in vitro* germination, and germination (%) was evaluated at 45 days. For shoot induction, explants from apical and cotyledonary nodal segments were inoculated in WPM culture medium supplemented with different concentrations (0, 2.5 and 5 µM) of 6-benzyladenine (BA). The induction, number and length of shoots were analyzed after 45 days, and samples were collected for PAs and proteomics analyses. Shoots obtained *in vitro* without and

with 2.5 µM of BA were rooted *ex vitro* with different concentrations (0, 100 and 500 µM) of indole-3-butyric acid (IBA). The best growth of seedlings was obtained in WPM culture medium compared to MS. The use of 2.5 µM benzilaminopurine (BA) provided the significantly higher length of shoots by alteration on free-Putrescine contents and proteomic profile. Treatment with benzyladenine showed differentially accumulated proteins associated with elongation of shoots when compared to treatments without benzyladenine. No significant differences of indole–3-butyric acid (IBA) concentration (0, 100 and 500 µM) on root induction from both type of explants was observed, being the root induction significant higher in shoots from both type explants grown without BA. This is the first study showing the relevance of cytokinin, polyamines and proteomic profile on *in vitro* shoot development, as well as, the auxin and cytokinin balance on *ex vitro* rooting in *D. nigra.*

Keywords Brazilian Atlantic Forest ● Shoot development ● cytokinin and auxin.

2.2. Introduction

Several native wood species from the Atlantic Rain Forest are endangered, including *Dalbergia nigra* (Vell.) Allemão ex Benth, commonly known as Jacarandá-da-Bahia. Due to the intense exploitation of woody, and the lack of reforestation programs, this species has been included as vulnerable on the Red List of the International Union for Conservation of Nature (International Union for Conservation of Nature and Natural Resources., 2017). Appropriate biotechnological and sustainable conservation strategies for many woody species needs further research and development, and *in vitro* propagation technologies can be applied for conservation, with a great going to a global economic and ecological impact on sustaining tropical forest woody biodiversity (Pijut et al. 2012).

Biotechnological tools, as micropropagation, has been applied in studies aiming the propagation of woody species (Perveen *et al.*, 2013; Fermino and Scherwinski-Pereira, 2012)(Perveen *et al.*, 2013). Micropropagation is the commercially efficient propagation of species in a short period of time (Gupta et al. 2014), enabling clonal production and conservation of germplasm (Giri et al. 2004; Shukla et al. 2009; Kodym and Leeb 2019). The knowledgment of biochemical and molecular aspects on *in vitro*

morphogenesis, such as the cellular mechanisms involved in the growth and development of these species, is necessary for the propagation and preservation of threatened species that difficulties on propagation by conventional methods (Fonseca et al. 1991; Pijut et al. 2007; Dias et al. 2012).

The steps of *in vitro* propagation involves manipulation of type of explants as well as the components of culture medium, as plant growth regulators (PGRs), to achieve an optimal condition for shoot multiplication and root induction (Bunn et al. 2011). Among the PGRs, cytokinins and auxins are the most used in plant tissue cultures for shoot and root development (Phillips and Garda 2019). In propagation of woody species, the 6-benzyladenine (BA) is the cytokinin most used to promote the development of axillary buds, breaking the apical dominance and stimulating shoot proliferation (Giri *et al.*, 2004; Pijut *et al.*, 2012). Studies has been showed the relationship of PGRs with other compounds, such as polyamines (PAs) on shoot development (Aragão *et al.*, 2016; 2017).

PAs are low molecular weight, aliphatic, polycationic compounds with positively charged nitrogen atoms naturally occurring in plants (Baron and Stasolla, 2008). These compounds can interact with negatively charged macromolecules, such as DNA, RNA, phospholipids, cell wall components, and proteins (Baron and Stasolla, 2008).Thus, PAs are essential for various physiological and developmental processes in plant (Santa-Catarina *et al.*, 2007; Dutra *et al.*, 2013), including the shoot development (Aragão *et al.*, 2017; Lerin *et al.*, 2019; Oliveira *et al.*, 2020). Changes in endogenous PAs contents induced by exogenous PAs, especially putrescine (Put), demonstrated its relevance for shoot development in *C. fissilis* (Aragão *et al.*, 2017).

In addition to PAs, specific proteins has been candidate markers associated with morphogenic competence during *in vitro* plant morphogenesis (Heringer *et al*., 2015, 2017; Reis *et al*., 2016). Proteomic studies revealed the involvement of multiple proteins with specific functions in competence for *in vitro* development of shoots (Mitrovic *et al.,* 2012; Ghosh and Pal 2013; Corredor-Prado *et al.,* 2016). Changes in accumulation of some proteins involved mainly in metabolic and cellular processes, as cell division, during *in vitro* shoot development induced or not by exogenous putrescine (Put), demonstrated an important relationship of specific proteins with shoot development in *C. fissilis* (Aragão *et al.,* 2016; 2017).

In addition to shoot development, the formation of adventitious root is an

essential step of *in vitro* plant propagation. The auxin plays an essential role on rooting, being the indole-3-butyric acid (IBA) the most commonly used due its higher root-inducing capacity and greater stability to light (Pacurar et al. 2014). The IBA use is well documented during *in vitro* and *ex vitro* rooting in several woody species (Pijut et al. 2012). The *ex vitro* rooting has advantage of lower cost, and save time, reducing the cost of a micropropagation protocol up to 70% compared to *in vitro* rooting (Yan et al. 2010; Ranaweera et al. 2013; Patel et al. 2014). In addition, another advantages of *ex vitro* rooting is that plantlets do not need additional acclimatization, exhibiting a well-root development and improved plantlet survival compared to *in vitro* rooting (Yan et al. 2010; Gupta et al. 2014).

Studies with *in vitro* propagation of *D. nigra* has been not developed yet. In this sense, the establishment of *in vitro* propagation for this species can contribute for conservation programs and reposition of impacted areas. In addition, biochemical and molecular approaches can improve the knowledgement for *in vitro* morphogenesis competence. Thus, the aim of this work was to establish the *in vitro* propagation and *ex vitro* rooting of *D. nigra*, and evaluated the alterations on PAs contents and protein profile during shoot development.

2.3. Materials and methods

2.3.1. Plant material

The mature seeds were obtained from Caiçara Comércio de Sementes LTDA located in Brejo Alegre, SP, Brazil (21º10'S and 50º10'W) were used. Forty-five-days-old seedlings were used as the source of apical and cotyledonary nodal explants for the shoot development experiments. Forty-five-day-old micropropagated shoots were used for the *ex vitro* rooting experiments.

2.3.2. Seed disinfection

Prior to inoculation, seeds were surface-disinfected according to Santa-Catarina et al. (2001), with modifications. Seeds were washed with 250 mL distilled water, followed by immersion in 70 % ethanol for 1 min, incubation in 2.5 % sodium

hypochlorite solution supplemented with the fungicide Derosal® 500 SC (Bayer; São Paulo, Brazil; Active ingredient carbendazim 500 g L^{-1}; 200 µL of commercial solution per liter of water) for 30 min. Seeds were washed five times, for 10 min each, in sterile distilled water in a flow chamber.

2.3.3. Effect of plant culture medium on seed germination

After disinfection, seeds were transferred to Murashige and Skoog (MS; Phytotechnology Lab, Overland Park, USA) (Murashige & Skoog, 1962) and Woody Plant Medium (WPM; Phytotechnology) (Lloyd and McCown 1981) culture media, both supplemented with 20 g L^{-1} sucrose (Synth; São Paulo, Brazil) and 2 g L^{-1} Phytagel® (Sigma-Aldrich, St. Louis, USA). The pH of the culture medium was adjusted to 5.7 before the use of Phytagel and autoclaved at 121 ºC for 15 min.

After, seeds were incubated in 16-h photoperiod, at light intensity of 55 µmol m^{-2} s^{-1}, and temperature of 25±2°C. Germination (%) and morphology of seedlings were analyzed after 30 days of incubation. Each treatment consisted of five repetitions, being 20 seeds of each repetition.

2.3.4. Effect of explant, plant culture medium and BA concentration on shoot development

Forty-five days old seedlings germinated *in vitro* were used as the source of explants (Fig. 2a). Apical (Fig. 2b) and cotyledonary (Fig. 2c) nodal segments (± 2 cm) were isolated from seedlings and cultured on MS and/or WPM culture medium, supplemented with 20 g L^{-1} sucrose, 2 g L^{-1} Phytagel® and different concentrations (0; 2.5 and 5 µM) of BA (Sigma-Aldrich). The pH of the culture medium was adjusted to 5.7 and autoclaved at 121 ºC for 15 min. The explants were transferred to the culture medium with different treatments and maintained at 16-h photoperiod, under light intensity of 55 µmol m^{-2} s^{-1}, and temperature of 25±2°C. Eight repetitions per treatment were used, with four explant of each repetition. The induction (%), number of shoots per explant and length of the first and second shoot were analyzed after 45 days of incubation. Samples were collected for PAs and proteomic analyses, being maintained in -80 °C until proceeding the analysis.

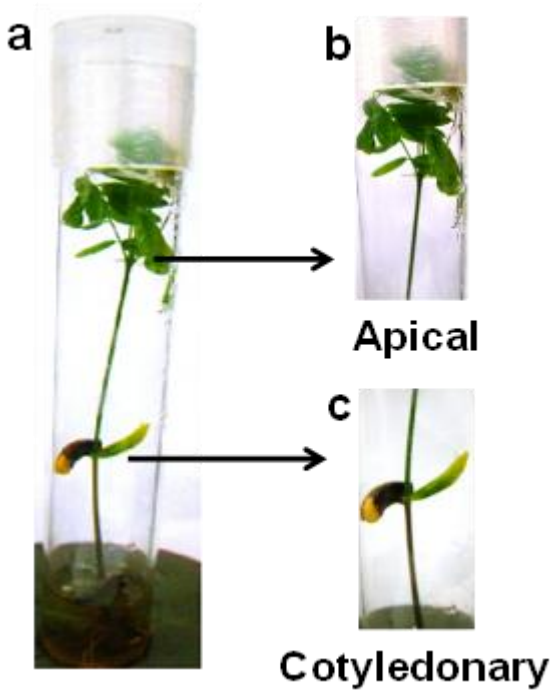

Fig.2: Forty-five days old seedlings of *D. nigra* germinated *in vitro* (a) and apical (b) and cotyledonary (c) nodal segments obtained from seedling.

2.3.5. Free PA determination

Determination of free PAs was performed according to Santa-Catarina et al. (2006) using samples of shoots from apical and cotyledonary nodal segments with 45 days of incubation without (control) and with 2.5 µM BA in WPM medium. Samples (200 mg fresh matter – FM – each, in triplicate) were grounded in 1.2 mL of 5% perchloric acid (Merck Millipore, Darmstadt, Germany). After 1 h of incubation at 4 °C, the samples were centrifuged for 20 min at 20,000×g at 4 °C. The supernatant was collected, and free-PAs were determined directly from the supernatant by derivatization with dansyl chloride (Merck Millipore) and identified by high-performance liquid chromatography (HPLC) (Shimadzu, Kyoto, Japan) using a 5-µm C18 reverse-phase column (Shimadzu Shin-pack CLC ODS). The HPLC column gradient was created by adding increasing volumes of absolute acetonitrile (Merck Millipore) to a 10% aqueous acetonitrile solution with the pH adjusted to 3.5 with hydrochloric acid (Merck Millipore). The absolute acetonitrile concentration was maintained at 65% for the first 10 min, increased from 65 to 100% between 10 and 13 min, and maintained at 100% between 13 and 21 min. The mobile phase was added at a flow rate of 1 mL

min^{-1} and 40 °C. The PA concentration was determined using a fluorescence detector at 340 nm (excitation) and 510 nm (emission). The peak areas and retention times of the samples were measured through comparisons with the standard PAs Put, Spd, and Spm (Sigma-Aldrich).

2.3.6 Protein extraction and digestion

Proteins were extracted from samples (tree biological triplicates, 300 mg FM each sample) of shoots from apical and cotyledonary nodal explants grown without (0 µM - control) and with 2.5 µM BA at 45 days of incubation in WPM medium. Proteins were extracted using the trichloroacetic acid (TCA)/acetone method with modifications (Damerval *et al.*, 1986). Initially, the samples were pulverized in liquid nitrogen using a ceramic mortar and pestle. The resulting powder was resuspended in 1 mL of chilled extraction buffer 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. Following, 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 complete protease inhibitor cocktail (Roche Diagnostics, Mannheim, Germany), being 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 2-D Quant Kit (GE Healthcare).

Before the trypsin digestion step, protein samples were precipitated using the methanol/chloroform methodology (Nanjo *et al.*, 2012). After protein precipitation, samples were resuspended in 7M urea/2M thiourea solution. Aliquots of 100 µg of protein were subjected to tryptic digestion using the filter-aided sample preparation (FASP) methodology (Botini *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.

2.3.7 Mass spectrometry analysis

Mass spectrometry was performed using a nanoAcquity UPLC connected to a Q-TOF SYNAPT G2-Si instrument (Waters, Manchester, UK). Runs consisted of three biological replicates of 1 µg of peptide samples. During separation, samples were loaded onto the nanoAcquity UPLC M-Class Symmetry C18 5 µm trap column (180 µm × 20 mm) at 5 $\mu L.min^{-1}$ during 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 (SigmaAldrich) 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 experiment at 120 min. Mass spectrometry was performed in positive and resolution mode (V mode), 35,000 full widths at half maximum, with ion mobility separation (IMS), and in data-independent acquisition mode ($HDMS^E$). The ion mobility wave was set to a velocity of 600 m s^{-1}; and a helium and IMS gas flow of 180 and 90 mL min^{-1}, respectively. The transfer collision energy ramped from 19 to 55 V in high-energy mode; the cone and capillary voltages were 30 and 2750 V, respectively; and the source temperature was 70 °C. Regarding time of flight (TOF) parameters, the scan time was set to 0.5 s in continuum mode with a mass range of 50 to 2000 Da. The human [Glu1]-fibrinopeptide B at 100 $fmol.\mu L^{-1}$ was used as an external calibrant and lock mass acquisition was performed every 30 s. Mass spectra were acquired by the MassLynx v4.0 software.

2.3.8 Proteomics data analysis

Spectra processing and database search conditions were performed using ProteinLynx Global Server (PLGS) software v.3.0.2 (Waters). The PLGS was processed by the following parameters: Apex3D of 150 counts for low-energy threshold, 50 counts for elevated-energy threshold, and 750 counts for intensity threshold; two missed cleavage; minimum fragment ions per peptide equal to three; minimum fragment ions per protein equal to seven; minimum peptides per protein equal to two; fixed modifications of carbamidomethyl (C) and variable modifications of

oxidation (M) and phosphoryl (STY); default false discovery rate (FDR) was set to a maximum of 1%. We used the *Arachis hypogaea* protein databank from UniProtKB (http://www.unipr ot.org) used for protein identification, as it is the largest databank with proximity to *D. nigra*. Label-free quantification analysis was performed using ISOQuant workflow software v.1.7 (Distler *et al.*, 2014). Briefly, the following parameters were used to identify proteins: FDR 1%, a peptide score greater than six, a minimum peptide length of six amino acids, and at least two peptides per protein were considered for label free quantitation using the TOP3 approach, followed by the multidimensional normalized process within ISOQuant (Distler *et al.*, 2014). To ensure the quality of the results after data processing, only the proteins that were either present or absent (for unique proteins) in all three biological replicates were considered for differential accumulation analysis. Data were analyzed using Student's t-test (two-tailed). Proteins with ANOVA ($P < 0.05$) were considered up-accumulated if the $\log_2$ value of the fold change (FC) was greater than 0.60 and down-accumulated if the $\log_2$ value of the FC was less than -0.60. Functional annotations were performed using OmicsBox software 1.0.34 and UniProtKB (http://www.uniprot.org).

2.3.9 Effect of IBA on ex vitro rooting of shoots and plant acclimatization

Shoots from apical and cotyledonary nodal segments (± 2 cm) cultured in WPM culture medium supplemented without and with 2.5 µM BA were used for shoot rooting. Shoots, containing the apical meristem and leaves, were treated during 30 s with different concentrations (0, 100 and 500 µM) of IBA (Sigma-Aldrich). After, shoots were transferred to 50 mL plastic pots containing a mixture of PlantMax substrate (DDL Agroindustria, Paulínia, Brazil) with vermiculite (2:1; v/v). The shoots were maintained in plastic trays covered with a plastic film to maintain the high humidity needed for root development during *ex vitro* rooting and acclimatization. These plastic trays were kept in the grow room, under 16-h photoperiod, a light intensity of 55 µmol m^{-2} s^{-1}, and temperature of 25±2 °C. After 30 days, the humidity was gradually reduced until 40 days, when rooted shoots were considered acclimatized. The induction of rooting (%), number of roots initiated per shoot and root length were recorded after 45 days. Each treatment consisted of eight repetitions, with four shoots in each repetition.

2.3.10. Data analyses

The experimental design was completely randomized. Data were analyzed using analysis of variance ($P < 0.05$) followed by the Student–Newman–Keuls (SNK) test (Sokal and Rohlf 1995) using the R program (R Foundation for Statistical Computing, version 3.4.4, 2018, Vienna, Austria).

2.4 Results

2.4.1. Effects of plant culture medium on germination and seedling development

Both culture media tested showed no significant difference on germination, resulting in similar percentage for MS (80%) and WPM (81%) (Fig. 3a). However, the seedlings obtained in the MS culture medium showed more senescence (Fig. 3b) compared to those of the WPM culture medium (Fig. 3c), which showed well-developed leaves.

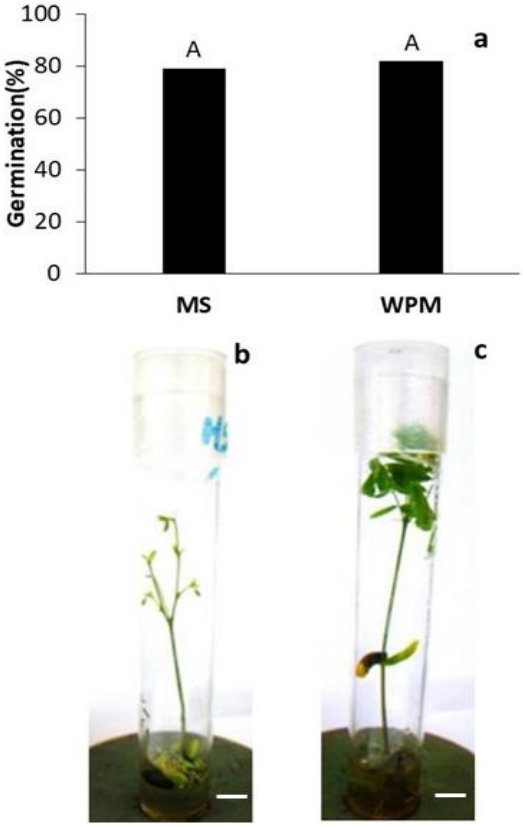

Fig. 3: Germination (%) of *Dalbergia nigra* seeds after 30 days of incubation in MS and WPM culture media (a) and morphological aspects of 30-day-old seedlings germinated

in MS (b) and WPM (c) culture media. (n = 5; Coefficient of variation = 13.18%). Bars in b and c = 1 cm.

2.4.2. Effects of explant, plant culture media and BA on shoot development

Due to the difference in length between the first (Fig. 4a and 4b) and second shoot (Fig. 4c and 4d) developed, they were measured separated. The BA addition promoted the elongation of first shoot developed from both type of explants, the apical and cotyledonary nodal segments, in both culture media, MS (Fig. 4a) and WPM (Fig. 4b), compared to shoots obtained without BA (control). Moreover, no significant difference was observed comparing the two types of explants in the same BA concentration and same culture medium, as well as comparing both culture media used (Fig. 4a and 4b). As BA is essential for shoot growth, and no significant differences on length of shoots between 2.5 and 5 µM BA in both culture media, the two types of explants can be used for *in vitro* propagation of *D. nigra*, considering the elongation of first shoot developed.

The second shoot showed lower elongation (Figs. 4d and 4e) compared to the first one (Figs. 4a and 4b). At MS culture medium, the BA concentration increased the length of second shoot from cotyledonary nodal segments compared to control, while no significant effects were observed in shoots from apical nodal segments (Fig. 4c). At WPM culture medium, the 2.5 µM BA treatment showed lower elongation of second shoots from cotyledonary nodal segments compared to control and 5 µM BA (Fig. 4d).

There were no significant differences for the number of shoots comparing the two types of explants, in each BA concentration (0 or 2.5µM) and also in both culture media, the MS (Fig. 4e) and WPM (Fig. 4f), except to apical explants in the control treatment (without BA) in MS culture medium which showed a significantly lower number of shoots (Fig. 4e). On the other hand, no significant differences were observed for the number of shoots from apical and cotyledonary nodal segments incubated with WPM culture medium (Fig. 4f).

For shoot induction, no significant differences were observed in both explant types, culture media and BA concentrations, showing 100% of shoot induction in all treatments (data not showed).

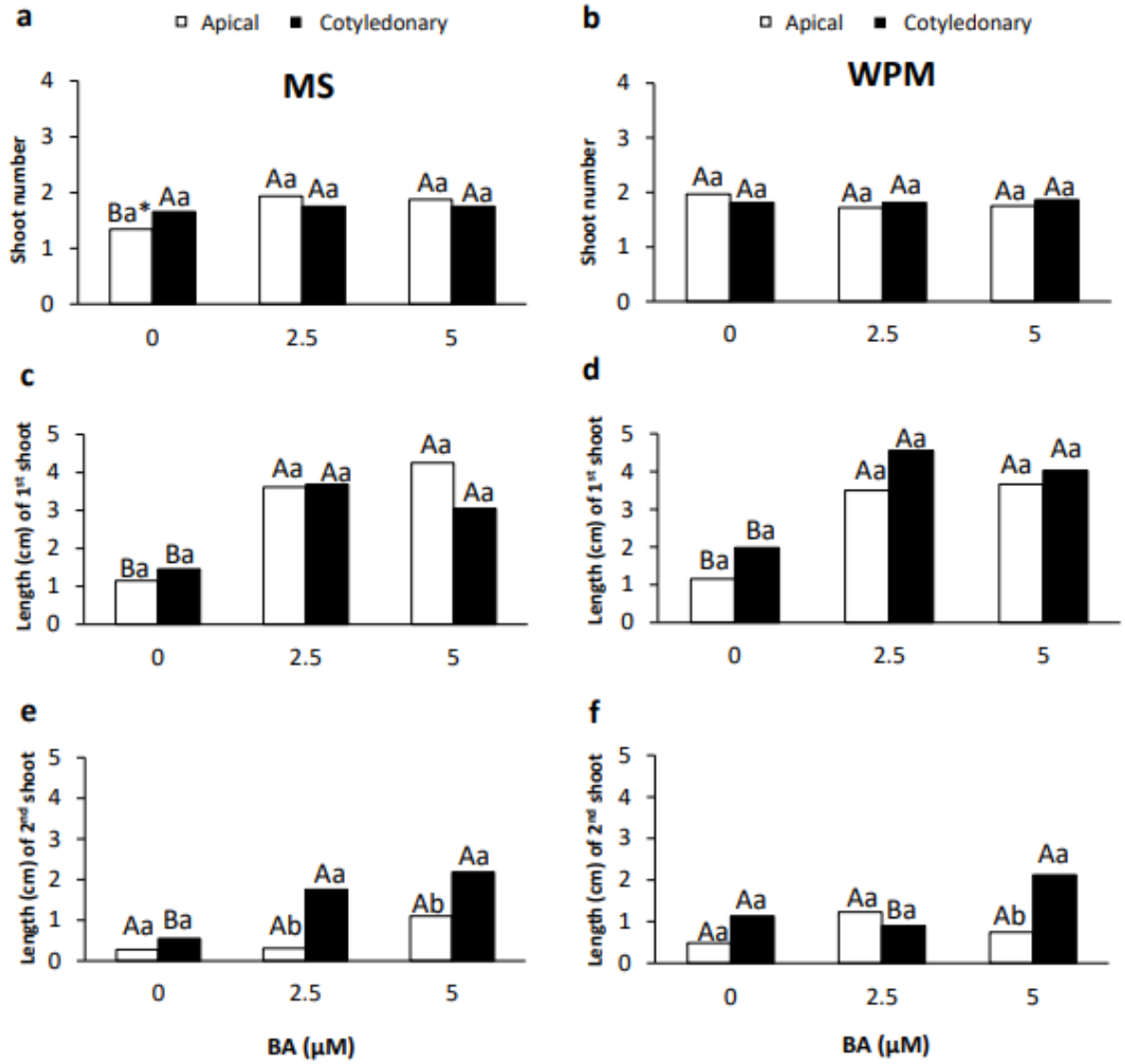

Fig. 4: Number of shoots (a and b) and length (cm) of first (c and d) and second (e and f) shoot obtained from apical and cotyledonary nodal segments of *Dalbergia nigra* after 45 days of incubation in the MS (a, c, and e) and WPM (b,d and f) culture media. Means followed by different letters are significantly different ($P < 0.05$) according to the SNK test. Capital letters denotes significant differences comparing the same type of explant (apical and cotyledonary) in different BA concentrations (0, 2.5 and 5 µM). Lowercase letters denotes significant differences comparing the two types of explants (apical and cotyledonary) in the same BA concentration (0, 2.5 or 5 µM). Asterisc (*) indicates significant differences comparing the MS and WPM culture media for apical nodal segment explant in the same BA concentration (0, 2.5 or 5 µM). CV = Coefficient of Variation. (n = 8; CV of shoot number = 21.13 %; CV of length of first shoot = 29.82%; CV of length of second shoot = 66.4%).

