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**Jorge Lepikson Neto**

# “Influência da suplementação por flavonóides na formação da madeira em Eucalipto“

*“Influence of Flavonoid supplementation on Eucalyptus Wood formation”*

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**Universidade Estadual de Campinas**

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**Orientador: Prof. Dr. Gonçalo Amarante Guimarães Pereira**

*"Influence of Flavonoid supplementation on Eucalyptus Wood formation"*

Tese de doutorado apresentada ao Programa de Pós Graduação em Biologia Funcional e Molecular do Instituto de Biologia da Universidade Estadual de Campinas para obtenção do titulo de Doutor em Biologia Funcional e Molecular, na área de Bioquímica.

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**Resumo:**

O *Eucalyptus* é o gênero florestal mais plantado no Brasil e no mundo. É composto por mais de 700 espécies, com numerosas subespécies, variedades botânicas e híbridos. O Brasil é atualmente o primeiro produtor de celulose de fibra curta do mundo, e décimo produtor de papel em 2010, além de estar na vanguarda do conhecimento de produção de bicombustíveis, sendo seu setor florestal altamente desenvolvido. Uma das principais limitações para o uso da biomassa lignocelulósica de eucalipto para a produção de energia e seu melhor aproveitamento na produção de papel vem da sua estruturação da parede celular, com a lignina impedindo o acesso a celulose. Para aperfeiçoar este processo é necessário estudar as características da parede celular e dos genes que controlam sua formação. Os flavonóides narigenin-chalcona e narigenin sintetizados respectivamente pelos genes chalcone synthase (CHS) e isomerase (CHI), tem comprovada influência na lignificação de diversas espécies vegetais e expressão diferencial observada em diferentes espécies de Eucalipto, sendo desta forma o estudo da sua influência na formação da madeira em Eucalipto um potencial ponto para o desenvolvimento de novos produtos para o setor florestal brasileiro visando o melhoramento do rendimento da espécie. Desta forma a presente tese de doutorado analisou a influência destes flavonóides na formação da madeira em um híbrido comercial de *Eucalipto grandis* x *Eucalipto Urophylla*, caracterizando quimicamente madeira e avaliando as alterações no perfil transcripcional de mudas suplementadas, estando assim seus resultados diretamente ligados a ambição do país, hoje maior produtor mundial de celulose, em permanecer como referencia no setor.

**Abstract:**

The genus Eucalyptus is the most planted forest in Brazil and worldwide. It comprises more than 700 species, with numerous subspecies, botanical varieties and hybrids. Brazil is currently the largest producer of hardwood pulp in the world, and tenth paper producer in 2010, in addition to being at the forefront of knowledge of biofuel production, with its highly developed forestry sector. A major limitation to the use of lignocellulosic biomass for the production of eucalyptus energy and its better use in paper production comes from its structure of the cell wall with lignin preventing access to cellulose. To optimize this process it is necessary to study the characteristics of the cell wall and the genes that control their formation. Flavonoids narigenin-chalcone and narigenin respectively synthesized by genes chalcone synthase (CHS) and isomerase (CHI), has proven influence on lignification in various plant species and differential expression observed in different species of Eucalyptus, and thus the study of their influence on wood formation in eucalyptus a potential for the development of new products for the Brazilian forest sector aimed at improving the performance of the species. Thus the present doctoral thesis examined the influence of these flavonoids in wood formation in a commercial hybrid *Eucalyptus grandis* x *Eucalyptus Urophylla*, characterizing its wood chemically and evaluating changes in the transcriptional profile of seedlings supplemented with flavonoids. Results are therefore directly linked to the ambition of the country, today world's largest producer of pulp, to remain as a reference in the sector.

# Sumário

# 1- Introdução

## 1.1. O Eucalipto e sua importância econômica

O gênero *Eucalyptus* é composto por cerca de 500 espécies e 200 híbridos, sendo endêmico da Austrália e Tasmânia, com poucas espécies ocorrendo naturalmente fora destes locais (Ladiges, Udovicic, & Nelson, 2003).

Os eucaliptos crescem rápido, suportam solos pobres em nutrientes e possuem madeira de boa qualidade, motivos pelos qual o *Eucalyptus* é o principal gênero cultivado nas plantações industriais existentes no mundo: cerca de 20 milhões de hectares plantados em mais 90 países (Paiva et al. 2011).

A maioria das espécies de *Eucalyptus* se caracteriza por serem árvores típicas de floresta altas, atingindo alturas que variam entre 30 e 50 metros. Algumas espécies podem atingir excepcionalmente 100 metros de altura, sendo consideradas as árvores florestais latifoliadas mais altas do mundo (Boland et al. 2006).

Outras espécies comuns de *Eucalyptus* são aquelas típicas de florestas abertas, com árvores menores que atingem de 10 a 25 metros (Boland et al. 2006)). Cerca de 30 a 40 espécies são arbustivas (conhecidas como “Malees”) e se caracterizam por possuírem diversos troncos oriundo de um único núcleo lenhoso subterrâneo. Apesar da grande variedade em relação ao habitat e aparência, todas as espécies de eucalipto devem possuir características comuns para serem classificadas dentro do gênero como, por exemplo, a presença de glândulas de óleo nas folhas, tipo de flores e frutos, entre outros descritores (Boland et al. 2006). Entretanto, a característica morfológica mais importante do eucalipto seja possivelmente a sua casca, sendo que os diversos tipos distintos de casca são capazes de caracterizar grupos de espécies estreitamente relacionadas (Boland et al. 2006).

Devido à grande quantidade de espécies, o gênero *Eucalyptus* possui uma alta gama de adaptações edafoclimáticas, podendo ser encontradas espécies que se adaptam bem tanto em temperaturas negativas (até -18 ºC) quanto em climas quentes (+35ºC), e em solos que apresentam uma variação desde arenosos a encharcados (Silva, 2001).

No Brasil, o eucalipto é responsável pelo abastecimento da maior parte do setor industrial de base florestal. Atualmente, existem cerca de 4,5 milhões de hectares de florestas plantadas de *Eucalyptus* no Brasil (Bracelpa, 2011). O segmento de celulose e papel é composto por aproximadamente 220 empresas distribuídas em 450 municípios, de 17 estados, e utiliza madeira exclusivamente de florestas plantadas. Segundo a Sociedade Brasileira de Silvicultura, em 2010 a produção de

papel alcançou 9,8 milhões de toneladas (aumento de 4,4% em relação ao ano anterior) e a de celulose 14 milhões de toneladas (aumento de 6,4% em relação ao ano anterior). Isso tornou o Brasil o maior produtor mundial de celulose de eucalipto (Bracelpa, 2011). No setor de carvão vegetal, a produção atinge anualmente a marca de 18,8 milhões de metros cúbicos (70% da produção nacional). Outro setor importante é o de chapa de fibra que tem uma produção anual de 558 mil $m^3$, dos quais a madeira de eucalipto é responsável por 100% da produção nacional (Bracelpa, 2011). No setor de chapas de fibra aglomerada, a produção perfaz 500 mil $m^3$, representando quase 30% da produção nacional (Bracelpa, 2011).

As receitas de exportação desses produtos florestais atingiram US$ 7,4 bilhões em 2007 e, apesar de apresentar grande queda devido à crise de 2009, em 2010 o setor deu sinais de recuperação com aumento de 33% em relação ao ano anterior nas exportações, totalizando US$ 6,7 bilhões. A receita de exportações de celulose registrou 41,2% de aumento em 2010, chegando a US$ 4,7 bilhões, contribuindo expressivamente na economia do país, uma vez que o setor de base florestal emprega, direta e indiretamente, 6,5 milhões de pessoas em todos os segmentos (Bracelpa 2011).

Outra característica importante da espécie é a alta capacidade de produção de biomassa - até 100 $m^3$/ha/ano de madeira rica em fibra de celulose (Bracelpa, 2011) - e uma considerável habilidade no seqüestro de carbono (10-14 ton/ha/ano), sendo que este saldo se mantém positivo mesmo quando considerada a emissão de $CO_2$ proveniente da produção de carvão e papel (Bracelpa, 2011).

Nos últimos anos a demanda por fontes de energia alternativa vem aumentando cada vez mais, principalmente devido à necessidade da substituição da plataforma petroquímica, com um desejo crescente por parte da sociedade, dos governos e da comunidade científica em se desenvolver fontes de energia sustentáveis (Pu et al. 2008). Dentre as principais alternativas para a produção de biocombustíveis, a biomassa lignocelulósica assume posição de destaque como umas das fontes de energia sustentável mais promissora, principalmente a madeira e fibras produzidas em áreas de silvicultura e em áreas agrícolas marginais (Mansfield 2009). A partir da biomassa é possível utilizar seus principais componentes (celulose, hemicelulose e lignina) como fonte de carbono para produção de biocombustíveis e, assim, substituir a utilização de combustíveis fosseis, complementando as culturas já existentes e aumentando a diversidade de matéria prima produtora de combustíveis ( Zhu and Pan 2010; Yáñez-S et al. 2012).

Espécies arbóreas de rápido crescimento como *Eucalyptus* e *Populus* tem enorme potencial para a aplicação na produção de combustível de segunda geração

(Carroll and Somerville 2009; Hinchee et al. 2009; Mansfield 2009; Richard 2010; Somerville et al. 2010; Mizrachi et al. 2011; Séguin 2011). *Eucalyptus* e seus híbridos estão entre os líderes mundiais de produção de biomassa e suas ótimas propriedades da madeira, alta produtividade e ampla adaptabilidade poderão permitir a produção sustentável e eficiente de etanol de segunda geração.

A principal limitação para o uso da biomassa lignocelulósica está na sua recalcitrância à degradação, ligada à estrutura e composição das paredes celulares lignificadas (Séguin 2011). A sua complexa estrutura e composição impedem o aproveitamento total dos açucares fermentáveis, sendo o processo de lignificação justamente um dos principais fatores que determinam tal complexidade. Sendo assim, vários esforços vêm sendo concentrados para melhor se compreender este processo e produzir árvores com menos lignina ou que sejam mais susceptíveis à degradação química (Weng et al. 2008; Mansfield 2009).

Atualmente a matéria prima utilizada para produção de biocombustiveis provém das culturas de cana de açúcar, milho e soja (Chisti 2007). Apesar de já estabelecida, esta parece não ser a melhor estratégia energética a longo prazo, uma vez que a atual capacidade de produção agrícola não é suficientemente capaz de suprir sustentavelmente a demanda, além de já existir uma competição por terras agriculturáveis para produção de alimentos (Mansfield et al. 2012).

Além disso, o Brasil possui altos níveis de produtividade de eucalipto comparados à média mundial devido, principalmente, às condições climáticas aliadas aos investimentos em pesquisa e desenvolvimento no setor, especialmente nas técnicas convencionais de melhoramento genético. Em 2010, a produtividade média da madeira proveniente de *Eucalyptus* alcançou a marca de 44 $m^3$/ha/ano, enquanto outros produtores, como Chile, África do Sul e Portugal, apresentaram níveis abaixo de 30 $m^3$/ha/ano (Bracelpa, 2011).

Sendo o Brasil o maior produtor mundial de celulose de eucalipto (Bracelpa, 2011) além de ser um dos maiores produtores mundiais de bioetanol - na safra de 2008/2009 produziu 27,5 bilhões de litros de etanol a partir do caldo da cana-de-açúcar (Unica, 2010) - é oportuno que a pesquisa científica do país direcione seus esforços a juntar e ampliar esses dois grandes mercados para continuar na vanguarda do conhecimento mundial. Para isso, é imprescindível a compreensão dos mecanismos de formação da parede celular e sua influência na composição final da madeira.

## 1.2. A parede celular

A parede celular do eucalipto é composta aproximadamente por 50% celulose, 25% hemicelulose e 25% lignina. Essa constituição química varia entre espécies do mesmo gênero e, em menor escala, entre os exemplares da mesma espécie (Kirst et al. 2004). Esses compostos são formados a partir da combinação de alguns elementos químicos, considerada como obedecendo à seguinte proporção geral: 50% de carbono, 44% de oxigênio, 6% de hidrogênio, 0,1% de nitrogênio e 0,3% de cinzas (material inorgânico) (Ragland et al. 1991).

A parede celular tem várias funções: regula a expansão celular, contribui para a adesão entre as células, funciona como barreira para potenciais patógenos e determina as propriedades físicas da planta, bem como a resistência mecânica que permite que algumas plantas alcancem grandes alturas (Boudet 2000; Grima-pettenati et al. 2012). A parede celular também atua como exoesqueleto, controlando a forma da árvore, e é necessária para regular as relações hídricas das plantas, pois determina a relação entre turgor e volume celular, sendo o crescimento vegetal limitado principalmente pela capacidade de expansão da parede celular. As células do xilema, tais como as encontradas na madeira, são notáveis por possuir parede secundária altamente espessada e reforçada por lignina (Fukuda 1996; Plomion et al. 2001).

O desenvolvimento do xilema secundário pode ser dividido em cinco eventos sequenciais: divisão celular, elongação, biossíntese da parede celular, lignificação e morte celular programada. Em cada fase, a expressão ordenada de famílias de genes é regulada por sinais ambientais e do desenvolvimento da planta, que influenciam a composição e a morfologia da parede celular das células do xilema, sendo assim o fator mais importante na determinação das propriedades da biomassa lignocelulósica (Chaffey et al. 2002).

As microfibrilas de celulose são estruturas rígidas que contribuem para a resistência e a disposição estrutural da parede celular. Os glucanos individuais que constituem as fibrilas estão firmemente alinhados e ligados entre si, formando uma fita altamente ordenada que exclui água e é relativamente inacessível ao ataque enzimático. Como resultado, a celulose é muito forte, muito estável e resistente à degradação (Fukuda 1996; Plomion et al. 2001; Mansfield 2009; Mansfield et al. 2012).

As diferentes funções da parede celular refletem sua composição entre os diferentes tipos celulares e processos de diferenciação celular. Acredita-se que até 15% dos genes contidos no genoma vegetal possam estar envolvidos com síntese da parede celular e sua regulação (Darley et al. 2001). Um grande número de genes também é necessário para a síntese de polímeros da parede celular, como lignina,

celulose, xilano, xiloglucano, pectinas, proteínas estruturais e outros componentes, bem como o envolvimento de genes relacionados a hormônios, citoesqueleto e sua regulação (Somerville et al. 2010). Figura 1.

Assim, para entender como as plantas constroem seus diferentes tipos de parede celular, é necessário conhecer os genes que participam das vias metabólicas de síntese e aqueles que participam da sua regulação, uma vez que a formação da parede celular secundária é finamente regulada por uma cascata de fatores de transcrição. (Demura and Fukuda 2007; Zhong et al. 2007; Zhong and Ye 2007; Zhong et al. 2008; Zhong et al. 2010; Zhang et al. 2011; Zhao and Dixon 2011).

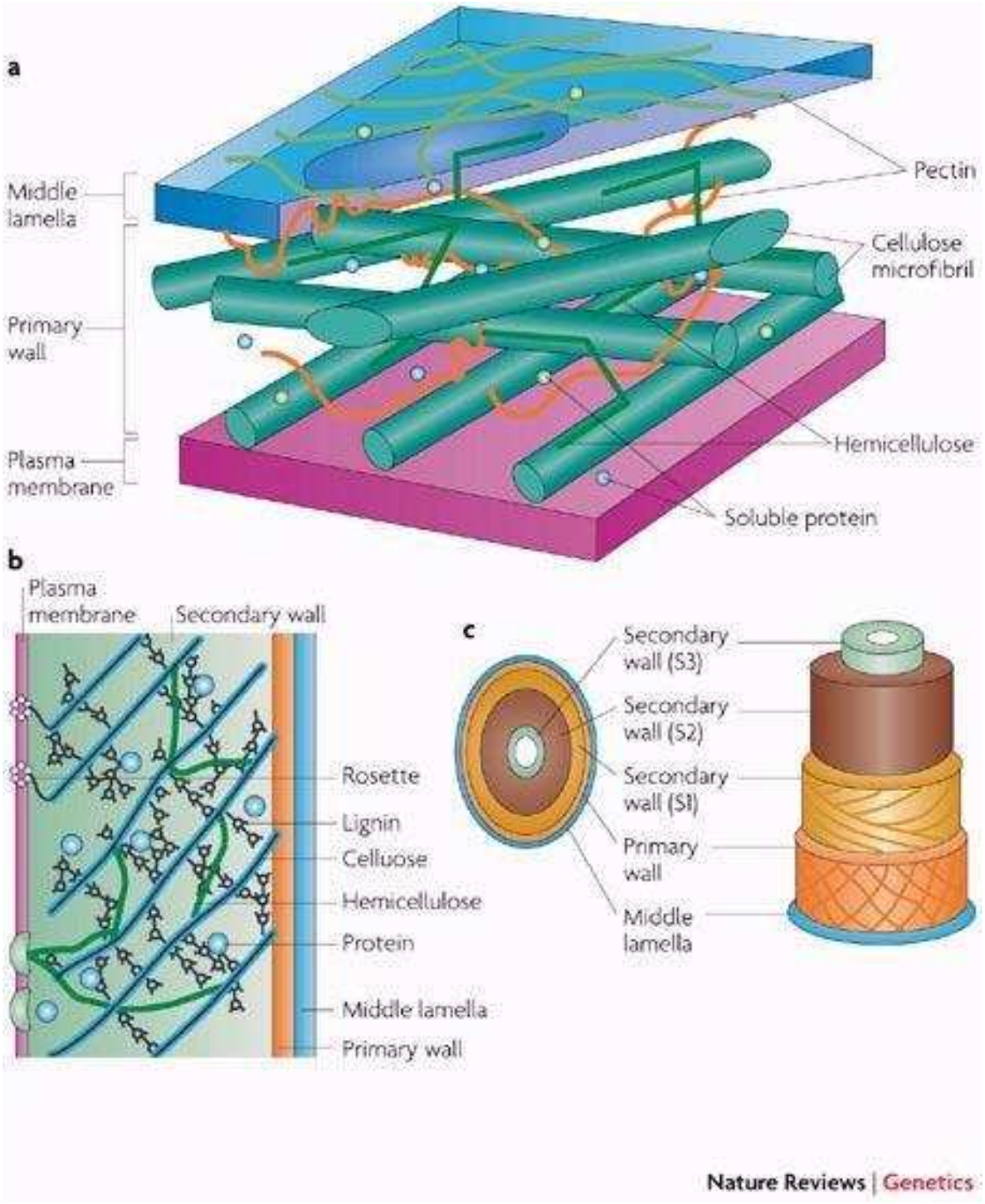


Figura 1: A) Parede celular contendo microfibrilas de celulose, hemicelulose, lignina, pectina e proteínas solúeis; B) Celulose sintáse em forma de complexos roseta; C) Lignificação ocorre nas camadas S1, S2 e S3 da parede celular; retirado de: Sticklen 2008.

### 1.3 A Lignina e a via de fenilpropanóides.

A lignina é um termo genérico para um grupo grande de polímeros aromáticos resultantes do acoplamento oxidativo combinatorial de fenilpropanóides específicos (4-*hydroxyphenylpropanoids)* (Boerjan et al. 2003; Ralph et al. 2004).

A lignina é encontrada na parede celular de vários tipos de tecidos de sustentação e vascular, especialmente traqueídes e elementos de vaso, correspondendo entre 15 a 35% do peso seco da madeira. Ela é depositada, sobretudo, no espessamento da parede secundária, mas também pode ocorrer na parede primária e na lamela média em íntimo contato com a celulose e hemicelulose presentes (Vanholme et al. 2010).

A composição química elementar da lignina inclui carbono, hidrogênio e oxigênio, mas a contribuição relativa destes elementos pode variar, principalmente se a lignina for obtida de coníferas ou de folhosas, além de depender do método de isolamento da mesma. A rigidez mecânica da lignina fortalece os caules e o tecido vascular, permitindo o crescimento ascendente e possibilitando que a água e os sais minerais sejam conduzidos através do xilema sob pressão negativa, sem haver colapso do tecido (Weng et al. 2010).

A sua estrutura química consiste de três monômeros que diferem entre si pelo grau de metilação, sendo eles: álcool trans-coniferílico, álcool trans-sinapílico e álcool para-trans-cumárico. Estes três álcoois levam a formação dos diferentes tipos de lignina: guaicílica (G), sinapílica (S) e cumarílica (H), respectivamente. Em angiospermas, a lignina S é predominantemente encontrada em fibras enquanto a G está mais presente em vasos, e a última lignina, H, é encontrada em quantidade muito inferior, sendo mais presente em gramíneas (Besseau et al. 2007; Vanholme et al. 2010; Grima-pettenati et al. 2012;).

A diferença na composição das ligninas e a quantidade de cada um dos tipos de lignina influem nas características da madeira (Kirst et al. 2004). Taxas elevadas de S/G são vantajosas para a produção de celulose, papel e bioenergia, devido a maiores taxas de deslignificação, gerando menor consumo de produtos químicos e rendimentos mais elevados (Rodrigues et al. 1999; Gomes et al. 2008;).

Uma grande quantidade de genes é atribuída como participante da formação da lignina e, apesar de sua maioria já ter sido caracterizada, a via é constantemente revisitada e ainda é motivo de grande debate em algum nível de sua síntese (Boerjan et al. 2003; Grima-pettenati et al. 2012).

A síntese de lignina envolve a via geral de fenilpropanóides, começando pela desaminação da fenilalanina levando a produção de ésteres de *hydroxycinnamoyl-CoA* (Grima-pettenati et al. 2012). As principais enzimas que participam desta cascata de

reações são: *phenylalanine ammonia-lyase* (PAL), *cinnamate 4-hydroxylase* (C4H) e *4-coumarate-CoA ligase* (4CL) e posteriormente, *ferulate 5-hydroxylase* (F5H), *cinnamoyl-Co-A* NADP *reductase* (CCR), *cinnamyl alcohol dehydrogenase* (CAD), que participam das reações da etapa que antecede à polimerização da lignina (Boudet 2000; Darley et al. 2001; Boudet et al. 2003;).

Apesar do esforço realizado na pesquisa, especialmente nos últimos anos, a regulação fisiológica das taxas de biossíntese e a disposição espacial e temporal das unidades monoméricas que compõem o polímero de lignina ainda continua pouco entendida, principalmente devido a existência de diversos grupos separados de enzimas relacionados com a sua produção, e a grande intersecção de vias metabólicas a estes relacionados. (Ferrer et al. 2008).

Além da deposição natural destes compostos, sua biossíntese pode também ser induzida por varias condições de estresses bióticos e abióticos, tais como infecção, ferimento, patógenos, estresse metabólico e perturbações na parede celular (Caño-Delgado et al. 2003; Tronchet et al. 2010).

As vias de flavonoides e lignina estão intimamente relacionadas, tendo enzimas e intermediários em comum. Fazem parte da via de fenilpropanóides, sintetizados em organismos vegetais a partir do aminoácido fenilalanina (Besseau et al. 2007) (ver Figura 2). O nome "fenilpropanóide" é derivado da junção do grupo fenila (anel aromático) e uma cadeia lateral de três carbonos (grupo propila).

Os flavonóides *narigenin-chalcone* e *naringenin* são intermediários do metabolismo de fenilpropanóides em plantas, sendo estes sintetizados pelas enzimas *chalcone sintase* (CHS) e *chalcone isomerase* (CHI), respectivamente. Existem estudos mostrando que estes flavonoides influenciam o crescimento de diferentes plantas inibindo a síntese de lignina (Chen et al. 2004; Deng et al. 2004; Chen et al. 2005; Chen et al. 2011), e estes efeitos parecem residir na inibição de enzimas chave da via de ligninas, principalmente a *4-coumarate CoA* Ligase sintetizada pelo gene 4Cl. O seu produto, *p-coumaroyl – CoA*, está situado na junção das rotas metabólicas levando a produção de flavonóides ou lignina *sensu stricto*, sendo o substrato comum a ambas (Voo et al. 1995; Campbell and Sederoff 1996; Besseau et al. 2007).

Estudos anteriores demonstraram que a quantidade e a composição monomérica da lignina pode ser reduzida e modificada pela inibição do gene 4CL (Lee et al. 1997; Tamagnone et al. 1998). Também foi demonstrado que *narigenin-chalcone* e *narigenin* inibem a atividade de 4CL *in vitro* e promovem a inibição do crescimento de diversas gramíneas, como milho (*Zea Mays*), arroz (*Oryza sativa*) e *Echinochloa oryzicola,* uma erva daninha (Deng et al 1999). Também foi demonstrado que, em

*Pinus,* a supressão do gene 4Cl afetou o fénotipo das plantas, resultando em plantas anãs (Wagner et al. 2009). Por outro lado, em *Aspen* ocorreu o efeito inverso, resultando em plantas com crescimento acelerado (Hu et al. 1999).

Dessa forma, fica claro que estes compostos contribuem para a formação e o desenvolvimento de diversos vegetais e que o estudo da sua suplementação em *Eucalyptus* é de fundamental importância no entendimento da lignificação do mesmo, permitindo uma análise ampla e integrada da influência destes flavonóides na composição química da madeira e na sua expressão gênica.

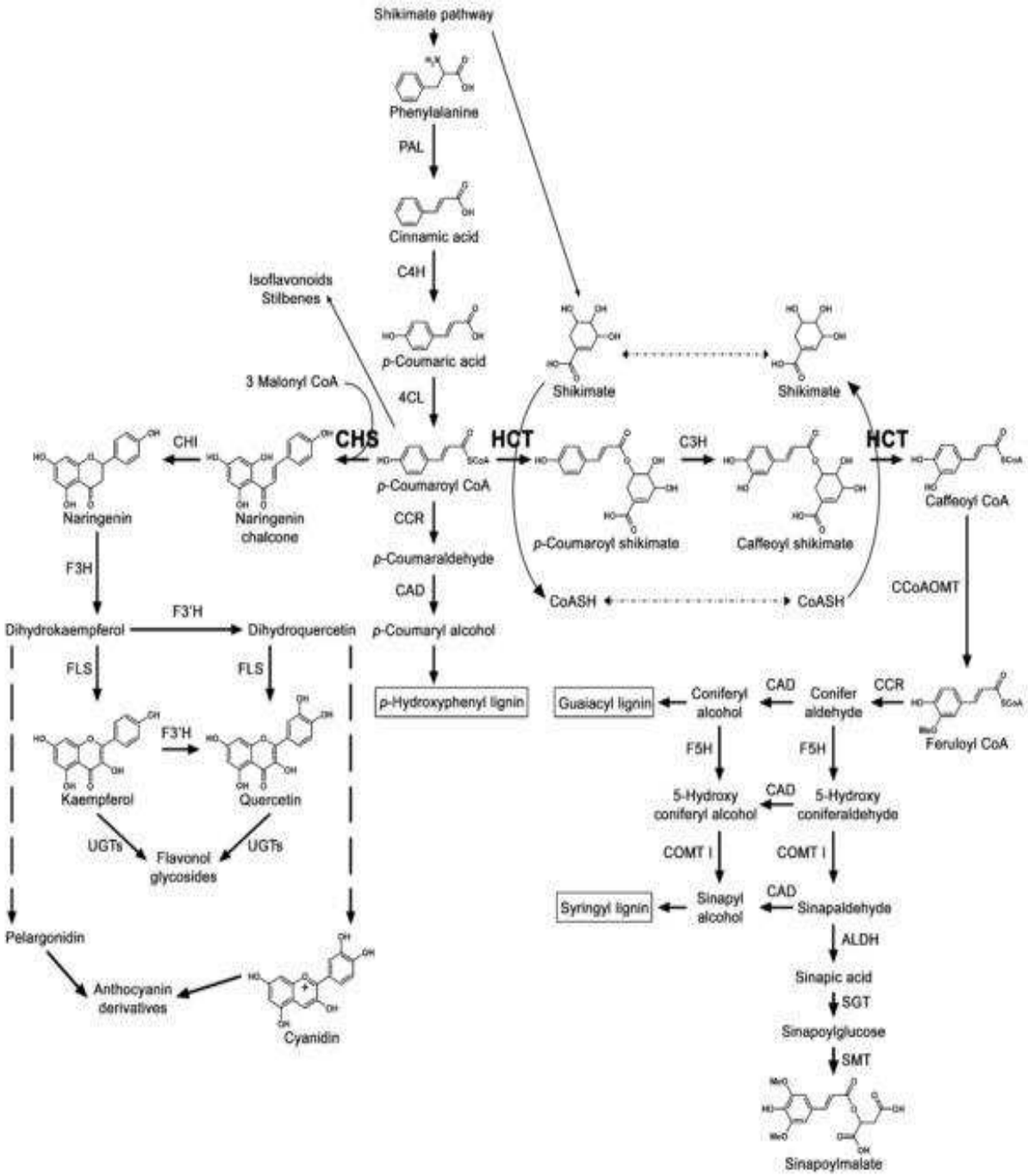


Figura 2: Vista conjunta das vias de flavonoides e lignina. Genes representados: ALDH, *aldehyde dehydrogenase*; C3H, *p-coumarate 3-hydroxylase*; C4H, *C4-hydroxylase*; F5H, *ferulate 5-hydroxylase*; CAD, *cinnamyl alcohol dehydrogenase*; CCoAOMT, *caffeoyl-CoA O-methyltransferase*; CCR, *cinnamoyl-CoA reductase*; CHI, *chalcone isomerase*; 4CL, *4-coumaroyl-CoA ligase*; COMT I, *caffeic acid O-methyltransferase*; F3H, *flavanone 3-hydroxylase*; F39H, *flavonoid 39-hydroxylase*; FLS, *flavonol synthase*; HCT, *hydroxycinnamoyl-CoA shikimate;* PAL, *phenylalanine ammonia lyase*; SGT, *sinapate UDPglucose sinapoyltransferase*; SMT, *sinapoylglucose malate sinapoyltransferase*; UGTs, *UDP sugar glycosyltransferases* (Retirado de Besseau, 2007).

### 1.4 Estresse, flavonídes e lignificação

Todos os fenilpropanóides são formados a partir do ácido cinâmico (cinamato) que, por sua vez, é formado a partir do aminoácido fenilalanina pela ação da enzima PAL (*phenylalanine ammonia lyase*) sendo o ponto de encontro entre o metabolismo primário (via do shikimato) e secundário (Dixon and Paiva 1995).

Muitos fenilpropanóides simples (com o esqueleto de carbono C6-C3 derivado da fenilalanina) são produzidos a partir do cinamato através de varias reações de hidroxilação, metilação e ou desidratação, ai se incluindo os precursores da lignina: álcool trans-coniferílico, álcool trans-sinapílico e álcool para-trans-cumárico (Dixon and Paiva 1995; Vanholme et al. 2010).

Estresse e a via de fenilpropanóides estão intimamente ligados com um grande número de fenilpropanóides sendo produzidos em resposta ao estresse (figura 3), sendo derivados do esqueleto C15 dos flavonóides e sintetizados via CHS (*chalcone synthase*) pela condensação de *p-coumaroyl-CoA* e três moléculas de *malonyl-CoA* (Harbone 1988).

A principal função deste fenilpropanóides é de proteção, estresses abióticos, como a seca, salinidade, temperaturas extremas, toxicidade química e estresse oxidativo são ameaças sérias para a agricultura sendo a principal causa de perda de culturas em todo o mundo, reduzindo o rendimento médio para a maioria das principais plantas de cultura por mais de 50% (Wang et al. 2004). Alguns compostos são induzidos em resposta a ferimentos ou alimentação causada por herbívoros, antocianinas e flavonas aumentam em resposta a altos níves de luz e irradiação ultravioleta induz a produção de flavonóides e de sinapato em arabidopsis (Dixon and Paiva 1995). Este ultimo é um intermediário na biossíntese da lignina siringil (S) em angiospermas, e em alguns taxóns serve como um precursor para a metabolitos secundários solúveis (Ruegger et al. 1999).

Também é sugerido que, em *arabidopsis*, o acúmulo de um ou mais intermediários da via de flavonóides promove a repressão de toda a via de fenilpropanoides ou de ramos da via, levando à produção de compostos específicos (Li et al. 1993). Esse mecanismo serviria para balancear a via e existem precedentes que demonstram que produtos da via podem regulá-la como, por exemplo, o ácido trans-cinâmico, produto de PAL, bloqueando a ação de CHS e da própia PAL (Bolwell et al. 1988; Mavandad et al. 1990), além da existência de *motifs* comuns aos promotores dos dois genes (Dixon and Harrison 1990). Esta flexibilidade seria importante para

promover alternativas biossintéticas diversas em resposta a diferentes estímulos ambientais e de desenvolvimento (Dixon and Paiva 1995).

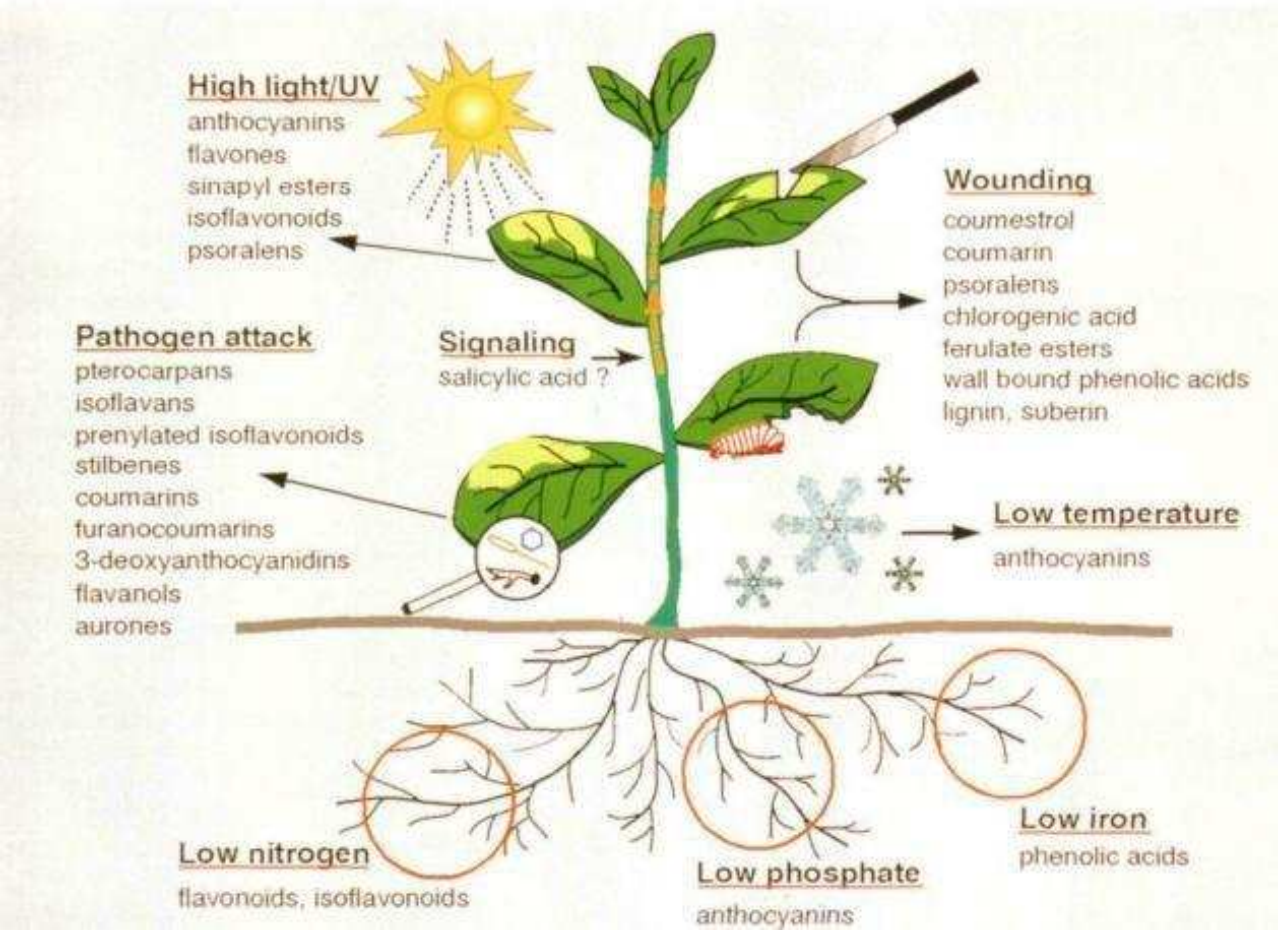


Figura 3: Exemplos de fenilpropanóides induzidos por estresse. Retirado de (Dixon and Paiva 1995)

Os flavonóides são um grupo grande e diversificado de importantes metabólitos, envolvidos com inúmeras funções no desenvolvimento e crescimento das plantas. Muitas dessas funções estão envolvidas com atração de vetores animais, polinização, dispersão de sementes e reabsorção de nutrientes minerais de folhas senescentes. Outras funções incluem promover vantagens competitivas para o crescimento em circunstâncias estressantes, como por exemplo, aumentar a tolerância a fatores abióticos, defesa contra herbívoros e patógenos. Devido a sua importância, esse grupo de metabólitos encontra-se presente em todo o reino vegetal, sendo investida grande energia metabólica para a sua produção (Andersen & Markham 2006).

Chalconas, dihidrochalconas e auronas são três grupos distintos que constituem mais de 900 flavonóides descritos e são mais conhecidos como pigmentos de coloração amarela e laranja em flores de plantas, mas que se distinguem de outros flavonóides devido a sua estrutura de cadeia aberta de três carbonos. Esses flavonóides não se restringem apenas às flores estando presente em diversos tecidos vegetais e são convertidos a sua respectiva flavona pela atuação da enzima *chalcone isomerase* (CHI). Central para estas reações e para o metabolismo dos flavonóides esta a formação da narigenin-chalcona através da condensação de três moléculas de malonyl-CoA e uma de p-coumaroyl-CoA catalisanda pela enzima *chalcone synthase* (CHS) (Andersen & Markham 2006).

Flavonóides são considerados reguladores naturais do fluxo de auxina em plantas, atuando junto a complexos de proteínas de membrana, e foi demonstrado em mutantes de *arabidopsis* que a acumulação de flavonóides era dependente das condições de luz e controlada pela expressão de CHS, com sua acumulação resultando em redução do crescimento da planta devido à inibção do transporte de auxina (Besseau et al 2007).

A expressão de genes que codificam enzimas da via de flavonóides também é dependente de luz, no entanto se acumulam em raízes de plantas sem acesso a luz se seus brotos estiverem expostos, podendo assim serem transportados pela planta. Da mesma forma, foi demonstrado que após a aplicação de flavonóides na raiz da planta estes podem ser transportados por longas distâncias para tecidos vasculares através de transporte de célula à célula.

Outro exemplo dessa flexibilidade é a via metabólica da raafinose, que é uma familia de oligossacarideos que atuam como transporte de carboidratos no floema, compostos de armazenamento e agentes metabólicos que combatem o estresse. Estudos recentes em *Populus thichocarpa* demonstram que a super-expressão dos genes dessa via *galactinol synhtase* (GolS) e *raafinose synthase* (RaFs) resultam em formação de madeira de tensão, maiores quantidades de celulose e aumento da biomassa total (Unda et al. 2012; Unda 2012).

Em suma, apesar do grande potencial de utilização do material lignocelulósico de origem florestal para a produção de energia, este processo ainda está longe de ser viável do ponto de vista econômico, existindo pouco conhecimento sobre os fatores genéticos envolvidos na formação destes tecidos (Plomion et al. 2001), principalmente os envolvidos na sua regulação transcricional (Legay et al. 2010).

Conforme mencionado anteriormente, a complexa estrutura e composição da parede celular impedem o aproveitamento total dos açúcares fermentáveis. Uma vez que o processo de lignificação constitui um dos principais fatores que determinam tal dificuldade, e a deslignificação da biomassa constitui um processo caro, vários esforços vêm sendo concentrados para melhor se compreender este processo e produzir árvores com menos lignina ou que sejam mais susceptíveis à degradação química (Weng et al. 2008; Mansfield 2009;).

Os principais esforços nesse sentido constituem na construção de plantas transgênicas com super-expressão ou repressão dos genes envolvidos com a formação da parede celular (Baucher et al. 2003; Goicoechea et al. 2005; Foucart et al. 2009). Entretanto, esta estratégia, além de ser demorada e trabalhosa, envolve um componente legal que muitas vezes dificulta a comercialização de produtos transgênicos, além de analisar apenas um conjunto pequeno de genes de cada vez.

Assim, é de interesse o desenvolvimento de estratégias alternativas para a obtenção de plantas otimizadas para os processos industriais como, no caso de *Eucalyptus*, seu uso na produção de celulose e papel e, também, como biomassa para geração de bioquímicos de segunda geração. Entre estas estratégias alternativas, metodologias de manejo sobressaem-se como poderosas ferramentas quando aliadas ao conhecimento da genética da espécie, especialmente aqueles genes que se traduzem efetivamente em fenótipos desejáveis.

Diante do que já se sabe sobre os efeitos dos flavonoides sobre o crescimento e desenvolvimento vegetal e seu potencial na regulação de eventos específicos à parede celular, como lignificação, o presente estudo buscou adotar a suplementação de *Eucalyptus* por flavonoides visando o melhoramento da qualidade da madeira para uso industrial.

## 2. Objetivos

Os objetivos da presente tese de doutorado compreendem o estudo do efeito da suplementação química dos flavonóides narigenin e narigenin-chalcona na formação da parede celular de Eucalipto.

### 2.1. Objetivos específicos:

- Caracterizar fenotipicamente a parede celular de mudas de Eucalipto, avaliando os efeitos da suplementação por flavonóides na sua composição química;
- Avaliar o efeito da suplementação por flavonóides no perfil de expressão gênica das mudas de Eucalipto;
- Associar as mudanças fisico-quimicas na composição da madeira de eucalipto ao perfil de expressão gênica;
- Verificar a suceptibilidade das plantas suplementadas à hidrólise enzimática, através da quantificação dos açúcares fermentescíveis presentes no hidrolisado;

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## 3. Material e métodos

### 3.1. Material Biológico e delineamento experimental.

Mudas de um clone comercial de um híbrido *E. urophylla x E. grandis* (*Eucalyptus urograndis)* com 6 meses de idade foram fornecidos pela International Paper (Mogi-Guaçu, Brasil) e cultivados em uma estufa (figura 4). As plântulas foram divididos em 5 grupos, de acordo com as condições de suplementação (para além da solução padrão nutricional fornecido para todos os grupos), como se segue: grupo controle (CT), grupo experimental 1 (CH), suplementado com 0,1 mmol de naringenina-chalcona durante 5 meses; grupo experimental 2 (NAR), suplementado com 0,1 mmol de naringenina, durante 5 meses, grupo experimental 3 (CHSTOP), suplementado com 0,1 mmol de naringenina-chalcona apenas para o primeiro mês, e grupo experimental 4 (NARSTOP), suplementado com 0,1 mmol de naringenina apenas o primeiro mês (figura 5). Todas as soluções foram administradas por aplicação na raiz a aproximadamente 100 a 150 mL por dia. Os tratamentos foram realizados durante 5 meses. A solução padrão nutricional foi composta como descrito previamente por (Sarruje 1975).

Todas as amostras foram analisadas de 5 meses após o início da experiência, independentemente da sua suplementação.

Para as análise químicas as hastes de madeira foram descascadas e moídas num moinho de Thomas-Wiley modelo ED-5 para passar de uma peneira de 1 mm e rastreada em um aparelho de crivagem vibratório, e de 40 a 60 mesh fracção farinha de madeira foram retidos para análise. Para análise histológica os caules foram conservados em solução de F.A.A (formalin:aceticacid: ethanol 50%, 1:1:18 v/v) e para as análises de expressão gênica, conservados imediatamente a -80° C.

Naringenina (4'-, 5 -, 7-trihidroxiflavanona, 95%) e naringenina-chalcona (1,3 - difenil-2-propen-1-ona, 97%) foram adquiridos da Sigma-Aldrich Co. (Tóquio, Japão) e AcrosOrganics Co. (Tóquio, Japão), respectivamente.

### 3.2. Análises químicas e histológica.

3.2.1. Histologia.

Três amostras por grupo após a colheita foram fixados em FAA (formalina: aceticacid: 50% de etanol, 1:01:18 v / v) durante pelo menos 24 horas (Johansen 1940). Todos os materiais foram desidratados utilizando o álcool butílico terciário série (Johansen, 1940), embebidos em parafina (paraplast Plus ® - Fischer) e seccionados a 12-14µm de espessura em micrótomo rotativo. Secções desparafinadas foram duplamente coradas com 1% de solução alcoólica safranina-O e 1% de Astral-blue (Gerlach 1969). As secções foram observadas com um microscópio Olympus BX51 sob luz branca, e as imagens foram obtidas com DP-72 da câmara digital e Image Pro Plus 6,3 software. Devido a limitação de tamanho de grupo, apenas os grupos de tratamento prolongado (CT, CH e NAR) foram analisados.

Figura 4. Mudas de *Eucalipto urograndis* na casa de vegetação. Ao fim dos 5 meses de suplementação as plantas alcançavam aproximadamente três metros, tocando no teto.

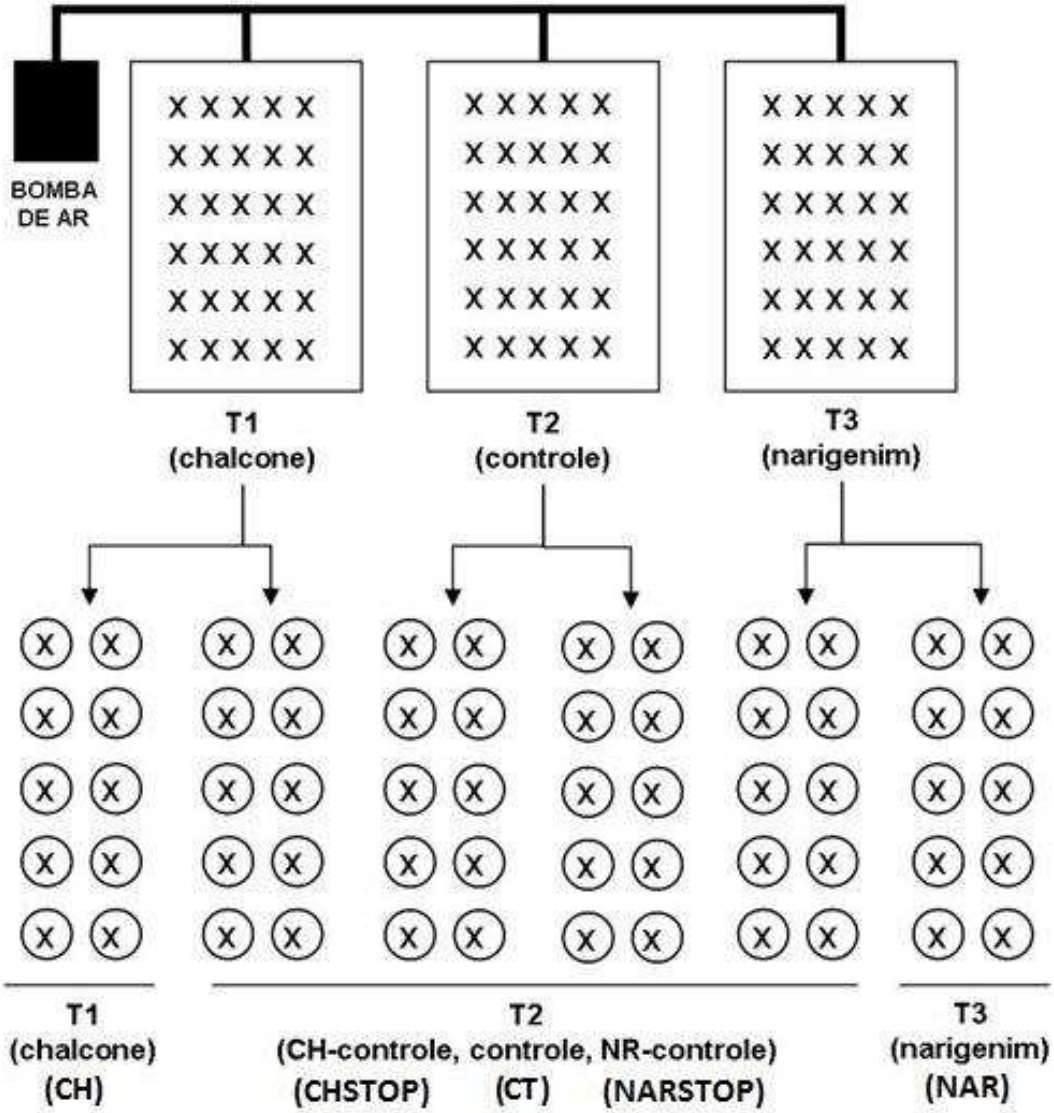


Figura 5. Representação ilustrativa do delineamento experimental da suplementação por flavonóides das mudas de *Eucalipto urograndis* em casa de vegetação. CT - suplementação apenas por solução nutritiva; CH - suplementação 5 meses narigenin-chalcona; NR - suplementação 5 meses narigenin; CHSTOP - suplementação 1 mês narigenin-chalcona, 4 meses solução nutritiva; NARSTOP - suplementação 1 mês narigenin, 4 meses solução nutritiva.

3.2.2 Medição do teor de extrativos.

Entre duas e oito amostras por grupo (0,3g, a 1,5 g) foram mantidos individualmente em sacos de filtro ( Ankon Technology, Nova Iorque, EUA) e extraiu-se sequencialmente durante 16 horas com etanol a 95%, seguido por um outras 16h em água destilada em um aparelho de Soxhlet de 125ml. Depois de cada extracção as amostras foram deixadas para secar *overnight* a temperatura ambiente e em seguida, secos a 60ºC *overnight*, seguido por 2 horas a 102 ± 2ºC. Os teores de extrativos foram avaliados pela perda de peso após cada passo (Alves et al. 2012). Apenas uma determinação por amostra foi possível devido à baixa quantidade de amostra disponível.

3.2.3. Médição dos teores de Lignina.

Para a análise dos teores de lignina, um *pool* de cinco indivíduos escolhidos aleatoriamente foram preparados por grupo de tratamento. Foram medidas a lignina Klason (lignina insolúvel em ácido) e lignina total (lignina insolúvel em ácido + lignina soluvel), valores da lignina Klason foram determinados de acordo com a normativa TAPPI T 222 om-02 de acordo com as modificações descritas por por Schwanninger e Hinterstoisser (Schwanninger, Manfred / Hinterstoisser 2002), valor de lignina solúvel foi determinado de acordo com a normativa TAPPI UM 157 250.

3.2.4.Pirólise Analítica.

Uma alíquota de 30 mg de cada amostra previamente extratada, foi moída num moinho vibratório (Mixer MM Mill, Retsch) durante 5 min e mantido em dessecador antes da análise por pirólise analítica. A pirólise analítica foi realizada utilizando uma Pyroprobe CDS 1000 com uma sonda de filamento conectado a um GC (Agilent 6890), com um detector de ionização de chama (FID), através de uma interface aquecida (270ºC). A pirólise foi realizada a 600ºC durante 5 segundos, utilizando-se 75-77 µg de cada amostra. Coluna capilar: DB1701 (60 mx 0,25 mm, 0,25 película um, J & W Scientific), Condições GC: injetor de 270ºC, detector de 270º C, temperatura de programa de 45ºC, 4 min isotérmica, seguida de aquecimento a taxa de 4ºC min-1 para 250 º C e 6ºC min-1 até 270ºC mantido por 8min (Alves et al. 2011; Rodrigues et al. 2001; Rodrigues et al. 1999).

Os picos produzidos pela pirólise foram analisádos com Chemstation Software (Agilent Technologies, Palo Alto, EUA) as relações S/G e H/G, foram calculadas a partir da soma das áreas dos picos dos produtos de pirólise atribuídos a fenóis de tipo siringil (S), guaiacil (G) e p-hidroxifenil (H). A proporção cP/cH foi calculado a partir da soma das áreas dos picos dos produtos de pirólise características de pentoses (cP) e hexoses (CH) e representa uma estimativa grosseira da proporção relativa de hemicelulose e celulose. Py-lignina foi calculada como a razão entre a soma das áreas dos picos a partir de produtos de lignina dividida pela soma da área de todos os picos utilizados (lignina e polissacarídeos, 75% da área total), multiplicado por 100% (Alves et al. 2006).

### 3.3. Extração de RNA e sequenciamento.

3.3.1. Extração de RNA

O RNA foi extraído de acordo com o protocolo descrito por (Zeng and Yang 2002) com as modificações propostas por (Le Provost et al. 2003), concentrações e qualidade foram medidas com Nanodrop 2000 (Thermo Scientific).

3.3.2. Sequenciamento de mRNA

O sequenciamento de RNA mensageiro foi feito na facility de seqüenciamento de nova geração do *Carolina Center for Genome Sciences* da Universidade da Carolina do Norte. Para cada biblioteca 10ug de RNA total foi usado para o seqüenciamento de acordo com o protocolo da Illumina. Controle e qualidade das amostras foram verificadas com o *Bioanalyzer Chip DNA 1000 series II* (Agilent). Para cada biblioteca foram seqüenciados fragmentos *single-end* de 36 ou 50 pares de base com *Illumina Genome Analyzer IIx.* Um total de 8 bibliotecas foram geradas, três réplicas biológicas do grupo controle (CT); duas réplicas biológicas do grupo suplementado cinco meses com narigenin (NAR); e uma biblioteca de cada grupo restante: cinco meses suplementação narigenin-chalcona (CH); um mês suplementação de narigenin (NARSTOP) e um mês suplementação narigenin-chalcona (CHSTOP). Cada biblioteca corresponde ao agrupamento de três amostras individuais.

3.3.3. Alinhamento

Os *reads* Illumina foram filtrados para excluir material ribossomal (utilizando a base de dados SILVA (Pruesse et al. 2007) e de baixa qualidade (Phred> = 20). Os restantes foram alinhados contra as variantes mais elevadas de transcritos do genoma de *Eucalyptus grandis* Phytozome 7,0 (44.974 sequências) utilizando o alinhador SOAP2 (Li et al. 2009). Para preparar os dados para análise Genebrowser, leituras foram alinhadas contra o genoma de *E. grandis* usando TopHat (Trapnell et al. 2009) para permitir a alinhamentos *spliced*. Ambos os programas foram configurados para permitir até dois *mismatches* (SNPs podem gerar desequilíbrios no alinhamento, especialmente nestes casos, porque as seqüências são de espécies diferentes), descartar seqüências com ambigüidades (Ns) e retornar apenas alinhamentos únicos.

3.3.4 Anotação

O programa Autofact (Koski et al. 2005) foi usado para realizar a anotação automática de todos os contigs EUCANEXT. A principal característica do Autofact é a sua capacidade para retomar a anotação com base em pesquisas de similaridade de seqüência em vários bancos de dados. BLASTx (Altschul et al. 1997) (valor de corte de 1e-5) foi utilizado para alinhar os contigs contra as seguintes bases de dados públicas: a base de dados não redundante (NR), do NCBI; Uniref90 e Uniref100 a base de dados de vias metabólicas KEGG (Kanehisa 2000), e TAIR (versão 10 do

banco de dados de proteínas Arabidopsis. Anotação funcional (GO) foi realizada utilizando BLAST2GO (Conesa et al. 2005), e Mapman software (Thimm et al. 2004) com os parâmetros padrão.

3.3.5 Determinação dos valores de expressão gênica

Os valores de expressão gênica foram medidos utilizando o *FPKM (fragments per kilobase of exon per million fragments mapped),* utilizando apenas alinhamentos únicos como descrito por (Mortazavi et al. 2008). Todos os transcritos e seus valores de expressão podem ser acessados no banco de dados EUCANEXT – www.lge.ibi.unicamp.br/eucalyptusdb

**3.4 Hidrólise enzimática**

3.4.1 Preparação do substrato

O material vegetal de xilema de Eucalipto foi congelado em nitrogênio liquido e liofilizado usando o FreeZone6 (Labconco) a - 51°C e 25 Pa durante 48 horas. Após a liofilização o material foi moído em um moinho de bola (MARCA) em um ciclo de 5 minutos.

3.4.2. Produção do Secretoma

A linhagem de *Neurospora crassa* St.L 74A (Missouri University, Kansas City, http://www.fgsc.net/) foi usada para a produção do secretoma. A preparação dos conídios foi realizada inoculado o fungo em 100ml de meio mínimo com sais de Vogel suplementados com 143uL de biotina ( 5mg, etanol 50% (v/v), 143uL de solução ( 5g de ácido cítrico, 5g ZnSO4. 7H20, 1g FE(NH4) .6H2O, 0,25g de CuSO4.5H2O, 0,05g MnSO4.H2O, 0,05g H3BO3, 0,05g Na2MoO4.2H2O, para 1000 mL), 1,5% de Agar, 2% de sacarose e crescido durante três dias a 30°C no escuro e depois por sete dias com presença de luz a 25°C. A suspensão de conídios foi inoculada em 100mL do mesmo meio de crescimento contendo 2% do material de eucalipto moído na contendo *E. grandis, E. urograndis* and *E. urophylla* na proporção de 3:3:1 como única fonte de carbono (Phillips et al. 2011).

3.4.3 Hidrólise

A hidrólise foi realizada de acordo com (Bragatto et al. 2012) com as seguintes modificações: utilizou-se tubos eppendorf de 2ml agitados a 1000 rpm a 30°C no *Thermomixer* (Eppendorf) durante 48 horas. Cerca de 10 mg do substrato foi diluído em 400 ul de tampão 50 mM acetato de sódio pH 5.5 e adicionado 100 uL do secretoma de *N. crassa* na concentração de 0,4 ug/uL determinada usando o *Bradford Kit assay* (BioRad) com BSA padrão. Todas as reações foram realizadas em triplicata. Para a determinação da concentração de açúcar redutor e produção de glicose, os

tubos de 2 mL foram centrifugados a 20.000g durante 10 minutos a 4°C, o sobrenadante foi recuperado e utilizou-se 100 uL para cada reação. Para a determinação do açúcar redutor foi adicionado ao sobrenadante 100 uL de *dinitrosalicylic acid assay* - DNS (Miller 1959), a reação foi aquecida a 99°C por 10 minutos e transferido 100 uL para uma placa ELISA e medida a absorbância a 540 nm (Tecan Infinite M200 instrument). Para o cálculo do conteúdo de glicose, 20 uL do sobrenadante dói adicionado a 100 uL de solução de trabalho do Kit *Glucose Oxidase* (Laborlab) em placas de ELISA e incubados a 37°C por 10 minutos e medida a absorbância a 505 nm.

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## 4. Apresentação dos trabalhos:

Este trabalho objetivou a avaliação da influência da suplementação pelos flavonóides narigenin-chalcona e narigenin, na formação da madeira do híbrido comercial *E. grandis* x *E. urophylla* extensamente plantado no Brasil. O trabalho foi organizado em dois capítulos respectivamente: :

**Capitulo 1**. **Caracterização química da parede celular de mudas de eucalipto suplementadas com flavonóides.** Para avaliar a influência da suplementação por flavonóides na composição química da parede celular, as mudas de eucalipto foram analisadas através métodos químicos tradicionais e da pirólise analítica, objetivando quantificar extrativos, pentoses, lignina e composição monomérica da mesma. Este trabalho foi realizado no estágio de doutorado sanduíche do autor, realizado no Instituto de Investigação Científico tropical da Universidade Técnica de Lisboa, sobre a supervisão do Dr. José Carlos Rodrigues.

