

DANÚBIA RODRIGUES ALVES

**CARACTERIZAÇÃO DE UMA REGIÃO GENÔMICA DO
HÍBRIDO DE TIMOR CIFC 832/2 ASSOCIADA À
RESISTÊNCIA À *Hemileia vastatrix***

Dissertação apresentada à Universidade Federal de Viçosa, como parte das exigências do Programa de Pós-Graduação em Genética e Melhoramento, para obtenção do título de *Magister Scientiae*.

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APROVADA: 31 de julho de 2019.



Tiago Antônio de Oliveira Mendes
(Coorientador)



Gilza Barcelos de Souza



Eveline Teixeira Caixeta
(Orientadora)

*A Deus, por guiar meus passos,
Aos meus pais, Irene e Pedro,
E ao Arthur,
Por todo amor e dedicação,
Dedico*

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A Deus, por iluminar o meu caminho.

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“A persistência é o menor caminho do êxito.”

Charles Chaplin

RESUMO

ALVES, Danúbia Rodrigues, M.Sc., Universidade Federal de Viçosa, julho de 2019. **Caracterização de uma região genômica do Híbrido de Timor CIFC 832/2 associada à resistência à *Hemileia vastatrix***. Orientadora: Eveline Teixeira Caixeta. Coorientadores: Dênia Pires de Almeida e Tiago Antônio de Oliveira Mendes.

A ferrugem do cafeeiro, causada pelo fungo biotrófico *Hemileia vastatrix* é a principal doença de importância econômica dessa cultura, sendo responsável por grandes prejuízos à cafeicultura mundial. Novas raças do patógeno têm surgido infectando cultivares de café comercializados como resistentes a essa doença. Desse modo, devido ao alto potencial adaptativo do fungo, a busca por cafeeiros resistentes a essa doença é uma atividade recorrente nos programas de melhoramento. Estudos com o Híbrido de Timor (HdT), tem sido realizados em pesquisas que visam resistência durável à ferrugem e outras doenças do cafeeiro. Compreender a natureza da resistência duradoura em genótipos do HdT e descrever os genes envolvidos na defesa das plantas é fundamental para o uso eficiente dos recursos disponíveis nesse híbrido natural. A utilização de ferramentas moleculares e de bioinformática tem mostrado resultados significativos para a ampliação do conhecimento dos genes envolvidos no patossistema *Coffea* - *H. vastatrix*. Desse modo, objetivou-se com esse estudo sequenciar e caracterizar, por meio de análises de bioinformática, uma região do genoma do Híbrido de Timor CIFC 832/2, que contém marcadores associados à resistência à *H. vastatrix*. Para isso foi realizado o sequenciamento do clone BAC 70-22F contendo a marca funcional de resistência, por meio da Plataforma Illumina MiSeq (*paired – end reads*). Posteriormente foi feita a montagem dos *contigs* e a predição dos genes. Realizou-se a anotação gênica com base nos genomas de *Coffea arabica*, *Coffea canephora* e *Coffea eugenioides*, utilizando a ferramenta BLAST. A anotação gênica revelou a presença de genes candidatos relacionados ao mecanismo de resistência de hospedeiros contra patógenos. Foram anotados 991 genes do clone BAC 70-22F. Desses genes, 340 foram anotados com similaridade com o genoma de *C. arabica* (var. Caturra), 337 com o genoma de *C. eugenioides* e 314 com o genoma de *C. canephora* (clone IF 200). Com base na anotação gênica foram selecionadas duas sequências de genes candidatos a receptores *like kinases* (RLK) e desenhados *primers* para estudo do perfil de expressão gênica durante a interação *Coffea* - *H. vastatrix*. Um possível gene de resistência, *LRR receptor-like serine/threonine-protein kinase* GSO2, foi descrito e apresentou um perfil

de expressão correspondente a uma resposta de resistência pré-haustorial. O outro possível receptor *like kinase* em estudo, apresentando um domínio *LRR*, exibiu uma diminuição na expressão gênica pré-haustorial em genótipos incompatíveis. As análises filogenéticas desses genes, bem como os estudos de identidade e similaridade genética da região genômica clonada, demonstraram uma relação mais próxima entre o clone BAC 70-22F e a espécie *C. arabica* e corroboram com a diversidade genética descrita para o HdT. Os resultados sugerem que a região genômica clonada do HdT CIFC 832/2 possui importantes genes candidatos a resistência do cafeeiro à *H. vastatrix* e apresentam informações relevantes para ampliar o conhecimento sobre o HdT, podendo contribuir para futuros planejamentos de estratégias de melhoramento do cafeeiro.

ABSTRACT

ALVES, Danúbia Rodrigues, M.Sc., Universidade Federal de Viçosa, July, 2019. **Characterization of a genomic region of the Híbrido de Timor CIFC 832/2 associated with resistance to *Hemileia vastatrix*.** Advisor: Eveline Teixeira Caixeta. Co-advisers: Dênia Pires de Almeida and Tiago Antônio de Oliveira Mendes.

Coffee leaf rust, caused by the biotrophic fungus *Hemileia vastatrix* is the main disease of economic importance of this crop, being responsible for major damages to world coffee. New races of the pathogen have emerged infecting coffee cultivars marketed as resistant to this disease. Thus, due to the high adaptive potential of the fungus, the search for coffee resistant to this disease is a recurrent activity in breeding programs. Studies with the Híbrido de Timor (HdT) have been conducted in research aimed at durable resistance to rust and other coffee diseases. Understanding the nature of enduring resistance in HdT genotypes and describing the genes involved in plant defense is critical to the efficient use of the resources available in this natural hybrid. The use of molecular and bioinformatics tools has shown significant results to increase the knowledge of the genes involved in the *Coffea - H. vastatrix* pathosystem. Thus, the aim of this study was to sequencing and characterize, through bioinformatics analysis, a region of the Híbrido de Timor CIFC 832/2 genome, which contains markers associated with resistance to *H. vastatrix*. For this, the sequencing of clone BAC 70-22F containing the functional resistance mark was performed by means of the Illumina MiSeq Platform (paired - end reads). Subsequently, the contigs were assembled and the genes predicted. Genic annotation was performed based on the genomes of *Coffea arabica*, *Coffea canephora* and *Coffea eugenioides*, using the BLAST tool. The gene annotation revealed the presence of candidate genes related to the mechanism of host resistance against pathogens. 991 genes of clone BAC 70-22F were noted. Of these genes, 340 were noted similarly with the *C. arabica* genome (var. Caturra), 337 with the *C. eugenioides* genome and 314 with the *C. canephora* genome (clone IF 200). Based on the gene annotation, two sequences of candidate genes receptor like kinases (RLK) were selected and primers designed to study the gene expression profile during the *Coffea - H. vastatrix* interaction. A possible resistance gene, receptor-like serine / threonine protein kinase GSR2 LRR, has been described and has an expression profile corresponding to a pre-haustorial resistance response. The other possible receptor like kinase under study, presenting an LRR domain, exhibited a decrease in pre-haustorial

gene expression in incompatible genotypes. Phylogenetic analyzes of these genes, as well as genetic identity and similarity studies of the cloned genomic region, demonstrated a closer relationship between clone BAC 70-22F and *C. arabica* and corroborated the genetic diversity described for HdT. The results suggest that the cloned genomic region of HdT CIFC 832/2 has important candidate genes for resistance to *H. vastatrix* coffee and presents relevant information to increase knowledge about HdT and may contribute to future planning of coffee breeding strategies.

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1. Introdução

As perdas na produção cafeeira é um dos problemas de destaque enfrentado pelos cafeicultores devido à suscetibilidade do café a diferentes doenças (CARVALHO *et al.*, 2012). A principal doença de importância econômica dessa cultura é a ferrugem, causada pelo fungo biotrófico *Hemileia vastatrix*, que ocasiona grandes prejuízos à cafeicultura mundial (AVELINO *et al.*, 2015; ZAMBOLIM, 2016). A maioria das variedades comerciais de *Coffea arabica*, espécie de grande valor econômico, é suscetível a essa doença (ZAMBOLIM, 2016; TALHINHAS *et al.*, 2017). A ferrugem do cafeeiro foi constatada pela primeira vez no Brasil no ano de 1970, na região sul do estado da Bahia. Quatro meses após a primeira observação da doença no país, a ferrugem foi encontrada em diferentes regiões produtoras de café. Hoje, a *H. vastatrix* está amplamente distribuída nas áreas cafeeiras em todo o mundo e novas raças do patógeno, capazes de suplantar a resistência, têm surgido. (CABRAL *et al.*, 2009; TALHINHAS *et al.*, 2017).

O sucesso da infecção do cafeeiro por esse patógeno depende da sua habilidade em suprimir as respostas da planta (JONES e DANGL, 2006). No processo de coevolução de plantas e patógenos, as plantas desenvolveram a capacidade de reconhecer padrões moleculares e efetores do patógeno, ativando uma resposta de defesa elaborada. De forma similar, os patógenos desenvolveram estratégias contra os mecanismos de defesa das plantas, havendo uma complexa dinâmica de evolução na interação planta-patógeno (JONES e DANGL, 2006; FRANTZESKAKIS *et al.*, 2019).

As ferrugens formam uma estrutura especializada, haustórios, no mesófilo das células dos seus hospedeiros durante o processo de infecção. Essa estrutura desempenha um papel importante na infecção, sendo responsável pela absorção de nutrientes a partir do hospedeiro. Além disso, induz mudanças estruturais na célula hospedeira, como o rearranjo do citoesqueleto, a migração do núcleo e a condensação da cromatina (MENDGEN e HAHN, 2002). Acredita-se que essas modificações são induzidas pela atuação de proteínas efetoras produzidas nos haustórios, que são secretadas na matriz extra-haustorial e translocadas para o interior da célula vegetal. A resposta de resistência às ferrugens normalmente é observada após a formação dos haustórios indicando que os genes Avr (Avr – avirulência) do patógeno são expressos nessa estrutura (DODDS *et al.*, 2009).

O sistema de defesa da planta pode ser representado por um sistema imune inato, constituído por duas linhas de defesa. Na primeira linha de defesa, há o reconhecimento do patógeno por padrões moleculares associados à patógenos (PAMPs – *Pathogen Associated Molecular Patterns*) ou por padrões moleculares associados à microrganismos (MAMPs – *Microbe Associated Molecular Patterns*) resultando a imunidade desencadeada por PAMPs/MAMPs (PTI - *Pathogen Triggered Immunity*) (JONES e DANGL, 2006). Os PAMPs/MAMPs são identificados por receptores de reconhecimento padrão (PRR - *Pattern Recognition Receptor*) localizados na superfície da membrana celular ou no interior da célula. Eles levam à formação de uma cascata de transdução de sinais ativando a resposta de defesa do hospedeiro. Geralmente os PRRs são proteínas transmembranas pertencentes à classe das proteínas semelhantes a receptores (RLPs) ou receptores do tipo quinases (RLKs) e apresentam repetições ricas em leucina (LRRs) ou motivo de lisina (LysM) no domínio extracelular, região responsável pelo reconhecimento de PAMPs (JONES e DANGL, 2006; BECK *et al.*, 2012).

Patógenos bem adaptados muitas vezes são capazes de suplantar a PTI por meio do transporte de proteínas efetoras para o citoplasma do hospedeiro. Dessa forma, uma segunda linha de defesa é ativada, a imunidade desencadeada por efetores (ETI - *Effector Triggered Immunity*). Essa é uma linha de defesa mais específica e eficaz para alguma(s) raça(s) do patógeno (JONES e DANGL, 2006). Na ETI, as plantas apresentam proteínas de resistência (R) que reconhecem os efetores do patógeno (Avr) resultando em resistência. O reconhecimento de efetores pelas proteínas R pode ser direto (modelo gene-a-gene) ou indireto (modelo guarda). No modelo gene-a-gene, o reconhecimento se dá de forma direta entre as proteínas R e Avr. Por sua vez, no modelo guarda o reconhecimento pelas proteínas R é realizado por meio do monitoramento de uma proteína acessória da planta hospedeira, alvo dos efetores do patógeno (SEKHWAL *et al.*, 2015; REDDY e NARESH, 2018).

A maioria dos genes *R* codificam proteínas que contêm um domínio C-terminal rico em repetições de leucina (LRR) e um domínio conservado contendo sítios de ligação a nucleotídeos (NBS), pertencendo à classe de genes de resistência NBS-LRR. O domínio LRR pode interagir com a proteína Avr ou com um complexo de proteínas formado pela Avr e outras proteínas do hospedeiro. O domínio NBS atua como sinalizadores celulares e provavelmente iniciam a resposta de resistência em plantas (RIBAS *et al.*, 2011; REDDY e NARESH, 2018). Os genes *R* de diferentes espécies de

plantas compartilham domínios conservados e podem ser usados para triagem de genomas de plantas para putativos genes de resistência (REDDY e NARESH, 2018). Análogos de genes de resistência (*RGAs*) conservam domínios e motivos proteicos que desempenham papéis específicos na defesa da planta contra patógenos (SEKHWAL *et al.*, 2015).

A resistência das plantas de cafeeiro na interação com o fungo *H. vastatrix* é condicionada por no mínimo nove genes dominantes de efeito maior (NORONHA e BETTENCOURT, 1967; BETTENCOURT *et al.*, 1988) e se baseia no modelo gene-a-gene, proposto por Flor (1971). De acordo com esse modelo, ocorre o reconhecimento dos genes *Avr* das diferentes raças de *H. vastatrix*, por parte dos fatores de resistência do cafeeiro. Seguindo o modelo gene-a-gene, foi inferida a existência de nove genes de virulência (*v1-v9*) em *H. vastatrix* (NORONHA e BETTENCOURT, 1967; BETTENCOURT *et al.*, 1988). Atualmente, o número de perfis de virulência da ferrugem do cafeeiro provavelmente vai muito além das raças caracterizadas (TALHINHAS *et al.*, 2017). A raça XXXIII de *H. vastatrix*, por exemplo, contém genes (*v5,7* ou *v5,7,9*) capazes de suplantar a resistência de algumas cultivares que foram inicialmente caracterizadas como resistentes ao fungo causador da ferrugem (CAPUCHO *et al.*, 2012). Dessa forma, a obtenção de cultivares com resistência durável tem sido um desafio para os melhoristas.

Estudos com o Híbrido de Timor (HdT), um híbrido interespecífico natural entre *Coffea arabica* e *Coffea canephora* (BETTENCOURT, 1973), tem sido de grande importância para os progressos alcançados em pesquisas visando a resistência do cafeeiro à *H. vastatrix*. O HdT e as progênies derivadas do seu cruzamento com outros cultivares vêm sendo estudados em diversas regiões produtoras de café no mundo (TALHINHAS *et al.*, 2017; SOUSA *et al.*, 2017; SILVA *et al.*, 2018). Esse germoplasma tem sido utilizado em programas de melhoramento que visam resistência durável à ferrugem e outras doenças do cafeeiro (SILVA *et al.*, 2018). Entretanto, o HdT ainda contém genes que não foram caracterizados (CAPUCHO *et al.*, 2009; DIOLA *et al.*, 2011; PESTANA *et al.*, 2015). Entre os derivados do HdT, CIFIC (Centro de Investigação das Ferrugens do Cafeeiro, Portugal) 832/1 e CIFIC 832/2 são de suma importância, pois unem a resistência à patógenos e boas características agronômicas. A resistência do HdT CIFIC 832/2 pode ser mais durável do que em outros genótipos de HdT e contém ainda respostas mais rápidas de resistência à ferrugem (BETTENCOURT, 1973; DINIZ *et al.*, 2012).

Compreender melhor a diversidade genética e a natureza da resistência duradoura em genótipos do HdT é fundamental para o uso eficiente dos recursos disponíveis nesse híbrido natural (SETOTAW *et al.*, 2010; TALHINHAS *et al.*, 2017). O estudo do perfil de expressão gênica durante a interação *Coffea* - *H. vastatrix* pode facilitar a identificação dos genes envolvidos na resistência e auxiliar na compreensão dos mecanismos de defesa da planta (BARKA *et al.*, 2017; FLOREZ *et al.*, 2017). Estudos com o objetivo de entender a diversidade genética do HdT também contribuem para o planejamento de estratégias de melhoramento (SETOTAW *et al.*, 2010).

A expansão das pesquisas genômicas, possibilitada pelo desenvolvimento de novas tecnologias, tem aumentado em larga escala a quantidade de informações biológicas disponíveis (ETIENNE *et al.*, 2002; MICHNO e STUPAR, 2018). Os avanços da biotecnologia em conjunto com os estudos de bioinformática, aplicados ao melhoramento, têm auxiliado na compreensão e manipulação gênica (EDWARDS e BATLEY, 2004; MICHNO e STUPAR, 2018). Essas ferramentas possibilitam a ampliação do conhecimento dos genes que estão envolvidos na resistência de *Coffea* à *H. vastatrix*, podendo levar a identificação e até mesmo a clonagem de genes essenciais para a resistência do cafeeiro (ETIENNE *et al.*, 2002; FERNANDES-BRUM *et al.*, 2017).

Utilizando essas ferramentas, o estudo do transcriptoma da interação *Coffea* - *H. vastatrix*, permitiu identificar genes candidatos, relacionados ao mecanismo de defesa do cafeeiro e caracterizar a expressão desses genes em interação compatível e incompatível (Florez *et al.*, 2017). Sendo relatados genes RLKs envolvidos na primeira resposta de defesa da planta. Essa resposta precoce é fundamental para introduzir cascatas de sinalização na PTI e posterior a expressão de genes envolvidos em mecanismos de defesa (KUMAR e KIRTI, 2011). Acredita-se que a resistência pré-haustorial, antes das 24 horas após a inoculação na interação cafeeiro – *H. vastatrix*, seja mais durável por envolver vários mecanismos de defesa do hospedeiro, consolidando a proteção da planta (HEATH, 2000; LOPES, 2015). O perfil de expressão do gene *putative probable receptor-like protein kinase At5g39020*, previamente identificado por Florez *et al.* (2017), mostrou uma resposta pré-haustorial no genótipo resistente e uma expressão mais tardia no genótipo suscetível. Os autores concluíram que esse gene provavelmente está relacionado ao reconhecimento do patógeno na primeira linha de defesa da planta. Assim, esse marcador apresenta

características significativas para o estudo da resistência de plantas no patossistema *Coffea - H. vastatrix*.

Desse modo, objetivou-se sequenciar e caracterizar uma região do genoma da principal fonte de resistência do cafeeiro à *Hemileia vastatrix*, o Híbrido de Timor CIFC 832/2, utilizando o marcador *putative probable receptor-like protein kinase At5g39020*. A identificação de genes nessa região será empregada para ampliar o conhecimento da resistência do cafeeiro a essa importante doença.

2. Material e Métodos

2.1. Rastreo e sequenciamento do clone BAC

Foi feito o rastreo de uma biblioteca de clones BAC (*Bacterial Artificial Chromosome*), mantida no Laboratório de Biotecnologia do Cafeeiro (Universidade Federal de Viçosa – MG), com o marcador *putative probable receptor-like protein kinase At5g3920*. Esta biblioteca foi construída a partir do cafeeiro HdT CIFC 832/2 (CAÇÃO *et al.*, 2013), genótipo portador de fatores genéticos que condicionam resistência a diferentes patógenos e boas características agronômicas (BETTENCOURT, 1973). A biblioteca contém 56.832 clones BAC em 148 placas de titulação de 384 poços. (CAÇÃO *et al.*, 2013).

Os clones foram replicados em placas de titulação de 384 poços contendo 70µl de meio LB fresco (com 12,5µgml⁻¹ Cloranfenicol), usando um replicador de placas esterilizado, sob capela de fluxo de ar laminar. A multiplicação da cultura foi feita por meio da incubação das placas em agitador com temperatura de 37°C durante 18h e velocidade de 180rpm. Após a incubação, com a finalidade de identificar os clones com a marca, foi utilizada a metodologia de decomposição do agrupamento das BAC. A placa foi dividida em duas parte e coletado o *pool* de cada parte. Posteriormente a meia placa da biblioteca contendo o marcador foi decomposta em quatro grupos de 48 clones, seguida da análise das colunas verticais até chegar a um único clone BAC (DIOLA, 2009). O DNA plasmidial do clone foi extraído com o *kit Wizard® Plus SV Minipreps DNA purification System* (Promega), seguindo as recomendações do fabricante. A quantificação foi realizada com o auxílio do Qubit dsDNA BR (*Life Technologies*) e espectrofotômetro NanoDrop™ (*Thermo Fisher Scientific*). A PCR foi otimizada contendo 50ng DNA plasmidial, 0,1µM de cada primer, 0,15mM de dNTP (Promega),

1,0mM MgCl₂, 1,0U de Taq *DNA polymerase* (Invitrogen), e 1X PCR reação buffer, com volume final de 20µL. O DNA foi amplificado em termociclador (PTC - 200 - MJ *Research and Veriti - Applied Biosystems*), programado com desnaturação inicial a 94°C por 10min, seguida por 35 ciclos desnaturação a 94°C por 30s, anelamento a 61°C por 30s e extensão a 72°C por 1min. Finalizando com uma extensão final de 72°C por 10min. O produto foi visualizado em gel de agarose (1,5%).

O clone identificado foi sequenciado por meio da plataforma Illumina MiSeq (*paired-end reads*). Para isso, 50ng de DNA plasmidial foi submetido a uma reação de fragmentação aleatória na qual o DNA foi fragmentado e ligado a adaptadores específicos utilizando o *kit Nextera® XT DNA Sample Preparation* (Illumina), conforme instrução do fabricante. Em seguida, o DNA purificado foi amplificado utilizando iniciadores complementares aos adaptadores. Os produtos foram quantificados por meio do espectrofotômetro Qubit DNA BR (*Life Technologies*). As bibliotecas foram diluídas em uma solução de Tris-HCl e Tween 0,1%, depositadas em uma *flowchip* e submetidas a 500 ciclos (2x250bp) de sequenciamento utilizando *MiSeq Reagent Kit v2* (Illumina).

2.2. Análises de bioinformática

2.2.1. Montagem de *contigs*

Após o sequenciamento, as *reads* geradas foram submetidas a análises de bioinformática para a edição, montagem e anotação dos *contigs*, com o intuito de interpretar o contexto biológico. Realizou-se uma avaliação de qualidade das *reads* sequenciadas utilizando o *software* FastQC (versão 0.11.5) (ANDREWS, 2010). Em seguida, foram removidas as sequências contaminantes e as de baixa qualidade por meio do *software* Trimmomatic (versão 0.36) (LOHSE *et al.*, 2012). Com base nas sequências selecionadas, realizou-se a montagem dos *contigs* e *scaffolds* usando o *software* SPAdes (BANKEVICH *et al.*, 2012), empregando a estratégia de montagem *de novo*. Efetuou-se uma avaliação de qualidade da montagem dos *scaffolds* utilizando a ferramenta de avaliação de montagem de genoma QUAST (versão 5.0.2) (MIKHEENKO *et al.*, 2018).

2.2.2. Predição gênica

Utilizando o *software* AUGUSTUS (<http://augustus.gobics.de/>), os genes foram preditos a partir dos *contigs* para a obtenção do número de exons, íntrons e transcritos (STANKE *et al.*, 2004). A predição gênica foi realizada com base no reconhecimento de regiões previamente caracterizadas de *Solanum lycopersicum*. Essa espécie foi usada como referência por ser geneticamente próxima ao gênero *Coffea* e assim, compartilharem repertórios de genes comuns (LIN *et al.*, 2005).

2.2.3. Anotação de genes

A anotação dos genes foi efetuada utilizando a ferramenta para busca de similaridade de sequência, BLASTp (*Basic Local Alignment Search Tool*) com *e-value* de 10^{-5} . Foi utilizada uma estratégia baseada em similaridade para identificar sequências relacionadas com funções já conhecidas em genoma de *C. arabica* (var. Caturra), *C. eugenioides* (NCBI - <https://www.ncbi.nlm.nih.gov/>) e *C. canephora* (clone IF 200) (COFFEE GENOME HUB - <http://coffee-genome.org/>). As sequências foram anotados a partir do melhor alinhamento (*best hit*) com cada genoma.

2.3. Análise de expressão gênica

Com base na anotação gênica foram selecionadas duas sequências de genes candidatos a *receptores like kinase (RLK)*. Para as duas sequências escolhidas foram desenhados *primers* utilizando o servidor *GenScript* (<https://www.genscript.com/>) e o programa *Oligo Explorer* (versão 1.5) (KUULASMAA, 2010). Foi desenhado um conjunto de *primers* para cada sequência de genes candidatos a *RLK*. Foram desenhados *primers* para o gene anotado como *LRR receptor-like serine/threonine-protein kinase GSO2* (Gene1: F: 5'-TGGCGGATCAAGTGCATCT-3'; 60,3°C - R: 5'-TCGTCTCCTTGAAACTCTTGC-3'; 58,3°C; 154pb). Também foram desenhados *primers* para o gene anotado como *putative receptor-like protein kinase At3g47110* (Gene2: F: 5'-GCCTTGGATTTGGCGATAA-3'; 56,8°C - R: 5'-CTGAGGAAGCATGAGACC-3', 57,1°C; 143pb). Os *primers* desenhados foram utilizados nas reações de PCR quantitativo em tempo real (RT-qPCR).

O experimento para a análise de expressão gênica foi conduzido em um delineamento experimental inteiramente casualizado, com três repetições biológicas.

Utilizaram-se plantas jovens *C. arabica* var. Caturra CIFC 19/1 (interação compatível) e Híbrido de Timor CIFC 832/1 (interação incompatível), as quais foram inoculadas com a raça XXXIII de *H. vastatrix*. A inoculação foi realizada como proposto por Capucho *et al.* (2009). Esses cafeeiros usados na análise de expressão gênica correspondem aos parentais da cultivar Oeiras MG 6851, que teve sua resistência suplantada pela raça XXXIII do patógeno. As amostras foram coletadas em 0, 12, 24 e 72 hai. Para a extração do RNA, as folhas inoculadas foram coletadas e maceradas em N₂ líquido. O RNA total foi extraído com 100mg de tecido macerado e *Rneasy Plant Mini Kit* (Qiagen), seguindo as recomendações do fabricante. A quantificação foi realizada com o uso do espectrofotômetro Qubit RNA BR (*Life Technologies*) e NanoDrop™ (*Thermo Fisher Scientific*). A integridade do RNA foi avaliada por eletroforese em gel de agarose (1,5%) corado com brometo de etídio. As amostras foram armazenadas em ultracongelamento a -80°C, até o uso. O cDNA foi sintetizado com 3µg de RNA total, pré-tratado com 1µl de DNase por 15min (50U/µL, DNaseI de Inversão, Invitrogen™) para remover possíveis contaminantes do DNA genômico. A primeira cadeia de cDNA foi sintetizada utilizando o *kit* de RT-PCR do Protocolo de Transcrição Reversa ImProm-II™ (Promega), de acordo com as orientações do fabricante e armazenada a -20°C até a utilização.

Para a realização da técnica de PCR quantitativo em tempo real, em aparelho 7500 Real Time PCR Systems (*Applied Biosystems*), foi utilizado o sistema de detecção de fluorescência SYBR Green I (*Applied Biosystems*, California, USA). Para cada reação utilizou-se 2µl da diluição da reação de síntese de cDNA de fita simples, 1µl de *primers forward* e *reverse*, 5µl de SYBR® Green PCR Master Mix (*Applied Biosystems*), 0,2µl de Dyer e 1µl de água estéril. Para um volume final de 10µl com 50ng/µl de cDNA e 100nM de *primers*. As condições da reação foram: 95°C por 10min para a desnaturação inicial, seguido por 40 ciclos de 95°C por 15s e 60°C por 1min. O nível de expressão dos genes foi calculado utilizando os valores médios de Ct, resultante de três réplicas biológicas e três réplicas técnicas.

Para a normalização dos dados foram utilizados dois genes constitutivos selecionados (Ubiquitina10 e Gliceraldeído-3-fosfato desidrogenase) cujas expressões foram encontradas estáveis (CRUZ *et al.*, 2009). As análises estatísticas foram realizadas utilizando o *software Prism 5* (versão 5.01) (MOTULSKY, 2007). Todos os dados são apresentados como média. A diferença no nível de expressão entre interações em uma mesma hora de mensuração foi calculada utilizando o teste o Teste de Tukey (p

< 0,05). A diferença no nível de expressão entre amostras não inoculadas e amostras inoculadas foi calculada utilizando ANOVA seguida pelo Teste de Tukey ($p < 0,05$).

2.4. Estudos filogenéticos

Foram efetuados estudos da relação genética do clone BAC selecionado (70-22F), utilizando *software* TopHat (versão 2.1.1) (TRAPNELL *et al.*, 2009), em comparação com quatro genomas de *Coffea*: *C. arabica*1 var. Caturra (NCBI - <https://www.ncbi.nlm.nih.gov/>); *C. arabica*2, var. Típica (dados não publicados); *C. arabica*3, var. Bourbon (WCR - <https://worldcoffeeresearch.org/>) e *Coffea canephora* clone IF 200 (COFFEE GENOME HUB - <http://coffee-genome.org/>). No *software* realizou-se uma busca de identidade genética entre as *reads* geradas pelo sequenciamento do clone BAC 70-22F e as variedades de *Coffea* em estudo. Também foi realizada uma busca de similaridade de sequências (BLASTp com *e-value* de 10^{-5}) entre o clone e os quatro genomas. A porcentagem de BLAST foi calculada a partir dos dois melhores alinhamentos, de cada genoma com cada sequência de *contigs*.

Além disso, também realizaram-se análises filogenéticas baseadas em alinhamentos de cinco sequências gênicas conservadas e de cópia única do clone BAC 70-22F e dos quatro genomas de *Coffea*. As análises foram realizadas utilizando o *software* MEGA-X-10.0.5 (KUMAR *et al.*, 2018). As cinco sequências gênicas conservadas, *3-oxoacyl-[acyl-carrier-protein] reductase 4*, *UDP-glucose 6-dehydrogenase 5-like*, *succinate-semialdehyde dehydrogenase%2C mitochondrial-like*, *asparagine synthetase [glutamine-hydrolyzing]* e *Enolase*, foram escolhidas com base na anotação gênica. A história evolutiva das sequências proteicas foi inferida utilizando o método *Maximum Likelihood*, baseado no modelo de Tamura-Nei com *bootstrap* de 1.000 réplicas (FELSENSTEIN, 1985; TAMURA e NEI, 1993).

Análises filogenéticas foram realizadas para os dois possíveis genes de resistência selecionados, *LRR receptor-like serine/threonine-protein kinase GSO2* (Gene1) e *putative receptor-like protein kinase At3g47110* (Gene2), utilizando o *software* MEGA-X-10.0.5 (KUMAR *et al.*, 2018). O estudo filogenético foi efetuado com base nos melhores alinhamentos (BLASTp com *e-value* de 10^{-5}) de sequências proteicas, dos dois genes com os quatro genomas de *Coffea*: *C. arabica*1 var. Caturra; *C. arabica*2, var. Típica; *C. arabica*3, var. Bourbon e *Coffea canephora* clone IF 200. A história evolutiva das sequências proteicas foi inferida utilizando o método *Maximum*

Likelihood, baseado no modelo de Tamura-Nei com *bootstrap* de 1.000 réplicas (FELSENSTEIN, 1985; TAMURA e NEI, 1993). Posteriormente, foram caracterizados os domínios das sequências proteicas do Gene1, do Gene2 e das sequências de *Coffea* que ficaram mais próximas na árvore filogenética desses dois genes de interesse. Essa análise foi executada no banco de dados de famílias proteicas Pfam (<https://pfam.xfam.org/search/sequence>) (FINN *et al.*, 2013).

3. Resultados

3.1. Rastreamento e sequenciamento do clone BAC

Para caracterização de uma região genômica com potencial associação à resistência do cafeeiro, o marcador molecular capaz de amplificar o gene *putative probable receptor-like protein kinase At5g39020* foi utilizado para analisar uma biblioteca de clones BAC do cafeeiro HdT CIFC 832/2 (CAÇÃO *et al.*, 2013). Após o rastreamento com o marcador, identificou-se o clone BAC 70-22F contendo a marca funcional desse gene (Figura 1). O fragmento de DNA do clone BAC 70-22F foi extraído e posteriormente sequenciado. Foram obtidas 122.273 *reads* de alta qualidade com o sequenciamento do clone BAC 70-22F.

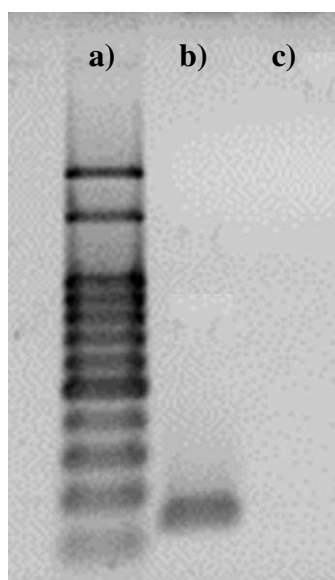


Figura 1. Produto de amplificação da biblioteca BAC (HdT CIFC 832/2). **a)** Marcador de peso molecular 100pb. **b)** Clone BAC 70-22F contendo a marca funcional do

putative probable receptor-like protein kinase At5g39020. c) Clone BAC 70-23F não apresentando a marca funcional do *putative probable receptor-like protein kinase* At5g39020.

3.2. Análises de bioinformática

Utilizando estratégias de bioinformática, foi realizada a montagem da sequência de DNA a partir das *reads* de qualidade obtidas com o sequenciamento do clone BAC 70-22F. A montagem resultou em 3.355 *scaffolds*. A região genômica montada apresentou um valor de N50 de 1.080 pb e L50 de 605 pb, a percentagem de CG foi de 43,43 (Tabela 1).

Tabela 1. Parâmetros estatísticos da montagem do clone BAC 70-22F.

| Características do genoma | Valores |
|--|----------------|
| <i>Reads</i> de alta qualidade | 122.273 |
| Número total de bases | 230.817 pb |
| Número de <i>scaffolds</i> | 3.355 |
| Maior <i>scaffold</i> | 6.472 pb |
| N50 | 1.080 pb |
| L50 | 605 pb |
| Número total de bases (* \geq 0 pb) | 1.080.585 pb |
| Número total de bases (* \geq 1.000 pb) | 1.17.713 pb |
| Número total de bases (* \geq 5.000 pb) | 24.466 pb |
| Número total de bases (* \geq 10.000 pb) | 0 |
| Número total de bases (* \geq 25.000 pb) | 0 |
| Número total de bases (* \geq 50.000 pb) | 0 |
| GC (%) | 43,43 |

*: *scaffolds*; pb: pares de bases.

Empregando a ferramenta para busca de similaridade de sequências (BLAST), foram anotados 991 genes a partir os genes preditos do clone BAC 70-22F. Desses genes, 340 foram anotados com similaridade com o base no genoma de *C. arabica* (var. Caturra), 337 com o genoma de *C. eugenioides* e 314 com o genoma de *C. canephora* (clone IF 200) (Apêndice A). Em relação aos genes anotados a partir do genoma de *C.*

arabica, 173 foram encontrados no subgenoma *C. eugenioides* (C^E), 152 no subgenoma *C. canephora* (C^C) e 15 com sequências não caracterizadas em cromossomos.

A anotação gênica revelou a presença de genes candidatos relacionados ao mecanismo de resistência de hospedeiros contra patógenos. Foram identificados genes como um análogo ao *putative late blight resistance protein homolog RIA-4*, *cysteine synthase*, entre outros possíveis genes envolvidos no mecanismo de defesa de plantas (Apêndice A).

3.3. Análise de expressão gênica

Foram selecionados dois genes análogos de resistência (*RGAs*), identificados na região genômica do HdT CIFC 832/2 (BAC 70-22F), para a análise de expressão. Os genes escolhidos, *LRR receptor-like serine/threonine-protein kinase GSO2* (Gene1) e *putative receptor-like protein kinase At3g47110* (Gene2), são candidatos a receptores *like kinase (RLK)*.

As análises de expressão gênica mostraram resultados significativos para os dois genes selecionados do clone BAC 70-22F. Na análise da expressão do Gene1 foram observadas diferenças significativas entre interação incompatível e compatível às 12 e 24 hai (Figura 2). Na interação compatível não houve diferença de expressão quando comparados os diferentes tempos após infecção. Na interação incompatível, observou-se um aumento de expressão do gene às 12 hai, momento em que também houve diferença significativa entre as interações incompatível e compatível (Figura 2).

LRR receptor-like serine/threonine-protein kinase GSO2

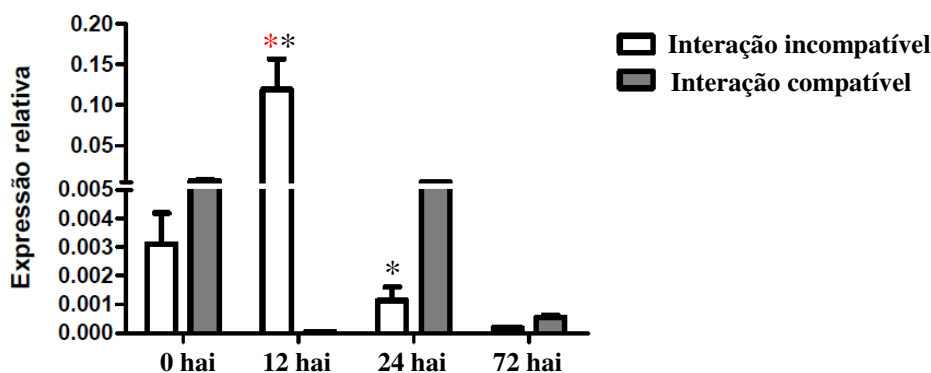


Figura 2. Análise de expressão por PCR em tempo real do Gene1. O padrão de expressão foi mensurado em 0 hora, amostras não inoculadas, 12, 24 e 72 horas após a

inoculação de urediniósporos frescos (*H. vastatrix* – raça XXXIII) em plantas incompatíveis (HdT CIFC 832/1) e compatíveis (*C. arabica* var. Caturra CIFC 19/1). (*) Diferença significativa no nível de expressão entre interações na mesma hai. (*) Diferença significativa em relação às amostras não inoculadas (0h) na mesma interação.

A expressão do gene Gene2 analisado entre interações incompatível e compatível e mensurados em horários iguais de infecção, revelou diferença significativa às 0 e 72 hai. Em ambos os horários, a interação incompatível apresentou maior expressão do gene (Figura 3). Na interação incompatível houve uma diminuição da expressão relativa do Gene2 em relação ao mesmo genótipo avaliado às 0h. A interação compatível revelou um aumento significativo de expressão do Gene2 às 24 hai (Figura 3).