2.4.3. Effect of BA and type of explant on endogenous PAs contents on shoot development

Free PAs were quantified in 45-days-old shoots from apical and cotyledonary nodal segments incubated without and with 2.5 µM BA and WPM culture medium (Fig. 5). Free-Put content was significantly higher when shoots were grown in 2.5 µM of BA compared to control in both type of explants, being significant higher in shoots from apical nodal segments compared to cotyledonary nodal segments (Fig. 5a). Higher free-Spd content was observed in shoots from apical explants grown in 2.5 µM BA, differing statistically from shoots in control treatment (Fig. 5b). Moreover, a higher free-Spm content was observed in shoots from cotyledonary nodal segments in 2.5 µM BA treatment compared to control (Fig. 5c). The content of total free-PAs was significantly higher in shoots from both type of explants incubated in 2.5 µM BA compared to shoots from control treatment (Fig. 5d).

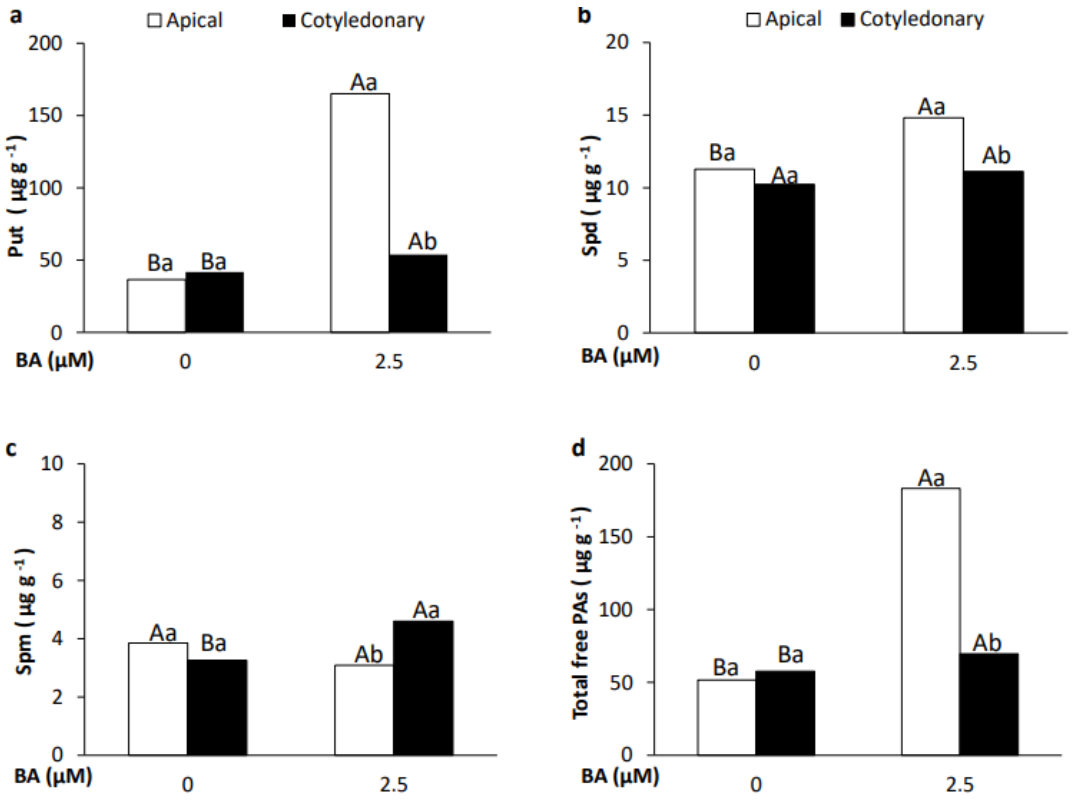

Fig. 5: Free Put (a), Spd (b) and Spm (c) contents (µg.g^{-1} FM) in shoots obtained from apical and cotyledonary nodal segments of *Dalbergia nigra* at 45 days of incubation on WPM culture medium without and with 2.5 µM BA. Means followed by different letters are significantly different ($P < 0.05$) according to the SNK test. Capital letters indicate significant differences between the same type of explant (apical or cotyledonary) in the

different BA concentration (0 and 2.5 µM). Lowercase letters denote significant differences between different type of explant (apical and cotyledonary) in the same BA concentration (0 or 2.5 µM). CV = Coefficient of Variation. (n = 3; CV of Put = 8.33%, CV of Spd = 10.99%, CV of Spm = 15.16%, CV of Total free PAs = 7.57%).

2.4.4. Effect of BA and type of explant on proteomic profile during shoot development

Proteomic analysis was performed comparing the effects of BA (by the comparisons BA2.5_Apical/BA0_Apical and BA2.5_Cotyledonary/BA0_Cotyledoenary) and type of explant (by the comparisons BA2.5_Cotyledonary/BA2.5_Apical and BA0_Cotyledonary/BA0_Apical) on shoot development. A total of 1232 proteins were identified (Supplementary table 1). Among the DAPs, some proteins were highlighted according to their relevance on cell division and growth of shoots. Proteins were selected according to the four comparisons performed. Thus, the proteins must repeat the same pattern in each comparison, without being classified as unchanged in any of the cases.

Comparing the BA concentrations (0 and 2.5µM) in shoots obtained from apical nodal segments (BA2.5_Apical/BA0_Apical) a total of 292 proteins were differentially accumulated (DAPs) and 923 unchanged. Among the DAPs, 93 proteins were up- and 158 down-accumulated, with 13 unique in shoots grown under BA2.5_Apical and 28 unique in shoots under BA0_Apical (Fig. 6a; Supplementary table 1). The comparison of BA concentrations treatment in shoots from cotyledonary nodal segment (BA2.5_Cotyledonary/BA0_Cotyledonary), a total of 374 proteins were DAPs and 846 unchanged. Among the DAPs, 179 were up- and 158 were down-accumulated. In addition, 18 proteins were unique in shoots from cotyledonary nodal segments incubated with 2.5µM BA (BA2.5_Cotyledonary) treatment and 19 proteins were unique in shoots from cotyledonary nodal segments without BA (BA0_Cotyledonary) treatment (Fig. 6b; Supplementary table 1).

Among these proteins, some were up-accumulated in shoots from both type of explants (apical and cotyledonary nodal segments) incubated with 2.5 BA, as the factor ATP-dependent RNA helicase DEAH7 (A0A444YGB9), calreticulin-3 (A0A445A993), and the protein elongation factor 1-alpha (A0A444Y7Y0). Other proteins that were up-accumulated in shoots from cotyledonary nodal segments incubated in 2.5 µM BA compared to shoots without BA (comparison BA2.5_Cotyledonary/BA0_Cotyledonary)

(Supplementary Table 1) were cell division cycle protein 48 homolog (A0A444Z3W1) and the aspartate aminotransferase 1 (A0A445B4C1) (Supplementary Table 1). In addition, the proteins phosphoenolpyruvate carboxylase 2 (A0A445BXQ0) phosphoribosylamine-glycine ligase (A0A445E7J0), FT-interacting protein (A0A444ZYV6), dolichyl-diphosphooligosaccharide-protein glycosyltransferase 48 kDa subunit (A0A445A8R7), citrate synthase mitochondrial (mtCS), phosphoribosylamine-glycine ligase (A0A445E7J0) and 60S ribosomal protein L35a-3 (A0A444ZT56) were up-accumulated in shoots from cotyledonary nodal segments incubated in 2.5 µM BA compared to shoots without BA (comparison BA2.5_Cotyledonary/BA0_Cotyledonary) (Supplementary Table 1).

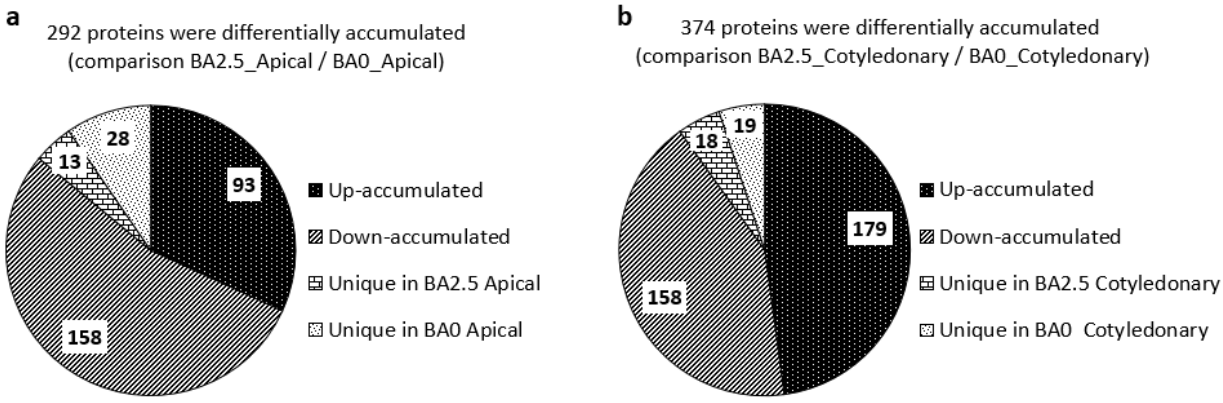

Fig. 6: Differentially accumulated proteins (DAPs) in 45-day-old shoots of *Dalbergia nigra* obtained from apical (a) and cotyledonary (b) nodal segments used as explants, comparing the two BA concentrations (0 or 2.5 µM) in the same type of explant with the comparisons: BA2.5_Apical/BA0_Apical (a) and BA2.5_Cotyledonary/BA0_Cotyledoenary (b).

The effect of explant type, in the same BA concentration, was evaluated on protein profile. Comparing shoots from cotyledonary with shoots from apical nodal segments incubated at 2.5 µM BA (comparison BA2.5_Cotyledonary/BA2.5_Apical), 242 proteins were DAPs and 973 unchanged. Among the DAPs, 154 were up- and 46 were down-accumulated, with 28 proteins unique in shoots at BA2.5_Cotyledonary treatment and 14 proteins unique in shoots from BA2.5_Apical (Fig. 7a). Comparing the shoots from cotyledonary to apical nodal segments incubated without BA (comparison BA0_Cotyledonary/BA0_Apical), a total of 231 proteins were DAP and 997 unchanged (Fig. 7b). Among the DAPs, 89 were up- and 90 down-accumulated, presenting 26

proteins unique in shoots from cotyledonary nodal segments without BA (BA0_Cotyledonary treatment) and 26 proteins unique in shoots from apical nodal segments without BA (BA0_Apical treatment) (Supplementary table 1). Among the DAPs, the malate dehydrogenase 2 (peroxisome) (A0A445DRP9), ATP synthase subunit beta, chloroplastic (A0A445AH22) proteins were up-accumulated in shoots from cotyledonary nodal segments compared to those from apical, in both BA concentration. The bifuncional dTDP-4-desidrorhamnose 3,5-epimerase/dTDP-4-desidrorhamnose reductase (A0A444Z945) protein was unique in *D. nigra* shoots from cotyledonary nodal segments BA-treated compared to shoots without BA (BA2.5_Cotyledonary/BA0_Cotyledonary) and to shoots from apical nodal segments BA-treated (BA2.5_Cotyledonary/BA2.5_Apical).

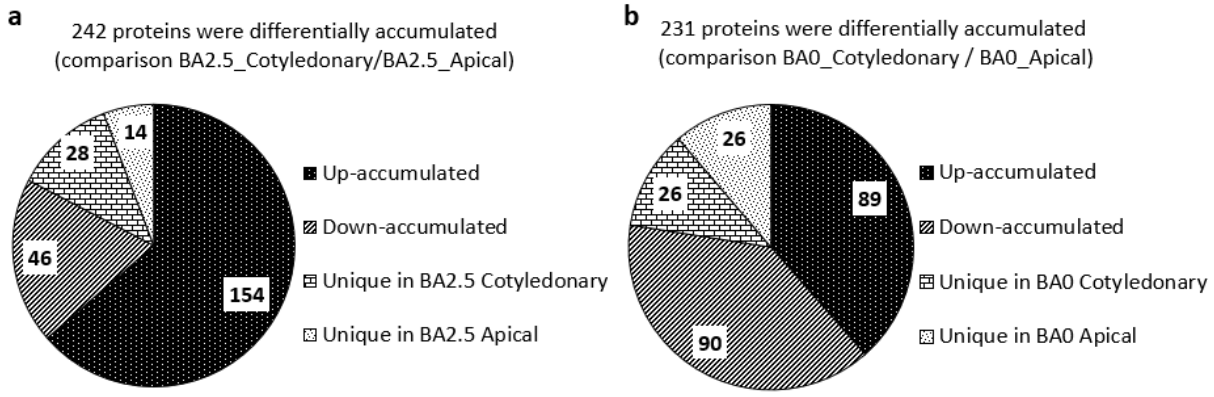

Fig. 7: Differentially accumulated proteins (DAPs) in 45-day-old shoots of *Dalbergia nigra* obtained from apical and cotyledonary nodal segments incubated with 2.5 µM (a) and without (0 µM) BA (b), comparing the two types of explants (apical and cotyledonary) in the same BA concentration (0 or 2.5µM), at the comparisons BA2.5_Cotyledonary/BA2.5_Apical (a) and BA0_Cotyledonary/BA0_Apical (b).

2.4.5. Effect of IBA on *ex vitro* rooting of shoots and acclimatization

The *ex vitro* root induction of shoots was not significantly affected by IBA concentrations and types of explants (Fig. 8). However, the induction of roots was significantly affected by BA supplementation on the culture medium of shoot development, being the induction of roots significantly higher in shoots grown in culture medium without BA (Fig. 8a) compared to 2.5 µM BA (Fig. 8b). The number of roots was also significantly affected by the BA concentration used on shoot multiplication,

being significantly higher in shoots multiplied without BA (Fig. 8c) compared to BA (Fig. 8d). The length of shoots was significantly affected by BA treatment during shoot multiplication, being significantly higher in shoots from cotyledonary nodal explants grown with BA (Fig. 8e and 8f). On the other hand, the length of roots was not significantly affected by IBA concentrations used in shoots from both type of explants used (Figs. 8e and 7f).

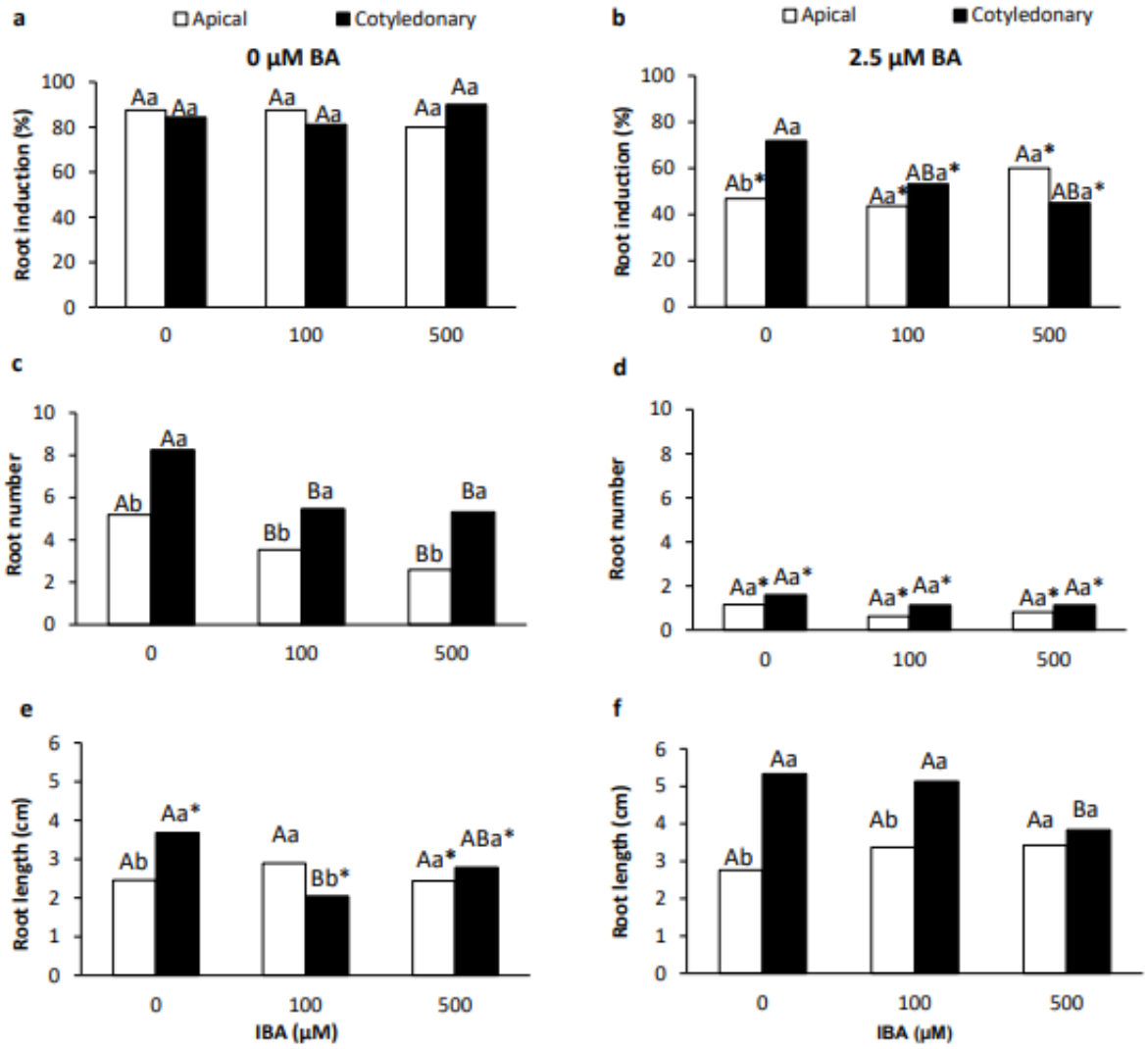

Fig. 8: Root induction (a, b), root number (c, d) and root length (cm) (e, f) in shoots from two types of explants (apical and cotyledonary nodal segments) of *Dalbergia nigra* obtained in WPM culture medium without and with 2.5 µM BA, at 45 days in acclimatization. Capital letters denotes significant differences comparing the same type of explant (shoots from apical or cotyledonary nodal segments) in different IBA concentrations. Lowercase letters denotes significant differences comparing shoots from the two types of explants (apical and cotyledonary nodal segments) in the same

IBA concentration. * Denotes significant differences for shoots from apical and cotyledonary nodal segments comparing the BA treatment (0 and 2.5 µM) at each IBA concentration. (n = 8; CV of root induction = 27.4 %; CV of root number = 24.92%; CV of root length = 24.4%).

2.5. Discussion

The establishment of the best culture medium for *in vitro* seed germination is relevant to obtain explants for micropropagation. Besides no significant differences in seed germination (Fig. 3a), the WPM culture medium resulted in seedlings with better growth (Fig. 3c). In *C. legalis*, the WPM culture medium improved the percentage of *in vitro* seed germination, being significantly higher compared to MS culture medium (Aragão et al. 2017). The WPM culture medium has only 25% of the concentrations of nitrate and ammonium ions present in MS culture medium, in addition to more potassium and a high level of sulfate ions, widely used for micropropagation of woody species (Hazubska-Przybył 2019). The less concentrations of total nitrogen and ammonium in WPM culture medium reduces the possibility of toxicity to ammonium, which can contribute to the development of seedlings in some woody species (Phillips and Garda 2019), as observed in *D. nigra* in the present work.

For shoot development, the BA is the most cytokinin used for proliferation of axillary buds in many plant species (Sahai and Shahzad, 2013), including several trees, such as *Santalum album* (Mujib, 2005), *Azadirachta excelsa* (Chiew and Othman, 2006), *Sapium sebiferum* and *Calophyllum brasiliensis* (Stein *et al.*, 2017). The structural stability of BA and the ability of plant cells to easily assimilate make this cytokinin stand out as an efficient promoter of plant development (Ahmad *et al.,* 2013). Our results showed that BA addition was essential to increase the length of shoots from both types of explants (apical and cotyledonary nodal segments) and culture media (MS and WPM) (Fig. 4) in *D. nigra*. The use of BA also promoted longer shoots in *Juglans nigra* (Stevens and Pijut, 2018) *Rauvolfia tetraphylla* (Hussain *et al.*, 2018). This promotion in the length of shoots BA-induced may be associated with effects of cytokinins in the control of cell division, providing greater growth and development (Anis *et al.*, 2009; Wybouw and De Rybel, 2019). Besides the positive effects of BA on shoot length, this cytokinin showed no effects on shoot induction (%) and number of shoots per explant (Fig. 4) in *D. nigra*. Similarly, no significant effects of BA on number

of shoots was also observed for *C. legalis* (Aragão *et al.*, 2017). On the other hand, in *Dalbergia sisso*, the use of 4.4 µM BA provided a greater number of shoots compared to the control (Sahu et al. 2014). These results show that the *in vitro* morphogenic response BA-induced is intrinsic to the species, and this response may be different even within species of the same genus as that observed between *D. nigra* and *D. sisso*.