Manuscrito: "**Flavonoid supplementation reduces the extractive content and increases the syringyl/guaiacyl ratio in Eucalyptus grandis x Eucalyptus urophylla hybrid trees"** Lepikson-Neto, Jorge ; Alves, A. ; Simoes, R. ; Deckmann, A. C. ; Camargo, E.L.O. ; Salazar, Marcela Mendes ; Rio,MCS ; Nascimento, LC ; Pereira, G. A. G. ; Rodrigues, J. C. Bioresources (Raleigh, N.C), v. 8, p. 1747-1757, 2013.

Data de submissão: 10/2012

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**Capitulo 2**. Análise da expressão gênica e hidrólise enzimática: Para verificar o impacto da suplementação por flavonóides na expressão gênica e obtenção de açucares das mudas previamente caracterizadas quimicamente, foi seqüenciado transcriptoma e realizada a hidrólise enzimática do material, no intuito de verificar os efeitos moleculares do processo e associar a sua expressão gênica e potencial obtenção de açucares fermentáveis as alterações da parede celular verificadas no primeiro capitulo do trabalho, de modo que estas informações completamente inéditas na literatura possam contribuir para futuros trabalhos de melhoramento genético da espécie.

Manuscrito: **"Flavonoid supplementation affects the gene expression of cell wall formation and lignification metabolisms and increases sugar content and saccharification levels in the fast growing Eucalyptus hybrid *E. urophylla x E. grandis***" Lepikson-Neto, J.[1], Nascimento L.C [1,], Salazar M.M.[1], Camargo E.L.O.[1] ,Cairo, J.P.F [2]; Teixeira P.J[1] , Marques, W.L[1] ; Squina F.M [2]; Mieczkowski, P [3].; Deckmann, A.C.[1]and Pereira, G.A.G.[1]

Data prevista para submissão; 06/2013

Devido aos resultados positivos obtidos, a patente da composição química utilizada para a suplementação dos eucaliptos foi depositada junto ao **INPI – BR1020120269813**, pelo autor do trabalho e seu orientador, juntamente com a parceria da International Paper do Brasil. A folha de rosto da mesma encontra-se no **anexo 1.**

# Capitulo 1: Caracterização química da parede celular de mudas de eucalipto suplementadas com flavonóides.

# Flavonoid Supplementation Reduces the Extractive Content and Increases the Syringyl/Guaiacyl Ratio in *Eucalyptus grandis x Eucalyptus urophylla* Hybrid Trees

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The *Eucalyptus* genus plays an important role in the worldwide forest industry, with highly productive plantations supplying high-quality raw material for pulp and paper, wood, and biomass that would otherwise come from native forests. Lignin and extractives are important components for wood structure and protection but they are disruptive elements with respect to some industrial processes involving paper, pulp, and biomass production. This work evaluated effects of supplementation of flavonoids on the wood composition of *Eucalyptus grandis* x *Eucalyptus urophylla* (*E. urograndis*), a commercial hybrid. The wood samples were analyzed for extractives and lignin contents by wet chemical analysis, and the composition of lignin monomers and the carbohydrate hexosan/pentosan ratio were determined by analytical pyrolysis. The results showed that supplementation with the flavonoids naringenin and naringenin-chalcone led to an overall reduction of the extractive content and altered the monomeric composition of lignins towards a higher syringyl content. Thus, the treatment of *Eucalyptus* with flavonoids results in the improvement of wood quality for technological purposes.

*Keywords: Eucalyptus; Extractives; Lignin; Flavonoids*

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## INTRODUCTION

Wood is a natural resource that forms the basis of a global industry producing fiber, timber, and energy, and it is the fifth most important world trade product (Foucart *et al.* 2009). Wood represents one of the most important sources of energy and biomass on Earth and constitutes an environmentally friendly and renewable alternative to fossil resources. Moreover, wood is an important natural sink for carbon dioxide, one of the major causes of global warming due to the greenhouse effect (Demura and Fukuda 2007).

The genus *Eucalyptus* is the most widely planted hardwood crop in the tropical and subtropical world due to its superior growth, broad adaptability, and multipurpose wood properties (Hu *et al.* 1999). Plantation-grown *Eucalyptus* supplies high-quality woody biomass for several industrial applications while reducing the pressure on tropical forests and their associated biodiversity (Hu *et al.* 1999).

The chemical composition of wood plays an important role in wood applications, especially in chemical conversion. Wood extractives, the non-cell wall components that can be removed by solvents, are necessary for protecting the living tree and derived wood products against disease; however, extractives can be detrimental to pulp and paper, paint, and varnish films and adhesives (Alves *et al.* 2012). Pulpwood from tropically grown eucalyptus trees, including those grown in Brazil, contains a higher content of extractives than those grown in Europe, accounting for a decrease of up to 4% in the pulping yield (Gomide *et al.* 2005). The extractive content is lower at a young harvesting age, and the content increases rapidly with aging (Gomide *et al.* 2005). Lignin composition is also a very important parameter. Eucalyptus lignins are composed of syringyl (S) and guaiacyl (G) units in varying proportions. High syringyl/guaiacyl (S/G) ratios are advantageous for pulp production due to higher delignification rates, reduced chemical consumption, and higher pulp yields (Rodrigues *et al.* 1999). Because of high tree-to-tree variation (Rodrigues *et al.* 1999) and low variation within a tree, lignin composition is a wood trait under strong genetic control (Stackpole *et al.* 2010) even when tension wood is present (Rodrigues *et al.* 2001). Therefore, extensive research efforts are focused on comprehending the lignification process in an effort to design trees through genetic engineering that either have reduced lignin content, produce lignins that are more susceptible to chemical degradation (Weng *et al.* 2008; Mansfield *et al.* 2009), or have altered lignin content (Valerio *et al.* 2003).

Lignin synthesis is a relatively well-established process that starts with the assemblage of radicals produced during the single-electron oxidation of monolignols (Baucher *et al.* 2003). The units resulting from the monolignols, when incorporated into the lignin polymer, are called guaiacyl (G), syringyl (S), and p-hydroxyphenyl (H) (Vanholme *et al.* 2010).

The monolignols are synthesized from the aminoacid phenylalanine through the phenylpropanoid and monolignol-specific pathways. Phenylalanine is derived from the shikimate biosynthetic pathway in the plastid (Boudet *et al.* 2003; Rippert *et al.* 2009), which is responsible for the synthesis of a wide variety of secondary metabolic compounds, including lignin and phenolic extractives (Dixon *et al.* 1996; Vogt *et al.* 2010).

The catalytic step performed by the enzyme 4-coumaroyl:CoA-ligase (4CL) likely represents the most important branch point within the central phenylpropanoid biosynthesis pathway in plants (Campbell and Sederoff 1996; Voo *et al.* 1995). Through 4CL activity, cells can produce the precursors for either flavonoid biosynthesis or guaiacyl (G) and syringyl (S) lignin units (Vogt, 2010). The product of 4CL, p-coumaroyl-CoA, is the substrate of the enzyme chalcone synthase(CHS) (Besseau *et al.* 2007), the committing step in flavonoid biosynthesis. This pathway is reviewed in detail elsewhere (Besseau *et al.* 2007; Vanholme *et al.* 2010).

The flavonoids naringenin-chalcone and naringenin, synthesized by the enzymes chalcone synthase (CHS) and chalcone isomerase (CHI), respectively, constitute the primary C15 intermediates in flavonoid biosynthesis (Moustafa 1967;Chen *et al.* 2011). Naringenin was reported to inhibit the activity of 4CL (Voo *et al.* 1995), and this inhibition is positively associated with naringenin sensitivity in several plant species (Deng*et al.* 2004; Yun *et al.* 2009).

The objective of the present work was to evaluate the effects of naringenin-chalcone and naringenin supplementation on the wood composition of *E.urophylla x E. grandis*, a commercial hybrid referred to hereafter as *E. urograndis*.

## EXPERIMENTAL

### Materials

Plantlets of a 6-month-old commercial clone of *Eucalyptus urograndis* were provided by International Paper (Mogi-Guaçu, Brazil) and grown in a greenhouse. The plantlets were divided into 5 groups, according to supplementation conditions (apart from the standard nutritional solution supplied to all groups) as follows: control group (CT); experimental group 1 (CH), supplemented with 0.1 mmol of naringenin-chalcone for 5 months; experimental group 2 (NAR), supplemented with 0.1 mmol of naringenin for 5 months; experimental group 3 (CHSTOP), supplemented with 0,1 mmol of naringenin-chalcone for only the first month; and experimental group 4 (NARSTOP), supplemented with 0.1 mmol naringenin for only the first month. All solutions were administered by root application at approximately 100 to 150 mL daily. The treatments lasted 5 months. The composition of the standard nutritional solution has been described previously (Sarruje 1975). At the end of the experiment, all 5 groups of plantlets were cut, and the stems were kept for analysis; no growth differences were observed between the control and the treatment groups. A total of 30 plantlets were individually analyzed; 9 were only used for histology and 21 for chemical analyses. The same extracted samples were used for pyrolysis. All samples were analyzed 5 months after the start of the experiment regardless of their supplementation. The main wood stems were debarked and ground in a Thomas–Wiley mill model ED-5 to pass a 1 mm sieve and screened in a vibratory sieving apparatus, and the 40 to 60 mesh wood meal fraction was retained for analysis.

Naringenin (4'-,5-,7-trihydroxyflavanone, 95%) and naringenin-chalcone (1,3-diphenyl-2-propen-1-one, 97%) were purchased from Sigma-Aldrich Co. (Tokyo, Japan) and AcrosOrganics Co. (Tokyo, Japan), respectively.

### Histology

After harvesting, three stem samples per group were fixed in FAA (formalin: acetic acid: 50% ethanol, 1:1:18 v/v) for at least 24 h (Johansen 1940). All materials were dehydrated using the tertiary butyl alcohol series (Johansen 1940), embedded in paraffin (Paraplast Plus® - Fischer), and sectioned into 12 to 14 µm thick sections with a rotary microtome (Model and brand). Deparaffinized sections were double stained with a 1% alcoholic solution of safranin-O and1% aqueous astral blue (Gerlach 1969). The sections were observed using an Olympus BX51 microscope under white light, and the images were obtained using a DP-72 digital camera and Image Pro Plus 6.3 software. Due to group size limitation, only the prolonged treatment groups (CT, CH, and NAR) were analyzed.

### ExtractivesContent

Between two and eight samples per group (0.3 to 1.5 g) were kept individually in Ankon filter bags (Ankon Technology, New York, USA) and sequentially extracted for 16h with 95% ethanol followed by another 16 h in distilled water in a 125 mL Soxhlet apparatus. Afterwards, the extracted samples were allowed to cool and dry under room conditions overnight and then dried at 60ºC overnight, followed by 2 hours at 102 ± 2ºC. The extractive content was assessed according to weight loss after each step (Alves *et al.* 2012). Only one determination per sample was possible due to the low amount of sample available.

## Lignin Content

For lignin analysis, a pool of five randomly selected individuals was prepared per group treatment, and Klason (acid-insoluble lignin) and total lignin content (acid-insoluble lignin plus acid-soluble lignin) were assessed using the averaged values based on the oven-dried, extractive-free weight of each pooled sample as determined using wet chemistry methods. Klason (acid-insoluble) lignin content was determined according to TAPPI T 222 om-02 following the modifications by Schwanninger and Hinterstoisser (2002), and the acid-soluble lignin content was determined according to TAPPI UM 250.

## Analytical Pyrolysis

A 30 mg aliquot of each extracted sample was further milled in a vibratory ball mill (Mixer Mill MM, Retsch) for 5 min and kept in desiccators prior to analysis by analytical pyrolysis. Analytical pyrolysis was performed using a CDS Pyroprobe 1000 with a coil filament probe connected to a gas chromatography (GC) unit (Agilent 6890) with a flame ionization detector (FID) using a heated interface (270ºC). The pyrolysis was carried out at 600ºC for 5 s using 75 to 77 µg of the extractive-free milled samples. Capillary column: DB1701 (60 m x 0.25 mm, 0.25 µm film, J&W Scientific). GC conditions: injector, 270ºC; detector, 270ºC; temperature program, 45ºC, 4 min isothermal, then heating rate 4ºCmin$^{-1}$ to 250ºC and 6ºC min$^{-1}$ to 270ºC, hold for 8 min (Rodrigues *et al.* 1999, 2001; Alves *et al.* 2011).

From the pyrolysis product peaks, the following ratios were computed using Chemstation Software (Agilent Technologies, Palo Alto, USA). S/G and H/G ratios were calculated from the sum of the peak areas of the pyrolysis products assigned to syringyl (S), guaiacyl (G), and p-hydroxyphenyl (H) type phenols. The cP/cH ratio was calculated from the sum of the peak areas of the characteristic pyrolysis products of pentosans (cP) and hexosans (cH) and represents a rough estimation of the relative proportion of hemi-celluloses and cellulose. Py-lignin was calculated as the ratio of the sum of the areas of the peaks from the lignin products divided by the sum of the area of all peaks used (lignin and polysaccharides, *ca*. 75% of the total area) multiplied by 100% (Alves *et al*. 2006a).

## Statistical analysis

To verify significant differences between the controls and the flavonoid-supplemented groups, a one way ANOVA test was performed between the control and each supplemented group. The results were considered significant if $p< 0.05$ and were classified as follows: *,$p< 0.05$; **, $p< 0.01$; and ***, $p< 0.001$. The correlation between ethanol and water extractives was also assessed. All statistics were performed using Analysis ToolPak for Excel 2007.

# RESULTS AND DISCUSSION

## Histochemical Analysis

The photomicrographs of the stained (astral blue-safranin) transverse section cuttings show that the treatment groups had a more pronounced blue coloration than the control group, especially evident in the NAR group (Fig. 1). These results suggest a relative decrease in the lignin content with a consequent increase in the polysaccharide fraction of the flavonoid-treated wood plantlets because astral blue-safranin dye confers a distinct coloration for carbohydrates and colors cellulose in the absence of lignin blue and

lignin-rich regions red. As shown later using wet chemical analysis, no significant changes in lignin content were found, whereas a clear reduction in the content of ethanol extractives seemed to indicate that the difference in the coloration could result from different amounts of ethanol extractives. Another possibility is the mobilization of the stained compounds during the preparation stages of the material. In fact, mobilization alone could account for the differences between the stain results and the analytical results.

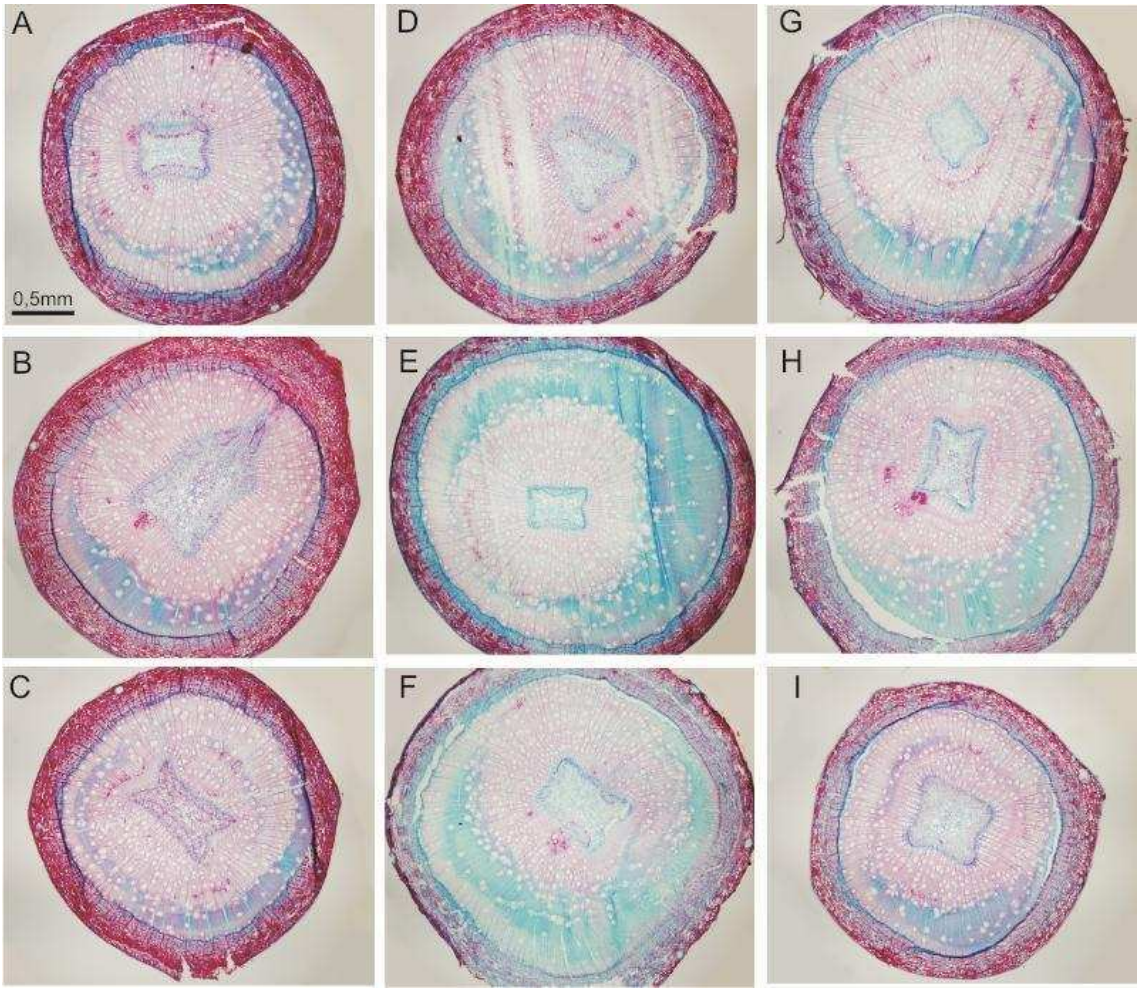


**Fig. 1.** Photomicrographs of the stained (astral blue-safranin) transverse section cuttings from the control (A-C) and the naringenin (D-F) and naringenin-chalcone (G-I) treatment groups

## Extractives and Lignin Content

A summary of results for the extractive and lignin content of the samples is given in Table 1.

Across groups and plants, the ethanol extractives content varied between 4.4% and 13.7% of the dry weight of the wood meal, representing between 51% and 83% of the total extractives content. After ethanol extraction, the water extractive content varied between 2.0% and 6.6% and represented between 26% and 41% of the total extractives content. The ethanol and water extractives contents were positively correlated ($r = 0.56$), and the correlation was highly significant ($p < 0.004$).

**Table 1.** Summary of the Results of the Extractive and Lignin (Klason and total) Contents

| | Extractives (%) | | | Lignin (%) | |
|---|---|---|---|---|---|
| | Ethanol | Water | Total | Klason | Total |
| CT | 10.3(0.34) | 3.8(1.09) | 14.2(1.25) | 22.6(0.03) | 26.7(0.01) |
| CH | 6.1(1.01) *** | 2.9(0.47) | 9.0(1.82) *** | 21.5(0.03) | 25.5(0.01) |
| CHSTOP | 7.1(0.23) *** | 3.4(0.44) | 10.5(1.31) ** | 22.6(0.14) | 26.6(0.03) |
| NAR | 7.6(1.57) *** | 4.2(0.14) | 11.8(0.90) * | 22.3(0.01) | 26.3(0.17) |
| NARSTOP | 6.9(0.99) ** | 2.5(0.28) | 9.4(0.19) ** | 22.5(0.02) | 26.2(0.40) |

Extractive data refer to the mean values of the individual samples from each group. Lignin data refer to the replicate analysis of a 5-sample pool per treatment. CT – control group; CH – 5 months naringenin-chalcone; CHSTOP – 1 month naringenin-chalcone; NAR – 5 months naringenin; NARSTOP- 1 month naringenin. Values in brackets refer to variance.

A decrease in the ethanol extractives content was observed for the flavonoid-treated plants. The average ethanol extractives content decreased from 10.3% (control group) to between 6.1% (CH) and 7.6% (NAR), representing a decrease of between 41% (CH) and 26% (NAR) compared with the control group. The water extractive content was also reduced with flavonoid treatment from 14% (CH) to 34% (NARSTOP), with the exception of the NAR-treated group, which showed an 11% increase compared with the control group. The total extractive content followed the same pattern as the ethanol extractives.

The extractive content of these plants was higher than the extractive content of *Eucalyptus urograndis* at the age of commercial pulpwood. The ethanol extractive content alone was above or close to the total extractive content of the heartwood (7.6%) and at least twice that of the total extractive content of the sapwood (3.7%) of 5.6-year-old trees from an *E. urograndis* clone in a commercial pulpwood plantation in Brazil (Gominho *et al.* 2001). These differences could be explained, at least in part, by the fact that living cells (developing xylem) filled with easily extractable metabolites (Paiva *et al.* 2008) represent a larger percentage of the stem at this age than at older ages.

The reduced extractive content due to flavonoid treatment will increase the productivity of pulping because a higher extractives content accounts for up to 4% of the losses to the kraft pulping yield of clonal eucalyptus in Brazil (Gomide *et al.* 2005).

The Klason and total lignin contents of these plantlets were lower than the reported values for *E. urograndis* at commercial age in Brazil (6 to 7 years old), ranging from 24.2% to 27.1% (Klason) and 27.5% to 30.6% (total) lignin content (Gomide *et al.* 2005). However, these results were obtained on a limited number of samples (7 clones, each a composite sample of three individuals).

The lignin content (Klason and total) was not affected by the flavonoid treatment (Table 1), which was unexpected in light of the histological results (Fig. 1). This result seems to indicate that, in addition to changing the extractive content, the flavonoid treatment could also have changed the extractive composition, accounting for the differences in coloration between the treated and control samples.

Alternatively, the flavonoid treatment could have altered the lignin composition results by making cellulose and other carbohydrates more accessible to the dye astral blue (Fig. 1).

## Analytical Pyrolysis

The summary of the analytical pyrolysis results is shown in Table 2. According to these results, flavonoid-treated plants showed a statistically significant increase in the S/G ratio (between 8 and 10% compared with the control) and a decrease in the H/G ratio (between 11 and 16%). Both changes have a favorable impact on pulping because of their effects on delignification rates, chemical consumption, and pulp yields (Rodrigues *et al*. 1999).

**Table 2.** Summary of the Analytical Pyrolysis Results

| | | cP/cH | H/G | S/G | Py-lignin% |
|---|---|---|---|---|---|
| CT | 5 | 26.8(1.6) | 0.092(0.008) | 1.41(0.05) | 23.2(0.6) |
| CH | 8 | 28.8(3.3) | 0.078(0.007) ** | 1.55(0.03)** | 23.7(0.8) |
| CHSTOP | 3 | 29.5(2.5) | 0.078(0.006) * | 1.55(0.03) ** | 24.2(0.3) |
| NAR | 3 | 28.2(1.2) | 0.077(0.004) * | 1.52(0.02) * | 24.1(0.7) |
| NARSTOP | 2 | 29.6(4.2) | 0.082(0.009) | 1.52(0.01) * | 23.0(0.1) |

The mean values and standard deviation (brackets) results of the analytical pyrolysis. The first column refers to the number of individual samples analyzed.

The syringyl/guaiacyl (S/G) ratio ranged from 1.41 (CT) to 1.52 (CH and NAR), representing an approximate 7.8% increase in syringyl lignins in the flavonoid treatment. The same result was observed in the short-term flavonoid supplementation groups: the S/G ratio increased to 1.52 and 1.53 in the CHSTOP and NARSTOP groups, respectively, which represents an approximately 7.8% (CHSTOP) and 8.5% (NARSTOP) increase. These values are lower than the values reported for this species (S/G ratio above 2) using analytical pyrolysis and nitrobenzene oxidation (Barbosa *et al*. 2008; Lima *et al*. 2008). However, the analytical pyrolysis results cannot be directly compared because differences in the pyrolysis instruments and columns will inevitably lead to different results.

The H/G ratio decreased from 0.092 (CT) to 0.078 for both CH and NAR groups and to 0.078 and 0.081 in the CHSTOP and NARSTOP groups, respectively, representing an approximate 15% decrease in the H/G ratio in the prolonged treatments (CH and NAR) and 15% (CHSTOP) and 12% (NARSTOP) in the short-term treatments. Interestingly, these H/G values are higher than the average H/G ratios for *Pinus pinaster* (0.64) (Alves *et al*. 2006b), *Pinus caribaea* (0.50) (Godoy *et al*. 2007), and *Picea abies* (0.50), all determined by analytical pyrolysis using the same methodology (Alves *et al*. 2009).

Because no changes in the total lignin content were observed and the S/G ratio increased while the H/G ratio decreased, a direct substitution of p-hydroxyphenyl and guaiacyl units by syringyl units in the composition of lignin is likely. This substitution is one of the key desired aspects of *Eucalyptus* plants (Baucher *et al.* 2003; Grattapaglia and Kirst, 2008; Jung *et al.* 2011), increasing lignin solubility and cellulose accessibility by promoting better delignification (Baucher *et al.* 2003; Huntley *et al.* 2003; Stewart *et al.* 2006). To explain this result, a change in the phenylpropanoid pathway is necessary, with a shift towards S lignin synthesis; expression analyses of supplemented eucalyptus might help elucidate this change.

Both the cP/cH ratio and the Py-lignin content showed no statistically significant differences between the control and treatment groups, although the cP/cH ratio was, on average, higher for all treated groups compared with the control.

In conclusion, it was demonstrated that flavonoid supplementation of *Eucalyptus urograndis* plantlets has a strong influence on its wood composition; the present results are preliminary but have great potential for the improvement of this species towards increased productivity. The addition of flavonoids to a common nutrient medium is inexpensive and easy to accomplish in a eucalyptus nursery. The fact that short-term supplementation (only 1 month) was enough to produce changes in wood composition 4 months later was encouraging, and longer experiments should be performed to determine the impact of supplementation on full-grown Eucalyptus.

## CONCLUSIONS

1. Root-applied flavonoid supplementation promotes a significant reduction in extractive content and increases the lignin monomeric composition (S/G ratio) of young *E. urograndis* trees.
2. These preliminary results indicate that flavonoid supplementation can potentially be used as a nutritional complement being a new, viable, and interesting method for improving *Eucalyptus* wood quality for its utilization by the paper and pulp industry and for biomass exploitation.

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# Capitulo 2: Análise da expressão gênica e hidrólise enzimática

# Flavonoid supplementation affects the expression of genes involved in cell wall formation and lignification metabolism and increases sugar content and saccharification in the fast-growing *Eucalyptus* hybrid *E. urophylla x E. grandis*

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**ABSTRACT**

*Eucalyptus* species are the most widely planted hardwood species in the world and are renowned for their rapid growth and adaptability. These species supply the timber industry with high-quality material for producing pulp, paper, wood and biomass while preserving natural forests. In Brazil, one of the most widely grown *Eucalyptus* cultivars is the fast-growing *Eucalyptus urophylla x Eucalyptus grandis* hybrid. In a previous study, we described a chemical characterization of these hybrids when subjected to flavonoid supplementation on 2 distinct timetables, and our results revealed marked differences between the wood composition of the treated and untreated trees. In this work, we report the transcriptional responses occurringin these trees that may be related to the observed chemical differences. Gene expression was analyzed through mRNAsequencing, and the results showed that the supplemented trees exhibit a distinct expression profile in comparison with the control group. Notably, compared to control trees, the treated trees display differential down-regulation of cell wall formation pathways such as phenylpropanoid metabolism as well as differential expression of genes involved in sucrose, starch and minor CHO metabolism and genes that play a role in several stress and environmental responses. Because phenylpropanoid metabolism is involved in lignin and flavonoid biosynthesis, these results may provide clues regarding the molecular events that determine wood quality in *Eucalyptus* trees. We also performed enzymatic hydrolysis of wood samples from the different treatments, and the results indicated higher sugar contents and glucose yields in the flavonoid-treated plants, further illustrating the potential use of flavonoids as a nutritional complement for modifying *Eucalyptus* wood.

**Keywords**: Eucalyptus; lignin, phenylpropanoid metabolism, syringyl/guaiacyl ratio, gene expression, hydrolysis.

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## Introduction

Trees constitute the majority of the lignocellulosic biomass on Earth and are expected to play a significant role in the future as a renewable and environmentally cost-effective alternative feedstock for biofuel production, a source of fibers and solid wood products and a major sink for excess atmospheric $CO_2$(Boudet et al. 2003; Plomion et al. 2001; Rengel et al. 2009). In Brazil, the pulp and paper industries have been efficiently fed by *Eucalyptus* forests due to their rapid growth, adaptability and wood quality, but with the dramatic increase in industrial demands and the interest in second-generation biofuels and renewable chemicals, the quality and quantity of wood produced must also increase (Paiva et al. 2011; Grattapaglia et al. 2012).

Wood is a highly variable material that differs among trees and is composed of the secondary xylem, a specialized type of conductive and structural support tissue produced through the lateral growth and differentiation of the meristematic vascular cambium (Fukuda 1996). Most of the genes expressed during the formation of the secondary xylem (xylogenesis) are involved in determining the physical and chemical properties of wood (Plomion et al. 2001; Paux et al. 2005). Despite the progress that has been made in defining the molecular and cellular events involved in xylogenesis, the mechanisms regulating the rate of this process and the variation in wood properties remain largely unknown ( Kirst et al. 2004; Foucart et al. 2009; Vanholme et al. 2010).

The secondary xylem cell wall of *Eucalyptus* trees is mostly composed by cellulose (β-1,4-glucan), lignin (a phenolic polymer) and hemicelluloses (heterogeneous polysaccharides), in an approximate ratio of 2:1:1(Hu et al. 1999). During tree growth, cellulose microfibrils give the cell walls tensile strength, and the lignin encasing the cellulose microfibrils imparts rigidity to the cell walls. Despite its importance during growth, lignin becomes problematic during postharvest, cellulose-based wood processing because it must be extracted during industrial handling through a complicated process, resulting in an enormous expenditure of energy and chemicals and strain on the environment (Hu et al. 1999; Fu et al. 2010). Thus, it is of major interest to investigate the molecular basis of lignification to further increase our overall comprehension of this metabolic process for better adaptation of industrial processes.

Lignin synthesis is a relatively well-understood process that begins with the assembly of radicals produced during the single-electron oxidation of monolignols (Baucher et al. 2003; Li et al. 2010; Vanholme et al. 2010). The industrial exploitation of wood to obtain cellulose depends mostly on the composition of lignins because lignins determine the rigidity of the wood and the feasibility of cellulose extraction, which are of major concern in the paper and pulp industries. In angiosperms, lignin is composed of 2 major units: the guaiacyl (G) and syringyl (S) units, which are derived from corresponding monolignol precursors, the coniferyl and sinapyl alcohols, respectively (Boudet 2000; Boudet et al. 2003). The S/G ratio dictates the degree and nature of polymeric cross-linking; an increased G content leads to highly cross-linked lignin (more rigid

wood), whereas S subunits are typically linked through more labile ether bonds at the 4-hydroxyl position (Dixon et al. 1996; Guo et al. 2001; Ferrer et al. 2008;). Thus, S-rich lignins are much easier to dissociate from cellulosic content, resulting in a much cleaner and cheaper process (Ferrer et al. 2008). The S/G ratio is variable among species and is commonly used to evaluate the quality of woodin commercial tree plantations (Rodrigues et al. 1999; Foelkel 2009;).

The formation of lignin monomers begins with the catalytic step performed by the 4-coumaroyl:CoA-ligase (4CL) enzyme, which likely represents the most important branch point in the central phenylpropanoid biosynthesis pathway in plants (Voo et al. 1995; Campbell and Sederoff 1996). Through 4CL activity, cells can produce the precursors for either flavonoids or the G and S lignin precursors (Vogt 2010). The product of 4CL, p-coumaroyl-CoA, is the substrate of the enzyme chalcone synthase (CHS) (Besseau et al. 2007), which carries out the committing step in flavonoid biosynthesis. This pathway is reviewed in detail elsewhere (Besseau et al. 2007; Vanholme et al. 2010).

The flavonoids naringenin-chalcone and naringenin, which are synthesized by the enzymes chalcone synthase (CHS) and chalcone isomerase (CHI), respectively, are the primary C15 intermediates in flavonoid biosynthesis (Moustafa 1967; Chen et al. 2011). This metabolic pathway appears to be a promising target for improving wood quality in *Eucalyptus* trees, as shown by our previous work (Lepikson-Neto et al 2013) demonstrating that flavonoid supplementation of the fast-growing *Eucalyptus urophylla x Eucalyptus grandis* hybrid, hereafter referred to as *E. urograndis,* changes its wood composition, reduces its extractive contents and alters its syringyl monomer composition.

In this context, the objective of the present work was to perform further studies on the effects of flavonoid supplementation on *E. urograndis* trees by analyzing gene expression in xylem tissue from treated and non-treated trees and by measuring the effect on sugar accessibility through enzymatic hydrolysis. We analyzed the obtained data with special emphasis on results that might be correlated with the previously observed changes in wood composition (Lepikson-Neto et al. 2013).

## Materials and Methods

### Plant materials and tissue harvesting

Plantlets of a 6-month-old commercial clone of *Eucalyptus urograndis* were provided by International Paper (Mogi-Guaçu, Brazil) and grown in a greenhouse.The plantlets were divided into 5 groups according to supplementation conditions (apart from the standard nutritional solution supplied to all groups), as follows: control group (CT); experimental group 1 (CH), supplemented with 0.1 mmol of naringenin-chalcone for 5 months; experimental group 2 (NAR), supplemented with 0.1 mmol of naringenin for 5 months; experimental group 3 (CHSTOP), supplemented with 0.1 mmol of naringenin-chalcone for only the first month and then given the standard nutrition solution for the next 5 months; and experimental group 4 (NARSTOP), supplemented with 0.1 mmol of naringenin for only the first month and then given the standard nutrition solution for the next 5 months. Approximately 100-150 mL of each solution was administered via root application daily. The treatments lasted 5 months. The composition of the standard nutritional solution has been described previously (Sarruje, 1975). At the end of the experiment, all 5 groups of plantlets were cut, and their stems were debarked, immediately frozen in liquid nitrogen and kept at -80ºC for analysis; no growth differences were observed between the control and treatment groups. All samples were analyzed 5 months after the beginning of the experiment, regardless of the applied supplementation.

Naringenin (4'-,5-,7-trihydroxyflavanone, 95%) and naringenin-chalcone (1,3-diphenyl-2-propen-1-one, 97%) were purchased from Sigma-Aldrich Co. (Tokyo, Japan) and AcrosOrganics Co. (Tokyo, Japan), respectively.

### Total RNA extraction

Total RNA was extracted according to the protocol described by Zeng and Yang (2002), with the modifications proposed by Le Provost et al. (2003). The obtained RNA concentration and quality were verified using a Nanodrop 2000 spectrophotometer (Thermo Scientific).

### mRNA sequencing

mRNA sequencing was performed at the High-Throughput Sequencing Facility of the Carolina Center for Genome Sciences (University of North Carolina, USA). From each xylem sample, 10 µg of total RNA was used to prepare an mRNAseq library according to the protocol provided by Illumina. The gel extraction step was modified by dissolving excised gel slices at room temperature to avoid underrepresentation of AT-rich sequences (Quail et al. 2008). Quality control and quantification of the libraries were performed using a DNA 1000 series II Bioanalyzer Chip (Agilent). For each library, single-end sequences of 36 or 50 bp were generated in a single lane using an Illumina Genome Analyzer IIx. A total of 8 libraries were generated: 3 biological replicates of the control group (CT); 2 biological replicates of the 5-month naringenin-supplemented groups (NAR); and 1 library for each remaining group (subjected to 1 month of supplementation with naringenin (NARSTOP), 5 months of supplementation with naringenin-chalcone (CH) or 1 month of supplementation with naringenin-chalcone (CHSTOP). Each library was constructed from a sample pooled from 3 individual trees.

### Read alignment

The obtained Illumina reads were filtered to exclude ribosomal sequences (using the SILVA database (Pruesse et al. 2007) and low quality reads (phred ≥ 20). The remaining reads were aligned against the greater splice variants of *E. grandis* transcripts from Phytozome 7.0 (44,974 sequences) using the SOAP2 alignment software package (Li et al. 2009). To prepare the data for Genebrowser analysis, the reads were aligned to the *E. grandis* genome using the TopHat aligner (Trapnell et al. 2009) to allow for spliced alignments. Both programs were configured to allow up two mismatches (because SNPs can generate mismatches in the alignments, especially in cases such as the present analysis, where the sequences come from different

species), discard sequences with ambiguities (Ns) and return only reads with unique alignments.

**Gene annotation**

The Autofact program (Koski et al. 2005) was used to perform an automatic annotation of all *E. grandis* transcripts. The main feature of Autofact is its ability to perform gene annotation based on sequence similarity searches of several databases. BLASTx (Altschul et al. 1997) (e-value cutoff of 1e-5) was used to align the obtained contigs against the following public databases: the *NCBI* non-redundant (NR) database; the Uniref90 and Uniref100databases, which contain clustered sets of proteins from Uniprot (Suzek et al. 2007); the KEGG database of metabolic pathways (Kanehisa 2000); and TAIR (version 10), an *Arabidopsis* proteins database. Functional annotation (GO) was performed using BLAST2GO (Conesa et al. 2005) and MaPMAN with the default parameters.

**Determination of gene expression levels**

Gene expression was measured via the FPKM (fragments per kilobase of exon per million fragments mapped) method using only one read alignment for each transcript, as described by Mortazavi et al. (2008). The FPKM values for all transcripts are available for searching in the EUCANEXT database (www.lge.ibi.unicamp.br/eucalyptusdb).

**Enzymatic Hydrolysis**

**Substrate preparation**

Samples from each Eucalyptus treatment were frozen in liquid nitrogen and then dried in FreeZone6 (Labconco) at - 51°C and 25 Pa for 48 hours. Subsequently, the lignocellulosic material was reduced through 1cycle of 5 minutes in a ball-milling reactor. The milled material was used as a substrate for fungal growth and hydrolysis assays.

**Secretome production for enzymatic hydrolysis**

The *Neurospora crassa* wide strain St.L. 74A (Missouri University, Kansas City, http://www.fgsc.net/) was used for secretome production. Conidia preparation was performed by inoculating the fungus in 100 mL of minimal medium plus Vogel's salts supplemented with 143 µL of biotin (biotin 5 mg, ethanol 50% (v/v), 143 µL of a trace element solution (5 g monohydrate citric acid, 5 g of ZnSO4.7H2O, 1 g of Fe(NH4)2.6H2O, 0.25 g of CuSO4.5H2O, 0.05 g MnSO4.H2O, 0.05 g H3BO3, 0.05 g Na2MoO4.2H2O, qsp 1,000 mL), 1.5% agar and 2% sucrose. The prepared samples were grown for 3 days at 30°C in the dark and then for 7 days in the light at 25°C. A conidial suspension was then inoculated in 100 mL of the same medium described above without agar (Phillips et al. 2011) containing as the only carbon source 2% of a substrate blend of 3 *Eucalyptus* species: *E. grandis*, *E. urograndis* and *E. urophylla*, in a ratio of 3:3:1,prepared as described above.

**Eucalyptus hydrolysis**

Hydrolysis was performed as described by Bragatto et al. (2012) with the following modifications: enzymatic hydrolysis was performed in 2 mL tubes shaken at 1,000 rpm at 30°C in a Thermomixer (Eppendorf) for 48 hours. Approximately 10 mg of substrate from each substrate preparation was diluted in 400 µL of 50 mM sodium acetate buffer pH 5.5, and 100 µL of the *N. crassa* secretome was then added. The protein concentration of the secretome was 0.4 µg/µL, as determined in a Bradford Kit assay (BioRad) with BSA as a standard. This temperature and pH were optimal for the hydrolysis of carboxymethyl cellulose, xylan and ß-

glucan, as determined by testing the temperatures of 25-40 °C and pH levels of 4.0−9.0. All hydrolysis reactions were performed in triplicate. For determination of the reducing sugar concentration and glucose production in supernatants derived from *Eucalyptus* hydrolysis, 2 mL tubes were centrifuged at 20,000 x g for 10 minutes at 4°C. The supernatant was then recovered, and 100 µL of each reaction was used to determine the content of reducing sugars by adding 100 µL of the dinitrosalicylic acid (DNS) assay reagent (Miller 1959) heated to 99 °C. A 100 µl aliquot of the sample was next transferred to an ELISA plate, and its absorbance was measured at 540 nm using a Tecan Infinite M200 microplate reader, referring to calibration curves generated from glucose solutions. To calculate glucose contents, 20 µL of the supernatant was added to 100 µL of a working solution from a Glucose Oxidase Kit (Laborlab) in ELISA plates. The reaction was subsequently incubated at 37°C for 10 minutes, and its absorbance and measured at 505 nm (in a Tecan Infinite M200 microplate reader). Glucose concentrationswere calculated with a factor referring to a standard solution of glucose at 1 mg/mL. A blank reaction containing only buffer and substrate was subtracted from the measurements obtained for each assay.

## Results

### RNA sequencing and differential gene expression

A total of over 335 million reads were generated from 8 samples: 3 samples from the control group (CT); 3 from the naringenin-supplemented groups (2 NAR and 1 NARSTOP); and 2 from the naringenin-chalcone supplemented groups (1 CH and 1 CHSTOP). The number of reads per sample ranged from 32 to 54 million (total) and 30 to 48 million (after filtering). The reads were mapped against the greater splice variants (44,974 sequences) of the *E.grandis* gene predictions from Phytozome 7.0 (54,935 transcripts) using the SOAP2 alignment software package (Li et al., 2009) (Supplementary file 1).

Heat map clustering of all transcripts was performed using Expander software (Shamir et al. 2005), resulting in 2 major groups: 1 formed by the 3 control sample replicates and the other by the flavonoid-supplemented samples (Figure 1).

The read counts from each sample were used to test the differential expression of the genes between the control (CT) and supplemented (CH, NAR, CHSTOP and NARSTOP) treatments using the baySeq package(Hardcastle and Kelly 2010). A total of 1,573 genes were considered to be differentially expressed (FDR < 0.01), which were distributed among the treatments (917 CH; 1,289 NAR; 268 CHSTOP; 47 NARSTOP) (Supplementary file 2).

The gene expression patterns observed for the supplemented and control groups were distinct, while similar profiles were observed within treatments, indicating similarities among the different types of flavonoid supplementation studied here. Most of the differences were observed in the long-term supplementation treatments, which comprised almost all of the genes that were differentially expressed in the short-term treatments as well. The NAR-supplemented plants displayed the greatest number of genes that were differentially expressed, while the NARSTOP-supplemented plants had fewer, which may indicate that naringenin supplementation has a strong, but short-lasting impact on gene expression, whereas naringenin-chalcone has a smaller but more durable impact.

### Functional analyses

To determine the biological functions of the genes responding to flavonoid supplementation, functional analyses were performed using the web-based tools Blast2GO and Mapman. The genes considered differentially expressed in each treatment were mapped to their corresponding metabolic pathways, and the treatments were tested for enrichment of particular metabolic responses.

Only 36 genes were differentially expressed in all four treatments, including genes encoding several heat-shock proteins, sequences with no hits and unknown proteins (Table 1).

Each supplemented group was analyzed individually. Common categories between different treatments are shown in Figure 2, and all affected GO categories are listed in Supplementary file 3.

Many of the down-regulated categories that were common to all treatments are involved in cell wall formation and development. On the other hand, the common up-regulated categories are all related to stress and environmental responses. Interestingly, NARSTOP, which resulted in fewer differentially expressed genes, only led to enriched GO categories among up-regulated genes.

Mapman analyses of all of the differentially expressed genes also indicated down-regulation of cell wall-related genes and phenylpropanoid pathways, whereas flavonoid, minor CHO and starch and sucrose metabolism and stress response were associated with the most genes up-regulated (Figure3).

**The phenylpropanoid genes**

To further analyze the impact of flavonoid supplementation on lignification, a broader analysis was performed on the genes from the phenylpropanoid pathway, especially those related to lignin biosynthesis.

Several phenylpropanoid genes were differentially expressed between the treated samples and controls (Table 2), including the following genes that are directly related to lignin synthesis: 4CL, HCT, 2 OMT-methyltransferases, CCR and 2 CAD genes; 4CL, HCT and CCR were down-regulated, while the 2 methyltransferases and CAD genes were up-regulated. Additionally, several laccases were down-regulated among the treatments. These results are highly significant in terms of explaining the higher S/G ratio found in supplemented plants.

Interestingly, no gene related to the phenylpropanoid pathway was differentially expressed as a result of NARSTOP treatment.

**Secondary cell wall genes**

In addition to genes from the phenylpropanoid pathway, many genes related to secondary cell wall formation were differentially expressed in response to flavonoid supplementation (Table 3). Among these genes, we observed sucrose synthases, cellulose synthases and many glucosylases and transferases, most of which were down-regulated following the prolonged supplementation treatments. However, we also observed the up-regulation of several genes related to secondary cell wall formation after both prolonged and short-term flavonoid supplementation, including galactinol synthase, stachyose synthase, raffinose synthase and starch synthase.

**Stress-related genes**

Some of the most differentially expressed genes belonged to stress-related gene categories, which were up-regulated in all of the supplemented groups. These genes included several encoding heat-shock proteins and UDP-glycosil transferases (Table 4).

**Enzymatic Hydrolysis**

To verify the effects of flavonoid supplementation on sugar yields and saccharificationin *Eucalyptus* wood, enzymatic hydrolysis was performed. The hydrolysates were analyzed for total sugar contents ('reduced sugars'), which included most of the pentoses and hexoses from the hemicellulose fraction, and glucose content ('glucose'), allowing an estimate of the percent of saccharification to be obtained.

Flavonoid-supplemented plantlets showed increased sugar and glucose values compared to the control groups. The reduced sugar content was increased from 50% (CH) to 250% (NARSTOP), and the glucose content was increased from 43% (CH) to 253% (NARSTOP). With the exception of the naringenin-chalcone prolonged supplementation treatment (CH), all of the treatment values were considered statistically significant (Table 5).

## Discussion

The metabolism of phenylpropanoids follows 2 main pathways: the lignin branch and the flavonoid branch. The two pathways share common substrates and enzymes, and these shared components lead to a high level of interdependence between the pathways. Considering the economic interest in *Eucalyptus* trees for paper and pulp production, and given that flavonoids are known to have a direct influence on lignification and wood formation in several species(Chen et al. 2004; Deng et al. 2004), including *Eucalyptus* species, as previously demonstrated by our group (Lepikson-Neto et al 2013), it is of high interest to verify the effects of flavonoid supplementation on gene expression, especially concerning genes related to wood formation. Additionally, there is a pressing interest in expanding the industrial uses of *Eucalyptus* because *Eucalyptus* forest cultures are well-established in Brazil and may affect other strategic sectors, such as second-generation biochemicals. In this case, *Eucalyptus* wood could be employed as lignocellulosic biomass for biological fermentation (Mizrachi et al. 2011; Mansfield et al. 2012).

With this objective, we designed the present work to investigate the molecular basis of the differences in wood observed in flavonoid-supplemented *E. urograndis* trees. Additionally, in light of our previous findings, we paid special attention to the expression of genes involved with lignin and secondary cell wall formation and to the possible association between gene expression and the chemical composition of wood in *Eucalyptus*.

We analyzed the whole genome (44,974 genes) of *Eucalyptus* plants following supplementation with different flavonoids. A total of 1,573 (3,5%) differentially expressedgenes were identified, which were distributed among the supplementation groups: 963 genes were down-regulated and 610 genes were up-regulated. Most of the differentially expressed genes were associated with the prolonged supplementation groups (1,289 for NAR and 917 for CH), while the short-term supplementation groups displayed fewer differentially expressed genes (268 for CHSTOP and 47 for NARSTOP). Most of the differentially expressed genes in the CHSTOP and NARSTOP groups were also differentially expressed in the NAR and CH groups. Thus, naringenin supplementation appears to have had a stronger but less durable effect, while naringenin-chalcone supplementation has a longer-lasting effect on gene expression.

GO enrichment analyses demonstrated that there were several categories involved in cell wall formation that were down-regulated in all of the supplemented groups, including the phenylpropanoid pathway in the NAR-supplemented samples. The up-regulated gene categories included many responses to stress and the environment as well as genes related to sugar alcohols, through being involved in polyol, hexitol and alditol metabolism (minor CHOs),in the CH group. This pattern could also be observed in the mapping analysis of differentially expressed genes performed using MapMan software, in which several pathways, most notably those associated with the cell wall and phenylpropanoids, were down-regulated, while the metabolic pathways associated withminor CHOs, flavonoids, sucrose and starch displayed up-regulated genes. Furthermore, there was strong evidence that stress may play a major role, as several stress-related gene categories were found to be enriched via GO analysis, even in the groups subjected to short-term supplementation.

It was therefore clear that lignification and the phenylpropanoid pathway are affected by a great number of factors, and we believe that our work can help to clarify some of these factors. The interdependence of the phenylpropanoid, flavonoid and lignin branches has been explored in other studies. For example, it has been reported that 4CL activity is inhibited by some flavonoids, such as naringenin-chalcone and naringenin, which are the products of the chalcone synthase (CHS) and chalcone isomerase (CHI) enzymes, respectively (Chen et al. 2004; Chen et al. 2005). The same study demonstrated that the administration of flavonoids suppressed the growth of 20 plant species, although the sensitivities of the plants to flavonoids were different.

In addition, the activation of the lignin precursor cinnamic acid (catalyzed by C4H) and p-coumaroyl-CoA (catalyzed by 4CL) is, to some extent, regulated by the activity of the CHS enzyme, which is involved in the first step of flavonoid biosynthesis (Chen et al. 2005). It has also been reported that CHS is associated with growth suppression via the regulation of 4CL. This association has major importance in lignin biosynthesis in a great number of species (Deng et al. 2004; Chen et al. 2005).

As demonstrated by our results, several genes involved in the phenylpropanoid pathway were differentially expressed in plants subjected to supplementation with flavonoids (Table 2; Figure3). Our most noteworthy findings revealed the differential expression of genes directly related to lignin synthesis. The NAR-supplemented group presented down-regulation of both the 4CL and CCR genes, whereas the ATOMT1 and 2 CAD genes were up-regulated. The CH-supplemented group exhibited HCT down-regulation and 1 CAD gene that was up-regulated. In the CHSTOP-supplemented group, 1 methyltransferase was up-regulated. No genes from the phenylpropanoid pathway were differentially expressed following supplementation with NARSTOP.

Surprisingly, the gene encoding F5H, which is one of the key enzymes involved in the synthesis of the monolignol sinapyl alcohol and, ultimately, the S lignin moiety, was not found to be differentially expressed on our analyses. This result is particularly interesting in light of our finding that the S/G ratios in all of the flavonoid-supplemented groups were higher than that of the control group. Thus, we expected a change in the expression of F5H following flavonoid treatment. Because phenylpropanoid metabolism is complex, it is likely that the differential regulation of other enzymatic steps, such as those encoded by the 4CL, HCT, CCR, ATOM1 and CAD genes, may underlie this response.

Some findings reported in the literature support this possibility. For example, 4CL plays a major role in phenylpropanoid metabolism, as its product, p-coumaroyl-CoA, is a substrate that is common to the flavonoid and lignin synthesis pathway. HCT silencing in *Arabidopsis* represses lignin synthesis and plant growth, and the metabolic flux is redirected toward flavonoids by chalcone synthase activity (Besseau et al. 2007). CCR catalyzes the reduction of hydroxycinnamoyl-CoA thioesters to the corresponding aldehydes; this reaction is considered to be a potential control point that regulates the overall carbon flux in favor of lignin (Lacombe et al. 1997). *Arabidopsis* ATOMT1 knock-out mutants lack S units (Goujon et al. 2003),and CAD catalyzes the reduction of cinnamaldehydes to cinnamyl alcohols, which is the last step in the biosynthesis of the monolignols, thus playing a pivotal role in determining the lignin monomer composition and increasing S contents (Baucher et al. 2003).

There are also several laccases that have been demonstrated to be involved in lignification (Berthet et al. 2011), and many laccases were found to be down-regulated in the NAR-, CH- and CHSTOP-supplemented samples.

Our results further corroborate those of Li et al. (1993), who suggested that *Arabidopsis* responds to the accumulation of 1 or more intermediates from the flavonoid pathway by down-regulating either the whole phenylpropanoid pathway or the specific branch leading to monocyclic phenolic compounds. According to our results, it is possible that the accumulation of naringenin-chalcone and naringenin, the products of CHS and CHI, respectively, due to exogenous supplementation, results in the down-regulation of genes from the phenylpropanoid

pathway, with the exception of 2 genes involved in the final steps of sinapilic acid synthesis (ATOMT1 and CAD).This down-regulation may at least partially explain the higher S/G ratios observed in the supplemented samples.

While the NARSTOP-supplemented plants did not show differential expression of any genes that are related to lignin synthesis according to our statistical analyses, they exhibited FPKM values that were similar to those of the NAR-, CH- and CHSTOP-supplemented groups, but closer to the control values than the other groups. This indicates that an early impact on gene expression may be sufficient to promote the phenotypic differences observed in this group.

Another possibility is that factors other than the genes from the lignification pathway *per se* influence the lignin monomer composition. Cook and collaborators (2012) reported that the levels of cellulose, xylan and lignin are not completely dependent on the transcription of the genes involved in these metabolic pathways. Thus, the regulation of cell wall biosynthesis occurs at different levels, not only at the transcriptional level(Cook et al. 2012).

Additionally, other genes that have not yet been discovered may be causing the observed differences, as many no hits and unknown proteins were found among the most differentially expressed genes following flavonoid treatment. The stress and environmental response pathways were significantly enriched and associated with lignification; thus, these pathways may play major roles in the alterations of lignin composition after flavonoid supplementation.

Stress and lignification are closely related. Many of the products of the phenylpropanoid pathway are induced by biotic and abiotic stress (Dixon and Paiva 1995). Both flavonoids and sinapate esters, which are used for lignin synthesis, are important for UV protection (Li et al. 1993). *Arabidopsis* mutants with reduced levels of CHS and CHI activity show up to 60% higher levels of sinapate esters (Li et al. 1993; Dixon et al 95).

Moreover, a large number of phenylpropanoids are induced by stress, such as those derived from the C15 flavonoid skeleton that are synthesized via the chalcone synthase (CHS)-mediated condensation of p-coumaroyl-coenzyme A (CoA) and three molecules of malonyl-CoA (Harbone 1988). In most plant families, the initial product of CHS is a tetrahydroxychalcone, which is further converted to other flavonoid classes, such as flavones, flavanones, flavanols, anthocyanins and 3-deoxyanthocyanidins, all of which are compounds that are important in the response to stress (Holton and Cornish 1995).

The observation that several genes related to stress responses are differentially expressed in flavonoid-supplemented trees confirms the importance of stress responses in defining *Eucalyptus* wood properties as has been previously shown by our group (Salazar et al 2013). In this work, a comparison between three *Eucalyptus* species revealed differential expression of stress-related genes in *E. urophylla, which* could explain the higher plasticity and

adaptability of this species compared to *E. grandis* and *E. globulus,* the two other studied species.

In the present study, the stress-related genes that were differentially expressed following flavonoid treatments included a noteworthy group composed of several UDP-glucosyltransferases (UGTs), which were up-regulated in all of our treatments. In plants, UGTs utilize UDP-glucose, UDP-galactose, and UDP-rhamnose as sugar donors and are involved in the modulation of plant architecture and the water stress response in *Arabidopsis* (Tognetti et al. 2010). The glucosylation of coniferyl aldehyde and sinapyl aldehyde may regulate both lignin biosynthesis and the metabolism of other phenylpropanoids, such as ferulic acid, 5-hydroxyferulic acid, sinapic acid and their derivatives (Lim et al. 2005). Thus, the presence of up-regulated UGTs in all of the groups is another interesting result that might help elucidate the chemical differences present in the flavonoid-supplemented trees.

Another notable finding regarding cell wall formation was the differential expression of genes involved in the metabolism of sucrose, starch, CHOs and minor sugars. Despite the down-regulation of sucrose synthase (Sus) and cellulose synthase (CesA), there were several other enzymes involved in this metabolic pathway that were up-regulated in the prolonged flavonoid treatments, even in the short-term treatments. Starting with galactinol synthase (GolS2), which was one of the most differentially expressed genes, all of the downstream genes in this pathway were differentially expressed (up-regulated), most of which were up-regulated after both the prolonged and short-term treatments.

The most notable of these genes was stachyose synthase (STS), which converts raafinose (a trisaccharide of galactose, fructose and glucose) into stachyose (a tetrasaccharide) by transferring a galactosyl moiety from galactinol, (Peterbauer et al. 2002). Raafinose synthase (RafS) was also differentially up-regulated. Additionally, sucrose phosphate synthase (SPS1F), which catalyses the conversion of UDP-glucose and D-fructose 6-phosphate into UDP and sucrose 6-phosphate (Chua et al. 2008), was also differentially up-regulated (Figure 4).

Starch synthase (SS) was up-regulated as well, as were enzymes involved in the degradation of starch into maltose (beta-amylase; BAM) and glucose (glycoside hydrolase; GH and phosphoglucan water dikinases; PWD). These results suggest a shift from sucrose and cellulose production to the synthesis of starch and minor sugars (galactinol, raffinose and stachyose).

Thus, to verify the possible effects of these transcriptional responses on cell wall formation and sugar accessibility, enzymatic hydrolysis was performed in wood samples from all of the experimental and control plants. The results revealed an increase in sugar contents (up to 250% in the NARSTOP group) and glucose yields of all of the flavonoid-supplemented *Eucalyptus* plants.

This may be the result of the plants producing more sugar or a result of the increased digestibility of lignin due to modifications of lignin structure and other cell wall components. The total values should increase exponentially with the use of pre-treatments and the extension of milling times (Chen and Dixon 2007; Inoue et al. 2008).

Galactinol, raffinose and stachyose have been described as being involved in freezing and stress tolerance (Saravitz et al. 1987; Taji et al. 2002). The levels of galactinol and raffinose are increased in the leaves of *Arabidops is* plants over-expressing HsfA2, a heat shock factor, suggesting a possible role for these compounds in protection from oxidative damage (Nishizawa et al. 2008). Moreover, this factor may also constitute another link between the stress response and cell wall formation in flavonoid-supplemented *Eucalyptus* plants because all of our treatment groups showed more than 1up-regulated HsfA2 gene.

Our results are also in agreement with those of Unda et al. (2012), who verified that in poplar trees, the over-expression of GolS and its product, galactinol, may serve as a molecular signal that initiates metabolic changes associated with combating stress, culminating in the formation of tension wood and increased glucose contents. Additionally, over-expression of raffinose synthase was found to result in increased biomass and total cellulose contents, while the total contents of lignin and xylose moieties were slightly reduced. Furthermore, the total amount of glucose was commensurately increased in the transgenic trees, by from ~1 to 4% (Unda et al 2012). Moreover, repression of the flavonoid pathway in *Arabidopsis* increases starch levels (Rubin et al. 2009), and a chalcone isomerase-deficient *Arabidopsis* mutant exhibits increased levels of starch and soluble sugars in its leaves.

Based on our results, flavonoid supplementation causes a stress response in *E. urograndis*, greatly affecting cell wall development, modifying lignification by affecting the expression of genes involved in the phenylpropanoid pathway and altering sugar metabolismin favor of starch and minor sugar synthesis, resulting in increased sugar accessibility and saccharification.