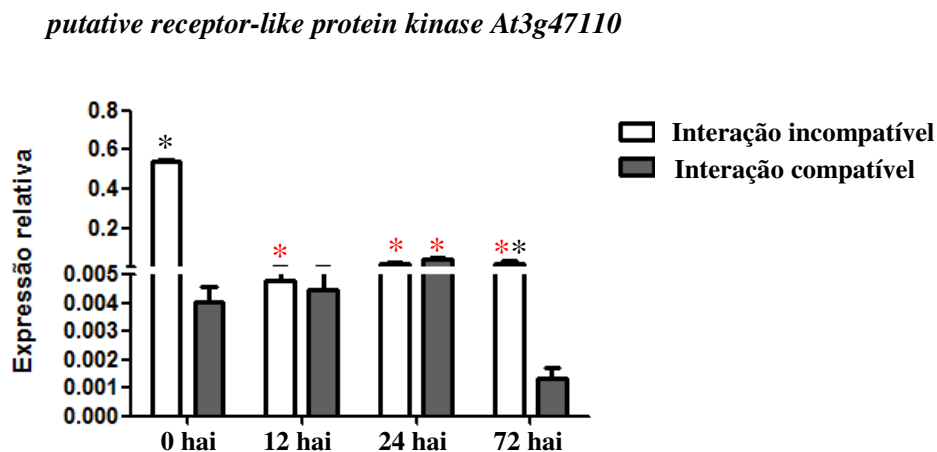


Figura 3. Análise de expressão por PCR em tempo real do Gene2. O padrão de expressão foi mensurado em 0 hora, amostras não inoculadas, 12, 24 e 72 horas após a inoculação de urediniósporos frescos (*H. vastatrix* – raça XXXIII) em plantas incompatíveis (HdT CIFC 832/1) e compatíveis (*C. arabica* var. Caturra CIFC 19/1). (*) Diferença significativa no nível de expressão entre interações na mesma hai. (*) Diferença significativa em relação às amostras não inoculadas (0h) na mesma interação.

3.4. Estudos filogenéticos

Análises filogenéticas foram realizadas para ampliar o conhecimento do clone BAC 70-22F. As *reads* obtidas no sequenciamento da BAC e os quatro genomas de *Coffea* foram submetidas a uma busca por identidade genética. Observou-se que as sequências

do clone BAC 70-22F possuem maior grau de identidade genética com o genoma de *C. arabica* var. Caturra (14,6%), seguida de *C. arabica* var. Típica (11,8%). A identidade genética com o genoma *C. arabica* var. Bourbon foi de 4,0 %. A menor identidade genética mensurada foi obtida em comparação com o genoma de *C. canephora* (0,2%) (Figura 4).

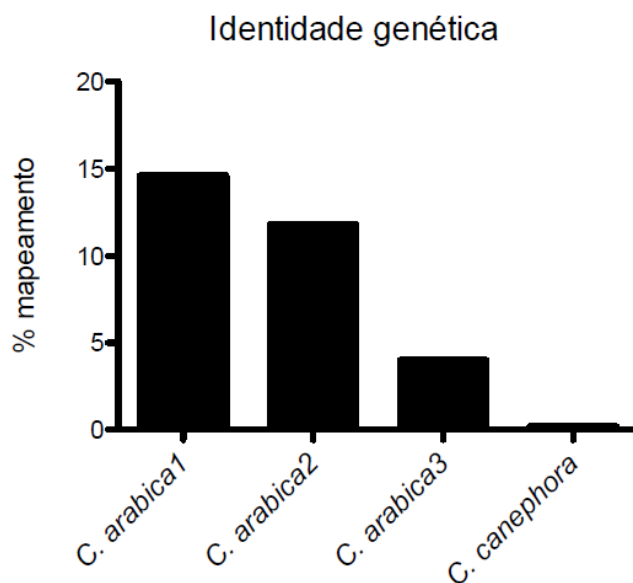


Figura 4. Identidade genética entre as *reads* geradas pelo sequenciamento do clone BAC 70-22F e as variedades Caturra (*C. arabica1*), Típica (*C. arabica2*), Bourbon (*C. arabica3*) e clone IF 200 (*C. canephora*).

Uma busca por similaridade de seqüências também foi realizada entre os *scaffolds* montados da BAC 70-22F e os quatro genomas de *Coffea*. Resultado semelhante ao encontrado com as *reads* foi observado. Nessa análise, maior similaridade foi observada para *C. arabica* var. Caturra (62,56%), seguida de *C. arabica* var. Típica (37,15%), *C. arabica* var. Bourbon (0,27%) e *C. canephora* (0,02%) (Figura 5).

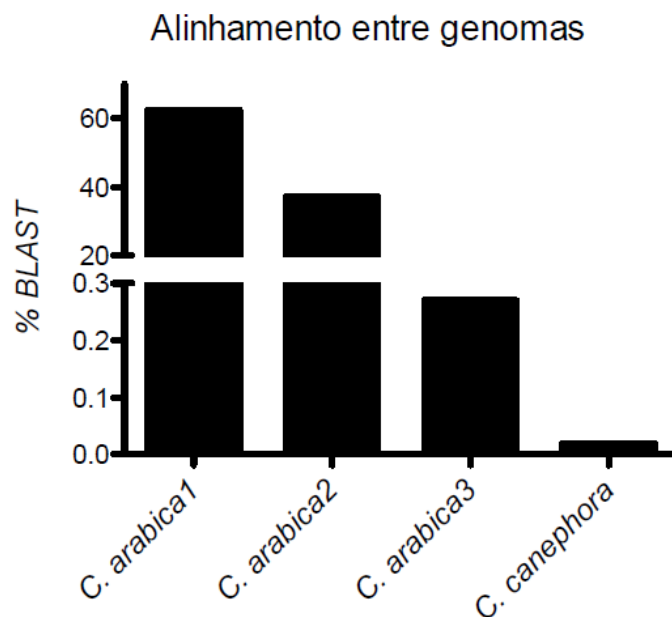


Figura 5. Similaridade de seqüências entre o clone BAC 70-22, montado em *contigs*, e as variedades Caturra (*C. arabica1*), Típica (*C. arabica2*), Bourbon (*C. arabica3*) e clone IF 200 *C. canephora*. A porcentagem de BLAST foi calculada a partir dos dois melhores alinhamentos de cada genoma com cada seqüência de *contigs*.

Na caracterização do clone BAC 70-22F foram ainda analisados alguns genes conservados, cópia única, encontrados na anotação gênica. Com base na análise filogenética das seqüências gênicas conservadas e dos quatro genomas de *Coffea*, o clone alinhou em diferentes grupos de acordo com o gene analisado (Figura 6).

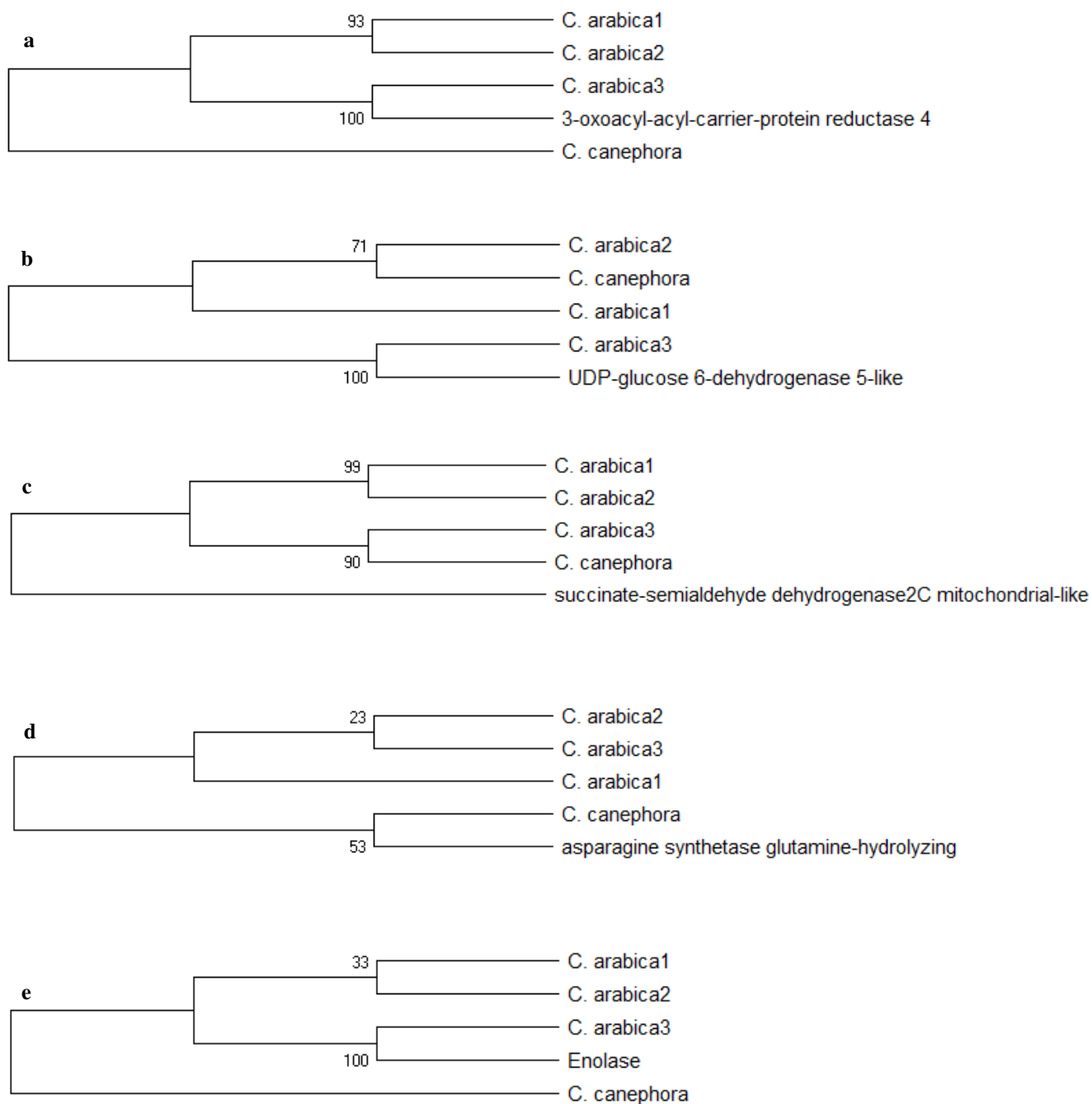


Figura 6. Árvores filogenéticas baseadas em alinhamento dos genomas *C. arabica* var. Caturra, *C. arabica*2 var. Típica, *C. arabica*3 var. Bourbon, *C. canephora* clone IF 200 e de sequências gênicas conservadas do clone BAC 70-22. **a)** *3-oxoacyl-[acyl-carrier-protein] reductase 4* (Gene1). **b)** *UDP-glucose 6-dehydrogenase 5-like* (Gene2). **c)** *succinate-semialdehyde dehydrogenase 2C mitochondrial-like* (Gene3). **d)** *asparagine synthetase [glutamine-hydrolyzing]* (Gene4). **e)** *Enolase* (Gene5).

Estudos filogenéticos foram efetuados para aumentar o conhecimento da possível origem dos dois genes selecionados do clone BAC 70-22F. O estudo foi baseado em alinhamentos de seqüências proteicas (Apêndice B) entre os dois genes (Gene1 e Gene2) e os quatro genomas de referência do gênero *Coffea* (*C. arabica*1 var. Caturra; *C. arabica*2, var. Típica; *C. arabica*3, var. Bourbon; *Coffea canephora* clone IF 200) (Figuras 7 e 8).

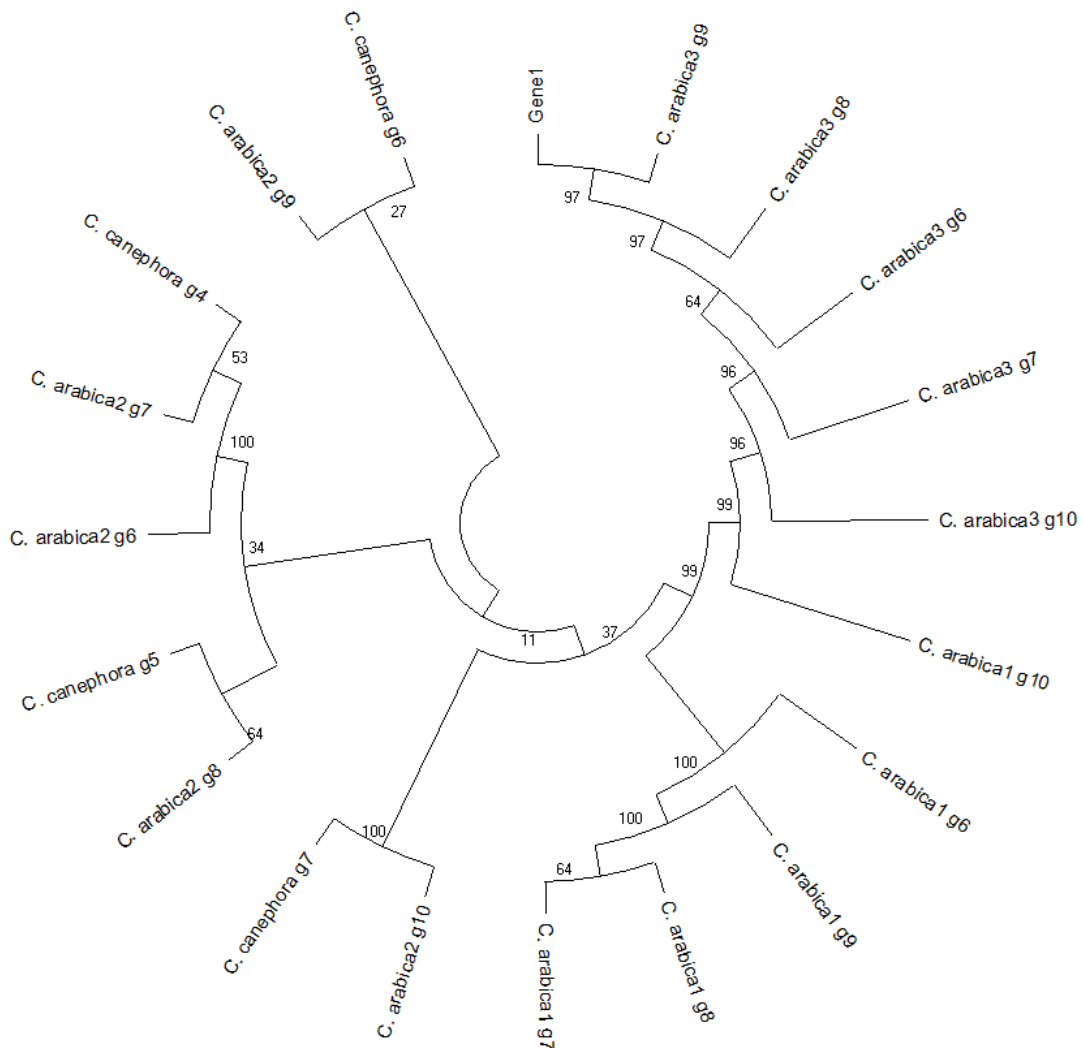


Figura 7. Árvore filogenética baseada em alinhamento de seqüências proteicas. Gene1: *LRR receptor-like serine/threonine-protein kinase GSO2*. *C. arabica*1: seqüências proteicas da variedade Caturra (NCBI). *C. arabica*2: seqüências proteicas da variedade Típica (dados não publicados). *C. arabica*3: seqüências proteicas da variedade Bourbon (WCR). *C. canephora*: seqüências proteicas do clone IF 200 (*Coffee Genome Hub*).

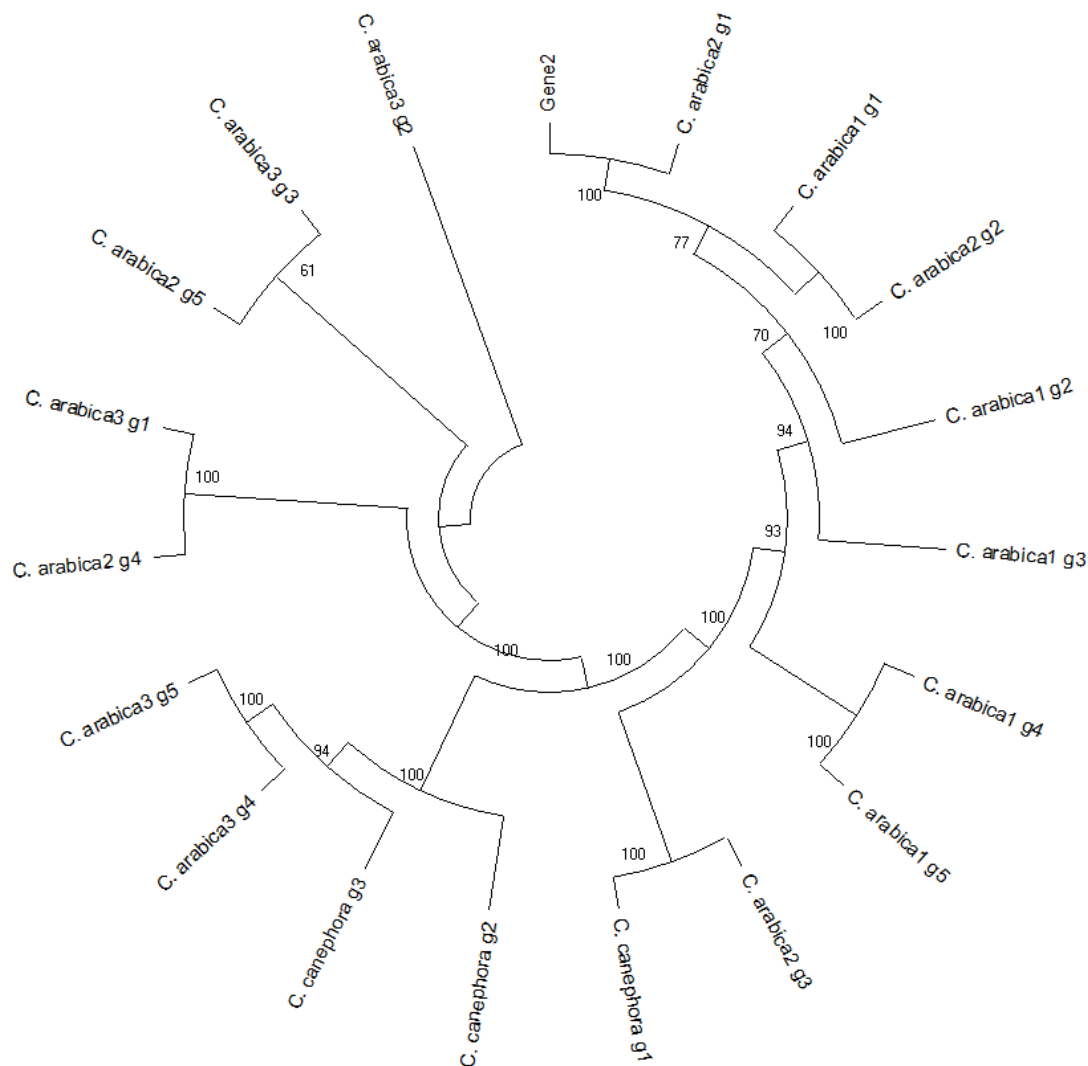


Figura 8. Árvore filogenética baseada em alinhamento de sequências proteicas. Gene2: *putative receptor-like protein kinase At3g47110*. *C. arabica1*: sequências proteicas da variedade Caturra (NCBI). *C. arabica2*: sequências proteicas da variedade Típica (dados não publicados). *C. arabica3*: sequências proteicas da variedade Bourbon (WCR). *C. canephora*: sequências proteicas do clone IF 200 (*Coffee Genome Hub*).

O Gene1 ficou no mesmo clado de quatro genes do genoma de *C. arabica3* var. Bourbon. De acordo com a anotação gênica, esses quatro genes são putativos: *LRR receptor-like serine/threonine-protein kinase GSO2* (*C. arabica3* g6), *uncharacterized protein LOC113703097* (*C. arabica3* g7), *LRR receptor-like serine/threonine-protein kinase GSO2* (*C. arabica3* g8) e *uncharacterized protein LOC113703097* (*C. arabica3* g9) (Tabela 2). Dentro do clado, o Gene1 ficou mais próximo de um gene não caracterizado de *C. arabica3* (g9) (Figura 7). Posteriormente, foi realizada a busca pelos

domínios proteicos das sequências desse clado utilizando o servidor Pfam. As sequências do clado, correspondentes aos cinco genomas, não apresentaram domínios proteicos caracterizados (Tabela 2).

Tabela 2. Características de sequências proteicas de *Coffea*. Sequência proteica do Gene1 e quatro sequências proteicas agrupadas em um mesmo clado na análise filogenética.

| Genoma | Sequência proteica | Anotação | Domínios |
|--------------------|---------------------------|---|-----------------|
| BAC 70-22F | Gene1 | <i>LRR receptor-like serine/threonine-protein kinase GSO2</i> | - |
| <i>C. arabica3</i> | g9-g19672.t1 | <i>uncharacterized protein LOC113703097</i> | - |
| <i>C. arabica3</i> | g8-g32952.t1 | <i>LRR receptor-like serine/threonine-protein kinase GSO2</i> | - |
| <i>C. arabica3</i> | g6-g6102.t1 | <i>LRR receptor-like serine/threonine-protein kinase GSO2</i> | - |
| <i>C. arabica3</i> | g7-g22356.t1 | <i>uncharacterized protein LOC113703097</i> | - |
| <i>C. arabica3</i> | g10-g5288.t1 | <i>uncharacterized protein LOC113703097</i> | - |

O Gene2 ficou agrupado em um clado com dois genes do genoma de *C. arabica2* (var. Típica) e um do genoma *C. arabica1* (var. Caturra). Os genes desse clado estão anotados como: *receptor-like serine threonine- kinase EFR* (*C. arabica2* g1), *putative receptor-like protein kinase At3g47110 isoform X1* (*C. arabica1* g1), *receptor-like serine threonine- kinase At3g47570* (*C. arabica2* g2) (Tabela 3). A partir de análises utilizando o servidor Pfam foi encontrado um domínio LRR1 na sequência proteica do Gene2. As outras três sequências do clado também apresentaram domínio LRR, mas LRR8 (Tabela 3). O gene *receptor-like serine threonine- kinase EFR* (*C. arabica2* g1), o qual mostrou-se mais próximo do Gene2 no clado (Figura 8), além do domínio LRR8, também possui domínio Pkinase e LRRNT2 .

Tabela 3. Características de sequências proteicas de *Coffea*. Sequência proteica do Gene2 e quatro sequências proteicas agrupadas em um mesmo clado na análise filogenética.

| Genoma | Sequência proteica | Anotação | Domínios |
|---------------------|--|---|-----------------------------------|
| BAC 70-22F | Gene2 | <i>putative receptor-like protein kinase At3g47110</i> | LRR1 |
| <i>C. arabica</i> 2 | (Scaffold4162HRSCAF 4163) gene-0.17 mRNA-1 | <i>receptor-like serine threonine-kinase EFR</i> | LRR8 LRRNT2 Pkinase |
| <i>C. arabica</i> 1 | XP027093211.1 | <i>putative receptor-like protein kinase At3g47110 isoform XI</i> | LRR8 LRRNT2 Pkinase |
| <i>C. arabica</i> 2 | (Scaffold4162HRSCAF 4163) gene-0.13 mRNA-1 | <i>receptor-like serine threonine-kinase At3g47570</i> | LRR8 LRRNT2 Pkinase |
| <i>C. arabica</i> 1 | g2-XP027093214.1 | <i>probable LRR receptor-like serine/threonine-protein kinase At3g47570</i> | LRRNT2 LRR8 LRR8 Pkinase |

4. Discussão

Por meio dos gráficos de análise de qualidade das sequências do clone BAC 70-22F, gerados pelo FastQC, observou-se que as *reads* obtidas pelo sequenciamento do clone BAC 70-22F apresentaram boa qualidade. O valor obtido de N50 mostra que 50% de toda a montagem está contida em *scaffolds* ≥ 1.080 pb. O N50 e o L50 da montagem são respectivamente a média dos maiores *scaffolds* até a metade do genoma (50%) e o número mínimo de *scaffolds* necessários para alcançar o valor N50 (GUREVICH e VYAHNI, 2013). Valores alto de N50 aumentam as chances de encontrar genes completos (LOPES, 2015; FLOREZ *et al.*, 2017).

A biblioteca BAC foi obtida a partir do cafeeiro CIFC 832/2 que corresponde a um híbrido interespecífico natural entre as espécies *C. arabica* e *C. canephora* (CAÇÃO *et al.*, 2013). A provável origem desse híbrido tetraploide fértil é a partir da fecundação de um gameta não reduzido de *C. canephora* com um gameta de *C. arabica* e posteriores eventos de retrocruzamentos com *C. arabica* (BETTENCOURT, 1973; LASHERMES *et al.*, 2000). Essa origem proposta para o HdT, corrobora para a maior similaridade de sequências encontradas entre o clone BAC e o genoma de *C. arabica*.

Entretanto, os genótipos derivados do Híbrido de Timor apresentam alta diversidade genética (SETOTAW *et al.*, 2010).

Foram anotados 173 genes em similaridade com o genoma de *C. arabica*. Em relação a esses genes, 173 foram encontrados no subgenoma *C. eugenioides* (C^E), 152 no subgenoma *C. canephora* (C^C) e 15 com sequências não caracterizadas em cromossomos. A espécie *C. arabica* possui dois subgenomas, pois é alotetraplóide (2n=44 cromossomos) (CLARINDO e CARVALHO, 2008) e tem origem da hibridação natural entre duas espécies diploides, *C. eugenioides* (2n=22 cromossomos) e *C. canephora* (2n=22 cromossomos) (LASHERMES *et al.*, 1999). Estudos sobre a origem de *C. arabica* sustentam a hipótese de que esse genoma resulta da associação dos subgenomas C^C e C^E, no entanto, afirmam que há limites taxonômicos entre *C. arabica* e *C. canephora*. Análises filogenéticas apresentam as três espécies em *clusters* distintos, sustentados por um alto valor de *bootstrap* (LASHERMES *et al.*, 1999).

Foram identificados no clone BAC 70-22F genes envolvidos na modulação da defesa em diferentes etapas da infecção e genes como um análogo ao *putative late blight resistance protein homolog RIA-4*, que desencadeia um sistema de defesa, incluindo uma resposta hipersensível que restringe o crescimento do patógeno (HR). Também foram identificados possíveis inibidores de proteases, envolvidos na morte programada ou apoptose controlada por sinalização (*cysteine synthase*) (TALHINHAS *et al.*, 2017), entre outros possíveis genes envolvidos no mecanismo de defesa de plantas (Apêndice A).

Genes candidatos relacionados a mecanismos de defesa semelhantes aos apresentados nesse trabalho, foram identificados por Florez *et al.* (2017). O transcriptoma da interação cafeeiro-*H. vastatrix*, foi analisado, considerando a interação compatível (*C. arabica* var. Caturra CIFC 19/1 inoculado com a raça XXXIII) e incompatível (HdT CIFC 832/1 inoculado com a raça XXXIII). Regiões gênicas com funções similares também foram descritas por Barka *et al.* (2017). Os autores analisaram uma biblioteca subtrativa e realizaram estudos de expressão gênica durante a interação incompatível (HdT CIFC 832/2) e compatível (*C. arabica* cv. Catuaí IAC 44) inoculados com a raça II de *H. vastatrix*. Esses trabalhos sustentam a hipótese de que a região do genoma do HdT CIFC 832/2 clonada e sequenciada no presente trabalho contém genes associados à resistência à *H. vastatrix*.

A partir da anotação dos genes presentes na região genômica do HdT CIFC 832/2 (BAC 70-22F), foram selecionados dois genes candidatos a receptores *like kinase*

(*RLKs*), para a análise de expressão gênica. Os *RLKs* são receptores de reconhecimento padrão (PRRs) que permitem a identificação de uma ampla gama de patógenos levando à PTI, constituindo a primeira linha de defesa da planta (SEKHWAL *et al.*, 2015).

O padrão de expressão do Gene1 sugere uma resistência pré-haustorial na interação incompatível, há reconhecimento do patógeno nas primeiras horas de infecção. O fungo *H. vastatrix* estabelece uma relação biotrófica com o seu hospedeiro em poucas horas após a inoculação, a produção de haustório ocorre logo que o fungo entra nos estômatos e, provavelmente, antes de chegar à cavidade subestomática, ou seja, aproximadamente às 24 hai (RAMIRO *et al.*, 2009).

Resistência pré-haustorial para o mesmo patossistema, genótipos resistente (HdT CIFC 832/2) e suscetível (*C. arabica* var. Caturra CIFC 19/1) inoculados com *H. vastatrix* raça XXXIII, foi observado em trabalhos de citologia (LOPES, 2015). Às 17h, após a inoculação, observaram-se as primeiras respostas citológicas induzidas pelo fungo, houve a morte celular nas células estomáticas de ambos os genótipos. Entretanto, os resultados sugerem impedimento do crescimento do fungo, no cafeeiro resistente, no estágio pré-haustorial, diferente do observado no cafeeiro suscetível. Na interação compatível, o fungo foi capaz de colonizar os tecidos do hospedeiro (LOPES, 2015).

Esse padrão de expressão observado para o Gene1, também foi descrito por Diniz *et al.* (2012), que sugerem uma rápida resposta de resistência em genótipos com interação incompatível. Entretanto, resistência pós-haustorial é geralmente a resposta descrita para a interação cafeeiro – *H. vastatrix*. O fungo cessa o seu crescimento em diferentes estágios da infecção, sendo mais frequentemente após a formação do primeiro haustório (SILVA *et al.*, 2002; RAMIRO *et al.*, 2009).

Já o padrão de expressão do Gene2, é uma diminuição da expressão no genótipo resistente que pode estar relacionada a uma resposta de defesa contra o patógeno. A maior expressão do gene pode cooperar de alguma forma com o sucesso da infecção pelo patógeno. Assim, em interações incompatíveis há a diminuição da expressão desse gene, como foi observado antes das 24 hai, sugerindo também uma defesa pré-haustorial. No genótipo suscetível observou-se um aumento da expressão do Gene2 às 24 hai, momento em que há a formação do haustório, o que pode estar permitindo maior adaptação do fungo. Padrão de expressão semelhante ao observado da expressão do Gene2 deste trabalho foi observado por BARROS (2016) em estudos do patossistema soja - *Phakopsora pachyrhiz* em que o fungo pode induzir respostas de defesa da planta nas horas iniciais do seu desenvolvimento, favorecendo o processo de infecção em

genótipos suscetíveis. No genótipo resistente vários genes foram reprimidos e no genótipo suscetível houve a indução na expressão de diferentes genes responsivos.

Para que ocorra uma resposta efetiva das plantas contra determinado estresse, diversos genes devem ser ativados e vários outros devem ser reprimidos. Os genes envolvidos na defesa contra patógeno, mesmo que tenham outra função na célula vegetal, só têm aumento no nível de expressão se for pertinente, evitando gasto de energia desnecessário para a célula (SREE *et al.*, 2015). Assim, outra hipótese para o padrão de expressão do Gene2 seria a diminuição da expressão de um gene que não auxilia nas respostas de defesa do cafeeiro durante a interação incompatível, permitindo o aumento eficiente da expressão de outros genes associados à resistência.

O perfil de expressão encontrado por Florez *et al.* (2017), em relação aos possíveis receptores *like kinase (RLK)*, durante a interação de *Coffea* com o fungo *H. vastatrix*, revelou que os *RLKs* tiveram uma diminuição na expressão relativa às 24 h durante a interação no genótipo resistente, em relação as amostras não inoculadas. No genótipo suscetível foi observado um pico de expressão às 24h após a infecção. Os autores relataram que os genes *RLKs* encontrados possivelmente estão envolvidos nas primeiras respostas de defesa da planta, PTI. O mesmo foi observado para o Gene2 nesse estudo. O reconhecimento do patógeno pelos receptores das plantas desencadeia uma cascata de sinalização para expressão de genes que resultam na PTI, em poucas horas após a infecção do fungo nas plantas (JONES e DANGL, 2006).

Nos estudos filogenéticos, o percentual de identidade genética entre as *reads* geradas pelo sequenciamento do clone BAC 70-22F e as variedade de *Coffea* mostrou valores baixos em relação a porcentagem de BLAST utilizando o genoma do clone montado em *contigs*. Com esses valores obtidos o indicado é a utilização da estratégia de montagem *de novo*. Pois os genomas de *Coffea* utilizados não são similares o suficiente com a região genômica sequenciada do HdT CIFC 832/2 para a realização da montagem por referência.

A similaridade genética entre o clone BAC 70-22F e a variedade Caturra (*C. arabica*1), a partir da porcentagem de BLAST entre os genomas, apresentou um valor alto em comparação com os outros resultados obtidos no alinhamento entre genomas. Já em relação à espécie *C. canephora*, os valores de similaridade e de identidade genética entre o clone BAC 70-22F e esse genoma apresentaram valores baixos. A análise de introgressão do genoma do HdT com os seus possíveis parentais, *C. canephora* var. Robusta e *C. arabica*, provou a existência de baixa introgressão de *C. canephora* no

HdT (SETOTAW *et al.*, 2010). A alta similaridade genética do HdT e *C. arabica* foram confirmadas por análise de introgressão do genoma, estudo da diversidade genética e análise de agrupamento, sustentando a hipótese de que o HdT é resultante de pelo menos dois retrocruzamentos com *C. arabica* (SETOTAW *et al.*, 2010). Além disso, o fenótipo do HdT é semelhante ao da espécie *C. arabica*, realizam autofecundação e contém um número tetraploide de cromossomos semelhante ao encontrado nessa espécie (HERRERA *et al.*, 2014).

Essas informações disponíveis na literatura corroboram as encontradas no presente trabalho. Entretanto, os genes de resistência (S_{H6} - S_{H9}) presentes no HdT, que ainda não foram suplantados (ZAMBOLIM, 2016), vieram da introgressão do genoma de *C. canephora* (HERRERA *et al.*, 2014). Os resultados observados podem indicar que o genoma utilizado *C. canephora* (clone IF 200) e o genoma *C. canephora* parental do HdT (CIFC 832/2) possuem ampla diversidade genética. Pois, dentro da espécie *C. canephora* há uma ampla base genética resultando em uma grande diversidade genética. A espécie possui diferentes grupos varietais, os quais provavelmente descendem da var. Robusta. *C. arabica* e o HdT apresentam maior similaridade com os genótipos do *C. canephora* var. Robusta do que com var. Conilon (SOUZA, 2011).

Na análise filogenética dos genes conservados, o clone alinhou em grupos diferentes de acordo com o gene estudado. Houve maior relação filogenética do clone BAC 70-22F com a variedade Boubon (*C. arabica*3), diferente dos dados encontrados em análises anteriores deste trabalho. No entanto, a menor similaridade foi com o genoma de *C. canephora*, em conformidade com resultados já apresentados.

Nem sempre é possível associar a filogenia detectada por um gene com a filogenia dos organismos. Fenômenos de duplicação, deleção e recombinação podem alterar significativamente a filogenia obtida. (CALDART *et al.*, 2016). Entretanto, as sequências utilizadas são de genes conservados e de cópia única, distribuídos em diferentes regiões do genoma do clone BAC 70-22F (HdT CIFC 832/2). Os resultados observados no estudo podem estar associados à diversidade genética apresentada pelo HdT. Setotaw *et al.* (2010), com o objetivo de investigar a diversidade genética do HdT, utilizando marcadores moleculares, concluíram ao analisarem 48 acessos de um banco de germoplasma, que o HdT apresenta considerável diversidade genética e ainda ampla variabilidade genética. Assim, além de ser uma importante fonte de genes para resistência a doenças, os genótipos do HdT possuem variações genéticas que são importantes no desenvolvimento de cultivares com resistência durável.

As árvores filogenéticas dos dois genes candidatos a RLKs, baseada no alinhamento de sequências proteicas dos genes e dos quatro genomas de *Coffea*, revelaram que o Gene1 e o Gene2 ficaram diferentes dos genes pertencentes ao genoma de *C. canephora*. Esses resultados sugerem que os dois genes pertencentes ao clone BAC 70-22F possuem relação filogenética mais próxima com os genes do genoma de *C. arabica*, assim como os resultados já apresentados neste trabalho.

O Gene2 e as três sequências agrupadas em um mesmo clado apresentaram domínios LRR. O domínio LRR possui importante função na defesa da planta contra patógenos, tem atuação tanto na PTI quanto na ETI. Na PTI os PRR localizados na superfície da membrana celular ou no interior da célula geralmente apresentam o domínio LRR. Além disso, o domínio LRR está envolvido no reconhecimento específico de efetores de patógenos, podendo interagir com a proteína Avr ou com um complexo de proteínas formado durante o processo de infecção (RAFIQI *et al.*, 2009; RIBAS *et al.*, 2011). No RT-qPCR apresentado nesse trabalho, o Gene2 apresentou alta expressão na interação incompatível (0 hai) e logo nas primeiras horas após a infecção o padrão de expressão diminuiu. Esse resultado pode estar relacionado com a atuação do gene no reconhecimento do patógeno no momento inicial da infecção. O mecanismo de defesa PTI ocorre imediatamente após o contato com o patógeno e é considerada a primeira linha de defesa induzida na planta, reconhecendo padrões moleculares conservados do patógeno (JONES e DANGL, 2006). Observou-se que na interação compatível houve um aumento da expressão do Gene2 após as 24 hai, momento em que o haustório já se formou. Essa defesa tardia no genótipo suscetível possivelmente está relacionada à suscetibilidade do genótipo, corroborando a importância da atuação de proteínas que contêm o domínio LRR no reconhecimento do patógeno.

5. Conclusões

As informações obtidas no presente trabalho são relevantes para ampliar o conhecimento sobre genes de resistência do cafeeiro à *H. vastatrix* e auxiliar na melhor compreensão da diversidade genética em genótipos do HdT. Pois, permitiram caracterizar uma região genômica do Híbrido de Timor CIFC 832/2, correspondente ao clone BAC 70-22F e potenciais genes com associação à resistência desse cafeeiro à *H. vastatrix* foram descritos. Dentre esses genes, dois genes se destacaram, sendo eles possíveis receptores *like kinases* (RLKs) com perfil de expressão correspondente a uma

resposta de resistência pré-haustorial. As análises de expressão gênica mostraram um perfil de expressão coerente com os já apresentados para o patossistema *Coffea – H. vastatrix*. As análises filogenéticas desses genes, bem como da região genômica clonada, demonstraram maior similaridade do clone BAC 70-22F com o genoma da espécie *C. arabica* e corroboraram a diversidade genética descrita para o HdT.

Referências Bibliográficas

ANDREWS, S. **FastQC: a quality control tool for high throughput sequence data**. 2010.

AUGUSTUS. Disponível em: <<http://augustus.gobics.de/>> Acesso em 20 de março de 2018.

AVELINO, J.; CRISTANCHO, M.; GEORGIU, S.; IMBACH, P.; AGUILAR, L.; BORNEMANN, G.; LÄDERACH, P.; ANZUETO, F.; HRUSKA, A.J.; MORALES, C. The coffee rust crises in Colombia and Central America (2008–2013): impacts, plausible causes and proposed solutions. **Food Security**, v. 7, n. 2, p. 303-321. 2015.

BANKEVICH, A.; NURK, S.; ANTIPOV, D.; ANTIPOV, D.; GUREVICH, A. A.; DVORKIN, M.; KULIKOV, A.S.; LESIN, V.M.; NIKOLENKO, S.I.; PHAM, S.; PRJIBELSKI, A.D.; PYSHKIN, A.V.; SIROTKIN, A.V.; VYAHHI, N.; TESLER, G.; ALEKSEYEV, M.A.; PEVZNER, P.A. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. **Journal of computational biology**, v. 19, n. 5, p. 455-477. 2012.