In addition to cytokinins, the PAs are involved in plant growth and development, once they can act in various physiological processes such as promotion of cell division, differentiation, and elongation, being essential to embryo development, germination, rhizogenesis (Santa-Catarina *et al.* 2006; Kusano *et al.* 2008; Pieruzzi *et al.* 2011; Gündeşli *et al.* 2019) and shoot development in woody plants (Aragão *et al.*, 2016; 2017; Lerin *et al.*, 2019). The higher content of free Put in shoots from cotyledonary and apical nodal segments incubated with BA was correlated with the higher length of shoots in *D. nigra* (Fig. 2). Similar results was observed during *in vitro* shoot development in other species, such as *Bixa orellana* (Parimalan *et al.*, 2011) and *C. fissilis* (Aragão *et al.*, 2016; Oliveira *et al.*, 2020). A high content of Put was shown directly related with cell cycle progression at the G1/S transition, stimulating synthesis of protein such as tubulins, which contribute to cell growth (Yamashita *et al*., 2013; Tiburcio *et al.,* 2014). Cross-talk among PAs and the other plant hormones, such as cytokinin, has been proposed, once BA can affect PA metabolism, and thereby their homeostasis, by changing the expression of the genes responsible for PA biosynthesis, catabolism, or both (Ahanger *et al.*, 2020). Therefore, the modulation of endogenous PA contents is relevant for shoot elongation in *D. nigra.*

Comparative proteomics is an important tool for the comprehension of physiologic and molecular processes during *in vitro* morphogenesis, once it is possible to compare DAPs under different treatments (Heringer *et al.*, 2017). This approach was applied in the present work aiming to comprehend the effects of BA and the type of explant (apical and cotyledonary nodal segments) (Figs. 6 and 7) on protein accumulation during shoot development in *D. nigra*. The accumulation of some proteins was significantly affected by BA addition in shoots of *D. nigra* from both type of explant (Supplementary Table 1). Among the DAPs, the up-accumulation of factor ATP-dependent RNA helicase DEAH7 (A0A444YGB9) could be relevant for shoot elongation induced by BA. This protein is involved in the expression of genes related to auxin-mediated development, such as the apical-basal standardization of embryonic

development and vascular development in *Arabidopsis* (Tsugeki and Terada 2015). Thus, the accumulation of this protein under BA treatment can improve the shoot elongation in *D. nigra* probably interacting with auxin metabolism as this protein is related to the auxin polar transport. The auxin polar transport is essential for cell elongation of the embryo scutellum owing to auxin-induced cell acidification and elongation to the plasma membrane enabling growth (Chen *et al.*, 2010).

The calreticulin is a molecular calcium-binding chaperone that promotes folding, oligomeric assembly and quality control in the endoplasmic reticulum through the calreticulin/calnexin cycle. Calcium is an important stabilizing agent in the control of plant cell metabolism, playing a role in the structure and permeability of cell membranes, cell division and elongation, translocation of carbohydrates and nitrogen metabolism, presenting direct effect on plant growth (Ahmad *et al.*, 2016). In this sense, the increase in the accumulation of calreticulin-3 (A0A445A993) protein BA-induced in shoots from both type of explants may be related with calcium and others compounds important for shoot elongation observed in *D. nigra.* In addition, the calreticulin proteins are able to transiently interact with almost all monoglucosylated glycoproteins necessary for the accumulation of elongation factor receptor (Ahmad *et al.*, 2016). In the present work, the up-accumulation of elongation factor 1-alpha (A0A444Y7Y0) protein in shoots from both type of explants under BA treatment compared to shoots grown without BA (Supplementary Table 1) could be relevant for the best shoot development in *D. nigra*. This protein works like a promoter of GTP-dependent binding of aminoacyl-tRNA to ribosome site during protein biosynthesis, an important process to growth and development (White et al. 2019). In addition, the up-accumulation of protein cell division cycle protein 48 homolog (A0A444Z3W1) in shoots from both type of explants could be relevant for the higher shoot elongation BA-induced in *D. nigra*. This protein is direct related to cell division, cytokinesis and growth processes in plants (Rancour *et al.*, 2002).

Nitrogen (N) is essential into carbon skeletons for the biosynthesis of the primary amino acids, glutamine and glutamate, which serve as N donors for the biosynthesis of major N compounds in plants, including other amino acids, nucleic acid bases, PAs, and chlorophylls (De La Torre *et al.,* 2014). The aspartate aminotransferase protein is important to aspartate biosynthesis and plays a key role in the metabolic regulation of carbon and nitrogen metabolism in all organisms (Cánovas

et al. 2007). The induced gene silencing of aspartate aminotransferase in *Nicotiana benthamiana* cause reduction in growth, chlorosis symptoms and decrease the levels of chlorophyll and lignin (De La Torre *et al.*, 2014). Moreover, the aspartate aminotransferase activity was involved with biomass increment in *Brassica napus* (McAllister et al. 2016). The up-accumulation of aspartate aminotransferase 1 (A0A445B4C1) protein in shoots from both type of explant grown under BA treatment (BA2.5_Apical/BA0_Apical and BA2.5_Cotyledonary/BA0_Cotyledonary comparisons) (Supplementary Table 1), may be important for the increment in biomass due to the higher length of shoots in *D. nigra* induced by BA.

The protein phosphoribosylamine-glycine ligase is associated with N-assimilation in bacterial nitrogen fixation (Resendis-Antonio *et al.,* 2011), and the accumulation of this protein (A0A445E7J0) in shoots from cotyledonary nodal segments BA-treated can promote the better elongation of *D. nigra* shoots altering nitrogen metabolism. In addition to nitrogen, the carbohydrate metabolism is essential for energy supply in plants. The phosphoenolpyruvate carboxylase protein is an important cytosolic enzyme situated at a crucial branch point of plant carbohydrate metabolism (Scholl *et al*., 2020). Phosphoenolpyruvate carboxylase 2 also fulfills essential non-photosynthetic functions, particularly the replenishment of tricarboxylic acid (TCA) cycle intermediates consumed during biosynthesis and N-assimilation (Scholl *et al.,* 2020). Some developmental or metabolic process that requires these organic acids will benefit from increased carbon flux through the phosphoenolpyruvate carboxylase 2 reaction (Willick *et al.*, 2019). Thus, the up-accumulation of phosphoenolpyruvate carboxylase 2 (A0A445BXQ0) could be relevant for elongation of shoots from cotyledonary nodal segments BA-treated compared to without BA in *D. nigra* (Supplementary Table 1). Other up-accumulated protein in shoots from cotyledonary nodal explants incubated with BA compared to those without BA was the FT-interacting protein (A0A444ZYV6) (Supplementary Table 1). This protein play an essential role in mediating proliferation and differentiation of shoot stem cells in *Arabidopsis* (Liu *et al.,* 2018). FT-interacting protein prevent intracellular trafficking of a key regulator, SHOOTMERISTEMLESS, to the plasma membrane in cells in the peripheral shoot meristem region. This facilitates SHOOTMERISTEMLESS recycling to the nucleus to maintain stem cells and accelerates stem cell differentiation *(Liu et*

al., 2018). In this sense, these proteins may be interesting to throw light on the BA signaling for the promotion of higher shoot elongation in *D. nigra*.

In addition, the dolichyl-diphosphooligosaccharide glycosyltransferase protein is known to be involved with protein glycosylation and protein modification, and participates in biological processes relevant for plant growth and development, such as mechanisms controlling the assembly of cell wall polymers, protein N-linked glycosylation through asparagine and cell growthparticipating in (Lerouxel *et al.*, 2005). An increase in the accumulation of dolichyl-diphosphooligosaccharide-protein glycosyltransferase 48 kDa subunit (A0A445A8R7) protein in shoots from cotyledonary nodal segments BA-treated can be related to the cytokinin promotion on the higher elongation of shoot in *D. nigra*.

The citrate synthase mitochondrial (mtCS) (A0A445EVE9 and A0A445CF35), other protein up-accumulated only in shoots from cotyledonary nodal segments BA-treated. The citrate synthase mitochondrial (mtCS) protein has an enhanced ability to excrete citric acid, the overexpression of mtCS in carrot cells results in better cell growth than wild type cells (Koyama *et al.*, 1999). It appears that the overexpression of citrate synthase in *Arabidopsis* improves growth in phosphorus-limited soils due to the increased excretion of citrate from the roots (Koyama *et al.*, 2000). These evidences may suggest that the increase in accumulation of citrate synthase mitochondrial (mtCS) (A0A445EVE9 and A0A445CF35) proteins in shoots from cotyledonary explants BA-treated can regulate the oxidative metabolism, promoting the elongation of shoots in *D. nigra*.

Other protein up-accumulated, the phosphoribosylamine-glycine ligase chloroplastic (A0A445E7J0), is involved in enzyme in the *de novo* purine biosynthesis pathway (Zhang *et al.,* 2018). Plants can degrade purines and the final products glyoxylate and ammonia are recovered to synthesize organic molecules for new growth (Amarante *et al.,* 2006). The increase on accumulation of this protein maybe involved with biosynthesis of organic molecules necessary to the higher growth of *D. nigra* shoots from cotyledonary nodal segments incubated with BA. The 60S ribosomal protein L35a-3 (A0A444ZT56) observed in *D. nigra* shoots from cotyledonary nodal segments treated with BA (Supplementary Table 1), is a structural constituent of ribosome and has as a biological function cytoplasmic translation and ribosomal large subunit biogenesis (Xiao *et al*., 2019). The eukaryotic ribosome is a complex structure

composed of several ribosomal RNAs and ribosomal proteins (r-proteins) (Taylor *et al*., 2009), which are responsible for protein synthesis necessary for cell growth, division, and development (Barakat *et al.*, 2001). It has been shown that genetic defects in ribosomal components, such as reduction on levels of individual r-proteins, can induce deleterious effects on the development of plants (Barakat *et al.*, 2001). Thus, a higher accumulation of 60S ribosomal protein L35a-3 (A0A444ZT56) could be relevant to maintain higher levels of r-proteins and consequently, higher elongation of *D. nigra* shoots from cotyledonary nodal segments incubated with BA.

The bifuncional dTDP-4-desidrorhamnose 3,5-epimerase/dTDP-4-desidrorhamnose reductase (A0A444Z945) protein was unique in *D. nigra* shoots from cotyledonary nodal segments BA-treated compared to shoots without BA (BA2.5_Cotyledonary/BA0_Cotyledonary) and to shoots from apical nodal segments BA-treated (BA2.5_Cotyledonary/BA2.5_Apical). This protein is involved in the dTDP-L-rhamnose biosynthesis, which is part of carbohydrate metabolism (Watt *et al*., 2004). The analysis of sugar composition and the study of gene expression at different stages of growth indicate that the synthesis of rhamnose-containing glycans is under specific tissue regulation (Martinez *et al.,* 2012). In addition, this protein is also present in the cell wall organization process, which can be an interesting factor to be associated with the differential elongation of *D. nigra* shoots incubated with BA.

Some proteins identified were associated with the type of explant, being more accumulated in shoots from cotyledonary nodal segments compared to apical, both with (BA2.5_Cotyledonary/BA2.5_apical comparison) or without BA (BA0_cotyledonary/BA0_apical comparison) (Supplementary Table 1). The malate dehydrogenase 2 protein catalyze a reversible NAD-dependent dehydrogenase reaction involved in central metabolism and redox homeostasis between organelle compartments (Tomaz *et al.,* 2010), and is also required for maintenance of photosynthetic rates under photorespiratory conditions (Cousins *et al.*, 2008). The ATP synthase subunit beta, chloroplastic (A0A445AH22) can be found in the plasma membrane of eubacteria, in thylakoids of chloroplast and in the inner mitochondrial membrane of eukaryotic cells (Mulkidjanian *et al.*, 2009). In loss of ATP synthase assembly defective in β subunit results in mitochondria deprived of cristae structures and when ATP2 was silenced cells show a peculiar organization of thylakoid stacks in the chloroplast with a reduced number of lamellae, as compared to the wild-type

harming plant development (Lapaille *et al.,* 2010). An up-accumulation of dehydrogenase 2 (peroxisome) (A0A445DRP9) and ATP synthase subunit beta, chloroplastic (A0A445AH22) in shoots of *D. nigra* from cotyledonary nodal segments, treated or not with BA, shows that this type of explant has a better regulation of redox homeostasis between organelle compartments and on ATP biosynthesis, an essential process for growth.

Rooting is a critical phase of *in vitro* propagation and overcome this phase can ensures the successful of process (Zeng *et al.*, 2019). Usually, exogenous auxins are necessary to promote root induction in some species, as observed for *Malus domestica* rootstocks (Meng *et al.*, 2019) and *Populus alba* (Zeng *et al.*, 2019). *Dalbergia nigra* has the possibility of propagation using the cutting method, however, reaching rates below 50%. Using the nebulization technique, it was possible to reach 42% of rooting, while only 32.5% of cuttings rooted in natural conditions. In both cases, the treatment used was 5000 ppm of IBA for juvenile cuttings up to one year old (Fonseca et al., 1991). In our work, the *ex vitro* rooting was efficient for plantlets production using shoots from both type of explants, with no necessity of IBA use (Fig. 6a and 6b) IBA was also not necessary to use for root induction and number of root in *Prunus persica* and *Prunus davidiana* (Zhou *et al.,* 2010).Thus, it was possible to reach a rate higher than 80% of rooting, showing better results when compared to the cutting technique used in the species.

Moreover, the balance between auxins and cytokinins is important for root induction (Jing and Strader, 2019; Růzǐčka *et al.*, 2009), and differences in rooting may occur due to the accumulation of cytokinins in plant tissues (da Costa *et al.*, 2013). In the present work, a comparison between shoots multiplied in culture medium without (control) and with 2.5 µM BA was performed to analyse if the shoot multiplication in BA concentrations affects the induction of root. The use of 2.5 µM BA is essential for shoot elongation, however the treatments with cytokinin significantly affect the root induction and number of roots in *D. nigra* compared to treatment without BA (Fig. 8c and 8d). In this way, we can infer that the balance between auxins and cytokinins influences *D. nigra* shoot rooting. This balance adjustment was also considered important in *Ceropegia bulbosa*, where different concentrations of cytokinin (BA) and auxins such as naphthalene acetic acid (NAA) and IBA were tested, demonstrating the importance of crosstalk among hormones (Phulwaria *et al.*, 2013). Unlike, in *Albizia lebbeck* the

use of 250 µM IBA promoted the largest number and higher length of roots from shoots grown under concentrations of the cytokinin thidiazuron (Perveen *et al.*, 2013), showing that endogenous hormone present in the explant that has an important role in plant organogenesis (Pal *et al.*, 2012; Zeng *et al.*, 2019). Thus, we can infer that the results obtained for rooting depends on the species and concentrations of PGRs to root induction, as well as, those used in the shoot multiplication step.

2.6. Conclusions

The WPM culture medium promoted the best seedling growth. The addition of BA is necessary to longer shoot lengths for both types of explants. BA addition promoted an increase in endogenous Put content, which induced the higher growth of shoots in both explants. Some proteins involved with central metabolism, redox homeostasis, maintenance of photosynthetic rates and carbon flow during photorespiration conditions were differentially accumulated in shoots from cotyledonary nodal explan, with and without BA, and are important for the growth of these shoots. *Ex vitro* rooting of shoots can be performed without IBA in both types of explants. This work enabled the production of seedlings that were directed to an ecological reserve. Furthermore, first results demonstrating the involvement of PAs and proteomic profile in the development of *D. nigra* shoots.

2.7. Acknowledgements

Acknowledgements Funding for this work was provided by the Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) (444453/2014-8 and 307596/2016-8) and the Fundação Carlos Chagas Filho de Amparo à Pesquisa no Estado do Rio de Janeiro (FAPERJ) (E26/202.969/2016; 202.533/2019). This study was also financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior—Brazil (CAPES)—Finance Code 001. LSP, KRS and VPMA acknowledge the scholarship funded by FAPERJ.

2.8. References

Aguiar, F., Tavares, A.R., Kanashiro, S., Baptista, P., Augusto, N. (2010) Germinação de sementes de *Dalbergia nigra* (Vell.) Allemao. Ciência e Agrotecnologia. 34(1), 1624–1629.

Ahanger, M.A., Aziz, U., Sahli, A. Al, Alyemeni, M.N., Ahmad, P. (2020) Combined Kinetin and Spermidine Treatments Ameliorate Growth and Photosynthetic Inhibition in *Vigna angularis* by Up-Regulating Antioxidant and Nitrogen Metabolism under Cadmium Stress. Biomolecules. 10(1), 1–21.

Ahmad, N., Javed, S. Bin, Khan, M.I., Anis, M. (2013) Rapid plant regeneration and analysis of genetic fidelity in micropropagated plants of *Vitex trifolia*: An important medicinal plant. Acta Physiologiae Plantarum. 35(8), 2493–2500.

Ahmad, P., Abdel Latef, A.A., Abd-Allah, E.F., Hashem, A., Sarwat, M., Anjum, N.A., Gucel, S. (2016) Calcium and potassium supplementation enhanced growth, osmolyte secondary metabolite production, and enzymatic antioxidant machinery in cadmium-exposed chickpea (*Cicer arietinum* L.). Frontiers in Plant Science. 7(APR2016), 1–12.

Amarante, L. do, Lima, J.D., Sodek, L. (2006) Growth and stress conditions cause similar changes in xylem amino acids for different legume species. Environmental and Experimental Botany. 58(1–3), 123–129.

Anis, M., Husain, M.K., Faisal, M., Shahzad, A., Ahmad, N., Siddique, I., Khan, H. (2009) *In vitro* approaches for plant regeneration and conservation of some potential medicinal plants. Molecular Markers Their Role in Crop Productivity. (November), 397–410.

Aragão, V.P.M., Navarro, B.V., Silva, A.T. da, Silveira, V., Santa-Catarina, C. (2017) Micropropagation of *Cariniana legalis* (Martius) O. Kuntze, an endangered hardwood tree from the Brazilian Atlantic Forest. Plant Cell Culture & Micropropagation. 13(2), 41–50.

Aragão, V.P.M., Reis, R.S., Silveira, V., Santa-Catarina, C. (2017) Putrescine promotes changes in the endogenous polyamine levels and proteomic profiles to regulate organogenesis in *Cedrela fissilis* Vellozo (Meliaceae). Plant Cell, Tissue and Organ Culture. 130(3), 495–505.

Aragão, V.P.M., de Souza Ribeiro, Y.R., Reis, R.S., Macedo, A.F., Floh, E.I.S., Silveira, V., Santa-Catarina, C. (2016) *In vitro* organogenesis of *Cedrela fissilis* Vell. (Meliaceae): the involvement of endogenous polyamines and carbohydrates on shoot development. Plant Cell, Tissue and Organ Culture. 124(3), 611–620.

Aragão, V.P.M., Trindade, B.M.C., Reis, R.S., Silveira, V., Santa-Catarina, C. (2019) Storage time affects the germination and proteomic profile of seeds of *Cariniana legalis* (Mart.) O. Kuntze (Lecythidaceae), an endangered tree species native to the Brazilian Atlantic Forest. Revista Brasileira de Botanica. 42(3), 407–419.

Barakat, A., Szick-Miranda, K., Chang, I.F., Guyot, R., Blanc, G., Cooke, R., Delseny,

M., Bailey-Serres, J. (2001) The organization of cytoplasmic ribosomal protein genes in the arabidopsis genome. Plant Physiology. 127(2), 398–415.

Baron, K., Stasolla, C. (2008) The role of polyamines during *in vivo* and *in vitro* development. In Vitro Cellular and Developmental Biology - Plant. 44(5), 384–395.

Botini, N., Almeida, F.A., Cruz, K.Z.C.M., Reis, R.S., Vale, E.M., Garcia, A.B., Santa-Catarina, C., Silveira, V. (2021) Stage-specific protein regulation during somatic embryo development of *Carica papaya* L. 'Golden.' Biochimica et Biophysica Acta - Proteins and Proteomics. 1869(2), 140561.

Bunn, E., Turner, S.R., Dixon, K.W. (2011) Biotechnology for saving rare and threatened flora in a biodiversity hotspot. *In Vitro* Cellular & Developmental Biology - Plant. 47, 188–200.

Cánovas, F.M., Avila, C., Cantón, F.R., Cañas, R.A., De La Torre, F. (2007) Ammonium assimilation and amino acid metabolism in conifers. Journal of of Experimental Botany , *58* (9), 2307-2318.

Chen, D., Ren, Y., Deng, Y., Zhao, J. (2010) Auxin polar transport is essential for the development of zygote and embryo in *Nicotiana tabacum* L. and correlated with ABP1 and PM H+-ATPase activities. Journal of Experimental Botany. 61(6), 1853–1867.

Chiew, F.C., Othman, Y.R. (2006) In vitro Direct Shoot Organogenesis and Regeneration of Plantlets from Leaf Explants of Sentang (*Azadirachta excelsa*). Biotechnology. 5(3), 337–340.

Corredor-Prado, J.P., De Conti, D., Cangahuala-Inocente, G.C., Guerra, M.P., Vesco, L.L.D., Pescador, R. (2016) Proteomic analysis in the induction of nodular cluster cultures in the bromeliad *Vriesea reitzii* Leme and Costa. Acta Physiologiae Plantarum. 38(130).

Cousins, A.B., Pracharoenwattana, I., Zhou, W., Smith, S.M., Badger, M.R. (2008) Peroxisomal malate dehydrogenase is not essential for photorespiration in arabidopsis but its absence causes an increase in the stoichiometry of photorespiratory CO2 release. Plant Physiology. 148(2), 786–795.

da Costa, C.T., de Almeida, M.R., Ruedell, C.M., Schwambach, J., Maraschin, F.S., Fett-Neto, A.G. (2013) When stress and development go hand in hand: Main hormonal controls of adventitious rooting in cuttings. Frontiers in Plant Science. 4(MAY), 1–19.

Damerval, C., De Vienne, D., Zivy, M., Thiellement, H. (1986) Technical improvements in two-dimensional electrophoresis increase the level of genetic variation detected in wheat-seedling proteins. Electrophoresis. 7(1), 52–54.

Debiasi C., B.C.F.G.P.P.L.I. (2007) Study of polyamines in the morphogenesis *in vitro* of *Hemerocallis* sp. Ciência Rural. 37(4), 1014–1020.

Dias, P.C., Oliveira, L.S. de, Xavier, A., Wendling, I. (2012) Estaquia e miniestaquia

de espécies florestais lenhosas do Brasil. Pesquisa Florestal Brasileira. 32(72), 453–462.

Distler, U., Kuharev, J., Navarro, P., Levin, Y., Schild, H., Tenzer, S. (2014) Drift time-specific collision energies enable independent acquisition proteomics. Nature Methods. 11(2), 167–177.

De La Torre, F., Cañas, R.A., Pascual, M.B., Avila, C., Cánovas, F.M. (2014) Plastidic aspartate aminotransferases and the biosynthesis of essential amino acids in plants. Journal of Experimental Botany. 65(19), 5527–5534.

Dutra, N.T., Silveira, V., de Azevedo, I.G., Gomes-Neto, L.R., Façanha, A.R., Steiner, N., Guerra, M.P., Floh, E.I.S., Santa-Catarina, C. (2013) Polyamines affect the cellular growth and structure of pro-embryogenic masses in *Araucaria angustifolia* embryogenic cultures through the modulation of proton pump activities and endogenous levels of polyamines. Physiologia Plantarum. 148(1), 121–132.

Fermino, P.C.P., Scherwinski-Pereira, J.E. (2012) Germinação e propagação *in vitro* de cerejeira (*Amburana acreana* (Ducke) A.C.Smith - Fabaceae). Ciência Florestal. 22(1), 1–9.

Fonseca, C. eduardo, Sperândio, J.P., Corrêa, M.P.F., Bueno, D.M., Lima, R. (1991) Propagação Vegetativa do Jacarandá-da-Baía através da estaquia. Pesquisa Agropecuária Brasileira. 26(1), 31–37.

Ghosh, S., Pal, A. (2013) Proteomic analysis of cotyledonary explants during shoot organogenesis in *Vigna radiata*. Plant Cell Tissue and Organ Culture. 115, 55–68.

Giri, C.C., Shyamkumar, B., Anjaneyulu, C. (2004) Progress in tissue culture, genetic transformation and applications of biotechnology to trees: an overview. Trees - Structure and Function. 18(2), 115–135.

Gündeşli, M.A., Kafkas, S., Zarifikhosroshahi, M., Kafkas, N.E. (2019) Role of endogenous polyamines in the alternate bearing phenomenon in pistachio. Turkish Journal of Agriculture and Forestry. 43(3), 265–274.