**Conclusion**

The effects of flavonoid supplementation on cell wall development in *Eucalyptus* plants are most likely due to a combination of transcriptional changes in several distinct pathways. The down-regulation of the phenylpropanoid pathway, combined with the up-regulation of ATOMT1 and CAD, results in a higher S/G ratio, which in turn, increases lignin solubility and facilitates access to cellulose and hemicellulose. Subsequently, as a result of the stress response, sugar metabolism is shifted towards starch and minor sugars, culminating in the increased sugar and saccharification levels identified due to hydrolysis.

Given the importance of *Eucalyptus* in several industrial sectors, there is great interest in expanding the use of these species as a resource for cellulose, paper and pulp production and as an alternative source of biomass for second-generation biochemicals. Our results contribute not only to our understanding of the molecular responses involved in wood formation but will also have a significant impact on the use of *Eucalyptus* as biomass. Finally, we expect our findings to guide future genetic manipulation and nutritional supplementation analyses of *Eucalyptus* trees aimed at achieving significant improvements in their productivity yields.

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## FIGURES AND TABLES

**Table 1. Gene ID, FPKM values and annotation of the 36 genes that found to bedifferentially expressed in all tested conditions.**

| Gene ID | Annotation | FPKM | | | | |
|---|---|---|---|---|---|---|
| | | CT | CH | NAR | CHSTOP | NARSTOP |
| Eucgr.F04479.1 | HSP20 | 0.12 | 35.55 | 40.44 | 23.84 | 57.92 |
| Eucgr.K02389.1 | unknown | 0.04 | 13.69 | 10.18 | 9.89 | 26.99 |
| Eucgr.K02399.1 | unknown | 0.08 | 18.09 | 18.67 | 19.48 | 53.82 |
| Eucgr.G01188.2 | EGY3 | 2.78 | 45.78 | 41.56 | 33.40 | 76.35 |
| Eucgr.J01979.1 | HSP18.2 | 0.34 | 17.61 | 19.94 | 14.63 | 27.21 |
| Eucgr.K02410.1 | unknown | 0.13 | 14.27 | 10.66 | 12.52 | 29.61 |
| Eucgr.J01980.1 | HSP18.2 | 0.02 | 12.20 | 11.59 | 9.15 | 26.39 |
| Eucgr.L02233.1 | no hit | 1.29 | 41.47 | 38.15 | 29.24 | 118.40 |
| Eucgr.F02898.1 | HSP20 | 2.76 | 525.99 | 343.17 | 280.68 | 342.59 |
| Eucgr.J01985.1 | HSP18.2 | 0.31 | 22.25 | 16.62 | 13.21 | 33.33 |
| Eucgr.K03553.1 | STS | 0.04 | 4.11 | 4.59 | 2.83 | 6.87 |
| Eucgr.L03261.1 | HSP18.2 | 1.44 | 47.41 | 27.81 | 19,98 | 75,67 |
| Eucgr.C03449.1 | HSFA2 | 0.29 | 14.55 | 12.98 | 14.36 | 18.58 |
| Eucgr.C00684.1 | HSP17.6II | 2.00 | 341.30 | 299.30 | 243.65 | 272.90 |
| Eucgr.K02384.1 | unknown | 0.07 | 14.56 | 10.59 | 10.60 | 27.23 |
| Eucgr.J01969.1 | HSP20 | 4.89 | 192.23 | 134.53 | 103.09 | 310.44 |
| Eucgr.K03472.1 | ARATH | 0.07 | 109.57 | 84.15 | 62.04 | 20.94 |
| Eucgr.H04513.1 | HSP70 | 0.23 | 15.72 | 18.79 | 11.56 | 21.62 |
| Eucgr.A00595.1 | PEBP | 0.10 | 81.17 | 76.66 | 57.33 | 98.83 |
| Eucgr.E02421.1 | unknown | 0.19 | 260.04 | 220.12 | 119.63 | 51.05 |
| Eucgr.H04692.1 | HSP21 | 2.97 | 83.31 | 59.57 | 43.11 | 313.22 |
| Eucgr.G02440.1 | UGT73B2 | 0.00 | 5.46 | 5.80 | 3.33 | 4.06 |
| Eucgr.G02259.1 | UGT73B3 | 0.00 | 2.73 | 2.14 | 1.18 | 3.10 |
| Eucgr.J01959.1 | HSP18.2 | 3.19 | 142.90 | 89.76 | 58.22 | 148.21 |
| Eucgr.K00295.1 | HSP90.1 | 2.11 | 46.13 | 38.25 | 35.52 | 62.69 |
| Eucgr.A01833.1 | AAC3 | 0.13 | 32.00 | 24.43 | 15.08 | 10.47 |
| Eucgr.C03071.1 | HSP17.6II | 3.64 | 517.08 | 509.51 | 451.66 | 324.54 |
| Eucgr.B03843.1 | no hit | 1.45 | 93.17 | 63.39 | 67.61 | 20.77 |
| Eucgr.C03320.1 | DUF1677 | 0.38 | 24.39 | 18.22 | 14.01 | 9.78 |
| Eucgr.B00176.2 | PIMT2 | 3.86 | 153.25 | 109.01 | 82.97 | 57.39 |
| Eucgr.J02588.1 | no hit | 3.20 | 225.90 | 182.76 | 194.01 | 130.04 |
| Eucgr.C00690.1 | HSP17.6II | 2.48 | 563.68 | 498.40 | 514.67 | 458.94 |
| Eucgr.K00237.1 | PEBP | 0.04 | 115.83 | 64.41 | 61.47 | 11.49 |
| Eucgr.F03196.1 | GSTU25 | 1.43 | 292.73 | 240.63 | 168.71 | 38.29 |
| Eucgr.I02136.1 | HSP20 | 1.68 | 226.73 | 147.43 | 90.02 | 259.35 |
| Eucgr.H04427.1 | MEE32 | 49.92 | 0.52 | 0.85 | 1.32 | 13.93 |

A total of 36 genes were differentially expressed in all four conditions. FPKM -fragments per kilobase of exon per million fragments mapped.All results are controlled for the FDR – false discovery rate ≤ 0.01. CT – control; CH – prolonged naringenin-chalcone supp; NAR – prolonged naringenin supp; CHSTOP- short-term naringenin-chalcone supp; NARSTOP – short-term naringenin supp. *HSP20– HSP20-like chaperone superfamily protein; unknown– unknown protein; EGY3–ethylene-dependent gravitropism-deficient and yellow-green-like 3; HSP18.2–heat shock protein 18.2; HSP20- HSP20-like chaperones superfamily protein; STS- stachyose synthase; HSFA2- heat shock transcription factor A2; HSP17.6II –17.6 kDa class II heat shock protein; ARATH –Adenine nucleotide alpha hydrolases-like superfamily protein; HSP70 –BIP1heat shock protein 70 family protein; PEBP – phosphatidylethanolamine-binding protein family protein; HSP21 –heat shock protein 21; UGT73B2 –UDP-glucosyltransferase 73B2; UGT73B3UDP – glucosyl transferase 73B3; HSP90.1 –heat shock protein 90.1; AAC3 – ADP/ATP carrier 3; DUF1677 –protein of unknown function; PIMT2 –protein-l-isoaspartate methyltransferase 2;*

*GSTU25 –glutathione S-transferase TAU 25; MEE32 dehydroquinate dehydratase, putative / shikimate dehydrogenase*

**Table 2. Differentially expressed phenylpropanoid-related genes**

| | | FPKM | | | | |
|---|---|---|---|---|---|---|
| **Gene ID** | **Annotation** | **CT** | **CH** | **NAR** | **CHSTOP** | **NARSTOP** |
| Eucgr.C00859.1 | U91A1 | 0.00 | 1.60* | 0.83 | 0.28 | 0.00 |
| Eucgr.K00903.1 | AAT | 0.38 | 3.91 | 4.61* | 3.45 | 1.26 |
| Eucgr.K00901.1 | AAT | 0.83 | 0.03* | 0.98 | 1.18 | 1.51 |
| Eucgr.E01250.1 | PRR1 | 38.77 | 3.72* | 4.68* | 7.66 | 21.15 |
| Eucgr.B03781.1 | AA | 24.04 | 0.04* | 0.86 | 1.39 | 9.77 |
| Eucgr.D02454.1 | DFR | 0.05 | 3.10* | 2.73* | 1.32 | 0.48 |
| Eucgr.G02325.1 | DFR | 2.51 | 28.24* | 20.16* | 21.06 | 9.55 |
| Eucgr.F04163.1 | LAC14 | 6.22 | 0.15 | 0.32* | 0.57 | 1.82 |
| Eucgr.F02646.1 | LAC14 | 1.99 | 0.00* | 0.02* | 0.06* | 0.44 |
| Eucgr.F04162.1 | LAC14 | 1.95 | 0.09 | 0.04* | 0.06 | 0.72 |
| Eucgr.H04937.1 | LAC14 | 13.67 | 0.02* | 0.15* | 0.21 | 4.66 |
| Eucgr.F04160.1 | LAC14 | 17.17 | 0.04* | 0.25* | 0.26* | 3.08 |
| Eucgr.F02674.1 | LAC14 | 7.13 | 0.28 | 0.27* | 0.42 | 2.90 |
| Eucgr.H04936.1 | LAC14 | 8.51 | 0.04* | 0.03* | 0.08 | 2.50 |
| Eucgr.B02796.1 | LAC4 | 12.04 | 0.28* | 1.95 | 3.31 | 5.69 |
| Eucgr.K00957.1 | ATOMT1 | 1.36 | 17.54 | 17.19* | 10.55 | 15.16 |
| Eucgr.A01877.1 | OMT-like | 0.00 | 0.31 | 0.79 | 1.75* | 0.22 |
| Eucgr.J00363.1 | HCT | 88.68 | 3.76* | 16.43 | 29.57 | 53.35 |
| Eucgr.B00137.1 | 4CL | 12.31 | 1.83 | 2.50* | 4.21 | 6.24 |
| Eucgr.E00270.1 | CCR | 30.29 | 3.21 | 3.29* | 4.03 | 8.00 |
| Eucgr.G01350.2 | CAD5 | 23.73 | 146.29* | 126.30* | 144.55 | 62.96 |
| Eucgr.E01110.2 | CAD1 | 4.34 | 59.21 | 49.17* | 51.45 | 27.12 |

*U91A1 –UDP-Glycosyltransferase superfamily protein; AAT –HXXXD-type acyl-transferase family protein; DFR –Dihydroflavonol-4-reductase; LAC14 –laccase 14; LAC4 –laccase 4; ATOMT1 –O-methyltransferase 1; OMT-like –O-methyltransferase family protein; HCT –hydroxycinnamoyl-CoA shikimate transferase; 4CL –4 coumarate CoA ligase; CCR–cinnamoyl-CoA reductase; CAD–cinnamyl alcohol dehydrogenase.*Denotes differential expression*

**Table 3. Differentially expressed secondary cell wall genes**

| Gene ID | Annotation | FPKM | | | | |
|---|---|---|---|---|---|---|
| | | CT | CH | NAR | CHSTOP | NARSTOP |
| Eucgr.C03199.1 | SUS4 | 1,532.75 | 66.91* | 100.38* | 132.04 | 213.15 |
| Eucgr.C01715.1 | SPS1F | 3.32 | 63.28* | 54.72 | 35.80* | 28.00 |
| Eucgr.F00464.1 | SUT4 | 28.18 | 85.70 | 85.04 | 82.49* | 36.89 |
| Eucgr.D01765.2 | CSLG3 | 0.07 | 3.26 | 6.28* | 7.07* | 1.24 |
| Eucgr.F04010.1 | CSLC05 | 7.51 | 0.11* | 0.35 | 0.47* | 3.06 |
| Eucgr.J00420.1 | CSLA2 | 41.08 | 2.63* | 5.07* | 5.87* | 25.59 |
| Eucgr.E00226.1 | CSLD3 | 10.13 | 0.53 | 0.78 | 0.68 | 2.11 |
| Eucgr.E00821.1 | CSLG2 | 3.07 | 0.38* | 0.35 | 0.78* | 3.03 |
| Eucgr.J02497.1 | AMR1 | 1.00 | 5.25 | 6.14 | 6.11* | 2.68 |
| Eucgr.J02407.1 | MUR1 | 74.28 | 18.89 | 17.82 | 19.95* | 38.28 |
| Eucgr.B03204.1 | MUR2 | 13.62 | 55.51 | 54.92 | 47.91* | 32.70 |
| Eucgr.J01663.1 | XTH5 | 97.41 | 1.21* | 1.87* | 3.31* | 75.71 |
| Eucgr.B03348.1 | XTH33 | 26.89 | 0.21 | 0.15* | 0.07* | 9.47 |
| Eucgr.K00883.2 | XTH9 | 607.60 | 16.06* | 29.74 | 37.61* | 288.85 |
| Eucgr.C00184.1 | XTH23 | 45.26 | 0.45 | 0.72* | 0.22* | 37.20 |
| Eucgr.H02634.1 | XTH16 | 386.73 | 21.78* | 47.14 | 72.69 | 396.09 |
| Eucgr.D01294.1 | XTH8 | 10.82 | 1.01 | 1.54 | 1.66* | 7.36 |
| Eucgr.J00827.1 | GSL12 | 0.04 | 0.90* | 1.56* | 0.98* | 0.76* |
| Eucgr.A02002.1 | GSL7 | 0.20 | 1.24 | 2.13 | 1.38* | 0.79 |
| Eucgr.A02008.1 | GSL7 | 0.16 | 1.07 | 1.89 | 1.66* | 0.83 |
| Eucgr.K02988.2 | GH | 16.20 | 90.51* | 69.09* | 53.94 | 47.27* |
| Eucgr.H00494.1 | PWD | 6.13 | 20.24 | 26.24* | 27.22 | 7.21 |
| Eucgr.H03767.1 | BAM9 | 39.25 | 225.21 | 235.09* | 217.12 | 115.07 |
| Eucgr.E00460.1 | TPS | 0.08 | 5.75* | 6.21* | 4.26 | 0.34 |
| Eucgr.K00387.1 | SS | 9.88 | 66.76* | 54.46* | 39.19 | 19.93 |
| Eucgr.C04266.1 | RafS | 26.09 | 1,317.97* | 1007.17 | 544.49 | 193.24 |
| Eucgr.K03553.1 | STS | 0.04 | 4.11* | 4.59* | 2.83* | 6.87* |
| Eucgr.H00997.1 | STS | 0.81 | 37.45* | 29.83* | 17.09* | 7.06* |
| Eucgr.K03563.1 | GoSL1 | 0.23 | 4.48 | 11.12* | 12.00 | 8.48* |
| Eucgr.L00249.1 | GoSL2 | 0.34 | 280.16* | 135.36* | 52.37* | 1.25 |
| Eucgr.L00243.1 | GoSL2 | 0.02 | 29.83* | 19.77* | 9.75* | 1.37* |
| Eucgr.L00251.1 | GoSL2 | 0.21 | 325.56* | 149.21* | 61.46* | 3.38 |
| Eucgr.L03245.1 | GoSL2 | 0.07 | 190.81* | 124.71* | 44.86* | 2.79* |
| Eucgr.L00240.1 | GoSL2 | 0.02 | 34.50* | 22.77* | 10.27* | 0.66 |
| Eucgr.L00248.1 | GoSL2 | 0.17 | 162.07* | 86.93* | 32.28* | 0.69 |
| Eucgr.L03244.1 | GoSL2 | 0.12 | 279.83* | 137.40* | 63.66* | 2.99* |
| Eucgr.L00235.1 | GosL2 | 0.04 | 73.19* | 38.88* | 15.60* | 0.03 |
| Eucgr.L00245.1 | GosL2 | 1.83 | 287.87* | 164.66 | 80.81* | 5.28 |
| Eucgr.F01661.1 | Invertase | 0.15 | 2.82* | 2.16 | 2.39* | 1.33 |
| Eucgr.J00457.2 | Invertase | 5.69 | 47.20* | 42.83 | 33.08* | 18.78 |
| Eucgr.G01751.1 | Invertase | 4.83 | 0.23* | 0.42 | 1.17* | 2.23 |
| Eucgr.A02888.1 | Invertase | 7.36 | 0.04* | 0.08* | 0.08* | 1.55 |

*Sus4 –sucrose synthase 4; SPS1F –sucrose phosphate synthase 1F; SUT4 –sucrose transporter 4; CSLG3 –cellulose synthase like G3; CSLD3 –cellulose synthase-like D3; CSLC05 –Cellulose-synthase-like C5; CSLA2 –cellulose synthase-like A02; CSLG2 –cellulose synthase like G2; CSLG3 –cellulose synthase like G3; CESA3 –cellulose synthase family protein; AMR1 –ascorbic acidmannose pathway regulator 1; GDP-mannose 4,6 dehydratase 2; MUR2 fucosyltransferase 1 ; XTH5 xyloglucan endotransglucosylase/hydrolase 5; XTH33 xyloglucosyl transferase 33; XTH9 xyloglucan endotransglucosylase/hydrolase 9; XTH23 xyloglucan endotransglycosylase 6; XTH16 xyloglucan endotransglucosylase/hydrolase 16; XTH8 xyloglucan endotransglucosylase/hydrolase 8; GSL12 glucan synthase-like 12; GSL7 glucan synthase-like 7; GH glycoside hydrolase;PWD phosphoglucan water dikinases; BAM9 beta-amylase 9 TPS trehalose-6-phosphate synthase; SS starch synthase; Rafs raafinose synthase; STS stachyose synthase; GoSL1 galactinol synthase 1; GoSL2 galactinol synthase 2. *Denotes differential expression*

**Table 4. Differentially expressed stress-related genes**

| Gene ID | Annotation | FPKM | | | | |
|---|---|---|---|---|---|---|
| | | CT | CH | NAR | CHSTOP | NARSTOP |
| Eucgr.H05081.4 | ALDH3I1 | 4.84 | 0.93* | 1.11* | 1.60 | 5.34 |
| Eucgr.C00112.1 | CIA2 | 0.70 | 12.29* | 14.05* | 17.42* | 3.57 |
| Eucgr.K01387.2 | COL9 | 3.33 | 26.78* | 22.63* | 18.02* | 2.56 |
| Eucgr.C03449.1 | HSFA2 | 0.29 | 14.55* | 12.98* | 14.36* | 18.58* |
| Eucgr.C03456.1 | HSFA2 | 0.09 | 2.67* | 3.64* | 2.25* | 1.45 |
| Eucgr.C00873.1 | HSFA2 | 1.92 | 24.38* | 18.82* | 14.75* | 7.94 |
| Eucgr.C03434.1 | HSFA2 | 0.31 | 6.75* | 6.22* | 6.19* | 2.03 |
| Eucgr.C01043.1 | HSFC1 | 2.92 | 122.26* | 116.87* | 96.98* | 13.96 |
| Eucgr.J01981.1 | HSP18.2 | 2.00 | 34.43 | 50.34 | 69.86* | 105.48* |
| Eucgr.J01980.1 | HSP18.2 | 0.02 | 12.20* | 11.59* | 9.15* | 26.39* |
| Eucgr.J01959.1 | HSP18.2 | 3.19 | 142.90* | 89.76* | 58.22* | 148.21* |
| Eucgr.J01958.1 | HSP18.2 | 2.68 | 115.32* | 90.34* | 65.56 | 100.03 |
| Eucgr.J01979.1 | HSP18.2 | 0.34 | 17.61* | 19.94* | 14.63* | 27.21* |
| Eucgr.J01958.1 | HSP18.2 | 2.68 | 115.32* | 90.34* | 65.56 | 100.03 |
| Eucgr.J01979.1 | HSP18.2 | 0.34 | 17.61* | 19.94* | 14.63* | 27.21* |
| Eucgr.J01977.1 | HSP18.2 | 0.37 | 9.43* | 8.59* | 7.08 | 19.26* |
| Eucgr.J01964.1 | HSP18.2 | 13.65 | 145.21* | 119.05* | 111.04 | 251.88* |
| Eucgr.J01985.1 | HSP18.2 | 0.31 | 22.25* | 16.62* | 13.21* | 33.33* |
| Eucgr.J01982.1 | HSP18.2 | 0.21 | 8.65* | 6.06* | 4.24 | 13.03* |
| Eucgr.F04479.1 | HSP20-like | 0.12 | 35.55* | 40.44* | 23.84* | 57.92* |
| Eucgr.I02136.1 | HSP20-like | 1.68 | 226.73* | 147.43* | 90.02* | 259.35* |
| Eucgr.J01969.1 | HSP20-like | 4.89 | 192.23* | 134.53* | 103.09* | 310.44* |
| Eucgr.G00061.1 | HSP20-like | 9.45 | 834.94* | 858.21* | 726.74* | 814.87 |
| Eucgr.E00433.1 | HSP20-like | 3.35 | 295.94 | 205.55* | 185.03 | 165.89 |
| Eucgr.F02898.1 | HSP20-like | 2.76 | 525.99* | 343.17* | 280.68* | 342.59* |
| Eucgr.A01416.1 | HSP21 | 0.08 | 12.40* | 7.60* | 4.34* | 0.29 |
| Eucgr.H04692.1 | HSP21 | 2.97 | 83.31* | 59.57* | 43.11* | 313.22* |
| Eucgr.J03127.1 | Hsp70b | 8.27 | 1576.75 | 1347.55* | 881.92 | 925.42 |
| Eucgr.H03518.1 | HSP70T-2 | 6.06 | 282.04* | 218.12* | 152.91 | 249.47 |
| Eucgr.K00295.1 | HSP90-1 | 2.11 | 46.13* | 38.25* | 35.52* | 62.69* |
| Eucgr.F03704.1 | MSL6 | 1.45 | 27.74* | 21.67* | 11.53* | 10.03 |
| Eucgr.H02896.1 | MYB305 | 0.07 | 6.57* | 8.20* | 6.34* | 1.14 |
| Eucgr.C00618.1 | Oleosin | 0.50 | 38.75* | 24.66* | 18.36* | 2.85 |
| Eucgr.F01003.1 | PAT1 | 2.30 | 43.54* | 47.40* | 43.89* | 6.02 |
| Eucgr.K00237.1 | PEBP | 0.04 | 115.83* | 64.41* | 61.47* | 11.49* |
| Eucgr.B00176.2 | PIMT2 | 3.86 | 153.25* | 109.01* | 82.97* | 57.39* |
| Eucgr.G01510.1 | RLK | 1.71 | 10.40* | 11.17* | 11.20* | 6.80 |
| Eucgr.F01854.1 | TRX1 | 4.16 | 598.03* | 295.93* | 191.61* | 25.01 |
| Eucgr.G02440.1 | UGT73B2 | 0.00 | 5.46* | 5.80* | 3.33* | 4.06* |
| Eucgr.L03261.1 | UGT73B3 | 1.44 | 47.41* | 27.81* | 19.98* | 75.67* |
| Eucgr.G02259.1 | UGT73B3 | 0.00 | 2.73* | 2.14* | 1.18* | 3.10* |
| Eucgr.I00409.1 | UGT73B3 | 0.06 | 3.27* | 4.18* | 2.91* | 0.60 |
| Eucgr.B02291.1 | UGT76E11 | 10.86 | 52.79* | 42.69* | 39.45 | 45.69 |

| | | | | | | |
|---|---|---|---|---|---|---|
| Eucgr.K01389.2 | XERICO | 19.81 | 1,348.64* | 796.35* | 569.70* | 120.14 |

*ALDH3I1 –aldehyde dehydrogenase 3I1; CIA2 –chloroplast import apparatus 2; COL9 –CONSTANS-like 9; HSFA2 –heat shock transcription factor A2; HSFC1 –heat shock transcription factor C1; HSP18.2 –heat shock protein 18.2; HSP20 like chaperones superfamily protein; HSP21 –heat shock protein 21; Hsp70b –heat shock protein 70B; HSP70T-2 –heat-shock protein 70T-2; HSP90.1 –heat shock protein 90.1; MSL6 – mechanosensitive channel of small conductance-like 6; MYB305 –myb domain protein 305; Oleosin family protein; PAT1 –GRAS family transcription factor; PEBP –phosphatidylethanolamine-binding protein family protein; RLK –receptor lectin kinase; TRX1 –thioredoxin H-type 1; UGT73B2 –UDP-glucosyltransferase 73B2; UGT73B3 –UDP-glucosyl transferase 73B3; UGT76E11 –UDP-glucosyl transferase 76E11; XERICO –RING/U-box superfamily protein*

**Table 5. Total sugar and glucose values**

| | n | Reduced sugars (mg/ml) | Reduced sugar Yield % | Glucose (mg/ml) | Saccharification % |
|---|---|---|---|---|---|
| CT | 7 | 1.17 (0.67) | 5.69 (3.23) | 0.39 (0.23) | 1.76 (1.13) |
| CH | 4 | 1.8 (0.33) | 9.06 (1.83) | 0.56 (0.07) | 2.59 (0.37) |
| NAR | 3 | 2.54 (0.005)** | 12.72 (0.66) ** | 0.87 (0.10) ** | 4.22 (0.5) ** |
| CHSTOP | 3 | 2.32 (0.24)* | 11.81 (1.08)* | 0.85 (0.29)* | 4.1 (1.46)* |
| NARSTOP | 3 | 3 (0.85) ** | 14.59 (4.34) ** | 0.99 (0.09) ** | 4.83 (0.46) ** |

Mean values and standard deviations (parentheses) for total sugar and glucose levels. n –number of biological replicates; CT – control; CH – prolonged naringenin-chalcone supp; N – prolonged naringenin supp; CHSTOP –short-termnaringenin-chalcone supp; NSTOP – short-termnaringenin supp. * p-value < 0.05; ** p-value < 0.01

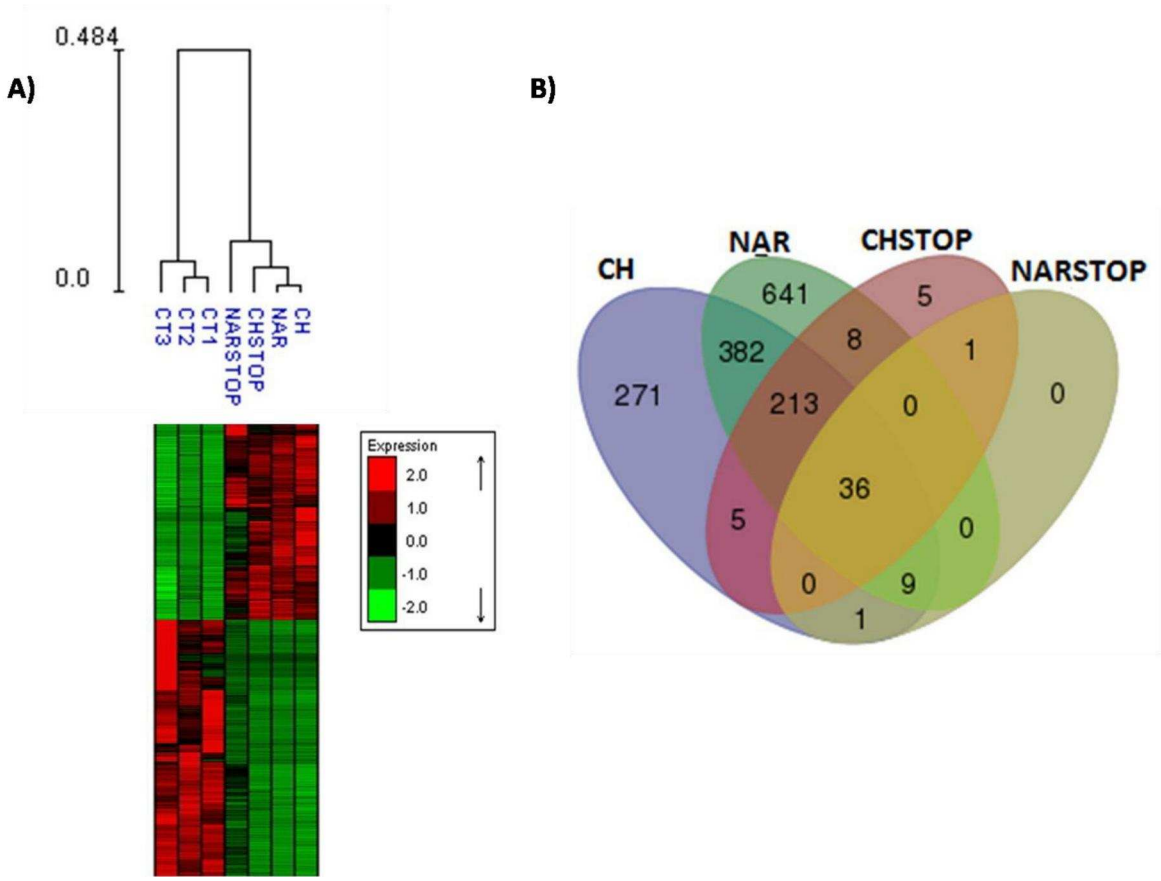


Figure 1. A) Heat map clustering of differentially expressed transcripts and comparison of the estimated log2 fold change correlations between each group subjected to differential expression analyses. B) Venn diagram of differentially expressed genes. CT – control; CH – prolonged naringenin-chalcone supp; NAR – prolonged naringenin supp; CHSTOP- short-term naringenin-chalcone supp; NARSTOP – short-termnaringenin supp

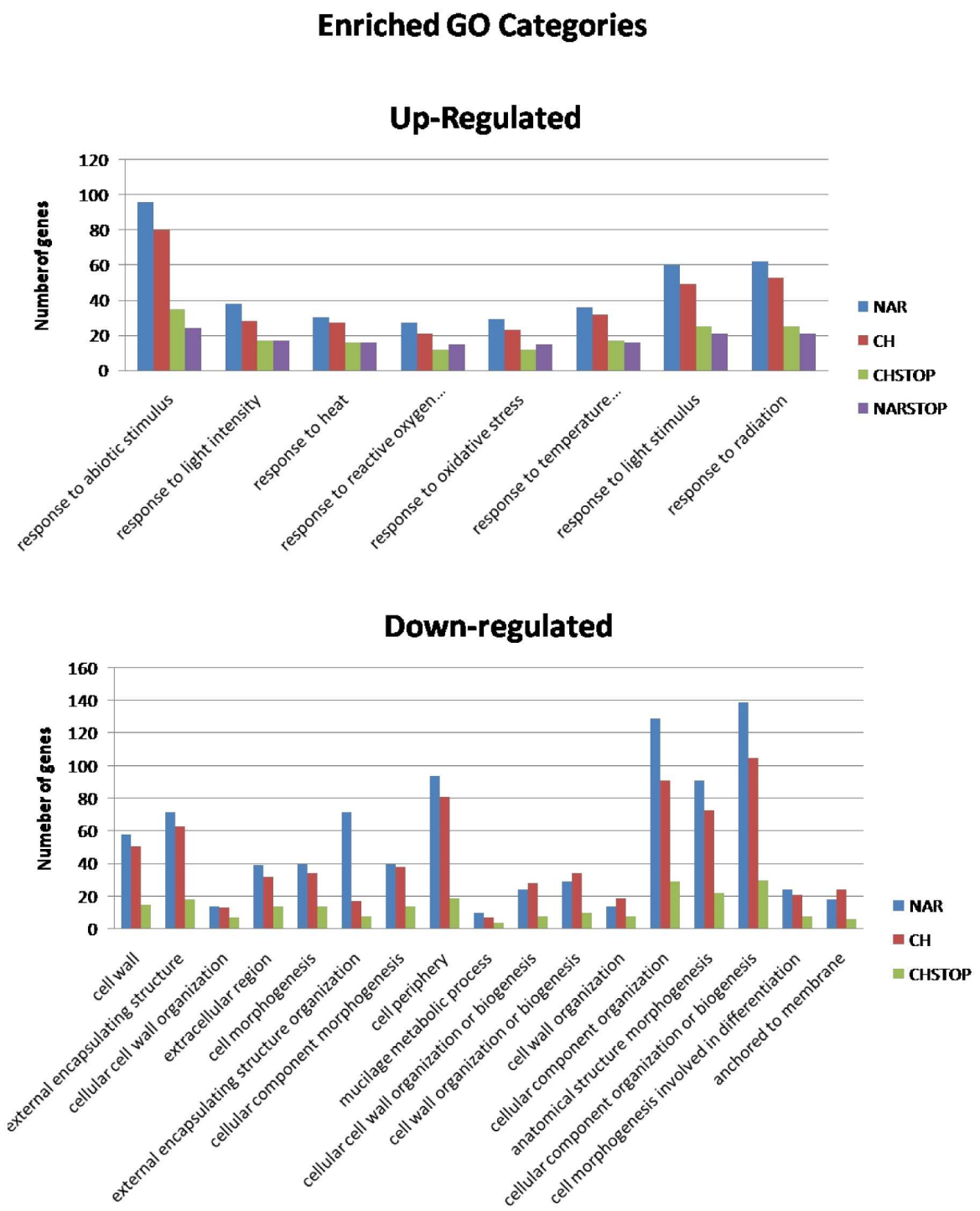


Figure 2. Common GO categories that were enriched (p-values ≤ 0.05) between treatments. CH – prolonged naringenin-chalcone supp; NAR – prolonged naringenin supp; CHSTOP- short term naringenin-chalcone supp; NARSTOP – short-term naringenin supplementation.

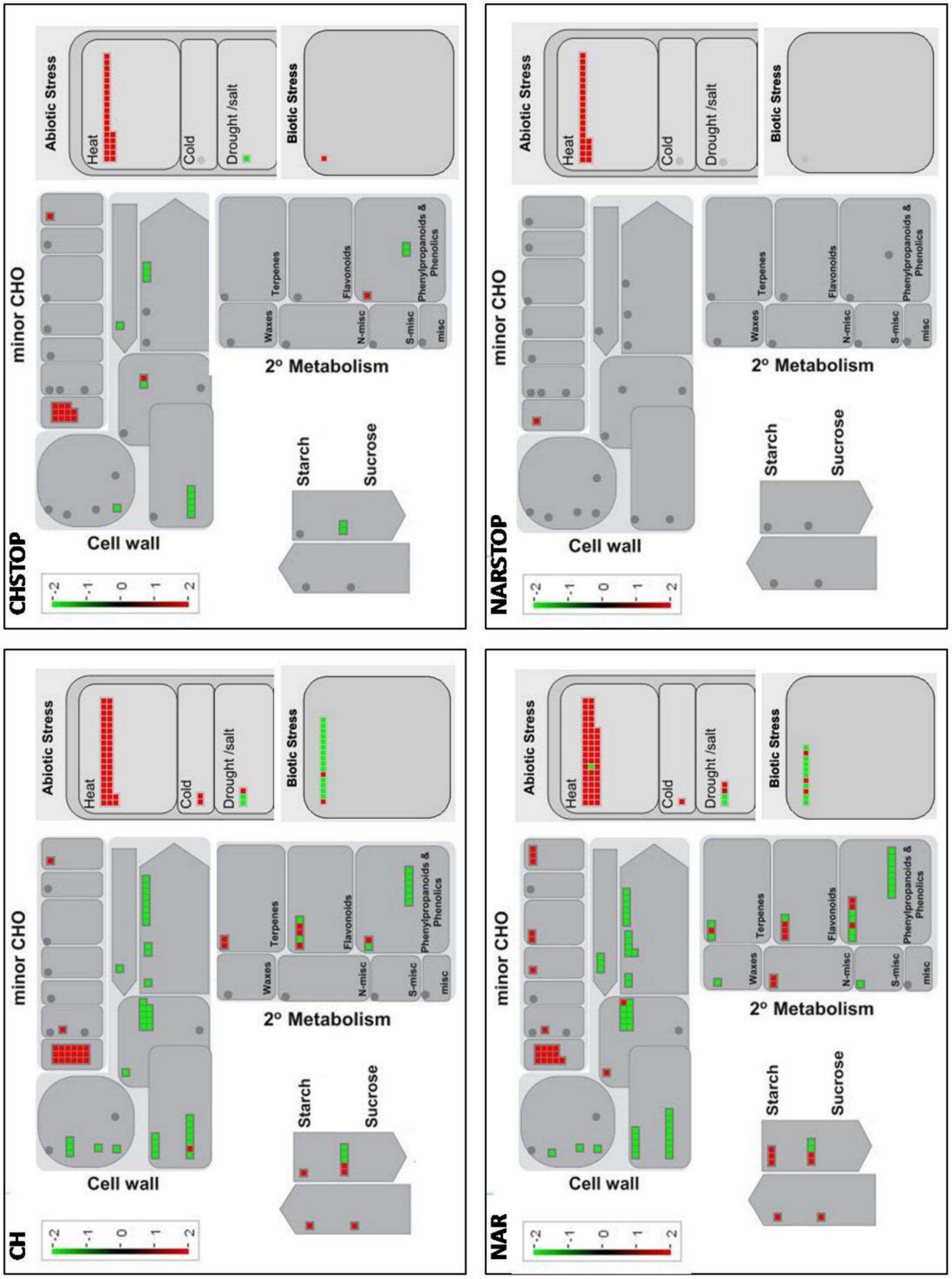


Figure 3. Mapman overview of the metabolism- and cellular response-related genes among the 1,573 genes that were differentially expressed under the four different flavonoid treatments. The presented values are the fold changes between the treatment and control groups. CH – prolonged naringenin-chalcone supp; NAR – prolonged naringenin supp; CHSTOP- short-term naringenin-chalcone supp; NARSTOP – short-term naringenin supp.

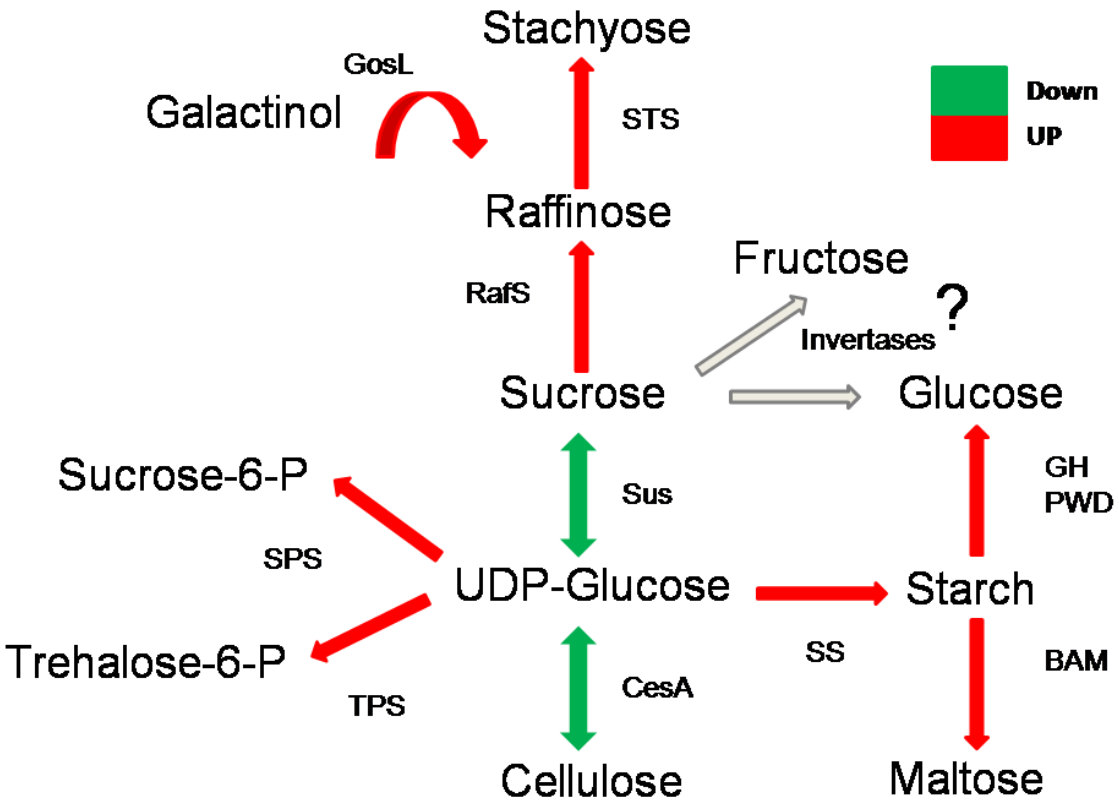


Figure 4. The effects of flavonoid supplementation on the expression of secondary cell wall-related genes.*Sus –sucrose synthase; SPS –sucrose phosphate synthase; CesA –cellulose synthase;; GH –glycoside hydrolase; PWD –phosphoglucan water dikinases; BAM –beta-amylase; TPS –trehalose-6-phosphate synthase; SS –starch synthase; Rafs – raafinose synthase; STS –stachyose synthase; GoSL –galactinol synthase*

## 5. Discussão

Para avaliar a influência da suplementação por flavonóides na formação da madeira em Eucalipto, mudas de um híbrido comercial de *E. urograndis*, foram suplementadas com os flavonóides narigenin e narigenin-chalcona, durante um ou cinco meses e após a suplementação foram analisadas quanto a composição química da sua parede celular, acessibilidade de enzimas hidrolíticas a seus açucares e expressão gênica. Todos os grupos tratados por flavonóides apresentaram diferenças fenotípicas em relação aos controles (não tratados), e os fenótipos dos grupos foram bastante semelhantes entre si, independentemente do tipo de flavonóide utilizado ou tempo de suplementação.

Após as análises químicas e de expressão gênica, fica claro que a suplementação por flavonóides exerce grande influência na formação da madeira em Eucalipto. Quimicamente, verifica-se uma redução bastante significativa na quantidade de extrativos, o que constitui um importante resultado uma vez que afeta a cor da pasta de papel. Apesar dos números totais do teor de lignina permanecerem semelhantes entre os grupos suplementados e os grupos controle, sua composição monomérica é significativamente alterada após suplementação pelos flavonóides, com favorecimento da via de produção de lignina siringílica (S) em detrimento da guaiacílica (G) e cumarílica (H). Este resultado também é bastante relevante, uma vez que estes monômeros, por fazerem menos ligações intermoméricas, são mais solúveis e, portanto, mais fáceis de serem removidos.

Ambos os resultados são de grande importância tanto para a indústria de papel e celulose, como para a utilização do Eucalipto como fonte de material lignocelulósico para obtenção de açucares fermentaveis para a produção de etanol de segunda geração. No caso de seu uso para produção de papel e celulose, o aumento da relação S/G pode significar um menor consumo de materiais químicos para a remoção da lignina da celulose usada para a fabricação de papel, sem comprometer o balanço energético da fábrica, uma vez que a lignina também é utilizada como fonte de energia para estas. Já para a produção de etanol de segunda geração, o fato da lignina estar mais “frouxa” significa maior acessibilidade das enzimas hidrolíticas à celulose e sua conseqüente quebra à açucares fermentaveis. Fato que se confirmou nos resultados da hidrólise enzimática do material, com aumento tanto dos açucares redutores totais quanto da quantidade de glicose encontrada nas mudas suplementadas.

Para melhor entender o que estaria causando estas modificações, analisamos a expressão gênica das mudas suplementadas através do seqüenciamento do seu transcriptoma, e verificamos a expressão diferencial de diversos genes e vias

metabólicas chaves para o desenvolvimento vegetal. Dentre os resultados mais relevantes, destacam-se a grande quantidade de genes relacionados a vias metabólicas de resposta ao estresse e às condições ambientais, todas induzidas nos grupos de suplementação por flavonoides em relação aos controles. Também foram diferencialmente expressos diversos genes relacionados à formação da parede celular e da via de fenílpropanóides, a qual inclui as rotas de síntese de lignina.

Olhando especificamente a via de formação de lignina, varios genes estão diferencialmente expressos entre os tratamentos. 4CL, HCT, diversas lacases e CCR estão reprimidos, enquanto duas metiltransferáses e dois genes da famílica CAD, estão induzidos nos grupos de suplementação por flavonóides. Este resultado é muito interessante por fornecer uma explicação, ainda que parcial, para o aumento da razão S/G nas plantas suplementadas. Consideramos que este resultado constitui uma explicação parcial porque, apesar de observamos valores de expressão (FPKM) semelhantes entre os grupos de suplementação, estes resultados só foram considerados estatisticamente significativos nos grupos que tiveram a suplementação prolongada (NAR e CH). Dessa forma, hipotetizamos que deve existir um controle mais complexo relacionado à síntese dos monômeros de lignina que poderia ser explicado pela presença de muitos genes sem identidade e função definida (*no hits;unknown function*) como diferencialmente expressos. Outra possibilidade é a contribuição de outras vias metabólicas.

Entre as vias que podem estar afetando a composição da madeira das plantas suplementadas em relação ao grupos controle, nos chamou a atenção as vias relacionadas com resposta a estresse. Diversos genes relacionados a estresse estão induzidos em todos os grupos de suplementação, independentemente do tipo ou duração do tratamento. Estresse e lignificação estão intimamente ligados, sendo esta uma resposta natural dos organismos vegetais. Os resultados deste trabalho indicam que existe uma ligação entre suplementação por flavonóides, estresse e consequentemente, modificação da composição monomérica da lignina e da parede celular.

Analisando os genes diferencialmente expressos relacionados com a formação da parede celular, verificamos que existe um desvio na síntese de açucares e polissacarídeos. Genes relacionados com a síntese da celulose e sacarose estão reprimidos, enquanto que estão induzidos, genes envolvidos com a síntese de amido (e de sua degradação em maltose e glicose) e açucares menores, estaquiose e rafinose. Genes desta via participam da resposta a estresse abióticos, seca e temperaturas baixas, mas também estão envolvidos com a formação de madeira de tensão, aumento de biomassa e do conteúdo celulósico. Além disso em plantas de

arabidopsis super-expressando o gene HsfA2 (Heat-shock factor A2), que também está induzido em todos os tratamentos, foi verificado um aumento dos níveis de rafinose.

Desta forma, os altos valores de FPKM encontrados em todos os grupos suplementados com flavonóides para os genes desta via, ligam à resposta ao estresse, que pode estar sendo causado pela simples adição destes flavonóides, aos resultados histológicos que demonstram uma aparente maior presença de madeira de tensão, aos resultados de expressão gênica e da hidrólise enzimática.

As diferenças fenotípicas encontradas são, provavelmente, resultado não de um desses fatores, mas sim de uma combinação dos mesmos. A suplementação por flavonóides seria o agente causador de estresse no organismo, e a resposta do vegetal envolveria a expressão de diversos genes e vias metabólicas, resultando numa redução de extrativos, modificação da composição monomérica da lignina, em uma possível maior produção e desvio da síntese de açucares e polissacarídeos na direção da formação de amido, estaquiose e rafinose, e a maior acessibilidade a estes.

Assim, a presente tese de doutorado abre novas perspectivas de pesquisa na área florestal e no melhoramento vegetal do Eucalipto. Testes mais amplos em campo são necessários para determinar a extensão do efeito da suplementação nas árvores adultas e para determinar a otimização dos flavonóides como composto nutricional, como por exemplo a concentração mais adequada, o tempo necessário de aplicação, idade correta das plantas para inicio e fim da aplicação, dentre outros. Além de serem necessários ensaios fermentativos e uma maior caracterização dos açucares obtidos na hidrólise para verificar o potencial da suplementação por flavonóides na produção de etanol.

Entretanto, a simples perspectiva de alcançar mudanças fenotípicas benéficas e significativas pela adição de um composto barato ao meio nutricional costumeiramente utilizado é muito favorável, especialmente em se tratando do melhoramento de um clone comercial, o qual já passou por inúmeras etapas de melhoramento clássico e tem sido amplamente selecionado devido a suas características ligadas a produtividade.

## 6. Conclusões

A suplementação de mudas de Eucalipto com flavonóides**:**

- Reduz a quantidade de extrativos em até 41%;
- Não altera as quantidades totais de lignina;
- Altera a composição monomérica da lignina, aumentando em até 8% a razão S/G e diminuindo a razão H/G em até 15%;
- Promove alterações transcricionais, modificando a expressão de genes presentes em vias de formação da parede celular e desenvolvimento vegetal, desviando a via para a formação e degradação de amido, além de carboidratos e açucares menores e de resposta ao estresse e ao meio ambiente;
- Melhora a acessibilidade de enzimas hidrolíticas aos açucares da parede celular;
- Aumenta a quantidade total de açucares e de glicose obtidos através da hidrólise enzimática;
- Os flavonóides narigenin-chalcona e narigenin tem potencial para serem utilizados pela indústria de papel, celulose e energia para aumentar o rendimento de suas plantações.

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**Anexo 1. Déposito patente INPI**

Folha de rosto do pedido de patente depositado junto ao INPI relativo à formulação de uma composição para a modificação química da madeira de eucalipto utilizando a suplementação por flavonóides.

< Uso exclusivo do INPI >

INPI INSTITUTO NACIONAL DE PROPRIEDADE INDUSTRIAL PROTOCOLO GERAL
mariengel 018120039306
22/10/2012 15:10 DESP
BR 10 2012 025981 3
Reservado ao protocolo

Espaço para etiqueta

## DEPÓSITO DE PEDIDO DE PATENTE OU DE CERTIFICADO DE ADIÇÃO

**Ao Instituto Nacional da Propriedade Industrial:**
O requerente solicita a concessão de um privilégio na natureza e nas condições abaixo indicadas

**1. Depositante (71):**

1.1 Nome: UNIVERSIDADE ESTADUAL DE CAMPINAS

1.2 Qualificação:

1.3 CNPJ/CPF: 46068425/0001-33

1.4 Endereço Completo:

1.5 CEP: 13083-970 1.6 Telefone: 19 3521-5015 1.7 Fax: 19 3521-5210

1.8 E-mail: patentes@inova.unicamp.br

☒ continua em folha anexa

**2. Natureza:** ◉ Invenção ○ Modelo de Utilidade ○ Certificado de Adição

Escreva, obrigatoriamente, e por extenso, a Natureza desejada:

**3. Título da Invenção ou Modelo de Utilidade ou Certificado de Adição(54):**
COMPOSIÇÃO PARA MODIFICAÇÃO QUÍMICA DA MADEIRA DE EUCALIPTOS, MÉTODO DE APLICAÇÃO E SEUS USOS

☐ continua em folha anexa

**4. Pedido de Divisão:** do pedido Nº Data de Depósito:

**5. Prioridade:** ☐ interna ☐ unionista

O depositante reivindica a(s) seguinte(s):

| País ou organização de origem | Número de depósito | Data do depósito |
|---|---|---|
| | | |
| | | |
| | | |

**6. Inventor (72):**

☐ Assinale aqui se o(s) mesmo(s) requer(em) a não divulgação de seu(s) nome(s)

6.1 Nome: GONÇALO AMARANTE GUIMARÃES PEREIRA

6.2 Qualificação: BRAS, CASADO, PROF. UNIVERSITARIO 6.3 CPF: 289.870.395-87

6.4 Endereço completo: RUA LAURO PIMENTEL, 323

6.5 CEP: 13083-250 6.6 Telefone: 19 3521-6237 6.7 Fax:

6.8 E-Mail: goncalo@unicamp.br

☒ continua em folha anexa

INPI Formulário 1.01 – Depósito de Pedido de Patente ou de Certificado de Adição (folha 1/2 )

**7. Declaração na forma do item 3.2 do Ato Normativo nº 127/97:**

☐ 7.1 Declaro que os dados fornecidos no presente formulário são idênticos ao da certidão de depósito ou documento equivalente do pedido cuja prioridade está sendo reivindicada.

☐ em anexo

**8. Declaração de divulgação anterior não prejudicial:** (Período de Graça):
(art. 12 da LPI e item 2 do AN nº 127/97) ☐ em anexo

**9. Procurador (74)**

9.1 Nome: FERNANDA LAVRAS COSTALLAT SILVADO

9.2 CNPJ/CPF: 295.166.068-57 9.3 API/OAB: 210.899

9.4 Endereço completo: PROCURADORIA GERAL DA UNICAMP, CAMPINAS - SP

9.5 CEP: 13083-970 9.6 Telefone: 19 3521-4771 9.7 Fax: 00 0000-0000

9.8 E-Mail: patentes@inova.unicamp.br

**10. Listagem de sequências Biológicas** (documentos anexados) (se houver):

☐ Listagem de sequências em arquivo eletrônico: nº de CDs ou DVDs (original e cópia).

☐ Código de controle alfanumérico no formato de código de barras: fl.

☐ Listagem de sequências em formato impresso: fls.

☐ Declaração de acordo com o artigo da Resolução INPI nº 228/09: fls.