BARKA, G. D.; CAIXETA, E. T.; de ALMEIDA, R. F.; ALVARENGA, S. M.; ZAMBOLIM, L. Differential expression of molecular rust resistance components have distinctive profiles in *Coffea arabica* - *Hemileia vastatrix* interactions. **European journal of plant pathology**, v. 149, n. 3, p.543-561. 2017.

BARROS, V. A. **Vias de sinalização mediadas por ácido salicílico e metil-jasmonato e papel de GmbZIP89 em resposta à infecção por *Phakopsora pachyrhizi* em genótipos contrastantes de soja**. Dissertação (Mestrado em Bioquímica Aplicada) – Departamento de Bioquímica e Biologia Molecular, Universidade Federal de Viçosa, Viçosa, MG. 2016.

BECK, M.; HEARD, W.; MBENGUE, M.; ROBATZEK, S. The INs and OUTs of pattern recognition receptors at the cell surface. **Current opinion in plant biology**, v. 15, n. 4, p. 367-374. 2012.

BETTENCOURT, A. J. **Considerações sobre o “Híbrido de Timor”**. Campinas: Instituto Agrônomo, 20p. (Circular n° 23). 1973.

BETTENCOURT, A. J.; RODRIGUES JÚNIOR, C.J. Principles and practice of coffee breeding for resistance to rust and other diseases In: CLARKE, R.J. and MACRAE, R (Ed.). Coffee: Volume 4 – Agronomy. London: **Elsevier Applied Science**, cap. 6, p.199-234. 1988.

CABRAL, P. G. C.; ZAMBOLIM, E. M.; ZAMBOLIM, L.; LELIS, T. P.; CAPUCHO, A. S & CAIXETA, E. T. Identification of a new race of *Hemileia vastatrix* in Brazil. **Australasian Plant Disease Notes**, v. 4, n. 1, p. 129–130. 2009.

CAÇÃO, S. M. B; SILVA, N. V.; DOMINGUES, D. S; VIEIRA, L. G. E.; DINIZ, L. E. C.; ALVEZ, C. S. G.; ANDRADE, A. C.; CARPETIERI-PIPOLO, V.; PEREIRA, L;F.P. Construction and characterization of a BAC library from the *Coffea arabica* genotype Timor Hybrid CIFC 832/2. **Genetica**, v. 141, n. 4-6, p. 217-226. 2013.

CALDART, E. T.; MATA, H.; CANAL, C. W.; RAVAZZOLO, A. P. Phylogenetic analysis: basic concepts and its use as a tool for virology and molecular epidemiology. **Acta Scientiae Veterinariae**, 44. 2016.

CAPUCHO, A. S.; CAIXETA, E. T.; ZAMBOLIM, E. M.; ZAMBOLIM, L. Herança da resistência do Híbrido de Timor UFV 443-03 à ferrugem do cafeeiro. **Pesq. Agrop. Bras.**, Brasília. 44: 276-282. 2009.

CAPUCHO, A. S.; MACIEL-ZAMBOLIM, E.; FREITAS, R.L.; HADDAD, F.; CAIXETA, E. T.; ZAMBOLIM, L. Identification of race XXXIII of *Hemileia vastatrix* on *Coffea arabica* Catimor derivatives in Brazil. **Austral Plant Dis Notes**, v. 7, p. 189–191. 2012.

CARVALHO, V. L.; CUNHA, R. L.; SILVA, N. R. N. Alternativas de controle de doenças do cafeeiro. **Coffee Science**, Lavras, v. 7, n. 1, p. 42-49, 2012.

CLARINDO, W. R.; CARVALHO, C. R. First *Coffea arabica* karyogram showing that this species is a true allotetraploid. **Plant Systematics and Evolution**. Sep 1;274(3-4):237. 2008.

COFFEE GENOME HUB. Disponível em: <<http://coffee-genome.org/coffeacanephora>> Acesso em 20 de março de 2018.

CRUZ, F.; KALAOUN, S.; NOBILE, P.; COLOMBO, C.; ALMEIDA, J.; BARROS, L.M.; ROMANO, E.; GROSSI-DE-SÁ, M.F.; VASLIN, M.; ALVES-FERREIRA, M. Evaluation of coffee reference genes for relative expression studies by quantitative real-time RT-PCR. **Molecular Breeding**. May 1;23(4):607-16. 2009.

DINIZ, I.; TALHINHAS, P.; AZINHEIRA, H. G.; VÁRZEA, V.; MEDEIRA, C.; MAIA, I.; PETITOT, A. S.; NICOLE, M.; FERNANDEZ, D.; do CÉU SILVA, M. Cellular and molecular analyses of coffee resistance to *Hemileia vastatrix* and nonhost resistance to *Uromyces vignae* in the resistance-donor genotype HDT832/2. **European journal of plant pathology**. May 1;133(1):141-57. 2012.

DIOLA, V. **Resistência à ferrugem do cafeeiro: mapeamento genético, físico e análise da expressão gênica em resposta a infecção de *H. vastatrix***. Tese (Doutorado em Fisiologia Vegetal) – Departamento de Biologia Vegetal, Universidade Federal de Viçosa, Viçosa, MG. 2009.

DIOLA, V.; DE BRITO, G. G.; CAIXETA, E. T.; MACIEL-ZAMBOLIM, E.; SAKIYAMA, N. S.; LOUREIRO, M. E.; High-density genetic mapping for coffee leaf rust resistance. **Tree genetics & genomes**, 7(6), pp.1199-1208. 2011.

DODDS, P. N.; RAFIQI, M.; GAN, P. H. P.; HARDHAM, A. R.; JONES, D. A.; ELLIS, E. G. Effectores of biotrophic fungi and oomycetes: pathogenicity factors and triggers of host resistance. **New Phytologist**. 183: 993-1000. 2009.

EDWARDS, D.; BATLEY, J. Plant bioinformatics: from genome to phenome. **Trends in biotechnology**, v. 22, n. 5, p. 232-237. 2004.

ETIENNE, H.; ANTHONY, F.; DUSSERT, S.; FERNANDEZ, D.; LASHERMES, P.; BERTRAND, B. Biotechnological applications for the improvement of coffee (*Coffea arabica* L.). **In Vitro Cellular & Developmental Biology-Plant**, v. 38, n. 2, p. 129-138. 2002.

FELSENSTEIN, J. Confidence Limits on Phylogenies: An Approach Using The Bootstrap. **Evolution** (N Y) 39:783–791. 1985.

FERNANDES-BRUM, C. N.; REZENDE, P. M.; RIBEIRO, T. H. C.; de OLIVEIRA, R. R.; de SOUZA CARDOSO, T. C.; do AMARAL, L. R. GOMES, M. S.; CHALFUN-JUNIOR, A. A genome-wide analysis of the RNA-guided silencing pathway in coffee reveals insights into its regulatory mechanisms. **PloS One**, v. 12, n. 4, p. e0176333. 2017.

FINN, R. D.; BATEMAN, A.; CLEMENTS, J.; COGGILL, P.; EBERHARDT, R. Y.; EDDY, S. R.; HEGER, A.; HETHETTINGTON, K; HOLM, L.; MISTRY, J.; SONNHAMMER, E. L. L., TADE, J.; PUNTA, M. Pfam: the protein families database. **Nucleic acids research**, v. 42, n. D1, p. D222-D230. 2013.

FLOR, H.H. Current status of the gene-for-gene concept. **Annual review of phytopathology**, v. 9, n. 1, p. 275-296. 1971.

FLOREZ, J. C.; MOFATTO, L. S.; DO LIVRAMENTO, R. F. L.; FERREIRA, S. S.; ZAMBOLIM, E. M.; CARAZZOLLE, M. F.; ZAMBOLIM, L.; CAIXETA, E. T. High throughput transcriptome analysis of coffee reveals prehaustorial resistance in response to *Hemileia vastatrix* infection. **Plant Molecular Biology**, v. 95, p. 607-623. 2017.

FRANTZESKAKIS, L.; DI PIETRO, A.; REP, M.; SCHIRAWSKI, J.; WU, C. H.; PANSTRUGA, R. Rapid evolution in plant–microbe interactions—a molecular genomics perspective. **New Phytologist**. 2019.

GEN SCRIPT. Disponível em: <<https://www.genscript.com/>> Acesso em 26 de fevereiro de 2019.

GUREVICH, A.; VYAHNI, N. QUAST: quality assessment tool for genome assemblies. **Bioinformatics**, v. 29, n. 8, p. 1072-1075. 2013.

HEATH, M. C. Nonhost resistance and nonspecific plant defenses. **Current opinion in plant biology**, v. 3, n. 4, p. 315-319. 2000.

HERRERA, J. C.; VILLEGAS, A. M.; GARCIA, F. A.; DEREPPER, A.; COMBES, M. C.; POSADA, H. E.; LASHERMES, P. Genomic relationships among different Timor hybrid (*Coffea* L.) accessions as revealed by SNP identification and RNA-Seq analysis. In: **Advances in Computational Biology**. Springer, Cham, p. 161-168. 2014.

JONES, J. D. G.; DANGL, J. L. The plant immune system. **Nature**, v. 444, n. 7117, p. 323. 2006.

KUULASMAA T. **Oligo Explorer** 1.5. University of Easter Finland, Kuopyo, Finland. 2010.

- KUMAR, K. R. R.; KIRTI, P. B. Differential gene expression in *Arachis diogenes* upon interaction with peanut late leaf spot pathogen, *Phaeoisariopsis personata* and characterization of a pathogen induced cyclophilin. **Plant Mol Biol**, v. 75:497–513. 2011.
- KUMAR, S.; STECHER, G.; LI, M.; KNYAZ, C.; TAMURA, K. MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. **Molecular Biology and Evolution**, 35:1547-1549. 2018.
- LASHERMES, P.; COMBES, M. C.; ROBERT, J.; TROUSLOT, P.; D'HONT, A.; ANTHONY, F.; CHARRIER, A. Molecular characterisation and origin of the *Coffea arabica* L. genome. **Molecular and General Genetics MGG**, v. 261, n. 2, p. 259-266. 1999.
- LASHERMES, P.; ANDRZEJEWSKI, S.; BERTRAND, B.; COMBES, M. C.; DUSSERT, S.; GRAZIOSI, G.; ANTHONY, F. Molecular analysis of introgressive breeding in coffee (*Coffea arabica* L.). **Theoretical and applied genetics**, v. 100, n. 1, p. 139-146. 2000.
- LIN, C.; MUELLER, L. A.; CARTHY, J. M.; CROUZILLAT, D.; PETIARD, D.; TANKSLEY, S. D. Coffee and tomato share common gene repertoires as revealed by deep sequencing of seed and cherry transcripts. **Theoretical and applied genetics**, v. 112, n. 1, p. 114-130. 2005.
- LOHSE, M.; BOLGER, A. M.; NAGEL, A.; FERNIE, A. R.; LUNN, J. E.; STITT, M.; USADEL, B. R. obi NA: a user-friendly, integrated software solution for RNA-Seq-based transcriptomics. **Nucleic Acids Res.**, v. 40, n.1, p. 622-627. 2012.
- LOPES, R. L. F. **Análise Citológica e Perfil de Expressão Gênica de *Hemileia vastatrix* (RaçaXXXIII) na Interação Com o Cafeeiro.** Tese (Doutorado em Genética e Melhoramento) – Departamento de Fitotecnia, Universidade Federal de Viçosa, Viçosa, MG. 2015.
- MENDGEN, K., HAHN, M. Plant infection and the establishment of fungal biotrophy. **Trends in plant science**, v. 7, n. 8, p. 352-356. 2002.
- MICHNO, J. M.; STUPAR, R. M. The importance of genotype identity, genetic heterogeneity, and bioinformatic handling for properly assessing genomic variation in transgenic plants. **BMC biotechnology**, v. 18, n. 1, p. 38. 2018.
- MIKHEENKO, A.; PRJIBELSKI, A.; SAVELIEV, V.; ANTIPOV, D.; GUREVICH, A. Avaliação de montagem de genoma versátil com QUAST-LG. **Bioinformática** 34 (13): i142-i150. 2018.
- MOTULSKY, H. J. **Prism 5 Statistics Guide, Software GraphPad.** Inc., San Diego CA. 2007.
- NATIONAL CENTER FOR BIOTECHNOLOGY INFORMATION. Disponível em: <<https://www.ncbi.nlm.nih.gov/>> Acesso em 20 de março de 2018.

NORONHA-WAGNER, M.; BETTENCOURT, A. Genetic study of the resistance of *coffea* spp. to leaf rust: i. identification and behavior of four factors conditioning disease reaction in *Coffea arabica* to twelve physiologic races of *Hemileia vastatrix*. **Canadian Journal of Botany**, v. 45, n. 11, p. 2021-2031. 1967.

PESTANA, K. N.; CAPUCHO, A. S.; CAIXETA, E. T.; DE ALMEIDA, D. P.; ZAMBOLIM, E. M.; CRUZ, C. D.; ZAMBOLIM, L.; PEREIRA, A. A.; OLIVEIRA, A. C. B.; SAKIYAMA, N. S. Inheritance study and linkage mapping of resistance loci to *Hemileia vastatrix* in Híbrido de Timor UFV 443-03. **Tree genetics & genomes**, v. 11, n. 4, p. 72. 2015.

RAFIQI, M.; BERNOUX, M.; ELLIS, J. G.; DODDS, P. N. In the trenches of plant pathogen recognition: Role of NB-LRR proteins. In: **Seminars in cell & developmental biology**. Academic Press, p. 1017-1024. 2009.

RAMIRO, D. A.; Escoute, J.; Petitot, A. S.; Nicole, M.; Maluf, M. P.; Fernandez, D. Biphasic haustorial differentiation of coffee rust (*Hemileia vastatrix* race II) associated with defence responses in resistant and susceptible coffee cultivars. **Plant Pathology**, v. 58, n. 5, p. 944-955. 2009.

REDDY, A. C.; NARESH, P. The crucial role of R-genes/RGAs in host-microbial interactions and plant immunity. **Research Journal of Biotechnology**, vol. v. 13, p. 4. 2018.

RIBAS, A. F.; CENCI, A.; COMBES, M. C.; ETIENNE, H.; LASHERMES, P. Organization and molecular evolution of a disease-resistance gene cluster in coffee trees. **BMC genomics**, v. 12, n. 1, p. 240. 2011.

SEKHWAL, M.; LI, P.; LAM, I.; WANG, X.; CLOUTIER, S.; YOU, F. Disease resistance gene analogs (RGAs) in plants. **International journal of molecular sciences**, v. 16, n. 8, p. 19248-19290. 2015.

SETOTAW, T. A.; TEXEIRA, C. E.; FERREIRE, P. G.; ZAMBOLIM, E. M.; PEREIRA, A. A.; SAKIYAMA, N. S. Breeding potential and genetic diversity of "Híbrido do Timor" coffee evaluated by molecular markers. **Crop breeding and applied biotechnology**, v. 10, n. 4, p. 298-304. 2010.

SILVA, M. C.; NICOLE, M.; GUERRA-GUIMARÃES, L.; RODRIGUES JR, C. J. Hypersensitive cell death and post-haustorial defence responses arrest the orange rust (*Hemileia vastatrix*) growth in resistant coffee leaves. **Physiological and Molecular Plant Pathology**, v. 60, n. 4, p. 169-183. 2002.

SILVA, R. A.; ZAMBOLIM, L.; CASTRO, I. S. L.; RODRIGUES, H. S.; CRUZ, C. D.; CAIXETA, E. T. The Híbrido de Timor germplasm: identification of molecular diversity and resistance sources to coffee berry disease and leaf rust. **Euphytica**, v. 214, n. 9, p. 153. 2018.

SOUZA, F. F. **Diversidade genética, estrutura populacional e mapeamento associativo em *Coffea canephora***. Tese (Doutorado em Genética e Melhoramento) – Departamento de Fitotecnia, Universidade Federal de Viçosa, Viçosa, MG. 2011.

SOUSA, T. V.; CAIXETA, E. T.; ALKIMIM, E. R.; DE OLIVEIRA, A. C. B.; PEREIRA, A. A.; SAKIYAMA, N. S. JÚNIOR, M. F. R. R.; ZAMBOLIM, L. Population structure and genetic diversity of coffee progenies derived from Catuaí and Híbrido de Timor revealed by genome-wide SNP marker. **Tree genetics & genomes**, v. 13, n. 6, p. 124. 2017.

SREE, K.; SOWJANYA; R. A. J. A. M.; MANCHIKATLA, V. Genetic engineering strategies for biotic stress tolerance in plants. In: **Plant Biology and Biotechnology**. Springer, New Delhi, p. 611-622. 2015.

STANKE, M.; STEINKAMP, R.; WAACK, S.; MORGENSTERN, B. AUGUSTUS: a web server for gene finding in eukaryotes. **Nucleic acids research**, v. 32, n. suppl 2, p. W309-W312. 2004.

TALHINHAS, P.; BATISTA, D.; DINIZ, I.; VIEIRA, A.; SILVA, D.N.; LOUREIRO, A., TAVERES, S.; PEREIRA, A.P.; AZINHEIRA, H. G.; GUERRERA-GUINARÃES, L.; VÁRZEA, V.; SILVA, M. C. The coffee leaf rust pathogen *Hemileia vastatrix*: one and a half centuries around the tropics. **Molecular plant pathology**, v. 18, n. 8, p. 1039-1051. 2017.

TAMURA, K.; NEI, M. Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. **Mol Biol Evol**. 1993.

TRAPNELL, C.; PACHTER, L.; SALZBERG, S. L. TopHat: discovering splice junctions with RNA-Seq. **Bioinformatics**, v. 25, n. 9, p. 1105-1111. 2009.

ZAMBOLIM, L. Current status and management of coffee leaf rust in Brazil. **Tropical Plant Pathology**, v. 41, n. 1, p. 1-8. 2016.

WORLD COFFEE RESEARCH. Disponível em: <<https://worldcoffeeresearch.org/>> Acesso em 20 de março de 2018.

Apêndice A. Anotação gênica do clone BAC 70-22F utilizando a ferramenta BLAST. Foram anotados 991 genes. 340 genes anotados em similaridade com *C. arabica* (var. Caturra). 337 genes anotados em similaridade com *C. eugenioides*.

314 genes anotados em similaridade com *C.canephora* (clone IF 200).

| ORFs | Locos | Genoma | %ID | E-value | Cobertura | Anotação |
|--|-------------------------|----------------|-------|-----------|-----------|---|
| NODE_1_length_6472_cov_8.48366:g1.t1 | NC_039902.1 3c | C. arabica | 49.55 | 0.0 | 98.00 | uncharacterized protein LOC113735882 |
| NODE_1_length_6472_cov_8.48366:g1.t1 | chr10 | C. canephora | 32.48 | 4,00E-26 | 15.00 | Putative Probable LRR receptor-like serine/threonine-protein kinase At4g08850 |
| NODE_1_length_6472_cov_8.48366:g1.t1 | NC_040035.1 1eu | C. eugenioides | 61.85 | 0.0 | 60.00 | uncharacterized protein LOC113769237 |
| NODE_1_length_6472_cov_8.48366:g1.t2 | NC_039902.1 3c | C. arabica | 57.96 | 0.0 | 61.00 | uncharacterized protein LOC113735882 |
| NODE_1_length_6472_cov_8.48366:g1.t2 | chr10 | C. canephora | 32.48 | 5,00E-26 | 15.00 | Putative Probable LRR receptor-like serine/threonine-protein kinase At4g08850 |
| NODE_1_length_6472_cov_8.48366:g1.t2 | NC_040035.1 1eu | C. eugenioides | 62.34 | 0.0 | 61.00 | uncharacterized protein LOC113769237 |
| NODE_2_length_6312_cov_4.20642:g2.t1 | NC_039915.1 9e | C. arabica | 75.38 | 1,00E-60 | 57.00 | uncharacterized protein LOC113709996 |
| NODE_2_length_6312_cov_4.20642:g2.t1 | chr0 | C. canephora | 58.33 | 8,00E-18 | 31.00 | Hypothetical protein |
| NODE_2_length_6312_cov_4.20642:g2.t1 | NC_040037.1 3eu | C. eugenioides | 73.61 | 9,00E-28 | 31.00 | uncharacterized protein LOC113766718 |
| NODE_10_length_2753_cov_2.94619:g8.t1 | NC_039902.1 3c | C. arabica | 65.03 | 0.0 | 95.00 | uncharacterized protein LOC113735882 |
| NODE_10_length_2753_cov_2.94619:g8.t1 | chr10 | C. canephora | 36.55 | 5,00E-27 | 25.00 | Putative Probable LRR receptor-like serine/threonine-protein kinase At4g08850 |
| NODE_10_length_2753_cov_2.94619:g8.t1 | NC_040036.1 2eu | C. eugenioides | 73.94 | 0.0 | 56.00 | uncharacterized protein LOC113760043 |
| NODE_12_length_2445_cov_5.93412:g9.t1 | NC_039901.1 2e | C. arabica | 61.18 | 1,00E-25 | 36.00 | uncharacterized protein LOC113729084 |
| NODE_12_length_2445_cov_5.93412:g9.t1 | NC_040036.1 2eu | C. eugenioides | 61.18 | 6,00E-26 | 36.00 | uncharacterized protein LOC113759824 |
| NODE_17_length_2074_cov_4.61592:g10.t1 | NC_039915.1 9e | C. arabica | 40.62 | 3,00E-40 | 44.00 | uncharacterized protein LOC113709957 |
| NODE_17_length_2074_cov_4.61592:g10.t1 | NW_020863778.1 scaffold | C. eugenioides | 42.55 | 2,00E-40 | 37.00 | uncharacterized protein LOC113757670 |
| NODE_17_length_2074_cov_4.61592:g10.t2 | NC_039915.1 9e | C. arabica | 40.62 | 2,00E-40 | 45.00 | uncharacterized protein LOC113709957 |
| NODE_17_length_2074_cov_4.61592:g10.t2 | NW_020863778.1 scaffold | C. eugenioides | 42.55 | 2,00E-40 | 37.00 | uncharacterized protein LOC113757670 |
| NODE_24_length_1689_cov_2.3995:g13.t1 | NC_039914.1 9c | C. arabica | 84.11 | 5,00E-84 | 53.00 | serologically defined colon cancer antigen 8 homolog |
| NODE_24_length_1689_cov_2.3995:g13.t1 | NC_040035.1 1eu | C. eugenioides | 60.56 | 4,00E-54 | 64.00 | uncharacterized protein LOC113770239 |
| NODE_24_length_1689_cov_2.3995:g13.t2 | NC_039914.1 9c | C. arabica | 84.11 | 1,00E-83 | 52.00 | serologically defined colon cancer antigen 8 homolog |
| NODE_24_length_1689_cov_2.3995:g13.t2 | NC_040035.1 1eu | C. eugenioides | 60.56 | 8,00E-54 | 63.00 | uncharacterized protein LOC113770239 |
| NODE_29_length_1476_cov_2.56469:g16.t1 | NC_039903.1 3e | C. arabica | 58.70 | 9,00E-167 | 100.00 | uncharacterized protein LOC113737292 |
| NODE_29_length_1476_cov_2.56469:g16.t1 | NC_040044.1 10eu | C. eugenioides | 60.22 | 7,00E-170 | 100.00 | uncharacterized protein LOC113750488 |
| NODE_29_length_1476_cov_2.56469:g16.t2 | NC_039903.1 3e | C. arabica | 58.70 | 1,00E-166 | 97.00 | uncharacterized protein LOC113737292 |
| NODE_29_length_1476_cov_2.56469:g16.t2 | NC_040044.1 10eu | C. eugenioides | 60.22 | 2,00E-169 | 97.00 | uncharacterized protein LOC113750488 |
| NODE_44_length_1234_cov_3.88678:g21.t1 | NC_039899.1 1e | C. arabica | 71.78 | 0.0 | 100.00 | uncharacterized protein LOC113692421 |
| NODE_44_length_1234_cov_3.88678:g21.t1 | NC_040035.1 1eu | C. eugenioides | 72.26 | 0.0 | 100.00 | uncharacterized protein LOC113768532 |
| NODE_61_length_936_cov_2.05937:g27.t1 | NC_039905.1 4e | C. arabica | 71.88 | 4,00E-88 | 100.00 | protein STRICTOSIDINE SYNTHASE-LIKE 12-like isoform X2 |

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|--|-------------------------|----------------|--------|----------|--------|--|
| NODE_61_length_936_cov_2.05937:g27.t1 | chr4 | C. canephora | 69.79 | 1,00E-81 | 100.00 | Putative Strictosidine synthase 1 |
| NODE_61_length_936_cov_2.05937:g27.t1 | NC_040038.1 4eu | C. eugenioides | 61.83 | 2,00E-69 | 96.00 | protein STRICTOSIDINE SYNTHASE-LIKE 11-like |
| NODE_61_length_936_cov_2.05937:g27.t2 | NC_039905.1 4e | C. arabica | 72.41 | 6,00E-96 | 93.00 | protein STRICTOSIDINE SYNTHASE-LIKE 12-like isoform X2 |
| NODE_61_length_936_cov_2.05937:g27.t2 | chr4 | C. canephora | 69.95 | 1,00E-82 | 88.00 | Putative Strictosidine synthase 1 |
| NODE_61_length_936_cov_2.05937:g27.t2 | NC_040038.1 4eu | C. eugenioides | 61.38 | 5,00E-71 | 87.00 | protein STRICTOSIDINE SYNTHASE-LIKE 11-like |
| NODE_62_length_907_cov_1.42651:g28.t1 | NC_039912.1 8e | C. arabica | 80.62 | 4,00E-48 | 100.00 | uncharacterized protein LOC113704544 |
| NODE_62_length_907_cov_1.42651:g28.t1 | chr0 | C. canephora | 67.16 | 2,00E-28 | 53.00 | Hypothetical protein |
| NODE_62_length_907_cov_1.42651:g28.t1 | NW_020864190.1 scaffold | C. eugenioides | 76.98 | 2,00E-47 | 100.00 | uncharacterized protein LOC113758088 |
| NODE_74_length_772_cov_1.49784:g29.t1 | NC_039904.1 4c | C. arabica | 100.00 | 1,00E-42 | 90.00 | diphthine methyltransferase homolog |
| NODE_74_length_772_cov_1.49784:g29.t1 | chr4 | C. canephora | 100.00 | 4,00E-43 | 90.00 | Putative WD repeat-containing protein 85 homolog |
| NODE_74_length_772_cov_1.49784:g29.t1 | NC_040038.1 4eu | C. eugenioides | 100.00 | 4,00E-43 | 90.00 | diphthine methyltransferase homolog isoform X2 |
| NODE_88_length_724_cov_1.32921:g35.t1 | NC_039913.1 8c | C. arabica | 58.33 | 9,00E-59 | 96.00 | delta-aminolevulinic acid dehydratase%2C chloroplastic-like |
| NODE_88_length_724_cov_1.32921:g35.t1 | chr8 | C. canephora | 58.33 | 3,00E-58 | 96.00 | Delta-aminolevulinic acid dehydratase%2C chloroplastic |
| NODE_88_length_724_cov_1.32921:g35.t1 | NC_040038.1 4eu | C. eugenioides | 58.33 | 5,00E-59 | 96.00 | delta-aminolevulinic acid dehydratase%2C chloroplastic-like |
| NODE_95_length_683_cov_1.15347:g39.t1 | NW_020850478.1 scaffold | C. arabica | 48.78 | 5,00E-27 | 50.00 | monothiol glutaredoxin-S7%2C chloroplastic |
| NODE_95_length_683_cov_1.15347:g39.t1 | chr7 | C. canephora | 48.78 | 1,00E-26 | 50.00 | Uncharacterized monothiol glutaredoxin ycf64-like |
| NODE_95_length_683_cov_1.15347:g39.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 48.78 | 3,00E-27 | 50.00 | monothiol glutaredoxin-S7%2C chloroplastic |
| NODE_100_length_671_cov_1.90741:g42.t1 | NC_039901.1 2e | C. arabica | 54.69 | 1,00E-18 | 44.00 | glycine-rich protein 2-like |
| NODE_100_length_671_cov_1.90741:g42.t1 | chr2 | C. canephora | 54.69 | 5,00E-19 | 44.00 | Glycine-rich protein 2b |
| NODE_100_length_671_cov_1.90741:g42.t1 | NC_040036.1 2eu | C. eugenioides | 54.69 | 8,00E-19 | 44.00 | glycine-rich protein 2 |
| NODE_104_length_660_cov_1.56261:g43.t1 | NC_039904.1 4c | C. arabica | 35.41 | 7,00E-29 | 95.00 | aldehyde dehydrogenase family 2 member B4%2C mitochondrial-like |
| NODE_104_length_660_cov_1.56261:g43.t1 | chr4 | C. canephora | 35.41 | 2,00E-29 | 95.00 | Aldehyde dehydrogenase family 2 member B4%2C mitochondrial |
| NODE_104_length_660_cov_1.56261:g43.t1 | NC_040038.1 4eu | C. eugenioides | 35.41 | 6,00E-29 | 95.00 | aldehyde dehydrogenase family 2 member B4%2C mitochondrial-like |
| NODE_105_length_656_cov_1.3886:g44.t1 | NC_039903.1 3e | C. arabica | 38.02 | 2,00E-21 | 93.00 | carboxyl-terminal-processing peptidase 2%2C chloroplastic-like isoform X1 |
| NODE_105_length_656_cov_1.3886:g44.t1 | chr3 | C. canephora | 38.54 | 3,00E-23 | 93.00 | Carboxyl-terminal-processing protease |
| NODE_105_length_656_cov_1.3886:g44.t1 | NC_040037.1 3eu | C. eugenioides | 38.54 | 4,00E-22 | 93.00 | carboxyl-terminal-processing peptidase 2%2C chloroplastic isoform X1 |
| NODE_110_length_645_cov_1.68486:g49.t1 | NC_039903.1 3e | C. arabica | 57.38 | 2,00E-17 | 75.00 | uncharacterized protein LOC113737438 |
| NODE_110_length_645_cov_1.68486:g49.t1 | NC_040041.1 7eu | C. eugenioides | 53.97 | 1,00E-17 | 77.00 | uncharacterized protein LOC113777170 |
| NODE_117_length_632_cov_2.09009:g53.t1 | NC_039907.1 5c | C. arabica | 29.58 | 3,00E-15 | 90.00 | probable lipid-A-disaccharide synthase%2C mitochondrial isoform X2 |
| NODE_117_length_632_cov_2.09009:g53.t1 | chr5 | C. canephora | 29.44 | 6,00E-16 | 90.00 | Putative Lipid-A-disaccharide synthase |
| NODE_117_length_632_cov_2.09009:g53.t1 | NC_040039.1 5eu | C. eugenioides | 29.11 | 5,00E-15 | 90.00 | probable lipid-A-disaccharide synthase%2C mitochondrial isoform X1 |
| NODE_118_length_632_cov_1.58378:g54.t1 | NC_039907.1 5c | C. arabica | 22.83 | 2,00E-10 | 96.00 | DUF21 domain-containing protein At1g55930%2C chloroplastic-like isoform X3 |
| NODE_118_length_632_cov_1.58378:g54.t1 | chr5 | C. canephora | 23.74 | 4,00E-10 | 87.00 | DUF21 domain-containing protein At1g55930%2C chloroplastic |
| NODE_118_length_632_cov_1.58378:g54.t1 | NC_040039.1 5eu | C. eugenioides | 25.73 | 9,00E-11 | 76.00 | putative DUF21 domain-containing protein At3g13070%2C chloroplastic isoform X2 |

| | | | | | | |
|--|-----------------------|----------------|--------|-----------|--------|---|
| NODE_128_length_614_cov_1.73557:g61.t1 | NC_039911.1 7e | C. arabica | 27.73 | 8,00E-08 | 99.00 | cellulose synthase A catalytic subunit 5 [UDP-forming]-like |
| NODE_128_length_614_cov_1.73557:g61.t1 | chr7 | C. canephora | 27.98 | 1,00E-09 | 98.00 | Cellulose synthase A catalytic subunit 5 [UDP-forming] |
| NODE_128_length_614_cov_1.73557:g61.t1 | NC_040041.1 7eu | C. eugenioides | 27.73 | 4,00E-08 | 99.00 | cellulose synthase A catalytic subunit 5 [UDP-forming]-like |
| NODE_129_length_613_cov_2.95522:g62.t1 | NC_039905.1 4e | C. arabica | 98.40 | 6,00E-54 | 100.00 | homeobox protein knotted-1-like 1 |
| NODE_129_length_613_cov_2.95522:g62.t1 | chr4 | C. canephora | 100.00 | 1,00E-45 | 86.00 | Putative uncharacterized protein |
| NODE_129_length_613_cov_2.95522:g62.t1 | NC_040038.1 4eu | C. eugenioides | 98.40 | 3,00E-54 | 100.00 | homeobox protein knotted-1-like 1 |
| NODE_132_length_607_cov_3.49811:g65.t1 | NC_039904.1 4c | C. arabica | 93.10 | 3,00E-48 | 97.00 | uncharacterized protein LOC113739892 isoform X1 |
| NODE_132_length_607_cov_3.49811:g65.t1 | chr4 | C. canephora | 93.10 | 1,00E-48 | 97.00 | unknown protein%3B FUNCTIONS IN |
| NODE_132_length_607_cov_3.49811:g65.t1 | NC_040038.1 4eu | C. eugenioides | 93.10 | 2,00E-48 | 97.00 | uncharacterized protein LOC113768344 isoform X1 |
| NODE_132_length_607_cov_3.49811:g65.t2 | NC_039904.1 4c | C. arabica | 100.00 | 8,00E-48 | 100.00 | uncharacterized protein LOC113739892 isoform X1 |
| NODE_132_length_607_cov_3.49811:g65.t2 | chr4 | C. canephora | 100.00 | 3,00E-48 | 100.00 | unknown protein%3B FUNCTIONS IN |
| NODE_132_length_607_cov_3.49811:g65.t2 | NC_040038.1 4eu | C. eugenioides | 100.00 | 4,00E-48 | 100.00 | uncharacterized protein LOC113768344 isoform X1 |
| NODE_140_length_596_cov_1.30829:g70.t1 | NC_039908.1 6c | C. arabica | 29.65 | 3,00E-21 | 93.00 | thioredoxin reductase NTRC-like |
| NODE_140_length_596_cov_1.30829:g70.t1 | chr6 | C. canephora | 29.65 | 9,00E-22 | 93.00 | NADPH-dependent thioredoxin reductase 3 |
| NODE_140_length_596_cov_1.30829:g70.t1 | NC_040040.1 6eu | C. eugenioides | 29.65 | 5,00E-22 | 93.00 | thioredoxin reductase NTRC |
| NODE_144_length_589_cov_2.50195:g74.t1 | NC_039918.1 11c | C. arabica | 29.56 | 2,00E-16 | 98.00 | spermidine synthase-like |
| NODE_144_length_589_cov_2.50195:g74.t1 | chr2 | C. canephora | 25.47 | 4,00E-12 | 96.00 | Spermine synthase |
| NODE_144_length_589_cov_2.50195:g74.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 28.93 | 7,00E-16 | 98.00 | spermidine synthase |
| NODE_146_length_588_cov_1.42661:g76.t1 | NC_039898.1 1c | C. arabica | 36.95 | 5,00E-31 | 95.00 | lysosomal beta glucosidase-like |
| NODE_146_length_588_cov_1.42661:g76.t1 | chr1 | C. canephora | 36.95 | 2,00E-31 | 95.00 | Putative Lysosomal beta glucosidase |
| NODE_146_length_588_cov_1.42661:g76.t1 | NC_040035.1 1eu | C. eugenioides | 37.50 | 7,00E-31 | 89.00 | lysosomal beta glucosidase-like |
| NODE_154_length_576_cov_1.46894:g81.t1 | NC_039900.1 2c | C. arabica | 27.98 | 1,00E-16 | 91.00 | ATP-dependent DNA helicase SRS2-like protein At4g25120 isoform X3 |
| NODE_154_length_576_cov_1.46894:g81.t1 | chr0 | C. canephora | 27.98 | 5,00E-17 | 91.00 | Putative ATP-dependent DNA helicase pcrA |
| NODE_154_length_576_cov_1.46894:g81.t1 | NC_040035.1 1eu | C. eugenioides | 27.98 | 3,00E-17 | 91.00 | ATP-dependent DNA helicase SRS2-like protein At4g25120 |
| NODE_168_length_551_cov_1.50422:g90.t1 | NC_039910.1 7c | C. arabica | 36.75 | 4,00E-14 | 59.00 | ATP-dependent 6-phosphofructokinase 5%2C chloroplastic-like |
| NODE_168_length_551_cov_1.50422:g90.t1 | chr7 | C. canephora | 36.75 | 1,00E-14 | 59.00 | 6-phosphofructokinase 5%2C chloroplastic |
| NODE_168_length_551_cov_1.50422:g90.t1 | NC_040041.1 7eu | C. eugenioides | 36.75 | 2,00E-14 | 59.00 | ATP-dependent 6-phosphofructokinase 5%2C chloroplastic |
| NODE_172_length_548_cov_3.2017:g92.t1 | NC_039905.1 4e | C. arabica | 95.45 | 1,00E-24 | 100.00 | uncharacterized protein LOC113742131 isoform X1 |
| NODE_172_length_548_cov_3.2017:g92.t1 | chr4 | C. canephora | 95.45 | 4,00E-25 | 100.00 | unknown protein%3B FUNCTIONS IN |
| NODE_172_length_548_cov_3.2017:g92.t1 | NC_040038.1 4eu | C. eugenioides | 95.45 | 9,00E-25 | 100.00 | uncharacterized protein LOC113768344 isoform X2 |
| NODE_173_length_548_cov_1.32696:g93.t1 | NC_039915.1 9e | C. arabica | 100.00 | 2,00E-100 | 100.00 | uncharacterized protein LOC113709986 |
| NODE_173_length_548_cov_1.32696:g93.t1 | chr2 | C. canephora | 53.30 | 2,00E-46 | 100.00 | Putative DNA helicase PIF1%2C ATP-dependent |
| NODE_173_length_548_cov_1.32696:g93.t1 | NC_040038.1 4eu | C. eugenioides | 100.00 | 5,00E-99 | 100.00 | uncharacterized protein LOC113769142 |
| NODE_174_length_548_cov_1.52654:g94.t1 | NC_039910.1 7c | C. arabica | 81.87 | 5,00E-110 | 100.00 | uncharacterized protein LOC113699534 |