Gupta, A.K., Harish, Rai, M.K., Phulwaria, M., Agarwal, T., Shekhawat, N.S. (2014) *In vitro* propagation, encapsulation, and genetic fidelity analysis of *Terminalia arjuna*: A cardioprotective medicinal tree. Applied Biochemistry and Biotechnology. 173(6), 1481–1494.

Hazubska-Przybył, T. (2019) Propagation of Juniper Species by Plant Tissue Culture: A Mini-Review. Forests. 10(11), 1028.

Heringer, A.S., Barroso, T., Macedo, A.F., Santa-Catarina, C., Henrique, G., Ferreira, M., Iochevet, E., Floh, S. (2015) Label-Free Quantitative Proteomics of Embryogenic and Non-Embryogenic Callus during Sugarcane Somatic Embryogenesis. Plos One, 1–23.

Heringer, A.S., Reis, R.S., Passamani, L.Z., de Souza-Filho, G.A., Santa-Catarina, C.,

Silveira, V. (2017) Comparative proteomics analysis of the effect of combined red and blue lights on sugarcane somatic embryogenesis. Acta Physiologiae Plantarum. 39(2), 52.

Hussain, S.A., Ahmad, N., Anis, M. (2018) Synergetic effect of TDZ and BA on minimizing the post-exposure effects on axillary shoot proliferation and assessment of genetic fidelity in *Rauvolfia tetraphylla* (L.). Rendiconti Lincei. 29(1), 109–115.

Jing, H., Strader, L.C. (2019) Interplay of auxin and cytokinin in lateral root development. International Journal of Molecular Sciences. 20(3).

Kodym, A., Leeb, C.J. (2019) Back to the roots : protocol for the photoautotrophic micropropagation of medicinal *Cannabis*. Plant Cell, Tissue and Organ Culture (PCTOC). 138(2), 399–402.

Koyama, H., Kawamura, A., Kihara, T., Hara, T., Takita, E., Shibata, D. (2000) Overexpression of mitochondrial citrate synthase in *Arabidopsis thaliana* improved growth on a phosphorus-limited soil. Plant and Cell Physiology. 41(9), 1030–1037.

Koyama, H., Takita, E., Kawamura, A., Hara, T., Shibata, D. (1999) Over expression of mitochondrial citrate synthase gene improves the growth of carrot cells in *Al-phosphate medium*. Plant and Cell Physiology. 40(5), 482–488.

Kusano, T., Berberich, T., Tateda, C., Takahashi, Y. (2008) Polyamines: essential factors for growth and survival. Planta. 228(3), 367–381.

Lapaille, M., Thiry, M., Perez, E., González-Halphen, D., Remacle, C., Cardol, P. (2010) Loss of mitochondrial ATP synthase subunit beta (Atp2) alters mitochondrial and chloroplastic function and morphology in *Chlamydomonas*. Biochimica et Biophysica Acta - Bioenergetics. 1797(8), 1533–1539.

Lerin, J., Aragão, V.P.M., Reis, R.S., Silveira, V., Santa-Catarina, C. (2019) Proteomic profile and polyamine contents are modulated by light source to promote *in vitro* shoot development in *Cariniana legalis* (Martius) O. Kuntze (Lecythidaceae). Plant Cell, Tissue and Organ Culture. 137(2), 329–342.

Liu, L., Li, C., Song, S., Teo, Z.W.N., Shen, L., Wang, Y., Jackson, D., Yu, H. (2018) FTIP-Dependent STM Trafficking Regulates Shoot Meristem Development in *Arabidopsis*. Cell Reports. 23(6), 1879–1890.

Martinez, V., Ingwers, M., Smith, J., Glushka, J., Yang, T., Bar-Peled, M. (2012) Biosynthesis of UDP-4-keto-6-deoxyglucose and UDP-rhamnose in pathogenic fungi *Magnaporthe grisea* and *Botryotinia fuckeliana*. Journal of Biological Chemistry. 287(2), 879–892.

McAllister, C.H., Wolansky, M., Good, A.G. (2016) The impact on nitrogen-efficient phenotypes when aspartate aminotransferase is expressed tissue-specifically in *Brassica napus*. New Negatives in Plant Science. 3–4, 1–9.

Meng, Y., Xing, L., Li, K., Wei, Y., Wang, H., Mao, J., Dong, F., Ma, D., Zhang, Z., Han,

M., Zhao, C., Tahir, M.M., Zhang, D. (2019) Genome-wide identification, characterization and expression analysis of novel long non-coding RNAs that mediate IBA-induced adventitious root formation in apple rootstocks. Plant Growth Regulation. 87(2), 287–302.

Mitrovi, A.Ć., Janoševi, D.Ć., Budimir, S., Pristov, J.B.Ć. (2012) Changes in antioxidative enzymes activities during *Tacitus bellus* direct shoot organogenesis. Biologia Plantarum. 56(2), 357–361.

Mujib, A. (2005) *In vitro* regeneration of sandal (Santalum album L.) from leaves. Turkish Journal of Botany. 29(1), 63–67.

Mulkidjanian, A.Y., Galperin, M.Y., Koonin, E. V. (2009) Co-evolution of primordial membranes and membrane proteins. Trends in Biochemical Sciences. 34(4), 206–215.

Murashige, T., Skoog, F. (1962) A Revised Medium for Rapid Growth and Bio Assays with *Tobacco* Tissue Cultures. Physiologia Plantarum. 15(3), 473–497.

Nanjo, Y., Skultety, L., Hajduch, M., Komatsu, S. (2012) Mass Spectrometry-Based Analysis of Proteomic Changes in the Root Tips of Flooded Soybean Seedlings. Journal of Geophysical Research. 11, 372–385.

Oliveira, T. dos R., Aragão, V.P.M., Moharana, K.C., Fedosejevs, E., do Amaral, F.P., Sousa, K.R., Thelen, J.J., Venâncio, T.M., Silveira, V., Santa-Catarina, C. (2020) Light spectra affect the *in vitro* shoot development of *Cedrela fissilis* Vell. (Meliaceae) by changing the protein profile and polyamine contents. Biochimica et Biophysica Acta - Proteins and Proteomics. 1868(12), 140529.

Pacurar, D.I., Perrone, I., Bellini, C. (2014) Auxin is a central player in the hormone cross-talks that control adventitious rooting. Physiologia Plantarum. 151(1), 83–96.

Pal, A.K., Acharya, K., Ahuja, P.S. (2012) Endogenous auxin level is a critical determinant for *in vitro* adventitious shoot regeneration in potato (Solanum tuberosum L.). Journal of Plant Biochemistry and Biotechnology. 21(2), 205–212.

Parimalan, R., Giridhar, P., Ravishankar, G.A. (2011) Enhanced shoot organogenesis in *Bixa orellana* L. in the presence of putrescine and silver nitrate. Plant Cell, Tissue and Organ Culture. 105(3), 285–290.

Patel, A.K., Phulwaria, M., Rai, M.K., Gupta, A.K., Shekhawat, S., Shekhawat, N.S. (2014) Scientia Horticulturae *In vitro* propagation and *ex vitro* rooting of *Caralluma edulis* (Edgew .) Benth . & Hook . f .: An endemic and endangered edible plant species of the Thar Desert. Scientia Horticulturae. 165, 175–180.

Perveen, S., Anis, M., Aref, I.M. (2013) Resource communication. *In vitro* plant regeneration of *Albizia lebbeck* (L.) Benth. from seed explants. Forest Systems. 22(2), 241–248.

Phillips, G.C., Garda, M. (2019) Plant tissue culture media and practices : an overview.

In Vitro Cellular & Developmental Biology - Plant. 55, 242–257.

Phulwaria, M., Shekhawat, N.S., Rathore, J.S., Singh, R.P. (2013) An efficient *in vitro* regeneration and *ex vitro* rooting of *Ceropegia bulbosa* Roxb. A threatened and pharmaceutical important plant of Indian Thar Desert. Industrial Crops and Products. 42(1), 25–29.

Pieruzzi, F.P., Dias, L.L.C., Balbuena, T.S., Santa-Catarina, C., Santos, A.L.W. dos, Floh, E.I.S. (2011) Polyamines, IAA and ABA during germination in two recalcitrant seeds: *Araucaria angustifolia* (Gymnosperm) and *Ocotea odorifera* (Angiosperm). Annals of Botany. 108(2), 337–345.

Pijut, P.M., Beasley, R.R., Lawson, S.S., Palla, K.J., Stevens, M.E., Wang, Y. (2012) *In vitro* propagation of tropical hardwood tree species – A review (2001-2011). Propagation of Ornamental Plants. 12(1), 25–51.

Pijut, P.M., Woeste, K.E., Vengadesan, G., Michler, C.H. (2007) Technological advances in temperate hardwood tree improvement including breeding and molecular marker applications. *In Vitro* Cellular & Developmental Biology - Plant. 43(4), 283–303.

Ranaweera, K.K., Gunasekara, M.T.K., Eeswara, J.P. (2013) Scientia Horticulturae *Ex vitro* rooting : A low cost micropropagation technique for Tea (*Camellia sinensis* (L .) O . Kuntz) hybrids. Scientia Horticulturae. 155, 8–14.

Rancour, D.M., Dickey, C.E., Park, S., Bednarek, S.Y. (2002) Characterization of AtCDC48. Evidence for multiple membrane fusion mechanisms at the plane of cell division in plants. Plant Physiology. 130(3), 1241–1253.

Reis, R.S., Vale, E. de M., Heringer, A.S., Santa-Catarina, C., Silveira, V. (2016) Putrescine induces somatic embryo development and proteomic changes in embryogenic callus of sugarcane. Journal of Proteomics. 130(1), 170–179.

Resendis-Antonio, O., Hernández, M., Salazar, E., Contreras, S., Batallar, G.M., Mora, Y., Encarnación, S. (2011) Systems biology of bacterial nitrogen fixation: High-throughput technology and its integrative description with constraint-based modeling. BMC Systems Biology. 5.

Růzička, K., Šimášková, M., Duclercq, J., Petrášek, J., Zažímalová, E., Simon, S., Friml, J., Van Montagu, M.C.E., Benková, E. (2009) Cytokinin regulates root meristem activity via modulation of the polar auxin transport. Proceedings of the National Academy of Sciences of the United States of America. 106(11), 4284–4289.

Sahai, A., Shahzad, A. (2013) High frequency *in vitro* regeneration system for conservation of *Coleus forskohlii*: a threatened medicinal herb. Acta Physiologiae Plantarum. 35(2), 473–481.

Sahu, J., Khan, S., Sahu, R.K., Roy, A. (2014) Micropropagation of *Dalbergia sissoo* Roxb. through tissue culture technique. Pakistan journal of biological sciences :

Santa-Catarina, C., Maciel, S. da C., Pedrotti, E.L. (2001) Germinação in vitro e

embriogênese somática a partir de embriões imaturos de canela sassafrás (*Ocotea odorifera* Mez). Revista Brasileira de Botânica. 24(4), 501–510.

Santa-Catarina, C., Silveira, V., Balbuena, T.S., Viana, A.M., Estelita, M.E.M., Handro, W., Floh, E.I.S. (2006) IAA, ABA, polyamines and free amino acids associated with zygotic embryo development of *Ocotea catharinensis*. Plant Growth Regulation. 49(2–3), 237–247.

Santa-Catarina, C., Silveira, V., Scherer, G.F.E., Floh, E.I.S. (2007) Polyamine and nitric oxide levels relate with morphogenetic evolution in somatic embryogenesis of *Ocotea catharinensis*. Plant Cell, Tissue and Organ Culture. 90(1), 93–101.

Scholl, J., Dengler, L., Bader, L., Forchhammer, K. (2020) Phosphoenolpyruvate carboxylase from the cyanobacterium Synechocystis sp. PCC 6803 is under global metabolic control by PII signaling. Molecular Microbiology. (February), 1–16.

Shukla, S., Shukla, S.K., Mishra, S.K. (2009) *In vitro* plant regeneration from seedling explants of Stereospermum personatum D . C .: a medicinal tree. Trees. 23, 409–413.

Silveira, V., Santa-Catarina, C., Tun, N.N., Scherer, G.F.E., Handro, W., Guerra, M.P., Floh, E.I.S. (2006) Polyamine effects on the endogenous polyamine contents, nitric oxide release, growth and differentiation of embryogenic suspension cultures of *Araucaria angustifolia* (Bert.) O. Ktze. Plant Science. 171(1), 91–98.

Stevens, M.E., Pijut, P.M. (2018) Rapid in vitro shoot multiplication of the recalcitrant species *Juglans nigra* L. *In Vitro* Cellular and Developmental Biology - Plant. 54(3), 309–317.

Taylor, D.J., Devkota, B., Huang, A.D., Topf, M., Narayanan, E., Sali, A., Harvey, S.C., Frank, J. (2009) Comprehensive Molecular Structure of the Eukaryotic Ribosome. Structure. 17(12), 1591–1604.

Tiburcio, A.F., Altabella, T., Bitrián, M., Alcázar, R. (2014) The roles of polyamines during the lifespan of plants: from development to stress. Planta. 240(1), 1–18.

Tomaz, T., Bagard, M., Pracharoenwattana, I., Lindén, P., Lee, C.P., Carroll, A.J., Ströher, E., Smith, S.M., Gardeström, P., Millar, A.H. (2010) Mitochondrial malate dehydrogenase lowers leaf respiration and alters photorespiration and plant growth in *Arabidopsis*. Plant Physiology. 154(3), 1143–1157.

Tsugeki, R., Terada, S. (2015) The *Arabidopsis* ortholog of the DEAH-box ATpase Prp16 influences auxin-mediated development. Plant Signaling and Behavior. 10(10), 23–26.

Watt, G., Leoff, C., Harper, A.D., Bar-Peled, M. (2004) A bifunctional 3,5-epimerase/4-keto reductase for nucleotide-rhamnose synthesis in arabidopsis. Plant Physiology. 134(4), 1337–1346.

White, J.T., Cato, T., Deramchi, N., Gabunilas, J., Roy, K.R., Wang, C., Chanfreau, G.F., Clarke, S.G. (2019) Protein Methylation and Translation: Role of Lysine

Modification on the Function of Yeast Elongation Factor 1A. Biochemistry. 58(49), 4997–5010.

Willick, I.R., Plaxton, W.C., Lolle, S.J., Macfie, S.M. (2019) Transcriptional and post-translational upregulation of phosphoenolpyruvate carboxylase in *Arabidopsis thaliana* (L. Heynh) under cadmium stress. Environmental and Experimental Botany. 164(April), 29–39.

Wybouw, B., De Rybel, B. (2019) Cytokinin – A Developing Story. Trends in Plant Science. 24(2), 177–185.

Xiao, R., Li, L., Ma, Y. (2019) A label-free proteomic approach differentiates between conventional and organic rice. Journal of Food Composition and Analysis. 80(April), 51–61.

Yan, H., Liang, C., Yang, L., Li, Y. (2010) *In vitro* and *ex vitro* rooting of Siratia grosvenorii , a traditional medicinal plant. Acta Physiologiae Plantarum. 32, 115–120.

Zeng, Q., Han, Z., Kang, X. (2019) Adventitious shoot regeneration from leaf , petiole and root explants in triploid (*Populus alba* × *P . glandulosa*) × *P . tomentosa.* Plant Cell, Tissue and Organ Culture (PCTOC). 138(1), 121–130.

Zhang, Ting, Feng, P., Li, Yunfeng, Yu, P., Yu, G., Sang, X., Ling, Y., Zeng, X., Li, Yidan, Huang, J., Zhang, Tianquan, Zhao, F., Wang, N., Zhang, C., Yang, Z., Wu, R., He, G. (2018) VIRESCENT-ALBINO LEAF 1 regulates leaf colour development and cell division in rice. Journal of Experimental Botany. 69(20), 4791–4804.

Zhou, H., Li, M., Zhao, X., Fan, X., Guo, A. (2010) Plant regeneration from *in vitro* leaves of the peach rootstock “Nemaguard” (*Prunus persica* × *P. davidiana*). Plant Cell, Tissue and Organ Culture. 101(1), 79–87.

2.9. Supplementary table 1. Differentially accumulated proteins identified in shoots of Dalbergia nigra comparing the effects of BA (by the comparisons BA2.5_Apical/BA0_Apical and BA2.5_Cotyledonary/BA0_Cotyledoenary) and type of explant on shoot development(by the comparisons BA2.5_Cotyledonary/BA2.5_Apical and BA0_Cotyledonary/BA0_Apical)

Accession	Reported peptides	Description	Differential accumulation			
			BA2.5_Apical/ BA0_Apical	BA2.5_Cotyledonary/ BA0_Cotyledonary	BA2.5_Cotyledonary/ BA2.5_Apical	BA0_Cotyledonary/ BA0_Apical
A0A445BSX1	5	photosystem II 32 kDa protein	UP	UP	UP	UP
A0A444YLN0	11	26S proteasome regulatory subunit 7	UP	UP	UP	UNCHANGED
A0A444Y820	3	histone H2A	UP	UP	UP	UNCHANGED
A0A445DYS8	3	universal stress protein PHOS32	UP	UP	UP	UNCHANGED
A0A444YGB9	4	ATP-dependent RNA helicase DEAH7	UP	UP	UP	UNCHANGED
A0A444Y7Y0	22	elongation factor 1-alpha	UP	UP	UNCHANGED	UNCHANGED
A0A444Y3F0	7	glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic	UP	UP	UNCHANGED	UNCHANGED
A0A444YKD2	7	probable aldo-keto reductase 1	UP	UP	UNCHANGED	UNCHANGED
A0A445A0E8	7	glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic	UP	UP	UNCHANGED	UNCHANGED
A0A445A3Z4	28	dolichol kinase EVAN isoform X1	UP	UP	UNCHANGED	UNCHANGED
A0A445A5D9	3	aldehyde dehydrogenase family 2 member C4	UP	UP	UNCHANGED	UNCHANGED
A0A445DLN8	16	peroxisomal (S)-2-hydroxy-acid oxidase	UP	UP	UNCHANGED	UNCHANGED
A0A445C479	7	protein argonaute 4	UP	UP	UNCHANGED	UNCHANGED
A0A445BGF3	21	pyruvate kinase 1, cytosolic	UP	UP	UNCHANGED	UNCHANGED
A0A445A993	2	calreticulin-3	UP	UP	UNCHANGED	UNCHANGED
A0A444ZKM6	9	cationic peroxidase 1-like	UP	UP	UNCHANGED	UNCHANGED
A0A444Y8T2	11	seed linoleate 9S-lipoxygenase-2	UP	UP	UNCHANGED	UNCHANGED
A0A445DE06	2	glycine-rich RNA-binding protein GRP1A	UP	UP	UNCHANGED	UNCHANGED
A0A444ZU45	4	eukaryotic peptide chain release factor GTP-binding subunit ERF3A isoform X1	UP	UP	UNCHANGED	UNCHANGED
A0A444Z3W1	12	cell division cycle protein 48 homolog	UP	UP	UNCHANGED	UNCHANGED
A0A444WNT6	7	probable aldo-keto reductase 2	UP	UP	UNCHANGED	UNCHANGED
A0A445EGE3	7	40S ribosomal protein SA isoform X1	UP	UP	UNCHANGED	UNCHANGED
A0A445DTN4	23	tubulin beta-1 chain	UP	UP	UNCHANGED	UNCHANGED
A0A445BBS5	15	pyruvate decarboxylase 1	UP	UP	UNCHANGED	UNCHANGED
A0A445EVE4	4	glucose-6-phosphate/phosphate translocator 1, chloroplastic	UP	UP	UNCHANGED	UNCHANGED
A0A445BH28	3	probable glutathione S-transferase	UP	UP	UNCHANGED	UNCHANGED
A0A444YIE4	18	sucrose synthase 2	UP	UP	UNCHANGED	UNCHANGED
A0A445CKC1	9	protein FAR1-RELATED SEQUENCE 5-like	UP	UP	UNCHANGED	UNCHANGED

A0A445EE69	6	glutathione S-transferase L3	UP	UP	UNCHANGED	UNCHANGED
A0A445C0I2	2	beta-glucosidase 12-like	UP	UP	UNCHANGED	UNCHANGED
A0A445E7V8	13	40S ribosomal protein S2-4	UP	UP	UNCHANGED	UNCHANGED
A0A445CD99	3	chlorophyll a-b binding protein CP26, chloroplastic-like	UP	UP	UNCHANGED	UNCHANGED
A0A445B7R0	8	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	UP	UP	UNCHANGED	UNCHANGED
A0A445AFG1	9	60S ribosomal protein L23	UP	UP	DOWN	UNCHANGED
A0A445A989	2	linoleate 13S-lipoxygenase 2-1, chloroplastic	UP	UP	UNCHANGED	DOWN
A0A445E6U4	6	40S ribosomal protein S23	UP	UP	UNCHANGED	DOWN
A0A444XPT6	8	probable aldo-keto reductase 1	UP	UP	UNCHANGED	DOWN
A0A445ALI9	10	glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform	UP	UP	UNCHANGED	DOWN
A0A445DHP6	5	peroxidase 16	UP	UP	UNCHANGED	DOWN
A0A444ZAV9	9	malate dehydrogenase, glyoxysomal	UP	UP	UNCHANGED	DOWN
A0A445B4C1	12	aspartate aminotransferase 1	UP	UP	UNCHANGED	DOWN
A0A445EBP2	10	heme-binding-like protein At3g10130, chloroplastic	UP	UP	UNCHANGED	DOWN
A0A445AV80	7	probable xyloglucan endotransglucosylase/hydrolase protein 23	UP	UP	DOWN	DOWN
A0A445BUY6	19	eukaryotic initiation factor 4A-10	UP	UP	DOWN	DOWN
A0A444Z6T1	6	ADP-ribosylation factor	UP	UP	DOWN	DOWN
A0A444ZDQ5	3	Peroxidase 15	Unique BA2.5_Apical	UP	UNCHANGED	Unique BA0_Cotyledonary
A0A445CFP3	27	eukaryotic initiation factor 4A-15	Unique BA0_Apical	UP	Unique BA2.5_Cotyledonary	DOWN
A0A444XX54	5	elongation factor 1-gamma	UNCHANGED	UP	UP	UNCHANGED
A0A444XUY6	29	transketolase, chloroplastic	UNCHANGED	UP	UP	UNCHANGED
A0A445D9X3	3	glycine--tRNA ligase, mitochondrial 1	UNCHANGED	UP	UP	UNCHANGED
A0A444ZT36	3	polygalacturonase inhibitor 2	UNCHANGED	UP	UP	UNCHANGED
A0A445ER05	2	rhicadhesin receptor	UNCHANGED	UP	UP	UNCHANGED
A0A444ZRH3	4	fasciclin-like arabinogalactan protein 11	UNCHANGED	UP	UP	UNCHANGED
A0A444ZDN9	2	peroxidase A2	UNCHANGED	UP	UP	UNCHANGED
A0A445AFH3	6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	UNCHANGED	UP	UP	UNCHANGED
A0A445C009	3	MLP-like protein 34	UNCHANGED	UP	UP	UNCHANGED
A0A444WYK7	3	ras-related protein RABA1f	UNCHANGED	UP	UP	UNCHANGED
A0A445BNU6	13	seed linoleate 9S-lipoxygenase-3	UNCHANGED	UP	UP	UNCHANGED
A0A445D565	5	NADH-plastoquinone oxidoreductase subunit I	UNCHANGED	UP	UP	UNCHANGED
A0A445B0H8	5	betaine aldehyde dehydrogenase 1, chloroplastic	UNCHANGED	UP	UP	UNCHANGED
A0A445C9G1	2	aspartyl protease AED3	UNCHANGED	UP	UP	UNCHANGED
A0A445A437	2	bifunctional nitrilase/nitrile hydratase NIT4A	UNCHANGED	UP	UP	UNCHANGED
A0A445DAZ1	23	6-phosphogluconate dehydrogenase, decarboxylating 3	UNCHANGED	UP	UP	UNCHANGED