**11. Documentos anexados** (assinale e indique também o número de folhas):
(Deverá ser indicado o nº total de somente uma das vias de cada documento)

| | | | | | |
|---|---|---|---|---|---|
| ☒ | 11.1 Guia de Recolhimento | 1 fls. | ☒ | 11.5 Relatório descritivo | 21 fls. |
| ☒ | 11.2 Procuração | 2 fls. | ☒ | 11.6 Reivindicações | 4 fls. |
| ☐ | 11.3 Documentos de Prioridade | fls. | ☐ | 11.7 Desenhos | fls. |
| ☐ | 11.4 Doc. de contrato de trabalho | fls. | ☒ | 11.8 Resumo | 1 fls. |
| ☐ | 11.9 Outros que não aqueles definidos no campo 11 (especificar)<br>ANEXOS | | | | 10 fls. |

**12. Total de folhas anexadas (referentes aos campos 10 e 11):** 39 fls.

**13. Declaro, sob penas da Lei, que todas as informações acima prestadas são completas e verdadeiras.**

CAMPINAS, SP, DE OUTUBRO DE 2012
Local e Data

Assinatura e Carimbo

Fernanda Lavras Costallat Silvado
Procuradora de Universidade Subchefe
Matrícula nº 28.574-2
OAB/SP nº 210.899

Anexo 2. Identidade, valores de expressão e anotação dos 1573 genes diferencialmente expressos.

| GENE ID | FPKM | | | | | Annotation |
|---|---|---|---|---|---|---|
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.F04479.1 | 0,12 | 35,55 | 40,44 | 23,84 | 57,92 | AT1G53540.1 \| Symbols: \| HSP20-like chaperones superfamily protein \| chr1:19980510-19980983 FORWARD LENGTH=157 |
| Eucgr.K02389.1 | 0,04 | 13,69 | 10,18 | 9,89 | 26,99 | AT3G10020.2 \| Symbols: \| unknown protein |
| Eucgr.K02399.1 | 0,08 | 18,09 | 18,67 | 19,48 | 53,82 | AT3G10020.1 \| Symbols: \| unknown protein |
| Eucgr.G01188.2 | 2,78 | 45,78 | 41,56 | 33,40 | 76,35 | AT1G17870.1 \| Symbols: ATEGY3, EGY3 \| ethylene-dependent gravitropism-deficient and yellow-green-like 3 \| |
| Eucgr.J01979.1 | 0,34 | 17,61 | 19,94 | 14,63 | 27,21 | AT5G59720.1 \| Symbols: HSP18.2 \| heat shock protein 18.2 \| chr5:24062632-24063117 FORWARD LENGTH=161 |
| Eucgr.K02410.1 | 0,13 | 14,27 | 10,66 | 12,52 | 29,61 | AT3G10020.1 \| Symbols: \| unknown protein |
| Eucgr.J01980.1 | 0,02 | 12,20 | 11,59 | 9,15 | 26,39 | AT5G59720.1 \| Symbols: HSP18.2 \| heat shock protein 18.2 \| chr5:24062632-24063117 FORWARD LENGTH=161 |
| Eucgr.L02233.1 | 1,29 | 41,47 | 38,15 | 29,24 | 118,40 | No hits found |
| Eucgr.C03056.2 | 4,97 | 32,66 | 25,61 | 15,26 | 91,38 | AT2G26150.1 \| Symbols: ATHSFA2, HSFA2 \| heat shock transcription factor A2 \| chr2:11135856-11137217 FORWARD LENGTH=345 |
| Eucgr.F02898.1 | 2,76 | 525,99 | 343,17 | 280,68 | 342,59 | AT5G37670.1 \| Symbols: \| HSP20-like chaperones superfamily protein \| chr5:14969035-14969448 FORWARD LENGTH=137 |
| Eucgr.J01985.1 | 0,31 | 22,25 | 16,62 | 13,21 | 33,33 | AT5G59720.1 \| Symbols: HSP18.2 \| heat shock protein 18.2 \| chr5:24062632-24063117 FORWARD LENGTH=161 |
| Eucgr.K03553.1 | 0,04 | 4,11 | 4,59 | 2,83 | 6,87 | AT4G01970.1 \| Symbols: AtSTS, STS \| stachyose synthase \| chr4:854073-856953 REVERSE LENGTH=876 |
| Eucgr.L03261.1 | 1,44 | 47,41 | 27,81 | 19,98 | 75,67 | AT5G59720.1 \| Symbols: HSP18.2 \| heat shock protein 18.2 \| chr5:24062632-24063117 FORWARD LENGTH=161 |
| Eucgr.C03449.1 | 0,29 | 14,55 | 12,98 | 14,36 | 18,58 | AT2G26150.1 \| Symbols: ATHSFA2, HSFA2 \| heat shock transcription factor A2 \| chr2:11135856-11137217 FORWARD LENGTH=345 |
| Eucgr.C00684.1 | 2,00 | 341,30 | 299,30 | 243,65 | 272,90 | AT5G12020.1 \| Symbols: HSP17.6II \| 17.6 kDa class II heat shock protein \| chr5:3882409-3882876 REVERSE LENGTH=155 |
| Eucgr.J01972.1 | 5,54 | 85,59 | 56,26 | 32,51 | 108,67 | AT5G59720.1 \| Symbols: HSP18.2 \| heat shock protein 18.2 \| chr5:24062632-24063117 FORWARD LENGTH=161 |
| Eucgr.K02384.1 | 0,07 | 14,56 | 10,59 | 10,60 | 27,23 | AT3G10020.1 \| Symbols: \| unknown protein |
| Eucgr.J01969.1 | 4,89 | 192,23 | 134,53 | 103,09 | 310,44 | AT2G29500.1 \| Symbols: \| HSP20-like chaperones superfamily protein \| chr2:12633279-12633740 REVERSE LENGTH=153 |
| Eucgr.K03472.1 | 0,07 | 109,57 | 84,15 | 62,04 | 20,94 | AT2G47710.1 \| Symbols: \| Adenine nucleotide alpha hydrolases-like superfamily protein \| |
| Eucgr.H04513.1 | 0,23 | 15,72 | 18,79 | 11,56 | 21,62 | AT5G28540.1 \| Symbols: BIP1 \| heat shock protein 70 (Hsp 70) family protein |
| Eucgr.A00595.1 | 0,10 | 81,17 | 76,66 | 57,33 | 98,83 | AT5G01300.1 \| Symbols: \| PEBP (phosphatidylethanolamine-binding protein) family protein |
| Eucgr.E02421.1 | 0,19 | 260,04 | 220,12 | 119,63 | 51,05 | AT1G30190.1 \| Symbols: \| unknown protein |
| Eucgr.H04692.1 | 2,97 | 83,31 | 59,57 | 43,11 | 313,22 | AT4G27670.1 \| Symbols: HSP21 \| heat shock protein 21 \| chr4:13819048-13819895 REVERSE LENGTH=227 |
| Eucgr.G02440.1 | 0,00 | 5,46 | 5,80 | 3,33 | 4,06 | AT4G34135.1 \| Symbols: UGT73B2 \| UDP-glucosyltransferase 73B2 \| chr4:16345476-16347016 REVERSE LENGTH=483 |
| Eucgr.J01978.1 | 1,35 | 36,39 | 28,77 | 20,90 | 71,33 | AT1G53540.1 \| Symbols: \| HSP20-like chaperones superfamily protein \| chr1:19980510-19980983 FORWARD LENGTH=157 |
| Eucgr.J01977.1 | 0,37 | 9,43 | 8,59 | 7,08 | 19,26 | AT5G59720.1 \| Symbols: HSP18.2 \| heat shock protein 18.2 \| chr5:24062632-24063117 FORWARD LENGTH=161 |
| Eucgr.G02259.1 | 0,00 | 2,73 | 2,14 | 1,18 | 3,10 | AT4G34131.1 \| Symbols: UGT73B3 \| UDP-glucosyl transferase 73B3 \| chr4:16343268-16344713 REVERSE LENGTH=481 |

| GENE ID | FPKM | | | | | Annotation |
|---|---|---|---|---|---|---|
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.J01959.1 | 3,19 | 142,90 | 89,76 | 58,22 | 148,21 | AT5G59720.1 \| Symbols: HSP18.2 \| heat shock protein 18.2 \| chr5:24062632-24063117 FORWARD LENGTH=161 |
| Eucgr.J01982.1 | 0,21 | 8,65 | 6,06 | 4,24 | 13,03 | AT5G59720.1 \| Symbols: HSP18.2 \| heat shock protein 18.2 \| chr5:24062632-24063117 FORWARD LENGTH=161 |
| Eucgr.K00295.1 | 2,11 | 46,13 | 38,25 | 35,52 | 62,69 | AT5G52640.1 \| Symbols: HSP81-1, ATHS83, HSP81.1, HSP83, ATHSP90.1, AtHsp90-1, HSP90.1 \| heat shock protein 90.1 \| |
| Eucgr.A01833.1 | 0,13 | 32,00 | 24,43 | 15,08 | 10,47 | AT4G28390.1 \| Symbols: AAC3, ATAAC3 \| ADP/ATP carrier 3 \| chr4:14041486-14042781 REVERSE LENGTH=379 |
| Eucgr.J01964.1 | 13,65 | 145,21 | 119,05 | 111,04 | 251,88 | AT5G59720.1 \| Symbols: HSP18.2 \| heat shock protein 18.2 \| chr5:24062632-24063117 FORWARD LENGTH=161 |
| Eucgr.C03071.1 | 3,64 | 517,08 | 509,51 | 451,66 | 324,54 | AT5G12020.1 \| Symbols: HSP17.6II \| 17.6 kDa class II heat shock protein \| chr5:3882409-3882876 REVERSE LENGTH=155 |
| Eucgr.B03843.1 | 1,45 | 93,17 | 63,39 | 67,61 | 20,77 | No hits found |
| Eucgr.I01982.1 | 13,71 | 110,50 | 95,01 | 54,71 | 184,40 | AT5G15450.1 \| Symbols: APG6, CLPB3, CLPB-P \| casein lytic proteinase B3 \| chr5:5014399-5018255 REVERSE LENGTH=968 |
| Eucgr.C03320.1 | 0,38 | 24,39 | 18,22 | 14,01 | 9,78 | AT5G20670.1 \| Symbols: \| Protein of unknown function (DUF1677) \| chr5:6993332-6993793 REVERSE LENGTH=153 |
| Eucgr.B00176.2 | 3,86 | 153,25 | 109,01 | 82,97 | 57,39 | AT5G50240.1 \| Symbols: PIMT2, AtPIMT2 \| protein-l-isoaspartate methyltransferase 2 \| |
| Eucgr.J02588.1 | 3,20 | 225,90 | 182,76 | 194,01 | 130,04 | No hits found |
| Eucgr.C00690.1 | 2,48 | 563,68 | 498,40 | 514,67 | 458,94 | AT5G12020.1 \| Symbols: HSP17.6II \| 17.6 kDa class II heat shock protein \| chr5:3882409-3882876 REVERSE LENGTH=155 |
| Eucgr.H01413.1 | 0,61 | 14,45 | 13,47 | 8,20 | 14,25 | AT1G03070.2 \| Symbols: \| Bax inhibitor-1 family protein \| chr1:730148-731379 FORWARD LENGTH=247 |
| Eucgr.H02887.1 | 4,80 | 37,80 | 28,32 | 19,46 | 30,12 | AT4G22340.1 \| Symbols: CDS2 \| cytidinediphosphate diacylglycerol synthase 2 \| chr4:11800150-11802549 REVERSE LENGTH=423 |
| Eucgr.G01414.1 | 0,04 | 1,91 | 1,28 | 1,10 | 2,80 | AT4G34131.1 \| Symbols: UGT73B3 \| UDP-glucosyl transferase 73B3 \| chr4:16343268-16344713 REVERSE LENGTH=481 |
| Eucgr.J01981.1 | 2,00 | 34,43 | 50,34 | 69,86 | 105,48 | AT5G59720.1 \| Symbols: HSP18.2 \| heat shock protein 18.2 \| chr5:24062632-24063117 FORWARD LENGTH=161 |
| Eucgr.K00237.1 | 0,04 | 115,83 | 64,41 | 61,47 | 11,49 | AT5G62040.1 \| Symbols: \| PEBP (phosphatidylethanolamine-binding protein) family protein \| |
| Eucgr.F03196.1 | 1,43 | 292,73 | 240,63 | 168,71 | 38,29 | AT1G17180.1 \| Symbols: ATGSTU25, GSTU25 \| glutathione S-transferase TAU 25 \| |
| Eucgr.I02136.1 | 1,68 | 226,73 | 147,43 | 90,02 | 259,35 | AT1G54050.1 \| Symbols: \| HSP20-like chaperones superfamily protein \| chr1:20179558-20180122 REVERSE LENGTH=155 |
| Eucgr.H04427.1 | 49,92 | 0,52 | 0,85 | 1,32 | 13,93 | AT3G06350.1 \| Symbols: EMB3004, MEE32 \| dehydroquinate dehydratase, putative / shikimate dehydrogenase, putative \| |
| Eucgr.L02860.1 | 2,44 | 408,70 | 383,21 | 397,30 | 273,12 | AT5G12020.1 \| Symbols: HSP17.6II \| 17.6 kDa class II heat shock protein \| chr5:3882409-3882876 REVERSE LENGTH=155 |
| Eucgr.B03280.1 | 0,36 | 165,28 | 127,02 | 117,88 | 51,95 | AT1G63840.1 \| Symbols: \| RING/U-box superfamily protein \| chr1:23689991-23690491 REVERSE LENGTH=166 |
| Eucgr.C04378.1 | 1,60 | 7,63 | 9,88 | 6,52 | 8,45 | AT1G50030.1 \| Symbols: TOR \| target of rapamycin \| chr1:18522626-18539619 REVERSE LENGTH=2481 |
| Eucgr.L01770.1 | 0,17 | 15,89 | 16,32 | 10,41 | 19,09 | AT5G28540.1 \| Symbols: BIP1 \| heat shock protein 70 (Hsp 70) family protein \| |
| Eucgr.L02697.1 | 0,02 | 1,00 | 1,30 | 0,92 | 1,27 | AT5G53990.1 \| Symbols: \| UDP-Glycosyltransferase superfamily protein \| chr5:21915707-21917050 REVERSE LENGTH=447 |
| Eucgr.H03046.1 | 1,04 | 8,76 | 4,89 | 4,14 | 11,58 | AT1G65660.1 \| Symbols: SMP1 \| Pre-mRNA splicing Prp18-interacting factor \| |
| Eucgr.L02363.1 | 0,24 | 39,93 | 126,78 | 154,82 | 28,88 | AT5G47550.1 \| Symbols: \| Cystatin/monellin superfamily protein \| chr5:19286596-19286964 REVERSE LENGTH=122 |
| Eucgr.K01389.2 | 19,81 | 1348,64 | 796,35 | 569,70 | 120,14 | AT2G04240.2 \| Symbols: XERICO \| RING/U-box superfamily protein \| chr2:1461816-1462304 REVERSE LENGTH=162 |
| Eucgr.D02334.1 | 1,64 | 250,51 | 223,70 | 129,50 | 253,35 | AT2G46240.1 \| Symbols: BAG6, ATBAG6 \| BCL-2-associated athanogene 6 \| |

| | | | | | | |
|---|---|---|---|---|---|---|
| Eucgr.H00118.1 | 27,73 | 1624,22 | 1433,16 | 1046,96 | 372,67 | AT1G04560.1 \| Symbols: \| AWPM-19-like family protein \| chr1:1245070-1245888 FORWARD LENGTH=186 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.B02743.1 | 0,06 | 5,44 | 6,05 | 6,01 | 10,26 | AT5G59720.1 \| Symbols: HSP18.2 \| heat shock protein 18.2 \| chr5:24062632-24063117 FORWARD LENGTH=161 |
| Eucgr.J02137.1 | 2,47 | 27,99 | 28,19 | 18,78 | 15,91 | AT5G15070.1 \| Symbols: \| Phosphoglycerate mutase-like family protein \| chr5:4876898-4885615 FORWARD LENGTH=1049 |
| Eucgr.F03363.1 | 1,18 | 115,06 | 100,03 | 71,61 | 51,24 | AT2G20900.2 \| Symbols: DGK5, ATDGK5 \| diacylglycerol kinase 5 \| chr2:8989794-8992798 REVERSE LENGTH=491 |
| Eucgr.K02873.1 | 0,31 | 9,45 | 11,35 | 7,36 | 4,06 | AT5G62890.3 \| Symbols: \| Xanthine/uracil permease family protein \| chr5:25243723-25247075 FORWARD LENGTH=532 |
| Eucgr.J01958.1 | 2,68 | 115,32 | 90,34 | 65,56 | 100,03 | AT5G59720.1 \| Symbols: HSP18.2 \| heat shock protein 18.2 \| chr5:24062632-24063117 FORWARD LENGTH=161 |
| Eucgr.K01402.1 | 0,68 | 489,73 | 335,43 | 243,43 | 159,69 | No hits found |
| Eucgr.H01638.1 | 7,89 | 123,54 | 93,85 | 65,50 | 121,11 | AT1G03070.2 \| Symbols: \| Bax inhibitor-1 family protein \| chr1:730148-731379 FORWARD LENGTH=247 |
| Eucgr.H03044.1 | 0,96 | 11,74 | 5,01 | 4,78 | 12,51 | AT1G65660.1 \| Symbols: SMP1 \| Pre-mRNA splicing Prp18-interacting factor \| chr1:24418295-24421231 REVERSE LENGTH=535 |
| Eucgr.B02244.1 | 0,12 | 11,57 | 8,11 | 6,82 | 11,20 | AT2G30000.1 \| Symbols: \| PHF5-like protein \| chr2:12804042-12804374 REVERSE LENGTH=110 |
| Eucgr.D01874.3 | 7,75 | 39,28 | 36,64 | 29,74 | 27,09 | AT1G12800.1 \| Symbols: \| Nucleic acid-binding, OB-fold-like protein \| chr1:4361778-4365189 REVERSE LENGTH=767 |
| Eucgr.A01806.1 | 17,58 | 0,52 | 1,62 | 3,50 | 4,84 | AT4G28250.1 \| Symbols: ATEXPB3, EXPB3, ATHEXP BETA 1.6 \| expansin B3 \| chr4:14000446-14001945 REVERSE LENGTH=264 |
| Eucgr.J00827.1 | 0,04 | 0,90 | 1,56 | 0,98 | 0,76 | AT5G13000.1 \| Symbols: ATGSL12, gsl12 \| glucan synthase-like 12 \| chr5:4110445-4121202 REVERSE LENGTH=1955 |
| Eucgr.K03563.1 | 0,23 | 4,48 | 11,12 | 12,00 | 8,48 | AT2G47180.1 \| Symbols: AtGolS1, GolS1 \| galactinol synthase 1 \| chr2:19369049-19370372 REVERSE LENGTH=344 |
| Eucgr.B03963.1 | 0,01 | 0,78 | 1,33 | 1,08 | 0,51 | AT3G62150.1 \| Symbols: PGP21 \| P-glycoprotein 21 \| chr3:23008755-23013579 REVERSE LENGTH=1296 |
| Eucgr.B02291.1 | 10,86 | 52,79 | 42,69 | 39,45 | 45,69 | AT3G46670.1 \| Symbols: UGT76E11 \| UDP-glucosyl transferase 76E11 \| chr3:17192795-17194227 REVERSE LENGTH=451 |
| Eucgr.E02947.1 | 0,37 | 8,89 | 9,66 | 7,62 | 7,69 | AT1G16770.1 \| Symbols: \| unknown protein |
| Eucgr.D00704.1 | 5,24 | 77,32 | 63,35 | 45,93 | 125,37 | AT1G61260.1 \| Symbols: \| Protein of unknown function (DUF761) \| chr1:22593756-22594986 REVERSE LENGTH=344 |
| Eucgr.D01410.1 | 25,73 | 0,43 | 0,86 | 1,34 | 6,87 | AT3G07880.1 \| Symbols: SCN1 \| Immunoglobulin E-set superfamily protein \| chr3:2514175-2515544 FORWARD LENGTH=240 |
| Eucgr.I02375.1 | 25,29 | 1,93 | 4,94 | 6,67 | 8,37 | AT5G66330.1 \| Symbols: \| Leucine-rich repeat (LRR) family protein \| chr5:26500531-26501787 REVERSE LENGTH=418 |
| Eucgr.G01464.1 | 0,16 | 19,83 | 11,39 | 8,24 | 8,14 | No hits found |
| Eucgr.J01960.1 | 4,43 | 365,87 | 267,66 | 190,17 | 357,50 | AT5G59720.1 \| Symbols: HSP18.2 \| heat shock protein 18.2 \| chr5:24062632-24063117 FORWARD LENGTH=161 |
| Eucgr.H03725.1 | 5,38 | 13,43 | 16,12 | 13,10 | 20,16 | AT4G13550.1 \| Symbols: \| triglyceride lipases;triglyceride lipases \| chr4:7871251-7876160 REVERSE LENGTH=715 |
| Eucgr.D01040.2 | 15,96 | 134,23 | 130,11 | 126,16 | 81,83 | AT5G22480.1 \| Symbols: \| ZPR1 zinc-finger domain protein \| chr5:7451643-7456168 REVERSE LENGTH=493 |
| Eucgr.A02381.1 | 4,49 | 172,85 | 136,95 | 91,17 | 101,55 | AT5G12840.3 \| Symbols: HAP2A, ATHAP2A, NF-YA1 \| nuclear factor Y, subunit A1 \| |
| Eucgr.I00312.1 | 2,82 | 14,42 | 15,28 | 12,03 | 15,91 | AT2G21860.1 \| Symbols: \| violaxanthin de-epoxidase-related \| chr2:9318333-9319990 REVERSE LENGTH=522 |
| Eucgr.H04079.1 | 9,38 | 74,45 | 65,19 | 42,14 | 40,33 | AT3G17180.1 \| Symbols: scpl33 \| serine carboxypeptidase-like 33 \| chr3:5855861-5859157 REVERSE LENGTH=478 |
| Eucgr.G02845.1 | 9,82 | 0,00 | 0,19 | 0,25 | 2,74 | AT5G03250.1 \| Symbols: \| Phototropic-responsive NPH3 family protein \| chr5:774591-776855 FORWARD LENGTH=592 |
| Eucgr.K02208.2 | 18,76 | 0,74 | 0,60 | 1,39 | 0,92 | AT5G35525.1 \| Symbols: \| PLAC8 family protein \| chr5:13707084-13707818 FORWARD LENGTH=152 |

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|---|---|---|---|---|---|---|
| Eucgr.G02748.1 | 17,47 | 0,31 | 0,44 | 0,60 | 5,40 | AT5G04310.1 \| Symbols: \| Pectin lyase-like superfamily protein \| chr5:1203356-1207352 REVERSE LENGTH=518 |
| Eucgr.F03704.1 | 1,45 | 27,74 | 21,67 | 11,53 | 10,03 | AT1G78610.1 \| Symbols: MSL6 \| mechanosensitive channel of small conductance-like 6 \| chr1:29569226-29572126 REVERSE LENGTH=856 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.I01368.1 | 4,42 | 135,89 | 110,06 | 83,93 | 39,49 | AT4G38810.2 \| Symbols: \| Calcium-binding EF-hand family protein \| chr4:18115607-18118860 REVERSE LENGTH=375 |
| Eucgr.D02073.1 | 24,48 | 469,78 | 380,75 | 330,52 | 1060,38 | AT4G25200.1 \| Symbols: ATHSP23.6-MITO, HSP23.6-MITO \| |
| Eucgr.G02781.1 | 0,16 | 80,65 | 61,04 | 42,50 | 3,75 | AT5G07330.1 \| Symbols: \| unknown protein |
| Eucgr.H03519.1 | 0,38 | 4,60 | 4,12 | 1,63 | 5,88 | No hits found |
| Eucgr.H03564.1 | 2,05 | 0,42 | 0,08 | 0,12 | 0,10 | AT5G19260.1 \| Symbols: \| Protein of unknown function (DUF3049) \| chr5:6479494-6480360 REVERSE LENGTH=288 |
| Eucgr.G01238.2 | 2,34 | 33,68 | 37,22 | 26,67 | 20,98 | AT3G18990.1 \| Symbols: VRN1, REM39 \| AP2/B3-like transcriptional factor family protein \| chr3:6549077-6551568 REVERSE LENGTH=341 |
| Eucgr.H04153.1 | 7,60 | 33,07 | 24,65 | 21,90 | 31,09 | AT3G17611.1 \| Symbols: ATRBL14, RBL14 \| RHOMBOID-like protein 14 \| chr3:6024946-6026173 FORWARD LENGTH=334 |
| Eucgr.H00260.2 | 4,36 | 52,47 | 46,33 | 43,37 | 29,63 | AT3G03080.1 \| Symbols: \| Zinc-binding dehydrogenase family protein \| chr3:698530-700278 REVERSE LENGTH=350 |
| Eucgr.B03897.1 | 11,62 | 57,07 | 44,48 | 34,48 | 68,19 | AT1G27650.1 \| Symbols: ATU2AF35A \| U2 snRNP auxiliary factor small subunit, putative \| chr1:9615152-9616042 FORWARD LENGTH=296 |
| Eucgr.D00856.1 | 24,31 | 247,98 | 198,32 | 196,32 | 181,11 | AT4G21320.1 \| Symbols: HSA32 \| Aldolase-type TIM barrel family protein \| chr4:11340492-11341732 FORWARD LENGTH=286 |
| Eucgr.C01031.1 | 2,73 | 476,52 | 301,85 | 296,55 | 156,41 | AT1G52240.2 \| Symbols: ATROPGEF11, ROPGEF11, PIRF1 \| RHO guanyl-nucleotide exchange factor 11 \| chr1:19458844-19459235 REVERSE LENGTH=94 |
| Eucgr.H03386.1 | 0,25 | 64,14 | 50,54 | 45,19 | 12,54 | No hits found |
| Eucgr.C00553.1 | 0,06 | 7,73 | 4,99 | 3,03 | 2,70 | AT4G32900.2 \| Symbols: \| Peptidyl-tRNA hydrolase II (PTH2) family protein \| chr4:15878944-15880979 REVERSE LENGTH=193 |
| Eucgr.E01440.1 | 15,55 | 311,66 | 257,44 | 211,20 | 244,86 | AT2G45380.1 \| Symbols: \| unknown protein |
| Eucgr.C03325.1 | 13,51 | 0,33 | 0,56 | 0,53 | 2,23 | AT2G05920.1 \| Symbols: \| Subtilase family protein \| chr2:2269831-2272207 REVERSE LENGTH=754 |
| Eucgr.L00243.1 | 0,02 | 29,83 | 19,77 | 9,75 | 1,37 | AT1G56600.1 \| Symbols: AtGolS2, GolS2 \| galactinol synthase 2 \| chr1:21207620-21209291 FORWARD LENGTH=335 |
| Eucgr.J03055.1 | 1,30 | 52,54 | 39,45 | 19,47 | 44,88 | AT1G80160.1 \| Symbols: \| Lactoylglutathione lyase / glyoxalase I family protein \| chr1:30151101-30151930 FORWARD LENGTH=167 |
| Eucgr.K00185.1 | 18,10 | 65,15 | 61,81 | 52,54 | 59,96 | AT5G51820.1 \| Symbols: PGM, ATPGMP, PGM1, STF1 \| phosphoglucomutase \| |
| Eucgr.B02319.1 | 1,11 | 62,29 | 41,02 | 20,31 | 18,83 | No hits found |
| Eucgr.J01986.1 | 15,59 | 1423,51 | 1288,64 | 1295,51 | 1725,77 | No hits found |
| Eucgr.F03317.1 | 7,94 | 99,41 | 63,55 | 61,29 | 61,03 | No hits found |
| Eucgr.H03518.1 | 6,06 | 282,04 | 218,12 | 152,91 | 249,47 | AT2G32120.2 \| Symbols: HSP70T-2 \| heat-shock protein 70T-2 \| chr2:13651720-13653411 REVERSE LENGTH=563 |
| Eucgr.H04961.1 | 0,09 | 83,28 | 46,51 | 26,22 | 2,80 | AT4G33467.2 \| Symbols: \| unknown protein |
| Eucgr.B03883.1 | 4,47 | 146,11 | 114,74 | 104,60 | 310,58 | AT4G21105.1 \| Symbols: \| cytochrome-c oxidases;electron carriers \| chr4:11266273-11266724 FORWARD LENGTH=68 |
| Eucgr.L03244.1 | 0,12 | 279,83 | 137,40 | 63,66 | 2,99 | AT1G56600.1 \| Symbols: AtGolS2, GolS2 \| galactinol synthase 2 \| chr1:21207620-21209291 FORWARD LENGTH=335 |

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|---|---|---|---|---|---|---|
| Eucgr.H03093.1 | 1,70 | 0,10 | 0,10 | 0,16 | 0,17 | AT2G39510.1 \| Symbols: \| nodulin MtN21 /EamA-like transporter family protein \| |
| Eucgr.H03531.1 | 74,41 | 0,51 | 2,84 | 6,02 | 12,22 | AT5G19530.1 \| Symbols: ACL5 \| S-adenosyl-L-methionine-dependent methyltransferases superfamily protein \| |
| Eucgr.C03260.1 | 25,50 | 0,97 | 1,08 | 1,41 | 4,84 | AT2G05920.1 \| Symbols: \| Subtilase family protein \| chr2:2269831-2272207 REVERSE LENGTH=754 |
| Eucgr.G02190.1 | 0,54 | 97,19 | 71,42 | 60,16 | 12,44 | No hits found |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.I01937.1 | 0,63 | 234,53 | 148,33 | 111,94 | 21,63 | No hits found |
| Eucgr.A01691.1 | 0,62 | 27,11 | 26,11 | 24,65 | 21,17 | AT2G36970.1 \| Symbols: \| UDP-Glycosyltransferase superfamily protein \| chr2:15529050-15530712 FORWARD LENGTH=490 |
| Eucgr.J02226.1 | 2,50 | 129,38 | 84,12 | 80,04 | 22,01 | AT5G40382.1 \| Symbols: \| Cytochrome c oxidase subunit Vc family protein \| chr5:16155486-16155683 REVERSE LENGTH=65 |
| Eucgr.H01945.1 | 6,14 | 62,68 | 72,80 | 52,36 | 31,27 | AT3G50380.1 \| Symbols: \| Protein of unknown function (DUF1162) \| chr3:18686527-18700533 REVERSE LENGTH=3072 |
| Eucgr.A02785.1 | 12,29 | 0,68 | 1,90 | 3,40 | 2,59 | AT3G48970.1 \| Symbols: \| Heavy metal transport/detoxification superfamily protein \| |
| Eucgr.K03449.2 | 8,93 | 62,92 | 60,36 | 43,02 | 30,45 | AT4G03200.1 \| Symbols: \| catalytics \| chr4:1408296-1412566 FORWARD LENGTH=818 |
| Eucgr.E02934.1 | 0,08 | 4,87 | 7,41 | 6,39 | 3,64 | AT1G16770.1 \| Symbols: \| unknown protein |
| Eucgr.L03214.1 | 24,68 | 888,01 | 641,74 | 501,21 | 1002,76 | AT1G53540.1 \| Symbols: \| HSP20-like chaperones superfamily protein \| chr1:19980510-19980983 FORWARD LENGTH=157 |
| Eucgr.F04333.1 | 2,83 | 0,05 | 0,29 | 0,41 | 0,38 | AT1G77400.1 \| Symbols: \| unknown protein |
| Eucgr.H02320.1 | 0,63 | 3,53 | 4,39 | 3,01 | 4,07 | AT5G65890.1 \| Symbols: ACR1 \| ACT domain repeat 1 \| chr5:26355701-26357721 FORWARD LENGTH=477 |
| Eucgr.B00140.1 | 15,42 | 176,75 | 142,66 | 163,92 | 115,92 | AT3G48510.1 \| Symbols: \| unknown protein |
| Eucgr.J01966.1 | 1,38 | 27,34 | 22,88 | 23,24 | 44,20 | AT1G53540.1 \| Symbols: \| HSP20-like chaperones superfamily protein \| chr1:19980510-19980983 FORWARD LENGTH=157 |
| Eucgr.K00957.1 | 1,36 | 17,54 | 17,19 | 10,55 | 15,16 | AT5G54160.1 \| Symbols: ATOMT1, OMT1 \| O-methyltransferase 1 \| chr5:21982075-21984167 FORWARD LENGTH=363 |
| Eucgr.I02689.1 | 21,71 | 218,24 | 199,47 | 162,07 | 136,90 | AT1G80670.1 \| Symbols: \| Transducin/WD40 repeat-like superfamily protein \| |
| Eucgr.C00370.2 | 57,14 | 230,72 | 219,00 | 189,70 | 274,04 | AT5G58070.1 \| Symbols: ATTIL, TIL \| temperature-induced lipocalin \| chr5:23500512-23501156 REVERSE LENGTH=186 |
| Eucgr.G00061.1 | 9,45 | 834,94 | 858,21 | 726,74 | 814,87 | AT4G10250.1 \| Symbols: ATHSP22.0 \| HSP20-like chaperones superfamily protein |
| Eucgr.H04349.1 | 0,10 | 0,48 | 1,13 | 0,87 | 0,99 | AT3G63380.1 \| Symbols: \| ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein \| |
| Eucgr.I02057.1 | 0,00 | 1,43 | 0,99 | 0,73 | 1,01 | AT3G30210.1 \| Symbols: ATMYB121, MYB121 \| myb domain protein 121 \| chr3:11838567-11840313 FORWARD LENGTH=276 |
| Eucgr.C03457.2 | 0,17 | 2,38 | 3,72 | 2,39 | 2,36 | AT2G26150.2 \| Symbols: ATHSFA2, HSFA2 \| heat shock transcription factor A2 \| |
| Eucgr.G01510.1 | 1,71 | 10,40 | 11,17 | 11,20 | 6,80 | AT2G37710.1 \| Symbols: RLK \| receptor lectin kinase \| chr2:15814934-15816961 REVERSE LENGTH=675 |
| Eucgr.C02666.1 | 11,79 | 71,43 | 66,15 | 46,70 | 55,43 | AT2G25140.1 \| Symbols: HSP98.7, CLPB-M, CLPB4 \| casein lytic proteinase B4 \| |
| Eucgr.L02232.1 | 0,02 | 0,81 | 0,48 | 0,27 | 0,82 | AT5G59720.1 \| Symbols: HSP18.2 \| heat shock protein 18.2 \| chr5:24062632-24063117 FORWARD LENGTH=161 |
| Eucgr.J02919.1 | 11,70 | 0,07 | 0,49 | 1,01 | 4,08 | AT2G19190.1 \| Symbols: FRK1 \| FLG22-induced receptor-like kinase 1 \| chr2:8326067-8329893 REVERSE LENGTH=876 |
| Eucgr.C03456.1 | 0,09 | 2,67 | 3,64 | 2,25 | 1,45 | AT2G26150.1 \| Symbols: ATHSFA2, HSFA2 \| heat shock transcription factor A2 |
| Eucgr.H00781.1 | 4,55 | 36,43 | 23,07 | 20,24 | 37,78 | AT3G07150.1 \| Symbols: \| unknown protein; |

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|---|---|---|---|---|---|---|
| Eucgr.K02521.1 | 48,86 | 363,27 | 336,91 | 234,15 | 831,75 | AT1G74310.1 \| Symbols: ATHSP101, HSP101, HOT1 \| heat shock protein 101 \| |
| Eucgr.B02460.3 | 41,11 | 1,17 | 2,07 | 2,91 | 10,24 | AT5G60210.2 \| Symbols: RIP5 \| ROP interactive partner 5 \| chr5:24243529-24245889 REVERSE LENGTH=564 |
| Eucgr.H01544.1 | 3,03 | 72,01 | 54,80 | 52,16 | 36,82 | AT4G02980.1 \| Symbols: ABP1, ABP \| endoplasmic reticulum auxin binding protein 1 \| |
| Eucgr.H03768.1 | 3,91 | 117,64 | 84,62 | 55,77 | 59,05 | No hits found |
| Eucgr.D00956.1 | 17,54 | 116,86 | 103,49 | 88,96 | 84,51 | AT5G47810.1 \| Symbols: PFK2 \| phosphofructokinase 2 \| chr5:19356569-19357989 REVERSE LENGTH=444 |
| Eucgr.H03959.1 | 5,98 | 0,07 | 0,05 | 0,07 | 0,61 | AT3G06840.1 \| Symbols: \| unknown protein; |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.G03295.1 | 4,33 | 0,00 | 0,01 | 0,03 | 0,13 | AT3G63470.1 \| Symbols: scpl40 \| serine carboxypeptidase-like 40 \| chr3:23438561-23440862 FORWARD LENGTH=502 |
| Eucgr.F01711.1 | 18,73 | 226,64 | 194,05 | 169,82 | 184,15 | AT5G20890.1 \| Symbols: \| TCP-1/cpn60 chaperonin family protein \| chr5:7087020-7089906 REVERSE LENGTH=527 |
| Eucgr.F01656.1 | 0,00 | 8,31 | 3,72 | 1,43 | 1,06 | AT1G75750.1 \| Symbols: GASA1 \| GAST1 protein homolog 1 \| chr1:28441813-28442284 REVERSE LENGTH=98 |
| Eucgr.K02988.2 | 16,21 | 90,52 | 69,09 | 53,94 | 47,28 | AT5G01260.1 \| Symbols: \| Carbohydrate-binding-like fold \| chr5:105367-106488 FORWARD LENGTH=306 |
| Eucgr.C00382.1 | 11,83 | 39,61 | 36,35 | 36,96 | 30,51 | AT5G58200.2 \| Symbols: \| Calcineurin-like metallo-phosphoesterase superfamily protein |
| Eucgr.F02405.1 | 0,08 | 1,19 | 2,13 | 1,16 | 0,98 | AT4G31940.1 \| Symbols: CYP82C4 \| cytochrome P450, family 82, subfamily C, polypeptide 4 |
| Eucgr.B03053.1 | 11,13 | 0,31 | 0,65 | 0,83 | 2,91 | AT1G25570.1 \| Symbols: \| Di-glucose binding protein with Leucine-rich repeat domain \| |
| Eucgr.G02214.1 | 0,04 | 42,30 | 20,44 | 13,24 | 1,86 | No hits found |
| Eucgr.G02673.1 | 0,51 | 13,39 | 10,33 | 7,14 | 3,98 | AT4G03320.1 \| Symbols: tic20-IV \| translocon at the inner envelope membrane of chloroplasts 20-IV |
| Eucgr.A01369.1 | 5,88 | 19,37 | 15,11 | 12,88 | 16,92 | AT1G04130.1 \| Symbols: TPR2, AtTPR2 \| Tetratricopeptide repeat (TPR)-like superfamily protein \| |
| Eucgr.B02930.1 | 0,16 | 1,00 | 1,20 | 1,11 | 1,20 | AT3G47570.1 \| Symbols: \| Leucine-rich repeat protein kinase family protein \| |
| Eucgr.I00418.1 | 21,92 | 0,86 | 1,80 | 2,35 | 7,81 | AT5G10150.1 \| Symbols: \| Domain of unknown function (DUF966) \| chr5:3182176-3183834 REVERSE LENGTH=414 |
| Eucgr.G01240.1 | 5,22 | 51,15 | 62,63 | 47,18 | 27,12 | AT3G18990.1 \| Symbols: VRN1, REM39 \| AP2/B3-like transcriptional factor family protein \| |
| Eucgr.F00083.2 | 5,75 | 30,30 | 23,10 | 18,30 | 15,70 | AT1G27840.1 \| Symbols: ATCSA-1 \| Transducin/WD40 repeat-like superfamily protein |
| Eucgr.H02860.1 | 275,17 | 0,98 | 4,25 | 5,40 | 27,03 | AT1G04680.1 \| Symbols: \| Pectin lyase-like superfamily protein \| chr1:1304052-1307780 REVERSE LENGTH=431 |
| Eucgr.G02722.2 | 6,40 | 71,75 | 59,67 | 48,41 | 39,53 | AT5G04520.1 \| Symbols: \| Protein of unknown function DUF455 \| chr5:1290012-1291063 REVERSE LENGTH=291 |
| Eucgr.I00519.1 | 31,40 | 3,85 | 4,68 | 5,80 | 10,85 | AT4G39980.1 \| Symbols: DHS1 \| 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 1 |
| Eucgr.H00997.1 | 0,81 | 37,45 | 29,83 | 17,09 | 7,06 | AT4G01970.1 \| Symbols: AtSTS, STS \| stachyose synthase \| chr4:854073-856953 REVERSE LENGTH=876 |
| Eucgr.G02747.1 | 26,28 | 0,69 | 1,15 | 1,75 | 11,16 | AT5G22930.1 \| Symbols: \| Protein of unknown function (DUF1635) \| chr5:7668229-7669315 REVERSE LENGTH=238 |
| Eucgr.H04537.3 | 25,06 | 97,97 | 79,89 | 63,75 | 86,77 | AT1G09140.2 \| Symbols: ATSRP30, SR30, At-SR30 \| SERINE-ARGININE PROTEIN 30 \| |
| Eucgr.E03920.1 | 0,60 | 180,55 | 135,44 | 120,35 | 24,55 | AT5G47550.1 \| Symbols: \| Cystatin/monellin superfamily protein \| chr5:19286596-19286964 REVERSE LENGTH=122 |
| Eucgr.F02056.1 | 38,09 | 1,81 | 3,39 | 5,42 | 14,84 | AT3G13130.1 \| Symbols: \| unknown protein; |
| Eucgr.A02615.1 | 0,54 | 0,00 | 0,02 | 0,00 | 0,00 | AT3G51680.1 \| Symbols: \| NAD(P)-binding Rossmann-fold superfamily protein \| |

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|---|---|---|---|---|---|---|
| Eucgr.F02145.1 | 0,45 | 20,73 | 14,00 | 6,64 | 6,80 | AT4G24540.1 \| Symbols: AGL24 \| AGAMOUS-like 24 \| chr4:12671160-12673645 REVERSE LENGTH=220 |
| Eucgr.G02938.1 | 48,93 | 2,52 | 5,91 | 9,39 | 13,24 | AT2G39700.1 \| Symbols: ATEXPA4, ATEXP4, ATHEXP ALPHA 1.6, EXPA4 \| expansin A4 \| |
| Eucgr.B02899.1 | 0,95 | 84,27 | 63,53 | 63,57 | 25,90 | AT1G71000.1 \| Symbols: \| Chaperone DnaJ-domain superfamily protein \| chr1:26769336-26770111 REVERSE LENGTH=165 |
| Eucgr.F03086.1 | 0,15 | 16,07 | 14,52 | 9,89 | 5,43 | AT4G26270.1 \| Symbols: PFK3 \| phosphofructokinase 3 \| chr4:13301094-13304030 REVERSE LENGTH=489 |
| Eucgr.H03385.1 | 6,95 | 375,36 | 306,61 | 226,60 | 105,02 | AT5G50850.1 \| Symbols: MAB1 \| Transketolase family protein \| chr5:20689671-20692976 FORWARD LENGTH=363 |
| Eucgr.L03245.1 | 0,07 | 190,81 | 124,71 | 44,86 | 2,79 | AT1G56600.1 \| Symbols: AtGolS2, GolS2 \| galactinol synthase 2 \| chr1:21207620-21209291 FORWARD LENGTH=335 |
| Eucgr.G02490.2 | 60,32 | 11,22 | 6,20 | 4,76 | 8,48 | AT1G69530.2 \| Symbols: ATEXPA1, EXP1, AT-EXP1, ATEXP1, ATHEXP ALPHA 1.2, EXPA1 \| expansin A1 |
| Eucgr.H03770.1 | 4,62 | 31,62 | 25,84 | 22,19 | 15,19 | AT4G15563.1 \| Symbols: \| unknown protein |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.D00485.1 | 0,00 | 0,82 | 0,69 | 0,20 | 0,74 | AT2G40330.1 \| Symbols: PYL6, RCAR9 \| PYR1-like 6 \| chr2:16845177-16845824 REVERSE LENGTH=215 |
| Eucgr.H02878.1 | 4,80 | 12,55 | 20,94 | 14,15 | 23,50 | AT4G13550.1 \| Symbols: \| triglyceride lipases;triglyceride lipases \| chr4:7871251-7876160 REVERSE LENGTH=715 |
| Eucgr.A01422.1 | 0,37 | 7,57 | 8,56 | 4,92 | 4,02 | AT3G49610.1 \| Symbols: \| Domain of unknown function (DUF313) \| chr3:18390413-18391417 REVERSE LENGTH=334 |
| Eucgr.F01661.1 | 0,15 | 2,82 | 2,16 | 2,39 | 1,33 | AT4G34860.2 \| Symbols: \| Plant neutral invertase family protein \| chr4:16609955-16612019 REVERSE LENGTH=571 |
| Eucgr.K02259.1 | 1,54 | 105,03 | 84,24 | 56,95 | 31,85 | AT1G18070.2 \| Symbols: \| Translation elongation factor EF1A/initiation factor IF2gamma family protein |
| Eucgr.H02522.1 | 19,02 | 1,51 | 3,06 | 4,33 | 8,82 | AT1G10750.1 \| Symbols: \| Protein of Unknown Function (DUF239) \| chr1:3574986-3578310 REVERSE LENGTH=467 |
| Eucgr.I01660.1 | 7,51 | 15,20 | 18,90 | 17,21 | 19,46 | AT3G01810.3 \| Symbols: \| unknown protein |
| Eucgr.I02316.4 | 7,86 | 33,41 | 27,76 | 28,59 | 19,16 | AT5G66090.1 \| Symbols: \| unknown protein |
| Eucgr.B01913.1 | 20,02 | 60,50 | 48,86 | 44,37 | 52,10 | AT3G05510.1 \| Symbols: \| Phospholipid/glycerol acyltransferase family protein \| |
| Eucgr.J01009.1 | 0,02 | 3,61 | 3,78 | 2,94 | 0,61 | AT5G65550.1 \| Symbols: \| UDP-Glycosyltransferase superfamily protein \| chr5:26198410-26199810 REVERSE LENGTH=466 |
| Eucgr.F02235.1 | 1,59 | 18,44 | 16,51 | 16,32 | 11,55 | AT5G48570.1 \| Symbols: ROF2, ATFKBP65, FKBP65 \| FKBP-type peptidyl-prolyl cis-trans isomerase family protein |
| Eucgr.E00235.1 | 28,49 | 88,82 | 70,95 | 60,97 | 69,20 | AT1G32260.1 \| Symbols: \| unknown protein |
| Eucgr.I01727.1 | 6,85 | 0,05 | 0,16 | 0,39 | 1,20 | AT5G14450.1 \| Symbols: \| GDSL-like Lipase/Acylhydrolase superfamily protein \| |
| Eucgr.K00423.1 | 11,57 | 550,59 | 437,13 | 391,96 | 619,70 | AT4G27670.1 \| Symbols: HSP21 \| heat shock protein 21 \| chr4:13819048-13819895 REVERSE LENGTH=227 |
| Eucgr.A02367.1 | 10,37 | 49,70 | 36,95 | 46,72 | 33,54 | AT1G01170.2 \| Symbols: \| Protein of unknown function (DUF1138) \| chr1:74105-74443 REVERSE LENGTH=83 |
| Eucgr.L00540.1 | 0,55 | 0,00 | 0,02 | 0,15 | 0,03 | AT3G51970.1 \| Symbols: ATSAT1, ASAT1, ATASAT1 \| acyl-CoA sterol acyl transferase 1 |
| Eucgr.K02328.1 | 1,09 | 45,53 | 43,31 | 28,73 | 7,18 | AT1G73390.3 \| Symbols: \| Endosomal targeting BRO1-like domain-containing protein \| |
| Eucgr.A00213.1 | 25,93 | 2,93 | 2,89 | 3,02 | 7,77 | AT1G05805.1 \| Symbols: \| basic helix-loop-helix (bHLH) DNA-binding superfamily protein \| |
| Eucgr.K01196.1 | 37,71 | 2,02 | 3,50 | 5,81 | 14,19 | AT1G78570.1 \| Symbols: RHM1, ROL1, ATRHM1 \| rhamnose biosynthesis 1 \| |
| Eucgr.J00195.1 | 0,78 | 96,37 | 68,50 | 50,25 | 7,59 | AT2G40170.1 \| Symbols: ATEM6, GEA6, EM6 \| Stress induced protein \| chr2:16779792-16780167 REVERSE LENGTH=92 |
| Eucgr.B03508.1 | 6,82 | 111,74 | 86,11 | 70,89 | 44,44 | AT1G27300.1 \| Symbols: \| unknown protein |

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|---|---|---|---|---|---|---|
| Eucgr.A02862.1 | 0,35 | 0,00 | 0,02 | 0,12 | 0,03 | AT2G28100.1 \| Symbols: ATFUC1, FUC1 \| alpha-L-fucosidase 1 \| chr2:11974803-11976489 FORWARD LENGTH=506 |
| Eucgr.H01377.1 | 0,46 | 65,76 | 46,42 | 35,69 | 12,76 | AT5G36100.1 \| Symbols: \| unknown protein |
| Eucgr.F03878.1 | 2,58 | 218,30 | 167,32 | 133,63 | 46,63 | AT1G80090.1 \| Symbols: \| Cystathionine beta-synthase (CBS) family protein \| |
| Eucgr.L03290.1 | 5,05 | 0,09 | 0,15 | 0,21 | 0,81 | AT2G05920.1 \| Symbols: \| Subtilase family protein \| chr2:2269831-2272207 REVERSE LENGTH=754 |
| Eucgr.I01700.1 | 25,91 | 0,69 | 1,52 | 3,71 | 6,37 | AT3G27350.2 \| Symbols: \| unknown protein |
| Eucgr.I00668.1 | 3,32 | 51,85 | 37,57 | 37,58 | 23,88 | AT2G14520.1 \| Symbols: \| CBS domain-containing protein with a domain of unknown function (DUF21) \| |
| Eucgr.C00873.1 | 1,92 | 24,38 | 18,82 | 14,75 | 7,94 | AT2G26150.1 \| Symbols: ATHSFA2, HSFA2 \| heat shock transcription factor A2 \| |
| Eucgr.H04478.1 | 0,03 | 13,41 | 9,75 | 7,19 | 0,81 | AT5G03250.1 \| Symbols: \| Phototropic-responsive NPH3 family protein \| chr5:774591-776855 FORWARD LENGTH=592 |
| Eucgr.C04178.1 | 3,48 | 0,13 | 0,31 | 0,61 | 0,48 | AT2G26700.1 \| Symbols: PID2 \| AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein \| |
| Eucgr.E00016.1 | 53,49 | 0,71 | 2,00 | 4,53 | 14,01 | AT3G61920.1 \| Symbols: \| unknown protein |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.I02204.1 | 3,39 | 12,91 | 15,79 | 15,47 | 10,98 | AT2G33620.4 \| Symbols: \| AT hook motif DNA-binding family protein \| chr2:14234749-14236563 FORWARD LENGTH=351 |
| Eucgr.G01537.1 | 0,42 | 0,00 | 0,00 | 0,00 | 0,00 | AT5G42650.1 \| Symbols: AOS, CYP74A, DDE2 \| allene oxide synthase \| chr5:17097803-17099359 REVERSE LENGTH=518 |
| Eucgr.E00433.1 | 3,35 | 295,94 | 205,55 | 185,03 | 165,89 | AT5G51440.1 \| Symbols: \| HSP20-like chaperones superfamily protein \| chr5:20891242-20892013 FORWARD LENGTH=210 |
| Eucgr.C01715.1 | 3,32 | 63,28 | 54,72 | 35,80 | 28,00 | AT5G20280.1 \| Symbols: ATSPS1F, SPS1F \| sucrose phosphate synthase 1F \| chr5:6844994-6849997 REVERSE LENGTH=1043 |
| Eucgr.C03454.1 | 0,92 | 10,40 | 10,94 | 6,71 | 5,80 | AT2G26150.1 \| Symbols: ATHSFA2, HSFA2 \| heat shock transcription factor A2 \| |
| Eucgr.A02804.1 | 24,80 | 78,79 | 76,07 | 72,67 | 89,08 | AT5G62020.1 \| Symbols: AT-HSFB2A, HSFB2A \| heat shock transcription factor B2A \| |
| Eucgr.H00812.1 | 38,28 | 1,20 | 2,33 | 3,34 | 8,92 | AT3G24660.1 \| Symbols: TMKL1 \| transmembrane kinase-like 1 \| chr3:9003641-9005751 FORWARD LENGTH=674 |
| Eucgr.H02278.1 | 2,17 | 60,73 | 55,26 | 50,88 | 24,61 | AT2G23110.2 \| Symbols: \| Late embryogenesis abundant protein, group 6 \| chr2:9840552-9840830 FORWARD LENGTH=92 |
| Eucgr.D02134.1 | 0,50 | 0,00 | 0,01 | 0,00 | 0,05 | AT3G10600.1 \| Symbols: CAT7 \| cationic amino acid transporter 7 \| chr3:3313969-3317162 FORWARD LENGTH=584 |
| Eucgr.A02658.1 | 11,73 | 0,29 | 0,65 | 1,52 | 1,91 | AT5G03870.1 \| Symbols: \| Glutaredoxin family protein \| chr5:1035813-1036967 REVERSE LENGTH=384 |
| Eucgr.C01043.1 | 2,92 | 122,26 | 116,87 | 96,98 | 13,96 | AT3G24520.1 \| Symbols: AT-HSFC1, HSFC1 \| heat shock transcription factor C1 \| |
| Eucgr.E00444.1 | 25,26 | 3,62 | 4,88 | 6,07 | 11,61 | AT4G17260.1 \| Symbols: \| Lactate/malate dehydrogenase family protein \| chr4:9674057-9675309 FORWARD LENGTH=353 |
| Eucgr.H04092.1 | 28,01 | 0,78 | 2,01 | 2,33 | 10,01 | AT1G48100.1 \| Symbols: \| Pectin lyase-like superfamily protein \| chr1:17766921-17769625 FORWARD LENGTH=475 |
| Eucgr.F03621.1 | 0,60 | 53,74 | 50,05 | 47,35 | 6,91 | AT1G21000.2 \| Symbols: \| PLATZ transcription factor family protein \| chr1:7338013-7339088 FORWARD LENGTH=243 |
| Eucgr.I02278.1 | 0,18 | 20,21 | 23,14 | 33,84 | 2,38 | AT4G35710.1 \| Symbols: \| Arabidopsis protein of unknown function (DUF241) \| chr4:16925301-16926152 FORWARD LENGTH=283 |
| Eucgr.F02505.1 | 14,04 | 0,07 | 0,31 | 0,42 | 5,27 | AT1G68360.1 \| Symbols: \| C2H2 and C2HC zinc fingers superfamily protein \| chr1:25621678-25622412 REVERSE LENGTH=244 |
| Eucgr.E02655.1 | 0,52 | 0,00 | 0,00 | 0,00 | 0,05 | AT2G34060.1 \| Symbols: \| Peroxidase superfamily protein \| chr2:14384914-14386530 FORWARD LENGTH=346 |
| Eucgr.I01669.1 | 3,07 | 67,66 | 79,13 | 75,99 | 34,25 | AT3G27250.1 \| Symbols: \| unknown protein |
| Eucgr.D00295.1 | 29,29 | 246,26 | 190,72 | 214,06 | 154,80 | AT1G30070.1 \| Symbols: \| SGS domain-containing protein \| chr1:10546794-10548072 REVERSE LENGTH=222 |

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|---|---|---|---|---|---|---|
| Eucgr.E00015.2 | 22,81 | 1,66 | 2,21 | 3,70 | 7,74 | No hits found |
| Eucgr.B02917.1 | 7,20 | 0,00 | 0,18 | 1,03 | 0,59 | AT4G14060.1 \| Symbols: \| Polyketide cyclase/dehydrase and lipid transport superfamily protein \| |
| Eucgr.H03952.1 | 0,45 | 0,00 | 0,01 | 0,00 | 0,05 | AT5G49130.1 \| Symbols: \| MATE efflux family protein \| chr5:19915904-19917525 FORWARD LENGTH=502 |
| Eucgr.L00240.1 | 0,02 | 34,50 | 22,77 | 10,27 | 0,66 | AT1G56600.1 \| Symbols: AtGolS2, GolS2 \| galactinol synthase 2 \| chr1:21207620-21209291 FORWARD LENGTH=335 |
| Eucgr.L03270.1 | 0,42 | 742,81 | 379,17 | 232,66 | 3,62 | AT4G33467.2 \| Symbols: \| unknown protein |
| Eucgr.K01431.1 | 1,67 | 34,99 | 28,93 | 27,47 | 15,68 | AT1G04520.1 \| Symbols: PDLP2 \| plasmodesmata-located protein 2 \| chr1:1231852-1233787 FORWARD LENGTH=307 |
| Eucgr.H00798.1 | 58,69 | 1,20 | 4,03 | 6,42 | 24,86 | AT5G48740.1 \| Symbols: \| Leucine-rich repeat protein kinase family protein \| chr5:19765324-19769314 REVERSE LENGTH=895 |
| Eucgr.D01780.1 | 7,62 | 1,87 | 1,71 | 1,79 | 2,13 | AT4G23720.1 \| Symbols: \| Protein of unknown function (DUF1191) \| chr4:12358707-12359648 FORWARD LENGTH=313 |
| Eucgr.J02951.1 | 0,48 | 0,00 | 0,00 | 0,02 | 0,03 | AT2G26490.1 \| Symbols: \| Transducin/WD40 repeat-like superfamily protein \| |
| Eucgr.D00534.1 | 0,00 | 0,90 | 1,04 | 0,71 | 0,29 | AT5G45910.1 \| Symbols: \| GDSL-like Lipase/Acylhydrolase superfamily protein \| |
| Eucgr.E00347.1 | 3,00 | 226,36 | 192,13 | 201,85 | 132,87 | AT4G33550.1 \| Symbols: \| Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein \| |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.D01202.1 | 29,79 | 1,29 | 1,68 | 2,32 | 15,49 | AT2G44690.1 \| Symbols: ARAC9, ATROP8, ROP8 \| Arabidopsis RAC-like 9 \| chr2:18429276-18430636 FORWARD LENGTH=209 |
| Eucgr.A02926.1 | 0,06 | 4,08 | 5,38 | 5,33 | 1,12 | AT5G07490.1 \| Symbols: \| unknown protein; |
| Eucgr.F03665.1 | 0,73 | 0,00 | 0,01 | 0,02 | 0,04 | AT5G59810.1 \| Symbols: ATSBT5.4, SBT5.4 \| Subtilase family protein \| chr5:24096895-24100387 REVERSE LENGTH=778 |
| Eucgr.L00251.1 | 0,21 | 325,56 | 149,21 | 61,46 | 3,38 | AT1G56600.1 \| Symbols: AtGolS2, GolS2 \| galactinol synthase 2 \| chr1:21207620-21209291 FORWARD LENGTH=335 |
| Eucgr.C02145.1 | 7,05 | 63,91 | 50,64 | 32,15 | 20,87 | AT4G31140.1 \| Symbols: \| O-Glycosyl hydrolases family 17 protein \| chr4:15141581-15143188 FORWARD LENGTH=484 |
| Eucgr.C00112.1 | 0,70 | 12,29 | 14,05 | 17,42 | 3,57 | AT5G57180.2 \| Symbols: CIA2 \| chloroplast import apparatus 2 \| chr5:23168393-23170763 FORWARD LENGTH=435 |
| Eucgr.B04029.1 | 1,08 | 5,43 | 5,54 | 4,24 | 4,75 | No hits found |
| Eucgr.K01574.1 | 2,12 | 14,23 | 17,44 | 12,16 | 9,54 | AT2G41510.1 \| Symbols: ATCKX1, CKX1 \| cytokinin oxidase/dehydrogenase 1 |
| Eucgr.J01011.1 | 24,97 | 0,49 | 1,02 | 2,06 | 5,93 | AT5G04660.1 \| Symbols: CYP77A4 \| cytochrome P450, family 77, subfamily A, polypeptide 4 \| |
| Eucgr.B01852.1 | 31,04 | 2,22 | 3,00 | 3,56 | 11,55 | AT1G09070.1 \| Symbols: SRC2, (AT)SRC2 \| soybean gene regulated by cold-2 \| chr1:2927767-2928741 FORWARD LENGTH=324 |
| Eucgr.D01381.1 | 17,58 | 1,64 | 1,70 | 1,92 | 4,85 | AT4G05520.1 \| Symbols: ATEHD2, EHD2 \| EPS15 homology domain 2 \| chr4:2804522-2807833 FORWARD LENGTH=546 |
| Eucgr.K02245.1 | 9,42 | 0,04 | 0,21 | 0,18 | 2,23 | AT3G18180.1 \| Symbols: \| Glycosyltransferase family 61 protein \| chr3:6230270-6231878 FORWARD LENGTH=470 |
| Eucgr.C02293.1 | 2,07 | 49,90 | 58,91 | 51,95 | 23,88 | AT5G57480.1 \| Symbols: \| P-loop containing nucleoside triphosphate hydrolases superfamily protein \| |
| Eucgr.G01235.1 | 3,36 | 40,19 | 40,09 | 43,38 | 22,26 | AT3G18990.1 \| Symbols: VRN1, REM39 \| AP2/B3-like transcriptional factor family protein \| |
| Eucgr.H02498.1 | 17,77 | 195,87 | 178,28 | 168,88 | 130,52 | AT1G59960.1 \| Symbols: \| NAD(P)-linked oxidoreductase superfamily protein \| |
| Eucgr.K01344.1 | 5,46 | 109,37 | 132,11 | 131,68 | 77,29 | AT3G12750.1 \| Symbols: ZIP1 \| zinc transporter 1 precursor \| chr3:4051950-4053156 REVERSE LENGTH=355 |
| Eucgr.A00215.1 | 35,20 | 7,54 | 7,19 | 9,01 | 17,55 | AT2G43130.1 \| Symbols: ARA4, ATRAB11F, ATRABA5C, ARA-4, RABA5C |
| Eucgr.H02273.1 | 0,11 | 17,75 | 13,64 | 12,12 | 2,51 | AT2G23120.1 \| Symbols: \| Late embryogenesis abundant protein, group 6 \| chr2:9842102-9842353 FORWARD LENGTH=83 |

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|---|---|---|---|---|---|---|
| Eucgr.E01133.2 | 5,10 | 36,15 | 34,71 | 36,12 | 27,09 | AT4G10430.3 \| Symbols: \| TMPIT-like protein \| chr4:6455110-6457996 REVERSE LENGTH=347 |
| Eucgr.K02872.1 | 0,00 | 1,89 | 2,16 | 1,86 | 0,66 | No hits found |
| Eucgr.G02197.1 | 8,32 | 23,70 | 36,64 | 34,02 | 25,13 | AT1G23010.1 \| Symbols: LPR1 \| Cupredoxin superfamily protein \| chr1:8147353-8149580 FORWARD LENGTH=581 |
| Eucgr.A02416.1 | 24,03 | 0,12 | 0,23 | 0,43 | 5,41 | AT3G57830.1 \| Symbols: \| Leucine-rich repeat protein kinase family protein \| |
| Eucgr.I01670.1 | 5,31 | 43,82 | 33,92 | 30,65 | 22,35 | AT3G48510.1 \| Symbols: \| unknown protein |
| Eucgr.B03684.1 | 49,42 | 9,83 | 22,21 | 38,16 | 22,44 | AT5G12870.1 \| Symbols: ATMYB46, MYB46 \| myb domain protein 46 \| chr5:4062939-4064939 REVERSE LENGTH=280 |
| Eucgr.K01425.1 | 10,37 | 0,33 | 0,93 | 1,13 | 5,35 | AT4G28650.1 \| Symbols: \| Leucine-rich repeat transmembrane protein kinase family protein \| |
| Eucgr.K03318.1 | 49,40 | 3,62 | 3,07 | 4,48 | 16,55 | AT3G54560.1 \| Symbols: HTA11 \| histone H2A 11 \| chr3:20196532-20197466 FORWARD LENGTH=136 |
| Eucgr.K00150.1 | 45,43 | 2,66 | 4,30 | 5,27 | 10,07 | AT5G51550.1 \| Symbols: EXL3 \| EXORDIUM like 3 \| chr5:20939793-20940806 REVERSE LENGTH=337 |
| Eucgr.I02678.1 | 6,78 | 34,08 | 31,69 | 27,68 | 25,32 | AT4G33500.1 \| Symbols: \| Protein phosphatase 2C family protein \| chr4:16112835-16116243 REVERSE LENGTH=724 |
| Eucgr.C03434.1 | 0,31 | 6,75 | 6,22 | 6,19 | 2,03 | AT2G26150.1 \| Symbols: ATHSFA2, HSFA2 \| heat shock transcription factor A2 \| |
| Eucgr.G02156.1 | 40,72 | 3,42 | 3,65 | 5,44 | 13,75 | AT1G14890.1 \| Symbols: \| Plant invertase/pectin methylesterase inhibitor superfamily protein |
| Eucgr.K03526.1 | 15,24 | 174,63 | 154,97 | 121,95 | 59,79 | AT4G02120.1 \| Symbols: \| CTP synthase family protein \| chr4:940873-944097 FORWARD LENGTH=556 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.A02229.1 | 34,74 | 0,51 | 1,19 | 1,73 | 4,71 | AT2G01420.1 \| Symbols: PIN4, ATPIN4 \| Auxin efflux carrier family protein \| chr2:180478-183199 REVERSE LENGTH=612 |
| Eucgr.F03514.1 | 189,06 | 3,00 | 6,50 | 5,98 | 31,95 | AT5G55410.2 \| Symbols: \| Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein \| |
| Eucgr.A02008.1 | 0,16 | 1,07 | 1,89 | 1,66 | 0,83 | AT1G06490.1 \| Symbols: ATGSL07, gsl07, atgsl7, GSL7 \| glucan synthase-like 7 \| |
| Eucgr.B00580.1 | 7,83 | 0,48 | 0,83 | 1,39 | 1,06 | AT5G07990.1 \| Symbols: TT7, CYP75B1, D501 \| Cytochrome P450 superfamily protein \| |
| Eucgr.E00360.1 | 5,58 | 623,57 | 416,31 | 243,00 | 88,39 | AT4G17030.1 \| Symbols: ATEXLB1, EXPR, AT-EXPR, ATEXPR1, ATHEXP BETA 3.1, EXLB1 \| expansin-like B1 |
| Eucgr.G03118.1 | 5,52 | 47,21 | 44,62 | 43,13 | 33,32 | No hits found |
| Eucgr.K02961.3 | 16,85 | 174,50 | 121,56 | 94,41 | 87,15 | AT2G40300.1 \| Symbols: ATFER4, FER4 \| ferritin 4 \| chr2:16831501-16833214 REVERSE LENGTH=259 |
| Eucgr.B00412.1 | 30,69 | 0,47 | 0,95 | 1,72 | 12,73 | AT5G62710.1 \| Symbols: \| Leucine-rich repeat protein kinase family protein \| chr5:25187438-25190325 FORWARD LENGTH=604 |
| Eucgr.B03008.1 | 62,99 | 475,02 | 399,93 | 377,86 | 240,60 | AT1G68300.1 \| Symbols: \| Adenine nucleotide alpha hydrolases-like superfamily protein \| chr1:25598518-25599261 REVERSE LENGTH=160 |
| Eucgr.G01728.1 | 3,87 | 0,06 | 0,25 | 0,35 | 1,00 | AT4G39010.1 \| Symbols: AtGH9B18, GH9B18 \| glycosyl hydrolase 9B18 \| chr4:18176162-18179102 REVERSE LENGTH=497 |
| Eucgr.J00457.2 | 5,69 | 47,20 | 42,83 | 33,08 | 18,78 | AT5G22510.1 \| Symbols: INV-E, At-A/N-InvE \| alkaline/neutral invertase \| chr5:7474974-7477479 REVERSE LENGTH=617 |
| Eucgr.C00218.1 | 61,73 | 8,50 | 11,31 | 12,67 | 24,16 | AT2G23810.1 \| Symbols: TET8 \| tetraspanin8 \| chr2:10135859-10137352 REVERSE LENGTH=273 |
| Eucgr.F00301.1 | 28,54 | 4,88 | 5,57 | 7,81 | 14,63 | AT1G78110.1 \| Symbols: \| unknown protein |
| Eucgr.K01055.1 | 42,72 | 337,71 | 362,68 | 582,22 | 200,35 | No hits found |
| Eucgr.G02495.1 | 16,31 | 0,79 | 1,91 | 3,33 | 7,13 | AT1G14190.1 \| Symbols: \| Glucose-methanol-choline (GMC) oxidoreductase family protein \| |
| Eucgr.H04815.2 | 8,01 | 133,50 | 102,82 | 79,74 | 77,03 | AT2G22240.1 \| Symbols: ATMIPS2, MIPS2, ATIPS2 \| myo-inositol-1-phosphate synthase 2 \| |