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|---|-------------------------|----------------|--------|-----------|--------|---|
| NODE_174_length_548_cov_1.52654:g94.t1 | chr10 | C. canephora | 40.00 | 6,00E-14 | 35.00 | Putative Probable LRR receptor-like serine/threonine-protein kinase At4g08850 |
| NODE_174_length_548_cov_1.52654:g94.t1 | NW_020862338.1 scaffold | C. eugenioides | 54.95 | 5,00E-74 | 100.00 | uncharacterized protein LOC113756011 |
| NODE_175_length_546_cov_1.54371:g95.t1 | NC_039900.1 2c | C. arabica | 34.57 | 3,00E-08 | 79.00 | LOW QUALITY PROTEIN: CLP protease regulatory subunit CLPX1%2C mitochondrial-like |
| NODE_175_length_546_cov_1.54371:g95.t1 | chr2 | C. canephora | 34.57 | 7,00E-09 | 79.00 | ATP-dependent Clp protease ATP-binding subunit ClpX |
| NODE_175_length_546_cov_1.54371:g95.t1 | NC_040036.1 2eu | C. eugenioides | 34.57 | 2,00E-08 | 79.00 | CLP protease regulatory subunit CLPX1%2C mitochondrial |
| NODE_176_length_545_cov_2.76282:g96.t1 | NC_039900.1 2c | C. arabica | 67.39 | 7,00E-38 | 100.00 | uncharacterized protein LOC113723844 |
| NODE_176_length_545_cov_2.76282:g96.t1 | chr2 | C. canephora | 49.45 | 3,00E-21 | 97.00 | Putative Pol-polyprotein |
| NODE_176_length_545_cov_2.76282:g96.t1 | NC_040035.1 1eu | C. eugenioides | 67.39 | 4,00E-37 | 100.00 | uncharacterized protein K02A2.6-like |
| NODE_185_length_535_cov_1.33188:g100.t1 | NC_039900.1 2c | C. arabica | 39.60 | 9,00E-18 | 93.00 | 3-methyl-2-oxobutanoate hydroxymethyltransferase 2%2C mitochondrial-like isoform X2 |
| NODE_185_length_535_cov_1.33188:g100.t1 | chr2 | C. canephora | 39.24 | 9,00E-18 | 98.00 | 3-methyl-2-oxobutanoate hydroxymethyltransferase |
| NODE_185_length_535_cov_1.33188:g100.t1 | NC_040036.1 2eu | C. eugenioides | 39.60 | 6,00E-18 | 93.00 | 3-methyl-2-oxobutanoate hydroxymethyltransferase 2%2C mitochondrial-like isoform X2 |
| NODE_186_length_534_cov_1.5186:g101.t1 | NC_039918.1 11c | C. arabica | 47.50 | 1,00E-17 | 64.00 | probable aquaporin NIP-type |
| NODE_186_length_534_cov_1.5186:g101.t1 | chr7 | C. canephora | 42.50 | 2,00E-16 | 64.00 | Probable aquaporin NIP-type |
| NODE_186_length_534_cov_1.5186:g101.t1 | NC_040036.1 2eu | C. eugenioides | 45.57 | 2,00E-17 | 63.00 | aquaporin NIP1-1-like |
| NODE_189_length_533_cov_1.01096:g103.t1 | NC_039906.1 5e | C. arabica | 29.38 | 7,00E-11 | 90.00 | aconitate hydratase%2C cytoplasmic |
| NODE_189_length_533_cov_1.01096:g103.t1 | chr5 | C. canephora | 29.38 | 3,00E-11 | 90.00 | Aconitate hydratase 2%2C mitochondrial |
| NODE_189_length_533_cov_1.01096:g103.t1 | NC_040039.1 5eu | C. eugenioides | 27.93 | 1,00E-10 | 92.00 | putative aconitate hydratase%2C cytoplasmic |
| NODE_192_length_532_cov_1.53407:g106.t1 | NW_020849470.1 scaffold | C. arabica | 100.00 | 2,00E-108 | 100.00 | uncharacterized protein LOC113720575 |
| NODE_192_length_532_cov_1.53407:g106.t1 | chr3 | C. canephora | 58.94 | 5,00E-58 | 85.00 | Hypothetical protein |
| NODE_192_length_532_cov_1.53407:g106.t1 | NC_040038.1 4eu | C. eugenioides | 98.30 | 6,00E-107 | 100.00 | uncharacterized protein LOC113769142 |
| NODE_204_length_525_cov_1.18973:g116.t1 | NC_039918.1 11c | C. arabica | 36.97 | 3,00E-09 | 72.00 | LOW QUALITY PROTEIN: inorganic phosphate transporter 2-1%2C chloroplastic-like |
| NODE_204_length_525_cov_1.18973:g116.t1 | chr11 | C. canephora | 41.76 | 8,00E-09 | 54.00 | Inorganic phosphate transporter 2-1%2C chloroplastic |
| NODE_204_length_525_cov_1.18973:g116.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 36.89 | 6,00E-09 | 62.00 | inorganic phosphate transporter 2-1%2C chloroplastic |
| NODE_207_length_522_cov_1.56404:g117.t1 | NC_039916.1 10e | C. arabica | 58.82 | 9,00E-58 | 100.00 | protein translocase subunit SECA2%2C chloroplastic-like |
| NODE_207_length_522_cov_1.56404:g117.t1 | chr10 | C. canephora | 58.82 | 1,00E-59 | 100.00 | Protein translocase subunit SECA2%2C chloroplastic |
| NODE_207_length_522_cov_1.56404:g117.t1 | NC_040035.1 1eu | C. eugenioides | 66.23 | 3,00E-60 | 92.00 | protein translocase subunit SecA%2C chloroplastic |
| NODE_211_length_520_cov_1.92325:g121.t1 | NC_039898.1 1c | C. arabica | 44.44 | 2,00E-07 | 36.00 | phosphomethylpyrimidine synthase%2C chloroplastic isoform X3 |
| NODE_211_length_520_cov_1.92325:g121.t1 | chr1 | C. canephora | 44.44 | 8,00E-08 | 36.00 | Phosphomethylpyrimidine synthase%2C chloroplastic |
| NODE_211_length_520_cov_1.92325:g121.t1 | NC_040035.1 1eu | C. eugenioides | 44.44 | 1,00E-07 | 36.00 | phosphomethylpyrimidine synthase%2C chloroplastic isoform X3 |
| NODE_213_length_518_cov_1.67574:g123.t1 | NC_039909.1 6e | C. arabica | 42.20 | 5,00E-23 | 94.00 | iron-sulfur assembly protein IscA-like 2%2C mitochondrial isoform X1 |
| NODE_213_length_518_cov_1.67574:g123.t1 | chr6 | C. canephora | 40.37 | 7,00E-23 | 94.00 | Iron-sulfur assembly protein IscA-like 2%2C mitochondrial |
| NODE_213_length_518_cov_1.67574:g123.t1 | NC_040040.1 6eu | C. eugenioides | 41.28 | 4,00E-23 | 94.00 | iron-sulfur assembly protein IscA-like 2%2C mitochondrial |
| NODE_216_length_517_cov_1.84091:g125.t1 | NC_039910.1 7c | C. arabica | 79.49 | 8,00E-15 | 37.00 | uncharacterized protein LOC113699907 |
| NODE_216_length_517_cov_1.84091:g125.t1 | NC_040042.1 8eu | C. eugenioides | 76.92 | 1,00E-12 | 37.00 | uncharacterized protein LOC113780732 |

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| NODE_217_length_515_cov_1.00457:g126.t1 | NC_039900.1 2c | C. arabica | 37.97 | 1,00E-31 | 99.00 | probable tRNA N6-adenosine threonylcarbamoyltransferase%2C mitochondrial |
| NODE_217_length_515_cov_1.00457:g126.t1 | chr2 | C. canephora | 37.97 | 3,00E-32 | 99.00 | Putative Probable tRNA threonylcarbamoyladenosine biosynthesis protein osgepl1 |
| NODE_217_length_515_cov_1.00457:g126.t1 | NC_040036.1 2eu | C. eugenioides | 37.97 | 7,00E-32 | 99.00 | probable tRNA N6-adenosine threonylcarbamoyltransferase%2C mitochondrial |
| NODE_222_length_512_cov_3.11034:g130.t1 | NC_039909.1 6e | C. arabica | 84.62 | 1,00E-95 | 99.00 | uncharacterized protein LOC113696749 |
| NODE_222_length_512_cov_3.11034:g130.t1 | chr7 | C. canephora | 64.71 | 9,00E-08 | 20.00 | Putative Late blight resistance protein R1 |
| NODE_222_length_512_cov_3.11034:g130.t1 | NW_020864084.1 scaffold | C. eugenioides | 84.62 | 3,00E-95 | 99.00 | uncharacterized protein LOC113758021 |
| NODE_228_length_508_cov_1.34339:g133.t1 | chr2 | C. canephora | 34.57 | 5,00E-08 | 98.00 | Putative Epimerase family protein slr1223 |
| NODE_228_length_508_cov_1.34339:g133.t1 | NC_040036.1 2eu | C. eugenioides | 34.57 | 1,00E-07 | 98.00 | epimerase family protein SDR39U1 homolog%2C chloroplastic isoform X1 |
| NODE_233_length_505_cov_1.89019:g135.t1 | NC_039902.1 3c | C. arabica | 42.01 | 4,00E-33 | 98.00 | probable uridine nucleosidase 2 isoform X1 |
| NODE_233_length_505_cov_1.89019:g135.t1 | chr3 | C. canephora | 42.01 | 2,00E-33 | 98.00 | Probable uridine nucleosidase 2 |
| NODE_233_length_505_cov_1.89019:g135.t1 | NC_040037.1 3eu | C. eugenioides | 42.60 | 1,00E-33 | 98.00 | probable uridine nucleosidase 2 |
| NODE_235_length_503_cov_1.07981:g137.t1 | NC_039900.1 2c | C. arabica | 55.38 | 1,00E-38 | 77.00 | glutamate synthase [NADH]%2C amyloplastic-like isoform X2 |
| NODE_235_length_503_cov_1.07981:g137.t1 | chr2 | C. canephora | 55.38 | 7,00E-39 | 77.00 | Glutamate synthase [NADH]%2C amyloplastic |
| NODE_235_length_503_cov_1.07981:g137.t1 | NC_040036.1 2eu | C. eugenioides | 55.38 | 9,00E-39 | 77.00 | glutamate synthase [NADH]%2C amyloplastic isoform X2 |
| NODE_239_length_501_cov_1.08726:g140.t1 | NC_039903.1 3e | C. arabica | 54.39 | 2,00E-14 | 41.00 | ribulose-phosphate 3-epimerase%2C cytoplasmic isoform-like |
| NODE_239_length_501_cov_1.08726:g140.t1 | chr4 | C. canephora | 45.59 | 6,00E-15 | 49.00 | Ribulose-phosphate 3-epimerase%2C chloroplastic (Fragment) |
| NODE_239_length_501_cov_1.08726:g140.t1 | NC_040037.1 3eu | C. eugenioides | 54.39 | 9,00E-15 | 41.00 | ribulose-phosphate 3-epimerase%2C cytoplasmic isoform-like |
| NODE_241_length_499_cov_1.38863:g142.t1 | NC_039901.1 2e | C. arabica | 35.35 | 1,00E-08 | 59.00 | D-xylose-proton symporter-like 2 |
| NODE_241_length_499_cov_1.38863:g142.t1 | chr2 | C. canephora | 35.35 | 4,00E-09 | 59.00 | D-xylose-proton symporter-like 2 |
| NODE_241_length_499_cov_1.38863:g142.t1 | NC_040036.1 2eu | C. eugenioides | 35.35 | 6,00E-09 | 59.00 | D-xylose-proton symporter-like 2 isoform X1 |
| NODE_244_length_496_cov_1.04535:g145.t1 | chr3 | C. canephora | 29.55 | 5,00E-06 | 77.00 | Pyruvate%2C phosphate dikinase%2C chloroplastic |
| NODE_244_length_496_cov_1.04535:g145.t1 | NC_040037.1 3eu | C. eugenioides | 29.55 | 7,00E-06 | 77.00 | pyruvate%2C phosphate dikinase%2C chloroplastic |
| NODE_248_length_494_cov_1.41487:g149.t1 | NC_039905.1 4e | C. arabica | 36.73 | 4,00E-12 | 67.00 | isochorismate synthase%2C chloroplastic-like |
| NODE_248_length_494_cov_1.41487:g149.t1 | chr4 | C. canephora | 36.73 | 2,00E-12 | 67.00 | Isochorismate synthase%2C chloroplastic |
| NODE_248_length_494_cov_1.41487:g149.t1 | NC_040038.1 4eu | C. eugenioides | 36.73 | 3,00E-12 | 67.00 | isochorismate synthase%2C chloroplastic |
| NODE_250_length_493_cov_1.4375:g151.t1 | NC_039917.1 10c | C. arabica | 98.16 | 2,00E-101 | 100.00 | putative receptor-like protein kinase At3g47110 isoform X1 |
| NODE_250_length_493_cov_1.4375:g151.t1 | chr10 | C. canephora | 82.21 | 1,00E-83 | 100.00 | Putative Probable LRR receptor-like serine/threonine-protein kinase At3g47570 |
| NODE_250_length_493_cov_1.4375:g151.t1 | NC_040044.1 10eu | C. eugenioides | 86.50 | 9,00E-90 | 100.00 | putative receptor-like protein kinase At3g47110 |
| NODE_254_length_489_cov_1.29369:g153.t1 | NC_039909.1 6e | C. arabica | 39.62 | 1,00E-07 | 55.00 | adenosine kinase 2 |
| NODE_254_length_489_cov_1.29369:g153.t1 | chr6 | C. canephora | 39.62 | 4,00E-08 | 55.00 | Adenosine kinase 2 |
| NODE_254_length_489_cov_1.29369:g153.t1 | NC_040040.1 6eu | C. eugenioides | 39.62 | 7,00E-08 | 55.00 | adenosine kinase 2 |
| NODE_255_length_488_cov_1.78589:g154.t1 | NC_039901.1 2e | C. arabica | 27.73 | 5,00E-08 | 72.00 | uncharacterized protein LOC113732124 |
| NODE_255_length_488_cov_1.78589:g154.t1 | chr6 | C. canephora | 27.78 | 2,00E-10 | 77.00 | Putative Phosphoglycerate kinase%2C cytosolic |
| NODE_255_length_488_cov_1.78589:g154.t1 | NC_040036.1 2eu | C. eugenioides | 27.73 | 3,00E-08 | 72.00 | uncharacterized protein LOC113762363 isoform X1 |

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| NODE_259_length_486_cov_1.25917:g157.t1 | NC_039900.1 2c | C. arabica | 37.40 | 3,00E-06 | 89.00 | NADPH-dependent aldehyde reductase 1%2C chloroplastic-like |
| NODE_259_length_486_cov_1.25917:g157.t1 | chr0 | C. canephora | 37.40 | 8,00E-07 | 89.00 | Glucose and ribitol dehydrogenase homolog 1 |
| NODE_264_length_486_cov_1.57702:g160.t1 | NC_039908.1 6c | C. arabica | 37.78 | 3,00E-24 | 83.00 | putative elongation factor TypA-like SVR3%2C chloroplastic isoform X3 |
| NODE_264_length_486_cov_1.57702:g160.t1 | chr6 | C. canephora | 36.96 | 1,00E-23 | 85.00 | GTP-binding protein TypA/BipA homolog |
| NODE_264_length_486_cov_1.57702:g160.t1 | NC_040040.1 6eu | C. eugenioides | 36.96 | 3,00E-23 | 85.00 | putative elongation factor TypA-like SVR3%2C chloroplastic |
| NODE_268_length_484_cov_1.33907:g162.t1 | NC_039919.1 11e | C. arabica | 72.22 | 2,00E-17 | 36.00 | 3-oxoacyl-[acyl-carrier-protein] reductase 4 |
| NODE_268_length_484_cov_1.33907:g162.t1 | chr11 | C. canephora | 72.22 | 7,00E-18 | 36.00 | 3-oxoacyl-[acyl-carrier-protein] reductase%2C chloroplastic |
| NODE_268_length_484_cov_1.33907:g162.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 72.22 | 1,00E-17 | 36.00 | 3-oxoacyl-[acyl-carrier-protein] reductase 4 |
| NODE_277_length_477_cov_1.4925:g168.t1 | NC_039913.1 8c | C. arabica | 40.32 | 3,00E-09 | 40.00 | histidine kinase 5-like |
| NODE_277_length_477_cov_1.4925:g168.t1 | chr8 | C. canephora | 40.32 | 9,00E-10 | 40.00 | Histidine kinase 5 |
| NODE_277_length_477_cov_1.4925:g168.t1 | NC_040042.1 8eu | C. eugenioides | 40.32 | 2,00E-09 | 40.00 | histidine kinase 5 |
| NODE_280_length_477_cov_1.7025:g170.t1 | NC_039919.1 11e | C. arabica | 56.52 | 1,00E-44 | 99.00 | glutamine--tRNA ligase-like |
| NODE_280_length_477_cov_1.7025:g170.t1 | chr11 | C. canephora | 55.80 | 1,00E-44 | 99.00 | Glutamine--tRNA ligase |
| NODE_280_length_477_cov_1.7025:g170.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 55.80 | 2,00E-44 | 99.00 | glutamine--tRNA ligase-like |
| NODE_284_length_474_cov_0.88665:g172.t1 | NC_039913.1 8c | C. arabica | 74.19 | 7,00E-66 | 100.00 | heat shock 70 kDa protein%2C mitochondrial-like |
| NODE_284_length_474_cov_0.88665:g172.t1 | chr7 | C. canephora | 74.19 | 2,00E-66 | 100.00 | Heat shock 70 kDa protein%2C mitochondrial |
| NODE_284_length_474_cov_0.88665:g172.t1 | NC_040036.1 2eu | C. eugenioides | 74.19 | 4,00E-66 | 100.00 | heat shock 70 kDa protein%2C mitochondrial-like |
| NODE_287_length_472_cov_2.37975:g174.t1 | NC_008535.1 chloroplast | C. arabica | 72.80 | 7,00E-61 | 91.00 | ribosomal protein S12 |
| NODE_287_length_472_cov_2.37975:g174.t1 | NC_040041.1 7eu | C. eugenioides | 57.26 | 3,00E-48 | 91.00 | uncharacterized protein LOC113777733 |
| NODE_295_length_468_cov_1.86189:g178.t1 | NC_039919.1 11e | C. arabica | 31.37 | 5,00E-10 | 94.00 | UDP-glucose 6-dehydrogenase 5-like |
| NODE_295_length_468_cov_1.86189:g178.t1 | chr7 | C. canephora | 32.03 | 2,00E-12 | 94.00 | UDP-glucose 6-dehydrogenase |
| NODE_295_length_468_cov_1.86189:g178.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 32.03 | 5,00E-12 | 94.00 | LOW QUALITY PROTEIN: UDP-glucose 6-dehydrogenase 3-like |
| NODE_297_length_468_cov_1.86701:g180.t1 | NC_039919.1 11e | C. arabica | 63.79 | 3,00E-18 | 75.00 | uncharacterized protein LOC113718566 |
| NODE_297_length_468_cov_1.86701:g180.t1 | NC_040038.1 4eu | C. eugenioides | 62.07 | 2,00E-17 | 75.00 | uncharacterized protein LOC113767831 |
| NODE_302_length_466_cov_1.98458:g185.t1 | NC_039903.1 3e | C. arabica | 37.41 | 2,00E-27 | 95.00 | succinate-semialdehyde dehydrogenase%2C mitochondrial-like |
| NODE_302_length_466_cov_1.98458:g185.t1 | chr5 | C. canephora | 36.73 | 2,00E-27 | 95.00 | Succinate-semialdehyde dehydrogenase%2C mitochondrial |
| NODE_302_length_466_cov_1.98458:g185.t1 | NC_040039.1 5eu | C. eugenioides | 37.41 | 1,00E-27 | 95.00 | succinate-semialdehyde dehydrogenase%2C mitochondrial |
| NODE_303_length_465_cov_1.1366:g186.t1 | NC_039909.1 6e | C. arabica | 33.98 | 2,00E-14 | 97.00 | L-2-hydroxyglutarate dehydrogenase%2C mitochondrial-like |
| NODE_303_length_465_cov_1.1366:g186.t1 | chr6 | C. canephora | 33.98 | 7,00E-15 | 97.00 | Putative L-2-hydroxyglutarate dehydrogenase%2C mitochondrial |
| NODE_303_length_465_cov_1.1366:g186.t1 | NC_040040.1 6eu | C. eugenioides | 33.98 | 9,00E-15 | 97.00 | L-2-hydroxyglutarate dehydrogenase%2C mitochondrial isoform X3 |
| NODE_306_length_463_cov_1.04922:g189.t1 | NC_039906.1 5e | C. arabica | 41.58 | 3,00E-20 | 100.00 | dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 2%2C mitochondrial-like |
| NODE_306_length_463_cov_1.04922:g189.t1 | chr2 | C. canephora | 40.74 | 9,00E-17 | 100.00 | Dihydrolipoyllysine-residue acetyltransferase component 1 of pyruvate dehydrogenase complex%2C mitochondrial |
| NODE_306_length_463_cov_1.04922:g189.t1 | NC_040039.1 5eu | C. eugenioides | 41.58 | 1,00E-20 | 100.00 | dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 2%2C mitochondrial |
| NODE_317_length_458_cov_1.74541:g195.t1 | NC_039911.1 7e | C. arabica | 38.75 | 2,00E-12 | 57.00 | tRNA threonylcarbamoyladenosine dehydratase-like isoform X2 |

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|--|-----------------------|----------------|-------|----------|--------|---|
| NODE_317_length_458_cov_1.74541:g195.t1 | chr7 | C. canephora | 40.00 | 2,00E-12 | 57.00 | Putative Uncharacterized protein YHR003C |
| NODE_317_length_458_cov_1.74541:g195.t1 | NC_040041.1 7eu | C. eugenioides | 38.75 | 1,00E-12 | 57.00 | tRNA threonylcarbamoyladenine dehydratase |
| NODE_328_length_452_cov_0.978667:g203.t1 | chr4 | C. canephora | 47.27 | 2,00E-07 | 85.00 | 30S ribosomal protein S15 |
| NODE_328_length_452_cov_0.978667:g203.t1 | NC_040038.1 4eu | C. eugenioides | 47.27 | 3,00E-08 | 85.00 | golgin subfamily A member 2 |
| NODE_334_length_449_cov_0.983871:g207.t1 | NC_039902.1 3c | C. arabica | 48.35 | 1,00E-24 | 73.00 | cryptochrome-1 isoform X1 |
| NODE_334_length_449_cov_0.983871:g207.t1 | chr3 | C. canephora | 48.35 | 5,00E-25 | 73.00 | Cryptochrome-2 |
| NODE_334_length_449_cov_0.983871:g207.t1 | NC_040037.1 3eu | C. eugenioides | 48.35 | 9,00E-25 | 73.00 | cryptochrome-1 |
| NODE_349_length_443_cov_0.808743:g218.t1 | NC_039911.1 7e | C. arabica | 29.68 | 6,00E-13 | 98.00 | xanthine dehydrogenase 1-like isoform X1 |
| NODE_349_length_443_cov_0.808743:g218.t1 | chr7 | C. canephora | 29.45 | 2,00E-12 | 93.00 | Xanthine dehydrogenase 1 |
| NODE_349_length_443_cov_0.808743:g218.t1 | NC_040041.1 7eu | C. eugenioides | 29.68 | 3,00E-13 | 98.00 | xanthine dehydrogenase 1-like isoform X1 |
| NODE_351_length_443_cov_1.59836:g219.t1 | NC_039901.1 2e | C. arabica | 31.91 | 2,00E-14 | 94.00 | 4-hydroxy-tetrahydronicotinate synthase%2C chloroplastic-like |
| NODE_351_length_443_cov_1.59836:g219.t1 | chr0 | C. canephora | 31.91 | 7,00E-15 | 94.00 | Dihydronicotinate synthase%2C chloroplastic |
| NODE_351_length_443_cov_1.59836:g219.t1 | NC_040036.1 2eu | C. eugenioides | 31.91 | 1,00E-14 | 94.00 | 4-hydroxy-tetrahydronicotinate synthase%2C chloroplastic-like |
| NODE_355_length_442_cov_1.27945:g221.t1 | NC_039919.1 11e | C. arabica | 35.54 | 1,00E-10 | 98.00 | 3-oxoacyl-[acyl-carrier-protein] reductase 4 |
| NODE_355_length_442_cov_1.27945:g221.t1 | chr11 | C. canephora | 35.54 | 4,00E-11 | 98.00 | 3-oxoacyl-[acyl-carrier-protein] reductase%2C chloroplastic |
| NODE_355_length_442_cov_1.27945:g221.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 35.54 | 9,00E-11 | 98.00 | 3-oxoacyl-[acyl-carrier-protein] reductase 4 |
| NODE_361_length_440_cov_2.02479:g225.t1 | NC_039915.1 9e | C. arabica | 55.03 | 7,00E-50 | 99.00 | leucine--tRNA ligase%2C chloroplastic/mitochondrial-like |
| NODE_361_length_440_cov_2.02479:g225.t1 | chr9 | C. canephora | 54.36 | 6,00E-50 | 99.00 | Leucine--tRNA ligase |
| NODE_361_length_440_cov_2.02479:g225.t1 | NC_040043.1 9eu | C. eugenioides | 55.03 | 4,00E-50 | 99.00 | leucine--tRNA ligase%2C chloroplastic/mitochondrial |
| NODE_364_length_439_cov_1.62707:g228.t1 | NC_039905.1 4e | C. arabica | 39.81 | 8,00E-20 | 92.00 | tropinone reductase homolog At5g06060-like |
| NODE_364_length_439_cov_1.62707:g228.t1 | chr4 | C. canephora | 39.81 | 2,00E-20 | 92.00 | Tropinone reductase homolog At1g07440 |
| NODE_364_length_439_cov_1.62707:g228.t1 | NC_040038.1 4eu | C. eugenioides | 39.81 | 4,00E-20 | 92.00 | tropinone reductase homolog At5g06060-like |
| NODE_365_length_438_cov_1.55956:g229.t1 | NC_039898.1 1c | C. arabica | 33.33 | 9,00E-13 | 93.00 | sorbitol dehydrogenase-like |
| NODE_365_length_438_cov_1.55956:g229.t1 | chr0 | C. canephora | 33.33 | 6,00E-14 | 93.00 | L-idonate 5-dehydrogenase |
| NODE_365_length_438_cov_1.55956:g229.t1 | NC_040035.1 1eu | C. eugenioides | 34.04 | 2,00E-13 | 93.00 | sorbitol dehydrogenase-like |
| NODE_384_length_429_cov_1.80682:g242.t1 | NC_039918.1 11c | C. arabica | 36.59 | 3,00E-24 | 100.00 | D-galacturonate reductase-like |
| NODE_384_length_429_cov_1.80682:g242.t1 | chr4 | C. canephora | 37.89 | 8,00E-25 | 100.00 | Putative Probable NAD(P)H-dependent oxidoreductase 1 |
| NODE_384_length_429_cov_1.80682:g242.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 37.80 | 2,00E-24 | 100.00 | D-galacturonate reductase-like |
| NODE_387_length_429_cov_2.01989:g245.t1 | NC_039916.1 10e | C. arabica | 37.23 | 9,00E-12 | 59.00 | RNA pseudouridine synthase 2%2C chloroplastic isoform X4 |
| NODE_387_length_429_cov_2.01989:g245.t1 | chr10 | C. canephora | 37.23 | 5,00E-12 | 59.00 | RNA pseudouridine synthase 2%2C chloroplastic |
| NODE_387_length_429_cov_2.01989:g245.t1 | NC_040044.1 10eu | C. eugenioides | 35.85 | 6,00E-13 | 68.00 | RNA pseudouridine synthase 2%2C chloroplastic isoform X2 |
| NODE_388_length_428_cov_1.22507:g246.t1 | NC_039904.1 4c | C. arabica | 35.29 | 2,00E-12 | 100.00 | DNA gyrase subunit B%2C chloroplastic/mitochondrial-like |
| NODE_388_length_428_cov_1.22507:g246.t1 | chr6 | C. canephora | 35.29 | 1,00E-12 | 100.00 | DNA gyrase subunit B%2C chloroplastic/mitochondrial |
| NODE_388_length_428_cov_1.22507:g246.t1 | NC_040040.1 6eu | C. eugenioides | 35.29 | 1,00E-12 | 100.00 | DNA gyrase subunit B%2C chloroplastic/mitochondrial-like |

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| NODE_398_length_424_cov_1.68876:g251.t1 | NC_039907.1 5c | C. arabica | 40.43 | 2,00E-11 | 92.00 | uncharacterized protein LOC113690691 isoform X1 |
| NODE_398_length_424_cov_1.68876:g251.t1 | chr5 | C. canephora | 40.43 | 1,00E-11 | 92.00 | Putative Ribosomal RNA small subunit methyltransferase B |
| NODE_398_length_424_cov_1.68876:g251.t1 | NC_040039.1 5eu | C. eugenioides | 40.43 | 9,00E-12 | 92.00 | uncharacterized protein LOC113772441 isoform X1 |
| NODE_401_length_424_cov_1.18732:g253.t1 | NC_039901.1 2e | C. arabica | 31.53 | 6,00E-08 | 90.00 | 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase%2C chloroplastic |
| NODE_401_length_424_cov_1.18732:g253.t1 | chr2 | C. canephora | 31.53 | 6,00E-08 | 90.00 | 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase%2C chloroplastic |
| NODE_401_length_424_cov_1.18732:g253.t1 | NC_040036.1 2eu | C. eugenioides | 31.53 | 4,00E-08 | 90.00 | 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase%2C chloroplastic |
| NODE_411_length_421_cov_0.860465:g259.t1 | NC_039916.1 10e | C. arabica | 41.56 | 7,00E-14 | 98.00 | fructose-1%2C6-bisphosphatase%2C cytosolic-like |
| NODE_411_length_421_cov_0.860465:g259.t1 | chr10 | C. canephora | 41.56 | 2,00E-14 | 98.00 | Fructose-1%2C6-bisphosphatase%2C cytosolic |
| NODE_411_length_421_cov_0.860465:g259.t1 | NC_040044.1 10eu | C. eugenioides | 41.56 | 3,00E-14 | 98.00 | fructose-1%2C6-bisphosphatase%2C cytosolic isoform X1 |
| NODE_415_length_420_cov_1.69679:g261.t1 | NC_039906.1 5e | C. arabica | 46.85 | 2,00E-32 | 79.00 | aspartate carbamoyltransferase 1%2C chloroplastic-like isoform X2 |
| NODE_415_length_420_cov_1.69679:g261.t1 | chr5 | C. canephora | 46.85 | 2,00E-32 | 79.00 | Aspartate carbamoyltransferase 1%2C chloroplastic |
| NODE_415_length_420_cov_1.69679:g261.t1 | NC_040039.1 5eu | C. eugenioides | 46.85 | 2,00E-32 | 79.00 | aspartate carbamoyltransferase 1%2C chloroplastic |
| NODE_417_length_420_cov_1.86297:g263.t1 | NC_039916.1 10e | C. arabica | 56.12 | 6,00E-35 | 98.00 | uncharacterized protein LOC113712777 |
| NODE_417_length_420_cov_1.86297:g263.t1 | chr10 | C. canephora | 56.12 | 2,00E-35 | 98.00 | Putative GTPase HflX |
| NODE_417_length_420_cov_1.86297:g263.t1 | NC_040044.1 10eu | C. eugenioides | 56.12 | 3,00E-35 | 98.00 | uncharacterized protein LOC113749927 |
| NODE_425_length_417_cov_0.911765:g267.t1 | NC_039902.1 3c | C. arabica | 66.67 | 1,00E-47 | 100.00 | biotin synthase%2C mitochondrial-like |
| NODE_425_length_417_cov_0.911765:g267.t1 | chr3 | C. canephora | 66.67 | 3,00E-48 | 100.00 | Biotin synthase |
| NODE_425_length_417_cov_0.911765:g267.t1 | NC_040037.1 3eu | C. eugenioides | 66.67 | 9,00E-50 | 100.00 | biotin synthase%2C mitochondrial-like |
| NODE_427_length_416_cov_1.41888:g268.t1 | NC_039898.1 1c | C. arabica | 35.76 | 6,00E-22 | 100.00 | LOW QUALITY PROTEIN: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (ferredoxin)%2C chloroplastic-like |
| NODE_427_length_416_cov_1.41888:g268.t1 | chr1 | C. canephora | 35.76 | 2,00E-22 | 100.00 | 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase%2C chloroplastic |
| NODE_427_length_416_cov_1.41888:g268.t1 | NC_040035.1 1eu | C. eugenioides | 35.76 | 4,00E-22 | 100.00 | 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (ferredoxin)%2C chloroplastic |
| NODE_433_length_415_cov_1.19822:g273.t1 | NC_039899.1 1e | C. arabica | 69.23 | 1,00E-64 | 100.00 | asparagine synthetase [glutamine-hydrolyzing] |
| NODE_433_length_415_cov_1.19822:g273.t1 | chr1 | C. canephora | 69.23 | 4,00E-65 | 100.00 | Asparagine synthetase [glutamine-hydrolyzing] |
| NODE_433_length_415_cov_1.19822:g273.t1 | NW_020862423.1 scaffold | C. eugenioides | 69.23 | 3,00E-66 | 100.00 | asparagine synthetase [glutamine-hydrolyzing]-like |
| NODE_437_length_415_cov_2.02367:g275.t1 | NC_039918.1 11c | C. arabica | 51.72 | 4,00E-25 | 96.00 | glutamate decarboxylase-like |
| NODE_437_length_415_cov_2.02367:g275.t1 | chr11 | C. canephora | 51.72 | 1,00E-25 | 96.00 | Glutamate decarboxylase |
| NODE_437_length_415_cov_2.02367:g275.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 51.72 | 2,00E-25 | 96.00 | glutamate decarboxylase-like |
| NODE_438_length_414_cov_1.75668:g276.t1 | NC_039913.1 8c | C. arabica | 39.44 | 8,00E-24 | 98.00 | formyltetrahydrofolate deformylase 1%2C mitochondrial-like isoform X2 |
| NODE_438_length_414_cov_1.75668:g276.t1 | chr8 | C. canephora | 36.60 | 2,00E-20 | 98.00 | Putative Formyltetrahydrofolate deformylase |
| NODE_438_length_414_cov_1.75668:g276.t1 | NC_040042.1 8eu | C. eugenioides | 39.44 | 4,00E-24 | 98.00 | formyltetrahydrofolate deformylase 1%2C mitochondrial isoform X2 |
| NODE_440_length_414_cov_2.21365:g278.t1 | NC_039900.1 2c | C. arabica | 55.66 | 6,00E-29 | 98.00 | uncharacterized protein LOC113723907 |
| NODE_440_length_414_cov_2.21365:g278.t2 | NC_039900.1 2c | C. arabica | 59.68 | 1,00E-39 | 99.00 | uncharacterized protein LOC113723907 |
| NODE_440_length_414_cov_2.21365:g278.t1 | chr2 | C. canephora | 39.74 | 3,00E-11 | 82.00 | Putative Pol-polyprotein |
| NODE_440_length_414_cov_2.21365:g278.t2 | chr2 | C. canephora | 41.67 | 1,00E-16 | 85.00 | Putative Pol-polyprotein |

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| NODE_440_length_414_cov_2.21365:g278.t1 | NC_040037.1 3eu | C. eugenoides | 50.41 | 9,00E-27 | 98.00 | uncharacterized protein LOC113766031 |
| NODE_440_length_414_cov_2.21365:g278.t2 | NC_040036.1 2eu | C. eugenoides | 53.24 | 9,00E-37 | 99.00 | uncharacterized protein LOC113759798 |
| NODE_446_length_412_cov_1.65075:g282.t1 | NC_039906.1 5e | C. arabica | 35.66 | 5,00E-14 | 93.00 | uncharacterized protein LOC113743442 |
| NODE_446_length_412_cov_1.65075:g282.t1 | chr5 | C. canephora | 34.88 | 2,00E-14 | 93.00 | Putative Release factor glutamine methyltransferase |
| NODE_446_length_412_cov_1.65075:g282.t1 | NC_040039.1 5eu | C. eugenoides | 34.88 | 7,00E-14 | 93.00 | uncharacterized protein LOC113770504 |
| NODE_449_length_410_cov_1.32733:g284.t1 | NC_039914.1 9c | C. arabica | 37.74 | 5,00E-11 | 100.00 | protein TRIGALACTOSYLDIACYLGLYCEROL 3%2C chloroplastic-like |
| NODE_449_length_410_cov_1.32733:g284.t1 | chr9 | C. canephora | 37.74 | 1,00E-11 | 100.00 | Protein TRIGALACTOSYLDIACYLGLYCEROL 3%2C chloroplastic |
| NODE_449_length_410_cov_1.32733:g284.t1 | NC_040043.1 9eu | C. eugenoides | 37.74 | 3,00E-11 | 100.00 | protein TRIGALACTOSYLDIACYLGLYCEROL 3%2C chloroplastic |
| NODE_456_length_409_cov_1.47289:g289.t1 | NC_039900.1 2c | C. arabica | 44.19 | 1,00E-26 | 94.00 | dicarboxylate transporter 2.1%2C chloroplastic-like |
| NODE_456_length_409_cov_1.47289:g289.t1 | chr2 | C. canephora | 44.19 | 4,00E-27 | 94.00 | 2-oxoglutarate/malate translocator%2C chloroplastic |
| NODE_456_length_409_cov_1.47289:g289.t1 | NC_040036.1 2eu | C. eugenoides | 44.19 | 6,00E-27 | 94.00 | dicarboxylate transporter 2.1%2C chloroplastic |
| NODE_466_length_406_cov_2.23708:g294.t1 | NC_039899.1 1e | C. arabica | 31.18 | 7,00E-07 | 69.00 | phosphatidylinositol N-acetylglucosaminyltransferase subunit A-like isoform X1 |
| NODE_466_length_406_cov_2.23708:g294.t1 | chr1 | C. canephora | 31.18 | 3,00E-07 | 69.00 | Phosphatidylinositol N-acetylglucosaminyltransferase subunit A |
| NODE_466_length_406_cov_2.23708:g294.t1 | NC_040035.1 1eu | C. eugenoides | 31.18 | 4,00E-07 | 69.00 | phosphatidylinositol N-acetylglucosaminyltransferase subunit A isoform X1 |
| NODE_470_length_405_cov_1.41463:g296.t1 | NC_008535.1 chloroplast | C. arabica | 50.00 | 2,00E-20 | 74.00 | RNA polymerase beta" subunit |
| NODE_470_length_405_cov_1.41463:g296.t1 | chr7 | C. canephora | 37.50 | 2,00E-06 | 45.00 | DNA-directed RNA polymerase II subunit RPB1 |
| NODE_470_length_405_cov_1.41463:g296.t1 | NC_040041.1 7eu | C. eugenoides | 39.06 | 7,00E-07 | 45.00 | DNA-directed RNA polymerase II subunit 1 |
| NODE_477_length_403_cov_2.00613:g300.t1 | NC_039912.1 8e | C. arabica | 97.74 | 1,00E-84 | 100.00 | uncharacterized protein LOC113703843 |
| NODE_477_length_403_cov_2.00613:g300.t1 | NW_020864630.1 scaffold | C. eugenoides | 91.67 | 6,00E-85 | 99.00 | uncharacterized protein LOC113758839 |
| NODE_485_length_401_cov_0.895062:g306.t1 | NC_039905.1 4e | C. arabica | 39.85 | 2,00E-20 | 100.00 | pre-mRNA-splicing factor ATP-dependent RNA helicase DEAH1-like |
| NODE_485_length_401_cov_0.895062:g306.t1 | chr2 | C. canephora | 39.85 | 3,00E-21 | 100.00 | Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 |
| NODE_485_length_401_cov_0.895062:g306.t1 | NC_040038.1 4eu | C. eugenoides | 39.85 | 9,00E-21 | 100.00 | pre-mRNA-splicing factor ATP-dependent RNA helicase DEAH1-like isoform X2 |
| NODE_487_length_401_cov_1.3642:g308.t1 | NC_039917.1 10c | C. arabica | 57.14 | 9,00E-08 | 47.00 | thylakoidal processing peptidase 1%2C chloroplastic-like |
| NODE_487_length_401_cov_1.3642:g308.t1 | chr10 | C. canephora | 48.78 | 1,00E-07 | 55.00 | Thylakoidal processing peptidase 1%2C chloroplastic |
| NODE_487_length_401_cov_1.3642:g308.t1 | NC_040044.1 10eu | C. eugenoides | 57.14 | 5,00E-08 | 47.00 | thylakoidal processing peptidase 1%2C chloroplastic-like |
| NODE_490_length_400_cov_1.36533:g309.t1 | NC_039902.1 3c | C. arabica | 78.79 | 8,00E-50 | 100.00 | MDIS1-interacting receptor like kinase 2-like |
| NODE_490_length_400_cov_1.36533:g309.t1 | NC_040039.1 5eu | C. eugenoides | 48.48 | 3,00E-24 | 100.00 | LRR receptor-like serine/threonine-protein kinase FLS2 |
| NODE_492_length_400_cov_1.50774:g311.t1 | NC_039908.1 6c | C. arabica | 34.62 | 1,00E-08 | 80.00 | protein DETOXIFICATION 16-like isoform X2 |
| NODE_492_length_400_cov_1.50774:g311.t1 | chr6 | C. canephora | 34.62 | 5,00E-09 | 80.00 | Putative MATE efflux family protein 7 |
| NODE_492_length_400_cov_1.50774:g311.t1 | NC_040040.1 6eu | C. eugenoides | 34.91 | 5,00E-09 | 81.00 | protein DETOXIFICATION 16-like isoform X2 |
| NODE_493_length_400_cov_1.59443:g312.t1 | NC_039919.1 11e | C. arabica | 38.40 | 9,00E-19 | 93.00 | pyruvate kinase%2C cytosolic isozyme-like |
| NODE_493_length_400_cov_1.59443:g312.t1 | chr11 | C. canephora | 38.40 | 7,00E-19 | 93.00 | Pyruvate kinase%2C cytosolic isozyme |
| NODE_493_length_400_cov_1.59443:g312.t1 | NC_040045.1 11eu 11eu | C. eugenoides | 38.40 | 5,00E-19 | 93.00 | pyruvate kinase%2C cytosolic isozyme |
| NODE_500_length_398_cov_1.14019:g318.t1 | NC_039898.1 1c | C. arabica | 46.40 | 2,00E-34 | 94.00 | ribosome-recycling factor%2C chloroplastic-like isoform X2 |