A0A444YZP2	3	hexokinase-1	UNCHANGED	UP	UP	UNCHANGED
A0A444X9R4	4	peroxidase 44-like	UNCHANGED	UP	UP	UNCHANGED
A0A444YMQ2	14	probable mediator of RNA polymerase II transcription subunit 37c	UNCHANGED	UP	UP	UNCHANGED
A0A445C6Y4	16	ubiquitin-activating enzyme E1 1	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444WXS0	31	heat shock 70 kDa protein, mitochondrial	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444WY58	23	quinone oxidoreductase PIG3 isoform X2	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444ZUU5	16	UDP-glucose 6-dehydrogenase 4	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444ZBG5	7	nitrile-specifier protein 5	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444WUY4	17	phosphoserine aminotransferase 2, chloroplastic-like	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445BGZ8	27	chaperonin CPN60-2, mitochondrial	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445AD89	2	hydroquinone glucosyltransferase	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444Y833	7	protein disulfide isomerase-like 1-4	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445ALK5	7	phospholipase D alpha 1	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445E5A7	9	40S ribosomal protein S5	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444ZYV6	13	FT-interacting protein	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445D3V5	28	pyruvate kinase, cytosolic isozyme	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445BRP0	22	catalase	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445DBF2	19	UDP-glucose 6-dehydrogenase 1	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445A755	6	prohibitin-1, mitochondrial	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444YP93	22	fructose-bisphosphate aldolase 6, cytosolic	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444XYJ3	5	probable aminotransferase TAT2	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445BVQ0	8	ADP,ATP carrier protein, mitochondrial	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445DL53	13	26S proteasome regulatory subunit 8 homolog A	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444Y4D9	3	stem-specific protein TSJT1	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444YWB9	4	3-oxo-Delta(4,5)-steroid 5-beta-reductase	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445EW60	16	alpha-glucan phosphorylase, H isozyme	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444YS81	14	V-type proton ATPase subunit C	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445EVE9	4	citrate synthase, mitochondrial	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445ADN6	12	NAD-dependent malic enzyme 59 kDa isoform, mitochondrial	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445D0R5	3	aldehyde dehydrogenase family 2 member B7, mitochondrial isoform X2	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445CF35	6	citrate synthase, mitochondrial	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445AKT4	5	ferritin-2, chloroplastic	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445BXQ0	18	phosphoenolpyruvate carboxylase 2	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445DW95	5	cinnamoyl-CoA reductase 1	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445A8R7	4	dolichyl-diphosphooligosaccharide-protein glycosyltransferase 48 kDa subunit	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445DRP4	9	NAD(P)H dehydrogenase (quinone) FQR1	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445E8V9	3	hypothetical protein Ahy_A02g006164 isoform A	UNCHANGED	UP	UNCHANGED	UNCHANGED

A0A445AWN5	6	pathogenesis-related protein 2-like	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445BLL2	15	pyruvate dehydrogenase E1 component subunit beta, mitochondrial	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445BPS9	2	mitochondrial-processing peptidase subunit alpha	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445BE06	15	2-oxoglutarate dehydrogenase, mitochondrial	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445DY27	2	scopoletin glucosyltransferase	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445BPL8	3	IAA-amino acid hydrolase ILR1-like 4	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444XG75	27	actin-1	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444ZLA4	24	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445E7J0	3	phosphoribosylamine--glycine ligase isoform X1	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444Z235	5	peptidyl-prolyl cis-trans isomerase CYP38, chloroplastic	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444YY24	27	enolase	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445BVN0	6	Glutelin type-A 1	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445AXE4	6	beta-glucosidase 46	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445B8N9	3	alcohol dehydrogenase 1-like	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445A9L1	12	UDP-glucuronic acid decarboxylase 6	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444ZT56	5	60S ribosomal protein L35a-3	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445CSS4	19	tubulin alpha-3 chain	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445A532	3	primary amine oxidase	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445CD88	4	chlorophyll a-b binding protein CP26, chloroplastic-like	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444XEU6	7	NAD-dependent malic enzyme 62 kDa isoform, mitochondrial	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445CNX2	8	probable ribose-5-phosphate isomerase 3, chloroplastic	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444Y5S7	3	peroxidase P7	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444XBS7	4	V-type proton ATPase subunit D	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445EC33	10	NADPH-dependent aldo-keto reductase, chloroplastic	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445CG11	7	annexin D1	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444WNM3	9	allene oxide cyclase, chloroplastic	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445AVY7	8	pyrophosphate-energized vacuolar membrane proton pump	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444YVR7	3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445BAT0	3	probable cinnamyl alcohol dehydrogenase 1	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445DJW8	3	dihydroxy-acid dehydratase, chloroplastic	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445DUT8	4	asparagine--tRNA ligase, cytoplasmic 1	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445E3Q0	7	isoflavone reductase homolog PCBER	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444Z2W0	14	phosphoglucomutase, cytoplasmic	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444Y3L6	15	phosphoenolpyruvate carboxylase	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445BP96	19	probable mediator of RNA polymerase II transcription subunit 37c	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444WVT0	7	phosphoenolpyruvate carboxykinase (ATP)	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445DNP8	7	alpha-1,4 glucan phosphorylase L-2 isozyme, chloroplastic/amyloplastic-like	UNCHANGED	UP	UNCHANGED	UNCHANGED

A0A445AKN0	5	inosine-5'-monophosphate dehydrogenase	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A445BN58	8	60S ribosomal protein L30	UNCHANGED	UP	UNCHANGED	UNCHANGED
A0A444WWG8	2	thioredoxin reductase NTRB-like	UNCHANGED	UP	DOWN	UNCHANGED
A0A444YL50	5	aspartyl protease family protein 2	UNCHANGED	UP	UP	DOWN
A0A444YT00	9	glyceraldehyde-3-phosphate dehydrogenase, cytosolic	UNCHANGED	UP	UP	DOWN
A0A445CME4	10	bifunctional protein FolD 2	UNCHANGED	UP	UNCHANGED	DOWN
A0A444YMD0	2	pyruvate kinase 1, cytosolic-like	UNCHANGED	UP	UNCHANGED	DOWN
T2B9M0	15	fructose-bisphosphate aldolase, cytoplasmic isozyme	UNCHANGED	UP	UNCHANGED	DOWN
A0A445BSX5	24	vacuolar protein sorting-associated protein 45 homolog	UNCHANGED	UP	UNCHANGED	DOWN
A0A445BF10	19	D-3-phosphoglycerate dehydrogenase 1, chloroplastic	UNCHANGED	UP	UNCHANGED	DOWN
A0A445BZ60	4	primary amine oxidase	UNCHANGED	UP	UNCHANGED	DOWN
A0A444XVW9	8	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	UNCHANGED	UP	UNCHANGED	DOWN
A0A445BH25	27	chaperonin CPN60-2, mitochondrial	UNCHANGED	UP	UNCHANGED	DOWN
A0A445DF95	11	pyruvate decarboxylase 2	UNCHANGED	UP	UNCHANGED	DOWN
A0A445CZL2	9	probable fructokinase-7 isoform X1	UNCHANGED	UP	UNCHANGED	DOWN
A0A445AKQ2	12	pyruvate decarboxylase 2	UNCHANGED	UP	UNCHANGED	DOWN
A0A445AAY3	3	bifunctional aspartokinase/homoserine dehydrogenase 1, chloroplastic	UNCHANGED	UP	UNCHANGED	DOWN
A0A445A8Z5	4	non-symbiotic hemoglobin 1	UNCHANGED	UP	UNCHANGED	DOWN
A0A445E1C3	37	aconitate hydratase, cytoplasmic	UNCHANGED	UP	UNCHANGED	DOWN
A0A445DV40	5	importin subunit beta-1	UNCHANGED	UP	UNCHANGED	DOWN
A0A444ZQ70	14	hypersensitive-induced response protein-like protein 2	UNCHANGED	UP	UNCHANGED	DOWN
A0A445AIW1	9	alcohol dehydrogenase 1	UNCHANGED	UP	UNCHANGED	DOWN
A0A445BH36	8	ATP-dependent 6-phosphofructokinase 4, chloroplastic isoform X1	UNCHANGED	UP	UNCHANGED	DOWN
A0A445CSV5	11	glutamate dehydrogenase 1	UNCHANGED	UP	UNCHANGED	DOWN
A0A445BS87	3	cytochrome b5	UNCHANGED	UP	UNCHANGED	DOWN
A0A444YTD7	2	heat shock cognate 70 kDa protein 2	UNCHANGED	UP	UNCHANGED	DOWN
A0A445B9L1	17	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	UNCHANGED	UP	UNCHANGED	DOWN
A0A444WTQ7	8	peroxidase 51	UNCHANGED	UP	UNCHANGED	DOWN
A0A445ETS0	3	isoflavone reductase homolog	UNCHANGED	UP	UNCHANGED	DOWN
A0A445DS99	4	alanine--glyoxylate aminotransferase 2 homolog 1, mitochondrial	UNCHANGED	UP	UNCHANGED	DOWN
A0A445E7K7	28	pyruvate kinase 1, cytosolic	UNCHANGED	UP	UNCHANGED	DOWN
A0A445DCW4	10	probable polygalacturonase	UNCHANGED	UP	UNCHANGED	DOWN
A0A444X4X2	14	peroxidase P7-like	UNCHANGED	UP	UNCHANGED	DOWN
A0A445D8X4	9	pyruvate dehydrogenase E1 component subunit alpha, mitochondrial	UNCHANGED	UP	UNCHANGED	DOWN
A0A445C521	10	peroxidase P7	UNCHANGED	UP	UNCHANGED	DOWN
A0A444X4V5	3	superoxide dismutase [Mn], mitochondrial	UNCHANGED	UP	UNCHANGED	DOWN
A0A445CFR2	5	isoflavone reductase	UNCHANGED	UP	UNCHANGED	DOWN

A0A445BR63	8	isoflavone reductase-like protein	UNCHANGED	UP	UNCHANGED	DOWN
A0A445EUA8	5	phospholipase D alpha 1	UNCHANGED	UP	DOWN	DOWN
A0A445B176	2	aspartyl protease AED3	DOWN	UP	UP	DOWN
A0A445D4K6	3	Eukaryotic translation initiation factor 6-2	DOWN	UP	DOWN	DOWN
A0A445EAI9	2	beta-glucosidase 11	-	UP	Unique BA2.5_Cotyledonary	Unique BA0_Cotyledonary
A0A445B0R4	15	pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha 2	UP	Unique BA2.5_Cotyledonary	UNCHANGED	Unique BA0_Apical
A0A444XRQ3	11	coatomer subunit alpha-2-like	UP	Unique BA2.5_Cotyledonary	UNCHANGED	Unique BA0_Apical
A0A444YN65	9	60S ribosomal protein L4	UP	Unique BA2.5_Cotyledonary	UNCHANGED	Unique BA0_Apical
A0A445BF91	19	tubulin alpha chain	UP	Unique BA2.5_Cotyledonary	DOWN	Unique BA0_Apical
A0A444X6X7	7	aspartate aminotransferase, cytoplasmic	Unique BA2.5_Apical	Unique BA2.5_Cotyledonary	UNCHANGED	-
A0A444XTJ0	4	polypyrimidine tract-binding protein homolog 3 isoform X1	Unique BA0_Apical	Unique BA2.5_Cotyledonary	Unique BA2.5_Cotyledonary	Unique BA0_Apical
A0A445CNX6	2	probable aldo-keto reductase 1	Unique BA0_Apical	Unique BA2.5_Cotyledonary	Unique BA2.5_Cotyledonary	Unique BA0_Apical
A0A445CSM6	4	hypothetical protein Ahy_A06g029154 isoform D	Unique BA0_Apical	Unique BA2.5_Cotyledonary	Unique BA2.5_Cotyledonary	Unique BA0_Apical
A0A445E8M5	2	hydroxyisourate hydrolase	Unique BA0_Apical	Unique BA2.5_Cotyledonary	Unique BA2.5_Cotyledonary	Unique BA0_Apical
A0A444WYB4	3	plasma membrane H+-ATPase	UNCHANGED	Unique BA2.5_Cotyledonary	UP	Unique BA0_Apical
A0A445ERW6	4	GTP-binding protein YPTM2	UNCHANGED	Unique BA2.5_Cotyledonary	UNCHANGED	Unique BA0_Apical
A0A445D343	4	probable caffeoyl-CoA O-methyltransferase At4g26220	UNCHANGED	Unique BA2.5_Cotyledonary	UNCHANGED	Unique BA0_Apical
A0A445A3B6	2	probable aminotransferase TAT2	UNCHANGED	Unique BA2.5_Cotyledonary	UNCHANGED	Unique BA0_Apical
A0A444YVU6	7	vacuolar-processing enzyme	UNCHANGED	Unique BA2.5_Cotyledonary	UNCHANGED	Unique BA0_Apical
A0A445CI73	5	14-3-3-like protein D	UNCHANGED	Unique BA2.5_Cotyledonary	UNCHANGED	Unique BA0_Apical
A0A445EF39	4	photosystem II CP47 chlorophyll apoprotein	UNCHANGED	Unique BA2.5_Cotyledonary	UNCHANGED	Unique BA0_Apical
A0A445B8L2	6	peroxidase P7	UNCHANGED	Unique BA2.5_Cotyledonary	UNCHANGED	Unique BA0_Apical
A0A444Z945	3	bifunctional dTDP-4-dehydrorhamnose 3,5-epimerase/dTDP-4-dehydrorhamnose reductase	-	Unique BA2.5_Cotyledonary	Unique BA2.5_Cotyledonary	-
A0A444YEA1	3	pathogenesis-related protein 2-like	UP	Unique BA0_Cotyledonary	Unique BA2.5_Apical	UNCHANGED

A0A444ZNM5	4	Heat shock 70 kDa 4 -like protein	Unique BA2.5_Apical	Unique BA0_Cotyledonary	Unique BA2.5_Apical	Unique BA0_Cotyledonary
A0A445ASQ8	11	elongation factor G-2, chloroplastic	Unique BA2.5_Apical	Unique BA0_Cotyledonary	Unique BA2.5_Apical	Unique BA0_Cotyledonary
A0A445BV01	14	linoleate 9S-lipoxygenase	Unique BA2.5_Apical	Unique BA0_Cotyledonary	Unique BA2.5_Apical	Unique BA0_Cotyledonary
A0A444XUW9	11	formate--tetrahydrofolate ligase	Unique BA0_Apical	Unique BA0_Cotyledonary	-	UNCHANGED
A0A444YVV0	7	vacuolar-processing enzyme	Unique BA0_Apical	Unique BA0_Cotyledonary	-	UNCHANGED
A0A445ELC9	4	glutamine synthetase leaf isozyme, chloroplastic	UNCHANGED	Unique BA0_Cotyledonary	Unique BA2.5_Apical	UP
A0A445CH39	9	ubiquitin-NEDD8-like protein RUB2	UNCHANGED	Unique BA0_Cotyledonary	Unique BA2.5_Apical	UNCHANGED
A0A445CLD1	2	ras-related protein RABA4d	UNCHANGED	Unique BA0_Cotyledonary	Unique BA2.5_Apical	DOWN
A0A445AXL4	3	L-ascorbate oxidase homolog	DOWN	Unique BA0_Cotyledonary	Unique BA2.5_Apical	UNCHANGED
A0A444ZQF9	10	subtilisin-like protease Glyma18g48580	DOWN	Unique BA0_Cotyledonary	Unique BA2.5_Apical	DOWN
A0A444XUU3	4	alpha-xylosidase 1	-	Unique BA0_Cotyledonary	-	Unique BA0_Cotyledonary
A0A444ZIA2	2	peroxidase 16	-	Unique BA0_Cotyledonary	-	Unique BA0_Cotyledonary
A0A445BXG9	9	ADP,ATP carrier protein 1, mitochondrial	-	Unique BA0_Cotyledonary	-	Unique BA0_Cotyledonary
A0A445DYY0	2	putative beta-glucosidase 41	-	Unique BA0_Cotyledonary	-	Unique BA0_Cotyledonary
A0A445DZL2	8	ras-related protein RABB1b	-	Unique BA0_Cotyledonary	-	Unique BA0_Cotyledonary
A0A445E4W3	7	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (ferredoxin), chloroplastic	-	Unique BA0_Cotyledonary	-	Unique BA0_Cotyledonary
A0A445EE30	2	probable methyltransferase PMT2	-	Unique BA0_Cotyledonary	-	Unique BA0_Cotyledonary
D8KXZ2	4	3-oxoacyl-[acyl-carrier-protein] reductase, chloroplastic	-	Unique BA0_Cotyledonary	-	Unique BA0_Cotyledonary
A0A445CL16	4	dirigent protein 22-like	UP	UNCHANGED	UNCHANGED	UP
A0A444XE84	3	2-alkenal reductase (NADP(+)-dependent) isoform X1	UP	UNCHANGED	UNCHANGED	UP
A0A445B020	7	hypersensitive-induced reaction 1 protein	UP	UNCHANGED	UNCHANGED	UP
A0A445BQM2	23	heat shock 70 kDa protein	UP	UNCHANGED	UNCHANGED	UP
A0A445D2U1	15	NADP-dependent malic enzyme	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XCH2	30	heat shock 70 kDa protein 15	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EX70	5	60S ribosomal protein L7-2 isoform X1	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CD40	3	1,4-alpha-glucan-branching enzyme 1, chloroplastic/amyloplastic	UP	UNCHANGED	UNCHANGED	UNCHANGED

A0A444ZXL4	2	60S ribosomal protein L6	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AJH5	12	NADPH-dependent aldo-keto reductase, chloroplastic	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A445ACY5	7	14-3-3-like protein D	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YGE5	10	AP-4 complex subunit mu	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DLC2	4	histidine kinase 3 isoform X1	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CIG2	5	60S ribosomal protein L8-3	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A445C4I2	2	ubiquitin carboxyl-terminal hydrolase 12-like isoform X1	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A445ALA3	3	60S ribosomal protein L8-3	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZWP4	2	40S ribosomal protein S6	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CM51	6	60S ribosomal protein L21-1	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BGH5	12	40S ribosomal protein S4-1	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XEA3	4	60S ribosomal protein L37a	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YJV3	4	60S ribosomal protein L18	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZQZ6	4	calreticulin-3	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YIB7	4	60S ribosomal protein L18	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Z1W0	2	protein argonaute 1	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZLL1	9	heat shock cognate 70 kDa protein	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A445D3X6	6	succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A0A6ZDS7	9	60S ribosomal protein L3	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZCB5	2	DUF1682 family protein	UP	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BU41	18	NADP-dependent malic enzyme isoform X2	UP	UNCHANGED	DOWN	UNCHANGED
A0A445EL83	6	glucose-1-phosphate adenylyltransferase large subunit 3, chloroplastic/amyloplastic isoform X1	UP	UNCHANGED	DOWN	UNCHANGED
A0A445CSH3	5	60S ribosomal protein L6-1	UP	UNCHANGED	DOWN	UNCHANGED
A0A445A9X6	21	actin	UP	UNCHANGED	DOWN	UNCHANGED
A0A444YS21	3	cytochrome b-c1 complex subunit Rieske-4, mitochondrial	UP	UNCHANGED	DOWN	UNCHANGED
A0A444ZXF0	3	inositol-3-phosphate synthase	UP	UNCHANGED	DOWN	UNCHANGED
A0A445CFQ1	30	eukaryotic initiation factor 4A-2-like	UP	UNCHANGED	DOWN	UNCHANGED
A0A445D410	2	cyanogenic beta-glucosidase isoform X1	UP	UNCHANGED	DOWN	UNCHANGED
A0A444XAV0	2	probable mediator of RNA polymerase II transcription subunit 37c	UP	UNCHANGED	DOWN	UNCHANGED
A0A444XR10	3	26S proteasome regulatory subunit 7	UP	UNCHANGED	DOWN	UNCHANGED
A0A444ZKN7	11	Peroxidase 68	UP	UNCHANGED	DOWN	DOWN
A0A444YBP0	2	cationic peroxidase 1	UP	UNCHANGED	DOWN	DOWN
A0A445DC87	10	subtilisin-like protease Glyma18g48580	Unique BA2.5_Apical	UNCHANGED	UP	Unique BA0_Cotyledonary
A0A445B2S1	5	UDP-arabinopyranose mutase 1	Unique BA2.5_Apical	UNCHANGED	UNCHANGED	Unique BA0_Cotyledonary

A0A445CE58	2	pyruvate kinase 1, cytosolic	Unique BA2.5_Apical	UNCHANGED	UNCHANGED	Unique BA0_Cotyledonary
A0A445EV57	3	cytochrome c1-2, heme protein, mitochondrial	Unique BA2.5_Apical	UNCHANGED	UNCHANGED	Unique BA0_Cotyledonary
A0A445B1Z1	6	glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform	Unique BA0_Apical	UNCHANGED	Unique BA2.5_Cotyledonary	UP
A0A445D7T0	9	glutamate--glyoxylate aminotransferase 2	Unique BA0_Apical	UNCHANGED	Unique BA2.5_Cotyledonary	UP
A0A444WNH1	16	Aldo/keto reductase	Unique BA0_Apical	UNCHANGED	Unique BA2.5_Cotyledonary	UNCHANGED
A0A444Y1W9	2	beta-glucosidase 12-like	Unique BA0_Apical	UNCHANGED	Unique BA2.5_Cotyledonary	UNCHANGED
A0A444YZ37	14	nuclear pore complex protein GP210 isoform X2	Unique BA0_Apical	UNCHANGED	Unique BA2.5_Cotyledonary	UNCHANGED
A0A444Z0F7	2	40S ribosomal protein S7	Unique BA0_Apical	UNCHANGED	Unique BA2.5_Cotyledonary	UNCHANGED
A0A444ZCQ1	5	dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 1, mitochondrial isoform X2	Unique BA0_Apical	UNCHANGED	Unique BA2.5_Cotyledonary	UNCHANGED
A0A445AX76	4	glutamine synthetase leaf isozyme, chloroplastic	Unique BA0_Apical	UNCHANGED	Unique BA2.5_Cotyledonary	UNCHANGED
A0A445BAI7	4	(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase	Unique BA0_Apical	UNCHANGED	Unique BA2.5_Cotyledonary	UNCHANGED
A0A445AFE6	8	60S ribosomal protein L23	Unique BA0_Apical	UNCHANGED	Unique BA2.5_Cotyledonary	DOWN
A0A445DRP9	5	malate dehydrogenase 2, peroxisoma	UNCHANGED	UNCHANGED	UP	UP
A0A444ZLJ1	6	fasciclin-like arabinogalactan protein 10	UNCHANGED	UNCHANGED	UP	UP
A0A444WXY5	5	soluble inorganic pyrophosphatase 6, chloroplastic	UNCHANGED	UNCHANGED	UP	UP
A0A445DQJ5	28	ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic	UNCHANGED	UNCHANGED	UP	UP
A0A445C8P8	19	NADP-dependent malic enzyme	UNCHANGED	UNCHANGED	UNCHANGED	UP
A0A445C2V5	7	fructose-bisphosphate aldolase, cytoplasmic isozyme 1	UNCHANGED	UNCHANGED	UNCHANGED	UP
A0A444XB73	5	putative complex I intermediate-associated protein	UNCHANGED	UNCHANGED	UNCHANGED	UP
A0A444YRR3	10	glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UP
A0A445B8R4	4	probable lactoylglutathione lyase, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UP
A0A445CG54	4	cytochrome c oxidase subunit 6b-1	UNCHANGED	UNCHANGED	UNCHANGED	UP
A0A445B6R7	13	caffeoyl-CoA O-methyltransferase	UNCHANGED	UNCHANGED	UNCHANGED	UP
A0A445AAD7	41	cell division cycle protein 48 homolog	UNCHANGED	UNCHANGED	UNCHANGED	UP
A0A444YIC8	11	bifunctional protein FolD 2	UNCHANGED	UNCHANGED	UNCHANGED	UP
A0A444X1G0	6	peroxidase P7-like	UNCHANGED	UNCHANGED	UNCHANGED	UP
A0A445EP01	3	peroxidase N	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A445CEI5	18	phosphoglycerate kinase, chloroplastic	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A444Y9V3	23	serine hydroxymethyltransferase, mitochondrial-like	UNCHANGED	UNCHANGED	UP	UNCHANGED