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|---|---|---|---|---|---|---|
| Eucgr.B00170.1 | 1,13 | 0,22 | 0,00 | 0,07 | 0,09 | No hits found |
| Eucgr.A02150.1 | 1,06 | 9,41 | 6,93 | 3,52 | 3,95 | AT1G69560.1 \| Symbols: MYB105, LOF2, ATMYB105 \| myb domain protein 105 \| |
| Eucgr.K01583.1 | 3,82 | 0,03 | 0,03 | 0,09 | 1,02 | AT1G17020.1 \| Symbols: SRG1, ATSRG1 \| senescence-related gene 1 \| chr1:5820258-5821741 FORWARD LENGTH=358 |
| Eucgr.K00778.1 | 2,61 | 0,06 | 0,26 | 0,71 | 0,60 | AT2G32540.1 \| Symbols: ATCSLB04, CSLB04, ATCSLB4 \| cellulose synthase-like B4 \| |
| Eucgr.I02514.1 | 3,73 | 0,20 | 0,33 | 0,38 | 0,53 | AT4G17000.1 \| Symbols: \| unknown protein; |
| Eucgr.K01967.1 | 26,89 | 1,99 | 3,68 | 4,77 | 10,23 | AT5G44530.1 \| Symbols: \| Subtilase family protein \| chr5:17937931-17941193 FORWARD LENGTH=840 |
| Eucgr.J00948.1 | 0,00 | 2,58 | 2,03 | 1,20 | 0,23 | AT2G28490.1 \| Symbols: \| RmlC-like cupins superfamily protein \| chr2:12178812-12180983 REVERSE LENGTH=511 |
| Eucgr.A01877.1 | 0,00 | 0,31 | 0,79 | 1,75 | 0,22 | AT4G35160.1 \| Symbols: \| O-methyltransferase family protein \| chr4:16730989-16732808 REVERSE LENGTH=382 |
| Eucgr.H00467.1 | 6,20 | 79,40 | 69,57 | 83,40 | 24,29 | AT1G60710.1 \| Symbols: ATB2 \| NAD(P)-linked oxidoreductase superfamily protein \| |
| Eucgr.F00649.1 | 1,21 | 0,06 | 0,13 | 0,17 | 0,23 | AT5G55250.1 \| Symbols: IAMT1 \| IAA carboxylmethyltransferase 1 \| chr5:22407589-22410854 REVERSE LENGTH=386 |
| Eucgr.A02858.1 | 0,77 | 45,90 | 34,68 | 20,99 | 8,40 | AT5G51760.1 \| Symbols: AHG1 \| Protein phosphatase 2C family protein \| chr5:21026916-21028912 FORWARD LENGTH=416 |
| Eucgr.H04619.1 | 0,34 | 29,24 | 24,75 | 23,01 | 2,43 | No hits found |
| Eucgr.K01580.1 | 3,13 | 16,92 | 16,68 | 21,70 | 10,45 | AT3G57190.1 \| Symbols: \| peptide chain release factor, putative \| chr3:21166468-21168198 FORWARD LENGTH=406 |
| Eucgr.A01798.3 | 12,42 | 0,13 | 0,53 | 0,87 | 5,37 | AT1G03620.1 \| Symbols: \| ELMO/CED-12 family protein \| chr1:904319-906013 REVERSE LENGTH=265 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.A02601.1 | 16,96 | 1,46 | 1,64 | 1,18 | 2,97 | AT3G52500.1 \| Symbols: \| Eukaryotic aspartyl protease family protein \| chr3:19465644-19467053 REVERSE LENGTH=469 |
| Eucgr.F01151.1 | 22,41 | 211,06 | 158,42 | 117,64 | 60,94 | AT4G27520.1 \| Symbols: ENODL2, AtENODL2 \| early nodulin-like protein 2 \| chr4:13750668-13751819 REVERSE LENGTH=349 |
| Eucgr.F02851.1 | 192,64 | 1,06 | 4,02 | 7,93 | 38,91 | AT2G30810.1 \| Symbols: \| Gibberellin-regulated family protein \| chr2:13127945-13128630 REVERSE LENGTH=106 |
| Eucgr.H02896.1 | 0,07 | 6,57 | 8,20 | 6,34 | 1,14 | AT3G24310.1 \| Symbols: MYB305, ATMYB71 \| myb domain protein 305 \| chr3:8811336-8812330 REVERSE LENGTH=269 |
| Eucgr.H02593.1 | 13,14 | 204,27 | 152,30 | 118,96 | 62,04 | AT1G60420.1 \| Symbols: \| DC1 domain-containing protein \| chr1:22261978-22264243 FORWARD LENGTH=578 |
| Eucgr.F02468.1 | 0,67 | 0,02 | 0,07 | 0,12 | 0,13 | AT5G45480.1 \| Symbols: \| Protein of unknown function (DUF594) \| chr5:18426296-18428929 REVERSE LENGTH=877 |
| Eucgr.B03303.1 | 43,12 | 3,33 | 6,88 | 9,78 | 19,35 | AT1G10750.1 \| Symbols: \| Protein of Unknown Function (DUF239) \| chr1:3574986-3578310 REVERSE LENGTH=467 |
| Eucgr.F03761.1 | 2,71 | 0,00 | 0,00 | 0,05 | 0,53 | AT5G08640.2 \| Symbols: FLS1 \| flavonol synthase 1 \| chr5:2804009-2805175 FORWARD LENGTH=336 |
| Eucgr.G00317.1 | 5,18 | 0,46 | 0,32 | 0,81 | 1,65 | AT1G09812.1 \| Symbols: \| unknown protein |
| Eucgr.H02966.1 | 24,69 | 0,87 | 1,27 | 1,73 | 3,30 | No hits found |
| Eucgr.I01646.1 | 48,55 | 1,72 | 2,40 | 2,82 | 14,36 | AT3G27060.1 \| Symbols: TSO2, ATTSO2 \| Ferritin/ribonucleotide reductase-like family protein |
| Eucgr.J01089.1 | 28,49 | 0,44 | 2,27 | 6,81 | 14,22 | AT2G39220.1 \| Symbols: PLP6, PLA IIB \| PATATIN-like protein 6 \| chr2:16375055-16376663 REVERSE LENGTH=499 |
| Eucgr.B00827.1 | 6,35 | 0,57 | 2,11 | 5,48 | 2,27 | No hits found |
| Eucgr.K01573.1 | 0,25 | 15,37 | 15,23 | 13,35 | 5,95 | No hits found |
| Eucgr.G01350.2 | 23,73 | 146,29 | 126,30 | 144,55 | 62,96 | AT4G34230.1 \| Symbols: CAD5, ATCAD5, CAD-5 \| cinnamyl alcohol dehydrogenase 5 \| |

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|---|---|---|---|---|---|---|
| Eucgr.F02055.1 | 2,82 | 0,21 | 0,18 | 0,43 | 0,66 | AT3G13130.1 \| Symbols: \| unknown protein |
| Eucgr.E01110.2 | 4,34 | 59,21 | 49,17 | 51,45 | 27,12 | AT1G72680.1 \| Symbols: ATCAD1, CAD1 \| cinnamyl-alcohol dehydrogenase \| chr1:27359346-27360876 REVERSE LENGTH=355 |
| Eucgr.I01013.1 | 8,29 | 0,08 | 0,65 | 1,64 | 1,01 | AT2G23610.1 \| Symbols: ATMES3, MES3 \| methyl esterase 3 \| chr2:10044410-10046403 REVERSE LENGTH=263 |
| Eucgr.A02860.1 | 4,54 | 0,07 | 0,11 | 0,14 | 0,99 | AT2G16280.1 \| Symbols: KCS9 \| 3-ketoacyl-CoA synthase 9 \| chr2:7051186-7052724 FORWARD LENGTH=512 |
| Eucgr.K01314.2 | 2,51 | 222,00 | 178,21 | 124,80 | 132,76 | AT3G08590.2 \| Symbols: \| Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent \| |
| Eucgr.F04059.1 | 20,67 | 2,20 | 3,84 | 5,47 | 10,52 | AT3G13000.2 \| Symbols: \| Protein of unknown function, DUF547 \| chr3:4158214-4160989 REVERSE LENGTH=582 |
| Eucgr.H03957.1 | 26,11 | 0,69 | 1,46 | 3,15 | 5,85 | AT4G02340.1 \| Symbols: \| alpha/beta-Hydrolases superfamily protein \| chr4:1035722-1037403 FORWARD LENGTH=324 |
| Eucgr.I01790.1 | 1,06 | 11,78 | 13,06 | 15,94 | 15,77 | AT3G01500.2 \| Symbols: CA1 \| carbonic anhydrase 1 \| chr3:194853-197873 REVERSE LENGTH=347 |
| Eucgr.G03283.1 | 6,98 | 23,73 | 17,15 | 14,04 | 15,53 | AT3G60910.1 \| Symbols: \| S-adenosyl-L-methionine-dependent methyltransferases superfamily protein \| |
| Eucgr.H03517.1 | 16,45 | 0,37 | 0,95 | 1,84 | 2,74 | AT1G05370.1 \| Symbols: \| Sec14p-like phosphatidylinositol transfer family protein \| |
| Eucgr.F03754.1 | 12,93 | 0,24 | 0,68 | 1,63 | 5,89 | AT1G38131.1 \| Symbols: \| O-fucosyltransferase family protein \| chr1:14293392-14296020 REVERSE LENGTH=589 |
| Eucgr.C00378.1 | 2,87 | 0,02 | 0,08 | 0,16 | 0,68 | AT2G24280.1 \| Symbols: \| alpha/beta-Hydrolases superfamily protein \| chr2:10334622-10336927 FORWARD LENGTH=494 |
| Eucgr.E00847.1 | 32,93 | 1,08 | 1,02 | 1,82 | 4,93 | AT4G23800.1 \| Symbols: \| HMG (high mobility group) box protein \| chr4:12390228-12392516 FORWARD LENGTH=456 |
| Eucgr.E00078.3 | 18,23 | 242,77 | 193,91 | 127,40 | 69,04 | AT2G46270.1 \| Symbols: GBF3 \| G-box binding factor 3 \| chr2:19000859-19002901 FORWARD LENGTH=382 |
| Eucgr.I01891.1 | 13,34 | 0,50 | 1,23 | 2,02 | 3,26 | AT3G28420.1 \| Symbols: \| Putative membrane lipoprotein \| chr3:10654674-10655324 REVERSE LENGTH=216 |
| Eucgr.D01765.2 | 0,07 | 3,26 | 6,28 | 7,07 | 1,24 | AT4G23990.1 \| Symbols: ATCSLG3, CSLG3 \| cellulose synthase like G3 \| chr4:12456491-12460498 FORWARD LENGTH=751 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.I00409.1 | 0,06 | 3,27 | 4,18 | 2,91 | 0,60 | AT4G34131.1 \| Symbols: UGT73B3 \| UDP-glucosyl transferase 73B3 \| chr4:16343268-16344713 REVERSE LENGTH=481 |
| Eucgr.G03282.1 | 0,09 | 10,41 | 8,85 | 6,96 | 1,53 | AT2G28420.1 \| Symbols: \| Lactoylglutathione lyase / glyoxalase I family protein \| |
| Eucgr.I01627.3 | 8,50 | 57,85 | 46,76 | 38,03 | 19,29 | AT3G01990.1 \| Symbols: ACR6 \| ACT domain repeat 6 \| chr3:330256-332066 FORWARD LENGTH=433 |
| Eucgr.J00303.1 | 7,16 | 0,14 | 0,37 | 0,57 | 0,98 | AT5G06470.1 \| Symbols: \| Glutaredoxin family protein \| chr5:1974659-1975378 REVERSE LENGTH=239 |
| Eucgr.C04221.1 | 1,01 | 0,00 | 0,02 | 0,00 | 0,11 | AT1G15360.1 \| Symbols: SHN1, WIN1 \| Integrase-type DNA-binding superfamily protein \| |
| Eucgr.G00501.1 | 0,71 | 0,03 | 0,02 | 0,07 | 0,09 | AT5G42650.1 \| Symbols: AOS, CYP74A, DDE2 \| allene oxide synthase \| chr5:17097803-17099359 REVERSE LENGTH=518 |
| Eucgr.C00666.1 | 5,19 | 63,12 | 75,80 | 71,30 | 30,32 | AT2G26170.2 \| Symbols: CYP711A1 \| cytochrome P450, family 711, subfamily A, polypeptide 1 |
| Eucgr.L02188.1 | 12,05 | 0,54 | 1,77 | 3,57 | 5,43 | AT5G11000.1 \| Symbols: \| Plant protein of unknown function (DUF868) \| chr5:3479166-3480335 REVERSE LENGTH=389 |
| Eucgr.B00302.1 | 27,47 | 0,98 | 1,66 | 2,43 | 6,41 | AT2G47160.1 \| Symbols: BOR1 \| HCO3- transporter family \| chr2:19357740-19360787 REVERSE LENGTH=704 |
| Eucgr.H01095.1 | 78,97 | 0,57 | 3,99 | 6,76 | 19,38 | AT4G02290.1 \| Symbols: AtGH9B13, GH9B13 \| glycosyl hydrolase 9B13 \| chr4:1002654-1005125 REVERSE LENGTH=516 |
| Eucgr.G03200.1 | 156,94 | 11,37 | 7,49 | 12,01 | 15,60 | AT5G07050.1 \| Symbols: \| nodulin MtN21 /EamA-like transporter family protein \| |
| Eucgr.K03469.1 | 56,95 | 1,15 | 2,72 | 3,54 | 10,39 | AT1G08560.1 \| Symbols: SYP111, KN, ATSYP111 \| syntaxin of plants 111 \| chr1:2709778-2710710 REVERSE LENGTH=310 |
| Eucgr.E00812.1 | 8,79 | 0,24 | 0,87 | 2,51 | 2,99 | AT1G64160.1 \| Symbols: \| Disease resistance-responsive (dirigent-like protein) family protein \| |

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|---|---|---|---|---|---|---|
| Eucgr.C01388.1 | 79,86 | 0,45 | 1,28 | 1,19 | 21,24 | AT2G10940.2 \| Symbols: \| Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein \| |
| Eucgr.J01066.1 | 37,91 | 812,10 | 857,97 | 610,25 | 159,86 | AT2G39130.1 \| Symbols: \| Transmembrane amino acid transporter family protein \| |
| Eucgr.H02629.1 | 20,89 | 306,08 | 289,19 | 273,68 | 273,55 | AT5G48570.1 \| Symbols: ROF2, ATFKBP65, FKBP65 \| FKBP-type peptidyl-prolyl cis-trans isomerase family protein \| |
| Eucgr.B01279.1 | 10,18 | 0,08 | 0,22 | 0,34 | 5,20 | AT3G26700.1 \| Symbols: \| Protein kinase superfamily protein \| chr3:9810669-9812356 FORWARD LENGTH=380 |
| Eucgr.K02082.1 | 161,54 | 0,89 | 2,95 | 5,95 | 52,84 | AT2G36570.1 \| Symbols: \| Leucine-rich repeat protein kinase family protein \| chr2:15335583-15337725 FORWARD LENGTH=672 |
| Eucgr.A02790.1 | 15,66 | 1398,81 | 1140,99 | 647,25 | 272,46 | AT5G52300.2 \| Symbols: RD29B, LTI65 \| CAP160 protein \| chr5:21237205-21239404 FORWARD LENGTH=618 |
| Eucgr.E00266.1 | 34,34 | 2,38 | 6,52 | 11,42 | 13,52 | No hits found |
| Eucgr.F02525.1 | 20,40 | 0,00 | 0,29 | 0,67 | 1,40 | No hits found |
| Eucgr.F02150.1 | 9,89 | 0,25 | 0,43 | 0,60 | 1,79 | AT5G60930.1 \| Symbols: \| P-loop containing nucleoside triphosphate hydrolases superfamily protein |
| Eucgr.H01202.1 | 12,87 | 0,05 | 0,33 | 2,39 | 1,37 | AT2G47880.1 \| Symbols: \| Glutaredoxin family protein \| chr2:19605124-19605432 FORWARD LENGTH=102 |
| Eucgr.I01639.1 | 11,06 | 69,22 | 57,03 | 66,79 | 28,53 | AT5G40960.1 \| Symbols: \| Protein of unknown function (DUF 3339) \| chr5:16412745-16412951 REVERSE LENGTH=68 |
| Eucgr.A02352.1 | 1,29 | 0,05 | 0,06 | 0,09 | 0,16 | AT2G41790.1 \| Symbols: \| Insulinase (Peptidase family M16) family protein \| chr2:17429453-17436110 REVERSE LENGTH=970 |
| Eucgr.K03244.2 | 29,50 | 382,43 | 351,93 | 254,16 | 266,20 | AT3G53420.2 \| Symbols: PIP2A, PIP2, PIP2;1 \| plasma membrane intrinsic protein 2A \| |
| Eucgr.E00450.1 | 16,88 | 2,16 | 2,89 | 4,73 | 7,62 | AT1G62520.1 \| Symbols: \| unknown protein |
| Eucgr.K01030.1 | 10,57 | 40,54 | 48,26 | 41,08 | 28,52 | AT4G03560.1 \| Symbols: ATTPC1, TPC1, ATCCH1, FOU2 \| two-pore channel 1 \| chr4:1580253-1585691 FORWARD LENGTH=733 |
| Eucgr.B02566.1 | 2,55 | 53,48 | 47,33 | 37,84 | 27,61 | AT1G24130.1 \| Symbols: \| Transducin/WD40 repeat-like superfamily protein \| chr1:8534183-8535430 REVERSE LENGTH=415 |
| Eucgr.K02050.1 | 309,22 | 1,77 | 6,92 | 12,73 | 116,05 | AT3G10080.1 \| Symbols: \| RmlC-like cupins superfamily protein \| chr3:3107476-3108159 REVERSE LENGTH=227 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.L02059.1 | 0,80 | 0,00 | 0,01 | 0,03 | 0,12 | AT3G63470.1 \| Symbols: scpl40 \| serine carboxypeptidase-like 40 \| chr3:23438561-23440862 FORWARD LENGTH=502 |
| Eucgr.H04021.1 | 5,29 | 0,08 | 0,17 | 0,19 | 0,34 | AT4G16120.1 \| Symbols: ATSEB1, COBL7, SEB1 \| COBRA-like protein-7 precursor \| |
| Eucgr.I00918.1 | 1,14 | 0,08 | 0,07 | 0,30 | 0,19 | AT4G36950.1 \| Symbols: MAPKKK21 \| mitogen-activated protein kinase kinase kinase 21 \| |
| Eucgr.F02209.1 | 11,50 | 101,96 | 92,75 | 54,42 | 38,58 | AT1G58520.1 \| Symbols: RXW8 \| lipases;hydrolases, acting on ester bonds |
| Eucgr.F03235.1 | 12,40 | 0,03 | 0,40 | 0,61 | 3,00 | AT1G29050.1 \| Symbols: TBL38 \| TRICHOME BIREFRINGENCE-LIKE 38 \| chr1:10136376-10139082 REVERSE LENGTH=380 |
| Eucgr.H00766.1 | 0,37 | 32,50 | 24,18 | 11,54 | 4,89 | AT3G07250.1 \| Symbols: \| nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein \| |
| Eucgr.H04224.1 | 6,87 | 0,05 | 0,08 | 0,35 | 0,69 | AT5G44040.1 \| Symbols: \| unknown protein |
| Eucgr.B03841.1 | 71,58 | 1,99 | 3,99 | 6,96 | 24,37 | AT5G22400.1 \| Symbols: \| Rho GTPase activating protein with PAK-box/P21-Rho-binding domain |
| Eucgr.K03042.1 | 15,22 | 268,45 | 224,70 | 203,87 | 53,05 | AT5G02020.1 \| Symbols: SIS \| Encodes a protein involved in salt tolerance, names SIS (Salt Induced Serine rich). \| |
| Eucgr.F02646.1 | 1,99 | 0,00 | 0,02 | 0,06 | 0,44 | AT5G09360.1 \| Symbols: LAC14 \| laccase 14 \| chr5:2906426-2908658 REVERSE LENGTH=569 |
| Eucgr.F04109.1 | 10,13 | 734,90 | 714,88 | 986,43 | 876,56 | AT4G10250.1 \| Symbols: ATHSP22.0 \| HSP20-like chaperones superfamily protein \| |
| Eucgr.A00276.1 | 0,08 | 2,08 | 1,68 | 1,14 | 1,33 | No hits found |

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|---|---|---|---|---|---|---|
| Eucgr.B03207.1 | 3,55 | 0,14 | 0,15 | 0,28 | 0,55 | AT1G26760.1 \| Symbols: ATXR1, SDG35 \| SET domain protein 35 \| chr1:9248304-9249941 REVERSE LENGTH=545 |
| Eucgr.A01770.1 | 0,00 | 0,51 | 0,72 | 0,38 | 0,12 | AT2G20340.1 \| Symbols: \| Pyridoxal phosphate (PLP)-dependent transferases superfamily protein |
| Eucgr.I01338.1 | 36,24 | 0,77 | 1,26 | 1,86 | 11,64 | AT4G34760.1 \| Symbols: \| SAUR-like auxin-responsive protein family \| chr4:16582471-16582794 REVERSE LENGTH=107 |
| Eucgr.E00448.1 | 580,44 | 10,96 | 19,88 | 34,02 | 221,46 | AT4G12510.1 \| Symbols: \| Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein \| |
| Eucgr.B02529.2 | 50,46 | 4,34 | 8,64 | 14,31 | 25,22 | AT5G60720.1 \| Symbols: \| Protein of unknown function, DUF547 \| chr5:24418436-24422177 REVERSE LENGTH=691 |
| Eucgr.A01357.2 | 31,33 | 1,48 | 1,95 | 2,58 | 3,04 | AT5G44040.1 \| Symbols: \| unknown protein |
| Eucgr.E01049.1 | 0,02 | 0,74 | 0,25 | 0,17 | 0,21 | AT4G00870.1 \| Symbols: \| basic helix-loop-helix (bHLH) DNA-binding superfamily protein \| |
| Eucgr.I02135.1 | 9,97 | 0,49 | 0,58 | 0,90 | 3,12 | AT1G72430.1 \| Symbols: \| SAUR-like auxin-responsive protein family \| chr1:27265150-27265509 REVERSE LENGTH=119 |
| Eucgr.A01957.1 | 0,58 | 0,00 | 0,03 | 0,02 | 0,08 | AT2G42800.1 \| Symbols: AtRLP29, RLP29 \| receptor like protein 29 \| chr2:17808157-17809545 REVERSE LENGTH=462 |
| Eucgr.J01883.1 | 36,93 | 10,59 | 10,01 | 8,15 | 17,05 | AT1G07220.1 \| Symbols: \| Arabidopsis thaliana protein of unknown function (DUF821) \| |
| Eucgr.J00621.1 | 21,67 | 0,30 | 0,32 | 0,70 | 8,21 | AT3G43720.2 \| Symbols: \| Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein \| |
| Eucgr.B03715.1 | 16,06 | 0,00 | 0,00 | 0,00 | 1,00 | AT1G74670.1 \| Symbols: \| Gibberellin-regulated family protein \| chr1:28053378-28053893 FORWARD LENGTH=101 |
| Eucgr.F02337.4 | 7,27 | 113,34 | 113,21 | 82,20 | 37,16 | AT1G45249.1 \| Symbols: ABF2, AREB1, ATAREB1 \| abscisic acid responsive elements-binding factor 2 \| |
| Eucgr.J03131.1 | 7,34 | 0,58 | 0,62 | 0,67 | 2,26 | AT1G79720.1 \| Symbols: \| Eukaryotic aspartyl protease family protein \| chr1:29997259-29998951 REVERSE LENGTH=484 |
| Eucgr.H00807.1 | 0,85 | 0,00 | 0,00 | 0,00 | 0,20 | AT3G24750.1 \| Symbols: \| unknown protein |
| Eucgr.D00426.1 | 11,10 | 0,28 | 0,39 | 0,45 | 1,34 | AT5G45700.1 \| Symbols: \| Haloacid dehalogenase-like hydrolase (HAD) superfamily protein \| |
| Eucgr.C01078.1 | 16,16 | 0,25 | 0,57 | 0,70 | 1,61 | AT4G13370.1 \| Symbols: \| Plant protein of unknown function (DUF936) \| chr4:7777916-7780334 REVERSE LENGTH=673 |
| Eucgr.F04387.1 | 2,85 | 0,40 | 0,33 | 0,49 | 0,87 | AT4G08550.1 \| Symbols: \| electron carriers;protein disulfide oxidoreductases \| |
| Eucgr.B01477.1 | 21,18 | 0,60 | 1,36 | 2,06 | 7,10 | AT3G63430.1 \| Symbols: \| unknown protein |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.H02960.1 | 122,70 | 2,60 | 7,75 | 12,67 | 57,78 | AT1G04040.1 \| Symbols: \| HAD superfamily, subfamily IIIB acid phosphatase \| chr1:1042564-1043819 REVERSE LENGTH=271 |
| Eucgr.F04160.1 | 17,17 | 0,04 | 0,25 | 0,26 | 3,08 | AT5G09360.1 \| Symbols: LAC14 \| laccase 14 \| chr5:2906426-2908658 REVERSE LENGTH=569 |
| Eucgr.G02547.1 | 0,01 | 1,16 | 0,81 | 0,39 | 0,24 | AT1G27040.1 \| Symbols: \| Major facilitator superfamily protein \| chr1:9386893-9390018 REVERSE LENGTH=567 |
| Eucgr.J03029.1 | 14,52 | 0,75 | 1,24 | 1,51 | 2,28 | AT3G15550.1 \| Symbols: \| unknown protein |
| Eucgr.D00307.4 | 6,66 | 36,15 | 33,90 | 37,67 | 19,08 | No hits found |
| Eucgr.I01402.1 | 289,10 | 9,62 | 19,51 | 27,72 | 61,09 | AT4G34980.1 \| Symbols: SLP2 \| subtilisin-like serine protease 2 \| chr4:16656929-16659223 REVERSE LENGTH=764 |
| Eucgr.J02407.1 | 74,28 | 18,89 | 17,82 | 19,95 | 38,28 | AT3G51160.1 \| Symbols: MUR1, MUR_1, GMD2 \| NAD(P)-binding Rossmann-fold superfamily protein \| |
| Eucgr.E04312.2 | 19,54 | 0,52 | 1,00 | 1,71 | 5,69 | AT4G20050.2 \| Symbols: QRT3 \| Pectin lyase-like superfamily protein \| chr4:10849911-10852090 REVERSE LENGTH=481 |
| Eucgr.H02465.1 | 4,88 | 30,26 | 28,79 | 18,16 | 13,32 | AT5G14420.2 \| Symbols: RGLG2 \| RING domain ligase2 \| chr5:4648355-4650563 REVERSE LENGTH=468 |
| Eucgr.K01841.1 | 203,66 | 9,77 | 11,72 | 14,99 | 51,74 | AT3G53750.1 \| Symbols: ACT3 \| actin 3 \| chr3:19915924-19917371 FORWARD LENGTH=377 |

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|---|---|---|---|---|---|---|
| Eucgr.G03262.1 | 7,68 | 0,49 | 0,53 | 0,77 | 0,76 | AT3G51930.1 \| Symbols: \| Transducin/WD40 repeat-like superfamily protein \| |
| Eucgr.J00777.1 | 4,31 | 0,15 | 0,16 | 0,28 | 1,60 | AT4G12620.1 \| Symbols: ORC1B, ATORC1B, UNE13 \| origin of replication complex 1B \| |
| Eucgr.D01627.1 | 90,32 | 2,93 | 4,91 | 8,21 | 19,08 | AT1G30690.2 \| Symbols: \| Sec14p-like phosphatidylinositol transfer family protein \| |
| Eucgr.I01996.1 | 77,43 | 0,73 | 1,68 | 3,88 | 31,92 | AT5G15350.1 \| Symbols: ENODL17, AtENODL17 \| early nodulin-like protein 17 \| chr5:4985184-4986154 REVERSE LENGTH=172 |
| Eucgr.I00988.1 | 287,18 | 3,87 | 5,41 | 6,76 | 52,68 | AT5G66920.1 \| Symbols: sks17 \| SKU5 similar 17 \| chr5:26722963-26725370 FORWARD LENGTH=546 |
| Eucgr.J02867.3 | 36,68 | 1,42 | 2,88 | 3,69 | 14,74 | AT3G13750.1 \| Symbols: BGAL1 \| beta galactosidase 1 \| chr3:4511192-4515756 FORWARD LENGTH=847 |
| Eucgr.F03122.1 | 7,77 | 1,04 | 1,61 | 1,76 | 2,53 | AT3G13690.1 \| Symbols: \| Protein kinase protein with adenine nucleotide alpha hydrolases-like domain \| |
| Eucgr.E02312.1 | 2,66 | 9,70 | 11,64 | 8,56 | 8,93 | AT4G12020.3 \| Symbols: WRKY19, ATWRKY19, MAPKKK11, MEKK4 \| protein kinase family protein \| |
| Eucgr.K02088.1 | 16,98 | 1,60 | 2,05 | 2,25 | 6,28 | AT5G48460.1 \| Symbols: \| Actin binding Calponin homology (CH) domain-containing protein \| |
| Eucgr.K02296.1 | 0,77 | 0,05 | 0,01 | 0,05 | 0,08 | AT1G14670.1 \| Symbols: \| Endomembrane protein 70 protein family \| chr1:5037669-5040199 FORWARD LENGTH=592 |
| Eucgr.C02605.1 | 5,32 | 0,00 | 0,19 | 0,53 | 0,72 | AT2G25060.1 \| Symbols: ENODL14, AtENODL14 \| early nodulin-like protein 14 \| |
| Eucgr.G02332.1 | 18,19 | 5,87 | 7,18 | 7,76 | 10,69 | AT3G25860.1 \| Symbols: LTA2, PLE2 \| 2-oxoacid dehydrogenases acyltransferase family protein \| |
| Eucgr.G02612.1 | 12,45 | 34,63 | 31,80 | 25,39 | 26,65 | AT5G23390.1 \| Symbols: \| Plant protein of unknown function (DUF639) \| chr5:7870719-7874283 REVERSE LENGTH=730 |
| Eucgr.H03764.1 | 26,53 | 6,32 | 6,53 | 8,88 | 14,82 | AT2G45140.1 \| Symbols: PVA12 \| plant VAP homolog 12 \| chr2:18611029-18612971 FORWARD LENGTH=239 |
| Eucgr.H02855.1 | 1,76 | 0,19 | 0,09 | 0,11 | 0,41 | AT1G61820.1 \| Symbols: BGLU46 \| beta glucosidase 46 \| chr1:22835452-22838444 FORWARD LENGTH=516 |
| Eucgr.F02578.1 | 20,17 | 0,22 | 0,70 | 0,50 | 2,27 | AT3G15540.1 \| Symbols: IAA19, MSG2 \| indole-3-acetic acid inducible 19 \| chr3:5264100-5265378 FORWARD LENGTH=197 |
| Eucgr.H02676.1 | 29,26 | 1,00 | 2,73 | 3,81 | 14,98 | AT4G13950.1 \| Symbols: RALFL31 \| ralf-like 31 \| chr4:8058268-8058609 REVERSE LENGTH=113 |
| Eucgr.H00764.1 | 3,75 | 44,29 | 39,82 | 29,85 | 27,21 | AT4G31940.1 \| Symbols: CYP82C4 \| cytochrome P450, family 82, subfamily C, polypeptide 4 \| |
| Eucgr.A02888.1 | 7,36 | 0,04 | 0,08 | 0,08 | 1,55 | AT1G62660.1 \| Symbols: \| Glycosyl hydrolases family 32 protein \| chr1:23199949-23203515 FORWARD LENGTH=648 |
| Eucgr.J00695.1 | 1,65 | 0,02 | 0,04 | 0,15 | 0,17 | AT5G19410.1 \| Symbols: \| ABC-2 type transporter family protein \| chr5:6545237-6547111 REVERSE LENGTH=624 |
| Eucgr.H00729.1 | 3,66 | 84,10 | 81,01 | 106,79 | 20,81 | No hits found |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.H04545.1 | 58,12 | 477,26 | 465,70 | 508,69 | 234,96 | AT1G56220.2 \| Symbols: \| Dormancy/auxin associated family protein \| chr1:21043414-21044381 FORWARD LENGTH=112 |
| Eucgr.A01499.1 | 0,25 | 7,54 | 6,14 | 3,12 | 1,56 | AT2G36270.1 \| Symbols: ABI5, GIA1 \| Basic-leucine zipper (bZIP) transcription factor family protein \| |
| Eucgr.D01440.1 | 52,51 | 560,58 | 442,94 | 396,48 | 159,63 | AT2G35760.1 \| Symbols: \| Uncharacterised protein family (UPF0497) \| chr2:15032059-15033094 FORWARD LENGTH=201 |
| Eucgr.A00686.1 | 15,75 | 0,93 | 1,89 | 2,82 | 5,55 | AT2G38370.1 \| Symbols: \| Plant protein of unknown function (DUF827) \| chr2:16072184-16074168 REVERSE LENGTH=522 |
| Eucgr.F02993.1 | 70,48 | 0,65 | 1,11 | 0,99 | 9,15 | AT1G72160.1 \| Symbols: \| Sec14p-like phosphatidylinositol transfer family protein \| |
| Eucgr.K02228.1 | 14,81 | 37,22 | 37,61 | 37,69 | 28,11 | AT1G48840.1 \| Symbols: \| Plant protein of unknown function (DUF639) \| chr1:18061931-18064811 FORWARD LENGTH=691 |
| Eucgr.B00987.1 | 2,83 | 0,05 | 0,06 | 0,37 | 0,82 | AT1G18290.1 \| Symbols: \| unknown protein |
| Eucgr.C00762.2 | 6,50 | 1,87 | 0,87 | 1,00 | 2,01 | AT5G20850.1 \| Symbols: ATRAD51, RAD51 \| RAS associated with diabetes protein 51 \| |

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|---|---|---|---|---|---|---|
| Eucgr.C04062.1 | 12,75 | 58,82 | 52,04 | 37,39 | 30,18 | AT5G35180.2 \| Symbols: \| Protein of unknown function (DUF1336) \| chr5:13424538-13432699 FORWARD LENGTH=778 |
| Eucgr.B00670.1 | 5,73 | 0,41 | 0,42 | 0,44 | 1,14 | AT1G18550.1 \| Symbols: \| ATP binding microtubule motor family protein \| chr1:6381656-6384340 REVERSE LENGTH=725 |
| Eucgr.I00528.1 | 4,99 | 0,36 | 0,46 | 0,72 | 1,49 | AT4G39630.1 \| Symbols: \| unknown protein |
| Eucgr.D01730.1 | 12,19 | 0,11 | 0,82 | 1,16 | 3,11 | AT4G23820.1 \| Symbols: \| Pectin lyase-like superfamily protein \| chr4:12397217-12400050 REVERSE LENGTH=444 |
| Eucgr.I01145.1 | 35,01 | 260,99 | 270,42 | 233,44 | 201,24 | AT4G34000.2 \| Symbols: ABF3, DPBF5 \| abscisic acid responsive elements-binding factor 3 \| |
| Eucgr.B03636.1 | 10,43 | 0,82 | 0,87 | 1,65 | 4,69 | AT5G06700.1 \| Symbols: TBR \| Plant protein of unknown function (DUF828) \| chr5:2063638-2065810 FORWARD LENGTH=608 |
| Eucgr.G02632.1 | 30,54 | 89,77 | 92,26 | 73,60 | 63,06 | AT3G20770.1 \| Symbols: EIN3, AtEIN3 \| Ethylene insensitive 3 family protein \| chr3:7260702-7262588 REVERSE LENGTH=628 |
| Eucgr.D00364.1 | 0,31 | 0,00 | 0,00 | 0,02 | 0,06 | AT4G19090.1 \| Symbols: \| Protein of unknown function (DUF594) \| chr4:10449900-10452757 FORWARD LENGTH=751 |
| Eucgr.B02141.1 | 11,41 | 69,23 | 81,64 | 86,64 | 39,43 | AT1G08650.1 \| Symbols: PPCK1, ATPPCK1 \| phosphoenolpyruvate carboxylase kinase 1 |
| Eucgr.J00083.1 | 1,09 | 0,08 | 0,02 | 0,05 | 0,23 | AT2G38720.1 \| Symbols: MAP65-5 \| microtubule-associated protein 65-5 \| chr2:16188047-16192102 FORWARD LENGTH=587 |
| Eucgr.C03733.1 | 0,00 | 1,53 | 1,26 | 1,02 | 0,39 | AT1G68180.1 \| Symbols: \| RING/U-box superfamily protein \| chr1:25554816-25555562 FORWARD LENGTH=248 |
| Eucgr.B02161.1 | 0,00 | 3,55 | 3,16 | 1,33 | 0,47 | AT5G18450.1 \| Symbols: \| Integrase-type DNA-binding superfamily protein \| chr5:6116097-6117020 REVERSE LENGTH=307 |
| Eucgr.I01246.1 | 46,83 | 0,15 | 0,47 | 0,71 | 8,11 | AT5G48485.1 \| Symbols: DIR1 \| Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein \| |
| Eucgr.H01151.1 | 115,54 | 644,91 | 537,09 | 547,36 | 429,41 | AT2G47710.1 \| Symbols: \| Adenine nucleotide alpha hydrolases-like superfamily protein \| |
| Eucgr.E00270.1 | 30,29 | 3,21 | 3,29 | 4,03 | 8,00 | AT2G23910.1 \| Symbols: \| NAD(P)-binding Rossmann-fold superfamily protein \| |
| Eucgr.B00229.1 | 27,71 | 1,88 | 5,18 | 8,16 | 11,72 | AT4G01680.3 \| Symbols: MYB55 \| myb domain protein 55 \| chr4:716401-717415 REVERSE LENGTH=241 |
| Eucgr.F04115.1 | 0,02 | 43,08 | 21,83 | 5,80 | 0,25 | AT1G72100.1 \| Symbols: \| late embryogenesis abundant domain-containing protein / LEA domain-containing protein \| |
| Eucgr.K02271.1 | 38,30 | 5,26 | 10,63 | 13,16 | 17,95 | AT1G73590.1 \| Symbols: PIN1, ATPIN1 \| Auxin efflux carrier family protein \| chr1:27659772-27662876 FORWARD LENGTH=622 |
| Eucgr.L01670.1 | 1,15 | 6,44 | 8,37 | 8,55 | 3,22 | AT4G11800.1 \| Symbols: \| Calcineurin-like metallo-phosphoesterase superfamily protein \| |
| Eucgr.B03139.1 | 36,26 | 0,41 | 1,99 | 4,46 | 15,63 | AT1G69160.1 \| Symbols: \| unknown protein |
| Eucgr.J00914.1 | 2,96 | 0,20 | 0,21 | 0,24 | 0,78 | AT2G28260.1 \| Symbols: ATCNGC15, CNGC15 \| cyclic nucleotide-gated channel 15 \| |
| Eucgr.B02031.1 | 78,79 | 15,93 | 17,53 | 19,21 | 33,16 | AT1G54690.1 \| Symbols: HTA3, H2AXB, G-H2AX, GAMMA-H2AX \| gamma histone variant H2AX \| |
| Eucgr.K00155.1 | 14,86 | 0,17 | 0,33 | 0,92 | 2,69 | AT5G62360.1 \| Symbols: \| Plant invertase/pectin methylesterase inhibitor superfamily protein \| |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.J02110.2 | 5,44 | 122,97 | 79,25 | 49,75 | 19,29 | AT1G07870.2 \| Symbols: \| Protein kinase superfamily protein \| chr1:2428942-2431843 REVERSE LENGTH=538 |
| Eucgr.F00384.1 | 3,20 | 31,55 | 40,06 | 36,29 | 18,56 | AT1G72200.1 \| Symbols: \| RING/U-box superfamily protein \| chr1:27169935-27171149 REVERSE LENGTH=404 |
| Eucgr.C00694.1 | 1,43 | 0,00 | 0,00 | 0,02 | 0,07 | AT5G51160.1 \| Symbols: \| Ankyrin repeat family protein \| chr5:20792280-20793681 FORWARD LENGTH=442 |
| Eucgr.C03431.1 | 2,27 | 18,52 | 21,95 | 26,89 | 18,38 | AT2G26150.1 \| Symbols: ATHSFA2, HSFA2 \| heat shock transcription factor A2 \| |
| Eucgr.K02165.1 | 35,62 | 0,61 | 2,12 | 3,43 | 15,72 | AT5G48800.1 \| Symbols: \| Phototropic-responsive NPH3 family protein \| chr5:19786881-19789003 FORWARD LENGTH=614 |
| Eucgr.F00651.1 | 5,56 | 35,29 | 26,29 | 19,95 | 17,25 | AT4G26780.1 \| Symbols: AR192 \| Co-chaperone GrpE family protein \| chr4:13485066-13486560 REVERSE LENGTH=327 |

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|---|---|---|---|---|---|---|
| Eucgr.F00721.2 | 10,47 | 2,01 | 2,11 | 3,28 | 5,55 | AT3G20420.1 \| Symbols: RTL2, ATRTL2 \| RNAse THREE-like protein 2 \| chr3:7119371-7120895 REVERSE LENGTH=391 |
| Eucgr.D02003.1 | 1,82 | 8,13 | 12,62 | 9,90 | 9,12 | AT4G13550.1 \| Symbols: \| triglyceride lipases;triglyceride lipases \| chr4:7871251-7876160 REVERSE LENGTH=715 |
| Eucgr.D01813.1 | 16,66 | 73,49 | 65,63 | 69,23 | 45,16 | AT5G41560.1 \| Symbols: \| unknown protein |
| Eucgr.J00194.1 | 0,05 | 46,26 | 27,67 | 16,03 | 0,76 | AT2G40170.1 \| Symbols: ATEM6, GEA6, EM6 \| Stress induced protein \| chr2:16779792-16780167 REVERSE LENGTH=92 |
| Eucgr.B00829.2 | 40,14 | 9,60 | 10,61 | 14,94 | 20,66 | AT1G73760.1 \| Symbols: \| RING/U-box superfamily protein \| chr1:27739366-27741161 REVERSE LENGTH=367 |
| Eucgr.A02029.1 | 7,37 | 1,21 | 0,84 | 0,95 | 1,45 | AT1G06660.1 \| Symbols: \| unknown protein |
| Eucgr.A01283.1 | 11,63 | 41,57 | 33,78 | 36,12 | 24,83 | AT2G37678.1 \| Symbols: FHY1, PAT3, FRY1 \| far-red elongated hypocotyl 1 \| chr2:15801689-15802696 REVERSE LENGTH=202 |
| Eucgr.F02300.1 | 15,32 | 0,62 | 0,79 | 1,36 | 1,68 | AT3G16150.1 \| Symbols: \| N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein \| |
| Eucgr.F03035.1 | 3,90 | 32,06 | 28,94 | 39,63 | 12,29 | AT1G52240.2 \| Symbols: ATROPGEF11, ROPGEF11, PIRF1 \| RHO guanyl-nucleotide exchange factor 11 \| |
| Eucgr.B03399.1 | 19,79 | 76,66 | 68,25 | 64,66 | 42,11 | AT1G27150.1 \| Symbols: \| Tetratricopeptide repeat (TPR)-like superfamily protein |
| Eucgr.C01731.1 | 18,89 | 101,85 | 127,26 | 132,48 | 46,83 | No hits found |
| Eucgr.I01495.1 | 7,74 | 1562,71 | 1211,97 | 880,37 | 92,12 | AT3G12500.1 \| Symbols: ATHCHIB, PR3, PR-3, CHI-B, B-CHI, HCHIB \| basic chitinase |
| Eucgr.B02467.1 | 5,95 | 19,77 | 20,56 | 15,35 | 12,74 | AT1G07910.2 \| Symbols: ATRNL, RNL, AtRLG1 \| RNAligase \| chr1:2446712-2454386 FORWARD LENGTH=1104 |
| Eucgr.F01003.1 | 2,30 | 43,54 | 47,40 | 43,89 | 6,02 | AT5G48150.2 \| Symbols: PAT1 \| GRAS family transcription factor \| chr5:19522497-19524053 REVERSE LENGTH=490 |
| Eucgr.D02320.1 | 24,92 | 79,39 | 63,57 | 56,94 | 53,81 | AT4G01280.2 \| Symbols: \| Homeodomain-like superfamily protein \| chr4:535288-536854 FORWARD LENGTH=303 |
| Eucgr.K03370.1 | 13,37 | 112,45 | 118,15 | 116,79 | 43,19 | AT3G63210.1 \| Symbols: MARD1 \| Protein of unknown function (DUF581) \| chr3:23354019-23354906 REVERSE LENGTH=263 |
| Eucgr.F02465.1 | 0,35 | 0,01 | 0,01 | 0,02 | 0,09 | AT3G46530.1 \| Symbols: RPP13 \| NB-ARC domain-containing disease resistance protein \| |
| Eucgr.G03232.1 | 16,14 | 0,72 | 1,57 | 2,15 | 5,91 | AT5G12330.1 \| Symbols: LRP1 \| Lateral root primordium (LRP) protein-related \| chr5:3987677-3989074 REVERSE LENGTH=320 |
| Eucgr.J02591.1 | 15,10 | 0,88 | 1,27 | 1,99 | 7,78 | AT1G53820.1 \| Symbols: \| RING/U-box superfamily protein \| chr1:20091491-20092423 FORWARD LENGTH=310 |
| Eucgr.F03575.1 | 62,99 | 0,76 | 1,47 | 2,24 | 19,19 | AT5G24318.1 \| Symbols: \| O-Glycosyl hydrolases family 17 protein \| chr5:8282285-8283956 REVERSE LENGTH=458 |
| Eucgr.F02000.1 | 6,72 | 0,16 | 0,26 | 0,40 | 0,90 | AT5G56120.1 \| Symbols: \| unknown protein; |
| Eucgr.B03665.1 | 41,27 | 4,87 | 5,22 | 4,68 | 13,19 | AT4G40030.2 \| Symbols: \| Histone superfamily protein \| chr4:18555840-18556827 REVERSE LENGTH=164 |
| Eucgr.C00665.1 | 5,03 | 53,29 | 66,19 | 45,36 | 24,04 | AT2G26170.1 \| Symbols: CYP711A1, MAX1 \| cytochrome P450, family 711, subfamily A, polypeptide 1 \| |
| Eucgr.K02533.1 | 8,40 | 0,86 | 0,73 | 0,93 | 2,34 | AT5G60980.1 \| Symbols: \| Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain \| |
| Eucgr.F01854.1 | 4,16 | 598,03 | 295,93 | 191,61 | 25,01 | AT3G51030.1 \| Symbols: ATTRX1, ATTRX H1, TRX1 \| thioredoxin H-type 1 \| chr3:18951123-18951955 REVERSE LENGTH=114 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.H01055.1 | 168,37 | 2,29 | 5,79 | 8,99 | 36,59 | AT1G02640.1 \| Symbols: BXL2, ATBXL2 \| beta-xylosidase 2 \| chr1:564293-567580 FORWARD LENGTH=768 |
| Eucgr.C00146.1 | 5,51 | 0,00 | 0,05 | 0,09 | 1,25 | AT1G73300.1 \| Symbols: scpl2 \| serine carboxypeptidase-like 2 \| chr1:27559673-27562048 REVERSE LENGTH=441 |
| Eucgr.I01275.1 | 6,36 | 0,00 | 0,03 | 0,05 | 0,51 | AT1G29420.1 \| Symbols: \| SAUR-like auxin-responsive protein family \| chr1:10301483-10301908 REVERSE LENGTH=141 |
| Eucgr.L02979.1 | 3,66 | 0,32 | 0,27 | 0,58 | 1,20 | AT3G20290.2 \| Symbols: ATEHD1, EHD1 \| EPS15 homology domain 1 \| chr3:7075057-7078655 REVERSE LENGTH=545 |

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|---|---|---|---|---|---|---|
| Eucgr.D01672.1 | 4,58 | 0,48 | 0,70 | 0,94 | 1,71 | AT4G10630.1 \| Symbols: \| Glutaredoxin family protein \| chr4:6566625-6567629 REVERSE LENGTH=334 |
| Eucgr.I01413.2 | 2,11 | 0,20 | 0,39 | 0,30 | 0,80 | AT2G20980.1 \| Symbols: MCM10 \| minichromosome maintenance 10 \| chr2:9011654-9013856 REVERSE LENGTH=396 |
| Eucgr.A02158.1 | 3,13 | 8,15 | 9,16 | 8,09 | 7,08 | AT3G03620.1 \| Symbols: \| MATE efflux family protein \| chr3:873904-876252 REVERSE LENGTH=500 |
| Eucgr.G02325.1 | 2,51 | 28,24 | 20,16 | 21,06 | 9,55 | AT1G68540.1 \| Symbols: \| NAD(P)-binding Rossmann-fold superfamily protein \| |
| Eucgr.I01172.2 | 11,08 | 34,85 | 26,74 | 24,74 | 22,72 | AT4G33940.1 \| Symbols: \| RING/U-box superfamily protein \| chr4:16266085-16267612 FORWARD LENGTH=262 |
| Eucgr.D02454.1 | 0,05 | 3,10 | 2,73 | 1,32 | 0,48 | AT2G45400.1 \| Symbols: BEN1 \| NAD(P)-binding Rossmann-fold superfamily protein \| |
| Eucgr.D02266.1 | 0,01 | 0,63 | 0,55 | 0,39 | 0,22 | AT3G61220.1 \| Symbols: \| NAD(P)-binding Rossmann-fold superfamily protein \| |
| Eucgr.C00147.1 | 10,43 | 0,02 | 0,09 | 0,16 | 2,72 | AT5G09640.1 \| Symbols: SNG2, SCPL19 \| serine carboxypeptidase-like 19 \| chr5:2988373-2990966 FORWARD LENGTH=465 |
| Eucgr.H00469.1 | 10,72 | 49,66 | 51,07 | 56,64 | 35,72 | AT1G60710.1 \| Symbols: ATB2 \| NAD(P)-linked oxidoreductase superfamily protein \| |
| Eucgr.B00095.1 | 7,72 | 26,19 | 28,29 | 26,11 | 15,98 | AT5G63520.1 \| Symbols: \| unknown protein |
| Eucgr.H00093.1 | 30,03 | 0,37 | 1,49 | 1,77 | 11,45 | AT4G13710.2 \| Symbols: \| Pectin lyase-like superfamily protein \| chr4:7962550-7966012 FORWARD LENGTH=451 |
| Eucgr.I00720.1 | 13,06 | 1,59 | 2,52 | 4,26 | 6,80 | AT4G24230.5 \| Symbols: ACBP3 \| acyl-CoA-binding domain 3 \| chr4:12567240-12568754 REVERSE LENGTH=362 |
| Eucgr.B02195.1 | 28,06 | 0,62 | 1,86 | 3,32 | 12,66 | AT5G26670.1 \| Symbols: \| Pectinacetylesterase family protein \| chr5:9318456-9320816 FORWARD LENGTH=416 |
| Eucgr.A01180.1 | 21,59 | 1072,43 | 901,04 | 862,26 | 494,83 | AT3G09640.2 \| Symbols: APX2, APX1B \| ascorbate peroxidase 2 \| chr3:2956301-2958163 FORWARD LENGTH=251 |
| Eucgr.F00208.1 | 17,00 | 0,40 | 1,14 | 1,46 | 9,35 | AT5G67090.1 \| Symbols: \| Subtilisin-like serine endopeptidase family protein \| |
| Eucgr.A02334.1 | 2,15 | 0,13 | 0,14 | 0,17 | 0,46 | AT3G10310.1 \| Symbols: \| P-loop nucleoside triphosphate hydrolases superfamily protein |
| Eucgr.B03598.1 | 14,71 | 2,15 | 2,68 | 3,16 | 7,56 | AT5G36110.1 \| Symbols: CYP716A1 \| cytochrome P450, family 716, subfamily A, polypeptide 1 \| |
| Eucgr.H01197.1 | 19,97 | 0,40 | 2,28 | 4,02 | 7,96 | AT1G03010.1 \| Symbols: \| Phototropic-responsive NPH3 family protein \| chr1:693480-696188 FORWARD LENGTH=634 |
| Eucgr.J02961.1 | 0,07 | 17,02 | 7,45 | 5,89 | 1,20 | No hits found |
| Eucgr.B00628.1 | 7,37 | 0,67 | 1,23 | 2,00 | 3,23 | AT3G02210.1 \| Symbols: COBL1 \| COBRA-like protein 1 precursor \| chr3:409352-411478 REVERSE LENGTH=452 |
| Eucgr.K02109.1 | 32,67 | 0,56 | 1,51 | 2,48 | 14,92 | AT3G07340.1 \| Symbols: \| basic helix-loop-helix (bHLH) DNA-binding superfamily protein \| |
| Eucgr.H01519.1 | 1,16 | 227,04 | 274,22 | 267,45 | 16,07 | AT3G63060.1 \| Symbols: EDL3 \| EID1-like 3 \| chr3:23300638-23301456 REVERSE LENGTH=272 |
| Eucgr.A02002.1 | 0,20 | 1,24 | 2,13 | 1,38 | 0,79 | AT1G06490.1 \| Symbols: ATGSL07, gsl07, atgsl7, GSL7 \| glucan synthase-like 7 \| |
| Eucgr.H01011.1 | 11,23 | 30,28 | 36,66 | 29,95 | 25,22 | AT4G02020.1 \| Symbols: EZA1, SWN, SDG10 \| SET domain-containing protein \| chr4:886693-891743 FORWARD LENGTH=856 |
| Eucgr.I02738.1 | 157,61 | 5,61 | 7,44 | 9,62 | 60,30 | AT2G46890.1 \| Symbols: \| Protein of unknown function (DUF1295) \| chr2:19266879-19268134 REVERSE LENGTH=322 |
| Eucgr.K03279.1 | 36,62 | 2,45 | 5,72 | 8,68 | 15,81 | AT5G51560.1 \| Symbols: \| Leucine-rich repeat protein kinase family protein \| |
| Eucgr.A01044.1 | 36,16 | 150,94 | 144,45 | 134,06 | 98,25 | AT3G07770.1 \| Symbols: Hsp89.1, AtHsp90.6, AtHsp90-6 \| HEAT SHOCK PROTEIN 89.1 \| |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.J02057.1 | 18,53 | 0,33 | 0,61 | 1,56 | 7,99 | AT5G02440.1 \| Symbols: \| unknown protein |
| Eucgr.I01789.4 | 3,31 | 41,00 | 42,66 | 37,20 | 18,16 | AT3G01510.1 \| Symbols: LSF1 \| like SEX4 1 \| chr3:198855-201682 REVERSE LENGTH=591 |