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| NODE_500_length_398_cov_1.14019:g318.t1 | chr1 | C. canephora | 46.40 | 2,00E-34 | 94.00 | Ribosome-recycling factor%2C chloroplastic (Fragment) |
| NODE_500_length_398_cov_1.14019:g318.t1 | NC_040035.1 1eu | C. eugenioides | 46.40 | 5,00E-35 | 94.00 | ribosome-recycling factor%2C chloroplastic isoform X2 |
| NODE_502_length_398_cov_2.23676:g319.t1 | NC_039909.1 6e | C. arabica | 37.59 | 4,00E-22 | 98.00 | DEAD-box ATP-dependent RNA helicase 37-like isoform X2 |
| NODE_502_length_398_cov_2.23676:g319.t1 | chr6 | C. canephora | 37.59 | 3,00E-22 | 98.00 | DEAD-box ATP-dependent RNA helicase 37 |
| NODE_502_length_398_cov_2.23676:g319.t1 | NC_040040.1 6eu | C. eugenioides | 37.59 | 5,00E-22 | 98.00 | DEAD-box ATP-dependent RNA helicase 37 |
| NODE_505_length_397_cov_1.57812:g321.t1 | NC_039909.1 6e | C. arabica | 45.97 | 1,00E-34 | 94.00 | enolase |
| NODE_505_length_397_cov_1.57812:g321.t1 | chr6 | C. canephora | 45.97 | 4,00E-35 | 94.00 | Enolase |
| NODE_505_length_397_cov_1.57812:g321.t1 | NC_040040.1 6eu | C. eugenioides | 45.97 | 7,00E-35 | 94.00 | enolase |
| NODE_509_length_397_cov_1.06563:g324.t1 | NC_039911.1 7e | C. arabica | 83.33 | 1,00E-50 | 100.00 | uncharacterized protein LOC113700707 |
| NODE_509_length_397_cov_1.06563:g324.t1 | NC_040035.1 1eu | C. eugenioides | 90.00 | 2,00E-53 | 100.00 | uncharacterized protein LOC113769237 |
| NODE_511_length_396_cov_1.83386:g325.t1 | NC_039909.1 6e | C. arabica | 92.17 | 4,00E-77 | 100.00 | uncharacterized protein LOC113696711 |
| NODE_511_length_396_cov_1.83386:g325.t1 | NC_040041.1 7eu | C. eugenioides | 93.04 | 1,00E-73 | 100.00 | uncharacterized protein LOC113777088 |
| NODE_516_length_395_cov_1.79874:g330.t1 | NC_039914.1 9c | C. arabica | 50.00 | 3,00E-07 | 27.00 | biotin carboxyl carrier protein of acetyl-CoA carboxylase%2C chloroplastic-like |
| NODE_516_length_395_cov_1.79874:g330.t1 | chr9 | C. canephora | 52.50 | 8,00E-09 | 30.00 | Biotin carboxyl carrier protein of acetyl-CoA carboxylase%2C chloroplastic |
| NODE_516_length_395_cov_1.79874:g330.t1 | NC_040043.1 9eu | C. eugenioides | 47.22 | 9,00E-07 | 27.00 | biotin carboxyl carrier protein of acetyl-CoA carboxylase%2C chloroplastic |
| NODE_519_length_395_cov_1.59434:g332.t1 | NC_008535.1 chloroplast | C. arabica | 42.11 | 9,00E-33 | 100.00 | RNA polymerase beta subunit |
| NODE_521_length_394_cov_1.39117:g334.t1 | NC_039913.1 8c | C. arabica | 48.96 | 8,00E-18 | 90.00 | uncharacterized protein LOC113706277 |
| NODE_521_length_394_cov_1.39117:g334.t1 | chr8 | C. canephora | 48.96 | 2,00E-18 | 90.00 | Putative 39S ribosomal protein L24%2C mitochondrial |
| NODE_521_length_394_cov_1.39117:g334.t1 | NC_040042.1 8eu | C. eugenioides | 48.96 | 5,00E-18 | 90.00 | uncharacterized protein LOC113780922 |
| NODE_525_length_393_cov_2.93038:g338.t1 | NC_039907.1 5c | C. arabica | 38.71 | 5,00E-07 | 62.00 | probable membrane metalloprotease ARASP2%2C chloroplastic |
| NODE_525_length_393_cov_2.93038:g338.t1 | chr5 | C. canephora | 38.71 | 1,00E-07 | 62.00 | Putative zinc metalloprotease slr1821 |
| NODE_525_length_393_cov_2.93038:g338.t1 | NC_040039.1 5eu | C. eugenioides | 32.26 | 3,00E-07 | 88.00 | probable membrane metalloprotease ARASP2%2C chloroplastic |
| NODE_530_length_391_cov_1.28662:g343.t1 | NC_039902.1 3c | C. arabica | 42.52 | 2,00E-30 | 97.00 | dihydrolipoyl dehydrogenase%2C mitochondrial-like |
| NODE_530_length_391_cov_1.28662:g343.t1 | chr3 | C. canephora | 42.52 | 6,00E-31 | 97.00 | Dihydrolipoyl dehydrogenase 1%2C mitochondrial |
| NODE_530_length_391_cov_1.28662:g343.t1 | NC_040037.1 3eu | C. eugenioides | 43.31 | 1,00E-30 | 97.00 | dihydrolipoyl dehydrogenase 1%2C mitochondrial-like |
| NODE_531_length_390_cov_1.18211:g344.t1 | NC_039914.1 9c | C. arabica | 33.03 | 3,00E-08 | 81.00 | LOW QUALITY PROTEIN: mitochondrial amidoxime reducing component 2-like |
| NODE_531_length_390_cov_1.18211:g344.t1 | chr9 | C. canephora | 33.03 | 1,00E-08 | 81.00 | Putative MOSC domain-containing protein 2%2C mitochondrial |
| NODE_531_length_390_cov_1.18211:g344.t1 | NC_040043.1 9eu | C. eugenioides | 28.24 | 7,00E-09 | 98.00 | mitochondrial amidoxime-reducing component 1-like |
| NODE_532_length_390_cov_1.48243:g345.t1 | NC_039912.1 8e | C. arabica | 36.79 | 2,00E-12 | 80.00 | ABC transporter B family member 10-like |
| NODE_532_length_390_cov_1.48243:g345.t1 | chr8 | C. canephora | 36.79 | 8,00E-13 | 80.00 | ABC transporter B family member 2 |
| NODE_532_length_390_cov_1.48243:g345.t1 | NC_040042.1 8eu | C. eugenioides | 36.79 | 1,00E-12 | 80.00 | ABC transporter B family member 10-like |
| NODE_546_length_386_cov_1.65696:g358.t1 | NC_039908.1 6c | C. arabica | 55.43 | 3,00E-31 | 93.00 | peroxiredoxin Q%2C chloroplastic |
| NODE_546_length_386_cov_1.65696:g358.t1 | chr6 | C. canephora | 55.43 | 9,00E-32 | 93.00 | Peroxiredoxin Q%2C chloroplastic |
| NODE_546_length_386_cov_1.65696:g358.t1 | NC_040040.1 6eu | C. eugenioides | 55.43 | 2,00E-31 | 93.00 | peroxiredoxin Q%2C chloroplastic |

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|---|-------------------------|----------------|--------|----------|--------|--|
| NODE_551_length_385_cov_1.23701:g362.t1 | NC_008535.1 chloroplast | C. arabica | 42.11 | 1,00E-08 | 75.00 | ribosomal protein L22 |
| NODE_553_length_385_cov_1.88961:g363.t1 | NC_039907.1 5c | C. arabica | 73.98 | 1,00E-53 | 100.00 | uncharacterized protein LOC113690699 |
| NODE_553_length_385_cov_1.88961:g363.t1 | NC_040043.1 9eu | C. eugenioides | 70.97 | 4,00E-41 | 75.00 | uncharacterized protein LOC113782301 |
| NODE_558_length_384_cov_1.43648:g367.t1 | NC_039906.1 5e | C. arabica | 41.10 | 1,00E-15 | 74.00 | DNA repair protein recA homolog 1%2C chloroplastic-like isoform X3 |
| NODE_558_length_384_cov_1.43648:g367.t1 | chr5 | C. canephora | 41.10 | 1,00E-15 | 74.00 | DNA repair protein recA homolog 1%2C chloroplastic |
| NODE_558_length_384_cov_1.43648:g367.t1 | NC_040039.1 5eu | C. eugenioides | 41.10 | 1,00E-15 | 74.00 | DNA repair protein recA homolog 1%2C chloroplastic isoform X1 |
| NODE_567_length_383_cov_1.44118:g372.t1 | NC_039904.1 4c | C. arabica | 30.48 | 3,00E-08 | 83.00 | peptidyl-prolyl cis-trans isomerase NIMA-interacting 4-like |
| NODE_567_length_383_cov_1.44118:g372.t1 | chr0 | C. canephora | 30.48 | 8,00E-09 | 83.00 | FKBP-like peptidyl-prolyl cis-trans isomerase family protein |
| NODE_567_length_383_cov_1.44118:g372.t1 | NC_040038.1 4eu | C. eugenioides | 30.48 | 2,00E-08 | 83.00 | peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 |
| NODE_581_length_380_cov_1.39604:g379.t1 | NC_008535.1 chloroplast | C. arabica | 43.90 | 1,00E-18 | 62.00 | RNA polymerase beta' subunit |
| NODE_591_length_378_cov_1.46844:g384.t1 | NC_039898.1 1c | C. arabica | 34.21 | 5,00E-15 | 89.00 | LOW QUALITY PROTEIN: 4-coumarate--CoA ligase-like 7 |
| NODE_591_length_378_cov_1.46844:g384.t1 | chr7 | C. canephora | 29.75 | 2,00E-09 | 95.00 | 4-coumarate--CoA ligase-like 1 |
| NODE_591_length_378_cov_1.46844:g384.t1 | NC_040035.1 1eu | C. eugenioides | 32.46 | 1,00E-14 | 89.00 | 4-coumarate--CoA ligase-like 7 |
| NODE_611_length_375_cov_1.91275:g394.t1 | NC_039915.1 9e | C. arabica | 43.59 | 1,00E-12 | 78.00 | riboflavin biosynthesis protein PYRR%2C chloroplastic-like |
| NODE_611_length_375_cov_1.91275:g394.t1 | chr9 | C. canephora | 43.59 | 3,00E-13 | 78.00 | Putative Riboflavin biosynthesis protein RibD |
| NODE_611_length_375_cov_1.91275:g394.t1 | NC_040043.1 9eu | C. eugenioides | 42.31 | 2,00E-12 | 78.00 | riboflavin biosynthesis protein PYRR%2C chloroplastic |
| NODE_614_length_375_cov_1.23154:g396.t1 | NC_039903.1 3e | C. arabica | 34.04 | 3,00E-09 | 75.00 | dihydroxy-acid dehydratase%2C chloroplastic-like |
| NODE_614_length_375_cov_1.23154:g396.t1 | chr3 | C. canephora | 32.98 | 5,00E-09 | 75.00 | Dihydroxy-acid dehydratase |
| NODE_614_length_375_cov_1.23154:g396.t1 | NC_040037.1 3eu | C. eugenioides | 32.98 | 1,00E-08 | 75.00 | dihydroxy-acid dehydratase%2C chloroplastic-like |
| NODE_621_length_374_cov_2.29966:g400.t1 | NC_039901.1 2e | C. arabica | 41.18 | 2,00E-23 | 95.00 | stromal 70 kDa heat shock-related protein%2C chloroplastic-like |
| NODE_621_length_374_cov_2.29966:g400.t1 | chr2 | C. canephora | 41.18 | 4,00E-24 | 95.00 | Stromal 70 kDa heat shock-related protein%2C chloroplastic |
| NODE_621_length_374_cov_2.29966:g400.t1 | NC_040036.1 2eu | C. eugenioides | 41.18 | 1,00E-23 | 95.00 | stromal 70 kDa heat shock-related protein%2C chloroplastic-like |
| NODE_629_length_372_cov_1.49831:g406.t1 | NC_039909.1 6e | C. arabica | 53.28 | 1,00E-38 | 99.00 | leucine aminopeptidase 1-like |
| NODE_629_length_372_cov_1.49831:g406.t1 | chr6 | C. canephora | 53.28 | 8,00E-39 | 99.00 | Leucine aminopeptidase 3%2C chloroplastic |
| NODE_629_length_372_cov_1.49831:g406.t1 | NC_040040.1 6eu | C. eugenioides | 53.28 | 8,00E-39 | 99.00 | leucine aminopeptidase 1-like |
| NODE_634_length_371_cov_1.7551:g411.t1 | NC_039908.1 6c | C. arabica | 36.67 | 6,00E-16 | 73.00 | D-lactate dehydrogenase [cytochrome]%2C mitochondrial |
| NODE_634_length_371_cov_1.7551:g411.t1 | chr6 | C. canephora | 34.21 | 1,00E-16 | 90.00 | D-lactate dehydrogenase [cytochrome]%2C mitochondrial |
| NODE_634_length_371_cov_1.7551:g411.t1 | NC_040040.1 6eu | C. eugenioides | 36.67 | 2,00E-17 | 73.00 | D-lactate dehydrogenase [cytochrome]%2C mitochondrial isoform X2 |
| NODE_635_length_371_cov_1.72109:g412.t1 | NW_020850478.1 scaffold | C. arabica | 35.77 | 9,00E-19 | 99.00 | LOW QUALITY PROTEIN: uncharacterized protein LOC113722974 |
| NODE_635_length_371_cov_1.72109:g412.t1 | chr7 | C. canephora | 37.40 | 8,00E-22 | 99.00 | Putative tRNA pseudouridine synthase B |
| NODE_635_length_371_cov_1.72109:g412.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 37.40 | 7,00E-21 | 99.00 | uncharacterized protein LOC113754167 |
| NODE_639_length_370_cov_2.49829:g416.t1 | NC_039912.1 8e | C. arabica | 99.15 | 6,00E-76 | 100.00 | uncharacterized protein LOC113703843 |
| NODE_639_length_370_cov_2.49829:g416.t1 | chr0 | C. canephora | 38.68 | 3,00E-18 | 88.00 | Putative uncharacterized protein |
| NODE_639_length_370_cov_2.49829:g416.t1 | NW_020863140.1 scaffold | C. eugenioides | 100.00 | 7,00E-77 | 100.00 | uncharacterized protein LOC113757037 |

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|---|-----------------------|----------------|-------|----------|--------|---|
| NODE_640_length_370_cov_2:g417.t1 | NC_039919.1 11e | C. arabica | 71.59 | 1,00E-40 | 98.00 | 1%2C4-dihydroxy-2-naphthoyl-CoA synthase%2C peroxisomal-like isoform X2 |
| NODE_640_length_370_cov_2:g417.t1 | chr11 | C. canephora | 71.59 | 7,00E-41 | 98.00 | 1%2C4-Dihydroxy-2-naphthoyl-CoA synthase%2C peroxisomal |
| NODE_640_length_370_cov_2:g417.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 71.59 | 1,00E-40 | 98.00 | 1%2C4-dihydroxy-2-naphthoyl-CoA synthase%2C peroxisomal |
| NODE_654_length_368_cov_2.03436:g427.t1 | NC_039909.1 6e | C. arabica | 81.01 | 2,00E-38 | 98.00 | uncharacterized protein LOC113696799 |
| NODE_654_length_368_cov_2.03436:g427.t1 | NC_040040.1 6eu | C. eugenioides | 71.01 | 3,00E-28 | 86.00 | uncharacterized protein LOC113774009 |
| NODE_666_length_367_cov_0.87931:g432.t1 | NC_039919.1 11e | C. arabica | 92.62 | 8,00E-76 | 100.00 | uncharacterized protein LOC113718074 |
| NODE_666_length_367_cov_0.87931:g432.t1 | NC_040042.1 8eu | C. eugenioides | 93.44 | 7,00E-75 | 100.00 | uncharacterized protein LOC113780676 |
| NODE_706_length_362_cov_1.01754:g456.t1 | NC_039907.1 5c | C. arabica | 46.46 | 8,00E-25 | 82.00 | glucose-1-phosphate adenyltransferase small subunit%2C chloroplastic/amyloplastic |
| NODE_706_length_362_cov_1.01754:g456.t1 | chr5 | C. canephora | 46.46 | 3,00E-25 | 82.00 | Glucose-1-phosphate adenyltransferase small subunit%2C chloroplastic |
| NODE_706_length_362_cov_1.01754:g456.t1 | NC_040039.1 5eu | C. eugenioides | 46.46 | 5,00E-25 | 82.00 | glucose-1-phosphate adenyltransferase small subunit%2C chloroplastic/amyloplastic |
| NODE_714_length_360_cov_1.53004:g460.t1 | NC_039917.1 10c | C. arabica | 48.33 | 5,00E-27 | 97.00 | glucose-6-phosphate isomerase%2C cytosolic |
| NODE_714_length_360_cov_1.53004:g460.t1 | chr10 | C. canephora | 48.33 | 6,00E-29 | 97.00 | Glucose-6-phosphate isomerase%2C cytosolic 1 |
| NODE_714_length_360_cov_1.53004:g460.t1 | NC_040044.1 10eu | C. eugenioides | 48.33 | 3,00E-27 | 97.00 | glucose-6-phosphate isomerase%2C cytosolic |
| NODE_719_length_360_cov_2.60071:g465.t1 | NC_039902.1 3c | C. arabica | 32.50 | 2,00E-07 | 100.00 | perakine reductase-like isoform X2 |
| NODE_719_length_360_cov_2.60071:g465.t1 | chr3 | C. canephora | 32.50 | 1,00E-07 | 100.00 | Perakine reductase |
| NODE_719_length_360_cov_2.60071:g465.t1 | NC_040037.1 3eu | C. eugenioides | 32.50 | 1,00E-07 | 100.00 | perakine reductase-like isoform X2 |
| NODE_723_length_359_cov_1.80496:g468.t1 | NC_039914.1 9c | C. arabica | 34.68 | 4,00E-10 | 100.00 | ABC transporter B family member 9-like |
| NODE_723_length_359_cov_1.80496:g468.t1 | chr0 | C. canephora | 37.17 | 1,00E-10 | 88.00 | Putative ABC transporter B family member 9 |
| NODE_723_length_359_cov_1.80496:g468.t1 | NC_040043.1 9eu | C. eugenioides | 37.17 | 5,00E-10 | 88.00 | ABC transporter B family member 4-like |
| NODE_738_length_357_cov_1.31071:g477.t1 | NC_039919.1 11e | C. arabica | 63.87 | 6,00E-49 | 100.00 | uracil-DNA glycosylase%2C mitochondrial-like |
| NODE_738_length_357_cov_1.31071:g477.t1 | chr11 | C. canephora | 63.03 | 9,00E-49 | 100.00 | Uracil-DNA glycosylase |
| NODE_738_length_357_cov_1.31071:g477.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 63.87 | 4,00E-49 | 100.00 | uracil-DNA glycosylase%2C mitochondrial |
| NODE_748_length_356_cov_1.5233:g482.t1 | NC_039901.1 2e | C. arabica | 61.29 | 9,00E-21 | 83.00 | DNA gyrase subunit A%2C chloroplastic/mitochondrial-like |
| NODE_748_length_356_cov_1.5233:g482.t1 | chr2 | C. canephora | 61.29 | 3,00E-21 | 83.00 | DNA gyrase subunit A%2C chloroplastic/mitochondrial |
| NODE_748_length_356_cov_1.5233:g482.t1 | NC_040036.1 2eu | C. eugenioides | 62.90 | 1,00E-21 | 83.00 | DNA gyrase subunit A%2C chloroplastic/mitochondrial |
| NODE_749_length_356_cov_1.17563:g483.t1 | NC_039904.1 4c | C. arabica | 35.48 | 1,00E-17 | 99.00 | uncharacterized protein LOC113738644 isoform X1 |
| NODE_749_length_356_cov_1.17563:g483.t1 | chr6 | C. canephora | 35.48 | 3,00E-18 | 99.00 | Putative Alpha-glucosidase yihQ |
| NODE_749_length_356_cov_1.17563:g483.t1 | NC_040040.1 6eu | C. eugenioides | 35.48 | 7,00E-18 | 99.00 | uncharacterized protein LOC113773196 |
| NODE_762_length_354_cov_1.59206:g493.t1 | chr0 | C. canephora | 34.69 | 7,00E-06 | 100.00 | 50S ribosomal protein L21 |
| NODE_762_length_354_cov_1.59206:g493.t1 | NC_040041.1 7eu | C. eugenioides | 28.57 | 1,00E-07 | 100.00 | 50S ribosomal protein L21%2C chloroplastic |
| NODE_765_length_354_cov_1.38628:g495.t1 | NC_039919.1 11e | C. arabica | 34.94 | 4,00E-11 | 70.00 | uncharacterized protein LOC113718834 |
| NODE_765_length_354_cov_1.38628:g495.t1 | chr11 | C. canephora | 34.94 | 1,00E-11 | 70.00 | phosphoglucomutase%2C putative / glucose phosphomutase%2C putative |
| NODE_765_length_354_cov_1.38628:g495.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 34.94 | 2,00E-11 | 70.00 | uncharacterized protein LOC113751259 |
| NODE_766_length_354_cov_1.22744:g497.t1 | NC_039906.1 5e | C. arabica | 35.83 | 8,00E-17 | 99.00 | putative DUF21 domain-containing protein At3g13070%2C chloroplastic isoform X2 |

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|---|-------------------------|----------------|-------|----------|--------|---|
| NODE_766_length_354_cov_1.22744:g497.t1 | chr5 | C. canephora | 35.29 | 2,00E-17 | 99.00 | DUF21 domain-containing protein At1g55930%2C chloroplastic |
| NODE_766_length_354_cov_1.22744:g497.t1 | NC_040039.1 5eu | C. eugenioides | 35.29 | 3,00E-17 | 99.00 | putative DUF21 domain-containing protein At3g13070%2C chloroplastic isoform X2 |
| NODE_774_length_352_cov_1.60364:g500.t1 | NC_039900.1 2c | C. arabica | 42.20 | 9,00E-24 | 93.00 | glycogen phosphorylase 1-like |
| NODE_774_length_352_cov_1.60364:g500.t1 | chr2 | C. canephora | 42.20 | 3,00E-24 | 93.00 | Glycogen phosphorylase 1 |
| NODE_774_length_352_cov_1.60364:g500.t1 | NC_040036.1 2eu | C. eugenioides | 42.20 | 5,00E-24 | 93.00 | glycogen phosphorylase 1-like isoform X3 |
| NODE_782_length_352_cov_1.52364:g505.t1 | NC_039917.1 10c | C. arabica | 60.42 | 1,00E-33 | 97.00 | alcohol dehydrogenase 1-like |
| NODE_782_length_352_cov_1.52364:g505.t1 | chr1 | C. canephora | 66.33 | 3,00E-40 | 100.00 | Alcohol dehydrogenase class-3 |
| NODE_782_length_352_cov_1.52364:g505.t1 | NC_040035.1 1eu | C. eugenioides | 66.33 | 6,00E-40 | 100.00 | alcohol dehydrogenase class-3 |
| NODE_788_length_351_cov_2.15328:g510.t1 | NC_039919.1 11e | C. arabica | 36.45 | 8,00E-20 | 92.00 | tryptophan synthase alpha chain-like |
| NODE_788_length_351_cov_2.15328:g510.t1 | chr11 | C. canephora | 35.51 | 2,00E-19 | 92.00 | Indole-3-glycerol phosphate lyase%2C chloroplastic |
| NODE_788_length_351_cov_2.15328:g510.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 36.45 | 4,00E-20 | 92.00 | tryptophan synthase alpha chain-like |
| NODE_802_length_350_cov_1.61538:g519.t1 | NC_039919.1 11e | C. arabica | 46.73 | 3,00E-21 | 92.00 | lipoyl synthase%2C chloroplastic-like |
| NODE_802_length_350_cov_1.61538:g519.t1 | chr11 | C. canephora | 46.73 | 1,00E-21 | 92.00 | Lipoyl synthase%2C chloroplastic |
| NODE_802_length_350_cov_1.61538:g519.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 46.73 | 3,00E-21 | 92.00 | lipoyl synthase%2C chloroplastic |
| NODE_804_length_350_cov_1.62637:g520.t1 | NC_008535.1 chloroplast | C. arabica | 58.18 | 2,00E-25 | 100.00 | ATP synthase CF1 beta subunit |
| NODE_804_length_350_cov_1.62637:g520.t1 | chr11 | C. canephora | 60.00 | 1,00E-25 | 100.00 | ATP synthase subunit beta |
| NODE_804_length_350_cov_1.62637:g520.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 60.00 | 2,00E-25 | 100.00 | ATP synthase subunit beta%2C mitochondrial |
| NODE_805_length_350_cov_2.24176:g521.t1 | NC_039910.1 7c | C. arabica | 30.36 | 3,00E-19 | 96.00 | uncharacterized protein LOC113698190 isoform X2 |
| NODE_805_length_350_cov_2.24176:g521.t1 | chr7 | C. canephora | 30.36 | 5,00E-20 | 96.00 | Putative Methionine aminotransferase |
| NODE_805_length_350_cov_2.24176:g521.t1 | NC_040041.1 7eu | C. eugenioides | 30.36 | 2,00E-19 | 96.00 | uncharacterized protein LOC113777435 isoform X2 |
| NODE_821_length_348_cov_1.29151:g530.t1 | NC_039914.1 9c | C. arabica | 48.31 | 5,00E-34 | 94.00 | glutamate--tRNA ligase%2C chloroplastic/mitochondrial-like |
| NODE_821_length_348_cov_1.29151:g530.t1 | chr9 | C. canephora | 48.31 | 2,00E-34 | 94.00 | Glutamate--tRNA ligase%2C chloroplastic/mitochondrial |
| NODE_821_length_348_cov_1.29151:g530.t1 | NC_040043.1 9eu | C. eugenioides | 46.61 | 1,00E-32 | 94.00 | glutamate--tRNA ligase%2C chloroplastic/mitochondrial-like isoform X1 |
| NODE_824_length_347_cov_2.09259:g532.t1 | NC_039916.1 10e | C. arabica | 52.08 | 4,00E-13 | 81.00 | serine--tRNA ligase%2C chloroplastic/mitochondrial-like isoform X1 |
| NODE_824_length_347_cov_2.09259:g532.t1 | chr10 | C. canephora | 52.08 | 1,00E-13 | 81.00 | Serine--tRNA ligase |
| NODE_824_length_347_cov_2.09259:g532.t1 | NC_040044.1 10eu | C. eugenioides | 52.08 | 3,00E-13 | 81.00 | serine--tRNA ligase%2C chloroplastic/mitochondrial isoform X1 |
| NODE_826_length_347_cov_1.0963:g534.t1 | NC_039903.1 3e | C. arabica | 34.25 | 2,00E-07 | 93.00 | bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase%2C chloroplastic isoform X2 |
| NODE_826_length_347_cov_1.0963:g534.t1 | chr3 | C. canephora | 34.25 | 5,00E-08 | 93.00 | Bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase%2C chloroplastic |
| NODE_836_length_346_cov_1.08922:g540.t1 | NC_039914.1 9c | C. arabica | 55.65 | 8,00E-48 | 100.00 | uncharacterized protein LOC113708912 isoform X2 |
| NODE_836_length_346_cov_1.08922:g540.t1 | chr9 | C. canephora | 55.65 | 5,00E-48 | 100.00 | Putative Uncharacterized protein yqjG |
| NODE_836_length_346_cov_1.08922:g540.t1 | NC_040043.1 9eu | C. eugenioides | 55.65 | 3,00E-48 | 100.00 | LOW QUALITY PROTEIN: uncharacterized protein LOC113783053 |
| NODE_842_length_345_cov_1.83955:g544.t1 | NC_039917.1 10c | C. arabica | 45.28 | 1,00E-08 | 45.00 | long chain acyl-CoA synthetase 9%2C chloroplastic-like |
| NODE_842_length_345_cov_1.83955:g544.t1 | chr9 | C. canephora | 29.13 | 2,00E-10 | 90.00 | 2-succinylbenzoate--CoA ligase%2C chloroplastic/peroxisomal |
| NODE_842_length_345_cov_1.83955:g544.t1 | NC_040043.1 9eu | C. eugenioides | 29.13 | 3,00E-10 | 90.00 | 2-succinylbenzoate--CoA ligase%2C chloroplastic/peroxisomal isoform X2 |

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|---|-----------------------|----------------|-------|----------|--------|---|
| NODE_844_length_344_cov_1.64419:g546.t1 | NC_039910.1 7c | C. arabica | 88.89 | 5,00E-39 | 94.00 | zinc finger protein GAI-ASSOCIATED FACTOR 1-like |
| NODE_844_length_344_cov_1.64419:g546.t1 | chr7 | C. canephora | 88.89 | 3,00E-39 | 94.00 | C2H2-like zinc finger protein |
| NODE_844_length_344_cov_1.64419:g546.t1 | NC_040041.1 7eu | C. eugenioides | 88.89 | 4,00E-39 | 94.00 | zinc finger protein GAI-ASSOCIATED FACTOR 1-like |
| NODE_856_length_344_cov_1.36704:g554.t1 | NC_039914.1 9c | C. arabica | 44.83 | 2,00E-10 | 82.00 | glutamate--tRNA ligase%2C chloroplastic/mitochondrial-like |
| NODE_856_length_344_cov_1.36704:g554.t1 | chr9 | C. canephora | 44.83 | 7,00E-11 | 82.00 | Glutamate--tRNA ligase%2C chloroplastic/mitochondrial |
| NODE_856_length_344_cov_1.36704:g554.t1 | NC_040043.1 9eu | C. eugenioides | 44.83 | 1,00E-10 | 82.00 | glutamate--tRNA ligase%2C chloroplastic/mitochondrial-like isoform X1 |
| NODE_863_length_343_cov_2.19549:g558.t1 | NC_039903.1 3e | C. arabica | 33.96 | 2,00E-10 | 93.00 | bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase%2C chloroplastic isoform X1 |
| NODE_863_length_343_cov_2.19549:g558.t1 | chr3 | C. canephora | 33.96 | 2,00E-10 | 93.00 | Bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase%2C chloroplastic |
| NODE_863_length_343_cov_2.19549:g558.t1 | NC_040037.1 3eu | C. eugenioides | 33.96 | 8,00E-11 | 93.00 | bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase%2C chloroplastic isoform X1 |
| NODE_864_length_343_cov_2.43609:g559.t1 | NC_039918.1 11c | C. arabica | 46.55 | 2,00E-09 | 58.00 | ATPase WRNIP1-like |
| NODE_864_length_343_cov_2.43609:g559.t1 | chr11 | C. canephora | 46.55 | 6,00E-10 | 58.00 | AAA-type ATPase family protein |
| NODE_864_length_343_cov_2.43609:g559.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 46.55 | 8,00E-10 | 58.00 | ATPase WRNIP1 |
| NODE_877_length_341_cov_1.79924:g568.t1 | NC_039912.1 8e | C. arabica | 54.29 | 4,00E-14 | 93.00 | uncharacterized protein LOC113703097 |
| NODE_877_length_341_cov_1.79924:g568.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 68.00 | 7,00E-25 | 100.00 | LRR receptor-like serine/threonine-protein kinase GSO2 |
| NODE_886_length_340_cov_1.11407:g574.t1 | chr9 | C. canephora | 28.99 | 3,00E-07 | 75.00 | Bifunctional dihydrofolate reductase-thymidylate synthase |
| NODE_886_length_340_cov_1.11407:g574.t1 | NC_040043.1 9eu | C. eugenioides | 28.99 | 1,00E-06 | 75.00 | putative bifunctional dihydrofolate reductase-thymidylate synthase |
| NODE_893_length_340_cov_1.68061:g577.t1 | NC_039911.1 7e | C. arabica | 41.59 | 9,00E-19 | 98.00 | phosphoenolpyruvate carboxykinase (ATP)-like |
| NODE_893_length_340_cov_1.68061:g577.t1 | chr7 | C. canephora | 42.48 | 1,00E-19 | 98.00 | Phosphoenolpyruvate carboxykinase [ATP] |
| NODE_893_length_340_cov_1.68061:g577.t1 | NC_040041.1 7eu | C. eugenioides | 41.59 | 5,00E-19 | 98.00 | phosphoenolpyruvate carboxykinase (ATP)-like |
| NODE_897_length_339_cov_1.60305:g578.t1 | NC_039903.1 3e | C. arabica | 38.39 | 3,00E-17 | 97.00 | ribulose-phosphate 3-epimerase%2C cytoplasmic isoform-like |
| NODE_897_length_339_cov_1.60305:g578.t1 | chr0 | C. canephora | 38.39 | 1,00E-17 | 97.00 | Ribulose-phosphate 3-epimerase%2C cytoplasmic isoform |
| NODE_897_length_339_cov_1.60305:g578.t1 | NC_040038.1 4eu | C. eugenioides | 31.82 | 3,00E-17 | 97.00 | ribulose-phosphate 3-epimerase%2C chloroplastic |
| NODE_899_length_339_cov_1.12595:g579.t1 | NC_039901.1 2e | C. arabica | 36.78 | 9,00E-09 | 97.00 | DNA damage-repair/toleration protein DRT102-like |
| NODE_899_length_339_cov_1.12595:g579.t1 | chr2 | C. canephora | 36.78 | 5,00E-09 | 97.00 | DNA-damage-repair/toleration protein DRT102 |
| NODE_899_length_339_cov_1.12595:g579.t1 | NC_040036.1 2eu | C. eugenioides | 36.78 | 6,00E-09 | 97.00 | DNA damage-repair/toleration protein DRT102 |
| NODE_903_length_339_cov_1.94656:g582.t1 | NC_039918.1 11c | C. arabica | 44.00 | 9,00E-16 | 100.00 | acetyl-coenzyme A synthetase%2C chloroplastic/glyoxysomal-like |
| NODE_903_length_339_cov_1.94656:g582.t1 | chr11 | C. canephora | 44.00 | 5,00E-16 | 100.00 | Acetate--CoA ligase ACS%2C chloroplastic/glyoxysomal |
| NODE_903_length_339_cov_1.94656:g582.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 44.00 | 1,00E-15 | 100.00 | acetyl-coenzyme A synthetase%2C chloroplastic/glyoxysomal-like |
| NODE_928_length_337_cov_1.11154:g593.t1 | NC_039908.1 6c | C. arabica | 46.67 | 2,00E-09 | 50.00 | uncharacterized protein LOC113691999 |
| NODE_928_length_337_cov_1.11154:g593.t1 | chr6 | C. canephora | 46.67 | 5,00E-10 | 50.00 | Putative D-alanine--D-alanine ligase A |
| NODE_928_length_337_cov_1.11154:g593.t1 | NC_040040.1 6eu | C. eugenioides | 46.67 | 9,00E-10 | 50.00 | uncharacterized protein LOC113775590 |
| NODE_930_length_336_cov_2.02317:g594.t1 | NC_039910.1 7c | C. arabica | 34.45 | 1,00E-11 | 100.00 | probable amino-acid acetyltransferase NAGS1%2C chloroplastic |
| NODE_930_length_336_cov_2.02317:g594.t1 | chr7 | C. canephora | 34.45 | 3,00E-12 | 100.00 | Putative Amino-acid acetyltransferase |
| NODE_930_length_336_cov_2.02317:g594.t1 | NC_040041.1 7eu | C. eugenioides | 34.45 | 2,00E-11 | 100.00 | probable amino-acid acetyltransferase NAGS1%2C chloroplastic |