A0A445CK24	12	26S proteasome regulatory subunit 10B homolog A	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A445ABP0	5	probable polygalacturonase	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A444ZU59	2	Aspartate-semialdehyde dehydrogenase	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A445CWQ9	14	aspartate--tRNA ligase 2, cytoplasmic	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A445CXA1	17	glycine dehydrogenase (decarboxylating), mitochondrial	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A445B448	7	proteasome subunit beta type-6	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A445A5R1	7	sulfite reductase [ferredoxin], chloroplastic	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A445BSR3	3	Ubiquitin-conjugating enzyme E2 10	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A445CH92	2	photosystem II 10 kDa polypeptide, chloroplastic	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A444YWA9	9	polyadenylate-binding protein 2-like	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A445DIG0	16	6-phosphogluconate dehydrogenase, decarboxylating 2, chloroplastic	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A445BMH6	22	linoleate 9S-lipoxygenase	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A444Z003	5	aldehyde dehydrogenase family 2 member C4	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A445D557	4	Photosystem II D2 protein	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A445E3K4	15	coatomer subunit gamma-2	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A445D9V5	3	2,3-dimethylmalate lyase isoform X2	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A444XIS0	2	protoporphyrinogen oxidase 1, chloroplastic	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A445DW24	3	peroxiredoxin Q, chloroplastic	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A445EUM0	6	proteasome subunit alpha type-7	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A444Y240	2	PsbA	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A445B682	5	stomatin-like protein 2, mitochondrial	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A444XDG9	22	eukaryotic initiation factor 4A-10	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A444XSB2	3	serine carboxypeptidase-like	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A444XBL2	5	photosystem I reaction center subunit V, chloroplastic	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A444XYG1	15	plasma membrane ATPase 4	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A444ZZK7	5	nucleoside diphosphate kinase III, chloroplastic/mitochondrial	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A444ZWP1	5	Actin-3	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A444YD85	4	probable aquaporin PIP-type 7a	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A445BRZ5	2	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase, chloroplastic/chromoplastic	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A444XEA9	10	2-alkenal reductase (NADP(+)-dependent)	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A444X9J0	3	beta-glucosidase 12	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A444Z7K3	9	cysteine synthase	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A444ZR23	2	photosystem I reaction center subunit XI, chloroplastic	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A445DJZ6	2	L-ascorbate oxidase homolog	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A445EVF8	5	peroxidase 4	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A444XD91	15	heat shock cognate 70 kDa protein-like	UNCHANGED	UNCHANGED	UP	UNCHANGED
A0A444ZDP0	6	peroxidase A2	UNCHANGED	UNCHANGED	UP	UNCHANGED

A0A444WV29	5	thioredoxin reductase NTRB-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A8G8	17	fructose-bisphosphate aldolase 1, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YF68	14	dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 2, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DMM1	7	beta-xylosidase/alpha-L-arabinofuranosidase 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZMJ2	15	bifunctional L-3-cyanoalanine synthase/cysteine synthase 1, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WWZ3	7	26S proteasome non-ATPase regulatory subunit 14 homolog	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445C4E1	22	T-complex protein 1 subunit eta	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EJG0	18	malate dehydrogenase, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EJP9	3	A0A445EJP9_ARAHY Uncharacterized protein OS=Arachis hypogaea OX=3818 GN=Ahy_A01g000115 PE=4 SV=1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Y1Z8	42	elongation factor 2 isoform X2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BQ71	7	coatomer subunit beta'-2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A372	7	mitochondrial-processing peptidase subunit alpha	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XZY0	4	beta-glucosidase 42	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E6W9	27	transketolase, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445ALB1	5	peroxidase P7-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WRN4	5	gamma carbonic anhydrase 1, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DJR7	6	fumarylacetoacetase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EUV7	12	ferredoxin--NADP reductase, leaf isozyme, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YHE1	2	polygalacturonase inhibitor-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DP66	3	eukaryotic translation initiation factor 2 subunit gamma isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WW04	39	probable cytosolic oligopeptidase A	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DA00	14	ribulose bisphosphate carboxylase small chain 1, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WQ52	4	photosystem II 22 kDa protein, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X3D0	14	polyadenylate-binding protein 8	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YEU5	6	ribose-phosphate pyrophosphokinase 4	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B2V7	13	UDP-glucose 6-dehydrogenase 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DK46	34	stromal 70 kDa heat shock-related protein, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A9D0	5	elongation factor 1-beta	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445ENL7	8	peroxidase 16	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZV53	16	aldehyde dehydrogenase family 2 member B7, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BE90	13	glycerate dehydrogenase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CHG7	31	ruBisCO large subunit-binding protein subunit beta, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CD15	15	glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445C9C1	8	glucose-6-phosphate isomerase 1, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZBY6	13	DEAD-box ATP-dependent RNA helicase 37	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DTP7	7	probable phospholipid hydroperoxide glutathione peroxidase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED

A0A444WZ23	15	chlorophyll a-b binding protein CP24 10A, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZM98	17	pyruvate dehydrogenase E1 component subunit beta, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CE24	7	glycine-rich RNA-binding, abscisic acid-inducible protein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XDI9	41	elongation factor 2 isoform X2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A8H5	3	glycine-rich protein 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DPP7	2	signal recognition particle receptor subunit beta	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DTR2	7	glutamate--cysteine ligase, chloroplastic isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YX87	3	plastidial pyruvate kinase 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XII0	5	pto-interacting protein 1-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZYG1	6	gamma carbonic anhydrase-like 2, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DBZ0	19	hypersensitive-induced response protein-like protein 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AHD7	6	3-ketoacyl-CoA thiolase 2, peroxisomal	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CRH1	15	2-Cys peroxiredoxin BAS1, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DDE6	4	DEAD-box ATP-dependent RNA helicase 8	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CH21	13	proteasome subunit alpha type-2-A	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CYF4	5	glutathione reductase, cytosolic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E2J6	8	gamma aminobutyrate transaminase 1, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Y8D3	9	triosephosphate isomerase, cytosolic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Z0T8	19	guanine nucleotide-binding protein subunit beta-like protein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZW85	9	cysteine synthase, chloroplastic/chromoplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YNV1	12	triosephosphate isomerase, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445D891	11	thiamine thiazole synthase 2, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XD25	9	probable mediator of RNA polymerase II transcription subunit 37c	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CMJ0	21	sucrose synthase 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZMP3	3	mitogen-activated protein kinase homolog MMK2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DY22	17	probable lactoylglutathione lyase, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X9W2	11	beta-glucosidase BoGH3B-like isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XDM4	9	ras-related protein RABD2a	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AFA1	8	succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EEI6	2	glycerol-3-phosphate dehydrogenase SDP6, mitochondrial isoform X2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AXK1	8	putative lactoylglutathione lyase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WW71	6	pectin acetylesterase 8	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CA13	14	probable L-ascorbate peroxidase 6, chloroplastic/mitochondrial isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BX16	8	cytochrome b6-f complex iron-sulfur subunit, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A190CSF1	19	eukaryotic initiation factor 4A-11	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445ED69	6	serine carboxypeptidase-like 45	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YZJ8	12	ATP-dependent 6-phosphofructokinase 3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED

A0A445AMM7	15	ubiquitin-activating enzyme E1 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AVN4	5	40S ribosomal protein S11	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XNX3	2	ras-related protein RABA5a	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Y1X8	14	isocitrate dehydrogenase [NADP]	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445C5M8	11	60S acidic ribosomal protein P0	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BNG4	3	probable linoleate 9S-lipoxygenase 5	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AM31	4	ribose-phosphate pyrophosphokinase 4	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B3H6	15	glucose-6-phosphate isomerase, cytosolic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WZ47	4	dynamin-related protein 3A	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DF26	7	aminoacylase-1 isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445C7D2	5	ATP synthase beta subunit	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E6W3	2	V-type proton ATPase subunit G	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WPU1	5	ATP synthase beta subunit	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BAE6	28	actin-7	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X0X3	8	prohibitin-1, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZRU7	24	adenosylhomocysteinase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EUE2	9	26S proteasome non-ATPase regulatory subunit 4 homolog isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A142F3D2	11	glutamate dehydrogenase 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZQI3	20	MDIS1-interacting receptor like kinase 2-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AGZ0	7	photosystem II protein D1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CMY6	2	uncharacterized protein LOC112695666	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Z848	4	porphobilinogen deaminase, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BKN6	17	26S proteasome regulatory subunit 6A homolog	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BTW6	2	GEM-like protein 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DNG7	4	26S proteasome non-ATPase regulatory subunit 1 homolog A	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DXV8	14	NADP-dependent malic enzyme	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XXV6	10	Phospholipase D alpha 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XX32	5	probable fructokinase-7	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445D826	8	cysteine synthase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BPA0	8	heat shock cognate 70 kDa protein-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E060	13	26S proteasome non-ATPase regulatory subunit 2 homolog A	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CCR6	26	tubulin beta chain	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X9B6	5	allene oxide cyclase, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X7K4	6	ATP synthase subunit gamma, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445ARD2	15	fumarate hydratase 1, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BN79	5	40S ribosomal protein S8	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YG83	23	prolyl endopeptidase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED

A0A445DRS8	4	methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Y4H6	3	probable phosphoribosylformylglycinamidine synthase, chloroplastic/mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DJL9	9	ATP synthase gamma chain, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BAQ8	44	DNA polymerase V	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EWB1	5	DNA damage-inducible protein 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Y1E4	5	DUF642 family protein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WQ31	7	photosystem II CP43 chlorophyll apoprotein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EBZ3	10	60S ribosomal protein L4	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Y324	9	trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Z9I7	16	isoflavone reductase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445C1N1	9	aspartyl protease family protein 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EQB3	2	40S ribosomal protein S10-1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445C1V2	25	chaperone protein ClpC, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZI83	16	plasma membrane ATPase 4	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CZP0	27	heat shock protein 90-5, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XC38	3	aromatic aminotransferase ISS1-like isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445C3A3	9	Phosphatidate cytidylyltransferase 3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZY15	7	phosphoribosylformylglycinamidine cyclo-ligase, chloroplastic/mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445D9X7	10	14-3-3-like protein A	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DTK9	5	40S ribosomal protein S11	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E214	3	protein transport protein SEC31 homolog B	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZBS6	19	adenosylhomocysteinase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YMI9	28	probable mediator of RNA polymerase II transcription subunit 37c	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DI38	11	ATP-dependent zinc metalloprotease FTSH 2, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZT52	10	40S ribosomal protein S14	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X9V2	21	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DK56	4	ras-related protein RABA2a	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BPM4	19	putative disease resistance protein At3g14460	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EX07	28	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YWX9	5	uncharacterized oxidoreductase At4g09670	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CKV5	25	elongation factor Tu, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BJK2	12	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445C427	12	Desiccation protectant protein Lea14-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E893	5	60S ribosomal protein L22-2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZQ84	6	outer plastidial membrane protein porin	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BF06	6	methylthioribose kinase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED

A0A445BZN2	3	allene oxide cyclase, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DS44	2	protein MET1, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BB34	4	probable NAD(P)H dehydrogenase (quinone) FQR1-like 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YF39	7	A0A444YF39_ARAHY Uncharacterized protein OS=Arachis hypogaea OX=3818 GN=Ahy_B07g088669 PE=4 SV=1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BWQ7	11	L-ascorbate oxidase homolog	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YL53	4	rhodanese-like domain-containing protein 4, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A9A5	34	elongation factor 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Y4E5	5	thioredoxin M4, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DA98	34	heat shock cognate 70 kDa protein 2-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A2S0	2	40S ribosomal protein S7	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AZP6	10	eukaryotic translation initiation factor 5A-2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZRY2	5	protein transport protein SEC23-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E9A2	8	proteasome subunit beta type-1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AA79	3	serine carboxypeptidase-like 51	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EHK0	14	26S proteasome regulatory subunit 7	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E5X8	6	UDP-glucuronic acid decarboxylase 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BPQ8	2	isocitrate dehydrogenase [NAD] catalytic subunit 5, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DRV6	14	guanosine nucleotide diphosphate dissociation inhibitor At5g09550	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CQ67	28	enolase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YS73	5	Uncharacterized protein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZB52	2	A0A444ZB52_ARAHY AMP-binding domain-containing protein OS=Arachis hypogaea OX=3818 GN=Ahy_B04g068938 PE=4 SV=1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CUR8	6	2-methylene-furan-3-one reductase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CYR7	9	chlorophyll a-b binding protein of LHCII type 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YUY3	6	A0A444YUY3_ARAHY Uncharacterized protein OS=Arachis hypogaea OX=3818 GN=Ahy_B06g085559 PE=4 SV=1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AAT1	6	beta-galactosidase 9	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E9D3	7	A0A445E9D3_ARAHY 3-phosphoshikimate 1-carboxyvinyltransferase OS=Arachis hypogaea OX=3818 GN=Ahy_A02g006334 PE=3 SV=1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XAE3	8	nascent polypeptide-associated complex subunit alpha-like protein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BEC7	10	coatomer subunit delta	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BPN2	12	isocitrate dehydrogenase [NAD] catalytic subunit 5, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WUB1	4	ADP-ribosylation factor-like protein 8a	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A7V7	4	A0A445A7V7_ARAHY Alanine--tRNA ligase OS=Arachis hypogaea OX=3818 GN=Ahy_B03g067845 PE=3 SV=1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AQW6	7	A0A445AQW6_ARAHY Peroxidase OS=Arachis hypogaea OX=3818 GN=Ahy_B01g053028 PE=3 SV=1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED

A0A444X0M6	2	A0A444X0M6_ARAHY Uncharacterized protein OS=Arachis hypogaea OX=3818 GN=Ahy_B10g101863 PE=3 SV=1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YAR2	7	hypothetical protein Ahy_B07g086888	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CR31	11	S-adenosylmethionine synthase 3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CA44	8	Methionine aminotransferase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Y0J8	20	phosphoglycerate kinase, cytosolic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YR98	3	4-alpha-glucanotransferase, chloroplastic/amyloplastic isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XEA4	6	Alcohol dehydrogenase superfamily	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X1J3	10	alpha-galactosidase 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445ACM0	7	A0A445ACM0_ARAHY Starch synthase, chloroplastic/amyloplastic OS=Arachis hypogaea OX=3818 GN=Ahy_B02g057701 PE=3 SV=1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E3J7	3	A0A445E3J7_ARAHY RRM domain-containing protein OS=Arachis hypogaea OX=3818 GN=Ahy_A03g016531 PE=4 SV=1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YMV2	3	glutathione S-transferase L3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X3L0	49	clathrin heavy chain 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WSL6	5	A0A444WSL6_ARAHY V-type proton ATPase subunit H OS=Arachis hypogaea OX=3818 GN=Ahy_Scaffold1g106846 PE=3 SV=1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WPW6	7	ATP synthase subunit beta, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XZI8	2	MLP-like protein 34	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E4E5	11	L-ascorbate peroxidase, cytosolic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XV97	16	fructose-bisphosphate aldolase 3, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XCP3	4	ABC transporter G family member 36	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BPZ0	3	ruvB-like protein 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CLS5	2	S-formylglutathione hydrolase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EN18	13	leucine aminopeptidase 1-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WRT6	3	isoflavone reductase-like protein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CLY7	15	ferredoxin-dependent glutamate synthase, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B027	8	ATPase 11, plasma membrane-type	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Y8S7	7	peroxiredoxin-2E, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BHY6	4	ureidoglycolate hydrolase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Z9I3	8	isoflavone reductase-like protein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CS26	6	peroxidase 44	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CGS6	6	photosystem I reaction center subunit II, chloroplastic-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445C3D7	14	oxygen-evolving enhancer protein 1, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YWV9	18	proteasome subunit alpha type-1-B-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CBX6	9	isoflavone reductase-like protein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X1R2	3	GDP-mannose 3,5-epimerase 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BME0	24	seed linoleate 9S-lipoxygenase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED

A0A445ESM3	11	26S proteasome regulatory subunit 6B homolog	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CPR8	3	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YHD7	2	ATOZI1, putative	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445C3V2	3	oxygen-evolving enhancer protein 2, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WYL4	3	acetolactate synthase 3, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BIX1	2	T-complex protein 1 subunit gamma	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EAC9	3	beta-glucosidase 11	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZK37	9	proteasome subunit alpha type-4	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A0P3	11	proteasome subunit beta type-2-A	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XZW0	4	MLP-like protein 34	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AVJ3	4	temperature-induced lipocalin-1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BEI9	2	Armadillo-like helical	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BRN9	15	L-ascorbate oxidase homolog	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BPG2	11	NADP-specific glutamate dehydrogenase isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E4L8	8	60S ribosomal protein L12	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XFL4	6	PSII 47kDa protein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YA80	6	60S ribosomal protein L10	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZC00	10	protein transport protein SEC23	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DJL0	12	putative lactoylglutathione lyase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZQB2	4	V-type proton ATPase subunit d2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WUR2	15	aconitate hydratase 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DMY3	5	ras-related protein Rab11A	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZV61	8	pyruvate dehydrogenase E1 component subunit alpha, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A120	19	sucrose synthase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XBQ6	4	coatomer subunit beta-1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CIL2	25	phospholipase D alpha 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A3G6	3	probable protein phosphatase 2C 39	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CTD3	4	40S ribosomal protein S27-2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DA80	18	heat shock cognate 70 kDa protein-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E7D6	8	adenosine kinase 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Y6B9	17	ADP,ATP carrier protein 3, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DHF2	14	pyruvate kinase, cytosolic isozyme	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZV18	3	probable inactive purple acid phosphatase 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B5D1	31	actin-7	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Y4X2	5	photosystem II 32 kDa protein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DCA2	2	subtilisin-like protease Glyma18g48580	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DIP1	4	peroxisomal fatty acid beta-oxidation multifunctional protein MFP2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED

A0A445CRL7	2	cytochrome P450 98A2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YJC8	5	rhicadhesin receptor	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EC54	2	alcohol dehydrogenase 1-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BUM7	5	adenine phosphoribosyltransferase 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Y6Y4	24	aconitate hydratase, cytoplasmic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BD24	3	serine carboxypeptidase-like 27	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A8F7	10	NADP-dependent D-sorbitol-6-phosphate dehydrogenase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445D1S9	3	eukaryotic peptide chain release factor GTP-binding subunit ERF3A	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445C2G3	8	isocitrate dehydrogenase [NAD] regulatory subunit 1, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CQC8	10	1,4-alpha-glucan-branching enzyme 1, chloroplastic/amyloplastic isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E437	36	elongation factor 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A444	3	probable histone H2A.1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZR08	3	putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EDU9	7	Histone H4	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
Q06H28	4	photosystem I reaction center subunit VI-2, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Y0G1	4	thiosulfate/3-mercaptopyruvate sulfurtransferase 1, mitochondrial isoform X2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DY01	8	mitochondrial-processing peptidase subunit alpha	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XR59	2	glutathione reductase, cytosolic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Z7M9	5	40S ribosomal protein S3a	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X3K8	12	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A3S6	8	malate dehydrogenase, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AAF6	9	lactoylglutathione lyase isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E1T5	4	serine carboxypeptidase-like 40	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B3G3	14	outer plastidial membrane protein porin	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YQ05	4	NADH dehydrogenase subunit 9	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XBH9	4	splicing factor U2af large subunit B isoform X6	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X1A7	14	caffeoyl-CoA O-methyltransferase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B963	6	agmatine deiminase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZIT0	4	glutathionyl-hydroquinone reductase YqjG	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EW07	3	peptidyl-prolyl cis-trans isomerase CYP19-4	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZHQ7	2	subtilisin-like protease SBT2.5	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EEN9	8	26S proteasome regulatory subunit 4 homolog A	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Y7T3	14	UDP-D-apiose/UDP-D-xylose synthase 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DA96	26	probable mediator of RNA polymerase II transcription subunit 37c	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EPK8	2	thiol protease aleurain-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DAA8	26	2-oxoglutarate dehydrogenase, mitochondrial-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A3U6	9	UBP1-associated protein 2C	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED

A0A444X8G9	26	alpha-1,4 glucan phosphorylase L isozyme, chloroplastic/amyloplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445APA9	13	dipeptidyl peptidase family member 6	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BKU9	19	calreticulin	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CWP3	2	pleiotropic drug resistance protein 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E872	2	pectinesterase-like isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DYD3	2	glycerophosphodiester phosphodiesterase GDPDL3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WUX6	5	isocitrate dehydrogenase [NAD] regulatory subunit 1, mitochondrial isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DUP5	9	xylose isomerase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A9G0	3	protein TOC75, chloroplastic isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YUK8	15	plasma membrane ATPase 4	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445D3E3	17	isocitrate dehydrogenase [NADP]	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WYH7	6	eukaryotic translation initiation factor 3 subunit D-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DF33	25	argininosuccinate synthase, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XYE0	12	GTP-binding nuclear protein Ran-3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CIR4	15	heat shock 70 kDa protein 5	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X199	10	proteasome subunit beta type-5	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BCY2	29	elongation factor 1-alpha	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A9Y6	31	heat shock cognate 70 kDa protein 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XJC4	9	photosystem II CP47 chlorophyll apoprotein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XKT9	5	translationally-controlled tumor protein homolog	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CG04	25	probable mitochondrial-processing peptidase subunit beta, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CQS8	4	secoisolariciresinol dehydrogenase-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445C618	5	photosystem II D2-reaction-center protein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Z1D2	13	glutamine synthetase nodule isozyme	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DCQ0	2	zinc finger CCCH domain-containing protein ZFN-like isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EH47	11	malate dehydrogenase, cytoplasmic isoform X2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YS80	11	mitochondrial phosphate carrier protein 3, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445ARZ8	2	Glutamate dehydrogenase 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BPI7	3	ubiquitin carboxyl-terminal hydrolase 6	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AW73	22	dihydrolipoyl dehydrogenase, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B220	10	splicing factor 3A subunit 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YW80	6	cysteine proteinase RD21A	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DJI2	12	ras-related protein RABB1c	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZF59	7	GTP-binding protein SAR1A	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XJ98	7	aspartic proteinase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B5H4	3	26S proteasome non-ATPase regulatory subunit 12 homolog A	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YDJ3	54	clathrin heavy chain 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED

A0A445A368	2	hexokinase-1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XAW9	15	pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BDL3	3	UPF0235 protein At5g63440 isoform X2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZRX9	3	xyloglucan endotransglucosylase/hydrolase 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445APT4	4	V-type proton ATPase subunit H	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZCQ0	18	aminomethyltransferase, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X3E3	6	40S ribosomal protein S16	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445C9Y8	18	protein disulfide-isomerase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YD70	4	hypothetical protein Ahy_B07g087884	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BQC1	3	Cytochrome c oxidase subunit 5b-2, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X8I3	6	40S ribosomal protein S19-1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EUW8	16	photosystem I P700 apoprotein A2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B683	14	caffeic acid 3-O-methyltransferase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DV73	29	luminal-binding protein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AKS9	9	proteasome subunit alpha type-4	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XI53	13	ADP-ribosylation factor 2 isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445ADV8	6	elongation factor 1-gamma	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DWK8	15	40S ribosomal protein S3-3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445D9Y2	10	T-complex protein 1 subunit zeta 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E0I3	2	probable 2-isopropylmalate synthase isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EWV7	9	protein transport protein SEC13 homolog B	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AQ01	2	L-ascorbate oxidase homolog	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EM30	8	galactokinase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YK12	2	mannosylglycoprotein endo-beta-mannosidase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZY94	14	chaperone protein ClpC, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XW77	34	ATP synthase subunit beta, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445C2K4	9	chlorophyll a-b binding protein 8, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B7R9	4	26S proteasome non-ATPase regulatory subunit 7 homolog A	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X337	8	PsbC	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WQJ4	8	photosystem II cp47 protein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CEU3	12	succinate-semialdehyde dehydrogenase, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E1I0	5	chloroplast envelope quinone oxidoreductase homolog	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445C6W9	34	clathrin heavy chain 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BUE9	5	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DEB0	8	alpha-galactosidase 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445D5H5	19	probable UDP-arabinopyranose mutase 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BUL7	9	photosystem I P700 apoprotein A2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED

A0A445BZ79	3	MLP-like protein 34	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DND4	25	protein PLASTID MOVEMENT IMPAIRED 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CCX1	14	catalase isozyme 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445ARH5	7	probable histone H2B.3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E6Z9	2	DEAD-box ATP-dependent RNA helicase 38	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WNG8	6	probable aldo-keto reductase 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B5L1	3	developmentally-regulated G-protein 3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A6Q1	5	BAG family molecular chaperone regulator 7	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X619	5	eukaryotic translation initiation factor 3 subunit B	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CMI3	2	serine/arginine-rich splicing factor SR34B isoform X2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B4I2	6	ER membrane protein complex subunit 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BG52	4	tripeptidyl-peptidase 2 isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EQU9	3	Programmed cell death protein 4	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WYK0	10	Polyphenol oxidase A1, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BPJ4	2	vacuolar protein sorting-associated protein 26A	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XNG6	2	phosphoribosylaminoimidazole carboxylase, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CG60	6	thylakoid lumenal 29 kDa protein, chloroplastic isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445D987	5	proteasome subunit beta type-4	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AAR7	12	selenium-binding protein 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X9N8	3	cytochrome c1-2, heme protein, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A8L0	3	U-box domain-containing protein 44	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B5Z3	3	probable chalcone--flavonone isomerase 3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZY78	14	ribonuclease TUDOR 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Y0B6	9	ubiquitin-NEDD8-like protein RUB2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445C9D4	11	14-3-3-like protein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZWU7	5	probable cinnamyl alcohol dehydrogenase 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445ED48	18	ATPase subunit 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CP77	5	peptidyl-prolyl cis-trans isomerase CYP19-3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DYK2	8	malate dehydrogenase, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BEK8	3	glutamine--tRNA ligase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZV91	8	hypersensitive-induced response protein 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XC07	11	phospholipase D alpha 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EPG6	5	betaine aldehyde dehydrogenase 1, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DU44	6	V-type proton ATPase subunit E	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZS36	7	lipoxygenase 6, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445D0T6	9	proteasome subunit beta type-3-A	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445D9F8	9	photosystem II protein D2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED

A0A445DGI7	3	NAD(P)-binding Rossmann-fold superfamily protein isoform 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CNH5	21	luminal-binding protein 5	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A6E4	18	patellin-3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EKG3	10	NAD-dependent malic enzyme 59 kDa isoform, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CYD6	2	chlorophyll a-b binding protein 6A, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CRD7	44	cell division cycle protein 48 homolog	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B8E4	2	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A8G9	4	coatomer subunit alpha-2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WNH7	2	eukaryotic translation initiation factor 3 subunit H	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CNY6	17	GDP-mannose 3,5-epimerase 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CJK2	15	L-ascorbate oxidase homolog	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A4L0	4	60S ribosomal protein L17-2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CIH8	23	heat shock 70 kDa protein 15	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DCC8	2	subtilisin-like protease Glyma18g48580	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WPH6	6	ferredoxin--NADP reductase, root isozyme, chloroplastic isoform X2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A5F9	6	sulfite reductase [ferredoxin], chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BVT7	4	protein TOC75-3, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CE47	11	GDP-mannose 3,5-epimerase 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B7Y7	2	phosphoinositide phospholipase C 2 isoform X2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BDU9	10	spliceosome-associated protein 130 A	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WXE2	11	NADH-cytochrome b5 reductase-like protein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B3Q5	2	Glycine-rich RNA-binding protein 3, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EUJ0	14	glucose-6-phosphate 1-dehydrogenase, cytoplasmic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZEL1	2	desiccation-related protein PCC13-62	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XXG6	5	adenylate kinase 4	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XVM3	14	40S ribosomal protein S15a-1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WUN5	9	3-dehydroquinate synthase, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XH79	8	dihydrolipoyllysine-residue acetyltransferase component 2 of pyruvate dehydrogenase complex, mitochondrial isoform X2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DQB8	17	NADH dehydrogenase [ubiquinone] iron-sulfur protein 1, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Y8T0	26	mitochondrial-processing peptidase subunit alpha	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZB47	39	V-type proton ATPase catalytic subunit A	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E446	3	cyanogenic beta-glucosidase isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BCL3	8	peptidyl-prolyl cis-trans isomerase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B669	2	nascent polypeptide-associated complex subunit alpha-like protein 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AV59	2	ADP-ribosylation factor 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445C2U4	16	heat shock protein 90-6, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED

A0A444XPX7	21	malate dehydrogenase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BKG6	8	mitochondrial Rho GTPase 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A2Y9	2	3-hydroxyisobutyryl-CoA hydrolase-like protein 3, mitochondrial isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BK83	10	60S ribosomal protein L11 isoform X2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XVQ8	8	proteasome subunit alpha type-5	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CNV7	25	putative aldo-keto reductase 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CCH7	27	endoplasmin homolog	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZVW6	4	glutathione S-transferase DHAR3, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZAX5	30	sucrose synthase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DJV5	6	plastid-lipid-associated protein, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BMH5	13	linoleate 9S-lipoxygenase 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BB06	4	multiple organellar RNA editing factor 9, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YUK5	5	peroxidase 16	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CWF5	25	aspartate aminotransferase P2, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B155	16	T-complex protein 1 subunit theta	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AA42	28	ruBisCO large subunit-binding protein subunit alpha	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DMI3	11	3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E4Q7	4	isovaleryl-CoA dehydrogenase, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XS90	9	peptidyl-prolyl cis-trans isomerase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Y8N8	7	threonine synthase, chloroplastic-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XW20	12	perakine reductase-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YYZ7	23	nuclear pore complex protein GP210 isoform X2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZFB8	3	beta-D-xylosidase 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YRQ2	5	eukaryotic peptide chain release factor subunit 1-3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZDI4	8	60S ribosomal protein L9	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YX51	10	fructose-1,6-bisphosphatase, cytosolic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E3M6	13	ras-related protein Rab7	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZYZ5	11	heat shock protein 83	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZKY1	26	receptor-like protein kinase FERONIA	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E2F5	12	cinnamoyl-CoA reductase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XWG6	14	glyceraldehyde-3-phosphate dehydrogenase, cytosolic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZB77	12	D-3-phosphoglycerate dehydrogenase 2, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DKC9	2	glucan endo-1,3-beta-glucosidase 4	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EGC3	7	40S ribosomal protein SA isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZC22	5	ATP phosphoribosyltransferase 2, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YKF2	12	DNA damage-repair/toleration protein DRT102	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZH12	12	eukaryotic initiation factor 4A-3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED

A0A444YRS0	3	probable xyloglucan endotransglucosylase/hydrolase protein B	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YDF4	18	receptor kinase-like protein Xa21	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YJ95	3	aspartic proteinase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Y0K0	16	glyceraldehyde-3-phosphate dehydrogenase GAPCP1, chloroplastic-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YNX7	16	pyruvate kinase 1, cytosolic isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WPT5	12	GTP-binding protein SAR1A	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445ETG3	2	subtilisin-like protease SBT1.7	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A3E8	2	profilin-1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CZE9	4	sorbitol dehydrogenase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AJ02	3	acylamino-acid-releasing enzyme isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BDU0	3	chalcone--flavonone isomerase 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DCU5	3	probable UDP-arabinopyranose mutase 5	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YCA5	20	isocitrate dehydrogenase [NADP]	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DGQ0	5	FK506-binding protein 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XWD3	2	cyclase-like protein 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EV37	5	CBS domain-containing protein CBSX3, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AAB1	7	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (ferredoxin), chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZZ22	20	puromycin-sensitive aminopeptidase isoform X2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BKU1	6	importin subunit alpha-2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E3G2	15	glucose-1-phosphate adenylyltransferase large subunit 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YMB1	9	alcohol dehydrogenase class-3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZBM0	5	protein transport protein SEC23	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DGU8	2	peptidyl-prolyl cis-trans isomerase FKBP62	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XDH8	15	seed linoleate 9S-lipoxygenase-3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WZY3	3	mediator of RNA polymerase II transcription subunit 36a	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YWV3	2	gamma carbonic anhydrase 1, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZDX5	3	obg-like ATPase 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A0X3	2	ATP synthase CF1 alpha subunit	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BP87	2	60S ribosomal protein L5	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CNY2	7	probable aldo-keto reductase 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CA43	3	TolB protein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AMC5	6	trans-cinnamate 4-monooxygenase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AF75	3	40S ribosomal protein S20-2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YCM7	8	probable fructokinase-6, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WS55	23	succinate dehydrogenase [ubiquinone] flavoprotein subunit 1, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DA81	7	probable mediator of RNA polymerase II transcription subunit 37c	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED

A0A445ANY1	14	proteasome subunit alpha type-6	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445D2M1	7	peroxiredoxin-2B	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZRW6	16	serine hydroxylmethyltransferase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EMG5	3	peroxidase 40	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BZY4	13	ADP,ATP carrier protein 1, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EC07	4	NADH dehydrogenase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZWW0	6	fructose-1,6-bisphosphatase, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DKT8	3	heat shock 70 kDa protein 17	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XBV8	4	pyrophosphate-energized vacuolar membrane proton pump	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BE69	27	V-type proton ATPase subunit B2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AWL1	11	ATP-citrate synthase beta chain protein 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BI73	18	malate dehydrogenase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WXU4	5	proline iminopeptidase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445D2N7	7	probable lactoylglutathione lyase, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CWK1	7	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A4W1	14	ketol-acid reductoisomerase, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DUQ9	8	xylose isomerase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DA87	10	heat shock cognate 70 kDa protein-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X2Q0	8	eukaryotic translation initiation factor 3 subunit F	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AA86	2	basic transcription factor 3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DN91	16	guanosine nucleotide diphosphate dissociation inhibitor 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DQH7	10	protease Do-like 7	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DAK6	13	F-box protein CPR1-like isoform X2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CBG9	3	serpin-ZX	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CXE9	6	aspartate--tRNA ligase 2, cytoplasmic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DMN9	8	beta-hydroxyacyl-ACP dehydrase 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BC65	5	pyridoxal 5'-phosphate synthase subunit PDX1.3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CB29	7	importin subunit beta-1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BQI5	2	3-isopropylmalate dehydratase small subunit 3-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B1A4	7	Bifunctional purine biosynthesis protein PurH	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZJQ9	7	ERBB-3 BINDING PROTEIN 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZMU5	5	proline iminopeptidase-like protein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EIW8	13	DEAD-box ATP-dependent RNA helicase 56 isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DQ58	23	UTP--glucose-1-phosphate uridylyltransferase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445D2Y2	14	photosystem II CP47 chlorophyll apoprotein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X4N2	4	chloroplastic import inner membrane translocase subunit HP30-2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XPN3	3	eukaryotic translation initiation factor 6-2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED

A0A445BF14	3	probable cinnamyl alcohol dehydrogenase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BGN3	12	coatomer subunit alpha-2-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WXJ6	6	serine-threonine kinase receptor-associated protein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BXJ4	3	fasciclin-like arabinogalactan protein 13	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DNF3	7	T-complex protein 1 subunit delta	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E7N6	18	monodehydroascorbate reductase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YBV0	9	CBS domain-containing protein CBSX3, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445D9W9	7	glycine--tRNA ligase, mitochondrial 1-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445ETR1	12	methylenetetrahydrofolate reductase 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E165	4	dnaJ protein homolog	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XDL1	6	nucleoside diphosphate kinase 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AXY9	3	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CTA4	15	probable alpha-mannosidase At5g13980	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AUI1	18	aldehyde dehydrogenase family 2 member B4, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AHX0	2	polygalacturonase inhibitor-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DTY1	14	monodehydroascorbate reductase 5, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YCC5	21	Glutamate decarboxylase 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B1X8	14	proteasome subunit alpha type-3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DTV1	7	puromycin-sensitive aminopeptidase isoform X3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X5B5	4	histone H3.2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XBQ4	9	mitochondrial dicarboxylate/tricarboxylate transporter DTC	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445C227	23	ribonuclease J isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X977	4	omega-amidase, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WPE0	2	glucan endo-1,3-beta-glucosidase, basic isoform	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YZE6	4	probable caffeoyl-CoA O-methyltransferase At4g26220	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WW48	14	pectin acetylesterase 8	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BYZ0	17	ADP,ATP carrier protein 1, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AND8	34	heat shock cognate protein 80	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EKD7	8	3-ketoacyl-CoA synthase 11	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BG04	5	zinc finger CCHC domain-containing protein 9	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CM38	24	rhomboid-like protein 15 isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XT34	2	ATP synthase subunit d, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445ACL3	9	calcium-transporting ATPase, endoplasmic reticulum-type	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZW17	11	probable cytosolic oligopeptidase A	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BMR3	4	peroxidase A2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A5Z7	3	Protein usf	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Y8X9	24	linoleate 9S-lipoxygenase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED

A0A444YR78	29	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YIK7	3	pectinesterase-like isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YVU0	3	far upstream element-binding protein 2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CFS4	7	glycine-rich RNA-binding protein	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YMM7	7	ras-related protein RABE1a	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZCV0	2	tropinone reductase-like 3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AHR4	7	pyruvate kinase 1, cytosolic-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Y8V2	25	ABC transporter G family member 36	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YFL6	32	heat shock cognate protein 80	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZU48	4	mitochondrial import receptor subunit TOM40-1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CWY8	2	ATP-dependent zinc metalloprotease FTSH 4, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E8C3	3	hydroxyisourate hydrolase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EEJ7	9	cyclin D1/2/4	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445C262	3	3-isopropylmalate dehydratase large subunit, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CS98	6	60S ribosomal protein L30	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445D9V9	20	transaldolase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YJU5	5	60S ribosomal protein L22-2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444WNW6	2	MFP1 attachment factor 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A908	9	allene oxide synthase 3	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BTV1	9	14-3-3-like protein B	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
Q45W77	7	ubiquitin-conjugating enzyme E2 36	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A3P9	16	phosphoenolpyruvate carboxylase, housekeeping isozyme	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AIA4	5	homoserine kinase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XM91	2	serine/threonine-protein phosphatase PP1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AYN0	3	cullin-associated NEDD8-dissociated protein 1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YFW7	7	oxygen-dependent coproporphyrinogen-III oxidase, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DY80	6	probable 3-hydroxyisobutyrate dehydrogenase-like 1, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BQ62	32	heat shock 70 kDa protein 15-like	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445EBY1	3	small nuclear ribonucleoprotein SmD3b	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445D768	3	photosystem II cytochrome b559 alpha subunit	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZFB4	5	importin subunit alpha-2	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YIZ9	11	proline--tRNA ligase, cytoplasmic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Z225	16	formate dehydrogenase, mitochondrial isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CRE7	3	pyridoxal kinase isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445D336	2	proteasome subunit beta type-7-B	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BDW2	11	formate--tetrahydrofolate ligase	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZPW4	2	chaperone protein ClpB3, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED

A0A445E5C3	8	40S ribosomal protein S28	UNCHANGED	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DAI2	27	Aldo/keto reductase	UNCHANGED	UNCHANGED	DOWN	UNCHANGED
A0A444Y659	14	heat shock cognate 70 kDa protein-like	UNCHANGED	UNCHANGED	DOWN	UNCHANGED
A0A445DW87	3	thiol protease aleurain-like	UNCHANGED	UNCHANGED	DOWN	UNCHANGED
A0A445BWT0	41	aconitate hydratase, cytoplasmic	UNCHANGED	UNCHANGED	DOWN	UNCHANGED
A0A445CNU0	7	proteasome subunit beta type-4	UNCHANGED	UNCHANGED	DOWN	UNCHANGED
A0A444Z767	15	glutamate--glyoxylate aminotransferase 2	UNCHANGED	UNCHANGED	DOWN	UNCHANGED
A0A444XGU2	25	linoleate 9S-lipoxygenase	UNCHANGED	UNCHANGED	DOWN	UNCHANGED
A0A444XDE6	10	seed linoleate 9S-lipoxygenase-3	UNCHANGED	UNCHANGED	DOWN	UNCHANGED
A0A445AFM7	7	alcohol dehydrogenase class-3	UNCHANGED	UNCHANGED	DOWN	UNCHANGED
A0A445E9E3	2	AT-hook motif nuclear-localized protein 7-like	UNCHANGED	UNCHANGED	DOWN	UNCHANGED
A0A445C6F7	5	ATPase subunit 8	UNCHANGED	UNCHANGED	DOWN	UNCHANGED
A0A445DEQ9	12	cationic peroxidase 1	UNCHANGED	UNCHANGED	DOWN	UNCHANGED
A0A445DYX7	3	receptor-like protein kinase THESEUS 1	UNCHANGED	UNCHANGED	DOWN	UNCHANGED
A0A445EHF2	6	pectinesterase	UNCHANGED	UNCHANGED	DOWN	UNCHANGED
A0A445E8M7	9	40S ribosomal protein S5	UNCHANGED	UNCHANGED	UNCHANGED	DOWN
A0A444ZP19	7	serine hydroxymethyltransferase 3, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	DOWN
A0A445EU47	2	endochitinase	UNCHANGED	UNCHANGED	UNCHANGED	DOWN
A0A445BXR7	19	heat shock cognate 70 kDa protein-like	UNCHANGED	UNCHANGED	UNCHANGED	DOWN
A0A445B037	16	probable aldehyde dehydrogenase isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	DOWN
A0A445DB36	5	UDP-arabinopyranose mutase 1	UNCHANGED	UNCHANGED	UNCHANGED	DOWN
A0A445BDT8	2	beta-hexosaminidase 1	UNCHANGED	UNCHANGED	UNCHANGED	DOWN
A0A444XRR8	27	chaperonin CPN60-2, mitochondrial	UNCHANGED	UNCHANGED	UNCHANGED	DOWN
A0A444XQF7	6	plastid-lipid-associated protein 6, chloroplastic	UNCHANGED	UNCHANGED	UNCHANGED	DOWN
A0A445D7V0	2	pectinesterase	UNCHANGED	UNCHANGED	UNCHANGED	DOWN
A0A445DW96	12	aldehyde dehydrogenase family 7 member A1	UNCHANGED	UNCHANGED	UNCHANGED	DOWN
A0A445BZV8	2	benzyl alcohol O-benzoyltransferase	UNCHANGED	UNCHANGED	UNCHANGED	DOWN
A0A445CZ04	9	Heat shock protein Hsp90	UNCHANGED	UNCHANGED	UNCHANGED	DOWN
A0A444XU44	2	hevamine-A	UNCHANGED	UNCHANGED	UNCHANGED	DOWN
A0A445BZL2	3	MLP-like protein 34	UNCHANGED	UNCHANGED	UNCHANGED	DOWN
A0A445DWR8	24	cell division cycle protein 48 homolog	UNCHANGED	UNCHANGED	UNCHANGED	DOWN
A0A444Y8L6	2	alcohol dehydrogenase 1	UNCHANGED	UNCHANGED	UNCHANGED	DOWN
A0A445BR12	2	glucose-1-phosphate adenylyltransferase large subunit 1 isoform X1	UNCHANGED	UNCHANGED	UNCHANGED	DOWN
A0A445AYA2	2	ATP-dependent 6-phosphofructokinase 2	UNCHANGED	UNCHANGED	UNCHANGED	DOWN
A0A444YYV3	8	2-hydroxyacyl-CoA lyase	UNCHANGED	UNCHANGED	UNCHANGED	DOWN
A0A444ZZV5	11	biotin carboxylase 2, chloroplastic	UNCHANGED	UNCHANGED	DOWN	DOWN
A0A444ZCE6	16	elongation factor Tu, mitochondrial	UNCHANGED	UNCHANGED	DOWN	DOWN

A0A444YFQ5	25	glucose-1-phosphate adenylyltransferase small subunit 2, chloroplastic	UNCHANGED	UNCHANGED	DOWN	DOWN
A0A444Y023	3	protein FAR1-RELATED SEQUENCE 5-like	UNCHANGED	UNCHANGED	DOWN	DOWN
A0A444ZBQ0	10	selenium-binding protein 1	UNCHANGED	UNCHANGED	DOWN	DOWN
A0A445D3G8	3	NADP-dependent malic enzyme	UNCHANGED	UNCHANGED	DOWN	DOWN
A0A444ZSR4	10	eukaryotic translation initiation factor 3 subunit I-like	UNCHANGED	UNCHANGED	DOWN	DOWN
A0A445C543	9	peroxidase P7-like	DOWN	UNCHANGED	UP	UNCHANGED
A0A445DT01	3	patellin-3	DOWN	UNCHANGED	UP	UNCHANGED
A0A445CE34	7	glucose-1-phosphate adenylyltransferase large subunit 1	DOWN	UNCHANGED	UP	UNCHANGED
A0A445CR15	12	triosephosphate isomerase, chloroplastic	DOWN	UNCHANGED	UP	UNCHANGED
A0A445B5D2	2	carbamoyl-phosphate synthase small chain, chloroplastic	DOWN	UNCHANGED	UP	UNCHANGED
A0A445ENA2	17	heat shock 70 kDa protein	DOWN	UNCHANGED	UP	UNCHANGED
A0A444YGN2	3	glutathione reductase, chloroplastic	DOWN	UNCHANGED	UP	UNCHANGED
A0A444ZDX1	33	tubulin beta chain	DOWN	UNCHANGED	UP	UNCHANGED
A0A445D168	16	glutamate decarboxylase-like	DOWN	UNCHANGED	UP	UNCHANGED
A0A445BU13	22	tubulin alpha chain	DOWN	UNCHANGED	UP	UNCHANGED
A0A444Y8R8	15	probable fructokinase-4	DOWN	UNCHANGED	UP	UNCHANGED
A0A445E3R9	12	glutamate-1-semialdehyde 2,1-aminomutase, chloroplastic	DOWN	UNCHANGED	UP	UNCHANGED
A0A445DCB5	2	2-dehydro-3-deoxyphosphooctonate aldolase	DOWN	UNCHANGED	UP	UNCHANGED
A0A445EAT1	8	chlorophyll a-b binding protein CP29.2, chloroplastic	DOWN	UNCHANGED	UP	UNCHANGED
A0A445BBW8	7	14-3-3-like protein C	DOWN	UNCHANGED	UP	UNCHANGED
A0A445D9Q8	3	hsp70-Hsp90 organizing protein 3-like	DOWN	UNCHANGED	UP	UNCHANGED
A0A444ZW26	4	glutamine synthetase nodule isozyme	DOWN	UNCHANGED	UP	UNCHANGED
A0A444ZB98	5	protein argonaute 4	DOWN	UNCHANGED	UP	UNCHANGED
A0A445D4N7	8	chlorophyll a-b binding protein CP26, chloroplastic	DOWN	UNCHANGED	UP	UNCHANGED
I6XQQ7	6	S-adenosylmethionine synthase 1	DOWN	UNCHANGED	UP	UNCHANGED
A0A445BEL0	2	dihydrolipoyllysine-residue acetyltransferase component 4 of pyruvate dehydrogenase complex, chloroplastic	DOWN	UNCHANGED	UP	UNCHANGED
A0A445E858	5	endoglucanase 17	DOWN	UNCHANGED	UP	UNCHANGED
A0A444WYJ8	2	allantoinase	DOWN	UNCHANGED	UP	UNCHANGED
A0A444Y536	2	probable NAD(P)H dehydrogenase (quinone) FQR1-like 1	DOWN	UNCHANGED	UP	UNCHANGED
A0A445CFC7	2	vicianin hydrolase	DOWN	UNCHANGED	UP	UNCHANGED
A0A445BFK3	15	photosystem I reaction center subunit II, chloroplastic	DOWN	UNCHANGED	UP	UNCHANGED
A0A444Y823	9	carbamoyl-phosphate synthase large chain, chloroplastic	DOWN	UNCHANGED	UP	UNCHANGED
A0A444X279	9	chlorophyll a-b binding protein CP29.3, chloroplastic	DOWN	UNCHANGED	UP	UNCHANGED
A0A444XQQ0	12	plastid-lipid-associated protein 6, chloroplastic	DOWN	UNCHANGED	UP	UNCHANGED
A0A445BDM9	5	2-isopropylmalate synthase 2, chloroplastic	DOWN	UNCHANGED	UP	UNCHANGED
A0A445DLK1	7	3-oxoacyl-[acyl-carrier-protein] reductase 4 isoform X1	DOWN	UNCHANGED	UP	UNCHANGED