| | | | | | | |
|---|---|---|---|---|---|---|
| Eucgr.G02817.1 | 14,61 | 0,63 | 0,65 | 0,69 | 5,55 | AT2G35770.1 \| Symbols: scpl28 \| serine carboxypeptidase-like 28 \| chr2:15034179-15036497 REVERSE LENGTH=462 |
| Eucgr.J03191.1 | 3,93 | 15,89 | 16,74 | 13,92 | 10,60 | AT1G78930.1 \| Symbols: \| Mitochondrial transcription termination factor family protein \| |
| Eucgr.F03345.1 | 22,16 | 1,38 | 1,91 | 2,12 | 9,18 | AT5G54380.1 \| Symbols: THE1 \| protein kinase family protein \| chr5:22077313-22079880 REVERSE LENGTH=855 |
| Eucgr.D00636.2 | 15,82 | 76,56 | 66,45 | 71,30 | 29,85 | AT3G47160.2 \| Symbols: \| RING/U-box superfamily protein \| chr3:17360238-17361879 REVERSE LENGTH=257 |
| Eucgr.B02770.1 | 13,08 | 2,54 | 3,55 | 4,43 | 6,83 | AT2G38040.2 \| Symbols: CAC3 \| acetyl Co-enzyme a carboxylase carboxyltransferase alpha subunit \| |
| Eucgr.E00105.1 | 77,46 | 1,55 | 4,11 | 6,21 | 19,93 | AT3G61490.3 \| Symbols: \| Pectin lyase-like superfamily protein \| chr3:22758439-22760137 FORWARD LENGTH=476 |
| Eucgr.F02730.1 | 5,89 | 54,46 | 61,88 | 65,31 | 29,37 | AT1G21360.1 \| Symbols: GLTP2 \| glycolipid transfer protein 2 \| chr1:7481365-7483237 FORWARD LENGTH=223 |
| Eucgr.B03070.1 | 2,83 | 0,16 | 0,05 | 0,09 | 0,33 | AT1G68740.1 \| Symbols: PHO1;H1 \| EXS (ERD1/XPR1/SYG1) family protein \| chr1:25812735-25816574 REVERSE LENGTH=784 |
| Eucgr.F00495.1 | 7,54 | 83,26 | 77,38 | 55,20 | 28,40 | No hits found |
| Eucgr.D01034.1 | 14,55 | 0,54 | 1,23 | 1,91 | 5,33 | AT3G54950.1 \| Symbols: PLP7, PLA IIIA \| patatin-like protein 6 \| chr3:20359076-20360774 REVERSE LENGTH=488 |
| Eucgr.A02438.1 | 4,71 | 0,34 | 0,59 | 0,95 | 1,89 | No hits found |
| Eucgr.A02689.1 | 1,92 | 0,07 | 0,05 | 0,06 | 0,69 | AT3G16520.1 \| Symbols: UGT88A1 \| UDP-glucosyl transferase 88A1 \| chr3:5618807-5620833 REVERSE LENGTH=451 |
| Eucgr.K03540.1 | 13,07 | 42,64 | 35,67 | 35,25 | 31,50 | AT4G02090.1 \| Symbols: \| unknown protein |
| Eucgr.F01784.1 | 3,28 | 10,77 | 10,55 | 9,53 | 8,03 | No hits found |
| Eucgr.K02134.1 | 31,03 | 0,45 | 1,05 | 2,38 | 10,49 | AT3G25130.1 \| Symbols: \| unknown protein |
| Eucgr.J00323.1 | 4,96 | 0,58 | 0,61 | 1,59 | 1,54 | AT5G23440.1 \| Symbols: FTRA1 \| ferredoxin/thioredoxin reductase subunit A (variable subunit) 1 \| |
| Eucgr.K01300.1 | 35,05 | 0,44 | 1,52 | 2,44 | 13,01 | AT3G08600.1 \| Symbols: \| Protein of unknown function (DUF1191) \| chr3:2612646-2613596 FORWARD LENGTH=316 |
| Eucgr.D02381.1 | 102,26 | 8,94 | 12,83 | 11,83 | 27,84 | AT1G01300.1 \| Symbols: \| Eukaryotic aspartyl protease family protein \| chr1:117065-118522 FORWARD LENGTH=485 |
| Eucgr.C00368.1 | 2,43 | 8,19 | 9,12 | 9,70 | 6,55 | AT5G58050.1 \| Symbols: SVL4 \| SHV3-like 4 \| chr5:23494498-23497386 REVERSE LENGTH=753 |
| Eucgr.B01111.1 | 58,85 | 12,93 | 15,61 | 17,59 | 32,48 | AT4G14220.1 \| Symbols: RHF1A \| RING-H2 group F1A \| chr4:8196012-8198240 FORWARD LENGTH=371 |
| Eucgr.G02550.2 | 20,18 | 102,70 | 103,74 | 103,49 | 56,62 | AT1G07040.1 \| Symbols: \| unknown protein |
| Eucgr.D00296.1 | 15,53 | 3,16 | 3,29 | 4,46 | 8,41 | AT2G34560.1 \| Symbols: \| P-loop containing nucleoside triphosphate hydrolases superfamily protein \| |
| Eucgr.H03285.1 | 53,31 | 489,01 | 664,72 | 513,12 | 242,38 | AT1G15690.1 \| Symbols: AVP1, ATAVP3, AVP-3, AtVHP1;1 \| Inorganic H pyrophosphatase family protein \| |
| Eucgr.B03561.1 | 28,70 | 3,74 | 3,91 | 4,74 | 11,45 | AT1G57820.1 \| Symbols: VIM1, ORTH2 \| Zinc finger (C3HC4-type RING finger) family protein \| |
| Eucgr.F01527.1 | 0,78 | 23,96 | 25,97 | 17,49 | 5,52 | AT1G47530.1 \| Symbols: \| MATE efflux family protein \| chr1:17451724-17454110 FORWARD LENGTH=484 |
| Eucgr.H04950.1 | 1,81 | 0,31 | 0,22 | 0,86 | 0,56 | AT1G77120.1 \| Symbols: ADH1, ADH, ATADH, ATADH1 \| alcohol dehydrogenase 1 |
| Eucgr.I01337.1 | 21,93 | 1,56 | 2,71 | 5,84 | 10,35 | AT4G34750.2 \| Symbols: \| SAUR-like auxin-responsive protein family \| chr4:16577566-16578018 FORWARD LENGTH=150 |
| Eucgr.F03278.2 | 36,02 | 5,60 | 6,03 | 8,41 | 16,58 | AT1G16920.1 \| Symbols: RAB11, ATRABA1B, RABA1b \| RAB GTPase homolog A1B \| |
| Eucgr.K01646.1 | 25,16 | 4,47 | 5,36 | 7,15 | 14,82 | AT3G56750.1 \| Symbols: \| unknown protein |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |

| | | | | | | |
|---|---|---|---|---|---|---|
| Eucgr.H03767.1 | 39,26 | 225,21 | 235,10 | 217,13 | 115,08 | AT5G18670.1 \| Symbols: BMY3, BAM9 \| beta-amylase 3 \| chr5:6226138-6227999 FORWARD LENGTH=536 |
| Eucgr.D01613.2 | 79,21 | 16,99 | 16,29 | 19,60 | 29,09 | AT2G34770.1 \| Symbols: FAH1, ATFAH1 \| fatty acid hydroxylase 1 \| chr2:14666776-14668061 FORWARD LENGTH=237 |
| Eucgr.B02615.1 | 7,49 | 0,32 | 0,25 | 0,36 | 2,19 | AT1G69770.1 \| Symbols: CMT3 \| chromomethylase 3 \| chr1:26248496-26253519 REVERSE LENGTH=839 |
| Eucgr.A01900.1 | 19,76 | 1,28 | 1,41 | 2,26 | 7,55 | AT2G42570.1 \| Symbols: TBL39 \| TRICHOME BIREFRINGENCE-LIKE 39 \| chr2:17717498-17719921 REVERSE LENGTH=367 |
| Eucgr.F04351.1 | 23,62 | 78,31 | 73,21 | 72,29 | 59,16 | AT1G21780.2 \| Symbols: \| BTB/POZ domain-containing protein \| chr1:7652476-7653866 FORWARD LENGTH=326 |
| Eucgr.H01465.1 | 0,00 | 2,60 | 2,10 | 0,55 | 0,14 | AT3G22490.1 \| Symbols: \| Seed maturation protein \| chr3:7969785-7970738 REVERSE LENGTH=262 |
| Eucgr.K01373.1 | 0,00 | 2,23 | 1,13 | 1,03 | 0,09 | No hits found |
| Eucgr.G01861.1 | 0,00 | 9,28 | 6,63 | 2,41 | 0,22 | AT2G23240.1 \| Symbols: \| Plant EC metallothionein-like protein, family 15 \| chr2:9895995-9896325 REVERSE LENGTH=85 |
| Eucgr.G00824.1 | 0,00 | 0,81 | 0,61 | 0,30 | 0,10 | AT5G45910.1 \| Symbols: \| GDSL-like Lipase/Acylhydrolase superfamily protein \| chr5:18620420-18622264 REVERSE LENGTH=372 |
| Eucgr.H04654.1 | 69,13 | 4,69 | 10,72 | 14,51 | 33,14 | AT1G67510.1 \| Symbols: \| Leucine-rich repeat protein kinase family protein \| chr1:25297477-25300184 REVERSE LENGTH=719 |
| Eucgr.G00172.1 | 3,61 | 10,52 | 12,37 | 12,56 | 10,02 | No hits found |
| Eucgr.H03574.1 | 7,17 | 0,47 | 0,87 | 1,20 | 3,68 | AT5G19160.1 \| Symbols: TBL11 \| TRICHOME BIREFRINGENCE-LIKE 11 \| chr5:6430725-6432456 FORWARD LENGTH=464 |
| Eucgr.A02652.1 | 3,53 | 0,24 | 0,86 | 1,17 | 1,59 | AT4G21580.1 \| Symbols: \| oxidoreductase, zinc-binding dehydrogenase family protein \| |
| Eucgr.C00351.1 | 28,09 | 1,62 | 3,25 | 4,69 | 11,75 | AT2G24230.1 \| Symbols: \| Leucine-rich repeat protein kinase family protein \| chr2:10301979-10304540 REVERSE LENGTH=853 |
| Eucgr.A00199.1 | 7,15 | 0,43 | 0,52 | 0,45 | 1,24 | AT3G58650.1 \| Symbols: \| unknown protein |
| Eucgr.I01272.1 | 19,58 | 2,97 | 3,65 | 3,72 | 7,31 | AT2G16250.1 \| Symbols: \| Leucine-rich repeat protein kinase family protein \| chr2:7039682-7042933 REVERSE LENGTH=915 |
| Eucgr.I02050.1 | 2,16 | 0,00 | 0,04 | 0,24 | 0,70 | No hits found |
| Eucgr.I02034.1 | 1,63 | 0,08 | 0,03 | 0,08 | 0,32 | AT3G02120.1 \| Symbols: \| hydroxyproline-rich glycoprotein family protein \| chr3:377122-377577 FORWARD LENGTH=126 |
| Eucgr.E03946.1 | 0,56 | 0,05 | 0,01 | 0,07 | 0,18 | AT1G21270.1 \| Symbols: WAK2 \| wall-associated kinase 2 \| chr1:7444997-7447345 FORWARD LENGTH=732 |
| Eucgr.G03101.1 | 0,10 | 0,95 | 1,31 | 1,00 | 0,41 | AT5G01660.1 \| Symbols: \| unknown protein |
| Eucgr.B02465.1 | 6,80 | 0,14 | 0,34 | 0,26 | 1,95 | AT1G07900.1 \| Symbols: LBD1 \| LOB domain-containing protein 1 \| chr1:2442624-2443631 FORWARD LENGTH=190 |
| Eucgr.C00688.1 | 1,89 | 0,00 | 0,00 | 0,06 | 0,12 | AT5G51160.1 \| Symbols: \| Ankyrin repeat family protein \| chr5:20792280-20793681 FORWARD LENGTH=442 |
| Eucgr.J01649.1 | 6,12 | 0,36 | 0,25 | 0,33 | 1,45 | AT5G37010.1 \| Symbols: \| unknown protein |
| Eucgr.B00858.1 | 2,37 | 0,22 | 0,14 | 0,13 | 0,78 | AT1G18090.1 \| Symbols: \| 5'-3' exonuclease family protein \| chr1:6224539-6227715 FORWARD LENGTH=577 |
| Eucgr.C00602.1 | 2,41 | 0,15 | 0,26 | 0,57 | 0,90 | AT5G25830.1 \| Symbols: GATA12 \| GATA transcription factor 12 \| chr5:9004398-9005502 REVERSE LENGTH=331 |
| Eucgr.H04126.1 | 0,21 | 116,86 | 67,26 | 27,17 | 1,14 | No hits found |
| Eucgr.F01532.1 | 3,53 | 0,55 | 0,25 | 0,49 | 0,60 | AT5G42610.1 \| Symbols: \| Protein of unknown function (DUF607) \| chr5:17062507-17063934 FORWARD LENGTH=293 |
| Eucgr.F03192.1 | 8,01 | 0,58 | 0,96 | 1,05 | 1,83 | AT1G72250.2 \| Symbols: \| Di-glucose binding protein with Kinesin motor domain \| |
| Eucgr.E03164.1 | 1,54 | 0,00 | 0,00 | 0,00 | 0,20 | AT2G34060.1 \| Symbols: \| Peroxidase superfamily protein \| chr2:14384914-14386530 FORWARD LENGTH=346 |
| Eucgr.D02141.1 | 49,41 | 4,95 | 8,75 | 12,20 | 28,73 | AT2G35190.1 \| Symbols: NPSN11, ATNPSN11, NSPN11 \| novel plant snare 11 \| |
| GENE ID | FPKM | | | | | Annotation |

| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
|---|---|---|---|---|---|---|
| Eucgr.H03412.1 | 2,02 | 25,37 | 23,40 | 18,00 | 8,94 | AT3G22830.1 \| Symbols: AT-HSFA6B, HSFA6B \| heat shock transcription factor A6B \| |
| Eucgr.E02751.1 | 9,90 | 1,01 | 1,14 | 1,18 | 3,04 | AT3G19390.1 \| Symbols: \| Granulin repeat cysteine protease family protein \| chr3:6723024-6724768 FORWARD LENGTH=452 |
| Eucgr.E00653.1 | 20,86 | 998,82 | 820,18 | 566,16 | 475,38 | AT5G52640.1 \| Symbols: HSP81-1, ATHS83, HSP81.1, HSP83, ATHSP90.1, AtHsp90-1, HSP90.1 \| heat shock protein 90.1 \| |
| Eucgr.K02631.1 | 3,76 | 0,12 | 0,20 | 0,24 | 1,03 | AT3G42660.1 \| Symbols: \| transducin family protein / WD-40 repeat family protein \| |
| Eucgr.H01935.1 | 0,21 | 16,09 | 12,48 | 11,36 | 1,34 | No hits found |
| Eucgr.H00738.1 | 19,53 | 1,56 | 3,65 | 5,56 | 7,38 | AT3G25290.2 \| Symbols: \| Auxin-responsive family protein \| chr3:9208955-9210353 FORWARD LENGTH=393 |
| Eucgr.C03734.2 | 21,41 | 114,73 | 107,58 | 113,74 | 67,99 | AT3G46500.1 \| Symbols: \| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein \| |
| Eucgr.A00685.1 | 4,91 | 0,77 | 0,36 | 1,25 | 1,12 | AT2G40475.1 \| Symbols: \| unknown protein; |
| Eucgr.G02914.1 | 2,55 | 0,04 | 0,04 | 0,03 | 0,28 | AT2G39510.1 \| Symbols: \| nodulin MtN21 /EamA-like transporter family protein \| |
| Eucgr.I02446.1 | 25,27 | 76,29 | 54,91 | 49,57 | 50,51 | AT5G13970.1 \| Symbols: \| unknown protein; |
| Eucgr.A01510.1 | 6,01 | 0,07 | 0,55 | 1,11 | 2,22 | AT3G52780.1 \| Symbols: ATPAP20, PAP20 \| Purple acid phosphatases superfamily protein \| |
| Eucgr.J03116.1 | 35,53 | 243,22 | 220,93 | 205,31 | 109,05 | AT5G25110.1 \| Symbols: CIPK25, SnRK3.25 \| CBL-interacting protein kinase 25 \| chr5:8657740-8659206 REVERSE LENGTH=488 |
| Eucgr.G01719.1 | 6,80 | 0,33 | 0,44 | 0,55 | 2,35 | AT2G21340.1 \| Symbols: \| MATE efflux family protein \| chr2:9132629-9136236 FORWARD LENGTH=559 |
| Eucgr.K01326.1 | 4,13 | 0,23 | 0,50 | 0,59 | 1,79 | AT1G47056.1 \| Symbols: VFB1 \| VIER F-box proteine 1 \| chr1:17276103-17277659 REVERSE LENGTH=518 |
| Eucgr.A02419.1 | 4,27 | 0,23 | 0,20 | 0,54 | 1,02 | AT2G42260.1 \| Symbols: UVI4, PYM \| uv-b-insensitive 4 \| chr2:17602240-17603283 REVERSE LENGTH=259 |
| Eucgr.F02608.1 | 40,99 | 0,88 | 1,99 | 3,75 | 19,27 | AT1G71970.1 \| Symbols: \| unknown protein |
| Eucgr.C03407.2 | 36,43 | 450,65 | 402,82 | 402,69 | 157,74 | AT1G17550.1 \| Symbols: HAB2 \| homology to ABI2 \| chr1:6034917-6036939 FORWARD LENGTH=511 |
| Eucgr.F03662.1 | 1,19 | 0,02 | 0,02 | 0,06 | 0,30 | AT5G59810.1 \| Symbols: ATSBT5.4, SBT5.4 \| Subtilase family protein \| chr5:24096895-24100387 REVERSE LENGTH=778 |
| Eucgr.G02658.1 | 20,17 | 0,47 | 1,02 | 1,26 | 3,58 | AT3G03130.1 \| Symbols: \| unknown protein |
| Eucgr.B02372.1 | 7,27 | 32,99 | 36,44 | 42,25 | 23,11 | AT3G46540.1 \| Symbols: \| ENTH/VHS family protein \| chr3:17134204-17135411 REVERSE LENGTH=307 |
| Eucgr.A01404.1 | 0,64 | 9,23 | 6,74 | 5,80 | 2,56 | AT5G53730.1 \| Symbols: \| Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family \| |
| Eucgr.A01247.1 | 1,43 | 0,14 | 0,08 | 0,07 | 0,51 | AT5G02540.1 \| Symbols: \| NAD(P)-binding Rossmann-fold superfamily protein \| chr5:568609-570720 FORWARD LENGTH=331 |
| Eucgr.K00764.1 | 0,95 | 7,77 | 4,52 | 3,85 | 3,04 | AT2G22475.1 \| Symbols: GEM \| GRAM domain family protein \| chr2:9541523-9544778 FORWARD LENGTH=299 |
| Eucgr.B02355.1 | 323,58 | 2,45 | 9,49 | 18,01 | 119,17 | AT2G39700.1 \| Symbols: ATEXPA4, ATEXP4, ATHEXP ALPHA 1.6, EXPA4 \| expansin A4 \| |
| Eucgr.A02869.1 | 21,72 | 5,23 | 5,88 | 8,03 | 13,66 | AT5G51710.2 \| Symbols: KEA5, ATKEA5 \| K+ efflux antiporter 5 \| chr5:21004566-21008580 REVERSE LENGTH=565 |
| Eucgr.G02884.1 | 22,55 | 0,40 | 0,29 | 1,47 | 10,73 | AT5G04310.1 \| Symbols: \| Pectin lyase-like superfamily protein \| chr5:1203356-1207352 REVERSE LENGTH=518 |
| Eucgr.J00542.1 | 101,89 | 11,05 | 9,82 | 10,65 | 36,38 | AT3G44220.1 \| Symbols: \| Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family \| |
| Eucgr.F01953.2 | 15,06 | 0,43 | 1,14 | 1,84 | 8,49 | AT1G21060.1 \| Symbols: \| Protein of unknown function, DUF547 \| chr1:7371799-7374085 FORWARD LENGTH=505 |
| Eucgr.D02489.1 | 4,28 | 0,46 | 0,40 | 0,64 | 1,17 | AT3G60660.1 \| Symbols: \| unknown protein; |
| Eucgr.J00903.1 | 13,90 | 0,47 | 0,99 | 1,29 | 7,35 | AT5G04250.2 \| Symbols: \| Cysteine proteinases superfamily protein \| chr5:1176397-1178492 FORWARD LENGTH=345 |

| | | | | | | |
|---|---|---|---|---|---|---|
| Eucgr.F03301.1 | 1,14 | 0,05 | 0,20 | 0,56 | 0,33 | No hits found |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.F02302.1 | 26,54 | 0,78 | 1,24 | 1,69 | 6,64 | AT4G34160.1 \| Symbols: CYCD3;1, CYCD3 \| CYCLIN D3;1 \| chr4:16357903-16359304 FORWARD LENGTH=376 |
| Eucgr.E02910.1 | 17,99 | 3,07 | 2,73 | 3,54 | 8,95 | No hits found |
| Eucgr.B01911.5 | 45,47 | 276,97 | 253,38 | 191,66 | 159,73 | AT1G09140.2 \| Symbols: ATSRP30, SR30, At-SR30 \| SERINE-ARGININE PROTEIN 30 \| |
| Eucgr.B00048.1 | 7,18 | 0,00 | 0,31 | 0,39 | 2,44 | AT1G72210.1 \| Symbols: \| basic helix-loop-helix (bHLH) DNA-binding superfamily protein \| |
| Eucgr.K02942.1 | 28,02 | 4,38 | 5,40 | 5,70 | 11,94 | AT5G01710.1 \| Symbols: \| methyltransferases \| chr5:263709-265250 REVERSE LENGTH=513 |
| Eucgr.J03133.1 | 3,45 | 0,08 | 0,16 | 0,33 | 0,80 | AT1G16070.1 \| Symbols: AtTLP8, TLP8 \| tubby like protein 8 \| chr1:5511899-5513779 REVERSE LENGTH=397 |
| Eucgr.H00185.1 | 0,46 | 0,00 | 0,00 | 0,14 | 0,11 | AT4G23990.1 \| Symbols: ATCSLG3, CSLG3 \| cellulose synthase like G3 \| chr4:12456491-12460498 FORWARD LENGTH=751 |
| Eucgr.K00751.1 | 7,65 | 0,04 | 0,15 | 0,10 | 0,83 | AT4G03965.1 \| Symbols: \| RING/U-box superfamily protein \| chr4:1889576-1890205 FORWARD LENGTH=209 |
| Eucgr.G02816.1 | 16,72 | 1,26 | 1,78 | 1,84 | 5,78 | AT3G07990.1 \| Symbols: SCPL27 \| serine carboxypeptidase-like 27 \| chr3:2552544-2554644 FORWARD LENGTH=459 |
| Eucgr.E03124.1 | 9,69 | 2,73 | 2,82 | 4,77 | 5,27 | AT4G04930.1 \| Symbols: DES-1-LIKE \| fatty acid desaturase family protein \| chr4:2509236-2510918 FORWARD LENGTH=332 |
| Eucgr.A01002.1 | 9,58 | 0,94 | 1,05 | 0,99 | 2,24 | AT4G01730.1 \| Symbols: \| DHHC-type zinc finger family protein \| chr4:749574-752034 FORWARD LENGTH=508 |
| Eucgr.J00148.1 | 2,63 | 0,18 | 0,09 | 0,08 | 0,58 | No hits found |
| Eucgr.D00751.1 | 0,02 | 7,90 | 3,84 | 1,41 | 0,21 | AT4G21440.1 \| Symbols: ATMYB102, ATM4, MYB102 \| MYB-like 102 \| chr4:11418425-11419652 REVERSE LENGTH=350 |
| Eucgr.G01894.3 | 28,14 | 3,39 | 3,61 | 5,80 | 12,54 | AT1G47740.2 \| Symbols: \| PPPDE putative thiol peptidase family protein \| chr1:17567903-17569035 FORWARD LENGTH=279 |
| Eucgr.K02233.1 | 7,39 | 0,26 | 0,40 | 0,40 | 1,27 | AT1G18370.1 \| Symbols: HIK, ATNACK1, NACK1 \| ATP binding microtubule motor family protein \| |
| Eucgr.D01694.1 | 15,86 | 131,02 | 112,03 | 96,82 | 79,44 | AT5G63830.1 \| Symbols: \| HIT-type Zinc finger family protein \| chr5:25543585-25544802 REVERSE LENGTH=405 |
| Eucgr.F03980.1 | 29,88 | 1058,66 | 920,98 | 642,11 | 1318,09 | AT3G12580.1 \| Symbols: HSP70, ATHSP70 \| heat shock protein 70 \| chr3:3991487-3993689 REVERSE LENGTH=650 |
| Eucgr.H04428.2 | 37,29 | 7,59 | 7,86 | 8,52 | 17,19 | AT3G06350.1 \| Symbols: EMB3004, MEE32 \| dehydroquinate dehydratase, putative / shikimate dehydrogenase, putative \| |
| Eucgr.G01342.1 | 193,47 | 1,29 | 2,45 | 4,01 | 67,16 | AT4G15480.1 \| Symbols: UGT84A1 \| UDP-Glycosyltransferase superfamily protein \| |
| Eucgr.D01985.1 | 4,75 | 0,07 | 0,11 | 0,07 | 0,89 | AT1G12370.2 \| Symbols: PHR1, UVR2 \| photolyase 1 \| chr1:4206500-4208842 REVERSE LENGTH=496 |
| Eucgr.L03161.1 | 0,71 | 0,11 | 0,03 | 0,04 | 0,18 | AT1G21270.1 \| Symbols: WAK2 \| wall-associated kinase 2 \| chr1:7444997-7447345 FORWARD LENGTH=732 |
| Eucgr.K01547.1 | 8,25 | 26,70 | 32,27 | 37,79 | 24,48 | AT1G08710.2 \| Symbols: \| F-box family protein \| chr1:2771720-2773011 FORWARD LENGTH=295 |
| Eucgr.G02912.1 | 3,83 | 0,04 | 0,03 | 0,10 | 0,37 | AT2G39510.1 \| Symbols: \| nodulin MtN21 /EamA-like transporter family protein \| |
| Eucgr.H00919.1 | 6,02 | 489,18 | 193,76 | 106,41 | 20,09 | AT4G08570.1 \| Symbols: \| Heavy metal transport/detoxification superfamily protein \| |
| Eucgr.A01714.1 | 39,83 | 7,62 | 9,46 | 11,10 | 22,23 | AT1G05210.1 \| Symbols: \| Transmembrane protein 97, predicted \| chr1:1510469-1511485 FORWARD LENGTH=168 |
| Eucgr.C01067.1 | 14,85 | 0,50 | 0,74 | 0,72 | 6,92 | AT3G24460.1 \| Symbols: \| Serinc-domain containing serine and sphingolipid biosynthesis protein \| |
| Eucgr.B00137.1 | 12,31 | 1,83 | 2,50 | 4,21 | 6,24 | AT5G63380.1 \| Symbols: \| AMP-dependent synthetase and ligase family protein \| |
| Eucgr.J00969.2 | 34,52 | 2,05 | 2,92 | 4,23 | 13,80 | AT2G39870.1 \| Symbols: \| unknown protein |

| | | | | | | |
|---|---|---|---|---|---|---|
| Eucgr.J00271.1 | 8,34 | 299,91 | 192,56 | 122,45 | 31,18 | AT5G04760.1 \| Symbols: \| Duplicated homeodomain-like superfamily protein \| chr5:1373752-1374529 REVERSE LENGTH=215 |
| Eucgr.L03024.1 | 1,02 | 0,00 | 0,02 | 0,03 | 0,24 | AT4G18780.1 \| Symbols: CESA8, IRX1, ATCESA8, LEW2 \| cellulose synthase family protein \| |
| Eucgr.C02352.1 | 11,51 | 0,00 | 0,19 | 0,14 | 2,09 | AT1G33540.1 \| Symbols: scpl18 \| serine carboxypeptidase-like 18 \| chr1:12162349-12164700 REVERSE LENGTH=446 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.F02338.1 | 0,42 | 11,09 | 6,84 | 6,32 | 2,78 | No hits found |
| Eucgr.E00226.1 | 10,13 | 0,53 | 0,78 | 0,68 | 2,11 | AT3G03050.1 \| Symbols: CSLD3, KJK, ATCSLD3 \| cellulose synthase-like D3 \| chr3:687873-691629 FORWARD LENGTH=1145 |
| Eucgr.K02618.1 | 2,22 | 0,26 | 0,18 | 0,32 | 0,64 | AT4G31400.1 \| Symbols: CTF7 \| damaged DNA binding;DNA-directed DNA polymerases |
| Eucgr.A00994.1 | 20,90 | 2,91 | 3,97 | 4,36 | 13,00 | AT2G46930.1 \| Symbols: \| Pectinacetylesterase family protein \| chr2:19283625-19286090 FORWARD LENGTH=416 |
| Eucgr.G00557.1 | 16,97 | 46,33 | 47,35 | 51,16 | 34,05 | AT1G60940.2 \| Symbols: SNRK2-10, SNRK2.10, SRK2B \| SNF1-related protein kinase 2.10 \| |
| Eucgr.H03092.1 | 6,20 | 0,10 | 0,16 | 0,39 | 2,08 | AT5G43420.1 \| Symbols: \| RING/U-box superfamily protein \| chr5:17451790-17452917 FORWARD LENGTH=375 |
| Eucgr.A00530.1 | 41,00 | 2,35 | 4,67 | 5,83 | 16,20 | AT5G01360.1 \| Symbols: TBL3 \| Plant protein of unknown function (DUF828) \| chr5:147608-149316 REVERSE LENGTH=434 |
| Eucgr.L00249.1 | 0,34 | 280,16 | 135,36 | 52,37 | 1,25 | AT1G56600.1 \| Symbols: AtGolS2, GolS2 \| galactinol synthase 2 \| chr1:21207620-21209291 FORWARD LENGTH=335 |
| Eucgr.A02410.1 | 25,38 | 1,89 | 3,12 | 5,75 | 12,43 | AT5G06940.1 \| Symbols: \| Leucine-rich repeat receptor-like protein kinase family protein \| |
| Eucgr.J00169.1 | 14,01 | 0,35 | 0,55 | 1,29 | 3,34 | AT2G38310.1 \| Symbols: PYL4, RCAR10 \| PYR1-like 4 \| chr2:16050251-16050874 FORWARD LENGTH=207 |
| Eucgr.E00402.1 | 12,99 | 40,59 | 41,66 | 32,07 | 27,12 | AT2G39810.1 \| Symbols: HOS1 \| ubiquitin-protein ligases \| chr2:16612941-16617802 FORWARD LENGTH=927 |
| Eucgr.C04023.1 | 5,44 | 20,57 | 21,03 | 21,19 | 11,05 | AT5G24970.2 \| Symbols: \| Protein kinase superfamily protein \| chr5:8604358-8608656 REVERSE LENGTH=761 |
| Eucgr.F00103.2 | 21,10 | 0,55 | 1,06 | 1,51 | 6,47 | AT1G58440.1 \| Symbols: XF1, SQE1 \| FAD/NAD(P)-binding oxidoreductase family protein |
| Eucgr.F02263.1 | 27,76 | 3,11 | 7,28 | 13,35 | 16,39 | AT1G49890.1 \| Symbols: QWRF2 \| Family of unknown function (DUF566) \| chr1:18470282-18473463 FORWARD LENGTH=659 |
| Eucgr.H03407.1 | 9,56 | 0,39 | 0,69 | 1,22 | 3,60 | No hits found |
| Eucgr.A02144.1 | 6,82 | 17,97 | 18,26 | 15,96 | 12,00 | AT3G09360.1 \| Symbols: \| Cyclin/Brf1-like TBP-binding protein \| chr3:2873796-2878432 FORWARD LENGTH=604 |
| Eucgr.F01560.1 | 37,72 | 2,92 | 4,59 | 6,97 | 19,00 | AT3G46940.1 \| Symbols: DUT1 \| DUTP-PYROPHOSPHATASE-LIKE 1 \| chr3:17288367-17288867 REVERSE LENGTH=166 |
| Eucgr.D01775.1 | 1,57 | 0,04 | 0,52 | 0,56 | 0,55 | AT4G23750.2 \| Symbols: CRF2, TMO3 \| cytokinin response factor 2 \| chr4:12376751-12377782 FORWARD LENGTH=343 |
| Eucgr.F02691.1 | 2,11 | 16,62 | 17,60 | 13,57 | 7,69 | AT5G50080.1 \| Symbols: ERF110 \| ethylene response factor 110 \| chr5:20365948-20366835 FORWARD LENGTH=220 |
| Eucgr.F01369.1 | 5,98 | 1,26 | 1,44 | 1,99 | 3,30 | AT1G78570.1 \| Symbols: RHM1, ROL1, ATRHM1 \| rhamnose biosynthesis 1 \| |
| Eucgr.B03763.1 | 6,04 | 0,07 | 0,22 | 0,52 | 1,83 | AT4G13870.2 \| Symbols: WRNEXO \| Werner syndrome-like exonuclease \| chr4:8023563-8025542 REVERSE LENGTH=288 |
| Eucgr.K00770.2 | 5,60 | 33,27 | 23,33 | 23,26 | 13,75 | AT2G32650.2 \| Symbols: \| RmlC-like cupins superfamily protein \| chr2:13851547-13851966 FORWARD LENGTH=139 |
| Eucgr.J01951.2 | 42,69 | 16,98 | 14,79 | 15,70 | 24,39 | AT2G29570.1 \| Symbols: PCNA2, ATPCNA2 \| proliferating cell nuclear antigen 2 \| |
| Eucgr.I02584.1 | 13,10 | 2,99 | 2,97 | 3,32 | 5,76 | AT2G04305.1 \| Symbols: \| Magnesium transporter CorA-like family protein \| chr2:1501679-1503448 REVERSE LENGTH=434 |
| Eucgr.B00246.1 | 22,27 | 63,49 | 52,27 | 51,95 | 41,44 | AT1G17100.1 \| Symbols: \| SOUL heme-binding family protein \| chr1:5844766-5845539 FORWARD LENGTH=232 |
| Eucgr.C00213.3 | 0,28 | 9,02 | 5,83 | 5,10 | 1,59 | No hits found |

| | | | | | | |
|---|---|---|---|---|---|---|
| Eucgr.J00420.1 | 41,08 | 2,63 | 5,07 | 5,87 | 25,59 | AT5G22740.1 \| Symbols: ATCSLA02, CSLA02, ATCSLA2, CSLA2 \| cellulose synthase-like A02 \| |
| Eucgr.K01046.1 | 19,54 | 2,24 | 2,77 | 4,55 | 8,76 | AT2G47070.1 \| Symbols: SPL1 \| squamosa promoter binding protein-like 1 \| |
| Eucgr.E00628.2 | 225,84 | 1457,57 | 1141,60 | 1015,46 | 836,98 | AT2G45960.3 \| Symbols: PIP1B, TMP-A, ATHH2, PIP1;2 \| plasma membrane intrinsic protein 1B \| |
| Eucgr.E02426.1 | 1,67 | 11,42 | 9,63 | 7,40 | 4,00 | AT1G30220.1 \| Symbols: ATINT2, INT2 \| inositol transporter 2 \| chr1:10632957-10635439 REVERSE LENGTH=580 |
| Eucgr.H00564.1 | 12,64 | 142,25 | 102,24 | 81,75 | 36,62 | AT1G68090.1 \| Symbols: ANNAT5, ANN5 \| annexin 5 \| chr1:25519442-25520774 REVERSE LENGTH=316 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.A01107.1 | 4,38 | 0,83 | 0,72 | 0,97 | 1,44 | AT2G32590.1 \| unknown protein |
| Eucgr.J01598.1 | 19,43 | 0,43 | 0,94 | 1,51 | 8,01 | AT5G16720.1 \| Symbols: \| Protein of unknown function, DUF593 \| |
| Eucgr.J01910.1 | 0,54 | 7,08 | 6,35 | 4,03 | 2,69 | No hits found |
| Eucgr.F01907.1 | 4,45 | 0,65 | 0,58 | 0,77 | 1,77 | AT1G75150.1 \| Symbols: \| unknown protein; |
| Eucgr.C03593.1 | 0,18 | 5,75 | 2,92 | 2,40 | 1,04 | AT5G20610.1 \| Symbols: \| unknown protein; |
| Eucgr.K01424.1 | 9,34 | 0,39 | 0,50 | 1,09 | 2,76 | AT4G28660.1 \| Symbols: PSB28 \| photosystem II reaction center PSB28 protein \| |
| Eucgr.C02424.1 | 10,48 | 0,92 | 2,11 | 3,12 | 6,60 | AT5G57670.2 \| Symbols: \| Protein kinase superfamily protein \| chr5:23360531-23363694 REVERSE LENGTH=579 |
| Eucgr.L03349.1 | 0,74 | 0,00 | 0,00 | 0,05 | 0,17 | AT3G63470.1 \| Symbols: scpl40 \| serine carboxypeptidase-like 40 \| chr3:23438561-23440862 FORWARD LENGTH=502 |
| Eucgr.A02688.1 | 9,29 | 0,07 | 0,53 | 0,38 | 2,14 | AT5G52860.1 \| Symbols: \| ABC-2 type transporter family protein \| chr5:21419776-21421545 REVERSE LENGTH=589 |
| Eucgr.I01972.1 | 6,97 | 0,28 | 0,69 | 0,81 | 1,90 | AT3G01015.1 \| Symbols: \| TPX2 (targeting protein for Xklp2) protein family \| chr3:1798-4017 REVERSE LENGTH=488 |
| Eucgr.I01041.1 | 8,13 | 0,05 | 0,04 | 0,05 | 0,84 | AT2G22990.1 \| Symbols: SNG1, SCPL8 \| sinapoylglucose 1 \| chr2:9786393-9789925 FORWARD LENGTH=433 |
| Eucgr.A01014.3 | 20,05 | 0,97 | 1,28 | 2,21 | 11,70 | AT1G75250.1 \| Symbols: ATRL6, RSM3, RL6 \| RAD-like 6 \| chr1:28245073-28245453 REVERSE LENGTH=126 |
| Eucgr.B03001.1 | 10,78 | 0,37 | 0,87 | 0,87 | 4,40 | AT1G68360.1 \| Symbols: \| C2H2 and C2HC zinc fingers superfamily protein \| chr1:25621678-25622412 REVERSE LENGTH=244 |
| Eucgr.I02165.1 | 7,24 | 0,37 | 0,64 | 1,20 | 2,81 | AT1G53820.1 \| Symbols: \| RING/U-box superfamily protein \| chr1:20091491-20092423 FORWARD LENGTH=310 |
| Eucgr.E02665.1 | 1,68 | 0,03 | 0,01 | 0,04 | 0,30 | AT1G53210.1 \| Symbols: \| sodium/calcium exchanger family protein / calcium-binding EF hand family protein \| |
| Eucgr.E03762.2 | 0,26 | 9,63 | 10,32 | 6,79 | 1,51 | AT4G05200.1 \| Symbols: CRK25 \| cysteine-rich RLK (RECEPTOR-like protein kinase) 25 |
| Eucgr.F03057.1 | 0,25 | 6,74 | 5,20 | 3,01 | 0,86 | AT3G11560.4 \| Symbols: \| LETM1-like protein \| chr3:3639553-3645506 FORWARD LENGTH=872 |
| Eucgr.E01053.1 | 56,62 | 8,07 | 14,73 | 24,68 | 31,55 | AT2G46770.1 \| Symbols: NST1, EMB2301, ANAC043 \| NAC (No Apical Meristem) domain transcriptional regulator superfamily protein \| |
| Eucgr.K02999.1 | 5,34 | 0,11 | 0,55 | 0,75 | 1,56 | AT5G38690.1 \| Symbols: \| Zinc-finger domain of monoamine-oxidase A repressor R1 protein \| |
| Eucgr.J00337.1 | 0,01 | 4,30 | 2,62 | 1,34 | 0,06 | AT4G27420.1 \| Symbols: \| ABC-2 type transporter family protein \| chr4:13712434-13714797 REVERSE LENGTH=638 |
| Eucgr.E01674.1 | 3,01 | 0,39 | 1,02 | 0,85 | 1,69 | AT4G08850.2 \| Symbols: \| Leucine-rich repeat receptor-like protein kinase family protein \| |
| Eucgr.C00887.2 | 6,39 | 16,34 | 16,37 | 15,88 | 12,10 | AT5G56900.2 \| Symbols: \| CwfJ-like family protein / zinc finger (CCCH-type) family protein \| |
| Eucgr.J00100.1 | 121,16 | 6,53 | 8,13 | 11,85 | 46,17 | AT5G58300.2 \| Symbols: \| Leucine-rich repeat protein kinase family protein \| |
| Eucgr.H01073.1 | 12,56 | 0,90 | 0,95 | 1,16 | 4,15 | No hits found |

| | | | | | | |
|---|---|---|---|---|---|---|
| Eucgr.G01011.1 | 1,43 | 0,02 | 0,13 | 0,29 | 0,62 | AT5G10530.1 \| Symbols: \| Concanavalin A-like lectin protein kinase family protein \| |
| Eucgr.G02554.1 | 0,56 | 17,38 | 14,94 | 10,37 | 3,41 | AT1G69850.1 \| Symbols: ATNRT1:2, NTL1, NRT1:2 \| nitrate transporter 1:2 \| chr1:26296945-26300407 REVERSE LENGTH=585 |
| Eucgr.D00605.1 | 9,78 | 0,45 | 0,64 | 0,98 | 3,08 | AT1G28340.1 \| Symbols: AtRLP4, RLP4 \| receptor like protein 4 \| chr1:9940175-9943252 FORWARD LENGTH=626 |
| Eucgr.B00988.1 | 8,49 | 1,21 | 1,60 | 2,75 | 4,84 | AT3G17950.1 \| Symbols: \| unknown protein |
| Eucgr.K03267.1 | 3,62 | 0,07 | 0,21 | 0,22 | 1,30 | AT5G43420.1 \| Symbols: \| RING/U-box superfamily protein \| chr5:17451790-17452917 FORWARD LENGTH=375 |
| Eucgr.B00599.1 | 8,10 | 0,19 | 0,43 | 0,79 | 3,02 | AT5G08020.1 \| Symbols: ATRPA70B, RPA70B \| RPA70-kDa subunit B \| chr5:2572107-2574879 FORWARD LENGTH=604 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.B00551.1 | 35,81 | 2,17 | 4,26 | 5,92 | 17,08 | AT1G18670.1 \| Symbols: IBS1 \| Protein kinase superfamily protein \| chr1:6427242-6430696 REVERSE LENGTH=709 |
| Eucgr.B01491.1 | 5,55 | 0,12 | 0,36 | 0,58 | 2,22 | AT3G54650.1 \| Symbols: FBL17 \| RNI-like superfamily protein \| chr3:20226004-20228882 REVERSE LENGTH=593 |
| Eucgr.E02340.1 | 1,98 | 0,13 | 0,08 | 0,15 | 0,36 | AT1G79740.1 \| Symbols: \| hAT transposon superfamily \| chr1:30004367-30006715 REVERSE LENGTH=651 |
| Eucgr.F02385.1 | 5,66 | 0,70 | 0,96 | 0,87 | 3,11 | AT1G06870.1 \| Symbols: \| Peptidase S24/S26A/S26B/S26C family protein \| chr1:2108832-2110642 FORWARD LENGTH=367 |
| Eucgr.E01067.3 | 79,45 | 2,95 | 7,99 | 12,36 | 30,56 | AT1G32860.1 \| Symbols: \| Glycosyl hydrolase superfamily protein \| chr1:11907308-11908803 REVERSE LENGTH=426 |
| Eucgr.K03005.1 | 78,79 | 14,60 | 19,22 | 25,88 | 44,34 | AT5G01090.1 \| Symbols: \| Concanavalin A-like lectin family protein \| chr5:33055-34116 FORWARD LENGTH=353 |
| Eucgr.B00050.1 | 49,41 | 3,54 | 5,42 | 8,21 | 18,44 | AT4G40080.1 \| Symbols: \| ENTH/ANTH/VHS superfamily protein \| chr4:18579371-18580542 FORWARD LENGTH=365 |
| Eucgr.J00390.1 | 23,19 | 0,68 | 0,47 | 1,32 | 6,52 | AT5G22880.1 \| Symbols: H2B, HTB2 \| histone B2 \| chr5:7652130-7652567 REVERSE LENGTH=145 |
| Eucgr.B00944.1 | 341,64 | 3,14 | 8,91 | 12,41 | 90,76 | AT1G73620.1 \| Symbols: \| Pathogenesis-related thaumatin superfamily protein |
| Eucgr.L00518.1 | 2,43 | 0,00 | 0,19 | 0,66 | 0,55 | AT2G02220.1 \| Symbols: ATPSKR1, PSKR1 \| phytosulfokin receptor 1 \| chr2:584098-587124 REVERSE LENGTH=1008 |
| Eucgr.L00984.1 | 3,73 | 0,25 | 0,85 | 1,07 | 1,57 | No hits found |
| Eucgr.B01142.1 | 22,88 | 0,88 | 1,77 | 2,57 | 8,87 | AT3G06130.2 \| Symbols: \| Heavy metal transport/detoxification superfamily protein \| |
| Eucgr.B02240.1 | 10,68 | 1,20 | 1,78 | 2,19 | 6,12 | AT5G58600.1 \| Symbols: PMR5, TBL44 \| Plant protein of unknown function (DUF828) |
| Eucgr.L01545.1 | 6,34 | 0,00 | 0,49 | 0,82 | 1,37 | AT5G27550.1 \| Symbols: \| P-loop containing nucleoside triphosphate hydrolases superfamily protein \| |
| Eucgr.C00641.1 | 21,35 | 84,20 | 73,78 | 62,26 | 47,57 | AT5G26040.2 \| Symbols: HDA2 \| histone deacetylase 2 \| chr5:9099321-9101598 REVERSE LENGTH=387 |
| Eucgr.B00321.1 | 0,32 | 0,02 | 0,00 | 0,03 | 0,07 | AT3G48150.1 \| Symbols: APC8, CDC23 \| anaphase-promoting complex subunit 8 \| |
| Eucgr.H01542.1 | 14,48 | 59,67 | 54,43 | 56,83 | 28,25 | AT1G03360.1 \| Symbols: ATRRP4, RRP4 \| ribosomal RNA processing 4 \| chr1:824653-826179 FORWARD LENGTH=322 |
| Eucgr.I01044.2 | 4,41 | 0,02 | 0,04 | 0,07 | 1,17 | AT1G33540.1 \| Symbols: scpl18 \| serine carboxypeptidase-like 18 \| chr1:12162349-12164700 REVERSE LENGTH=446 |
| Eucgr.D01652.1 | 48,33 | 5,47 | 3,89 | 5,24 | 13,63 | AT5G59970.1 \| Symbols: \| Histone superfamily protein \| chr5:24146352-24146663 REVERSE LENGTH=103 |
| Eucgr.J02063.1 | 71,85 | 5,51 | 6,10 | 9,94 | 33,73 | No hits found |
| Eucgr.A02875.1 | 13,92 | 0,77 | 0,89 | 1,23 | 3,14 | AT5G51600.1 \| Symbols: PLE, ATMAP65-3, MAP65-3 \| Microtubule associated protein (MAP65/ASE1) family protein \| |
| Eucgr.C00778.1 | 6,85 | 0,47 | 1,06 | 1,55 | 3,55 | AT1G74960.3 \| Symbols: FAB1 \| fatty acid biosynthesis 1 \| chr1:28152564-28155948 REVERSE LENGTH=541 |
| Eucgr.I01037.1 | 40,91 | 0,25 | 0,80 | 1,36 | 16,04 | AT1G73270.1 \| Symbols: scpl6 \| serine carboxypeptidase-like 6 \| chr1:27549021-27552517 REVERSE LENGTH=452 |

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|---|---|---|---|---|---|---|
| Eucgr.A02902.1 | 129,32 | 3,58 | 9,45 | 11,21 | 44,80 | AT5G61480.1 \| Symbols: PXY \| Leucine-rich repeat protein kinase family protein \| |
| Eucgr.C02505.1 | 9,97 | 37,74 | 33,87 | 37,48 | 23,55 | AT2G24060.1 \| Symbols: \| Translation initiation factor 3 protein \| chr2:10229453-10231390 FORWARD LENGTH=312 |
| Eucgr.B02268.1 | 2,01 | 0,00 | 0,10 | 0,19 | 0,55 | AT2G29680.2 \| Symbols: CDC6, ATCDC6 \| cell division control 6 \| chr2:12689586-12692854 FORWARD LENGTH=508 |
| Eucgr.D00303.1 | 33,81 | 91,21 | 90,91 | 113,92 | 75,66 | AT1G53560.1 \| Symbols: \| Ribosomal protein L18ae family \| chr1:19984908-19985960 REVERSE LENGTH=153 |
| Eucgr.F03082.1 | 4,20 | 0,09 | 0,20 | 0,20 | 0,95 | No hits found |
| Eucgr.H04906.1 | 9,33 | 0,25 | 0,09 | 0,34 | 2,38 | No hits found |
| Eucgr.D01657.1 | 22,49 | 2,42 | 3,36 | 5,01 | 11,02 | AT1G32930.1 \| Symbols: \| Galactosyltransferase family protein \| chr1:11931980-11934399 REVERSE LENGTH=399 |
| Eucgr.F02441.1 | 16,28 | 0,11 | 0,50 | 0,79 | 6,95 | AT1G78060.1 \| Symbols: \| Glycosyl hydrolase family protein \| chr1:29349796-29352868 REVERSE LENGTH=767 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.E01240.1 | 20,81 | 3,31 | 4,90 | 5,37 | 12,01 | AT1G31850.2 \| Symbols: \| S-adenosyl-L-methionine-dependent methyltransferases superfamily protein \| |
| Eucgr.F03071.1 | 26,13 | 1,39 | 4,09 | 6,57 | 18,16 | AT1G79760.1 \| Symbols: DTA4 \| downstream target of AGL15-4 \| chr1:30012054-30013042 FORWARD LENGTH=299 |
| Eucgr.K00289.1 | 9,82 | 0,57 | 0,69 | 1,25 | 2,03 | No hits found |
| Eucgr.E00787.1 | 106,55 | 5,93 | 6,54 | 10,79 | 18,83 | AT2G46150.1 \| Symbols: \| Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family \| |
| Eucgr.F01793.1 | 113,75 | 0,78 | 1,54 | 3,30 | 23,64 | AT1G42970.1 \| Symbols: GAPB \| glyceraldehyde-3-phosphate dehydrogenase B subunit \| |
| Eucgr.I01534.1 | 41,79 | 346,80 | 294,74 | 241,43 | 181,85 | AT4G35300.5 \| Symbols: TMT2 \| tonoplast monosaccharide transporter2 \| chr4:16796432-16798332 REVERSE LENGTH=542 |
| Eucgr.A02961.1 | 5,51 | 0,48 | 0,37 | 0,33 | 1,37 | AT1G50240.2 \| Symbols: FU \| Protein kinase family protein with ARM repeat domain \| |
| Eucgr.C02984.1 | 8,40 | 0,14 | 0,20 | 0,70 | 1,62 | AT3G16500.1 \| Symbols: PAP1, IAA26 \| phytochrome-associated protein 1 \| chr3:5612801-5614208 REVERSE LENGTH=269 |
| Eucgr.A02093.1 | 4,34 | 0,48 | 0,42 | 0,38 | 1,38 | AT1G54385.2 \| Symbols: \| ARM repeat superfamily protein \| chr1:20301289-20303048 REVERSE LENGTH=560 |
| Eucgr.B03344.1 | 9,80 | 0,49 | 0,67 | 0,85 | 2,25 | AT1G23790.1 \| Symbols: \| Plant protein of unknown function (DUF936) \| chr1:8410099-8411917 FORWARD LENGTH=518 |
| Eucgr.F02669.1 | 45,30 | 4,39 | 6,46 | 6,83 | 21,01 | AT1G14290.1 \| Symbols: SBH2 \| sphingoid base hydroxylase 2 \| chr1:4880307-4881784 REVERSE LENGTH=259 |
| Eucgr.G03410.1 | 0,88 | 0,00 | 0,00 | 0,00 | 0,13 | AT2G27660.1 \| Symbols: \| Cysteine/Histidine-rich C1 domain family protein \| chr2:11798694-11800850 REVERSE LENGTH=718 |
| Eucgr.D02102.1 | 3,92 | 52,28 | 42,04 | 29,15 | 15,81 | AT2G35700.1 \| Symbols: ATERF38, ERF38 \| ERF family protein 38 \| chr2:15005205-15005789 FORWARD LENGTH=194 |
| Eucgr.G00453.1 | 18,24 | 5,14 | 4,28 | 4,15 | 11,06 | AT3G18830.1 \| Symbols: ATPLT5, PMT5, ATPMT5 \| polyol/monosaccharide transporter 5 \| |
| Eucgr.G02470.1 | 50,46 | 5,37 | 8,59 | 14,80 | 31,89 | No hits found |
| Eucgr.G03393.1 | 274,46 | 0,82 | 7,50 | 13,54 | 89,26 | AT3G20820.1 \| Symbols: \| Leucine-rich repeat (LRR) family protein \| chr3:7280930-7282027 FORWARD LENGTH=365 |
| Eucgr.J02497.1 | 1,00 | 5,25 | 6,14 | 6,11 | 2,68 | AT1G65770.1 \| Symbols: AMR1 \| ascorbic acid mannose pathway regulator 1 \| |
| Eucgr.B03204.1 | 13,62 | 55,51 | 54,92 | 47,91 | 32,70 | AT2G03220.1 \| Symbols: FT1, ATFUT1, ATFT1, MUR2 \| fucosyltransferase 1 \| chr2:970401-972353 REVERSE LENGTH=558 |
| Eucgr.F03752.1 | 2,46 | 0,00 | 0,07 | 0,31 | 0,83 | AT1G75710.1 \| Symbols: \| C2H2-like zinc finger protein \| chr1:28428806-28431128 FORWARD LENGTH=462 |
| Eucgr.F04123.1 | 4,43 | 24,12 | 27,70 | 19,16 | 14,12 | AT1G35660.1 \| Symbols: \| unknown protein; |
| Eucgr.K02028.1 | 8,68 | 1,99 | 1,26 | 1,40 | 4,76 | AT4G18590.1 \| Symbols: \| Nucleic acid-binding, OB-fold-like protein \| chr4:10236524-10236940 FORWARD LENGTH=106 |

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|---|---|---|---|---|---|---|
| Eucgr.A02614.1 | 25,53 | 108,74 | 109,69 | 117,90 | 62,20 | AT5G06260.1 \| Symbols: \| TLD-domain containing nucleolar protein \| chr5:1902755-1904835 REVERSE LENGTH=424 |
| Eucgr.A02807.2 | 29,92 | 7,05 | 7,88 | 8,57 | 19,60 | AT5G07240.1 \| Symbols: IQD24 \| IQ-domain 24 \| chr5:2272028-2274051 FORWARD LENGTH=401 |
| Eucgr.G02888.1 | 2,51 | 0,28 | 0,23 | 0,25 | 1,09 | AT5G13550.1 \| Symbols: SULTR4;1 \| sulfate transporter 4.1 \| chr5:4355412-4359490 REVERSE LENGTH=685 |
| Eucgr.D01969.1 | 10,57 | 0,00 | 0,03 | 0,07 | 1,75 | AT4G22790.1 \| Symbols: \| MATE efflux family protein \| chr4:11975153-11976628 REVERSE LENGTH=491 |
| Eucgr.B00460.1 | 35,05 | 2,61 | 4,89 | 9,65 | 16,17 | AT5G08139.1 \| Symbols: \| RING/U-box superfamily protein \| chr5:2616487-2617617 FORWARD LENGTH=376 |
| Eucgr.C01259.2 | 28,79 | 0,38 | 2,46 | 4,27 | 19,92 | AT2G46225.2 \| Symbols: ABIL1 \| ABI-1-like 1 \| chr2:18982113-18984074 FORWARD LENGTH=329 |
| Eucgr.C03720.3 | 12,49 | 64,35 | 70,19 | 66,15 | 36,01 | AT5G19740.1 \| Symbols: \| Peptidase M28 family protein \| chr5:6673986-6676767 FORWARD LENGTH=681 |
| Eucgr.F04353.1 | 31,13 | 7,91 | 6,54 | 7,72 | 14,84 | AT1G21830.1 \| Symbols: \| unknown protein; |
| Eucgr.B02400.1 | 8,24 | 1,05 | 1,31 | 1,44 | 4,26 | AT5G59790.1 \| Symbols: \| Domain of unknown function (DUF966) \| chr5:24090950-24092804 FORWARD LENGTH=423 |
| Eucgr.K02419.1 | 12,75 | 57,17 | 49,61 | 53,84 | 27,59 | AT5G03560.1 \| Symbols: \| Tetratricopeptide repeat (TPR)-like superfamily protein \| |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.B00609.1 | 5,22 | 0,40 | 0,87 | 1,10 | 2,48 | AT1G74160.1 \| Symbols: \| unknown protein |
| Eucgr.C00618.1 | 0,50 | 38,75 | 24,66 | 18,36 | 2,85 | AT2G25890.1 \| Symbols: \| Oleosin family protein \| chr2:11037435-11037884 FORWARD LENGTH=149 |
| Eucgr.F04267.1 | 0,80 | 0,04 | 0,13 | 0,10 | 0,28 | AT4G25980.1 \| Symbols: \| Peroxidase superfamily protein \| chr4:13189393-13191507 FORWARD LENGTH=371 |
| Eucgr.G01567.1 | 10,72 | 58,84 | 37,89 | 28,81 | 20,54 | AT5G67210.1 \| Symbols: \| Protein of unknown function (DUF579) \| chr5:26819019-26819972 FORWARD LENGTH=317 |
| Eucgr.K01750.1 | 14,82 | 1,65 | 3,32 | 4,93 | 8,91 | AT2G41820.1 \| Symbols: \| Leucine-rich repeat protein kinase family protein \| |
| Eucgr.D02018.1 | 15,80 | 0,35 | 1,46 | 1,50 | 5,99 | AT4G12390.1 \| Symbols: PME1 \| pectin methylesterase inhibitor 1 \| chr4:7336553-7337173 FORWARD LENGTH=206 |
| Eucgr.G02689.1 | 8,40 | 50,00 | 41,57 | 43,99 | 26,38 | AT2G25100.1 \| Symbols: \| Polynucleotidyl transferase, ribonuclease H-like superfamily protein \| |
| Eucgr.H03461.1 | 0,03 | 5,99 | 4,21 | 1,81 | 0,31 | AT3G22490.1 \| Symbols: \| Seed maturation protein \| chr3:7969785-7970738 REVERSE LENGTH=262 |
| Eucgr.L00712.1 | 7,42 | 0,38 | 0,48 | 0,71 | 2,38 | AT4G19840.1 \| Symbols: ATPP2-A1, ATPP2A-1, PP2-A1 \| phloem protein 2-A1 \| |
| Eucgr.D00432.1 | 30,00 | 1,79 | 4,78 | 8,24 | 14,94 | AT1G17030.1 \| Symbols: \| unknown protein; |
| Eucgr.C02127.1 | 4,43 | 0,00 | 0,05 | 0,21 | 0,44 | AT4G31330.1 \| Symbols: \| Protein of unknown function, DUF599 \| chr4:15202354-15203151 FORWARD LENGTH=239 |
| Eucgr.K01221.2 | 23,90 | 2,62 | 4,73 | 7,69 | 14,67 | AT3G59110.1 \| Symbols: \| Protein kinase superfamily protein \| chr3:21855673-21857847 FORWARD LENGTH=512 |
| Eucgr.K03427.1 | 21,62 | 0,93 | 1,17 | 1,68 | 6,20 | AT4G03100.1 \| Symbols: \| Rho GTPase activating protein with PAK-box/P21-Rho-binding domain \| |
| Eucgr.B03400.1 | 16,70 | 0,75 | 1,37 | 1,78 | 7,96 | AT1G69910.1 \| Symbols: \| Protein kinase superfamily protein \| chr1:26330166-26332076 FORWARD LENGTH=636 |
| Eucgr.H04811.1 | 6,24 | 0,71 | 0,65 | 0,83 | 2,40 | AT5G10110.1 \| Symbols: \| unknown protein; |
| Eucgr.F03619.1 | 24,87 | 0,35 | 1,11 | 1,61 | 10,18 | AT2G33570.1 \| Symbols: \| Domain of unknown function (DUF23) \| chr2:14217361-14219043 FORWARD LENGTH=496 |
| Eucgr.H03555.1 | 15,82 | 0,81 | 1,89 | 2,64 | 8,84 | AT1G47480.1 \| Symbols: \| alpha/beta-Hydrolases superfamily protein \| chr1:17417623-17419296 FORWARD LENGTH=314 |
| Eucgr.D01977.1 | 20,18 | 62,67 | 46,61 | 52,79 | 34,33 | AT1G12340.1 \| Symbols: \| Cornichon family protein \| chr1:4197396-4198032 FORWARD LENGTH=129 |
| Eucgr.I00628.1 | 137,65 | 23,23 | 26,89 | 21,21 | 51,74 | AT4G37870.1 \| Symbols: PCK1, PEPCK \| phosphoenolpyruvate carboxykinase 1 \| |