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| NODE_952_length_333_cov_1.59375:g609.t1 | NC_039916.1 10e | C. arabica | 61.47 | 9,00E-40 | 99.00 | glutamate-1-semialdehyde 2%2C1-aminomutase%2C chloroplastic-like |
| NODE_952_length_333_cov_1.59375:g609.t1 | chr10 | C. canephora | 61.47 | 3,00E-40 | 99.00 | Glutamate-1-semialdehyde 2%2C1-aminomutase%2C chloroplastic |
| NODE_952_length_333_cov_1.59375:g609.t1 | NC_040044.1 10eu | C. eugenioides | 61.47 | 9,00E-40 | 99.00 | glutamate-1-semialdehyde 2%2C1-aminomutase%2C chloroplastic-like |
| NODE_954_length_333_cov_1.61328:g610.t1 | NC_039908.1 6c | C. arabica | 49.14 | 2,00E-30 | 100.00 | probable polyribonucleotide nucleotidyltransferase 1%2C chloroplastic |
| NODE_954_length_333_cov_1.61328:g610.t1 | chr6 | C. canephora | 49.14 | 4,00E-31 | 100.00 | Putative Polyribonucleotide nucleotidyltransferase |
| NODE_954_length_333_cov_1.61328:g610.t1 | NC_040040.1 6eu | C. eugenioides | 49.14 | 6,00E-31 | 100.00 | probable polyribonucleotide nucleotidyltransferase 1%2C chloroplastic |
| NODE_959_length_332_cov_1.15294:g612.t1 | NC_039914.1 9c | C. arabica | 42.05 | 9,00E-16 | 88.00 | adenylosuccinate synthetase 2%2C chloroplastic-like |
| NODE_959_length_332_cov_1.15294:g612.t1 | chr6 | C. canephora | 42.05 | 2,00E-16 | 88.00 | Adenylosuccinate synthetase%2C chloroplastic |
| NODE_959_length_332_cov_1.15294:g612.t1 | NC_040040.1 6eu | C. eugenioides | 42.05 | 5,00E-16 | 88.00 | adenylosuccinate synthetase 2%2C chloroplastic |
| NODE_961_length_332_cov_1.16078:g614.t1 | NC_039899.1 1e | C. arabica | 27.12 | 1,00E-06 | 99.00 | choline monooxygenase%2C chloroplastic-like |
| NODE_961_length_332_cov_1.16078:g614.t1 | chr1 | C. canephora | 27.12 | 5,00E-07 | 99.00 | Choline monooxygenase%2C chloroplastic |
| NODE_961_length_332_cov_1.16078:g614.t1 | NC_040035.1 1eu | C. eugenioides | 27.12 | 7,00E-07 | 99.00 | choline monooxygenase%2C chloroplastic |
| NODE_976_length_331_cov_2.02756:g621.t1 | NC_039900.1 2c | C. arabica | 45.22 | 1,00E-20 | 100.00 | 3-phosphoshikimate 1-carboxyvinyltransferase 2 isoform X2 |
| NODE_976_length_331_cov_2.02756:g621.t1 | chr2 | C. canephora | 45.22 | 6,00E-21 | 100.00 | 3-phosphoshikimate 1-carboxyvinyltransferase%2C chloroplastic |
| NODE_976_length_331_cov_2.02756:g621.t1 | NC_040036.1 2eu | C. eugenioides | 45.22 | 6,00E-21 | 100.00 | 3-phosphoshikimate 1-carboxyvinyltransferase 2 |
| NODE_981_length_330_cov_0.873518:g624.t1 | NC_039908.1 6c | C. arabica | 40.00 | 2,00E-08 | 77.00 | uncharacterized protein LOC113691859 |
| NODE_981_length_330_cov_0.873518:g624.t1 | chr6 | C. canephora | 40.00 | 1,00E-08 | 77.00 | Putative Alpha-glucosidase yihQ |
| NODE_981_length_330_cov_0.873518:g624.t1 | NC_040040.1 6eu | C. eugenioides | 40.00 | 2,00E-08 | 77.00 | uncharacterized protein LOC113773196 |
| NODE_983_length_330_cov_1.22134:g626.t1 | NC_008535.1 chloroplast | C. arabica | 44.55 | 8,00E-24 | 99.00 | RNA polymerase beta subunit |
| NODE_985_length_330_cov_2.33202:g628.t1 | NC_039914.1 9c | C. arabica | 41.75 | 7,00E-24 | 95.00 | leucine--tRNA ligase%2C chloroplastic/mitochondrial-like |
| NODE_985_length_330_cov_2.33202:g628.t1 | chr9 | C. canephora | 41.75 | 2,00E-24 | 95.00 | Leucine--tRNA ligase |
| NODE_985_length_330_cov_2.33202:g628.t1 | NC_040043.1 9eu | C. eugenioides | 41.75 | 6,00E-24 | 95.00 | leucine--tRNA ligase%2C chloroplastic/mitochondrial |
| NODE_1013_length_326_cov_2.93574:g640.t1 | NC_039909.1 6e | C. arabica | 64.52 | 1,00E-22 | 82.00 | S-formylglutathione hydrolase-like isoform X1 |
| NODE_1013_length_326_cov_2.93574:g640.t1 | chr6 | C. canephora | 65.57 | 5,00E-23 | 81.00 | S-formylglutathione hydrolase |
| NODE_1013_length_326_cov_2.93574:g640.t1 | NC_040040.1 6eu | C. eugenioides | 64.52 | 8,00E-23 | 82.00 | S-formylglutathione hydrolase isoform X1 |
| NODE_1014_length_326_cov_1.40562:g641.t1 | NC_039914.1 9c | C. arabica | 30.49 | 3,00E-09 | 79.00 | ABC transporter C family member 12-like isoform X1 |
| NODE_1014_length_326_cov_1.40562:g641.t1 | chr2 | C. canephora | 33.33 | 2,00E-09 | 78.00 | ABC transporter C family member 9 |
| NODE_1014_length_326_cov_1.40562:g641.t1 | NC_040043.1 9eu | C. eugenioides | 30.49 | 2,00E-09 | 79.00 | ABC transporter C family member 12-like |
| NODE_1019_length_325_cov_1.5:g643.t1 | NC_039905.1 4e | C. arabica | 42.50 | 4,00E-13 | 97.00 | ABC transporter I family member 17-like isoform X1 |
| NODE_1019_length_325_cov_1.5:g643.t1 | chr4 | C. canephora | 42.50 | 3,00E-13 | 97.00 | ABC transporter I family member 17 |
| NODE_1019_length_325_cov_1.5:g643.t1 | NC_040035.1 1eu | C. eugenioides | 45.68 | 3,00E-13 | 100.00 | ABC transporter B family member 25%2C mitochondrial isoform X1 |
| NODE_1021_length_325_cov_1.67742:g644.t1 | NC_039901.1 2e | C. arabica | 59.22 | 8,00E-41 | 100.00 | glycine--tRNA ligase%2C chloroplastic/mitochondrial 2-like isoform X2 |
| NODE_1021_length_325_cov_1.67742:g644.t1 | chr2 | C. canephora | 59.22 | 3,00E-41 | 100.00 | Glycine--tRNA ligase 2%2C chloroplastic/mitochondrial |
| NODE_1021_length_325_cov_1.67742:g644.t1 | NC_040036.1 2eu | C. eugenioides | 59.22 | 5,00E-41 | 100.00 | LOW QUALITY PROTEIN: glycine--tRNA ligase%2C chloroplastic/mitochondrial 2 |

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|---|-------------------------|----------------|-------|----------|--------|---|
| NODE_1023_length_325_cov_1.78226:g645.t1 | NC_039916.1 10e | C. arabica | 33.72 | 5,00E-11 | 93.00 | uncharacterized protein LOC113711900 |
| NODE_1023_length_325_cov_1.78226:g645.t1 | chr10 | C. canephora | 33.72 | 2,00E-11 | 93.00 | Putative Hypoxanthine-guanine phosphoribosyltransferase |
| NODE_1023_length_325_cov_1.78226:g645.t1 | NC_040044.1 10eu | C. eugenioides | 32.56 | 4,00E-11 | 93.00 | uncharacterized protein LOC113749350 |
| NODE_1033_length_324_cov_0.898785:g650.t1 | NC_039909.1 6e | C. arabica | 37.14 | 8,00E-15 | 98.00 | glutathione hydrolase 3 isoform X2 |
| NODE_1033_length_324_cov_0.898785:g650.t1 | chr6 | C. canephora | 37.14 | 2,00E-15 | 98.00 | Putative Gamma-glutamyltranspeptidase 1 |
| NODE_1033_length_324_cov_0.898785:g650.t1 | NC_040040.1 6eu | C. eugenioides | 37.14 | 3,00E-15 | 98.00 | glutathione hydrolase 3 |
| NODE_1037_length_323_cov_1.20325:g653.t1 | NC_039907.1 5c | C. arabica | 41.67 | 2,00E-07 | 78.00 | elongation factor Ts%2C mitochondrial isoform X1 |
| NODE_1037_length_323_cov_1.20325:g653.t1 | chr6 | C. canephora | 52.33 | 3,00E-15 | 79.00 | Elongation factor Ts |
| NODE_1037_length_323_cov_1.20325:g653.t1 | NC_040040.1 6eu | C. eugenioides | 52.33 | 2,00E-15 | 79.00 | uncharacterized protein LOC113775676 isoform X3 |
| NODE_1054_length_322_cov_1.90612:g660.t1 | NW_020849470.1 scaffold | C. arabica | 94.38 | 5,00E-36 | 95.00 | uncharacterized protein LOC113720575 |
| NODE_1054_length_322_cov_1.90612:g660.t1 | NC_040038.1 4eu | C. eugenioides | 94.38 | 3,00E-36 | 95.00 | uncharacterized protein LOC113769142 |
| NODE_1065_length_321_cov_1.30738:g665.t1 | NC_039906.1 5e | C. arabica | 42.70 | 2,00E-18 | 93.00 | imidazole glycerol phosphate synthase hisHF%2C chloroplastic-like |
| NODE_1065_length_321_cov_1.30738:g665.t1 | NC_040039.1 5eu | C. eugenioides | 42.70 | 8,00E-19 | 93.00 | imidazole glycerol phosphate synthase hisHF%2C chloroplastic |
| NODE_1066_length_321_cov_2.06967:g666.t1 | NC_039904.1 4c | C. arabica | 37.96 | 4,00E-14 | 100.00 | isochorismate synthase%2C chloroplastic-like |
| NODE_1066_length_321_cov_2.06967:g666.t1 | chr4 | C. canephora | 39.18 | 7,00E-12 | 87.00 | Isochorismate synthase%2C chloroplastic |
| NODE_1066_length_321_cov_2.06967:g666.t1 | NC_040038.1 4eu | C. eugenioides | 37.96 | 2,00E-14 | 100.00 | isochorismate synthase%2C chloroplastic |
| NODE_1077_length_319_cov_1.21074:g671.t1 | NC_039907.1 5c | C. arabica | 32.69 | 1,00E-17 | 99.00 | ubiquinone biosynthesis O-methyltransferase%2C mitochondrial-like |
| NODE_1077_length_319_cov_1.21074:g671.t1 | chr5 | C. canephora | 34.38 | 4,00E-17 | 91.00 | Putative 3-demethylubiquinone-9 3-methyltransferase |
| NODE_1077_length_319_cov_1.21074:g671.t1 | NC_040039.1 5eu | C. eugenioides | 34.38 | 9,00E-17 | 91.00 | ubiquinone biosynthesis O-methyltransferase%2C mitochondrial |
| NODE_1087_length_318_cov_1.73444:g679.t1 | NC_039916.1 10e | C. arabica | 75.61 | 5,00E-42 | 100.00 | carbamoyl-phosphate synthase large chain%2C chloroplastic-like |
| NODE_1087_length_318_cov_1.73444:g679.t1 | chr10 | C. canephora | 75.61 | 2,00E-42 | 100.00 | Carbamoyl-phosphate synthase large chain |
| NODE_1087_length_318_cov_1.73444:g679.t1 | NC_040044.1 10eu | C. eugenioides | 75.61 | 3,00E-42 | 100.00 | carbamoyl-phosphate synthase large chain%2C chloroplastic |
| NODE_1089_length_318_cov_1.41079:g681.t1 | NC_039898.1 1c | C. arabica | 75.47 | 4,00E-50 | 100.00 | phosphomethylpyrimidine synthase%2C chloroplastic isoform X3 |
| NODE_1089_length_318_cov_1.41079:g681.t1 | chr1 | C. canephora | 75.47 | 5,00E-49 | 100.00 | Phosphomethylpyrimidine synthase%2C chloroplastic |
| NODE_1089_length_318_cov_1.41079:g681.t1 | NC_040035.1 1eu | C. eugenioides | 75.47 | 3,00E-50 | 100.00 | phosphomethylpyrimidine synthase%2C chloroplastic isoform X3 |
| NODE_1108_length_316_cov_2.12552:g688.t1 | NC_039914.1 9c | C. arabica | 45.97 | 2,00E-28 | 100.00 | putative bifunctional dihydrofolate reductase-thymidylate synthase isoform X2 |
| NODE_1108_length_316_cov_2.12552:g688.t1 | chr9 | C. canephora | 46.34 | 6,00E-30 | 99.00 | Bifunctional dihydrofolate reductase-thymidylate synthase 2 |
| NODE_1108_length_316_cov_2.12552:g688.t1 | NC_040043.1 9eu | C. eugenioides | 46.34 | 9,00E-29 | 99.00 | putative bifunctional dihydrofolate reductase-thymidylate synthase |
| NODE_1116_length_314_cov_1.87342:g692.t1 | NC_039902.1 3c | C. arabica | 41.27 | 3,00E-11 | 82.00 | uncharacterized protein LOC113733856 |
| NODE_1116_length_314_cov_1.87342:g692.t1 | chr3 | C. canephora | 41.27 | 1,00E-11 | 82.00 | Putative 30S ribosomal protein S6 |
| NODE_1116_length_314_cov_1.87342:g692.t1 | NC_040037.1 3eu | C. eugenioides | 39.68 | 3,00E-11 | 82.00 | uncharacterized protein LOC113765091 |
| NODE_1119_length_314_cov_2.18565:g694.t1 | NC_039910.1 7c | C. arabica | 42.86 | 3,00E-08 | 70.00 | zinc transporter 5 |
| NODE_1119_length_314_cov_2.18565:g694.t1 | chr7 | C. canephora | 42.86 | 9,00E-09 | 70.00 | Metal tolerance protein 12 |
| NODE_1119_length_314_cov_2.18565:g694.t1 | NC_040041.1 7eu | C. eugenioides | 42.86 | 1,00E-08 | 70.00 | zinc transporter 5 |

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| NODE_1132_length_313_cov_2:g703.t1 | NC_039916.1 10e | C. arabica | 31.73 | 4,00E-11 | 95.00 | ABC transporter B family member 13-like |
| NODE_1132_length_313_cov_2:g703.t1 | chr10 | C. canephora | 31.73 | 1,00E-11 | 95.00 | ABC transporter B family member 13 |
| NODE_1132_length_313_cov_2:g703.t1 | NC_040044.1 10eu | C. eugenioides | 31.73 | 9,00E-12 | 95.00 | ABC transporter B family member 13-like isoform X1 |
| NODE_1150_length_311_cov_1.26068:g711.t1 | NC_039910.1 7c | C. arabica | 46.15 | 3,00E-20 | 100.00 | L-aspartate oxidase%2C chloroplastic-like |
| NODE_1150_length_311_cov_1.26068:g711.t1 | chr7 | C. canephora | 46.15 | 9,00E-21 | 100.00 | Putative L-aspartate oxidase |
| NODE_1150_length_311_cov_1.26068:g711.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 45.19 | 3,00E-20 | 100.00 | L-aspartate oxidase%2C chloroplastic |
| NODE_1152_length_311_cov_1.25214:g712.t1 | NC_039910.1 7c | C. arabica | 66.34 | 1,00E-28 | 98.00 | probable 1-deoxy-D-xylulose-5-phosphate synthase 2%2C chloroplastic |
| NODE_1152_length_311_cov_1.25214:g712.t1 | chr7 | C. canephora | 66.34 | 4,00E-29 | 98.00 | Probable 1-deoxy-D-xylulose-5-phosphate synthase 2%2C chloroplastic |
| NODE_1152_length_311_cov_1.25214:g712.t1 | NC_040041.1 7eu | C. eugenioides | 66.34 | 7,00E-29 | 98.00 | probable 1-deoxy-D-xylulose-5-phosphate synthase 2%2C chloroplastic |
| NODE_1167_length_310_cov_2.54077:g723.t1 | NC_039916.1 10e | C. arabica | 46.94 | 6,00E-23 | 96.00 | uncharacterized protein LOC113712902 |
| NODE_1167_length_310_cov_2.54077:g723.t1 | chr10 | C. canephora | 46.94 | 9,00E-24 | 96.00 | Putative Methionine aminotransferase |
| NODE_1167_length_310_cov_2.54077:g723.t1 | NC_040044.1 10eu | C. eugenioides | 46.94 | 3,00E-23 | 96.00 | uncharacterized protein LOC113748699 |
| NODE_1168_length_310_cov_1.09442:g724.t1 | NC_039907.1 5c | C. arabica | 40.20 | 1,00E-15 | 97.00 | phosphoglycerate kinase%2C chloroplastic-like |
| NODE_1168_length_310_cov_1.09442:g724.t1 | chr5 | C. canephora | 40.20 | 3,00E-16 | 97.00 | Phosphoglycerate kinase%2C cytosolic |
| NODE_1168_length_310_cov_1.09442:g724.t1 | NC_040039.1 5eu | C. eugenioides | 38.24 | 4,00E-15 | 97.00 | exocyst complex component EXO70B1-like |
| NODE_1170_length_309_cov_1.90517:g725.t1 | NC_039898.1 1c | C. arabica | 82.95 | 2,00E-48 | 86.00 | elongation factor Tu%2C mitochondrial-like |
| NODE_1170_length_309_cov_1.90517:g725.t1 | chr1 | C. canephora | 82.95 | 7,00E-49 | 86.00 | Elongation factor Tu%2C mitochondrial |
| NODE_1170_length_309_cov_1.90517:g725.t1 | NC_040035.1 1eu | C. eugenioides | 82.95 | 2,00E-48 | 86.00 | elongation factor Tu%2C mitochondrial |
| NODE_1181_length_309_cov_2.00862:g731.t1 | NC_039917.1 10c | C. arabica | 100.00 | 4,00E-56 | 100.00 | probable LRR receptor-like serine/threonine-protein kinase At3g47570 |
| NODE_1181_length_309_cov_2.00862:g731.t1 | chr10 | C. canephora | 96.59 | 6,00E-54 | 100.00 | Putative Probable LRR receptor-like serine/threonine-protein kinase At3g47570 |
| NODE_1181_length_309_cov_2.00862:g731.t1 | NC_040044.1 10eu | C. eugenioides | 96.59 | 1,00E-56 | 100.00 | receptor kinase-like protein Xa21 |
| NODE_1198_length_307_cov_1.25217:g740.t1 | NC_039910.1 7c | C. arabica | 63.16 | 6,00E-29 | 93.00 | translation factor GUF1 homolog%2C mitochondrial isoform X1 |
| NODE_1198_length_307_cov_1.25217:g740.t1 | chr7 | C. canephora | 63.16 | 2,00E-29 | 93.00 | Translation factor GUF1 homolog%2C mitochondrial |
| NODE_1198_length_307_cov_1.25217:g740.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 63.16 | 3,00E-29 | 93.00 | translation factor GUF1 homolog%2C mitochondrial isoform X1 |
| NODE_1207_length_306_cov_2.26201:g747.t1 | NC_039904.1 4c | C. arabica | 43.56 | 4,00E-23 | 100.00 | aldehyde dehydrogenase family 2 member C4-like |
| NODE_1207_length_306_cov_2.26201:g747.t1 | chr4 | C. canephora | 40.00 | 7,00E-21 | 100.00 | Aldehyde dehydrogenase family 2 member C4 |
| NODE_1207_length_306_cov_2.26201:g747.t1 | NC_040038.1 4eu | C. eugenioides | 43.56 | 2,00E-23 | 100.00 | aldehyde dehydrogenase family 2 member C4-like |
| NODE_1226_length_305_cov_1.26754:g758.t1 | NC_008535.1 chloroplast | C. arabica | 52.78 | 9,00E-26 | 99.00 | NADH dehydrogenase subunit 5 |
| NODE_1228_length_304_cov_1.95595:g760.t1 | NC_039903.1 3e | C. arabica | 34.85 | 6,00E-15 | 96.00 | ubiquinone biosynthesis monooxygenase COQ6%2C mitochondrial-like isoform X1 |
| NODE_1228_length_304_cov_1.95595:g760.t1 | chr3 | C. canephora | 34.09 | 5,00E-15 | 96.00 | Putative Ubiquinone biosynthesis monooxygenase COQ6 |
| NODE_1228_length_304_cov_1.95595:g760.t1 | NC_040037.1 3eu | C. eugenioides | 34.09 | 2,00E-14 | 96.00 | ubiquinone biosynthesis monooxygenase COQ6%2C mitochondrial |
| NODE_1235_length_304_cov_0.964758:g763.t1 | NC_039919.1 11e | C. arabica | 58.54 | 4,00E-21 | 86.00 | succinate--CoA ligase [ADP-forming] subunit alpha-2%2C mitochondrial |
| NODE_1235_length_304_cov_0.964758:g763.t1 | chr11 | C. canephora | 58.54 | 1,00E-21 | 86.00 | Succinyl-CoA ligase [ADP-forming] subunit alpha-1%2C mitochondrial |
| NODE_1235_length_304_cov_0.964758:g763.t1 | NW_020863752.1 scaffold | C. eugenioides | 59.76 | 1,00E-21 | 86.00 | succinate--CoA ligase [ADP-forming] subunit alpha%2C mitochondrial |

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|---|-------------------------|----------------|-------|----------|--------|--|
| NODE_1236_length_304_cov_1.91189:g764.t1 | NC_039909.1 6e | C. arabica | 54.02 | 1,00E-21 | 84.00 | S-adenosylmethionine synthase 3 |
| NODE_1236_length_304_cov_1.91189:g764.t1 | chr6 | C. canephora | 54.02 | 5,00E-22 | 84.00 | S-adenosylmethionine synthase 2 |
| NODE_1236_length_304_cov_1.91189:g764.t1 | NC_040040.1 6eu | C. eugenioides | 54.02 | 8,00E-22 | 84.00 | S-adenosylmethionine synthase 3 |
| NODE_1243_length_304_cov_2.15859:g768.t1 | NC_039913.1 8c | C. arabica | 56.44 | 8,00E-30 | 100.00 | elongation factor G-2%2C chloroplastic-like |
| NODE_1243_length_304_cov_2.15859:g768.t1 | chr8 | C. canephora | 56.44 | 3,00E-30 | 100.00 | Elongation factor G%2C chloroplastic |
| NODE_1243_length_304_cov_2.15859:g768.t1 | NC_040042.1 8eu | C. eugenioides | 54.46 | 5,00E-29 | 100.00 | elongation factor G-2%2C chloroplastic isoform X2 |
| NODE_1250_length_303_cov_1.50885:g769.t1 | NC_039904.1 4c | C. arabica | 30.38 | 3,00E-06 | 77.00 | aldehyde dehydrogenase family 2 member B4%2C mitochondrial-like |
| NODE_1250_length_303_cov_1.50885:g769.t1 | chr4 | C. canephora | 30.38 | 1,00E-06 | 77.00 | Aldehyde dehydrogenase family 2 member B4%2C mitochondrial |
| NODE_1250_length_303_cov_1.50885:g769.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 29.63 | 2,00E-06 | 79.00 | aldehyde dehydrogenase family 2 member B7%2C mitochondrial-like |
| NODE_1261_length_302_cov_1.2:g777.t1 | NC_039911.1 7e | C. arabica | 54.72 | 5,00E-12 | 63.00 | uncharacterized protein LOC113701027 |
| NODE_1261_length_302_cov_1.2:g777.t1 | chr7 | C. canephora | 56.60 | 6,00E-13 | 63.00 | GTPase Der |
| NODE_1261_length_302_cov_1.2:g777.t1 | NC_040041.1 7eu | C. eugenioides | 56.60 | 1,00E-12 | 63.00 | uncharacterized protein LOC113778856 |
| NODE_1267_length_302_cov_1.38667:g781.t1 | chr2 | C. canephora | 44.12 | 3,00E-21 | 99.00 | Putative Allantoinase |
| NODE_1267_length_302_cov_1.38667:g781.t1 | NC_040036.1 2eu | C. eugenioides | 44.12 | 1,00E-20 | 99.00 | LOW QUALITY PROTEIN: uncharacterized protein LOC113763476 |
| NODE_1269_length_301_cov_1.32143:g783.t1 | NC_039919.1 11e | C. arabica | 34.33 | 6,00E-08 | 74.00 | aldehyde dehydrogenase family 2 member B7%2C mitochondrial-like |
| NODE_1269_length_301_cov_1.32143:g783.t1 | chr11 | C. canephora | 34.33 | 2,00E-08 | 74.00 | Aldehyde dehydrogenase family 2 member B7%2C mitochondrial |
| NODE_1269_length_301_cov_1.32143:g783.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 34.33 | 3,00E-08 | 74.00 | aldehyde dehydrogenase family 2 member B7%2C mitochondrial-like |
| NODE_1270_length_301_cov_0.986607:g784.t1 | NC_039901.1 2e | C. arabica | 48.81 | 7,00E-18 | 84.00 | uncharacterized protein LOC113730254 isoform X2 |
| NODE_1270_length_301_cov_0.986607:g784.t1 | chr2 | C. canephora | 48.81 | 1,00E-18 | 84.00 | Macro domain-containing protein XCC3184 |
| NODE_1270_length_301_cov_0.986607:g784.t1 | NC_040036.1 2eu | C. eugenioides | 48.81 | 4,00E-18 | 84.00 | uncharacterized protein LOC113763385 |
| NODE_1274_length_301_cov_0.910714:g785.t1 | NC_039919.1 11e | C. arabica | 76.83 | 2,00E-38 | 82.00 | succinate--CoA ligase [ADP-forming] subunit alpha-2%2C mitochondrial |
| NODE_1274_length_301_cov_0.910714:g785.t1 | chr11 | C. canephora | 76.83 | 5,00E-39 | 82.00 | Succinyl-CoA ligase [ADP-forming] subunit alpha-1%2C mitochondrial |
| NODE_1274_length_301_cov_0.910714:g785.t1 | NW_020863752.1 scaffold | C. eugenioides | 76.83 | 2,00E-39 | 82.00 | succinate--CoA ligase [ADP-forming] subunit alpha%2C mitochondrial |
| NODE_1279_length_301_cov_1.45982:g789.t1 | NC_039901.1 2e | C. arabica | 33.33 | 2,00E-09 | 72.00 | bifunctional phosphatase IMPL2%2C chloroplastic-like |
| NODE_1279_length_301_cov_1.45982:g789.t1 | chr2 | C. canephora | 33.33 | 6,00E-10 | 72.00 | Bifunctional phosphatase IMPL2%2C chloroplastic |
| NODE_1279_length_301_cov_1.45982:g789.t1 | NC_040036.1 2eu | C. eugenioides | 31.87 | 7,00E-10 | 90.00 | bifunctional phosphatase IMPL2%2C chloroplastic |
| NODE_1285_length_300_cov_2.30045:g794.t1 | NC_039918.1 11c | C. arabica | 39.78 | 6,00E-12 | 94.00 | folate synthesis bifunctional protein%2C mitochondrial-like isoform X2 |
| NODE_1285_length_300_cov_2.30045:g794.t1 | chr11 | C. canephora | 39.78 | 2,00E-12 | 94.00 | Putative Folic acid synthesis protein fol1 |
| NODE_1285_length_300_cov_2.30045:g794.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 39.78 | 3,00E-12 | 94.00 | folate synthesis bifunctional protein%2C mitochondrial isoform X2 |
| NODE_1286_length_300_cov_1.97309:g795.t1 | NC_039906.1 5e | C. arabica | 98.59 | 3,00E-44 | 76.00 | uncharacterized protein LOC113687576 |
| NODE_1286_length_300_cov_1.97309:g795.t1 | NC_040039.1 5eu | C. eugenioides | 98.59 | 2,00E-44 | 76.00 | uncharacterized protein LOC113771774 |
| NODE_1287_length_300_cov_1.82063:g796.t1 | NC_039912.1 8e | C. arabica | 47.37 | 7,00E-22 | 100.00 | puromycin-sensitive aminopeptidase-like isoform X2 |
| NODE_1287_length_300_cov_1.82063:g796.t1 | chr8 | C. canephora | 47.37 | 1,00E-21 | 100.00 | Putative Aminopeptidase N |
| NODE_1287_length_300_cov_1.82063:g796.t1 | NC_040042.1 8eu | C. eugenioides | 47.37 | 8,00E-22 | 100.00 | puromycin-sensitive aminopeptidase isoform X1 |

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| NODE_1291_length_299_cov_1.32883:g798.t1 | chr11 | C. canephora | 47.62 | 9,00E-06 | 42.00 | Putative Uncharacterized protein ypgQ |
| NODE_1319_length_297_cov_1.64091:g809.t1 | NC_039900.1 2c | C. arabica | 37.50 | 9,00E-09 | 81.00 | 2-oxoglutarate dehydrogenase%2C mitochondrial-like |
| NODE_1319_length_297_cov_1.64091:g809.t1 | chr2 | C. canephora | 37.50 | 3,00E-09 | 81.00 | 2-oxoglutarate dehydrogenase%2C mitochondrial |
| NODE_1319_length_297_cov_1.64091:g809.t1 | NC_040043.1 9eu | C. eugenioides | 37.50 | 5,00E-09 | 81.00 | 2-oxoglutarate dehydrogenase%2C mitochondrial-like |
| NODE_1324_length_297_cov_2:g812.t1 | NC_039911.1 7e | C. arabica | 47.27 | 3,00E-09 | 61.00 | LOW QUALITY PROTEIN: NAD-dependent protein deacylase SRT2-like |
| NODE_1324_length_297_cov_2:g812.t1 | chr7 | C. canephora | 45.45 | 1,00E-09 | 61.00 | NAD-dependent protein deacetylase SRT2 |
| NODE_1324_length_297_cov_2:g812.t1 | NC_040041.1 7eu | C. eugenioides | 45.45 | 2,00E-09 | 61.00 | NAD-dependent protein deacylase SRT2 isoform X1 |
| NODE_1334_length_296_cov_1.3379:g817.t1 | NC_039910.1 7c | C. arabica | 36.36 | 3,00E-12 | 100.00 | ATP-dependent RNA helicase DEAH12%2C chloroplastic-like |
| NODE_1334_length_296_cov_1.3379:g817.t1 | chr7 | C. canephora | 36.36 | 8,00E-13 | 100.00 | Putative uncharacterized protein At4g01020%2C chloroplastic |
| NODE_1334_length_296_cov_1.3379:g817.t1 | NC_040041.1 7eu | C. eugenioides | 36.36 | 1,00E-12 | 100.00 | ATP-dependent RNA helicase DEAH12%2C chloroplastic-like isoform X2 |
| NODE_1340_length_296_cov_1.43836:g821.t1 | NC_039899.1 1e | C. arabica | 45.57 | 1,00E-14 | 80.00 | LOW QUALITY PROTEIN: 3-ketoacyl-CoA thiolase 2%2C peroxisomal |
| NODE_1340_length_296_cov_1.43836:g821.t1 | chr1 | C. canephora | 45.57 | 3,00E-15 | 80.00 | 3-ketoacyl-CoA thiolase 2%2C peroxisomal |
| NODE_1340_length_296_cov_1.43836:g821.t1 | NC_040035.1 1eu | C. eugenioides | 45.57 | 7,00E-15 | 80.00 | 3-ketoacyl-CoA thiolase 2%2C peroxisomal |
| NODE_1343_length_295_cov_2.01376:g823.t1 | NC_039911.1 7e | C. arabica | 43.86 | 1,00E-09 | 83.00 | ABC transporter F family member 5-like |
| NODE_1343_length_295_cov_2.01376:g823.t1 | chr7 | C. canephora | 45.61 | 5,00E-11 | 83.00 | ABC transporter F family member 5 |
| NODE_1343_length_295_cov_2.01376:g823.t1 | NC_040041.1 7eu | C. eugenioides | 45.61 | 1,00E-10 | 83.00 | ABC transporter F family member 5 |
| NODE_1348_length_295_cov_1.9633:g828.t1 | NC_039908.1 6c | C. arabica | 57.89 | 2,00E-35 | 100.00 | probable lactoylglutathione lyase%2C chloroplastic isoform X1 |
| NODE_1348_length_295_cov_1.9633:g828.t1 | chr6 | C. canephora | 57.89 | 7,00E-36 | 100.00 | Probable lactoylglutathione lyase%2C chloroplast |
| NODE_1348_length_295_cov_1.9633:g828.t1 | NC_040040.1 6eu | C. eugenioides | 57.89 | 1,00E-35 | 100.00 | probable lactoylglutathione lyase%2C chloroplastic isoform X2 |
| NODE_1372_length_293_cov_2.71759:g836.t1 | NC_008535.1 chloroplast | C. arabica | 39.39 | 8,00E-15 | 91.00 | NADH dehydrogenase subunit 5 |
| NODE_1374_length_293_cov_1.36574:g837.t1 | NC_039901.1 2e | C. arabica | 39.39 | 2,00E-09 | 86.00 | thiamine biosynthetic bifunctional enzyme TH1%2C chloroplastic |
| NODE_1374_length_293_cov_1.36574:g837.t1 | chr2 | C. canephora | 37.88 | 2,00E-08 | 86.00 | Putative Thiamine biosynthesis bifunctional protein ThiED |
| NODE_1374_length_293_cov_1.36574:g837.t1 | NC_040036.1 2eu | C. eugenioides | 39.39 | 1,00E-09 | 86.00 | thiamine biosynthetic bifunctional enzyme TH1%2C chloroplastic |
| NODE_1377_length_293_cov_1.27315:g839.t1 | NC_039912.1 8e | C. arabica | 58.16 | 2,00E-31 | 100.00 | uncharacterized protein LOC113704260 |
| NODE_1377_length_293_cov_1.27315:g839.t1 | chr8 | C. canephora | 56.12 | 8,00E-31 | 100.00 | GMP synthase [glutamine-hydrolyzing] |
| NODE_1377_length_293_cov_1.27315:g839.t1 | NC_040042.1 8eu | C. eugenioides | 58.16 | 1,00E-31 | 100.00 | uncharacterized protein LOC113779135 |
| NODE_1416_length_289_cov_1.04245:g861.t1 | NC_039916.1 10e | C. arabica | 48.86 | 5,00E-18 | 96.00 | carbamoyl-phosphate synthase large chain%2C chloroplastic-like |
| NODE_1416_length_289_cov_1.04245:g861.t1 | chr10 | C. canephora | 48.86 | 1,00E-18 | 96.00 | Carbamoyl-phosphate synthase large chain |
| NODE_1416_length_289_cov_1.04245:g861.t1 | NC_040044.1 10eu | C. eugenioides | 48.86 | 3,00E-18 | 96.00 | carbamoyl-phosphate synthase large chain%2C chloroplastic |
| NODE_1418_length_289_cov_0.966981:g862.t1 | NC_039898.1 1c | C. arabica | 37.37 | 9,00E-11 | 98.00 | LOW QUALITY PROTEIN: uncharacterized protein LOC113742966 |
| NODE_1418_length_289_cov_0.966981:g862.t1 | chr1 | C. canephora | 38.38 | 2,00E-12 | 98.00 | Putative Malonyl-CoA-acyl carrier protein transacylase%2C mitochondrial |
| NODE_1418_length_289_cov_0.966981:g862.t1 | NC_040035.1 1eu | C. eugenioides | 37.37 | 5,00E-11 | 98.00 | uncharacterized protein LOC113779717 |
| NODE_1442_length_287_cov_1.7619:g877.t1 | NC_039908.1 6c | C. arabica | 44.71 | 1,00E-19 | 89.00 | probable polyribonucleotide nucleotidyltransferase 1%2C chloroplastic |
| NODE_1442_length_287_cov_1.7619:g877.t1 | chr6 | C. canephora | 44.71 | 3,00E-20 | 89.00 | Putative Polyribonucleotide nucleotidyltransferase |

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| NODE_1442_length_287_cov_1.7619:g877.t1 | NC_040040.1 6eu | C. eugenioides | 43.53 | 9,00E-20 | 89.00 | probable polyribonucleotide nucleotidyltransferase 1%2C chloroplastic |
| NODE_1443_length_287_cov_1.40476:g878.t1 | chr10 | C. canephora | 38.20 | 4,00E-10 | 87.00 | Probable beta-D-xylosidase 5 |
| NODE_1456_length_285_cov_1.41346:g885.t1 | NC_039905.1 4e | C. arabica | 35.48 | 5,00E-13 | 96.00 | uncharacterized protein LOC113741957 |
| NODE_1456_length_285_cov_1.41346:g885.t1 | chr4 | C. canephora | 34.41 | 1,00E-12 | 96.00 | Putative Uncharacterized oxidoreductase ygbJ |
| NODE_1456_length_285_cov_1.41346:g885.t1 | NC_040038.1 4eu | C. eugenioides | 35.48 | 3,00E-13 | 96.00 | uncharacterized protein LOC113768766 |
| NODE_1457_length_285_cov_2.21154:g886.t1 | NC_039919.1 11e | C. arabica | 42.86 | 2,00E-12 | 67.00 | 3-oxoacyl-[acyl-carrier-protein] reductase 4 |
| NODE_1457_length_285_cov_2.21154:g886.t1 | chr11 | C. canephora | 42.86 | 6,00E-13 | 67.00 | 3-oxoacyl-[acyl-carrier-protein] reductase%2C chloroplastic |
| NODE_1457_length_285_cov_2.21154:g886.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 42.86 | 1,00E-12 | 67.00 | 3-oxoacyl-[acyl-carrier-protein] reductase 4 |
| NODE_1461_length_285_cov_1.74038:g888.t1 | NC_039900.1 2c | C. arabica | 40.28 | 2,00E-08 | 70.00 | ATP-dependent DNA helicase SRS2-like protein At4g25120 isoform X2 |
| NODE_1461_length_285_cov_1.74038:g888.t1 | chr0 | C. canephora | 40.28 | 6,00E-09 | 70.00 | Putative ATP-dependent DNA helicase pcrA |
| NODE_1461_length_285_cov_1.74038:g888.t1 | NC_040035.1 1eu | C. eugenioides | 42.03 | 6,00E-08 | 65.00 | ATP-dependent DNA helicase SRS2-like protein At4g25120 |
| NODE_1481_length_284_cov_2.00966:g895.t1 | NC_039912.1 8e | C. arabica | 53.23 | 6,00E-14 | 81.00 | uncharacterized protein LOC113704029 |
| NODE_1481_length_284_cov_2.00966:g895.t1 | chr5 | C. canephora | 56.45 | 5,00E-17 | 81.00 | Translation initiation factor IF-2%2C chloroplastic |
| NODE_1481_length_284_cov_2.00966:g895.t1 | NC_040039.1 5eu | C. eugenioides | 56.45 | 9,00E-17 | 81.00 | translation initiation factor IF-2%2C chloroplastic |
| NODE_1490_length_283_cov_1.7767:g901.t1 | NC_039898.1 1c | C. arabica | 32.00 | 3,00E-10 | 92.00 | uncharacterized protein LOC113731733 |
| NODE_1490_length_283_cov_1.7767:g901.t1 | chr1 | C. canephora | 32.00 | 9,00E-11 | 92.00 | Putative ATP-dependent DNA helicase recQ |
| NODE_1490_length_283_cov_1.7767:g901.t1 | NC_040035.1 1eu | C. eugenioides | 32.00 | 2,00E-10 | 92.00 | uncharacterized protein LOC113781413 |
| NODE_1493_length_283_cov_1.78641:g903.t1 | NC_039901.1 2e | C. arabica | 57.41 | 3,00E-14 | 100.00 | intermediate cleaving peptidase 55%2C mitochondrial-like |
| NODE_1493_length_283_cov_1.78641:g903.t1 | chr2 | C. canephora | 57.41 | 1,00E-14 | 100.00 | Putative Probable Xaa-Pro aminopeptidase 3 |
| NODE_1493_length_283_cov_1.78641:g903.t1 | NC_040036.1 2eu | C. eugenioides | 57.41 | 2,00E-14 | 100.00 | intermediate cleaving peptidase 55%2C mitochondrial |
| NODE_1507_length_282_cov_1.40976:g909.t1 | NC_039901.1 2e | C. arabica | 41.25 | 1,00E-10 | 84.00 | ABC transporter G family member 8-like |
| NODE_1507_length_282_cov_1.40976:g909.t1 | chr0 | C. canephora | 41.25 | 5,00E-11 | 84.00 | ABC transporter G family member 8 |
| NODE_1507_length_282_cov_1.40976:g909.t1 | NC_040036.1 2eu | C. eugenioides | 41.25 | 8,00E-11 | 84.00 | ABC transporter G family member 8 |
| NODE_1517_length_281_cov_1.29412:g916.t1 | NC_039917.1 10c | C. arabica | 51.09 | 2,00E-24 | 98.00 | uncharacterized protein LOC113713612 |
| NODE_1517_length_281_cov_1.29412:g916.t1 | chr10 | C. canephora | 50.00 | 7,00E-24 | 98.00 | Putative tRNA modification GTPase MnmE |
| NODE_1517_length_281_cov_1.29412:g916.t1 | NC_040044.1 10eu | C. eugenioides | 51.09 | 1,00E-24 | 98.00 | uncharacterized protein LOC113749318 |
| NODE_1519_length_281_cov_2.83333:g918.t1 | NC_039911.1 7e | C. arabica | 47.19 | 2,00E-22 | 95.00 | lysine--tRNA ligase%2C cytoplasmic-like isoform X2 |
| NODE_1519_length_281_cov_2.83333:g918.t1 | chr7 | C. canephora | 47.19 | 7,00E-23 | 95.00 | Lysine--tRNA ligase |
| NODE_1519_length_281_cov_2.83333:g918.t1 | NC_040041.1 7eu | C. eugenioides | 47.19 | 1,00E-22 | 95.00 | lysine--tRNA ligase isoform X2 |
| NODE_1540_length_280_cov_0.955665:g929.t1 | NC_039904.1 4c | C. arabica | 51.85 | 4,00E-20 | 97.00 | glycerol kinase-like |
| NODE_1540_length_280_cov_0.955665:g929.t1 | chr4 | C. canephora | 51.85 | 1,00E-20 | 97.00 | Glycerol kinase |
| NODE_1540_length_280_cov_0.955665:g929.t1 | NC_040038.1 4eu | C. eugenioides | 51.85 | 2,00E-20 | 97.00 | glycerol kinase |
| NODE_1575_length_278_cov_1.47264:g944.t1 | NC_039916.1 10e | C. arabica | 98.91 | 4,00E-47 | 100.00 | DEAD-box ATP-dependent RNA helicase 21-like |
| NODE_1575_length_278_cov_1.47264:g944.t1 | chr10 | C. canephora | 98.91 | 1,00E-47 | 100.00 | DEAD-box ATP-dependent RNA helicase 21 |