A0A445E7W0	17	LL-diaminopimelate aminotransferase, chloroplastic	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DQ85	21	glutamate decarboxylase	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A3J6	7	ankyrin repeat and zinc finger domain-containing protein 1	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DA67	28	actin-11	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CII9	8	coatomer subunit beta'-2 isoform X1	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BYE8	4	chlorophyll a-b binding protein 13, chloroplastic	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CLH1	2	proliferating cell nuclear antigen	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A9Q0	5	ras-related protein Rab11C	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445A495	7	thiamine thiazole synthase, chloroplastic	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BK32	11	cysteine synthase	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DVJ9	29	hypothetical chloroplast RF21	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E0E4	13	equilibrative nucleotide transporter 3	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
D8KXZ7	13	enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic-like	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B9I7	4	GDSL esterase/lipase At5g14450	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E514	26	ruBisCO large subunit-binding protein subunit alpha	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445ERM0	11	elongation factor G-2, chloroplastic	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
L7PCI4	2	ras-related protein Rab7	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E7A3	3	phenylalanine ammonia-lyase	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445C8X3	5	phosphoenolpyruvate carboxykinase (ATP)	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A444YZP0	16	NADP-dependent malic enzyme	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DSZ0	2	Succinate-semialdehyde dehydrogenase (acetylating)	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZHU9	3	transcription factor Pur-alpha 1	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DC80	7	subtilisin-like protease Glyma18g48580	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445E4X9	17	UDP-D-apiose/UDP-D-xylose synthase 2	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Y924	5	phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic-like	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445CS70	4	ATP-dependent Clp protease proteolytic subunit 5, chloroplastic	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A444Z364	19	alpha-xylosidase 1	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BYQ2	4	probable bifunctional methylthioribulose-1-phosphate dehydratase/enolase-phosphatase E1	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A444ZJY2	3	adenylosuccinate synthetase 2, chloroplastic	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A444XBV0	2	40S ribosomal protein S12	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A444X596	2	photosystem I reaction center subunit N, chloroplastic	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445D2F3	2	aldehyde dehydrogenase family 2 member C4 isoform X1	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445BWX1	16	peroxidase 3	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445AD29	5	oxygen-evolving enhancer protein 3-2, chloroplastic	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445B636	3	stomatin-like protein 2, mitochondrial	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445DIV1	23	Peroxidase 15	DOWN	UNCHANGED	UNCHANGED	UNCHANGED

A0A444XB67	20	tubulin alpha-3 chain	DOWN	UNCHANGED	UNCHANGED	UNCHANGED
A0A445ETS2	7	ADP-ribosylation factor 1-like isoform X1	DOWN	UNCHANGED	UP	DOWN
A0A445DYP5	22	dolichol kinase EVAN isoform X1	DOWN	UNCHANGED	UNCHANGED	DOWN
A0A444Y732	7	fatty acid hydroperoxide lyase, chloroplastic	DOWN	UNCHANGED	UNCHANGED	DOWN
A0A444X9W6	22	Lysosomal beta glucosidase	DOWN	UNCHANGED	UNCHANGED	DOWN
A0A445BJM5	8	probable aldo-keto reductase 1	DOWN	UNCHANGED	UNCHANGED	DOWN
A0A445ELZ8	2	dihydrolipoyl dehydrogenase 2, chloroplastic	DOWN	UNCHANGED	UNCHANGED	DOWN
A0A444XWM2	4	ribonuclease TUDOR 1	-	UNCHANGED	Unique BA2.5_Cotyledonary	Unique BA0_Cotyledonary
A0A445AUL4	6	eukaryotic initiation factor 4A-6	-	UNCHANGED	Unique BA2.5_Cotyledonary	Unique BA0_Cotyledonary
A0A445BVW9	7	protein disulfide isomerase-like 1-4	-	UNCHANGED	Unique BA2.5_Cotyledonary	Unique BA0_Cotyledonary
A0A445DAH2	9	probable aldo-keto reductase 2 isoform X1	-	UNCHANGED	Unique BA2.5_Cotyledonary	Unique BA0_Cotyledonary
A0A445DG07	7	serine hydroxymethyltransferase 3, chloroplastic	-	UNCHANGED	Unique BA2.5_Cotyledonary	Unique BA0_Cotyledonary
A0A445D0Z0	9	carbonic anhydrase, chloroplastic isoform X2	UP	DOWN	UNCHANGED	UP
A0A444YX30	5	polypyrimidine tract-binding protein homolog 3 isoform X1	UP	DOWN	DOWN	UP
A0A445B253	10	ribulose bisphosphate carboxylase small chain 1, chloroplastic	UP	DOWN	DOWN	UP
A0A444XZJ1	2	MLP-like protein 34	Unique BA2.5_Apical	DOWN	UNCHANGED	Unique BA0_Cotyledonary
A0A445CXW8	7	polyadenylate-binding protein 2-like	Unique BA2.5_Apical	DOWN	UNCHANGED	Unique BA0_Cotyledonary
A0A444ZH18	11	ATP-dependent zinc metalloprotease FTSH 2, chloroplastic	Unique BA0_Apical	DOWN	Unique BA2.5_Cotyledonary	UP
A0A444Y881	3	UDP-glucuronic acid decarboxylase 6	Unique BA0_Apical	DOWN	Unique BA2.5_Cotyledonary	UNCHANGED
A0A445C024	2	Beta-glucosidase 13	Unique BA0_Apical	DOWN	Unique BA2.5_Cotyledonary	UNCHANGED
A0A445DBR9	2	ATP-dependent zinc metalloprotease FTSH 6, chloroplastic	Unique BA0_Apical	DOWN	Unique BA2.5_Cotyledonary	UNCHANGED
A0A445EHL4	9	chloroplast stem-loop binding protein of 41 kDa b, chloroplastic	UNCHANGED	DOWN	UP	UP
A0A445DYJ7	5	ankyrin repeat and zinc finger domain-containing protein 1	UNCHANGED	DOWN	UP	UP
A0A445DYM5	7	protochlorophyllide reductase, chloroplastic	UNCHANGED	DOWN	UP	UP
A0A444XZI9	2	MLP-like protein 34	UNCHANGED	DOWN	UP	UP
A0A445DW27	9	20 kDa chaperonin, chloroplastic	UNCHANGED	DOWN	UNCHANGED	UP
A0A445DRP2	14	LL-diaminopimelate aminotransferase, chloroplastic	UNCHANGED	DOWN	UNCHANGED	UP
A0A444Y7V9	7	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (ferredoxin), chloroplastic	UNCHANGED	DOWN	UNCHANGED	UP
A0A445EF65	20	ATP synthase beta subunit	UNCHANGED	DOWN	UNCHANGED	UP

A0A444YDT6	11	uroporphyrinogen decarboxylase	UNCHANGED	DOWN	UNCHANGED	UP
A0A445EDG2	8	Cytochrome b6	UNCHANGED	DOWN	UNCHANGED	UP
A0A445CJP2	6	thioredoxin-like protein CDSP32, chloroplastic	UNCHANGED	DOWN	UNCHANGED	UP
A0A444ZVK9	20	serine hydroxymethyltransferase, mitochondrial	UNCHANGED	DOWN	UNCHANGED	UP
A0A445EQM5	11	hypothetical chloroplast RF21	UNCHANGED	DOWN	UNCHANGED	UP
A0A445ADB6	15	ketol-acid reductoisomerase, chloroplastic	UNCHANGED	DOWN	UNCHANGED	UP
A0A445A189	17	20 kDa chaperonin, chloroplastic	UNCHANGED	DOWN	UNCHANGED	UP
A0A445BWH0	38	cell division cycle protein 48 homolog	UNCHANGED	DOWN	UNCHANGED	UP
A0A445D9A2	2	cysteine synthase isoform X1	UNCHANGED	DOWN	UNCHANGED	UP
A0A445DJX1	14	glutamine synthetase leaf isozyme, chloroplastic	UNCHANGED	DOWN	UNCHANGED	UP
A0A444YG88	26	tubulin beta chain	UNCHANGED	DOWN	UNCHANGED	UP
A0A445BP53	2	beta-galactosidase 1	UNCHANGED	DOWN	UNCHANGED	UP
A0A444XGR5	4	photosystem I subunit VII	UNCHANGED	DOWN	UNCHANGED	UP
A0A444YVR3	23	glycine dehydrogenase (decarboxylating), mitochondrial	UNCHANGED	DOWN	UNCHANGED	UP
A0A445ESG6	2	ubiquinone biosynthesis protein COQ9, mitochondrial isoform X1	UNCHANGED	DOWN	UNCHANGED	UP
A0A445DRB1	6	polyphenol oxidase A1, chloroplastic	UNCHANGED	DOWN	UNCHANGED	UP
A0A445DQU5	8	magnesium-chelatase subunit ChlI, chloroplastic	UNCHANGED	DOWN	UNCHANGED	UP
A0A445BWT3	5	40S ribosomal protein S27-2	UNCHANGED	DOWN	UNCHANGED	UP
A0A444ZMW4	2	peroxidase 3	UNCHANGED	DOWN	UNCHANGED	UP
A0A444YWW5	2	uncharacterized oxidoreductase At4g09670	UNCHANGED	DOWN	UNCHANGED	UP
A0A445BUM3	13	photosystem I P700 apoprotein A1	UNCHANGED	DOWN	UNCHANGED	UP
A0A444X1T0	5	GDP-mannose 3,5-epimerase	UNCHANGED	DOWN	UP	UNCHANGED
A0A445D6R8	2	uncharacterized protein LOC107488444	UNCHANGED	DOWN	UP	UNCHANGED
A0A445BCE7	9	peroxisomal (S)-2-hydroxy-acid oxidase	UNCHANGED	DOWN	UP	UNCHANGED
A0A444YPK8	5	monodehydroascorbate reductase	UNCHANGED	DOWN	UP	UNCHANGED
A0A445EJM7	7	UDP-glucose 6-dehydrogenase 1	UNCHANGED	DOWN	UP	UNCHANGED
A0A445D3V7	27	actin-1	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A444Y2S5	23	ruBisCO large subunit-binding protein subunit beta, chloroplastic	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A444Y0E3	8	proteasome subunit alpha type-2-A	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A445A6V2	3	hypothetical protein Ahy_B03g067459	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A445CIS5	6	D-3-phosphoglycerate dehydrogenase 2, chloroplastic-like	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A444YIF5	8	ATP synthase CF1 alpha subunit	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A445AVM3	3	temperature-induced lipocalin-1	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A445D367	13	biotin carboxylase 1, chloroplastic	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A445DDG6	4	phosphomannomutase	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A445AI36	4	serine carboxypeptidase-like	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A445E7J6	3	ubiquitin-conjugating enzyme E2 variant 1D	UNCHANGED	DOWN	UNCHANGED	UNCHANGED

A0A445BAJ7	3	cationic peroxidase 2	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A445CXG6	7	vacuolar-processing enzyme	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A445AD05	6	pectinesterase	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A444Z2A3	2	protease Do-like 1, chloroplastic	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A445CZ80	32	tubulin beta-1 chain	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A445A7D9	8	protein EXPORTIN 1A	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A445BDQ8	28	transketolase, chloroplastic	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A444ZM03	20	NAD-dependent malic enzyme 59 kDa isoform, mitochondrial	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A445DC61	7	subtilisin-like protease Glyma18g48580	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A444X7Z1	16	hypersensitive-induced response protein-like protein 2	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A445AP00	2	aspartyl protease family protein At5g10770	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A444YKC5	6	probable ribose-5-phosphate isomerase 3, chloroplastic	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A445DI23	2	ATP synthase CF1 alpha subunit	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A444X980	19	6-phosphogluconate dehydrogenase, decarboxylating 3	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A445AVK1	18	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A445A8V9	7	isoflavone reductase homolog PCBER	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A445D5C7	18	UDP-glucose 6-dehydrogenase 4	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A444YQU9	6	peroxidase 44	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
G3F840	6	2-methyl-6-phytyl-1,4-hydroquinone methyltransferase, chloroplastic	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A444ZDQ2	9	Lysosomal beta glucosidase	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A444WYZ1	8	magnesium-chelatase subunit ChlI, chloroplastic	UNCHANGED	DOWN	UNCHANGED	UNCHANGED
A0A445DPL3	7	carbonic anhydrase 2 isoform X1	UNCHANGED	DOWN	DOWN	UNCHANGED
A0A445BUX1	11	seed linoleate 9S-lipoxygenase-2	UNCHANGED	DOWN	DOWN	UNCHANGED
A0A445E885	4	putative disease resistance RPP13-like protein 1 isoform X1	UNCHANGED	DOWN	UNCHANGED	DOWN
A0A444Y4T5	4	universal stress protein PHOS32 isoform X1	UNCHANGED	DOWN	DOWN	DOWN
A0A445ENE7	4	xylose isomerase	DOWN	DOWN	UP	UP
A0A444ZV87	3	2-methylene-furan-3-one reductase	DOWN	DOWN	UP	UP
A0A444YCV3	23	ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic	DOWN	DOWN	UP	UP
A0A445DVU6	17	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	DOWN	DOWN	UP	UP
A0A444ZW91	24	ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic	DOWN	DOWN	UP	UP
A0A445AH22	30	ATP synthase subunit beta, chloroplastic	DOWN	DOWN	UP	UP
A0A445BBL2	3	30S ribosomal protein S5, chloroplastic	DOWN	DOWN	UP	UP
A0A445C7I8	12	sedoheptulose-1,7-bisphosphatase, chloroplastic	DOWN	DOWN	UP	UP
A0A445BHJ0	14	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	DOWN	DOWN	UP	UP
A0A445CJL4	12	ATP-dependent zinc metalloprotease FTSH, chloroplastic	DOWN	DOWN	UP	UP
A0A445DQJ9	4	ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic	DOWN	DOWN	UP	UP
A0A445DGE4	5	fructose-1,6-bisphosphatase, chloroplastic	DOWN	DOWN	UP	UP

A0A445A943	6	linoleate 13S-lipoxygenase 2-1, chloroplastic	DOWN	DOWN	UP	UP
A0A445AD56	8	chloroplast stem-loop binding protein of 41 kDa b, chloroplastic	DOWN	DOWN	UP	UP
A0A445DIV4	4	photosystem I reaction center subunit III, chloroplastic	DOWN	DOWN	UP	UP
A0A444WVN0	3	bifunctional pinoresinol-lariciresinol reductase 2-like	DOWN	DOWN	UP	UP
A0A445AKK6	3	flagellar radial spoke protein 5 isoform X2	DOWN	DOWN	UP	UP
A0A445E3Z0	6	beta-glucosidase 12	DOWN	DOWN	UP	UP
A0A444XLM2	6	UPF0603 protein At1g54780, chloroplastic	DOWN	DOWN	UP	UP
A0A445DJ87	3	phosphoglycolate phosphatase 2	DOWN	DOWN	UP	UP
A0A445C3P5	4	chloroplastic lipocalin	DOWN	DOWN	UP	UP
A0A444Z0X0	12	beta-glucosidase 44	DOWN	DOWN	UP	UP
A0A445CIM7	2	methyl-CpG-binding domain-containing protein 11	DOWN	DOWN	UP	UP
A0A445AJD1	25	ribulose bisphosphate carboxylase/oxygenase activase 2, chloroplastic isoform X1	DOWN	DOWN	UNCHANGED	UP
A0A444X9J3	9	ras-related protein RABB1b	DOWN	DOWN	UNCHANGED	UP
A0A445BGN5	5	malate dehydrogenase [NADP], chloroplastic	DOWN	DOWN	UNCHANGED	UP
A0A445DC02	3	atpA	DOWN	DOWN	UNCHANGED	UP
A0A445CHH2	21	(S)-2-hydroxy-acid oxidase GLO1	DOWN	DOWN	UNCHANGED	UP
A0A445E402	5	linoleate 13S-lipoxygenase 2-1, chloroplastic	DOWN	DOWN	UNCHANGED	UP
A0A445ATT0	15	elongation factor Tu, chloroplastic	DOWN	DOWN	UNCHANGED	UP
A0A445DWP1	5	28 kDa ribonucleoprotein, chloroplastic	DOWN	DOWN	UNCHANGED	UP
A0A444YMB3	2	photosystem I reaction center subunit IV, chloroplastic	DOWN	DOWN	UNCHANGED	UP
A0A445D4K5	2	beta-glucosidase 12	DOWN	DOWN	UNCHANGED	UP
A0A444XIZ7	2	DEAD-box ATP-dependent RNA helicase 3, chloroplastic	DOWN	DOWN	UNCHANGED	UP
A0A444YVA2	11	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	DOWN	DOWN	UP	UNCHANGED
A0A445CR60	4	phenylalanine ammonia-lyase 1	DOWN	DOWN	UP	UNCHANGED
A0A445DM32	22	ATP-dependent zinc metalloprotease FTSH 2, chloroplastic	DOWN	DOWN	UP	UNCHANGED
A0A444YP33	2	cytochrome f	DOWN	DOWN	UP	UNCHANGED
D8KXY7	2	malonyl-CoA:ACP transacylase 1-3	DOWN	DOWN	UP	UNCHANGED
A0A445BSX3	8	delta-aminolevulinic acid dehydratase, chloroplastic	DOWN	DOWN	UP	UNCHANGED
A0A444XC48	11	DEAD-box ATP-dependent RNA helicase 56 isoform X2	DOWN	DOWN	UP	UNCHANGED
A0A445EKE3	6	S-adenosylmethionine synthase	DOWN	DOWN	UP	UNCHANGED
A0A445BUJ9	34	ATP synthase CF1 beta subunit	DOWN	DOWN	UP	UNCHANGED
A0A445EC49	5	UDP-sulfoquinovose synthase, chloroplastic	DOWN	DOWN	UP	UNCHANGED
A0A445AM91	3	probable histone H2A.5	DOWN	DOWN	UP	UNCHANGED
A0A445AB33	21	elongation factor Tu, chloroplastic	DOWN	DOWN	UP	UNCHANGED
A0A445C4T5	3	plastocyanin	DOWN	DOWN	UP	UNCHANGED
A0A444ZAX2	4	peroxiredoxin Q, chloroplastic	DOWN	DOWN	UP	UNCHANGED

A0A445DM62	3	NAD-binding Rossmann-fold superfamily protein	DOWN	DOWN	UP	UNCHANGED
A0A444ZSQ9	7	Cytochrome f	DOWN	DOWN	UP	UNCHANGED
A0A445EUB7	11	alpha-mannosidase	DOWN	DOWN	UP	UNCHANGED
A0A445A0S5	5	ATP synthase CF1 alpha subunit	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A444YIX8	19	S-adenosylmethionine synthase	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A445E8D9	3	soluble inorganic pyrophosphatase 6, chloroplastic	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A444WUG6	17	ferredoxin--NADP reductase, leaf isozyme, chloroplastic	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A444WVJ5	14	phosphoribulokinase, chloroplastic	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A445EBD9	7	N-carbamoylputrescine amidase	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A445C4F8	16	beta-glucosidase BoGH3B-like	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A444Z503	6	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A445D060	18	alpha-xylosidase 1	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A445E7B3	9	fructose-bisphosphate aldolase 6, cytosolic-like	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A444X7E6	9	enolase 1, chloroplastic	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A445AZM4	5	ribulose-phosphate 3-epimerase, chloroplastic	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A445BZ81	6	protochlorophyllide reductase, chloroplastic	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A444X314	7	probable N-acetyl-gamma-glutamyl-phosphate reductase, chloroplastic	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A445DR20	3	non-classical arabinogalactan protein 31	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A444Y7Y6	7	beta-galactosidase 8-like	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A445EE78	3	photosystem I subunit VII	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A445ANU8	14	oxygen-evolving enhancer protein 1, chloroplastic	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A444X1D5	2	carbamoyl-phosphate synthase small chain, chloroplastic	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A445AV19	20	plasma membrane ATPase 4	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A445AU23	7	glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A445C3W2	6	oxygen-evolving enhancer protein 2, chloroplastic	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A445AN70	2	neutral ceramidase 1	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A445E2S4	13	photosystem II stability/assembly factor HCF136, chloroplastic	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A444XEE9	7	2-alkenal reductase (NADP(+)-dependent)	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A445AKJ4	3	beta-glucosidase 11-like isoform X2	DOWN	DOWN	UNCHANGED	UNCHANGED
A0A445C5W3	2	ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic	-	DOWN	Unique BA2.5_Cotyledonary	Unique BA0_Cotyledonary
A0A445EWM0	4	ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic	-	DOWN	Unique BA2.5_Cotyledonary	Unique BA0_Cotyledonary
A0A444ZTA5	3	NAD-binding Rossmann-fold superfamily protein	Unique BA2.5_Apical	-	Unique BA2.5_Apical	-
A0A444ZZ40	2	mitogen-activated protein kinase homolog MMK2	Unique BA2.5_Apical	-	Unique BA2.5_Apical	-
A0A444YVI6	11	60S acidic ribosomal protein P0	Unique BA0_Apical	-	-	Unique BA0_Apical
A0A444ZSC8	12	(S)-2-hydroxy-acid oxidase GLO1	Unique BA0_Apical	-	-	Unique BA0_Apical
A0A445B4X1	2	CHD3-type chromatin-remodeling factor PICKLE	Unique BA0_Apical	-	-	Unique BA0_Apical

A0A445CDQ7	2	dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 2, mitochondrial	Unique BA0_Apical	-	-	Unique BA0_Apical
A0A445CFW5	2	plastid-lipid-associated protein 6, chloroplastic	Unique BA0_Apical	-	-	Unique BA0_Apical
A0A445DXU1	11	NADP-dependent malic enzyme	Unique BA0_Apical	-	-	Unique BA0_Apical
A0A445EUH3	4	6-phosphogluconate dehydrogenase, decarboxylating 1	Unique BA0_Apical	-	-	Unique BA0_Apical
A0A445ETU5	12	pectin acetylesterase 8	DOWN	-	Unique BA2.5_Apical	Unique BA0_Apical
A0A444XCD2	5	ras-related protein Rab7	DOWN	-	Unique BA2.5_Apical	Unique BA0_Apical
A0A445EGD1	11	40S ribosomal protein SA isoform X2	DOWN	-	Unique BA2.5_Apical	Unique BA0_Apical