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|---|---|---|---|---|---|---|
| Eucgr.C02915.1 | 0,61 | 0,00 | 0,02 | 0,00 | 0,17 | AT4G28890.1 \| Symbols: \| RING/U-box superfamily protein \| chr4:14256437-14257735 REVERSE LENGTH=432 |
| Eucgr.A02622.1 | 22,15 | 3,41 | 5,48 | 8,14 | 14,02 | AT3G11590.1 \| Symbols: \| unknown protein; |
| Eucgr.E00596.1 | 22,69 | 1,22 | 4,29 | 7,27 | 14,35 | AT4G11450.1 \| Symbols: \| Protein of unknown function (DUF3527) \| chr4:6959065-6961223 REVERSE LENGTH=694 |
| Eucgr.G02657.1 | 13,90 | 3,76 | 5,04 | 5,27 | 9,26 | AT5G04885.1 \| Symbols: \| Glycosyl hydrolase family protein \| chr5:1423369-1426628 FORWARD LENGTH=665 |
| Eucgr.E01250.1 | 38,77 | 3,72 | 4,68 | 7,66 | 21,15 | AT1G32100.1 \| Symbols: ATPRR1, PRR1 \| pinoresinol reductase 1 \| chr1:11546472-11547953 REVERSE LENGTH=317 |
| Eucgr.F02355.1 | 8,00 | 0,84 | 0,74 | 0,60 | 2,71 | AT4G33400.1 \| Symbols: \| Vacuolar import/degradation, Vid27-related protein \| |
| Eucgr.C03813.1 | 25,83 | 0,97 | 1,63 | 1,95 | 12,67 | AT4G28950.1 \| Symbols: ARAC7, ATROP9, ATRAC7, RAC7, ROP9 \| RHO-related protein from plants 9 \| |
| Eucgr.C00897.1 | 14,21 | 0,15 | 0,62 | 1,14 | 8,51 | AT4G29720.1 \| Symbols: ATPAO5, PAO5 \| polyamine oxidase 5 \| chr4:14553456-14555057 REVERSE LENGTH=533 |
| Eucgr.G02614.1 | 16,98 | 56,10 | 45,29 | 57,33 | 33,72 | AT5G63670.1 \| Symbols: SPT42 \| SPT4 homolog 2 \| chr5:25488012-25489247 FORWARD LENGTH=116 |
| Eucgr.G00958.1 | 31,51 | 9,46 | 10,73 | 12,03 | 19,74 | AT2G07050.1 \| Symbols: CAS1 \| cycloartenol synthase 1 \| chr2:2924629-2930295 FORWARD LENGTH=759 |
| Eucgr.C03290.1 | 3,32 | 0,04 | 0,12 | 0,11 | 0,81 | AT5G20740.1 \| Symbols: \| Plant invertase/pectin methylesterase inhibitor superfamily protein \| |
| Eucgr.I01487.1 | 0,83 | 0,00 | 0,00 | 0,00 | 0,21 | AT1G29420.1 \| Symbols: \| SAUR-like auxin-responsive protein family \| chr1:10301483-10301908 REVERSE LENGTH=141 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.C00584.1 | 12,41 | 1,03 | 1,94 | 2,62 | 8,01 | AT1G27600.2 \| Symbols: IRX9-L, I9H \| Nucleotide-diphospho-sugar transferases superfamily protein \| |
| Eucgr.H01480.1 | 10,18 | 0,38 | 0,60 | 0,98 | 3,18 | AT4G02800.1 \| Symbols: \| unknown protein; |
| Eucgr.K01099.1 | 14,76 | 131,81 | 86,85 | 75,72 | 59,12 | AT2G31090.1 \| Symbols: \| unknown protein; |
| Eucgr.G01371.1 | 72,90 | 1,90 | 2,04 | 2,42 | 31,30 | AT5G67260.1 \| Symbols: CYCD3;2 \| CYCLIN D3;2 \| chr5:26836313-26837665 FORWARD LENGTH=367 |
| Eucgr.I02121.1 | 19,90 | 1,50 | 2,61 | 4,64 | 9,95 | AT5G38560.1 \| Symbols: \| Protein kinase superfamily protein \| chr5:15439844-15443007 FORWARD LENGTH=681 |
| Eucgr.I02501.1 | 7,81 | 1,31 | 1,75 | 2,21 | 5,01 | AT3G22960.1 \| Symbols: PKP1, PKP-ALPHA \| Pyruvate kinase family protein \| chr3:8139369-8141771 FORWARD LENGTH=596 |
| Eucgr.F01814.1 | 28,79 | 3,70 | 3,66 | 4,57 | 10,92 | AT1G20930.1 \| Symbols: CDKB2;2 \| cyclin-dependent kinase B2;2 \| chr1:7292752-7294664 REVERSE LENGTH=315 |
| Eucgr.J02626.1 | 11,01 | 1,99 | 3,04 | 3,28 | 5,86 | AT5G25170.1 \| Symbols: \| PPPDE putative thiol peptidase family protein \| chr5:8693257-8694438 FORWARD LENGTH=218 |
| Eucgr.K02806.1 | 25,05 | 1,53 | 4,51 | 7,19 | 13,06 | AT5G26660.1 \| Symbols: ATMYB86, MYB86 \| myb domain protein 86 \| chr5:9331775-9333044 REVERSE LENGTH=352 |
| Eucgr.H00370.1 | 124,23 | 5,85 | 6,17 | 6,60 | 26,26 | AT2G43290.1 \| Symbols: MSS3 \| Calcium-binding EF-hand family protein \| chr2:17991308-17991955 REVERSE LENGTH=215 |
| Eucgr.J01835.1 | 20,45 | 2,30 | 3,74 | 3,92 | 11,45 | AT1G60630.1 \| Symbols: \| Leucine-rich repeat protein kinase family protein \| chr1:22334754-22336785 REVERSE LENGTH=652 |
| Eucgr.H04041.1 | 1,64 | 0,21 | 0,12 | 0,19 | 0,82 | AT3G17030.1 \| Symbols: \| Nucleic acid-binding proteins superfamily \| chr3:5804509-5808462 REVERSE LENGTH=668 |
| Eucgr.D01080.1 | 6,28 | 0,25 | 0,65 | 0,89 | 2,36 | AT5G17670.1 \| Symbols: \| alpha/beta-Hydrolases superfamily protein \| chr5:5821082-5822600 FORWARD LENGTH=309 |
| Eucgr.H00778.1 | 2,36 | 0,19 | 0,19 | 0,15 | 0,81 | AT3G25100.1 \| Symbols: CDC45 \| cell division cycle 45 \| chr3:9144292-9146082 FORWARD LENGTH=596 |
| Eucgr.K03502.1 | 3,70 | 0,30 | 0,21 | 0,33 | 1,06 | AT2G47560.1 \| Symbols: \| RING/U-box superfamily protein \| chr2:19511934-19512617 REVERSE LENGTH=227 |
| Eucgr.G02798.1 | 22,08 | 0,71 | 0,34 | 0,26 | 4,04 | AT3G54770.1 \| Symbols: \| RNA-binding (RRM/RBD/RNP motifs) family protein \| |
| Eucgr.A02602.2 | 4,29 | 0,73 | 0,82 | 0,92 | 1,96 | AT2G36010.1 \| Symbols: E2F3, ATE2FA \| E2F transcription factor 3 \| chr2:15119688-15122893 FORWARD LENGTH=483 |

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|---|---|---|---|---|---|---|
| Eucgr.F04077.1 | 0,56 | 0,01 | 0,01 | 0,02 | 0,12 | AT3G47570.1 \| Symbols: \| Leucine-rich repeat protein kinase family protein \| |
| Eucgr.G00446.1 | 23,59 | 3,61 | 5,87 | 10,39 | 14,73 | AT4G34500.1 \| Symbols: \| Protein kinase superfamily protein \| chr4:16488005-16490792 REVERSE LENGTH=437 |
| Eucgr.J03181.2 | 11,88 | 0,27 | 0,79 | 1,67 | 6,76 | AT3G20260.1 \| Symbols: \| Protein of unknown function (DUF1666) \| chr3:7064190-7065751 REVERSE LENGTH=437 |
| Eucgr.C04266.1 | 26,09 | 1317,97 | 1007,17 | 544,49 | 193,24 | AT5G20250.4 \| Symbols: DIN10 \| Raffinose synthase family protein \| chr5:6833730-6836635 FORWARD LENGTH=844 |
| Eucgr.I00199.1 | 3,29 | 0,98 | 0,83 | 0,63 | 2,04 | AT4G33440.1 \| Symbols: \| Pectin lyase-like superfamily protein \| chr4:16092020-16094732 FORWARD LENGTH=475 |
| Eucgr.B02583.1 | 2,50 | 0,15 | 0,18 | 0,22 | 1,22 | AT5G23400.1 \| Symbols: \| Leucine-rich repeat (LRR) family protein \| chr5:7880603-7882372 FORWARD LENGTH=589 |
| Eucgr.I00804.1 | 15,40 | 1,60 | 3,13 | 5,42 | 9,10 | AT3G19420.1 \| Symbols: ATPEN2, PEN2 \| PTEN 2 \| chr3:6731824-6735354 FORWARD LENGTH=611 |
| Eucgr.B03781.1 | 24,04 | 0,04 | 0,86 | 1,39 | 9,77 | AT5G21105.1 \| Symbols: \| Plant L-ascorbate oxidase \| chr5:7172727-7177409 FORWARD LENGTH=588 |
| Eucgr.F04121.1 | 58,25 | 2,56 | 4,77 | 3,79 | 29,98 | AT1G71970.1 \| Symbols: \| unknown protein; |
| Eucgr.H01238.1 | 1,46 | 8,25 | 10,40 | 11,71 | 5,19 | AT4G36790.1 \| Symbols: \| Major facilitator superfamily protein \| chr4:17336360-17338304 FORWARD LENGTH=489 |
| Eucgr.D00086.1 | 5,95 | 0,22 | 0,63 | 1,05 | 2,53 | AT4G20840.1 \| Symbols: \| FAD-binding Berberine family protein \| chr4:11157916-11159535 FORWARD LENGTH=539 |
| Eucgr.J00152.1 | 7,28 | 0,10 | 0,32 | 0,98 | 2,78 | AT3G28050.1 \| Symbols: \| nodulin MtN21 /EamA-like transporter family protein \| |
| Eucgr.J03121.1 | 12,12 | 130,82 | 102,99 | 110,44 | 30,65 | AT1G80920.1 \| Symbols: J8 \| Chaperone DnaJ-domain superfamily protein \| chr1:30403863-30404549 REVERSE LENGTH=163 |
| Eucgr.B03123.1 | 3,73 | 0,63 | 0,61 | 0,54 | 1,47 | AT3G45070.1 \| Symbols: \| P-loop containing nucleoside triphosphate hydrolases superfamily protein \| |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.H05115.1 | 149,35 | 0,20 | 0,11 | 0,27 | 2,51 | AT5G63850.1 \| Symbols: AAP4 \| amino acid permease 4 \| chr5:25551494-25553374 FORWARD LENGTH=466 |
| Eucgr.G02452.1 | 21,00 | 1,74 | 2,89 | 4,40 | 11,03 | AT1G18650.1 \| Symbols: PDCB3 \| plasmodesmata callose-binding protein 3 \| chr1:6419036-6420413 REVERSE LENGTH=184 |
| Eucgr.J01238.1 | 4,12 | 217,96 | 126,49 | 113,37 | 21,22 | AT5G02220.1 \| Symbols: \| unknown protein; |
| Eucgr.J00928.1 | 1,04 | 69,46 | 45,49 | 33,12 | 5,61 | AT5G60680.1 \| Symbols: \| Protein of unknown function, DUF584 \| chr5:24386247-24386738 FORWARD LENGTH=163 |
| Eucgr.D00683.1 | 12,88 | 0,48 | 1,07 | 1,27 | 3,31 | AT1G11090.1 \| Symbols: \| alpha/beta-Hydrolases superfamily protein \| chr1:3702655-3703629 FORWARD LENGTH=324 |
| Eucgr.G01236.1 | 0,07 | 0,60 | 1,10 | 0,40 | 0,42 | AT3G18990.1 \| Symbols: VRN1, REM39 \| AP2/B3-like transcriptional factor family protein \| |
| Eucgr.J00232.1 | 3,18 | 28,72 | 28,58 | 31,82 | 10,29 | AT5G05700.1 \| Symbols: ATE1, DLS1, ATATE1 \| arginine-tRNA protein transferase 1 \| |
| Eucgr.F04216.1 | 4,65 | 0,38 | 1,33 | 1,70 | 2,82 | AT5G64740.1 \| Symbols: CESA6, IXR2, E112, PRC1 \| cellulose synthase 6 \| chr5:25881555-25886333 FORWARD LENGTH=1084 |
| Eucgr.I01414.1 | 139,72 | 25,94 | 32,98 | 41,76 | 80,52 | AT1G75840.1 \| Symbols: ARAC5, ATGP3, ROP4, ATROP4 \| RAC-like GTP binding protein 5 |
| Eucgr.A02452.1 | 6,84 | 0,27 | 0,57 | 0,83 | 1,82 | No hits found |
| Eucgr.G01455.1 | 5,99 | 0,26 | 0,30 | 0,29 | 1,55 | AT3G19184.1 \| Symbols: \| AP2/B3-like transcriptional factor family protein \| chr3:6637555-6639035 FORWARD LENGTH=277 |
| Eucgr.G01601.1 | 5,84 | 0,00 | 0,02 | 0,00 | 1,03 | AT4G13440.1 \| Symbols: \| Calcium-binding EF-hand family protein \| chr4:7810215-7810679 FORWARD LENGTH=154 |
| Eucgr.F02674.1 | 7,13 | 0,28 | 0,27 | 0,42 | 2,90 | AT5G09360.1 \| Symbols: LAC14 \| laccase 14 \| chr5:2906426-2908658 REVERSE LENGTH=569 |
| Eucgr.C02185.1 | 31,19 | 0,49 | 0,36 | 0,65 | 7,61 | AT1G73270.1 \| Symbols: scpl6 \| serine carboxypeptidase-like 6 \| chr1:27549021-27552517 REVERSE LENGTH=452 |
| Eucgr.K02684.1 | 0,94 | 59,52 | 31,31 | 17,24 | 6,17 | AT5G23660.1 \| Symbols: MTN3, SWEET12, AtSWEET12 \| homolog of Medicago truncatula MTN3 \| |

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|---|---|---|---|---|---|---|
| Eucgr.K02629.1 | 0,50 | 16,38 | 15,25 | 13,46 | 3,42 | AT5G23680.1 \| Symbols: \| Sterile alpha motif (SAM) domain-containing protein \| |
| Eucgr.F03763.1 | 0,73 | 0,00 | 0,02 | 0,11 | 0,26 | AT5G08640.2 \| Symbols: FLS1 \| flavonol synthase 1 \| chr5:2804009-2805175 FORWARD LENGTH=336 |
| Eucgr.F01637.1 | 43,10 | 5,05 | 6,51 | 7,10 | 25,95 | AT1G19920.1 \| Symbols: APS2, ASA1 \| Pseudouridine synthase/archaeosine transglycosylase-like family protein \| |
| Eucgr.I02055.1 | 3,60 | 0,19 | 0,30 | 0,17 | 2,00 | AT3G02230.1 \| Symbols: RGP1, ATRGP1 \| reversibly glycosylated polypeptide 1 \| chr3:415463-417304 FORWARD LENGTH=357 |
| Eucgr.C01038.1 | 3,90 | 0,24 | 0,40 | 0,49 | 1,46 | AT3G18830.1 \| Symbols: ATPLT5, PMT5, ATPMT5 \| polyol/monosaccharide transporter 5 \| |
| Eucgr.F03951.1 | 4,70 | 0,00 | 0,03 | 0,12 | 1,68 | AT5G10970.1 \| Symbols: \| C2H2 and C2HC zinc fingers superfamily protein \| chr5:3469268-3470086 FORWARD LENGTH=272 |
| Eucgr.E02613.1 | 0,00 | 3,87 | 2,70 | 1,43 | 0,08 | AT1G16770.1 \| Symbols: \| unknown protein; |
| Eucgr.B02320.1 | 0,00 | 3,18 | 1,89 | 0,55 | 0,17 | No hits found |
| Eucgr.C00635.1 | 3,82 | 0,61 | 0,64 | 1,09 | 2,15 | AT5G26010.1 \| Symbols: \| Protein phosphatase 2C family protein \| chr5:9085512-9087372 REVERSE LENGTH=331 |
| Eucgr.F01221.1 | 42,25 | 141,23 | 147,83 | 152,96 | 85,38 | AT1G53280.1 \| Symbols: \| Class I glutamine amidotransferase-like superfamily protein \| |
| Eucgr.F00754.1 | 1,41 | 0,00 | 0,10 | 0,05 | 0,51 | No hits found |
| Eucgr.H04911.1 | 16,40 | 0,46 | 0,83 | 0,93 | 4,06 | No hits found |
| Eucgr.F04010.1 | 7,51 | 0,11 | 0,35 | 0,47 | 3,06 | AT4G31590.1 \| Symbols: ATCSLC05, CSLC05, ATCSLC5, CSLC5 \| Cellulose-synthase-like C5 \| |
| Eucgr.H02961.1 | 0,18 | 7,69 | 3,40 | 1,03 | 0,81 | AT5G55240.1 \| Symbols: ATPXG2 \| ARABIDOPSIS THALIANA PEROXYGENASE 2 \| |
| Eucgr.D01317.1 | 27,91 | 2,38 | 4,44 | 6,21 | 16,79 | AT1G61900.1 \| Symbols: \| unknown protein |
| Eucgr.I01535.1 | 19,28 | 108,99 | 123,16 | 78,86 | 61,15 | AT3G51490.2 \| Symbols: TMT3 \| tonoplast monosaccharide transporter3 \| chr3:19105018-19107562 REVERSE LENGTH=737 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.B03167.1 | 2,47 | 0,13 | 0,22 | 0,15 | 0,70 | AT5G61210.1 \| Symbols: SNAP33, ATSNAP33, SNP33, ATSNAP33B \| soluble N-ethylmaleimide-sensitive factor |
| Eucgr.E00809.1 | 194,46 | 4,98 | 18,64 | 36,55 | 66,93 | AT4G23690.1 \| Symbols: \| Disease resistance-responsive (dirigent-like protein) family protein \| |
| Eucgr.F03961.1 | 3,47 | 13,71 | 15,61 | 13,14 | 7,88 | AT2G07680.1 \| Symbols: ATMRP11, MRP11, ABCC13 \| multidrug resistance-associated protein 11 \| |
| Eucgr.H00187.1 | 0,35 | 0,00 | 0,01 | 0,04 | 0,11 | AT4G23990.1 \| Symbols: ATCSLG3, CSLG3 \| cellulose synthase like G3 \| chr4:12456491-12460498 FORWARD LENGTH=751 |
| Eucgr.K00318.2 | 62,82 | 6,58 | 10,43 | 15,19 | 31,35 | AT5G53320.1 \| Symbols: \| Leucine-rich repeat protein kinase family protein \| chr5:21636453-21638337 REVERSE LENGTH=601 |
| Eucgr.G03039.1 | 0,61 | 15,02 | 13,01 | 13,13 | 2,67 | AT1G07280.3 \| Symbols: \| Tetratricopeptide repeat (TPR)-like superfamily protein \| |
| Eucgr.J00985.1 | 370,20 | 7,20 | 9,95 | 17,02 | 101,82 | AT3G54260.1 \| Symbols: TBL36 \| TRICHOME BIREFRINGENCE-LIKE 36 \| chr3:20085097-20086745 REVERSE LENGTH=379 |
| Eucgr.B00868.1 | 59,93 | 3,14 | 6,95 | 12,15 | 32,19 | AT3G18050.1 \| Symbols: \| unknown protein; |
| Eucgr.K02307.1 | 28,04 | 0,00 | 0,03 | 0,03 | 1,42 | AT1G73220.1 \| Symbols: AtOCT1, 1-Oct \| organic cation/carnitine transporter1 \| |
| Eucgr.H04662.1 | 18,11 | 1,66 | 3,61 | 5,89 | 11,65 | AT1G67560.1 \| Symbols: LOX6 \| PLAT/LH2 domain-containing lipoxygenase family protein \| |
| Eucgr.J02055.1 | 51,01 | 4,70 | 4,54 | 8,98 | 21,07 | AT4G40030.2 \| Symbols: \| Histone superfamily protein \| chr4:18555840-18556827 REVERSE LENGTH=164 |
| Eucgr.H01659.1 | 0,01 | 6,56 | 3,62 | 1,26 | 0,09 | AT4G34410.1 \| Symbols: RRTF1 \| redox responsive transcription factor 1 \| chr4:16451992-16452798 FORWARD LENGTH=268 |
| Eucgr.L01090.1 | 2,86 | 0,17 | 0,62 | 0,86 | 1,55 | AT4G36890.1 \| Symbols: IRX14 \| Nucleotide-diphospho-sugar transferases superfamily protein \| |

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|---|---|---|---|---|---|---|
| Eucgr.F03342.1 | 15,40 | 2,69 | 3,79 | 4,30 | 9,01 | AT5G54400.1 \| Symbols: \| S-adenosyl-L-methionine-dependent methyltransferases superfamily protein \| |
| Eucgr.D01942.1 | 17,85 | 0,09 | 0,73 | 1,24 | 7,34 | AT4G22900.1 \| Symbols: \| Protein of unknown function (DUF1191) \| chr4:12010221-12011252 FORWARD LENGTH=343 |
| Eucgr.H01211.1 | 5,26 | 0,65 | 0,67 | 1,50 | 1,87 | AT1G48910.1 \| Symbols: YUC10 \| Flavin-containing monooxygenase family protein \| |
| Eucgr.J01214.2 | 27,51 | 0,61 | 2,09 | 2,85 | 13,06 | AT3G28860.1 \| Symbols: ATMDR1, ATMDR11, PGP19, MDR11, MDR1, ATPGP19, ABCB19, ATABCB19 \| ATP binding cassette subfamily B19 \| |
| Eucgr.F02624.1 | 27,85 | 1,84 | 2,97 | 3,43 | 13,17 | AT5G54160.1 \| Symbols: ATOMT1, OMT1 \| O-methyltransferase 1 \| chr5:21982075-21984167 FORWARD LENGTH=363 |
| Eucgr.A01822.1 | 23,85 | 0,24 | 0,74 | 1,63 | 10,18 | AT4G28310.1 \| Symbols: \| unknown protein |
| Eucgr.L02974.1 | 6,42 | 0,24 | 0,21 | 0,55 | 2,80 | AT3G07880.1 \| Symbols: SCN1 \| Immunoglobulin E-set superfamily protein \| chr3:2514175-2515544 FORWARD LENGTH=240 |
| Eucgr.F01185.1 | 3,31 | 38,69 | 29,25 | 22,48 | 7,98 | AT5G54080.2 \| Symbols: HGO \| homogentisate 1,2-dioxygenase \| chr5:21945920-21948070 FORWARD LENGTH=461 |
| Eucgr.B02771.1 | 16,28 | 0,60 | 1,42 | 1,49 | 4,75 | AT1G58170.1 \| Symbols: \| Disease resistance-responsive (dirigent-like protein) family protein \| |
| Eucgr.I00910.1 | 4,61 | 0,17 | 0,17 | 0,32 | 1,58 | AT5G67090.1 \| Symbols: \| Subtilisin-like serine endopeptidase family protein \| |
| Eucgr.K01836.1 | 0,22 | 140,01 | 103,05 | 43,74 | 1,07 | AT5G06760.1 \| Symbols: LEA4-5 \| Late Embryogenesis Abundant 4-5 \| chr5:2089754-2090313 REVERSE LENGTH=158 |
| Eucgr.H04042.1 | 8,92 | 0,60 | 0,92 | 1,36 | 5,22 | AT3G17040.1 \| Symbols: HCF107 \| high chlorophyll fluorescent 107 \| chr3:5809378-5812605 REVERSE LENGTH=652 |
| Eucgr.F00115.1 | 21,48 | 0,63 | 0,63 | 0,79 | 6,99 | AT3G49940.1 \| Symbols: LBD38 \| LOB domain-containing protein 38 \| chr3:18514465-18515302 FORWARD LENGTH=247 |
| Eucgr.H02335.1 | 7,53 | 0,15 | 0,46 | 1,08 | 5,03 | AT4G37750.1 \| Symbols: ANT, DRG, CKC, CKC1 \| Integrase-type DNA-binding superfamily protein \| |
| Eucgr.H00130.1 | 21,52 | 3,91 | 4,30 | 6,49 | 14,76 | AT1G04520.1 \| Symbols: PDLP2 \| plasmodesmata-located protein 2 \| chr1:1231852-1233787 FORWARD LENGTH=307 |
| Eucgr.L03019.1 | 10,25 | 235,23 | 141,29 | 102,84 | 25,65 | No hits found |
| Eucgr.C03048.1 | 1,24 | 0,00 | 0,01 | 0,09 | 0,31 | AT4G26150.1 \| Symbols: CGA1, GATA22, GNL \| cytokinin-responsive gata factor 1 \| |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.G03115.1 | 3,08 | 0,00 | 0,03 | 0,03 | 0,62 | AT2G40435.1 \| Symbols: \| unknown protein |
| Eucgr.C02213.1 | 1,49 | 20,95 | 15,36 | 12,22 | 5,48 | No hits found |
| Eucgr.H04937.1 | 13,67 | 0,02 | 0,15 | 0,21 | 4,66 | AT5G09360.1 \| Symbols: LAC14 \| laccase 14 \| chr5:2906426-2908658 REVERSE LENGTH=569 |
| Eucgr.C02874.1 | 158,39 | 1402,30 | 1448,07 | 1241,28 | 372,50 | AT5G25560.2 \| Symbols: \| CHY-type/CTCHY-type/RING-type Zinc finger protein \| |
| Eucgr.I02220.2 | 27,62 | 84,32 | 76,11 | 78,92 | 49,88 | AT4G35510.1 \| Symbols: \| unknown protein; |
| Eucgr.K02439.1 | 45,53 | 0,30 | 1,32 | 1,18 | 13,64 | No hits found |
| Eucgr.C00963.1 | 1,30 | 23,61 | 22,96 | 34,80 | 2,98 | AT5G56550.1 \| Symbols: OXS3, ATOXS3 \| oxidative stress 3 \| chr5:22895847-22896502 REVERSE LENGTH=172 |
| Eucgr.H02314.1 | 34,55 | 1,35 | 5,36 | 11,28 | 18,37 | AT5G67620.1 \| Symbols: \| unknown protein; |
| Eucgr.B00846.1 | 4,78 | 0,00 | 0,05 | 0,10 | 1,19 | AT1G16390.1 \| Symbols: ATOCT3, 3-Oct \| organic cation/carnitine transporter 3 \| chr1:5602921-5604477 FORWARD LENGTH=518 |
| Eucgr.G01751.1 | 4,83 | 0,23 | 0,42 | 1,17 | 2,23 | AT4G34860.2 \| Symbols: \| Plant neutral invertase family protein \| chr4:16609955-16612019 REVERSE LENGTH=571 |
| Eucgr.D01066.2 | 13,54 | 0,35 | 0,26 | 1,08 | 4,77 | AT1G54730.2 \| Symbols: \| Major facilitator superfamily protein \| chr1:20424471-20429978 FORWARD LENGTH=470 |
| Eucgr.A02407.1 | 13,58 | 4,89 | 4,17 | 5,41 | 8,98 | AT3G12170.1 \| Symbols: \| Chaperone DnaJ-domain superfamily protein \| chr3:3881021-3882655 FORWARD LENGTH=262 |

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|---|---|---|---|---|---|---|
| Eucgr.D01021.1 | 4,04 | 0,52 | 0,34 | 0,41 | 1,37 | AT3G25690.3 \| Symbols: CHUP1 \| Hydroxyproline-rich glycoprotein family protein \| |
| Eucgr.E03592.1 | 10,80 | 0,87 | 0,79 | 0,72 | 3,77 | AT4G21270.1 \| Symbols: ATK1, KATA, KATAP \| kinesin 1 \| chr4:11329579-11333884 REVERSE LENGTH=793 |
| Eucgr.K00540.1 | 0,31 | 4,88 | 2,14 | 1,31 | 1,08 | AT1G28200.1 \| Symbols: FIP1 \| FH interacting protein 1 \| chr1:9850395-9852300 REVERSE LENGTH=259 |
| Eucgr.J03010.1 | 1,00 | 0,00 | 0,03 | 0,00 | 0,34 | AT1G12663.1 \| Symbols: \| Predicted to encode a PR (pathogenesis-related) protein. |
| Eucgr.H04817.1 | 8,33 | 0,08 | 0,15 | 0,58 | 1,43 | No hits found |
| Eucgr.K00711.1 | 40,24 | 2,52 | 3,47 | 3,51 | 21,20 | AT2G04780.2 \| Symbols: FLA7 \| FASCICLIN-like arabinoogalactan 7 \| chr2:1677488-1678252 FORWARD LENGTH=254 |
| Eucgr.B00946.1 | 52,67 | 1,74 | 2,12 | 2,74 | 11,37 | AT3G18000.1 \| Symbols: NMT1, XPL1, PEAMT \| S-adenosyl-L-methionine-dependent methyltransferases superfamily protein \| |
| Eucgr.J00336.1 | 14,73 | 0,87 | 1,28 | 1,61 | 8,15 | AT5G23420.1 \| Symbols: HMGB6 \| high-mobility group box 6 \| chr5:7888712-7890111 REVERSE LENGTH=241 |
| Eucgr.C03199.1 | 1532,75 | 66,91 | 100,38 | 132,04 | 213,15 | AT3G43190.1 \| Symbols: SUS4, ATSUS4 \| sucrose synthase 4 \| chr3:15179204-15182577 REVERSE LENGTH=808 |
| Eucgr.J02706.1 | 1,92 | 0,22 | 0,14 | 0,16 | 0,61 | AT3G21340.1 \| Symbols: \| Leucine-rich repeat protein kinase family protein \| chr3:7511848-7515937 REVERSE LENGTH=899 |
| Eucgr.K01509.1 | 0,01 | 0,74 | 0,64 | 0,62 | 0,09 | AT5G13530.2 \| Symbols: KEG \| protein kinases;ubiquitin-protein ligases \| chr5:4345618-4354369 FORWARD LENGTH=1624 |
| Eucgr.B01598.1 | 2,74 | 0,05 | 0,07 | 0,13 | 1,07 | AT3G06880.2 \| Symbols: \| Transducin/WD40 repeat-like superfamily protein \| chr3:2170516-2175686 REVERSE LENGTH=1264 |
| Eucgr.F01224.1 | 25,24 | 5,69 | 7,57 | 9,15 | 18,62 | AT1G53290.1 \| Symbols: \| Galactosyltransferase family protein \| chr1:19871353-19873251 FORWARD LENGTH=345 |
| Eucgr.A02891.1 | 173,15 | 26,43 | 29,77 | 40,45 | 84,89 | AT5G62390.1 \| Symbols: ATBAG7, BAG7 \| BCL-2-associated athanogene 7 \| chr5:25052377-25054170 REVERSE LENGTH=446 |
| Eucgr.J00806.1 | 39,40 | 2,72 | 3,85 | 4,81 | 15,48 | AT4G40030.2 \| Symbols: \| Histone superfamily protein \| chr4:18555840-18556827 REVERSE LENGTH=164 |
| Eucgr.B02618.1 | 4,68 | 0,26 | 0,46 | 0,52 | 1,43 | AT5G13770.1 \| Symbols: \| Pentatricopeptide repeat (PPR-like) superfamily protein \| |
| Eucgr.J02473.1 | 8,98 | 0,98 | 1,05 | 1,19 | 4,88 | AT4G35930.1 \| Symbols: \| F-box family protein \| chr4:17019482-17020744 FORWARD LENGTH=321 |
| Eucgr.B03097.1 | 23,63 | 1,21 | 2,42 | 4,46 | 13,02 | AT1G13600.1 \| Symbols: AtbZIP58, bZIP58 \| basic leucine-zipper 58 \| chr1:4650787-4651377 REVERSE LENGTH=196 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.H00477.2 | 0,92 | 7,81 | 5,01 | 4,89 | 2,28 | AT1G60730.2 \| Symbols: \| NAD(P)-linked oxidoreductase superfamily protein \| |
| Eucgr.D00242.1 | 5,10 | 0,16 | 0,38 | 0,49 | 2,13 | AT4G21070.1 \| Symbols: ATBRCA1, BRCA1 \| breast cancer susceptibility1 \| chr4:11248174-11252633 FORWARD LENGTH=941 |
| Eucgr.I00230.1 | 22,65 | 0,47 | 0,71 | 1,18 | 9,99 | AT5G64660.1 \| Symbols: ATCMPG2, CMPG2 \| CYS, MET, PRO, and GLY protein 2 \| |
| Eucgr.E00451.1 | 76,23 | 1,41 | 2,25 | 4,56 | 23,37 | AT4G22570.1 \| Symbols: APT3 \| adenine phosphoribosyl transferase 3 \| chr4:11882310-11885250 REVERSE LENGTH=183 |
| Eucgr.A00251.1 | 5,80 | 13,10 | 15,00 | 16,71 | 9,66 | AT1G54380.1 \| Symbols: \| spliceosome protein-related \| chr1:20298287-20300899 REVERSE LENGTH=515 |
| Eucgr.F00117.1 | 12,69 | 136,40 | 99,45 | 101,62 | 35,23 | AT5G43150.1 \| Symbols: \| unknown protein |
| Eucgr.I01724.1 | 15,71 | 1,14 | 2,53 | 3,07 | 9,24 | AT5G14430.1 \| Symbols: \| S-adenosyl-L-methionine-dependent methyltransferases superfamily protein |
| Eucgr.B03932.1 | 29,45 | 0,53 | 1,78 | 3,44 | 15,22 | AT5G22930.1 \| Symbols: \| Protein of unknown function (DUF1635) \| chr5:7668229-7669315 REVERSE LENGTH=238 |
| Eucgr.K02904.1 | 1,98 | 7,48 | 10,54 | 8,73 | 5,68 | AT1G74780.1 \| Symbols: \| Nodulin-like / Major Facilitator Superfamily protein \| |
| Eucgr.K01906.1 | 1,50 | 10,21 | 11,04 | 11,74 | 3,25 | AT3G11900.1 \| Symbols: ANT1 \| aromatic and neutral transporter 1 \| chr3:3758523-3760103 FORWARD LENGTH=432 |
| Eucgr.K00555.1 | 11,03 | 0,48 | 0,80 | 0,96 | 4,23 | AT4G01680.3 \| Symbols: MYB55 \| myb domain protein 55 \| chr4:716401-717415 REVERSE LENGTH=241 |

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|---|---|---|---|---|---|---|
| Eucgr.I02367.1 | 8,30 | 0,45 | 0,78 | 0,58 | 3,89 | AT4G36180.1 \| Symbols: \| Leucine-rich receptor-like protein kinase family protein \| |
| Eucgr.F01871.2 | 9,90 | 25,92 | 27,07 | 24,94 | 17,41 | AT4G39170.1 \| Symbols: \| Sec14p-like phosphatidylinositol transfer family protein \| |
| Eucgr.H00932.1 | 6,18 | 17,51 | 17,06 | 16,40 | 10,28 | AT1G11320.1 \| Symbols: \| unknown protein |
| Eucgr.F02126.1 | 15,99 | 81,63 | 67,38 | 51,81 | 31,20 | AT5G10940.2 \| Symbols: \| transducin family protein / WD-40 repeat family protein \| |
| Eucgr.J00665.1 | 5,19 | 62,07 | 49,09 | 40,77 | 13,36 | AT5G54620.1 \| Symbols: \| Ankyrin repeat family protein \| chr5:22187761-22189746 REVERSE LENGTH=431 |
| Eucgr.C03057.1 | 2,25 | 0,18 | 0,19 | 0,21 | 0,72 | AT2G26180.1 \| Symbols: IQD6 \| IQ-domain 6 \| chr2:11143433-11144982 REVERSE LENGTH=416 |
| Eucgr.D00880.2 | 46,25 | 3,29 | 4,19 | 6,79 | 27,71 | AT5G54530.1 \| Symbols: \| Protein of unknown function, DUF538 \| chr5:22152781-22154201 FORWARD LENGTH=161 |
| Eucgr.J02310.1 | 0,80 | 6,66 | 5,90 | 2,79 | 1,78 | AT5G40840.2 \| Symbols: SYN2 \| Rad21/Rec8-like family protein \| chr5:16359611-16363722 REVERSE LENGTH=810 |
| Eucgr.D00630.1 | 6,01 | 0,44 | 0,87 | 1,34 | 3,37 | AT3G15390.1 \| Symbols: SDE5 \| silencing defective 5 \| chr3:5196689-5199531 REVERSE LENGTH=490 |
| Eucgr.F02356.1 | 1,39 | 37,24 | 36,27 | 28,89 | 5,34 | No hits found |
| Eucgr.I00289.1 | 61,48 | 8,05 | 14,85 | 22,70 | 40,70 | AT1G43130.1 \| Symbols: LCV2 \| like COV 2 \| chr1:16228661-16231158 REVERSE LENGTH=261 |
| Eucgr.A01591.1 | 0,52 | 0,02 | 0,10 | 0,04 | 0,20 | AT2G36660.1 \| Symbols: PAB7 \| poly(A) binding protein 7 \| chr2:15361476-15364398 REVERSE LENGTH=609 |
| Eucgr.A01425.1 | 40,21 | 145,93 | 147,06 | 122,53 | 77,73 | AT5G24400.1 \| Symbols: EMB2024, PGL3 \| NagB/RpiA/CoA transferase-like superfamily protein \| |
| Eucgr.B03382.1 | 32,12 | 1,67 | 3,57 | 5,27 | 16,24 | AT1G27210.1 \| Symbols: \| ARM repeat superfamily protein \| chr1:9455669-9457917 REVERSE LENGTH=625 |
| Eucgr.H01670.1 | 1,88 | 0,07 | 0,08 | 0,10 | 0,56 | AT5G42930.1 \| Symbols: \| alpha/beta-Hydrolases superfamily protein \| chr5:17210738-17214152 REVERSE LENGTH=467 |
| Eucgr.C03762.1 | 0,30 | 4,85 | 4,09 | 2,70 | 0,94 | AT2G19900.1 \| Symbols: ATNADP-ME1, NADP-ME1 \| NADP-malic enzyme 1 \| chr2:8592106-8595403 REVERSE LENGTH=581 |
| Eucgr.A01776.1 | 5,58 | 0,43 | 0,64 | 0,75 | 2,38 | AT4G28230.1 \| Symbols: \| unknown protein; |
| Eucgr.E01169.1 | 69,42 | 4,13 | 5,46 | 6,43 | 17,75 | AT4G19420.1 \| Symbols: \| Pectinacetylesterase family protein \| chr4:10587504-10589807 REVERSE LENGTH=397 |
| Eucgr.A01210.1 | 2,39 | 22,87 | 13,48 | 11,77 | 1,30 | AT2G37330.1 \| Symbols: ALS3 \| aluminum sensitive 3 \| chr2:15669190-15670172 FORWARD LENGTH=273 |
| Eucgr.F02576.1 | 1,50 | 15,27 | 13,34 | 11,80 | 6,16 | No hits found |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.J02380.1 | 0,08 | 41,16 | 23,60 | 6,95 | 0,59 | No hits found |
| Eucgr.J01346.1 | 5,03 | 23,40 | 19,88 | 12,57 | 9,84 | AT3G28960.1 \| Symbols: \| Transmembrane amino acid transporter family protein \| |
| Eucgr.G03057.2 | 6,66 | 0,46 | 0,60 | 0,88 | 3,69 | AT3G55490.1 \| Symbols: \| GINS complex protein \| chr3:20572171-20573415 REVERSE LENGTH=185 |
| Eucgr.B01816.1 | 4,00 | 0,82 | 0,55 | 0,47 | 1,58 | AT1G09450.1 \| Symbols: \| Protein kinase superfamily protein \| chr1:3049066-3052858 FORWARD LENGTH=599 |
| Eucgr.J02488.1 | 0,26 | 4,09 | 3,62 | 2,37 | 1,00 | AT4G35830.1 \| Symbols: ACO1 \| aconitase 1 \| chr4:16973007-16977949 REVERSE LENGTH=898 |
| Eucgr.I02362.1 | 2,24 | 19,84 | 25,59 | 13,16 | 5,81 | No hits found |
| Eucgr.I01253.1 | 2,11 | 0,00 | 0,00 | 0,00 | 0,41 | AT1G29460.1 \| Symbols: \| SAUR-like auxin-responsive protein family \| chr1:10307609-10308055 REVERSE LENGTH=148 |
| Eucgr.B03096.1 | 3,63 | 0,23 | 0,40 | 0,86 | 2,13 | AT1G26220.1 \| Symbols: \| Acyl-CoA N-acyltransferases (NAT) superfamily protein \| |
| Eucgr.E03345.1 | 4,48 | 28,75 | 25,03 | 19,54 | 10,67 | AT3G47160.1 \| Symbols: \| RING/U-box superfamily protein \| chr3:17360238-17361879 REVERSE LENGTH=245 |

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|---|---|---|---|---|---|---|
| Eucgr.B00548.1 | 63,74 | 3,94 | 17,82 | 25,52 | 37,72 | AT5G61340.1 \| Symbols: \| unknown protein; |
| Eucgr.A02895.1 | 3,55 | 0,44 | 0,35 | 0,23 | 1,65 | AT5G62410.1 \| Symbols: SMC2, TTN3, ATCAP-E1, ATSMC4 \| structural maintenance of chromosomes 2 \| |
| Eucgr.D01982.1 | 45,48 | 5,08 | 7,26 | 9,83 | 28,05 | No hits found |
| Eucgr.B04023.1 | 14,16 | 0,76 | 2,41 | 4,46 | 10,39 | AT1G06920.1 \| Symbols: ATOFP4, OFP4 \| ovate family protein 4 \| chr1:2124854-2125801 REVERSE LENGTH=315 |
| Eucgr.A02076.1 | 8,53 | 42,73 | 39,27 | 27,33 | 17,59 | AT1G09230.1 \| Symbols: \| RNA-binding (RRM/RBD/RNP motifs) family protein \| chr1:2979637-2982563 REVERSE LENGTH=442 |
| Eucgr.J01549.1 | 3,52 | 0,40 | 1,27 | 2,00 | 2,35 | AT5G37790.1 \| Symbols: \| Protein kinase superfamily protein \| chr5:15008433-15011025 REVERSE LENGTH=552 |
| Eucgr.F04163.1 | 6,22 | 0,15 | 0,32 | 0,57 | 1,82 | AT5G09360.1 \| Symbols: LAC14 \| laccase 14 \| chr5:2906426-2908658 REVERSE LENGTH=569 |
| Eucgr.E02407.1 | 38,10 | 0,67 | 4,63 | 7,79 | 25,72 | AT4G18260.1 \| Symbols: \| Cytochrome b561/ferric reductase transmembrane protein family \| |
| Eucgr.J01393.1 | 50,50 | 3,41 | 9,74 | 12,85 | 28,42 | AT5G15630.1 \| Symbols: COBL4, IRX6 \| COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored protein family \| |
| Eucgr.A00785.1 | 22,93 | 1,66 | 4,06 | 6,20 | 12,75 | AT5G58300.2 \| Symbols: \| Leucine-rich repeat protein kinase family protein |
| Eucgr.K02087.4 | 6,80 | 27,91 | 26,92 | 24,77 | 15,29 | AT3G25410.1 \| Symbols: \| Sodium Bile acid symporter family \| chr3:9214565-9216331 REVERSE LENGTH=431 |
| Eucgr.C02095.1 | 13,35 | 0,28 | 0,63 | 0,53 | 6,51 | AT2G24490.2 \| Symbols: RPA2, ATRPA2, ROR1, ATRPA32A, RPA32A \| replicon protein A2 \| |
| Eucgr.H00371.1 | 30,04 | 1,31 | 1,37 | 1,51 | 6,47 | AT3G59400.1 \| Symbols: GUN4 \| enzyme binding;tetrapyrrole binding \| chr3:21948881-21949678 REVERSE LENGTH=265 |
| Eucgr.J01789.1 | 133,07 | 11,99 | 12,71 | 14,40 | 54,74 | AT1G58170.1 \| Symbols: \| Disease resistance-responsive (dirigent-like protein) family protein \| |
| Eucgr.G02893.1 | 14,23 | 63,60 | 65,88 | 61,38 | 27,70 | AT2G39450.1 \| Symbols: MTP11, ATMTP11 \| Cation efflux family protein \| chr2:16471744-16473735 REVERSE LENGTH=394 |
| Eucgr.B03492.1 | 6,01 | 36,52 | 38,76 | 40,11 | 17,67 | AT1G67340.1 \| Symbols: \| HCP-like superfamily protein with MYND-type zinc finger \| |
| Eucgr.D00694.1 | 3,64 | 0,04 | 0,14 | 0,09 | 1,26 | AT1G11125.1 \| Symbols: \| unknown protein; |
| Eucgr.G00872.1 | 29,17 | 3,70 | 6,80 | 10,08 | 22,79 | AT5G39420.1 \| Symbols: cdc2cAt \| CDC2C \| chr5:15772232-15774929 FORWARD LENGTH=644 |
| Eucgr.J01624.1 | 14,50 | 0,60 | 0,58 | 0,57 | 3,57 | AT1G66150.1 \| Symbols: TMK1 \| transmembrane kinase 1 \| chr1:24631503-24634415 FORWARD LENGTH=942 |
| Eucgr.G01704.2 | 13,07 | 1,85 | 3,60 | 3,66 | 9,66 | AT1G45130.1 \| Symbols: BGAL5 \| beta-galactosidase 5 \| chr1:17065447-17069110 FORWARD LENGTH=732 |
| Eucgr.F00716.1 | 0,20 | 14,38 | 5,01 | 1,52 | 0,05 | No hits found |
| Eucgr.E01665.1 | 2,29 | 0,00 | 0,25 | 0,71 | 1,11 | No hits found |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.F03030.1 | 15,78 | 1,87 | 2,56 | 3,48 | 8,19 | AT2G25737.1 \| Symbols: \| Sulfite exporter TauE/SafE family protein \| chr2:10977174-10979677 FORWARD LENGTH=476 |
| Eucgr.J00771.1 | 25,63 | 2,00 | 4,00 | 8,36 | 15,61 | AT2G17380.1 \| Symbols: AP19 \| associated protein 19 \| chr2:7553122-7554887 FORWARD LENGTH=161 |
| Eucgr.G02194.1 | 40,97 | 3,97 | 5,52 | 5,11 | 21,61 | AT1G71020.1 \| Symbols: \| ARM repeat superfamily protein \| chr1:26790825-26793105 REVERSE LENGTH=628 |
| Eucgr.B00537.2 | 12,12 | 52,77 | 53,21 | 46,71 | 7,08 | AT5G61380.1 \| Symbols: TOC1, APRR1, PRR1, AtTOC1 \| CCT motif -containing response regulator protein \| |
| Eucgr.E02713.1 | 12,05 | 0,32 | 1,00 | 0,93 | 7,19 | AT1G29050.1 \| Symbols: TBL38 \| TRICHOME BIREFRINGENCE-LIKE 38 \| chr1:10136376-10139082 REVERSE LENGTH=380 |
| Eucgr.C01116.1 | 2,78 | 0,51 | 0,07 | 0,57 | 0,71 | No hits found |
| Eucgr.A01406.1 | 4,55 | 52,32 | 50,28 | 61,46 | 9,65 | AT5G24490.1 \| Symbols: \| 30S ribosomal protein, putative \| chr5:8365690-8367178 FORWARD LENGTH=308 |

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|---|---|---|---|---|---|---|
| Eucgr.K00387.1 | 9,89 | 66,76 | 54,47 | 39,19 | 19,93 | AT5G24300.2 \| Symbols: SSI1 \| Glycogen/starch synthases, ADP-glucose type \| |
| Eucgr.E00328.1 | 29,66 | 4,61 | 4,12 | 5,48 | 15,95 | AT4G17670.1 \| Symbols: \| Protein of unknown function (DUF581) \| chr4:9833948-9834663 REVERSE LENGTH=159 |
| Eucgr.G03331.1 | 27,98 | 0,22 | 0,44 | 0,41 | 9,29 | AT5G12470.1 \| Symbols: \| Protein of unknown function (DUF3411) \| chr5:4044950-4047290 REVERSE LENGTH=386 |
| Eucgr.G01113.1 | 13,11 | 0,09 | 0,35 | 0,14 | 4,96 | AT5G09640.1 \| Symbols: SNG2, SCPL19 \| serine carboxypeptidase-like 19 \| chr5:2988373-2990966 FORWARD LENGTH=465 |
| Eucgr.D00356.1 | 3,25 | 0,25 | 0,48 | 0,48 | 1,53 | AT1G29630.2 \| Symbols: \| 5'-3' exonuclease family protein \| chr1:10349587-10353538 FORWARD LENGTH=735 |
| Eucgr.G01940.1 | 32,36 | 9,37 | 12,12 | 14,28 | 23,17 | AT1G12850.1 \| Symbols: \| Phosphoglycerate mutase family protein \| chr1:4380022-4381577 REVERSE LENGTH=405 |
| Eucgr.A01839.1 | 0,02 | 15,06 | 6,70 | 2,41 | 0,05 | AT1G03790.1 \| Symbols: SOM \| Zinc finger C-x8-C-x5-C-x3-H type family protein \| |
| Eucgr.C01876.1 | 80,43 | 21,36 | 19,01 | 30,24 | 41,50 | AT5G24930.1 \| Symbols: ATCOL4, COL4 \| CONSTANS-like 4 \| chr5:8589325-8590949 FORWARD LENGTH=406 |
| Eucgr.E01075.1 | 22,00 | 1,02 | 0,93 | 1,08 | 6,25 | AT5G59970.1 \| Symbols: \| Histone superfamily protein \| chr5:24146352-24146663 REVERSE LENGTH=103 |
| Eucgr.J02275.1 | 20,40 | 1,65 | 2,51 | 3,90 | 11,31 | AT3G27350.2 \| Symbols: \| unknown protein; |
| Eucgr.D01068.1 | 0,86 | 0,00 | 0,00 | 0,04 | 0,29 | AT1G54730.2 \| Symbols: \| Major facilitator superfamily protein \| chr1:20424471-20429978 FORWARD LENGTH=470 |
| Eucgr.E01150.1 | 5,09 | 1,09 | 0,72 | 1,50 | 2,41 | AT4G19350.1 \| Symbols: EMB3006 \| embryo defective 3006 \| chr4:10562214-10563676 REVERSE LENGTH=180 |
| Eucgr.A02408.1 | 1,36 | 0,05 | 0,05 | 0,07 | 0,66 | AT1G51200.4 \| Symbols: \| A20/AN1-like zinc finger family protein \| chr1:18985690-18986211 FORWARD LENGTH=173 |
| Eucgr.C00929.1 | 1,58 | 11,43 | 10,95 | 8,31 | 4,05 | AT4G29420.1 \| Symbols: \| F-box/RNI-like superfamily protein \| chr4:14470715-14472204 REVERSE LENGTH=446 |
| Eucgr.F01593.1 | 0,11 | 2,13 | 1,96 | 2,03 | 0,40 | AT3G50940.1 \| Symbols: \| P-loop containing nucleoside triphosphate hydrolases superfamily protein \| |
| Eucgr.K03212.1 | 49,08 | 6,21 | 13,83 | 27,31 | 33,81 | AT2G37080.1 \| Symbols: RIP3 \| ROP interactive partner 3 \| chr2:15581565-15584057 REVERSE LENGTH=583 |
| Eucgr.F02437.1 | 1,95 | 0,16 | 0,06 | 0,08 | 0,64 | AT1G78110.1 \| Symbols: \| unknown protein; |
| Eucgr.H02125.1 | 16,00 | 2,32 | 5,62 | 10,27 | 10,47 | AT5G67210.1 \| Symbols: \| Protein of unknown function (DUF579) \| chr5:26819019-26819972 FORWARD LENGTH=317 |
| Eucgr.E03246.1 | 586,63 | 21,03 | 39,85 | 53,99 | 216,49 | No hits found |
| Eucgr.J00068.2 | 29,62 | 1,64 | 1,20 | 0,88 | 20,52 | No hits found |
| Eucgr.K02905.1 | 2,66 | 10,24 | 11,71 | 9,55 | 5,16 | AT3G28580.1 \| Symbols: \| P-loop containing nucleoside triphosphate hydrolases superfamily protein |
| Eucgr.E00030.1 | 15,04 | 73,32 | 53,16 | 49,43 | 31,23 | AT3G61860.1 \| Symbols: ATRSP31, RSP31, At-RS31, RS31 \| RNA-binding (RRM/RBD/RNP motifs) family protein \| |
| Eucgr.H02448.1 | 4,40 | 0,03 | 0,08 | 0,12 | 1,43 | AT1G67750.1 \| Symbols: \| Pectate lyase family protein \| chr1:25401660-25403165 FORWARD LENGTH=408 |
| Eucgr.G00300.1 | 7,14 | 0,39 | 1,63 | 3,01 | 4,16 | AT2G21100.1 \| Symbols: \| Disease resistance-responsive (dirigent-like protein) family protein |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.F01447.1 | 26,34 | 272,06 | 261,70 | 274,46 | 81,80 | AT1G79040.1 \| Symbols: PSBR \| photosystem II subunit R \| chr1:29736085-29736781 FORWARD LENGTH=140 |
| Eucgr.A02608.1 | 1,74 | 0,21 | 0,14 | 0,14 | 0,82 | AT2G36026.1 \| Symbols: \| Ovate family protein \| chr2:15127265-15127816 FORWARD LENGTH=183 |
| Eucgr.B03728.1 | 4,92 | 0,39 | 1,24 | 1,26 | 3,07 | AT5G12340.1 \| Symbols: \| unknown protein; |
| Eucgr.D01823.1 | 0,27 | 27,86 | 24,42 | 19,89 | 1,52 | AT4G25700.1 \| Symbols: BETA-OHASE 1, B1, chy1, BCH1 \| beta-hydroxylase 1 |
| Eucgr.A02792.1 | 37,93 | 177,95 | 127,38 | 112,79 | 61,23 | AT4G25570.1 \| Symbols: ACYB-2 \| Cytochrome b561/ferric reductase transmembrane protein family \| |

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|---|---|---|---|---|---|---|
| Eucgr.K00285.1 | 0,37 | 0,02 | 0,02 | 0,04 | 0,16 | AT5G23940.1 \| Symbols: EMB3009, PEL3, DCR \| HXXXD-type acyl-transferase family protein \| |
| Eucgr.F02906.1 | 10,02 | 80,27 | 56,19 | 35,86 | 22,01 | AT5G17300.1 \| Symbols: RVE1 \| Homeodomain-like superfamily protein \| chr5:5690435-5692435 REVERSE LENGTH=387 |
| Eucgr.H01043.1 | 9,20 | 0,13 | 0,47 | 0,60 | 4,58 | AT4G02060.2 \| Symbols: PRL \| Minichromosome maintenance (MCM2/3/5) family protein \| |
| Eucgr.K02355.1 | 5,36 | 0,03 | 0,04 | 0,04 | 2,50 | AT2G43840.2 \| Symbols: UGT74F1 \| UDP-glycosyltransferase 74 F1 \| chr2:18157681-18159166 FORWARD LENGTH=449 |
| Eucgr.B02731.1 | 55,61 | 3,86 | 9,99 | 14,59 | 35,60 | AT5G02010.1 \| Symbols: ATROPGEF7, ROPGEF7 \| RHO guanyl-nucleotide exchange factor 7 \| |
| Eucgr.J01060.1 | 2,42 | 0,15 | 0,05 | 0,07 | 0,41 | AT3G07510.2 \| Symbols: \| unknown protein |
| Eucgr.G03227.1 | 79,40 | 0,86 | 1,85 | 1,91 | 31,98 | AT5G07030.1 \| Symbols: \| Eukaryotic aspartyl protease family protein \| chr5:2183600-2185717 REVERSE LENGTH=455 |
| Eucgr.E02770.1 | 8,60 | 0,25 | 0,26 | 0,27 | 5,12 | No hits found |
| Eucgr.C00451.1 | 13,11 | 75,21 | 62,76 | 49,39 | 25,17 | AT2G12400.1 \| Symbols: \| unknown protein; |
| Eucgr.B02321.1 | 0,02 | 3,51 | 1,36 | 0,32 | 0,09 | AT2G29090.2 \| Symbols: CYP707A2 \| cytochrome P450, family 707, subfamily A, polypeptide 2 \| |
| Eucgr.H03469.1 | 59,65 | 3,72 | 4,50 | 5,26 | 30,06 | AT4G03500.1 \| Symbols: \| Ankyrin repeat family protein \| chr4:1553453-1556571 FORWARD LENGTH=652 |
| Eucgr.G00575.1 | 4,29 | 0,94 | 0,59 | 0,85 | 2,55 | AT1G61000.1 \| Symbols: \| unknown protein |
| Eucgr.A01897.1 | 0,11 | 82,14 | 33,20 | 9,83 | 0,61 | No hits found |
| Eucgr.K00573.1 | 6,39 | 0,60 | 1,09 | 1,72 | 3,91 | AT3G62150.1 \| Symbols: PGP21 \| P-glycoprotein 21 \| chr3:23008755-23013579 REVERSE LENGTH=1296 |
| Eucgr.G02934.1 | 43,45 | 2,01 | 5,66 | 12,10 | 29,12 | AT3G55420.1 \| Symbols: \| unknown protein; |
| Eucgr.L00248.1 | 0,17 | 162,07 | 86,93 | 32,28 | 0,69 | AT1G56600.1 \| Symbols: AtGolS2, GolS2 \| galactinol synthase 2 \| chr1:21207620-21209291 FORWARD LENGTH=335 |
| Eucgr.B02197.1 | 7,47 | 0,13 | 0,37 | 0,41 | 3,11 | AT1G09540.1 \| Symbols: MYB61, ATMYB61 \| myb domain protein 61 \| chr1:3086333-3087689 FORWARD LENGTH=366 |
| Eucgr.F00501.1 | 2,52 | 0,06 | 0,05 | 0,19 | 1,40 | AT1G33110.1 \| Symbols: \| MATE efflux family protein \| chr1:12005084-12008618 FORWARD LENGTH=494 |
| Eucgr.K01667.2 | 64,37 | 4,52 | 11,87 | 23,49 | 35,51 | AT3G56480.1 \| Symbols: \| myosin heavy chain-related \| chr3:20936480-20938986 REVERSE LENGTH=490 |
| Eucgr.B03348.1 | 26,89 | 0,21 | 0,15 | 0,07 | 9,47 | AT1G10550.1 \| Symbols: XTH33, XET \| xyloglucan:xyloglucosyl transferase 33 \| chr1:3479257-3480957 REVERSE LENGTH=310 |
| Eucgr.D00321.1 | 127,97 | 0,75 | 1,93 | 4,91 | 23,84 | AT2G34430.1 \| Symbols: LHB1B1, LHCB1.4 \| light-harvesting chlorophyll-protein complex II subunit B1 \| |
| Eucgr.G03135.1 | 10,32 | 1,20 | 2,05 | 2,76 | 6,88 | AT2G40620.1 \| Symbols: \| Basic-leucine zipper (bZIP) transcription factor family protein |
| Eucgr.F03950.1 | 38,76 | 1,85 | 3,23 | 5,43 | 26,47 | AT1G80690.1 \| Symbols: \| PPPDE putative thiol peptidase family protein \| chr1:30329283-30330524 REVERSE LENGTH=227 |
| Eucgr.L00055.1 | 2,70 | 13,38 | 11,22 | 10,11 | 6,18 | AT5G16990.1 \| Symbols: \| Zinc-binding dehydrogenase family protein \| chr5:5581831-5583849 REVERSE LENGTH=343 |
| Eucgr.E04043.2 | 12,23 | 1,97 | 3,14 | 4,28 | 8,85 | AT1G11790.1 \| Symbols: ADT1 \| arogenate dehydratase 1 \| chr1:3981476-3984962 FORWARD LENGTH=392 |
| Eucgr.J02569.1 | 0,21 | 2,64 | 2,68 | 2,34 | 0,63 | AT1G20925.1 \| Symbols: \| Auxin efflux carrier family protein \| chr1:7289973-7292507 FORWARD LENGTH=472 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.A02086.1 | 23,71 | 7,91 | 6,93 | 8,18 | 17,77 | AT4G32890.1 \| Symbols: GATA9 \| GATA transcription factor 9 \| chr4:15875598-15876615 FORWARD LENGTH=308 |
| Eucgr.B02796.1 | 12,04 | 0,28 | 1,95 | 3,31 | 5,69 | AT2G38080.1 \| Symbols: IRX12, LAC4, ATLMCO4, LMCO4 \| Laccase/Diphenol oxidase family protein \| |
| Eucgr.J00113.1 | 3,97 | 0,40 | 0,49 | 0,48 | 1,68 | AT5G05240.1 \| Symbols: \| Uncharacterised conserved protein (UCP030365) \| chr5:1554023-1556230 REVERSE LENGTH=530 |