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|---|------------------|----------------|--------|----------|--------|--|
| NODE_1575_length_278_cov_1.47264:g944.t1 | NC_040044.1 10eu | C. eugenioides | 98.91 | 2,00E-47 | 100.00 | DEAD-box ATP-dependent RNA helicase 21-like |
| NODE_1576_length_278_cov_1.10448:g945.t1 | NC_039905.1 4e | C. arabica | 47.37 | 7,00E-20 | 83.00 | probable GTP diphosphokinase RSH2%2C chloroplastic isoform X1 |
| NODE_1576_length_278_cov_1.10448:g945.t1 | chr4 | C. canephora | 47.37 | 4,00E-20 | 83.00 | RELA/SPOT homolog 3 |
| NODE_1576_length_278_cov_1.10448:g945.t1 | NC_040038.1 4eu | C. eugenioides | 47.37 | 6,00E-20 | 83.00 | probable GTP diphosphokinase RSH2%2C chloroplastic |
| NODE_1589_length_278_cov_2.87562:g950.t1 | NC_039901.1 2e | C. arabica | 60.76 | 8,00E-26 | 85.00 | uncharacterized protein LOC113728817 |
| NODE_1589_length_278_cov_2.87562:g950.t1 | NC_040036.1 2eu | C. eugenioides | 62.03 | 1,00E-26 | 85.00 | uncharacterized protein LOC113759417 |
| NODE_1590_length_278_cov_1.42786:g951.t1 | NC_039910.1 7c | C. arabica | 42.03 | 7,00E-08 | 75.00 | uncharacterized protein LOC113698054 |
| NODE_1590_length_278_cov_1.42786:g951.t1 | chr7 | C. canephora | 42.03 | 1,00E-08 | 75.00 | Putative IMPACT family member HI_0722 |
| NODE_1590_length_278_cov_1.42786:g951.t1 | NC_040041.1 7eu | C. eugenioides | 42.03 | 3,00E-08 | 75.00 | uncharacterized protein LOC113778220 |
| NODE_1599_length_277_cov_2.1:g956.t1 | NC_039911.1 7e | C. arabica | 42.37 | 3,00E-10 | 92.00 | ABC transporter F family member 5-like |
| NODE_1599_length_277_cov_2.1:g956.t1 | chr7 | C. canephora | 40.68 | 3,00E-10 | 92.00 | ABC transporter F family member 5 |
| NODE_1599_length_277_cov_2.1:g956.t1 | NC_040041.1 7eu | C. eugenioides | 40.68 | 5,00E-10 | 92.00 | ABC transporter F family member 5 |
| NODE_1604_length_277_cov_1.46:g958.t1 | NC_039912.1 8e | C. arabica | 53.26 | 3,00E-20 | 98.00 | uncharacterized protein LOC113704029 |
| NODE_1604_length_277_cov_1.46:g958.t1 | chr8 | C. canephora | 53.26 | 9,00E-21 | 98.00 | Putative Translation initiation factor IF-2%2C mitochondrial |
| NODE_1604_length_277_cov_1.46:g958.t1 | NC_040042.1 8eu | C. eugenioides | 53.26 | 2,00E-20 | 98.00 | uncharacterized protein LOC113781276 |
| NODE_1609_length_277_cov_1.47:g962.t1 | NC_039905.1 4e | C. arabica | 49.21 | 2,00E-12 | 71.00 | ABC transporter A family member 2-like isoform X3 |
| NODE_1609_length_277_cov_1.47:g962.t1 | chr4 | C. canephora | 49.21 | 5,00E-13 | 71.00 | ABC transporter A family member 2 |
| NODE_1609_length_277_cov_1.47:g962.t1 | NC_040038.1 4eu | C. eugenioides | 47.83 | 1,00E-12 | 76.00 | ABC transporter A family member 2-like |
| NODE_1628_length_276_cov_0.743719:g972.t1 | NC_039917.1 10c | C. arabica | 61.54 | 3,00E-28 | 85.00 | CLP protease regulatory subunit CLPX3%2C mitochondrial-like isoform X2 |
| NODE_1628_length_276_cov_0.743719:g972.t1 | chr10 | C. canephora | 61.54 | 3,00E-29 | 85.00 | ATP-dependent Clp protease |
| NODE_1628_length_276_cov_0.743719:g972.t1 | NC_040044.1 10eu | C. eugenioides | 61.54 | 2,00E-28 | 85.00 | CLP protease regulatory subunit CLPX3%2C mitochondrial isoform X2 |
| NODE_1636_length_276_cov_1.0804:g977.t1 | NC_039914.1 9c | C. arabica | 37.63 | 4,00E-08 | 100.00 | ABC transporter B family member 9-like |
| NODE_1636_length_276_cov_1.0804:g977.t1 | chr0 | C. canephora | 37.63 | 9,00E-09 | 100.00 | ABC transporter B family member 9 |
| NODE_1636_length_276_cov_1.0804:g977.t1 | NC_040039.1 5eu | C. eugenioides | 39.08 | 2,00E-08 | 94.00 | ABC transporter G family member 10 |
| NODE_1637_length_276_cov_1.47739:g978.t1 | NC_039901.1 2e | C. arabica | 57.14 | 3,00E-23 | 100.00 | 50S ribosomal protein L1%2C chloroplastic-like |
| NODE_1637_length_276_cov_1.47739:g978.t1 | chr2 | C. canephora | 57.14 | 9,00E-24 | 100.00 | 50S ribosomal protein L1%2C chloroplastic |
| NODE_1637_length_276_cov_1.47739:g978.t1 | NC_040036.1 2eu | C. eugenioides | 57.14 | 2,00E-23 | 100.00 | 50S ribosomal protein L1%2C chloroplastic |
| NODE_1644_length_276_cov_1.75879:g980.t1 | NC_039910.1 7c | C. arabica | 40.24 | 9,00E-11 | 97.00 | uncharacterized protein LOC113697941 isoform X1 |
| NODE_1644_length_276_cov_1.75879:g980.t1 | chr7 | C. canephora | 40.24 | 3,00E-11 | 97.00 | Putative Methionyl-tRNA formyltransferase |
| NODE_1644_length_276_cov_1.75879:g980.t1 | NC_040036.1 2eu | C. eugenioides | 40.24 | 1,00E-10 | 97.00 | uncharacterized protein LOC113760375 |
| NODE_1647_length_276_cov_1.11558:g981.t1 | NC_039905.1 4e | C. arabica | 52.50 | 6,00E-08 | 51.00 | putative D-cysteine desulfhydrase 1%2C mitochondrial |
| NODE_1647_length_276_cov_1.11558:g981.t1 | chr4 | C. canephora | 52.50 | 2,00E-08 | 51.00 | Putative 1-aminocyclopropane-1-carboxylate deaminase |
| NODE_1647_length_276_cov_1.11558:g981.t1 | NC_040038.1 4eu | C. eugenioides | 52.50 | 3,00E-08 | 51.00 | putative D-cysteine desulfhydrase 1%2C mitochondrial |
| NODE_1665_length_275_cov_0.742424:g989.t1 | NC_039909.1 6e | C. arabica | 100.00 | 8,00E-33 | 100.00 | uncharacterized protein LOC113696623 |

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| NODE_1665_length_275_cov_0.742424:g989.t1 | chr10 | C. canephora | 62.26 | 3,00E-18 | 98.00 | Putative Probable LRR receptor-like serine/threonine-protein kinase At4g08850 |
| NODE_1665_length_275_cov_0.742424:g989.t1 | NC_040040.1 6eu | C. eugenioides | 100.00 | 4,00E-33 | 100.00 | uncharacterized protein LOC113774031 |
| NODE_1668_length_275_cov_1.48485:g991.t1 | NC_039919.1 11e | C. arabica | 32.35 | 3,00E-08 | 100.00 | protein lojap-related%2C mitochondrial |
| NODE_1668_length_275_cov_1.48485:g991.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 32.35 | 1,00E-08 | 100.00 | protein lojap-related%2C mitochondrial |
| NODE_1691_length_274_cov_1.50254:g1003.t1 | NC_039919.1 11e | C. arabica | 34.72 | 4,00E-09 | 85.00 | glyceraldehyde-3-phosphate dehydrogenase 2%2C cytosolic |
| NODE_1691_length_274_cov_1.50254:g1003.t1 | chr11 | C. canephora | 34.72 | 2,00E-09 | 85.00 | Glyceraldehyde-3-phosphate dehydrogenase%2C cytosolic |
| NODE_1691_length_274_cov_1.50254:g1003.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 34.72 | 2,00E-09 | 85.00 | glyceraldehyde-3-phosphate dehydrogenase 2%2C cytosolic |
| NODE_1694_length_274_cov_0.746193:g1004.t1 | NC_039912.1 8e | C. arabica | 83.72 | 6,00E-45 | 97.00 | puromycin-sensitive aminopeptidase-like isoform X1 |
| NODE_1694_length_274_cov_0.746193:g1004.t1 | chr8 | C. canephora | 83.72 | 5,00E-47 | 97.00 | Peptidase M1 family protein |
| NODE_1694_length_274_cov_0.746193:g1004.t1 | NC_040042.1 8eu | C. eugenioides | 83.72 | 3,00E-45 | 97.00 | puromycin-sensitive aminopeptidase isoform X1 |
| NODE_1701_length_274_cov_2.19289:g1008.t1 | chr8 | C. canephora | 42.62 | 2,00E-07 | 66.00 | Phosphorylase superfamily protein |
| NODE_1747_length_272_cov_1.50769:g1027.t1 | NC_039906.1 5e | C. arabica | 38.37 | 1,00E-17 | 95.00 | uroporphyrinogen decarboxylase 1%2C chloroplastic-like |
| NODE_1747_length_272_cov_1.50769:g1027.t1 | chr5 | C. canephora | 38.37 | 3,00E-18 | 95.00 | Uroporphyrinogen decarboxylase 1%2C chloroplastic |
| NODE_1747_length_272_cov_1.50769:g1027.t1 | NC_040039.1 5eu | C. eugenioides | 38.37 | 6,00E-18 | 95.00 | uroporphyrinogen decarboxylase 1%2C chloroplastic isoform X2 |
| NODE_1776_length_271_cov_1.13402:g1042.t1 | NC_039903.1 3e | C. arabica | 38.64 | 7,00E-09 | 92.00 | GTP-binding protein OBGC%2C chloroplastic |
| NODE_1776_length_271_cov_1.13402:g1042.t1 | chr3 | C. canephora | 42.05 | 3,00E-06 | 92.00 | Putative GTPase obg |
| NODE_1777_length_271_cov_1.13918:g1043.t1 | NC_039919.1 11e | C. arabica | 50.56 | 9,00E-25 | 98.00 | biotin carboxylase 1%2C chloroplastic-like |
| NODE_1777_length_271_cov_1.13918:g1043.t1 | chr11 | C. canephora | 50.56 | 3,00E-25 | 98.00 | Biotin carboxylase 1%2C chloroplastic |
| NODE_1777_length_271_cov_1.13918:g1043.t1 | NW_020862338.1 scaffold | C. eugenioides | 50.56 | 5,00E-25 | 98.00 | biotin carboxylase 1%2C chloroplastic |
| NODE_1782_length_271_cov_0.762887:g1045.t1 | NC_039919.1 11e | C. arabica | 100.00 | 9,00E-29 | 100.00 | putative late blight resistance protein homolog R1A-4 |
| NODE_1782_length_271_cov_0.762887:g1045.t1 | chr11 | C. canephora | 93.88 | 2,00E-27 | 100.00 | Putative Disease resistance protein (CC-NBS-LRR class) family |
| NODE_1782_length_271_cov_0.762887:g1045.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 100.00 | 5,00E-29 | 100.00 | putative late blight resistance protein homolog R1A-4 |
| NODE_1794_length_270_cov_1.87047:g1051.t1 | NC_039900.1 2c | C. arabica | 58.54 | 2,00E-12 | 100.00 | glutamine--fructose-6-phosphate aminotransferase [isomerizing] 2-like |
| NODE_1794_length_270_cov_1.87047:g1051.t1 | chr2 | C. canephora | 56.10 | 3,00E-12 | 100.00 | Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 2 |
| NODE_1794_length_270_cov_1.87047:g1051.t1 | NC_040036.1 2eu | C. eugenioides | 56.10 | 4,00E-12 | 100.00 | glutamine--fructose-6-phosphate aminotransferase [isomerizing] 2 |
| NODE_1804_length_270_cov_0.766839:g1055.t1 | NC_039900.1 2c | C. arabica | 50.57 | 3,00E-23 | 97.00 | LOW QUALITY PROTEIN: riboflavin biosynthesis protein PYRD%2C chloroplastic-like |
| NODE_1804_length_270_cov_0.766839:g1055.t1 | chr2 | C. canephora | 50.57 | 1,00E-23 | 97.00 | Putative Riboflavin biosynthesis protein RibD |
| NODE_1804_length_270_cov_0.766839:g1055.t1 | NC_040036.1 2eu | C. eugenioides | 50.57 | 2,00E-23 | 97.00 | riboflavin biosynthesis protein PYRD%2C chloroplastic |
| NODE_1807_length_270_cov_0.761658:g1058.t1 | NC_039904.1 4c | C. arabica | 52.54 | 2,00E-15 | 65.00 | DNA gyrase subunit B%2C chloroplastic/mitochondrial-like |
| NODE_1807_length_270_cov_0.761658:g1058.t1 | chr6 | C. canephora | 51.67 | 1,00E-15 | 66.00 | DNA gyrase subunit B%2C chloroplastic/mitochondrial |
| NODE_1807_length_270_cov_0.761658:g1058.t1 | NC_040040.1 6eu | C. eugenioides | 51.67 | 2,00E-15 | 66.00 | DNA gyrase subunit B%2C chloroplastic/mitochondrial-like |
| NODE_1824_length_269_cov_1.54167:g1066.t1 | NC_039901.1 2e | C. arabica | 54.84 | 1,00E-17 | 80.00 | aspartate--tRNA ligase%2C chloroplastic/mitochondrial isoform X1 |
| NODE_1824_length_269_cov_1.54167:g1066.t1 | chr2 | C. canephora | 54.84 | 4,00E-18 | 80.00 | Aspartate--tRNA ligase |
| NODE_1824_length_269_cov_1.54167:g1066.t1 | NC_040036.1 2eu | C. eugenioides | 54.84 | 9,00E-18 | 80.00 | aspartate--tRNA ligase%2C chloroplastic/mitochondrial isoform X4 |

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| NODE_1840_length_268_cov_1.54974:g1071.t1 | NC_039915.1 9e | C. arabica | 40.00 | 2,00E-10 | 96.00 | dihydropyrimidinase-like isoform X2 |
| NODE_1840_length_268_cov_1.54974:g1071.t1 | chr0 | C. canephora | 40.00 | 3,00E-09 | 96.00 | Putative Dihydropyrimidinase |
| NODE_1840_length_268_cov_1.54974:g1071.t1 | NC_040038.1 4eu | C. eugenioides | 40.00 | 1,00E-10 | 96.00 | LOW QUALITY PROTEIN: dihydropyrimidinase-like |
| NODE_1845_length_268_cov_1.90576:g1073.t1 | NC_039900.1 2c | C. arabica | 38.64 | 6,00E-13 | 100.00 | 4-hydroxy-tetrahydrodipicolinate synthase%2C chloroplastic-like |
| NODE_1845_length_268_cov_1.90576:g1073.t1 | chr0 | C. canephora | 38.64 | 2,00E-13 | 100.00 | Dihydrodipicolinate synthase%2C chloroplastic |
| NODE_1845_length_268_cov_1.90576:g1073.t1 | NC_040036.1 2eu | C. eugenioides | 38.64 | 3,00E-13 | 100.00 | 4-hydroxy-tetrahydrodipicolinate synthase%2C chloroplastic-like |
| NODE_1880_length_267_cov_2.25263:g1093.t1 | NC_039912.1 8e | C. arabica | 52.63 | 9,00E-24 | 98.00 | uncharacterized protein LOC113704260 |
| NODE_1880_length_267_cov_2.25263:g1093.t1 | chr8 | C. canephora | 52.63 | 4,00E-24 | 98.00 | GMP synthase [glutamine-hydrolyzing] |
| NODE_1880_length_267_cov_2.25263:g1093.t1 | NC_040042.1 8eu | C. eugenioides | 52.63 | 5,00E-24 | 98.00 | uncharacterized protein LOC113779135 |
| NODE_1882_length_266_cov_1.16931:g1094.t1 | NC_039916.1 10e | C. arabica | 42.25 | 6,00E-10 | 85.00 | carbamoyl-phosphate synthase large chain%2C chloroplastic-like |
| NODE_1882_length_266_cov_1.16931:g1094.t1 | chr10 | C. canephora | 42.25 | 2,00E-10 | 85.00 | Carbamoyl-phosphate synthase large chain |
| NODE_1882_length_266_cov_1.16931:g1094.t1 | NC_040044.1 10eu | C. eugenioides | 42.25 | 4,00E-10 | 85.00 | carbamoyl-phosphate synthase large chain%2C chloroplastic |
| NODE_1898_length_266_cov_1.55556:g1101.t1 | NC_039901.1 2e | C. arabica | 49.44 | 4,00E-23 | 100.00 | serine--tRNA ligase-like |
| NODE_1898_length_266_cov_1.55556:g1101.t1 | chr2 | C. canephora | 49.44 | 1,00E-23 | 100.00 | Serine--tRNA ligase |
| NODE_1898_length_266_cov_1.55556:g1101.t1 | NC_040036.1 2eu | C. eugenioides | 49.44 | 2,00E-23 | 100.00 | serine--tRNA ligase |
| NODE_1899_length_266_cov_0.772487:g1102.t1 | NC_039905.1 4e | C. arabica | 48.24 | 1,00E-14 | 95.00 | aldehyde dehydrogenase family 2 member B4%2C mitochondrial-like |
| NODE_1899_length_266_cov_0.772487:g1102.t1 | chr4 | C. canephora | 48.24 | 4,00E-15 | 95.00 | Aldehyde dehydrogenase family 2 member B4%2C mitochondrial |
| NODE_1899_length_266_cov_0.772487:g1102.t1 | NC_040038.1 4eu | C. eugenioides | 48.24 | 7,00E-15 | 95.00 | aldehyde dehydrogenase family 2 member B4%2C mitochondrial-like |
| NODE_1901_length_266_cov_1.93651:g1104.t1 | NC_039909.1 6e | C. arabica | 35.16 | 2,00E-08 | 93.00 | uncharacterized protein LOC113694619 |
| NODE_1901_length_266_cov_1.93651:g1104.t1 | chr6 | C. canephora | 35.16 | 7,00E-09 | 93.00 | Putative UPF0098 protein MTH_273 |
| NODE_1901_length_266_cov_1.93651:g1104.t1 | NC_040040.1 6eu | C. eugenioides | 35.16 | 1,00E-08 | 93.00 | uncharacterized protein LOC113776159 |
| NODE_1921_length_265_cov_1.48936:g1114.t1 | NC_039919.1 11e | C. arabica | 28.24 | 6,00E-10 | 97.00 | LOW QUALITY PROTEIN: methylenetetrahydrofolate reductase 1-like |
| NODE_1921_length_265_cov_1.48936:g1114.t1 | NW_020863270.1 scaffold | C. eugenioides | 28.24 | 9,00E-10 | 97.00 | methylenetetrahydrofolate reductase 2-like |
| NODE_1937_length_264_cov_1.17647:g1120.t1 | NC_039909.1 6e | C. arabica | 46.91 | 2,00E-19 | 93.00 | acetate/butyrate--CoA ligase AAE7%2C peroxisomal-like |
| NODE_1937_length_264_cov_1.17647:g1120.t1 | chr0 | C. canephora | 46.91 | 7,00E-20 | 93.00 | Acetate/butyrate--CoA ligase AAE7%2C peroxisomal |
| NODE_1937_length_264_cov_1.17647:g1120.t1 | NC_040037.1 3eu | C. eugenioides | 46.91 | 2,00E-19 | 93.00 | acetate/butyrate--CoA ligase AAE7%2C peroxisomal |
| NODE_1940_length_264_cov_1.58289:g1122.t1 | NC_039911.1 7e | C. arabica | 48.28 | 9,00E-17 | 100.00 | geranylgeranyl pyrophosphate synthase 7%2C chloroplastic-like |
| NODE_1940_length_264_cov_1.58289:g1122.t1 | chr7 | C. canephora | 47.13 | 9,00E-17 | 100.00 | Geranylgeranyl pyrophosphate synthase%2C chloroplastic |
| NODE_1940_length_264_cov_1.58289:g1122.t1 | NC_040041.1 7eu | C. eugenioides | 47.13 | 2,00E-16 | 100.00 | geranylgeranyl pyrophosphate synthase 7%2C chloroplastic-like |
| NODE_1943_length_264_cov_1.55615:g1124.t1 | NC_039918.1 11c | C. arabica | 41.10 | 6,00E-10 | 88.00 | nicotinate-nucleotide pyrophosphorylase [carboxylating]%2C chloroplastic-like |
| NODE_1943_length_264_cov_1.55615:g1124.t1 | chr11 | C. canephora | 41.10 | 2,00E-10 | 88.00 | Putative Probable nicotinate-nucleotide pyrophosphorylase [carboxylating] |
| NODE_1943_length_264_cov_1.55615:g1124.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 41.10 | 3,00E-10 | 88.00 | nicotinate-nucleotide pyrophosphorylase [carboxylating]%2C chloroplastic |
| NODE_1949_length_263_cov_1.5914:g1127.t1 | NC_039914.1 9c | C. arabica | 40.00 | 1,00E-06 | 91.00 | protein TRIGALACTOSYLDIACYLGLYCEROL 3%2C chloroplastic-like |
| NODE_1949_length_263_cov_1.5914:g1127.t1 | chr9 | C. canephora | 40.00 | 4,00E-07 | 91.00 | Protein TRIGALACTOSYLDIACYLGLYCEROL 3%2C chloroplastic |

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| NODE_1949_length_263_cov_1.5914:g1127.t1 | NC_040043.1 9eu | C. eugenioides | 40.00 | 7,00E-07 | 91.00 | protein TRIGALACTOSYLDIACYLGLYCEROL 3%2C chloroplastic |
| NODE_1960_length_263_cov_2.03226:g1133.t1 | NC_039909.1 6e | C. arabica | 47.50 | 2,00E-19 | 90.00 | arginine--trRNA ligase%2C cytoplasmic-like isoform X1 |
| NODE_1960_length_263_cov_2.03226:g1133.t1 | chr6 | C. canephora | 46.25 | 1,00E-18 | 90.00 | Putative Arginine--trRNA ligase |
| NODE_1960_length_263_cov_2.03226:g1133.t1 | NC_040040.1 6eu | C. eugenioides | 47.50 | 9,00E-20 | 90.00 | arginine--trRNA ligase%2C cytoplasmic-like isoform X1 |
| NODE_1966_length_262_cov_0.794595:g1137.t1 | NC_039903.1 3e | C. arabica | 42.68 | 1,00E-18 | 94.00 | LOW QUALITY PROTEIN: primary amine oxidase-like |
| NODE_1966_length_262_cov_0.794595:g1137.t1 | chr3 | C. canephora | 41.46 | 3,00E-18 | 94.00 | Primary amine oxidase |
| NODE_1966_length_262_cov_0.794595:g1137.t1 | NC_040037.1 3eu | C. eugenioides | 42.68 | 3,00E-19 | 94.00 | primary amine oxidase-like |
| NODE_1974_length_262_cov_1.2:g1143.t1 | NC_039916.1 10e | C. arabica | 53.12 | 2,00E-21 | 96.00 | uncharacterized protein LOC113712290 isoform X1 |
| NODE_1974_length_262_cov_1.2:g1143.t1 | chr10 | C. canephora | 55.74 | 5,00E-22 | 92.00 | UPF0047 protein yjbQ |
| NODE_1974_length_262_cov_1.2:g1143.t1 | NC_040044.1 10eu | C. eugenioides | 55.74 | 9,00E-22 | 92.00 | uncharacterized protein LOC113750884 isoform X2 |
| NODE_1997_length_261_cov_1.19565:g1157.t1 | NC_039904.1 4c | C. arabica | 44.16 | 1,00E-13 | 100.00 | betaine aldehyde dehydrogenase 1%2C chloroplastic-like |
| NODE_1997_length_261_cov_1.19565:g1157.t1 | chr4 | C. canephora | 44.16 | 4,00E-14 | 100.00 | Betaine aldehyde dehydrogenase 1%2C chloroplastic |
| NODE_1997_length_261_cov_1.19565:g1157.t1 | NC_040038.1 4eu | C. eugenioides | 44.16 | 6,00E-14 | 100.00 | betaine aldehyde dehydrogenase 1%2C chloroplastic-like |
| NODE_2008_length_261_cov_1.58696:g1162.t1 | NC_039901.1 2e | C. arabica | 41.43 | 5,00E-15 | 85.00 | intermediate cleaving peptidase 55%2C mitochondrial-like |
| NODE_2008_length_261_cov_1.58696:g1162.t1 | chr2 | C. canephora | 41.43 | 4,00E-15 | 85.00 | Putative Probable Xaa-Pro aminopeptidase 3 |
| NODE_2008_length_261_cov_1.58696:g1162.t1 | NC_040036.1 2eu | C. eugenioides | 41.43 | 3,00E-15 | 85.00 | intermediate cleaving peptidase 55%2C mitochondrial |
| NODE_2019_length_260_cov_2:g1169.t1 | NC_008535.1 chloroplast | C. arabica | 69.77 | 3,00E-34 | 100.00 | ATP synthase CF1 alpha subunit |
| NODE_2029_length_260_cov_2.39891:g1174.t1 | NC_039914.1 9c | C. arabica | 42.50 | 2,00E-11 | 95.00 | probable 3-hydroxyisobutyrate dehydrogenase%2C mitochondrial isoform X1 |
| NODE_2029_length_260_cov_2.39891:g1174.t1 | chr9 | C. canephora | 42.50 | 5,00E-12 | 95.00 | Probable 3-hydroxyisobutyrate dehydrogenase%2C mitochondrial |
| NODE_2029_length_260_cov_2.39891:g1174.t1 | NC_040043.1 9eu | C. eugenioides | 42.50 | 9,00E-12 | 95.00 | probable 3-hydroxyisobutyrate dehydrogenase%2C mitochondrial isoform X1 |
| NODE_2033_length_260_cov_0.803279:g1175.t1 | NC_039900.1 2c | C. arabica | 59.02 | 4,00E-17 | 70.00 | NAD(P)H dehydrogenase (quinone) FQR1-like |
| NODE_2033_length_260_cov_0.803279:g1175.t1 | chr2 | C. canephora | 59.02 | 1,00E-17 | 70.00 | Flavoprotein WrbA |
| NODE_2033_length_260_cov_0.803279:g1175.t1 | NC_040036.1 2eu | C. eugenioides | 59.02 | 3,00E-17 | 70.00 | NAD(P)H dehydrogenase (quinone) FQR1-like |
| NODE_2038_length_260_cov_0.808743:g1177.t1 | NC_039906.1 5e | C. arabica | 98.82 | 1,00E-56 | 100.00 | fatty acid desaturase 4%2C chloroplastic-like |
| NODE_2038_length_260_cov_0.808743:g1177.t1 | chr5 | C. canephora | 95.29 | 3,00E-54 | 100.00 | fatty acid desaturase A |
| NODE_2038_length_260_cov_0.808743:g1177.t1 | NC_040039.1 5eu | C. eugenioides | 98.82 | 8,00E-57 | 100.00 | fatty acid desaturase 4%2C chloroplastic-like |
| NODE_2048_length_259_cov_1.59341:g1180.t1 | NC_039911.1 7e | C. arabica | 56.99 | 7,00E-30 | 100.00 | chaperone protein ClpB3%2C chloroplastic-like |
| NODE_2048_length_259_cov_1.59341:g1180.t1 | chr7 | C. canephora | 56.99 | 2,00E-30 | 100.00 | Chaperone protein ClpB3%2C chloroplastic |
| NODE_2048_length_259_cov_1.59341:g1180.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 58.06 | 3,00E-30 | 100.00 | chaperone protein ClpB3%2C chloroplastic |
| NODE_2053_length_259_cov_1.61538:g1182.t1 | NC_039909.1 6e | C. arabica | 37.35 | 5,00E-12 | 94.00 | ferredoxin-dependent glutamate synthase%2C chloroplastic-like |
| NODE_2053_length_259_cov_1.61538:g1182.t1 | chr6 | C. canephora | 37.35 | 2,00E-12 | 94.00 | Ferredoxin-dependent glutamate synthase 1%2C chloroplastic |
| NODE_2053_length_259_cov_1.61538:g1182.t1 | NC_040040.1 6eu | C. eugenioides | 37.35 | 3,00E-12 | 94.00 | ferredoxin-dependent glutamate synthase%2C chloroplastic |
| NODE_2063_length_259_cov_1.83516:g1186.t1 | NC_039904.1 4c | C. arabica | 100.00 | 3,00E-55 | 100.00 | uncharacterized protein LOC113739892 isoform X1 |
| NODE_2063_length_259_cov_1.83516:g1186.t1 | chr4 | C. canephora | 100.00 | 1,00E-55 | 100.00 | unknown protein%3B FUNCTIONS IN |

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| NODE_2063_length_259_cov_1.83516:g1186.t1 | NC_040038.1 4eu | C. eugenioides | 98.84 | 9,00E-55 | 100.00 | uncharacterized protein LOC113768344 isoform X1 |
| NODE_2090_length_258_cov_1.70166:g1197.t1 | NC_039919.1 11e | C. arabica | 100.00 | 3,00E-38 | 100.00 | uncharacterized protein LOC113718104 |
| NODE_2090_length_258_cov_1.70166:g1197.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 98.78 | 8,00E-38 | 100.00 | uncharacterized protein LOC113751355 |
| NODE_2107_length_257_cov_1.63333:g1209.t1 | chr2 | C. canephora | 41.38 | 7,00E-07 | 100.00 | Nudix hydrolase 15%2C mitochondrial |
| NODE_2112_length_257_cov_0.966667:g1212.t1 | NC_039917.1 10c | C. arabica | 41.67 | 1,00E-13 | 91.00 | gamma carbonic anhydrase 1%2C mitochondrial-like |
| NODE_2112_length_257_cov_0.966667:g1212.t1 | chr10 | C. canephora | 41.67 | 4,00E-14 | 91.00 | Gamma carbonic anhydrase 1%2C mitochondrial |
| NODE_2112_length_257_cov_0.966667:g1212.t1 | NC_040044.1 10eu | C. eugenioides | 41.67 | 2,00E-13 | 91.00 | gamma carbonic anhydrase 1%2C mitochondrial |
| NODE_2127_length_256_cov_1.65363:g1220.t1 | NC_039905.1 4e | C. arabica | 45.45 | 3,00E-09 | 96.00 | 4-hydroxybenzoate polyprenyltransferase%2C mitochondrial-like |
| NODE_2127_length_256_cov_1.65363:g1220.t1 | chr4 | C. canephora | 45.45 | 9,00E-10 | 96.00 | 4-hydroxybenzoate polyprenyltransferase%2C mitochondrial |
| NODE_2127_length_256_cov_1.65363:g1220.t1 | NC_040038.1 4eu | C. eugenioides | 47.06 | 1,00E-09 | 94.00 | 4-hydroxybenzoate geranyltransferase 2-like |
| NODE_2135_length_256_cov_1.64246:g1225.t1 | NC_039905.1 4e | C. arabica | 44.05 | 4,00E-15 | 97.00 | acetylornithine aminotransferase%2C mitochondrial-like |
| NODE_2135_length_256_cov_1.64246:g1225.t1 | chr4 | C. canephora | 44.05 | 2,00E-15 | 97.00 | Acetylornithine aminotransferase%2C mitochondrial |
| NODE_2135_length_256_cov_1.64246:g1225.t1 | NC_040038.1 4eu | C. eugenioides | 44.05 | 3,00E-15 | 97.00 | acetylornithine aminotransferase%2C mitochondrial |
| NODE_2139_length_256_cov_2.41341:g1230.t1 | NC_039905.1 4e | C. arabica | 43.48 | 7,00E-11 | 79.00 | ABC transporter A family member 7-like |
| NODE_2139_length_256_cov_2.41341:g1230.t1 | chr4 | C. canephora | 43.48 | 2,00E-11 | 79.00 | ABC transporter A family member 7 |
| NODE_2139_length_256_cov_2.41341:g1230.t1 | NC_040038.1 4eu | C. eugenioides | 43.48 | 4,00E-11 | 79.00 | ABC transporter A family member 7-like |
| NODE_2162_length_255_cov_1.6236:g1243.t1 | NC_039900.1 2c | C. arabica | 41.18 | 2,00E-07 | 80.00 | LOW QUALITY PROTEIN: transketolase%2C chloroplastic-like |
| NODE_2162_length_255_cov_1.6236:g1243.t1 | chr2 | C. canephora | 41.18 | 6,00E-08 | 80.00 | Transketolase%2C chloroplastic |
| NODE_2162_length_255_cov_1.6236:g1243.t1 | NC_040036.1 2eu | C. eugenioides | 41.18 | 1,00E-07 | 80.00 | transketolase%2C chloroplastic |
| NODE_2166_length_255_cov_1.64045:g1245.t1 | chr3 | C. canephora | 45.83 | 1,00E-07 | 87.00 | Probable uridine nucleosidase 2 |
| NODE_2166_length_255_cov_1.64045:g1245.t1 | NC_040037.1 3eu | C. eugenioides | 47.92 | 5,00E-08 | 87.00 | probable uridine nucleosidase 2 |
| NODE_2186_length_254_cov_1.24294:g1249.t1 | NC_039915.1 9e | C. arabica | 52.87 | 1,00E-24 | 98.00 | leucine--tRNA ligase%2C chloroplastic/mitochondrial-like |
| NODE_2186_length_254_cov_1.24294:g1249.t1 | chr9 | C. canephora | 52.87 | 4,00E-25 | 98.00 | Leucine--tRNA ligase |
| NODE_2186_length_254_cov_1.24294:g1249.t1 | NC_040043.1 9eu | C. eugenioides | 52.87 | 7,00E-25 | 98.00 | leucine--tRNA ligase%2C chloroplastic/mitochondrial |
| NODE_2187_length_254_cov_1.41243:g1250.t1 | NC_039914.1 9c | C. arabica | 49.37 | 2,00E-21 | 96.00 | peptide chain release factor PrfB1%2C chloroplastic isoform X2 |
| NODE_2187_length_254_cov_1.41243:g1250.t2 | NC_039914.1 9c | C. arabica | 49.37 | 2,00E-21 | 96.00 | peptide chain release factor PrfB1%2C chloroplastic isoform X2 |
| NODE_2187_length_254_cov_1.41243:g1250.t1 | chr9 | C. canephora | 49.37 | 7,00E-22 | 96.00 | Peptide chain release factor 2 |
| NODE_2187_length_254_cov_1.41243:g1250.t2 | chr9 | C. canephora | 49.37 | 7,00E-22 | 96.00 | Peptide chain release factor 2 |
| NODE_2187_length_254_cov_1.41243:g1250.t1 | NC_040043.1 9eu | C. eugenioides | 49.37 | 1,00E-21 | 96.00 | peptide chain release factor PrfB1%2C chloroplastic |
| NODE_2187_length_254_cov_1.41243:g1250.t2 | NC_040043.1 9eu | C. eugenioides | 49.37 | 1,00E-21 | 96.00 | peptide chain release factor PrfB1%2C chloroplastic |
| NODE_2200_length_253_cov_1.25:g1255.t1 | NC_039908.1 6c | C. arabica | 37.29 | 1,00E-08 | 71.00 | LOW QUALITY PROTEIN: ABC transporter A family member 1-like |
| NODE_2200_length_253_cov_1.25:g1255.t1 | chr6 | C. canephora | 40.74 | 4,00E-09 | 65.00 | ABC transporter A family member 1 |
| NODE_2200_length_253_cov_1.25:g1255.t1 | NC_040040.1 6eu | C. eugenioides | 37.29 | 6,00E-09 | 71.00 | ABC transporter A family member 1 isoform X2 |
| NODE_2207_length_253_cov_1.68182:g1257.t1 | NC_039903.1 3e | C. arabica | 46.67 | 2,00E-15 | 100.00 | glutathione reductase%2C chloroplastic |

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| NODE_2207_length_253_cov_1.68182:g1257.t1 | chr1 | C. canephora | 55.00 | 7,00E-16 | 80.00 | Glutathione reductase%2C chloroplastic (Fragment) |
| NODE_2207_length_253_cov_1.68182:g1257.t1 | NC_040037.1 3eu | C. eugenioides | 47.95 | 1,00E-15 | 97.00 | glutathione reductase%2C chloroplastic |
| NODE_2214_length_252_cov_1.68:g1259.t1 | NC_039917.1 10c | C. arabica | 45.00 | 8,00E-08 | 71.00 | probable beta-D-xylosidase 7 |
| NODE_2214_length_252_cov_1.68:g1259.t1 | chr10 | C. canephora | 45.00 | 3,00E-08 | 71.00 | Probable beta-D-xylosidase 7 |
| NODE_2214_length_252_cov_1.68:g1259.t1 | NC_040044.1 10eu | C. eugenioides | 45.00 | 5,00E-08 | 71.00 | probable beta-D-xylosidase 7 |
| NODE_2257_length_250_cov_2.18497:g1280.t1 | chr3 | C. canephora | 36.54 | 5,00E-07 | 62.00 | Putative 30S ribosomal protein S1 |
| NODE_2275_length_250_cov_1.68208:g1286.t1 | NC_039918.1 11c | C. arabica | 34.88 | 4,00E-15 | 100.00 | 6-phosphogluconate dehydrogenase%2C decarboxylating 1 |
| NODE_2275_length_250_cov_1.68208:g1286.t1 | chr11 | C. canephora | 34.88 | 2,00E-15 | 100.00 | 6-phosphogluconate dehydrogenase%2C decarboxylating |
| NODE_2275_length_250_cov_1.68208:g1286.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 34.88 | 2,00E-15 | 100.00 | 6-phosphogluconate dehydrogenase%2C decarboxylating 1-like |
| NODE_2298_length_249_cov_0.854651:g1297.t1 | NC_039912.1 8e | C. arabica | 47.46 | 2,00E-11 | 69.00 | glycine dehydrogenase (decarboxylating)%2C mitochondrial-like isoform X2 |
| NODE_2298_length_249_cov_0.854651:g1297.t1 | NC_040042.1 8eu | C. eugenioides | 47.46 | 9,00E-12 | 69.00 | glycine dehydrogenase (decarboxylating)%2C mitochondrial |
| NODE_2321_length_249_cov_1.69767:g1305.t1 | NC_039905.1 4e | C. arabica | 32.39 | 6,00E-09 | 80.00 | long chain base biosynthesis protein 2a |
| NODE_2321_length_249_cov_1.69767:g1305.t1 | chr4 | C. canephora | 32.39 | 2,00E-09 | 80.00 | Serine palmitoyltransferase 2 |
| NODE_2321_length_249_cov_1.69767:g1305.t1 | NC_040038.1 4eu | C. eugenioides | 32.39 | 3,00E-09 | 80.00 | long chain base biosynthesis protein 2a |
| NODE_2327_length_248_cov_1.47368:g1307.t1 | NC_039918.1 11c | C. arabica | 44.58 | 2,00E-13 | 100.00 | ATPase WRNIP1-like |
| NODE_2327_length_248_cov_1.47368:g1307.t1 | chr11 | C. canephora | 44.58 | 6,00E-14 | 100.00 | AAA-type ATPase family protein |
| NODE_2327_length_248_cov_1.47368:g1307.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 44.58 | 7,00E-14 | 100.00 | ATPase WRNIP1 |
| NODE_2353_length_247_cov_0.858824:g1314.t1 | NC_039901.1 2e | C. arabica | 47.56 | 4,00E-19 | 100.00 | glycerol-3-phosphate dehydrogenase [NAD(+)] 2%2C chloroplastic-like isoform X2 |
| NODE_2353_length_247_cov_0.858824:g1314.t1 | chr2 | C. canephora | 47.56 | 5,00E-19 | 100.00 | Putative Glycerol-3-phosphate dehydrogenase [NAD(P)] |
| NODE_2353_length_247_cov_0.858824:g1314.t1 | NC_040036.1 2eu | C. eugenioides | 47.56 | 2,00E-19 | 100.00 | glycerol-3-phosphate dehydrogenase [NAD(+)] 2%2C chloroplastic isoform X2 |
| NODE_2362_length_247_cov_2.61176:g1320.t1 | NC_039911.1 7e | C. arabica | 77.36 | 6,00E-23 | 100.00 | chaperone protein ClpB3%2C chloroplastic-like |
| NODE_2362_length_247_cov_2.61176:g1320.t2 | NC_039905.1 4e | C. arabica | 74.39 | 1,00E-35 | 100.00 | chaperone protein ClpB1 |
| NODE_2362_length_247_cov_2.61176:g1320.t1 | chr7 | C. canephora | 77.36 | 2,00E-23 | 100.00 | Chaperone protein ClpB3%2C chloroplastic |
| NODE_2362_length_247_cov_2.61176:g1320.t2 | chr4 | C. canephora | 74.39 | 4,00E-36 | 100.00 | Chaperone protein ClpB1 |
| NODE_2362_length_247_cov_2.61176:g1320.t1 | NC_040045.1 11eu 11eu | C. eugenioides | 77.36 | 4,00E-23 | 100.00 | chaperone protein ClpB3%2C chloroplastic |
| NODE_2362_length_247_cov_2.61176:g1320.t2 | NC_040045.1 11eu 11eu | C. eugenioides | 70.73 | 2,00E-36 | 100.00 | chaperone protein ClpB3%2C chloroplastic |
| NODE_2373_length_247_cov_0.864706:g1327.t1 | NC_039899.1 1e | C. arabica | 34.57 | 1,00E-06 | 97.00 | dicarboxylate transporter 1%2C chloroplastic-like |
| NODE_2373_length_247_cov_0.864706:g1327.t1 | chr8 | C. canephora | 34.57 | 4,00E-07 | 97.00 | 2-oxoglutarate/malate translocator%2C chloroplastic |
| NODE_2373_length_247_cov_0.864706:g1327.t1 | NC_040035.1 1eu | C. eugenioides | 34.57 | 6,00E-07 | 97.00 | dicarboxylate transporter 1%2C chloroplastic |
| NODE_2378_length_247_cov_1.83529:g1329.t1 | NC_039905.1 4e | C. arabica | 64.56 | 8,00E-32 | 97.00 | 1-deoxy-D-xylulose 5-phosphate reductoisomerase%2C chloroplastic-like |
| NODE_2378_length_247_cov_1.83529:g1329.t1 | chr4 | C. canephora | 64.56 | 3,00E-32 | 97.00 | 1-deoxy-D-xylulose 5-phosphate reductoisomerase%2C chloroplastic |
| NODE_2378_length_247_cov_1.83529:g1329.t1 | NC_040038.1 4eu | C. eugenioides | 64.56 | 4,00E-32 | 97.00 | 1-deoxy-D-xylulose 5-phosphate reductoisomerase%2C chloroplastic-like |
| NODE_2392_length_246_cov_1.71598:g1336.t1 | NC_039906.1 5e | C. arabica | 54.35 | 5,00E-09 | 85.00 | LOW QUALITY PROTEIN: dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 1%2C mitochondrial-like |
| NODE_2392_length_246_cov_1.71598:g1336.t1 | NC_040039.1 5eu | C. eugenioides | 54.35 | 3,00E-09 | 85.00 | dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 2%2C mitochondrial |

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| NODE_2418_length_245_cov_2.24405:g1347.t1 | chr2 | C. canephora | 56.06 | 1,00E-07 | 88.00 | Cysteine synthase |
| NODE_2418_length_245_cov_2.24405:g1347.t1 | NC_040036.1 2eu | C. eugenioides | 55.07 | 3,00E-07 | 92.00 | cysteine synthase-like isoform X1 |
| NODE_2419_length_245_cov_1.7619:g1348.t1 | NC_039917.1 10c | C. arabica | 36.07 | 4,00E-08 | 91.00 | gamma carbonic anhydrase 1%2C mitochondrial-like |
| NODE_2419_length_245_cov_1.7619:g1348.t1 | chr7 | C. canephora | 34.38 | 2,00E-08 | 95.00 | Gamma carbonic anhydrase 1%2C mitochondrial |
| NODE_2419_length_245_cov_1.7619:g1348.t1 | NC_040044.1 10eu | C. eugenioides | 36.07 | 3,00E-08 | 91.00 | gamma carbonic anhydrase 1%2C mitochondrial |
| NODE_2420_length_245_cov_1.55952:g1349.t1 | NC_039898.1 1c | C. arabica | 41.98 | 8,00E-14 | 98.00 | LOW QUALITY PROTEIN: lysine--tRNA ligase%2C chloroplastic/mitochondrial-like |
| NODE_2420_length_245_cov_1.55952:g1349.t2 | NC_039898.1 1c | C. arabica | 42.50 | 1,00E-13 | 98.00 | LOW QUALITY PROTEIN: lysine--tRNA ligase%2C chloroplastic/mitochondrial-like |
| NODE_2420_length_245_cov_1.55952:g1349.t1 | chr1 | C. canephora | 41.98 | 6,00E-14 | 98.00 | Lysine--tRNA ligase |
| NODE_2420_length_245_cov_1.55952:g1349.t2 | chr1 | C. canephora | 42.50 | 9,00E-14 | 98.00 | Lysine--tRNA ligase |
| NODE_2420_length_245_cov_1.55952:g1349.t1 | NC_040035.1 1eu | C. eugenioides | 41.98 | 1,00E-13 | 98.00 | lysine--tRNA ligase%2C chloroplastic/mitochondrial |
| NODE_2420_length_245_cov_1.55952:g1349.t2 | NC_040035.1 1eu | C. eugenioides | 42.50 | 2,00E-13 | 98.00 | lysine--tRNA ligase%2C chloroplastic/mitochondrial |
| NODE_2450_length_244_cov_1.59281:g1359.t1 | NC_039911.1 7e | C. arabica | 54.55 | 2,00E-11 | 95.00 | probable phosphoribosylformylglycinamide synthase%2C chloroplastic/mitochondrial |
| NODE_2450_length_244_cov_1.59281:g1359.t1 | chr7 | C. canephora | 54.55 | 7,00E-12 | 95.00 | Probable phosphoribosylformylglycinamide synthase%2C chloroplastic/mitochondrial |
| NODE_2450_length_244_cov_1.59281:g1359.t1 | NC_040041.1 7eu | C. eugenioides | 54.55 | 1,00E-11 | 95.00 | LOW QUALITY PROTEIN: probable phosphoribosylformylglycinamide synthase%2C chloroplastic/mitochondrial |
| NODE_2451_length_244_cov_0.886228:g1360.t1 | NC_039905.1 4e | C. arabica | 40.51 | 8,00E-08 | 92.00 | uncharacterized protein LOC113742678 |
| NODE_2451_length_244_cov_0.886228:g1360.t1 | chr4 | C. canephora | 37.33 | 1,00E-07 | 92.00 | Putative Uncharacterized RNA methyltransferase CT0009 |
| NODE_2451_length_244_cov_0.886228:g1360.t1 | NC_040038.1 4eu | C. eugenioides | 40.51 | 5,00E-08 | 92.00 | uncharacterized protein LOC113767750 |
| NODE_2456_length_244_cov_1.30539:g1362.t1 | NC_039904.1 4c | C. arabica | 48.72 | 3,00E-21 | 97.00 | adenylate kinase 4 |
| NODE_2456_length_244_cov_1.30539:g1362.t1 | chr4 | C. canephora | 48.72 | 1,00E-21 | 97.00 | Adenylate kinase B |
| NODE_2456_length_244_cov_1.30539:g1362.t1 | NC_040038.1 4eu | C. eugenioides | 48.72 | 2,00E-21 | 97.00 | adenylate kinase 4 |
| NODE_2465_length_243_cov_1.60241:g1366.t1 | NC_039906.1 5e | C. arabica | 53.75 | 4,00E-22 | 100.00 | aconitate hydratase%2C cytoplasmic |
| NODE_2465_length_243_cov_1.60241:g1366.t1 | chr5 | C. canephora | 53.75 | 1,00E-22 | 100.00 | Aconitate hydratase 2%2C mitochondrial |
| NODE_2465_length_243_cov_1.60241:g1366.t1 | NC_040039.1 5eu | C. eugenioides | 53.75 | 2,00E-22 | 100.00 | aconitate hydratase%2C cytoplasmic isoform X2 |
| NODE_2469_length_243_cov_0.891566:g1368.t1 | NC_039909.1 6e | C. arabica | 36.84 | 5,00E-10 | 95.00 | acetolactate synthase 2%2C chloroplastic-like |
| NODE_2469_length_243_cov_0.891566:g1368.t1 | chr10 | C. canephora | 36.84 | 1,00E-10 | 95.00 | Acetolactate synthase 2%2C chloroplastic |
| NODE_2469_length_243_cov_0.891566:g1368.t1 | NC_040040.1 6eu | C. eugenioides | 36.84 | 2,00E-10 | 95.00 | acetolactate synthase 2%2C chloroplastic |
| NODE_2471_length_243_cov_1.75904:g1370.t1 | NC_039900.1 2c | C. arabica | 51.72 | 7,00E-15 | 98.00 | peptide methionine sulfoxide reductase A1-like |
| NODE_2471_length_243_cov_1.75904:g1370.t2 | NC_039900.1 2c | C. arabica | 55.56 | 6,00E-26 | 100.00 | peptide methionine sulfoxide reductase A1-like |
| NODE_2471_length_243_cov_1.75904:g1370.t1 | chr2 | C. canephora | 51.72 | 1,00E-15 | 98.00 | Peptide methionine sulfoxide reductase |
| NODE_2471_length_243_cov_1.75904:g1370.t2 | chr2 | C. canephora | 55.56 | 5,00E-27 | 100.00 | Peptide methionine sulfoxide reductase |
| NODE_2471_length_243_cov_1.75904:g1370.t1 | NC_040035.1 1eu | C. eugenioides | 51.72 | 3,00E-15 | 98.00 | peptide methionine sulfoxide reductase A1-like |
| NODE_2471_length_243_cov_1.75904:g1370.t2 | NC_040035.1 1eu | C. eugenioides | 55.56 | 2,00E-26 | 100.00 | peptide methionine sulfoxide reductase A1-like |
| NODE_2478_length_243_cov_0.891566:g1372.t1 | NC_039903.1 3e | C. arabica | 41.38 | 6,00E-10 | 100.00 | ATP-dependent Clp protease ATP-binding subunit ClpA homolog CD4B%2C chloroplastic-like |
| NODE_2478_length_243_cov_0.891566:g1372.t1 | chr0 | C. canephora | 41.38 | 4,00E-10 | 100.00 | ATP-dependent Clp protease ATP-binding subunit clpA homolog CD4B%2C chloroplastic |

| | | | | | | |
|--|-----------------|----------------|--------|----------|--------|--|
| NODE_2478_length_243_cov_0.891566:g1372.t1 | NC_040037.1 3eu | C. eugenioides | 40.23 | 7,00E-10 | 100.00 | ATP-dependent Clp protease ATP-binding subunit ClpA homolog CD4B%2C chloroplastic-like |
| NODE_2483_length_243_cov_1.63855:g1374.t1 | NC_039898.1 1c | C. arabica | 100.00 | 4,00E-34 | 98.00 | uncharacterized protein LOC113739227 |
| NODE_2483_length_243_cov_1.63855:g1374.t1 | NC_040036.1 2eu | C. eugenioides | 92.98 | 1,00E-29 | 98.00 | uncharacterized protein LOC113759946 |
| NODE_2488_length_243_cov_1.31928:g1376.t1 | NC_039903.1 3e | C. arabica | 67.57 | 3,00E-29 | 100.00 | cysteine synthase%2C chloroplastic/chromoplastic-like isoform X2 |
| NODE_2488_length_243_cov_1.31928:g1376.t1 | chr3 | C. canephora | 67.57 | 1,00E-29 | 100.00 | Cysteine synthase%2C chloroplastic/chromoplastic |
| NODE_2488_length_243_cov_1.31928:g1376.t1 | NC_040037.1 3eu | C. eugenioides | 67.57 | 2,00E-29 | 100.00 | cysteine synthase%2C chloroplastic/chromoplastic-like isoform X2 |
| NODE_2533_length_241_cov_1.80488:g1394.t1 | NC_039900.1 2c | C. arabica | 50.67 | 3,00E-21 | 93.00 | LOW QUALITY PROTEIN: transketolase%2C chloroplastic-like |
| NODE_2533_length_241_cov_1.80488:g1394.t1 | chr2 | C. canephora | 50.67 | 1,00E-21 | 93.00 | Transketolase%2C chloroplastic |
| NODE_2533_length_241_cov_1.80488:g1394.t1 | NC_040036.1 2eu | C. eugenioides | 52.00 | 8,00E-22 | 93.00 | transketolase%2C chloroplastic-like |
| NODE_2536_length_241_cov_0.896341:g1396.t1 | NC_039911.1 7e | C. arabica | 69.49 | 3,00E-25 | 100.00 | lysine--tRNA ligase%2C cytoplasmic-like isoform X2 |
| NODE_2536_length_241_cov_0.896341:g1396.t1 | chr4 | C. canephora | 69.49 | 1,00E-26 | 100.00 | Putative Lysyl-tRNA synthetase%2C class II |
| NODE_2536_length_241_cov_0.896341:g1396.t1 | NC_040041.1 7eu | C. eugenioides | 69.49 | 1,00E-25 | 100.00 | lysine--tRNA ligase isoform X2 |
| NODE_2538_length_241_cov_1.80488:g1398.t1 | NC_039904.1 4c | C. arabica | 39.39 | 7,00E-09 | 89.00 | peptide deformylase 1A%2C chloroplastic-like |
| NODE_2538_length_241_cov_1.80488:g1398.t1 | chr4 | C. canephora | 39.39 | 5,00E-09 | 89.00 | Peptide deformylase 1A%2C chloroplastic |
| NODE_2538_length_241_cov_1.80488:g1398.t1 | NC_040038.1 4eu | C. eugenioides | 39.39 | 1,00E-08 | 89.00 | peptide deformylase 1A%2C chloroplastic |
| NODE_2540_length_241_cov_2.68902:g1400.t1 | NC_039898.1 1c | C. arabica | 46.43 | 3,00E-20 | 100.00 | alpha-glucan phosphorylase%2C H isozyme |
| NODE_2540_length_241_cov_2.68902:g1400.t1 | chr1 | C. canephora | 46.43 | 1,00E-20 | 100.00 | Alpha-glucan phosphorylase%2C H isozyme |
| NODE_2540_length_241_cov_2.68902:g1400.t1 | NC_040035.1 1eu | C. eugenioides | 46.43 | 2,00E-20 | 100.00 | alpha-glucan phosphorylase%2C H isozyme |
| NODE_2557_length_240_cov_1.39877:g1411.t1 | NC_039913.1 8c | C. arabica | 60.76 | 4,00E-20 | 100.00 | ATP-dependent zinc metalloprotease FTSH 4%2C mitochondrial-like isoform X2 |
| NODE_2557_length_240_cov_1.39877:g1411.t1 | chr8 | C. canephora | 60.76 | 2,00E-20 | 100.00 | ATP-dependent zinc metalloprotease FTSH 4%2C mitochondrial |
| NODE_2557_length_240_cov_1.39877:g1411.t1 | NC_040042.1 8eu | C. eugenioides | 60.76 | 3,00E-20 | 100.00 | ATP-dependent zinc metalloprotease FTSH 4%2C mitochondrial isoform X2 |
| NODE_2577_length_239_cov_1.80247:g1424.t1 | NC_039908.1 6c | C. arabica | 34.94 | 1,00E-08 | 100.00 | preprotein translocase subunit SECY%2C chloroplastic-like isoform X1 |
| NODE_2577_length_239_cov_1.80247:g1424.t1 | chr6 | C. canephora | 34.94 | 5,00E-09 | 100.00 | Preprotein translocase subunit SCY1%2C chloroplastic |
| NODE_2577_length_239_cov_1.80247:g1424.t1 | NC_040040.1 6eu | C. eugenioides | 34.94 | 8,00E-09 | 100.00 | preprotein translocase subunit SECY%2C chloroplastic |
| NODE_2594_length_239_cov_3.22222:g1430.t1 | NC_039907.1 5c | C. arabica | 44.62 | 5,00E-11 | 82.00 | trifunctional UDP-glucose 4%2C6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3%2C5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM1-like |
| NODE_2594_length_239_cov_3.22222:g1430.t1 | chr5 | C. canephora | 44.62 | 2,00E-11 | 82.00 | Probable rhamnose biosynthetic enzyme 1 |
| NODE_2594_length_239_cov_3.22222:g1430.t1 | NC_040039.1 5eu | C. eugenioides | 44.62 | 3,00E-11 | 82.00 | trifunctional UDP-glucose 4%2C6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3%2C5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM1-like |
| NODE_2603_length_239_cov_1.49383:g1434.t1 | NC_039912.1 8e | C. arabica | 50.00 | 3,00E-21 | 98.00 | LOW QUALITY PROTEIN: ribose-phosphate pyrophosphokinase 1-like |
| NODE_2603_length_239_cov_1.49383:g1434.t1 | chr2 | C. canephora | 50.62 | 2,00E-21 | 100.00 | Ribose-phosphate pyrophosphokinase 5%2C chloroplastic |
| NODE_2603_length_239_cov_1.49383:g1434.t1 | NC_040036.1 2eu | C. eugenioides | 50.62 | 4,00E-21 | 100.00 | ribose-phosphate pyrophosphokinase 1-like |
| NODE_2638_length_238_cov_2.07453:g1445.t1 | NC_039899.1 1e | C. arabica | 44.83 | 2,00E-11 | 75.00 | iron-sulfur protein NUBPL-like |
| NODE_2638_length_238_cov_2.07453:g1445.t2 | NC_039899.1 1e | C. arabica | 44.83 | 2,00E-11 | 75.00 | iron-sulfur protein NUBPL-like |
| NODE_2638_length_238_cov_2.07453:g1445.t1 | chr1 | C. canephora | 44.83 | 5,00E-12 | 75.00 | Iron-sulfur protein NUBPL |
| NODE_2638_length_238_cov_2.07453:g1445.t2 | chr1 | C. canephora | 44.83 | 5,00E-12 | 75.00 | Iron-sulfur protein NUBPL |

| | | | | | | |
|--|-------------------------|----------------|-------|----------|--------|---|
| NODE_2638_length_238_cov_2.07453:g1445.t1 | NC_040035.1 1eu | C. eugenioides | 44.83 | 1,00E-11 | 75.00 | iron-sulfur protein NUBPL |
| NODE_2638_length_238_cov_2.07453:g1445.t2 | NC_040035.1 1eu | C. eugenioides | 44.83 | 1,00E-11 | 75.00 | iron-sulfur protein NUBPL |
| NODE_2681_length_236_cov_1.84906:g1463.t1 | NC_008535.1 chloroplast | C. arabica | 43.42 | 1,00E-12 | 97.00 | acetyl-CoA carboxylase beta subunit |
| NODE_2696_length_236_cov_2.13836:g1473.t1 | NC_039904.1 4c | C. arabica | 38.96 | 2,00E-10 | 89.00 | uncharacterized protein LOC113739385 |
| NODE_2696_length_236_cov_2.13836:g1473.t1 | chr4 | C. canephora | 38.96 | 6,00E-11 | 89.00 | Putative Oxygen-independent coproporphyrinogen-III oxidase-like protein sll1917 |
| NODE_2696_length_236_cov_2.13836:g1473.t1 | NC_040038.1 4eu | C. eugenioides | 38.96 | 1,00E-10 | 89.00 | uncharacterized protein LOC113768482 |
| NODE_2701_length_235_cov_1.86076:g1475.t1 | NC_039910.1 7c | C. arabica | 36.47 | 1,00E-09 | 92.00 | xanthine dehydrogenase 1-like isoform X1 |
| NODE_2701_length_235_cov_1.86076:g1475.t1 | chr1 | C. canephora | 36.84 | 1,00E-09 | 92.00 | Aldehyde oxidase 4 |
| NODE_2701_length_235_cov_1.86076:g1475.t1 | NC_040041.1 7eu | C. eugenioides | 36.47 | 8,00E-10 | 92.00 | xanthine dehydrogenase 1-like isoform X1 |
| NODE_2703_length_235_cov_0.936709:g1476.t1 | NC_039905.1 4e | C. arabica | 66.23 | 1,00E-20 | 100.00 | ruBisCO large subunit-binding protein subunit beta%2C chloroplastic-like |
| NODE_2703_length_235_cov_0.936709:g1476.t1 | chr1 | C. canephora | 66.67 | 2,00E-21 | 74.00 | Chaperonin CPN60-2%2C mitochondrial |
| NODE_2703_length_235_cov_0.936709:g1476.t1 | NC_040038.1 4eu | C. eugenioides | 66.23 | 8,00E-21 | 100.00 | ruBisCO large subunit-binding protein subunit beta%2C chloroplastic |
| NODE_2705_length_235_cov_1.44304:g1477.t1 | NC_039905.1 4e | C. arabica | 37.66 | 2,00E-09 | 98.00 | NADP-specific glutamate dehydrogenase isoform X1 |
| NODE_2705_length_235_cov_1.44304:g1477.t1 | chr4 | C. canephora | 38.96 | 2,00E-10 | 98.00 | Putative NADP-specific glutamate dehydrogenase |
| NODE_2705_length_235_cov_1.44304:g1477.t1 | NC_040038.1 4eu | C. eugenioides | 37.66 | 9,00E-10 | 98.00 | NADP-specific glutamate dehydrogenase isoform X1 |
| NODE_2714_length_234_cov_3.57962:g1482.t1 | NC_039911.1 7e | C. arabica | 35.90 | 2,00E-12 | 97.00 | octanoyltransferase LIP2p%2C chloroplastic-like isoform X3 |
| NODE_2714_length_234_cov_3.57962:g1482.t1 | chr7 | C. canephora | 35.90 | 1,00E-12 | 97.00 | Plastidial lipoyltransferase 2 |
| NODE_2714_length_234_cov_3.57962:g1482.t1 | NC_040041.1 7eu | C. eugenioides | 34.62 | 2,00E-11 | 97.00 | octanoyltransferase LIP2p%2C chloroplastic-like isoform X2 |
| NODE_2721_length_234_cov_0.936306:g1485.t1 | NC_039908.1 6c | C. arabica | 41.51 | 2,00E-07 | 80.00 | uracil phosphoribosyltransferase isoform X2 |
| NODE_2721_length_234_cov_0.936306:g1485.t1 | chr6 | C. canephora | 41.51 | 5,00E-08 | 80.00 | Uracil phosphoribosyltransferase |
| NODE_2721_length_234_cov_0.936306:g1485.t1 | NC_040040.1 6eu | C. eugenioides | 41.51 | 2,00E-07 | 80.00 | uracil phosphoribosyltransferase |
| NODE_2763_length_233_cov_1.94872:g1498.t1 | NC_039917.1 10c | C. arabica | 55.56 | 5,00E-19 | 93.00 | bifunctional aspartokinase/homoserine dehydrogenase 1%2C chloroplastic-like |
| NODE_2763_length_233_cov_1.94872:g1498.t1 | chr10 | C. canephora | 55.56 | 2,00E-19 | 93.00 | Bifunctional aspartokinase/homoserine dehydrogenase%2C chloroplastic (Fragment) |
| NODE_2763_length_233_cov_1.94872:g1498.t1 | NC_040036.1 2eu | C. eugenioides | 55.56 | 3,00E-19 | 93.00 | bifunctional aspartokinase/homoserine dehydrogenase 1%2C chloroplastic-like |
| NODE_2764_length_232_cov_2.83871:g1499.t1 | NC_039908.1 6c | C. arabica | 33.80 | 6,00E-07 | 93.00 | D-lactate dehydrogenase [cytochrome]%2C mitochondrial |
| NODE_2764_length_232_cov_2.83871:g1499.t1 | chr6 | C. canephora | 32.88 | 1,00E-07 | 96.00 | D-lactate dehydrogenase [cytochrome]%2C mitochondrial |
| NODE_2764_length_232_cov_2.83871:g1499.t1 | NC_040040.1 6eu | C. eugenioides | 32.88 | 8,00E-08 | 96.00 | D-lactate dehydrogenase [cytochrome]%2C mitochondrial isoform X2 |
| NODE_2769_length_232_cov_2.73548:g1501.t1 | NC_039901.1 2e | C. arabica | 40.38 | 6,00E-08 | 68.00 | delta-1-pyrroline-5-carboxylate synthase |
| NODE_2769_length_232_cov_2.73548:g1501.t1 | chr2 | C. canephora | 40.38 | 2,00E-08 | 68.00 | Delta-1-pyrroline-5-carboxylate synthase |
| NODE_2769_length_232_cov_2.73548:g1501.t1 | NC_040036.1 2eu | C. eugenioides | 40.38 | 3,00E-08 | 68.00 | delta-1-pyrroline-5-carboxylate synthase isoform X2 |
| NODE_2784_length_232_cov_0.948387:g1508.t1 | NC_039909.1 6e | C. arabica | 60.47 | 3,00E-13 | 55.00 | acetolactate synthase 2%2C chloroplastic-like |
| NODE_2784_length_232_cov_0.948387:g1508.t1 | chr10 | C. canephora | 60.47 | 8,00E-14 | 55.00 | Acetolactate synthase 2%2C chloroplastic |
| NODE_2784_length_232_cov_0.948387:g1508.t1 | NC_040040.1 6eu | C. eugenioides | 60.47 | 1,00E-13 | 55.00 | acetolactate synthase 2%2C chloroplastic |
| NODE_2817_length_231_cov_1.91558:g1524.t1 | NC_039908.1 6c | C. arabica | 33.33 | 9,00E-09 | 98.00 | ferredoxin-dependent glutamate synthase%2C chloroplastic |

| | | | | | | |
|---|-----------------|----------------|-------|----------|--------|---|
| NODE_2817_length_231_cov_1.91558:g1524.t1 | chr6 | C. canephora | 33.33 | 3,00E-09 | 98.00 | Ferredoxin-dependent glutamate synthase 1%2C chloroplastic |
| NODE_2817_length_231_cov_1.91558:g1524.t1 | NC_040040.1 6eu | C. eugenioides | 32.00 | 2,00E-08 | 98.00 | ferredoxin-dependent glutamate synthase%2C chloroplastic |
| NODE_2850_length_230_cov_1.04575:g1539.t1 | NC_039904.1 4c | C. arabica | 42.50 | 1,00E-12 | 100.00 | uncharacterized protein LOC113739699 isoform X1 |
| NODE_2850_length_230_cov_1.04575:g1539.t1 | chr4 | C. canephora | 42.50 | 5,00E-13 | 100.00 | Putative D-tagatose-1%2C6-bisphosphate aldolase subunit GatY |
| NODE_2850_length_230_cov_1.04575:g1539.t1 | NC_040038.1 4eu | C. eugenioides | 42.50 | 7,00E-13 | 100.00 | uncharacterized protein LOC113768766 |
| NODE_2860_length_229_cov_1.58553:g1544.t1 | NC_039906.1 5e | C. arabica | 71.43 | 3,00E-10 | 46.00 | dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 2%2C mitochondrial-like |
| NODE_2860_length_229_cov_1.58553:g1544.t1 | NC_040039.1 5eu | C. eugenioides | 71.43 | 2,00E-10 | 46.00 | dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 2%2C mitochondrial |
| NODE_2866_length_229_cov_2.88158:g1549.t1 | NC_039908.1 6c | C. arabica | 30.77 | 1,00E-08 | 100.00 | 2-Cys peroxiredoxin BAS1%2C chloroplastic |
| NODE_2866_length_229_cov_2.88158:g1549.t1 | chr6 | C. canephora | 30.77 | 5,00E-09 | 100.00 | Putative 1-cysteine peroxiredoxin 1 |
| NODE_2866_length_229_cov_2.88158:g1549.t1 | NC_040040.1 6eu | C. eugenioides | 30.77 | 8,00E-09 | 100.00 | uncharacterized protein LOC113774880 |

Apêndice B. Características de sequências proteicas de *Coffea*. Gene1: *LRR receptor-like serine/threonine-protein kinase GSO2*. Gene2: *putative receptor-like protein kinase At3g47110*. *C. arabica1*: sequências proteicas da variedade Caturra (NCBI). *C. arabica2*: sequências proteicas da variedade Típica (dados não publicados). *C. arabica3*: sequências proteicas da variedade Bourbon (WCR). *C. canephora*: sequências proteicas do clone IF 200 (*Coffee Genome Hub*).

| Genoma | Sequência proteica | Anotação | Domínios |
|---------------------|--|---|---|
| BAC 70-22F | Gene2 | <i>putative receptor-like protein kinase At3g47110</i> | LRR1 |
| <i>C. arabica2</i> | g1- (Scaffold4162HRSCAF 4163) gene-0.17 mRNA-1 | <i>receptor-like serine threonine-kinase EFR</i> | LRR8 LRRNT2 Pkinase Pkinase |
| <i>C. arabica1</i> | g1-XP027093211.1 | <i>putative receptor-like protein kinase At3g47110 isoform X1</i> | LRR8 LRR8 LRRNT2 Pkinase |
| <i>C. arabica2</i> | g2- (Scaffold4162HRSCAF 4163) gene-0.13 mRNA-1 | <i>receptor-like serine threonine-kinase At3g47570</i> | LRR8 LRR8 LRRNT2 Pkinase |
| <i>C. arabica1</i> | g2-XP027093214.1 | <i>probable LRR receptor-like serine/threonine-protein kinase At3g47570</i> | LRRNT2 LRR8 LRR8 Pkinase |
| <i>C. arabica1</i> | g3- XP027090481.1 | <i>putative receptor-like protein kinase At3g47110</i> | LRRNT2 LRR8 LRR8 Pkinase |
| <i>C. arabica1</i> | g4- XP027090966.1 | <i>putative receptor-like protein kinase At3g47110 isoform X2</i> | LRRNT2 LRR1 LRR8 LRR8 Pkinase |
| <i>C. arabica1</i> | g5- XP027090965.1 | <i>putative receptor-like protein kinase At3g47110 isoform X1</i> | LRRNT2 LRR1 LRR8 LRR8 Pkinase |
| <i>C. arabica2</i> | g3- g4- (Scaffold5;HRSCAF=6) snap gene-90.101-mRNA-1 | <i>receptor-like serine threonine-kinase</i> | 6x LRRNT2 12x LRR8 9x Pkinase |
| <i>C. canephora</i> | g1-Cc10g13960 | <i>Putative Probable LRR receptor-like serine/threonine-</i> | LRRNT2 LRR8 |

| | | | |
|---------------------|--|--|---|
| | | <i>protein kinase At3g47570</i> | LRR8 Pkinase |
| <i>C. arabica2</i> | g4- (Scaffold34;HRSCAF=35)) snap-gene-17.62-mRNA-1 | <i>receptor-like serine threonine-kinase At3g47570</i> | LRRNT2 LRR8 LRR8 Pkinase |
| <i>C. arabica3</i> | g1- g35710.t1 | receptor kinase-like protein Xa21 isoform X1 | LRRNT2 LRR8 LRR8 Pkinase |
| <i>C. arabica3</i> | g2- g31764.t1 | receptor kinase-like protein Xa21 isoform X1 | LRRNT2 LRR8 LRR8 LRR8 Pkinase |
| <i>C. arabica2</i> | g5- (Scaffold35;HRSCAF=36)) augustus-gene-17.115-mRNA-1 | <i>probable LRR receptor-like serine threonine-kinase At3g47570 isoform X1</i> | LRRNT2 LRR8 LRR8 LRR8 Pkinase |
| <i>C. arabica3</i> | g3-g631.t1 | receptor kinase-like protein Xa21 isoform X1 | LRRNT2 LRR8 LRR8 LRR8 Pkinase |
| <i>C. canephora</i> | g2- Cc00g00860 | <i>Putative Probable LRR receptor-like serine/threonine-protein kinase At3g47570</i> | LRRNT2 LRR1 LRR8 Pkinase Tyr |
| <i>C. canephora</i> | g3- Cc08g08750 | <i>Putative LRR receptor-like serine/threonine-protein kinase EFR</i> | LRR8 LRR8 Pkinase |
| <i>C. arabica3</i> | g4-g21521.t1 | uncharacterized protein LOC113708477 | RVT_1 zf_RVT RVT_3 LRRNT2 Pkinase |
| <i>C. arabica3</i> | g5-g17545.t1 | uncharacterized protein LOC113708477 | RVT_1 zf_RVT RVT_3 LRRNT2 Pkinase |
| <i>C. canephora</i> | g4- Cc07g11480 | <i>Putative Cation/H(+) antiporter 2</i> | Na_H_Exchange |
| <i>C. arabica2</i> | g6- (Scaffold28;HRSCAF=29)) gene-24.49-mRNA-1 | <i>H(+) antiporter 2-like isoform X1</i> | Na_H_Exchange |
| <i>C. arabica2</i> | g7- (Scaffold25;HRSCAF=26)) gene-28.30-mRNA-1 | <i>H(+) antiporter 2-like isoform X1</i> | Na_H_Exchange |

| | | | |
|---------------------|--|---|---|
| <i>C. canephora</i> | g5- Cc07g04300 | <i>Putative uncharacterized protein</i> | TCP |
| <i>C. canephora</i> | g6- Cc08g14420 | <i>Putative Myosin heavy chain-related protein</i> | NT_C2 |
| <i>C. arabica2</i> | g8- (Scaffold2407;HRSCAF=2408) snap-gene-0.13-mRNA-1 | <i>calmodulin-binding transcription activator 3-like isoform X1</i> | CG-1 |
| <i>C. arabica2</i> | g9- (Scaffold24;HRSCAF=25) gene-17.117-mRNA-1 | <i>uncharacterized</i> | N6-adenineMlase |
| <i>C. arabica2</i> | g10- (Scaffold28;HRSCAF=29) gene-20.62-mRNA-1 | <i>guanine nucleotide-binding alpha-1 subunit isoform X2</i> | HECT_2 |
| <i>C. canephora</i> | g7- Cc07g10020 | <i>Putative CONTAINS InterPro DOMAIN/s</i> | HECT_2 |
| <i>C. arabica1</i> | g6- XP027120379.1 | <i>uncharacterized protein</i> LOC113737329 | rve |
| <i>C. arabica1</i> | g7- XP027102262.1 | <i>uncharacterized protein</i> LOC113737329 | Retrotrans gag rve |
| <i>C. arabica1</i> | g8- XP027064319.1 | <i>uncharacterized protein</i> LOC113690552 | Retrotrans gag RT RNaseH Integrase H2C2 rve |
| <i>C. arabica1</i> | g9- XP027118312.1 | <i>uncharacterized protein</i> LOC113735511 | Retrotrans gag RT RNaseH Integrase H2C2 rve |
| <i>C. arabica3</i> | g6-g6102.t1 | <i>LRR serine/threonine-protein kinase</i> GSO2 | - |
| <i>C. arabica3</i> | g7-g22356.t1 | <i>uncharacterized protein</i> LOC113703097 | - |
| <i>C. arabica3</i> | g8-g32952.t1 | <i>LRR serine/threonine-protein kinase</i> GSO2 | - |
| BAC 70-22F | Gene1 | <i>LRR serine/threonine-protein kinase</i> GSO2 | - |
| <i>C. arabica3</i> | g9-g19672.t1 | <i>uncharacterized protein</i> LOC113703097 | - |
| <i>C. arabica1</i> | g10- XP027080133.1 | <i>uncharacterized protein</i> LOC113703097 | - |
| <i>C. arabica3</i> | g10-g5288.t1 | <i>uncharacterized protein</i> LOC113703097 | - |