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|---|---|---|---|---|---|---|
| Eucgr.C04217.1 | 39,42 | 3,74 | 7,46 | 12,21 | 22,98 | AT5G15050.1 \| Symbols: \| Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein |
| Eucgr.D01955.1 | 0,05 | 0,17 | 0,84 | 0,76 | 0,22 | AT2G45570.1 \| Symbols: CYP76C2 \| cytochrome P450, family 76, subfamily C, polypeptide 2 \| |
| Eucgr.K02638.1 | 3,52 | 0,78 | 0,21 | 0,50 | 1,74 | AT5G35520.1 \| Symbols: MIS12, ATMIS12 \| minichromosome instability 12 (mis12)-like \| |
| Eucgr.D00088.1 | 123,26 | 5,66 | 10,29 | 15,33 | 55,67 | AT1G30760.1 \| Symbols: \| FAD-binding Berberine family protein \| chr1:10918321-10920441 FORWARD LENGTH=534 |
| Eucgr.H02338.1 | 131,39 | 30,24 | 33,82 | 38,59 | 75,02 | AT3G49720.2 \| Symbols: \| unknown protein; |
| Eucgr.C03090.1 | 0,21 | 0,02 | 0,00 | 0,01 | 0,07 | AT1G79670.1 \| Symbols: RFO1, WAKL22 \| Wall-associated kinase family protein \| |
| Eucgr.D00322.1 | 364,73 | 15,53 | 18,75 | 41,58 | 83,31 | AT2G34430.1 \| Symbols: LHB1B1, LHCB1.4 \| light-harvesting chlorophyll-protein complex II subunit B1 \| |
| Eucgr.H04549.1 | 2,07 | 0,03 | 0,19 | 0,46 | 0,82 | AT4G15920.1 \| Symbols: SWEET17, AtSWEET17 \| Nodulin MtN3 family protein \| chr4:9030742-9033343 REVERSE LENGTH=241 |
| Eucgr.L03123.1 | 2,67 | 17,17 | 14,83 | 13,58 | 5,36 | AT4G29420.1 \| Symbols: \| F-box/RNI-like superfamily protein \| chr4:14470715-14472204 REVERSE LENGTH=446 |
| Eucgr.A02140.1 | 4,04 | 14,31 | 15,72 | 13,30 | 7,22 | AT3G03710.1 \| Symbols: RIF10, PNP \| polyribonucleotide nucleotidyltransferase, putative \| |
| Eucgr.F01611.1 | 418,71 | 48,29 | 107,92 | 147,05 | 182,78 | AT1G75500.2 \| Symbols: WAT1 \| Walls Are Thin 1 \| chr1:28338282-28340091 REVERSE LENGTH=389 |
| Eucgr.I01231.1 | 2,43 | 160,13 | 93,47 | 46,77 | 8,13 | AT2G15970.2 \| Symbols: COR413-PM1 \| cold regulated 413 plasma membrane 1 \| |
| Eucgr.D01441.2 | 12,88 | 36,00 | 35,04 | 32,63 | 21,09 | AT4G16440.1 \| Symbols: \| ferredoxin hydrogenases \| chr4:9269263-9271510 REVERSE LENGTH=474 |
| Eucgr.K02422.1 | 3,70 | 20,83 | 17,92 | 15,51 | 7,45 | AT5G03560.1 \| Symbols: \| Tetratricopeptide repeat (TPR)-like superfamily protein \| |
| Eucgr.J02173.1 | 77,27 | 4,25 | 5,33 | 4,84 | 37,11 | AT5G40150.1 \| Symbols: \| Peroxidase superfamily protein \| chr5:16059750-16060736 REVERSE LENGTH=328 |
| Eucgr.B02382.1 | 0,24 | 6,79 | 4,92 | 3,65 | 0,93 | AT1G07645.1 \| Symbols: ATDSI-1VOC, DSI-1VOC \| dessication-induced 1VOC superfamily protein \| |
| Eucgr.H00791.1 | 7,86 | 0,92 | 1,30 | 2,29 | 5,65 | AT5G48720.2 \| Symbols: XRI, XRI1 \| x-ray induced transcript 1 \| chr5:19759233-19761621 FORWARD LENGTH=300 |
| Eucgr.J02841.1 | 3,06 | 0,67 | 0,34 | 0,92 | 1,71 | AT1G17520.1 \| Symbols: \| Homeodomain-like/winged-helix DNA-binding family protein \| chr1:6024959-6027224 REVERSE LENGTH=296 |
| Eucgr.D01777.1 | 3,63 | 0,14 | 0,17 | 0,24 | 1,36 | AT4G23740.1 \| Symbols: \| Leucine-rich repeat protein kinase family protein \| chr4:12367063-12369159 FORWARD LENGTH=638 |
| Eucgr.H04936.1 | 8,51 | 0,04 | 0,03 | 0,08 | 2,50 | AT5G09360.1 \| Symbols: LAC14 \| laccase 14 \| chr5:2906426-2908658 REVERSE LENGTH=569 |
| Eucgr.J01431.1 | 11,18 | 0,12 | 0,16 | 0,31 | 3,93 | AT3G30530.1 \| Symbols: ATBZIP42, bZIP42 \| basic leucine-zipper 42 \| chr3:12139512-12140033 FORWARD LENGTH=173 |
| Eucgr.K00151.4 | 15,32 | 2,94 | 3,48 | 4,89 | 11,48 | AT4G25290.1 \| Symbols: \| DNA photolyases;DNA photolyases \| chr4:12941486-12944994 REVERSE LENGTH=692 |
| Eucgr.G03233.1 | 7,44 | 0,38 | 0,69 | 0,51 | 3,70 | No hits found |
| Eucgr.B01963.1 | 0,36 | 0,00 | 0,00 | 0,06 | 0,13 | AT3G14620.1 \| Symbols: CYP72A8 \| cytochrome P450, family 72, subfamily A, polypeptide 8 \| |
| Eucgr.H01495.1 | 3,96 | 0,04 | 0,10 | 0,23 | 1,46 | AT3G53810.1 \| Symbols: \| Concanavalin A-like lectin protein kinase family protein \| |
| Eucgr.F04162.1 | 1,95 | 0,09 | 0,04 | 0,06 | 0,72 | AT5G09360.1 \| Symbols: LAC14 \| laccase 14 \| chr5:2906426-2908658 REVERSE LENGTH=569 |
| Eucgr.C01045.1 | 11,70 | 0,52 | 1,49 | 2,57 | 8,06 | AT4G32350.1 \| Symbols: \| Regulator of Vps4 activity in the MVB pathway protein \| |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.A02929.1 | 45,35 | 195,33 | 180,49 | 171,77 | 70,43 | AT4G25130.1 \| Symbols: PMSR4 \| peptide met sulfoxide reductase 4 \| chr4:12898802-12899998 REVERSE LENGTH=258 |
| Eucgr.A02121.2 | 41,44 | 3,24 | 6,66 | 12,13 | 26,68 | AT5G32450.1 \| Symbols: \| RNA binding (RRM/RBD/RNP motifs) family protein \| |

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|---|---|---|---|---|---|---|
| Eucgr.E00070.1 | 32,68 | 1,90 | 4,13 | 6,97 | 20,34 | AT1G01430.1 \| Symbols: TBL25 \| TRICHOME BIREFRINGENCE-LIKE 25 \| chr1:156953-158536 REVERSE LENGTH=456 |
| Eucgr.K00075.1 | 14,32 | 44,40 | 42,17 | 39,60 | 22,57 | AT5G16750.1 \| Symbols: TOZ \| Transducin family protein / WD-40 repeat family protein \| |
| Eucgr.K01353.1 | 1,93 | 12,72 | 12,64 | 11,28 | 4,29 | AT5G60870.1 \| Symbols: \| Regulator of chromosome condensation (RCC1) family protein \| |
| Eucgr.E01876.1 | 3,68 | 39,38 | 33,04 | 35,68 | 9,70 | AT5G45040.1 \| Symbols: \| Cytochrome c \| chr5:18175566-18176851 REVERSE LENGTH=175 |
| Eucgr.B00601.1 | 2,95 | 0,16 | 0,23 | 0,35 | 1,44 | AT5G08020.1 \| Symbols: ATRPA70B, RPA70B \| RPA70-kDa subunit B \| chr5:2572107-2574879 FORWARD LENGTH=604 |
| Eucgr.G03122.1 | 259,31 | 5,64 | 10,62 | 21,19 | 94,55 | AT2G40480.1 \| Symbols: \| Plant protein of unknown function (DUF827) \| chr2:16910425-16912444 FORWARD LENGTH=518 |
| Eucgr.J03127.1 | 8,27 | 1576,75 | 1347,55 | 881,92 | 925,42 | AT1G16030.1 \| Symbols: Hsp70b \| heat shock protein 70B \| chr1:5502386-5504326 REVERSE LENGTH=646 |
| Eucgr.K00315.1 | 0,76 | 0,10 | 0,05 | 0,07 | 0,29 | AT5G52950.1 \| Symbols: \| unknown protein; |
| Eucgr.E00460.1 | 0,08 | 7,37 | 6,22 | 4,26 | 0,35 | AT4G12430.1 \| Symbols: TPPF \| Haloacid dehalogenase-like hydrolase (HAD) superfamily protein \| |
| Eucgr.J02714.1 | 0,74 | 0,13 | 0,00 | 0,09 | 0,28 | AT2G19190.1 \| Symbols: FRK1 \| FLG22-induced receptor-like kinase 1 \| chr2:8326067-8329893 REVERSE LENGTH=876 |
| Eucgr.G03078.1 | 35,58 | 1,80 | 4,90 | 11,75 | 22,17 | AT3G11090.1 \| Symbols: LBD21 \| LOB domain-containing protein 21 \| chr3:3475036-3475533 FORWARD LENGTH=165 |
| Eucgr.A01720.1 | 8,57 | 0,69 | 0,78 | 1,00 | 3,94 | AT1G01380.1 \| Symbols: ETC1 \| Homeodomain-like superfamily protein \| chr1:147267-147740 FORWARD LENGTH=83 |
| Eucgr.F03729.1 | 0,77 | 0,03 | 0,07 | 0,11 | 0,40 | AT4G08500.1 \| Symbols: MEKK1, ATMEKK1, MAPKKK8, ARAKIN \| MAPK/ERK kinase kinase 1 \| |
| Eucgr.E03922.1 | 7,89 | 119,99 | 97,52 | 76,35 | 18,49 | No hits found |
| Eucgr.H01054.1 | 4,39 | 0,00 | 0,04 | 0,39 | 1,57 | AT4G02090.1 \| Symbols: \| unknown protein; |
| Eucgr.I00191.1 | 18,91 | 304,30 | 179,39 | 171,43 | 32,65 | AT5G64530.1 \| Symbols: ANAC104, XND1 \| xylem NAC domain 1 \| chr5:25795360-25796699 FORWARD LENGTH=187 |
| Eucgr.D01367.1 | 2,05 | 0,00 | 0,00 | 0,00 | 0,62 | AT5G01840.1 \| Symbols: ATOFP1, OFP1 \| ovate family protein 1 \| chr5:324552-325364 FORWARD LENGTH=270 |
| Eucgr.D01770.1 | 9,52 | 146,22 | 130,43 | 116,67 | 25,55 | AT4G24015.1 \| Symbols: \| RING/U-box superfamily protein \| chr4:12469887-12471197 REVERSE LENGTH=174 |
| Eucgr.K02218.1 | 33,80 | 4,07 | 3,06 | 6,15 | 18,24 | No hits found |
| Eucgr.B03813.1 | 16,93 | 52,12 | 51,45 | 58,11 | 24,66 | AT5G22100.1 \| Symbols: \| RNA cyclase family protein \| chr5:7329015-7330718 FORWARD LENGTH=375 |
| Eucgr.J01834.1 | 9,39 | 3,15 | 3,11 | 3,89 | 6,70 | AT3G02820.1 \| Symbols: \| zinc knuckle (CCHC-type) family protein \| chr3:611573-613294 FORWARD LENGTH=282 |
| Eucgr.G01707.1 | 11,60 | 0,20 | 0,68 | 0,95 | 6,59 | AT2G16440.1 \| Symbols: MCM4 \| Minichromosome maintenance (MCM2/3/5) family protein \| |
| Eucgr.H03450.2 | 16,30 | 1,23 | 2,24 | 3,51 | 10,18 | AT3G22550.1 \| Symbols: \| Protein of unknown function (DUF581) \| chr3:7991827-7992805 REVERSE LENGTH=267 |
| Eucgr.K01388.2 | 14,26 | 52,88 | 45,91 | 42,56 | 23,17 | AT5G48240.3 \| Symbols: \| unknown protein; |
| Eucgr.K00903.1 | 0,38 | 3,91 | 4,61 | 3,45 | 1,26 | AT1G03940.1 \| Symbols: \| HXXXD-type acyl-transferase family protein \| chr1:1009542-1010951 REVERSE LENGTH=469 |
| Eucgr.G01683.1 | 15,59 | 1,40 | 2,46 | 3,13 | 10,99 | AT4G34530.1 \| Symbols: CIB1 \| cryptochrome-interacting basic-helix-loop-helix 1 \| |
| Eucgr.I00196.1 | 14,36 | 0,40 | 0,47 | 0,67 | 5,42 | AT1G49780.1 \| Symbols: PUB26 \| plant U-box 26 \| chr1:18429024-18430289 REVERSE LENGTH=421 |
| Eucgr.B02755.1 | 22,23 | 1,12 | 1,22 | 3,87 | 8,75 | AT3G54050.2 \| Symbols: HCEF1 \| high cyclic electron flow 1 \| chr3:20016951-20018527 FORWARD LENGTH=417 |
| Eucgr.D00371.1 | 0,17 | 0,00 | 0,00 | 0,03 | 0,07 | AT4G19090.1 \| Symbols: \| Protein of unknown function (DUF594) \| chr4:10449900-10452757 FORWARD LENGTH=751 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |

| | | | | | | |
|---|---|---|---|---|---|---|
| Eucgr.B00072.1 | 4,34 | 0,24 | 0,30 | 0,28 | 2,65 | AT2G31900.1 \| Symbols: XIF, ATXIF, ATMYO5 \| myosin-like protein XIF \| chr2:13560760-13569623 REVERSE LENGTH=1556 |
| Eucgr.G01052.1 | 19,72 | 2,20 | 3,15 | 4,89 | 13,64 | AT4G17980.1 \| Symbols: anac071, NAC071 \| NAC domain containing protein 71 \| |
| Eucgr.H01669.1 | 5,20 | 0,09 | 0,39 | 0,93 | 2,37 | AT5G67050.1 \| Symbols: \| alpha/beta-Hydrolases superfamily protein \| chr5:26759482-26761165 REVERSE LENGTH=477 |
| Eucgr.G01558.1 | 0,26 | 0,00 | 0,00 | 0,06 | 0,10 | AT5G10770.1 \| Symbols: \| Eukaryotic aspartyl protease family protein \| chr5:3403331-3405331 REVERSE LENGTH=474 |
| Eucgr.D01019.1 | 58,87 | 10,87 | 11,41 | 15,76 | 36,62 | AT3G23290.2 \| Symbols: LSH4 \| Protein of unknown function (DUF640) \| chr3:8326958-8328010 FORWARD LENGTH=195 |
| Eucgr.B00238.2 | 5,78 | 0,61 | 0,51 | 1,16 | 2,96 | AT4G24670.2 \| Symbols: TAR2 \| tryptophan aminotransferase related 2 \| chr4:12727940-12730694 REVERSE LENGTH=440 |
| Eucgr.H05117.4 | 3,47 | 0,98 | 0,88 | 1,11 | 2,44 | AT5G63860.1 \| Symbols: UVR8 \| Regulator of chromosome condensation (RCC1) family protein \| |
| Eucgr.F01643.1 | 3,53 | 0,00 | 0,17 | 0,36 | 2,30 | AT1G75710.1 \| Symbols: \| C2H2-like zinc finger protein \| chr1:28428806-28431128 FORWARD LENGTH=462 |
| Eucgr.E04300.1 | 14,03 | 37,96 | 39,12 | 36,51 | 23,84 | AT2G35060.1 \| Symbols: KUP11 \| K+ uptake permease 11 \| chr2:14775184-14778184 REVERSE LENGTH=792 |
| Eucgr.G02143.1 | 0,03 | 4,40 | 1,90 | 1,18 | 0,04 | AT1G14870.1 \| Symbols: PCR2 \| PLANT CADMIUM RESISTANCE 2 \| chr1:5128591-5129458 REVERSE LENGTH=152 |
| Eucgr.H02450.1 | 18,67 | 76,82 | 72,34 | 64,69 | 35,91 | AT1G13160.1 \| Symbols: \| ARM repeat superfamily protein \| chr1:4484634-4488388 FORWARD LENGTH=804 |
| Eucgr.F03668.1 | 39,12 | 1,79 | 5,22 | 7,67 | 22,63 | AT3G44730.1 \| Symbols: ATKP1, KP1 \| kinesin-like protein 1 \| chr3:16285888-16290852 FORWARD LENGTH=1087 |
| Eucgr.D02639.1 | 0,40 | 37,14 | 14,82 | 4,44 | 1,20 | AT5G62150.1 \| Symbols: \| peptidoglycan-binding LysM domain-containing protein \| |
| Eucgr.J01777.2 | 22,81 | 2,90 | 5,14 | 7,05 | 16,94 | AT2G02170.2 \| Symbols: \| Remorin family protein \| chr2:556595-558610 REVERSE LENGTH=486 |
| Eucgr.A01623.1 | 10,29 | 25,55 | 28,96 | 25,95 | 16,84 | AT4G39160.2 \| Symbols: \| Homeodomain-like superfamily protein \| chr4:18236828-18240433 FORWARD LENGTH=624 |
| Eucgr.F04485.1 | 0,10 | 11,70 | 7,83 | 4,51 | 0,42 | AT2G21820.1 \| Symbols: \| unknown protein; |
| Eucgr.K00648.1 | 14,25 | 0,45 | 0,21 | 0,76 | 4,92 | AT5G35740.1 \| Symbols: \| Carbohydrate-binding X8 domain superfamily protein \| |
| Eucgr.K02300.1 | 29,89 | 4,72 | 6,31 | 10,05 | 21,14 | AT3G48750.1 \| Symbols: CDKA;1, CDC2AAT, CDK2, CDC2, CDC2A, CDKA1 \| cell division control 2 \| |
| Eucgr.C01575.1 | 3,50 | 0,09 | 0,11 | 0,09 | 1,44 | AT5G25580.1 \| Symbols: \| unknown protein |
| Eucgr.A00208.1 | 0,02 | 3,66 | 1,60 | 0,24 | 0,06 | AT3G62560.1 \| Symbols: \| Ras-related small GTP-binding family protein \| chr3:23137539-23138880 FORWARD LENGTH=193 |
| Eucgr.D00412.1 | 0,02 | 1,92 | 1,24 | 0,20 | 0,05 | AT5G45690.1 \| Symbols: \| Protein of unknown function (DUF1264) \| chr5:18535139-18536259 REVERSE LENGTH=247 |
| Eucgr.K01851.1 | 0,01 | 0,83 | 0,66 | 0,28 | 0,03 | AT2G41970.1 \| Symbols: \| Protein kinase superfamily protein \| chr2:17520517-17522304 REVERSE LENGTH=365 |
| Eucgr.G03284.1 | 0,01 | 0,88 | 0,67 | 0,79 | 0,04 | AT5G13790.1 \| Symbols: AGL15 \| AGAMOUS-like 15 \| chr5:4449128-4450802 REVERSE LENGTH=268 |
| Eucgr.F00591.1 | 0,02 | 2,18 | 1,55 | 0,20 | 0,05 | AT1G75750.1 \| Symbols: GASA1 \| GAST1 protein homolog 1 \| chr1:28441813-28442284 REVERSE LENGTH=98 |
| Eucgr.A00995.1 | 7,47 | 98,88 | 59,96 | 43,40 | 13,77 | AT2G46940.1 \| Symbols: \| unknown protein; |
| Eucgr.D00583.1 | 16,76 | 0,59 | 0,95 | 1,93 | 8,70 | No hits found |
| Eucgr.H02351.1 | 21,03 | 3,01 | 6,16 | 6,08 | 14,74 | AT5G65710.1 \| Symbols: HSL2 \| HAESA-like 2 \| chr5:26292372-26295440 FORWARD LENGTH=993 |
| Eucgr.K02329.1 | 4,76 | 23,72 | 33,52 | 24,98 | 12,17 | AT1G73380.1 \| Symbols: \| unknown protein; |
| Eucgr.C00156.1 | 19,40 | 0,91 | 1,38 | 2,83 | 12,05 | AT4G30230.1 \| Symbols: \| unknown protein; |
| Eucgr.K02060.1 | 4,73 | 21,67 | 20,39 | 19,59 | 8,75 | AT1G19490.1 \| Symbols: \| Basic-leucine zipper (bZIP) transcription factor family protein \| |
| Eucgr.B02239.1 | 1,35 | 372,30 | 180,88 | 56,90 | 3,52 | AT3G47340.1 \| Symbols: ASN1, DIN6, AT-ASN1 \| glutamine-dependent asparagine synthase 1 \| |

| GENE ID | FPKM | | | | | Annotation |
|---|---|---|---|---|---|---|
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.F02999.1 | 13,23 | 0,37 | 1,71 | 2,57 | 7,82 | AT1G22610.1 \| Symbols: \| C2 calcium/lipid-binding plant phosphoribosyltransferase family protein \| |
| Eucgr.E00446.1 | 10,53 | 0,08 | 0,53 | 0,74 | 4,93 | AT1G62500.1 \| Symbols: \| Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein \| |
| Eucgr.D00059.1 | 7,86 | 22,20 | 23,11 | 21,70 | 12,79 | AT5G18820.1 \| Symbols: EMB3007 \| TCP-1/cpn60 chaperonin family protein \| chr5:6271549-6274153 FORWARD LENGTH=575 |
| Eucgr.F03226.1 | 3,54 | 0,51 | 0,59 | 1,04 | 2,37 | AT3G14740.2 \| Symbols: \| RING/FYVE/PHD zinc finger superfamily protein \| chr3:4952185-4953306 REVERSE LENGTH=343 |
| Eucgr.D02618.1 | 18,64 | 41,27 | 44,62 | 39,80 | 29,03 | AT4G31120.1 \| Symbols: SKB1, ATPRMT5 \| SHK1 binding protein 1 \| chr4:15132185-15136568 REVERSE LENGTH=642 |
| Eucgr.A01416.1 | 0,08 | 12,40 | 7,60 | 4,34 | 0,29 | AT4G27670.1 \| Symbols: HSP21 \| heat shock protein 21 \| chr4:13819048-13819895 REVERSE LENGTH=227 |
| Eucgr.E02733.1 | 0,90 | 0,00 | 0,03 | 0,02 | 0,40 | AT3G49340.1 \| Symbols: \| Cysteine proteinases superfamily protein \| chr3:18293347-18294577 REVERSE LENGTH=341 |
| Eucgr.B01665.1 | 7,24 | 0,70 | 1,44 | 1,58 | 4,68 | AT3G62630.1 \| Symbols: \| Protein of unknown function (DUF1645) \| chr3:23163937-23165079 REVERSE LENGTH=380 |
| Eucgr.F01247.1 | 62,51 | 5,65 | 5,19 | 8,11 | 34,14 | AT1G78780.2 \| Symbols: \| pathogenesis-related family protein \| chr1:29621447-29622431 REVERSE LENGTH=238 |
| Eucgr.J01592.1 | 3,62 | 0,18 | 0,17 | 0,45 | 1,49 | AT1G70780.1 \| Symbols: \| unknown protein; |
| Eucgr.F02449.1 | 0,21 | 0,00 | 0,00 | 0,05 | 0,09 | AT1G02390.1 \| Symbols: ATGPAT2, GPAT2 \| glycerol-3-phosphate acyltransferase 2 \| |
| Eucgr.I01944.1 | 0,07 | 1,86 | 2,17 | 1,75 | 0,27 | AT5G39785.1 \| Symbols: \| Protein of unknown function (DUF1666) \| chr5:15929257-15932215 FORWARD LENGTH=606 |
| Eucgr.D01116.1 | 2,47 | 0,11 | 0,03 | 0,18 | 0,78 | AT3G17350.1 \| Symbols: \| unknown protein |
| Eucgr.H02856.1 | 0,36 | 0,00 | 0,01 | 0,00 | 0,15 | AT1G61820.1 \| Symbols: BGLU46 \| beta glucosidase 46 \| chr1:22835452-22838444 FORWARD LENGTH=516 |
| Eucgr.C04122.1 | 13,12 | 1,84 | 1,88 | 3,31 | 7,45 | AT3G24460.1 \| Symbols: \| Serinc-domain containing serine and sphingolipid biosynthesis protein \| |
| Eucgr.I01141.1 | 1,91 | 0,04 | 0,00 | 0,00 | 0,58 | AT5G49730.1 \| Symbols: ATFRO6, FRO6 \| ferric reduction oxidase 6 \| chr5:20201355-20204455 REVERSE LENGTH=738 |
| Eucgr.L00250.1 | 0,08 | 24,46 | 8,06 | 2,35 | 0,03 | AT1G56600.1 \| Symbols: AtGolS2, GolS2 \| galactinol synthase 2 \| chr1:21207620-21209291 FORWARD LENGTH=335 |
| Eucgr.I02395.1 | 36,67 | 7955,76 | 4612,95 | 3696,64 | 424,49 | No hits found |
| Eucgr.I01970.1 | 1,48 | 0,02 | 0,14 | 0,12 | 0,81 | AT3G29060.1 \| Symbols: \| EXS (ERD1/XPR1/SYG1) family protein \| chr3:11044990-11048465 REVERSE LENGTH=800 |
| Eucgr.K02663.1 | 4,01 | 55,92 | 37,45 | 23,69 | 8,00 | AT1G73920.1 \| Symbols: \| alpha/beta-Hydrolases superfamily protein \| chr1:27791194-27794698 FORWARD LENGTH=704 |
| Eucgr.F03947.1 | 12,82 | 0,29 | 0,60 | 0,85 | 5,97 | AT5G25190.1 \| Symbols: \| Integrase-type DNA-binding superfamily protein \| chr5:8707007-8707655 REVERSE LENGTH=181 |
| Eucgr.F02971.1 | 9,35 | 27,60 | 31,49 | 27,79 | 16,25 | AT1G71490.1 \| Symbols: \| Tetratricopeptide repeat (TPR)-like superfamily protein \| |
| Eucgr.G02591.1 | 14,31 | 50,74 | 52,41 | 62,14 | 23,31 | AT5G08520.1 \| Symbols: \| Duplicated homeodomain-like superfamily protein \| chr5:2755470-2757741 REVERSE LENGTH=298 |
| Eucgr.G02992.1 | 2,45 | 0,00 | 0,08 | 0,11 | 1,25 | AT2G37820.1 \| Symbols: \| Cysteine/Histidine-rich C1 domain family protein \| |
| Eucgr.J02002.1 | 13,21 | 0,81 | 0,99 | 1,03 | 6,89 | AT1G07420.1 \| Symbols: ATSMO2, SMO2-1 \| sterol 4-alpha-methyl-oxidase 2-1 \| |
| Eucgr.D02220.1 | 10,52 | 0,86 | 1,06 | 1,60 | 5,86 | AT1G32250.1 \| Symbols: \| Calcium-binding EF-hand family protein \| chr1:11639843-11640343 FORWARD LENGTH=166 |
| Eucgr.H03598.1 | 26,97 | 1,37 | 3,01 | 6,08 | 17,56 | AT3G06145.1 \| Symbols: \| unknown protein; |
| Eucgr.K00264.1 | 1191,00 | 71,53 | 132,92 | 190,87 | 475,74 | AT5G23860.2 \| Symbols: TUB8 \| tubulin beta 8 \| chr5:8042962-8044528 FORWARD LENGTH=449 |
| Eucgr.J02238.1 | 2,25 | 0,29 | 0,13 | 0,21 | 1,36 | AT3G27640.1 \| Symbols: \| Transducin/WD40 repeat-like superfamily protein \| |

| | | | | | | |
|---|---|---|---|---|---|---|
| Eucgr.G03119.1 | 52,32 | 0,71 | 0,44 | 0,43 | 12,97 | AT2G40460.1 \| Symbols: \| Major facilitator superfamily protein \| chr2:16897123-16901171 FORWARD LENGTH=583 |
| Eucgr.B00615.2 | 11,42 | 0,62 | 0,78 | 1,56 | 4,90 | AT1G26355.1 \| Symbols: SP1L1 \| SPIRAL1-like1 \| chr1:9117950-9118611 REVERSE LENGTH=113 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.H00748.1 | 40,86 | 3,51 | 3,54 | 3,08 | 24,78 | AT3G07340.1 \| Symbols: \| basic helix-loop-helix (bHLH) DNA-binding superfamily protein \| |
| Eucgr.L00235.1 | 0,04 | 73,19 | 38,88 | 15,60 | 0,03 | AT1G56600.1 \| Symbols: AtGolS2, GolS2 \| galactinol synthase 2 \| chr1:21207620-21209291 FORWARD LENGTH=335 |
| Eucgr.F01599.1 | 18,17 | 0,64 | 0,62 | 0,66 | 8,13 | AT1G75390.1 \| Symbols: AtbZIP44, bZIP44 \| basic leucine-zipper 44 \| chr1:28292224-28292745 FORWARD LENGTH=173 |
| Eucgr.F00741.2 | 49,64 | 158,03 | 144,26 | 149,25 | 88,78 | AT1G11910.1 \| Symbols: APA1, ATAPA1 \| aspartic proteinase A1 \| chr1:4017119-4019874 REVERSE LENGTH=506 |
| Eucgr.B02318.1 | 3,10 | 0,14 | 0,04 | 0,00 | 1,34 | AT2G29125.1 \| Symbols: RTFL2, DVL13 \| ROTUNDIFOLIA like 2 \| chr2:12523472-12523819 FORWARD LENGTH=115 |
| Eucgr.I01316.1 | 12,00 | 2,71 | 2,61 | 4,89 | 7,64 | AT4G34660.1 \| Symbols: \| SH3 domain-containing protein \| chr4:16545595-16548294 REVERSE LENGTH=368 |
| Eucgr.A01602.1 | 45,92 | 4,95 | 10,83 | 17,13 | 31,40 | AT1G63300.1 \| Symbols: \| Myosin heavy chain-related protein \| chr1:23482193-23486067 FORWARD LENGTH=1029 |
| Eucgr.K01496.1 | 0,04 | 0,59 | 1,21 | 2,78 | 0,02 | AT1G55370.2 \| Symbols: NDF5 \| NDH-dependent cyclic electron flow 5 \| chr1:20674852-20676071 FORWARD LENGTH=354 |
| Eucgr.K01352.1 | 338,38 | 22,20 | 30,35 | 15,76 | 184,16 | AT3G22120.1 \| Symbols: CWLP \| cell wall-plasma membrane linker protein \| chr3:7795283-7796287 REVERSE LENGTH=334 |
| Eucgr.E02410.1 | 0,00 | 32,77 | 24,51 | 6,33 | 0,10 | AT1G07900.1 \| Symbols: LBD1 \| LOB domain-containing protein 1 \| chr1:2442624-2443631 FORWARD LENGTH=190 |
| Eucgr.L03254.1 | 0,00 | 2,32 | 1,51 | 0,40 | 0,04 | AT1G73190.1 \| Symbols: ALPHA-TIP, TIP3;1 \| Aquaporin-like superfamily protein \| |
| Eucgr.B03510.1 | 9,53 | 159,19 | 65,25 | 39,11 | 19,24 | AT3G48660.1 \| Symbols: \| Protein of unknown function (DUF 3339) \| chr3:18029659-18030133 FORWARD LENGTH=89 |
| Eucgr.I01142.1 | 4,35 | 0,03 | 0,08 | 0,03 | 1,54 | AT5G49740.1 \| Symbols: ATFRO7, FRO7 \| ferric reduction oxidase 7 \| chr5:20205549-20208628 REVERSE LENGTH=747 |
| Eucgr.E03147.1 | 2,67 | 26,90 | 16,87 | 14,49 | 6,25 | AT3G47160.2 \| Symbols: \| RING/U-box superfamily protein \| chr3:17360238-17361879 REVERSE LENGTH=257 |
| Eucgr.D01150.1 | 2,55 | 0,06 | 0,09 | 0,39 | 1,38 | AT2G44580.1 \| Symbols: \| zinc ion binding \| chr2:18402081-18403412 REVERSE LENGTH=386 |
| Eucgr.F03300.1 | 13,76 | 1,85 | 1,93 | 2,95 | 7,82 | AT5G53900.2 \| Symbols: \| Serine/threonine-protein kinase WNK (With No Lysine)-related |
| Eucgr.G02154.1 | 0,09 | 3,17 | 1,68 | 1,45 | 0,05 | AT1G14870.1 \| Symbols: PCR2 \| PLANT CADMIUM RESISTANCE 2 \| chr1:5128591-5129458 REVERSE LENGTH=152 |
| Eucgr.B03746.1 | 45,97 | 0,29 | 0,54 | 0,50 | 12,30 | AT5G07990.1 \| Symbols: TT7, CYP75B1, D501 \| Cytochrome P450 superfamily protein \| |
| Eucgr.E04058.1 | 36,99 | 2,23 | 1,91 | 2,85 | 62,13 | No hits found |
| Eucgr.B02749.1 | 5,57 | 1,08 | 1,14 | 1,82 | 4,23 | AT4G03120.1 \| Symbols: \| C2H2 and C2HC zinc fingers superfamily protein \| chr4:1385747-1387331 FORWARD LENGTH=207 |
| Eucgr.E01278.1 | 25,24 | 2,15 | 3,90 | 6,43 | 18,03 | AT3G07040.1 \| Symbols: RPM1, RPS3 \| NB-ARC domain-containing disease resistance protein \| |
| Eucgr.B00857.1 | 5,71 | 19,53 | 23,20 | 19,36 | 10,32 | AT3G18100.1 \| Symbols: MYB4R1, AtMYB4R1 \| myb domain protein 4r1 \| chr3:6200689-6204583 FORWARD LENGTH=847 |
| Eucgr.A00596.1 | 1,52 | 9,49 | 13,79 | 14,11 | 3,29 | AT2G38290.1 \| Symbols: ATAMT2, AMT2;1, AMT2 \| ammonium transporter 2 |
| Eucgr.B00330.1 | 24,60 | 0,65 | 2,92 | 6,17 | 15,66 | AT1G12220.2 \| Symbols: RPS5 \| Disease resistance protein (CC-NBS-LRR class) family \| |
| Eucgr.G03123.1 | 1,81 | 0,08 | 0,04 | 0,05 | 0,81 | AT5G05330.1 \| Symbols: \| HMG-box (high mobility group) DNA-binding family protein \| |
| Eucgr.I02361.1 | 5,43 | 55,55 | 51,56 | 32,51 | 12,50 | No hits found |
| Eucgr.E03059.1 | 3,55 | 0,42 | 0,23 | 0,37 | 1,85 | No hits found |

| | | | | | | |
|---|---|---|---|---|---|---|
| Eucgr.B02000.1 | 31,38 | 0,43 | 0,84 | 2,08 | 13,48 | AT1G72210.1 \| Symbols: \| basic helix-loop-helix (bHLH) DNA-binding superfamily protein \| |
| Eucgr.F03538.2 | 110,08 | 2,56 | 3,99 | 4,35 | 61,28 | AT1G76160.1 \| Symbols: sks5 \| SKU5 similar 5 \| chr1:28578211-28581020 REVERSE LENGTH=541 |
| Eucgr.B00523.1 | 77,15 | 4,49 | 6,63 | 14,78 | 44,66 | AT3G47470.1 \| Symbols: LHCA4, CAB4 \| light-harvesting chlorophyll-protein complex I subunit A4 \| |
| Eucgr.J01663.1 | 97,41 | 1,21 | 1,87 | 3,31 | 75,71 | AT5G13870.1 \| Symbols: EXGT-A4, XTH5 \| xyloglucan endotransglucosylase/hydrolase 5 \| |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.F03555.1 | 13,95 | 1,61 | 1,58 | 2,17 | 7,86 | No hits found |
| Eucgr.A02867.1 | 21,50 | 77,97 | 60,27 | 57,79 | 33,36 | AT5G62200.1 \| Symbols: \| Embryo-specific protein 3, (ATS3) \| chr5:24984463-24985674 REVERSE LENGTH=190 |
| Eucgr.H02220.1 | 18,05 | 0,74 | 0,78 | 1,29 | 10,03 | AT1G47128.1 \| Symbols: RD21, RD21A \| Granulin repeat cysteine protease family protein \| |
| Eucgr.D00363.1 | 0,44 | 0,09 | 0,04 | 0,09 | 0,24 | AT5G45470.1 \| Symbols: \| Protein of unknown function (DUF594) \| chr5:18422164-18424764 REVERSE LENGTH=866 |
| Eucgr.I01755.1 | 2,80 | 56,99 | 38,16 | 17,61 | 1,21 | AT5G40390.1 \| Symbols: SIP1 \| Raffinose synthase family protein \| chr5:16161720-16165085 FORWARD LENGTH=783 |
| Eucgr.H03017.2 | 43,78 | 3,51 | 4,59 | 5,87 | 21,12 | AT3G23410.1 \| Symbols: ATFAO3, FAO3 \| fatty alcohol oxidase 3 \| chr3:8382860-8386024 FORWARD LENGTH=746 |
| Eucgr.H02628.2 | 25,01 | 3,03 | 4,72 | 4,59 | 16,98 | AT5G48560.1 \| Symbols: \| basic helix-loop-helix (bHLH) DNA-binding superfamily protein \| |
| Eucgr.G02193.1 | 4,85 | 0,09 | 0,39 | 0,56 | 2,25 | AT2G01340.1 \| Symbols: At17.1 \| Encodes a protein whose expression is responsive to nematode infection. \| |
| Eucgr.G02743.1 | 1,23 | 16,29 | 14,12 | 10,00 | 2,99 | AT5G03530.1 \| Symbols: ATRAB ALPHA, ATRAB, ATRAB18B, ATRABC2A, RABC2A \| RAB GTPase homolog C2A \| |
| Eucgr.J00363.1 | 88,68 | 3,76 | 16,43 | 29,57 | 53,35 | AT5G41040.1 \| Symbols: \| HXXXD-type acyl-transferase family protein \| chr5:16431448-16433086 FORWARD LENGTH=457 |
| Eucgr.C00061.1 | 7,18 | 0,77 | 0,94 | 0,91 | 3,86 | AT2G07170.1 \| Symbols: \| ARM repeat superfamily protein \| chr2:2975565-2978692 FORWARD LENGTH=820 |
| Eucgr.F01455.1 | 36,69 | 6,23 | 9,26 | 12,83 | 29,36 | AT5G45030.2 \| Symbols: \| Trypsin family protein \| chr5:18172981-18175238 FORWARD LENGTH=607 |
| Eucgr.L03276.1 | 1,64 | 0,10 | 0,00 | 0,40 | 0,66 | No hits found |
| Eucgr.C03867.1 | 6,81 | 0,81 | 1,11 | 1,30 | 3,93 | AT3G24460.1 \| Symbols: \| Serinc-domain containing serine and sphingolipid biosynthesis protein \| |
| Eucgr.I02197.1 | 15,27 | 1,38 | 2,05 | 1,80 | 10,08 | AT1G20925.1 \| Symbols: \| Auxin efflux carrier family protein \| chr1:7289973-7292507 FORWARD LENGTH=472 |
| Eucgr.H01385.1 | 19,50 | 0,96 | 1,35 | 1,75 | 14,54 | AT1G65295.1 \| Symbols: \| unknown protein; |
| Eucgr.J00741.2 | 10,27 | 0,13 | 0,71 | 0,82 | 6,34 | AT3G51950.2 \| Symbols: \| Zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein \| |
| Eucgr.G00858.1 | 0,54 | 0,05 | 0,02 | 0,17 | 0,25 | AT2G34690.1 \| Symbols: ACD11 \| Glycolipid transfer protein (GLTP) family protein |
| Eucgr.I01042.1 | 1,98 | 0,00 | 0,00 | 0,02 | 0,70 | AT2G22990.1 \| Symbols: SNG1, SCPL8 \| sinapoylglucose 1 \| chr2:9786393-9789925 FORWARD LENGTH=433 |
| Eucgr.K00901.1 | 0,83 | 0,03 | 0,98 | 1,18 | 1,51 | AT1G03940.1 \| Symbols: \| HXXXD-type acyl-transferase family protein \| chr1:1009542-1010951 REVERSE LENGTH=469 |
| Eucgr.E03836.1 | 23,59 | 3,23 | 5,20 | 10,23 | 17,29 | AT5G47770.1 \| Symbols: FPS1 \| farnesyl diphosphate synthase 1 \| chr5:19345297-19347415 FORWARD LENGTH=384 |
| Eucgr.D00128.1 | 5,05 | 0,18 | 0,46 | 0,86 | 3,25 | AT4G20940.1 \| Symbols: \| Leucine-rich receptor-like protein kinase family protein \| |
| Eucgr.G02320.1 | 54,05 | 12,58 | 15,55 | 26,78 | 45,51 | AT1G13380.1 \| Symbols: \| Protein of unknown function (DUF1218) \| chr1:4589218-4590362 REVERSE LENGTH=188 |
| Eucgr.J01387.1 | 112,85 | 18,00 | 22,85 | 43,46 | 75,96 | AT1G26355.1 \| Symbols: SP1L1 \| SPIRAL1-like1 \| chr1:9117950-9118611 REVERSE LENGTH=113 |
| Eucgr.H04935.1 | 1,58 | 0,00 | 0,03 | 0,17 | 0,89 | No hits found |

| | | | | | | |
|---|---|---|---|---|---|---|
| Eucgr.J00011.1 | 8,59 | 1,18 | 1,09 | 1,64 | 6,23 | AT3G12530.1 \| Symbols: PSF2 \| PSF2 \| chr3:3972604-3973864 REVERSE LENGTH=210 |
| Eucgr.F04412.1 | 0,55 | 0,06 | 0,02 | 0,00 | 0,25 | AT4G09770.2 \| Symbols: \| TRAF-like family protein \| chr4:6154534-6155859 REVERSE LENGTH=297 |
| Eucgr.E00641.1 | 1,91 | 0,00 | 0,03 | 0,24 | 0,84 | AT3G61460.1 \| Symbols: BRH1 \| brassinosteroid-responsive RING-H2 \| chr3:22741701-22742213 REVERSE LENGTH=170 |
| Eucgr.I01393.1 | 2,27 | 156,93 | 131,40 | 134,97 | 6,62 | AT2G17880.1 \| Symbols: \| Chaperone DnaJ-domain superfamily protein \| chr2:7767176-7767658 REVERSE LENGTH=160 |
| Eucgr.F04055.2 | 102,46 | 11,17 | 19,96 | 31,01 | 67,83 | AT3G13040.2 \| Symbols: \| myb-like HTH transcriptional regulator family protein \| |
| Eucgr.I01737.1 | 24,79 | 140,09 | 119,59 | 108,71 | 45,70 | AT5G14500.1 \| Symbols: \| aldose 1-epimerase family protein \| chr5:4674503-4676368 REVERSE LENGTH=306 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.K02704.1 | 0,05 | 0,88 | 0,69 | 0,56 | 0,06 | AT5G50700.1 \| Symbols: HSD1 \| hydroxysteroid dehydrogenase 1 \| chr5:20623259-20624995 REVERSE LENGTH=349 |
| Eucgr.B01107.1 | 170,31 | 16,77 | 31,62 | 65,19 | 105,63 | AT3G06035.1 \| Symbols: \| Glycoprotein membrane precursor GPI-anchored \| chr3:1823172-1824110 REVERSE LENGTH=200 |
| Eucgr.F02909.1 | 0,66 | 0,00 | 0,02 | 0,03 | 1,35 | AT1G65920.1 \| Symbols: \| Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain \| |
| Eucgr.G01970.1 | 1,27 | 12,23 | 6,28 | 3,64 | 2,57 | AT5G13330.1 \| Symbols: Rap2.6L \| related to AP2 6l \| chr5:4272384-4274461 FORWARD LENGTH=212 |
| Eucgr.E00177.1 | 2,68 | 12,37 | 11,79 | 9,56 | 4,38 | AT1G01770.1 \| Symbols: \| unknown protein; |
| Eucgr.J01448.1 | 293,20 | 54,21 | 46,52 | 29,50 | 177,22 | AT3G25572.1 \| Symbols: CPuORF11 \| conserved peptide upstream open reading frame 11 \| |
| Eucgr.H04687.1 | 0,92 | 0,00 | 0,00 | 0,02 | 0,32 | AT1G24430.1 \| Symbols: \| HXXXD-type acyl-transferase family protein \| chr1:8658190-8659497 REVERSE LENGTH=435 |
| Eucgr.J00984.1 | 5,33 | 0,07 | 0,16 | 0,51 | 2,90 | AT3G10080.1 \| Symbols: \| RmlC-like cupins superfamily protein \| chr3:3107476-3108159 REVERSE LENGTH=227 |
| Eucgr.H04601.1 | 5,36 | 0,12 | 0,72 | 2,17 | 2,67 | AT5G14070.1 \| Symbols: ROXY2 \| Thioredoxin superfamily protein \| chr5:4541915-4542337 FORWARD LENGTH=140 |
| Eucgr.H00446.1 | 12,90 | 0,94 | 1,77 | 3,32 | 8,62 | AT5G12890.1 \| Symbols: \| UDP-Glycosyltransferase superfamily protein \| chr5:4069658-4071124 REVERSE LENGTH=488 |
| Eucgr.I02753.1 | 49,34 | 6,76 | 9,82 | 18,33 | 37,24 | AT1G58070.1 \| Symbols: \| unknown protein; |
| Eucgr.C03749.1 | 2,33 | 14,24 | 13,94 | 10,11 | 5,14 | AT1G35190.2 \| Symbols: \| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein \| |
| Eucgr.C03181.1 | 30,87 | 83,50 | 73,81 | 89,50 | 25,44 | AT5G20885.1 \| Symbols: \| RING/U-box superfamily protein \| chr5:7084133-7084663 REVERSE LENGTH=176 |
| Eucgr.L00245.1 | 1,83 | 287,87 | 164,66 | 80,81 | 5,28 | AT1G56600.1 \| Symbols: AtGolS2, GolS2 \| galactinol synthase 2 \| chr1:21207620-21209291 FORWARD LENGTH=335 |
| Eucgr.H02635.1 | 6,82 | 0,04 | 0,35 | 0,43 | 3,64 | AT3G23740.1 \| Symbols: \| unknown protein; |
| Eucgr.J01371.2 | 4,99 | 0,70 | 1,03 | 1,45 | 3,69 | AT5G15530.1 \| Symbols: BCCP2, CAC1-B \| biotin carboxyl carrier protein 2 \| chr5:5038955-5040437 FORWARD LENGTH=255 |
| Eucgr.H01080.1 | 0,60 | 6,95 | 6,64 | 8,41 | 1,61 | AT1G24020.2 \| Symbols: MLP423 \| MLP-like protein 423 \| chr1:8500653-8501458 REVERSE LENGTH=155 |
| Eucgr.I01757.1 | 1,24 | 15,94 | 10,85 | 4,78 | 0,59 | AT5G40390.1 \| Symbols: SIP1 \| Raffinose synthase family protein \| chr5:16161720-16165085 FORWARD LENGTH=783 |
| Eucgr.L03103.1 | 4,74 | 0,00 | 0,09 | 0,47 | 2,39 | AT1G12663.1 \| Symbols: \| Predicted to encode a PR (pathogenesis-related) protein. |
| Eucgr.L02809.1 | 3,37 | 0,21 | 0,81 | 1,00 | 2,25 | AT5G26910.1 \| Symbols: \| unknown protein; |
| Eucgr.D02595.1 | 93,74 | 5,16 | 8,96 | 13,91 | 65,47 | AT4G19120.2 \| Symbols: ERD3 \| S-adenosyl-L-methionine-dependent methyltransferases superfamily protein \| |
| Eucgr.G02484.1 | 8,11 | 0,04 | 0,24 | 0,38 | 4,24 | AT1G26761.1 \| Symbols: \| Arabinanase/levansucrase/invertase \| chr1:9250269-9251603 REVERSE LENGTH=444 |
| Eucgr.D01668.1 | 63,62 | 0,94 | 2,21 | 3,72 | 41,65 | AT1G32860.1 \| Symbols: \| Glycosyl hydrolase superfamily protein \| chr1:11907308-11908803 REVERSE LENGTH=426 |

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|---|---|---|---|---|---|---|
| Eucgr.H03535.1 | 23,32 | 2,21 | 3,07 | 2,75 | 17,46 | AT3G22400.1 \| Symbols: LOX5 \| PLAT/LH2 domain-containing lipoxygenase family protein \| |
| Eucgr.H03413.1 | 0,22 | 9,42 | 7,54 | 6,04 | 0,54 | AT2G26400.1 \| Symbols: ARD, ATARD3, ARD3 \| acireductone dioxygenase 3 \| chr2:11232058-11233274 REVERSE LENGTH=199 |
| Eucgr.H01468.1 | 26,78 | 2,36 | 3,11 | 4,58 | 19,24 | AT3G04860.1 \| Symbols: \| Plant protein of unknown function (DUF868) \| chr3:1339349-1340218 REVERSE LENGTH=289 |
| Eucgr.B01196.1 | 1,29 | 0,02 | 0,09 | 0,32 | 0,68 | AT3G52970.1 \| Symbols: CYP76G1 \| cytochrome P450, family 76, subfamily G, polypeptide 1 \| |
| Eucgr.I00200.3 | 47,74 | 3,92 | 3,37 | 6,51 | 24,57 | AT5G64040.1 \| Symbols: PSAN \| photosystem I reaction center subunit PSI-N, chloroplast, putative / PSI-N, putative (PSAN) \| |
| Eucgr.E03364.1 | 30,20 | 0,87 | 0,81 | 1,36 | 17,97 | AT1G11120.2 \| Symbols: \| unknown protein; |
| Eucgr.K02869.1 | 32,32 | 4,32 | 8,35 | 11,07 | 25,57 | AT3G48040.1 \| Symbols: ARAC8, ATROP10, ROP10, ATRAC8 \| RHO-related protein from plants 10 |
| Eucgr.K02974.1 | 109,96 | 5,80 | 13,01 | 25,21 | 62,01 | AT5G01360.1 \| Symbols: TBL3 \| Plant protein of unknown function (DUF828) \| chr5:147608-149316 REVERSE LENGTH=434 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.C02732.1 | 33,22 | 0,68 | 2,05 | 3,07 | 23,80 | AT2G25270.1 \| Symbols: \| unknown protein; |
| Eucgr.C00797.1 | 72,88 | 7,59 | 11,44 | 10,90 | 34,37 | AT2G05920.1 \| Symbols: \| Subtilase family protein \| chr2:2269831-2272207 REVERSE LENGTH=754 |
| Eucgr.G02493.1 | 13,14 | 4,01 | 3,24 | 2,52 | 19,02 | AT5G39660.2 \| Symbols: CDF2 \| cycling DOF factor 2 \| chr5:15878920-15880712 FORWARD LENGTH=457 |
| Eucgr.J00105.1 | 2,70 | 20,19 | 18,01 | 14,17 | 5,09 | AT2G38560.1 \| Symbols: TFIIS \| transcript elongation factor IIS \| chr2:16134802-16136319 FORWARD LENGTH=378 |
| Eucgr.H01622.1 | 0,31 | 0,00 | 0,00 | 0,02 | 0,14 | AT4G12910.1 \| Symbols: scpl20 \| serine carboxypeptidase-like 20 \| chr4:7550576-7553051 REVERSE LENGTH=497 |
| Eucgr.A01860.1 | 6,07 | 0,07 | 0,25 | 0,34 | 3,31 | AT5G46090.1 \| Symbols: \| Protein of unknown function (DUF679) \| chr5:18693485-18694129 FORWARD LENGTH=214 |
| Eucgr.F03309.1 | 1,53 | 0,00 | 0,04 | 0,57 | 0,85 | AT5G53850.2 \| Symbols: \| haloacid dehalogenase-like hydrolase family protein \| |
| Eucgr.D01819.1 | 80,34 | 4,38 | 7,93 | 13,49 | 59,59 | AT1G63910.1 \| Symbols: AtMYB103, MYB103 \| myb domain protein 103 \| chr1:23719968-23721625 REVERSE LENGTH=370 |
| Eucgr.B02453.1 | 13,56 | 1,98 | 3,25 | 3,47 | 10,76 | AT2G28550.3 \| Symbols: RAP2.7 \| related to AP2.7 \| chr2:12226168-12228251 REVERSE LENGTH=464 |
| Eucgr.K01387.2 | 3,33 | 26,78 | 22,63 | 18,02 | 2,56 | AT3G07650.4 \| Symbols: COL9 \| CONSTANS-like 9 \| chr3:2442494-2443901 FORWARD LENGTH=372 |
| Eucgr.I02211.1 | 1,65 | 70,32 | 142,40 | 284,67 | 0,90 | AT1G20823.1 \| Symbols: \| RING/U-box superfamily protein \| chr1:7238880-7239473 FORWARD LENGTH=197 |
| Eucgr.C00728.1 | 38,12 | 1,77 | 4,02 | 6,06 | 26,18 | AT1G02180.1 \| Symbols: \| ferredoxin-related \| chr1:413619-414505 REVERSE LENGTH=226 |
| Eucgr.B03079.1 | 0,46 | 7,39 | 8,38 | 9,72 | 1,15 | AT1G13480.1 \| Symbols: \| Protein of unknown function (DUF1262) \| chr1:4622783-4624043 REVERSE LENGTH=387 |
| Eucgr.L01116.1 | 3,48 | 0,20 | 0,43 | 0,79 | 2,08 | AT5G44530.1 \| Symbols: \| Subtilase family protein \| chr5:17937931-17941193 FORWARD LENGTH=840 |
| Eucgr.B03117.1 | 4,21 | 0,11 | 0,15 | 0,41 | 2,33 | No hits found |
| Eucgr.K03327.1 | 2,94 | 7,53 | 10,15 | 7,92 | 5,01 | AT3G63340.2 \| Symbols: \| Protein phosphatase 2C family protein \| chr3:23392181-23397999 REVERSE LENGTH=1075 |
| Eucgr.D01344.1 | 9,02 | 0,04 | 0,07 | 0,04 | 4,47 | AT4G22010.1 \| Symbols: sks4 \| SKU5 similar 4 \| chr4:11663429-11666463 FORWARD LENGTH=541 |
| Eucgr.D00234.3 | 23,67 | 0,91 | 0,97 | 3,13 | 10,72 | AT1G30380.1 \| Symbols: PSAK \| photosystem I subunit K \| chr1:10722325-10723013 FORWARD LENGTH=130 |
| Eucgr.H01314.3 | 81,51 | 4,51 | 13,74 | 28,23 | 51,70 | AT1G56720.3 \| Symbols: \| Protein kinase superfamily protein \| chr1:21263630-21265559 REVERSE LENGTH=492 |
| Eucgr.K03183.1 | 1,01 | 0,00 | 0,28 | 0,35 | 1,90 | AT2G37330.1 \| Symbols: ALS3 \| aluminum sensitive 3 \| chr2:15669190-15670172 FORWARD LENGTH=273 |
| Eucgr.B03111.1 | 6,22 | 0,15 | 0,91 | 1,39 | 3,83 | AT3G30380.2 \| Symbols: \| alpha/beta-Hydrolases superfamily protein \| chr3:11974424-11976571 FORWARD LENGTH=377 |

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|---|---|---|---|---|---|---|
| Eucgr.K01639.1 | 47,77 | 8,08 | 7,88 | 10,74 | 38,75 | AT3G57040.1 \| Symbols: ARR9, ATRR4 \| response regulator 9 \| chr3:21110059-21111228 FORWARD LENGTH=234 |
| Eucgr.K01853.1 | 15,53 | 0,92 | 1,43 | 1,67 | 10,58 | AT3G58060.1 \| Symbols: \| Cation efflux family protein \| chr3:21497778-21499676 REVERSE LENGTH=411 |
| Eucgr.E02504.1 | 2,20 | 0,00 | 0,09 | 0,13 | 1,42 | No hits found |
| Eucgr.C00826.1 | 13,21 | 0,89 | 0,69 | 0,73 | 9,60 | AT1G22640.1 \| Symbols: ATMYB3, MYB3 \| myb domain protein 3 \| chr1:8006289-8007219 FORWARD LENGTH=257 |
| Eucgr.I02368.2 | 31,02 | 10,48 | 7,28 | 6,84 | 45,32 | AT4G38960.1 \| Symbols: \| B-box type zinc finger family protein \| chr4:18161576-18163045 FORWARD LENGTH=183 |
| Eucgr.I01572.1 | 2,80 | 0,46 | 0,51 | 0,47 | 1,99 | AT3G26680.3 \| Symbols: SNM1 \| DNA repair metallo-beta-lactamase family protein \| |
| Eucgr.F01077.1 | 50,23 | 2,67 | 3,23 | 4,98 | 29,15 | AT5G54270.1 \| Symbols: LHCB3, LHCB3*1 \| light-harvesting chlorophyll B-binding protein 3 \| |
| Eucgr.H02038.1 | 1,00 | 0,00 | 0,02 | 0,21 | 0,55 | AT5G42930.1 \| Symbols: \| alpha/beta-Hydrolases superfamily protein \| chr5:17210738-17214152 REVERSE LENGTH=467 |
| Eucgr.K00655.1 | 13,42 | 1,65 | 2,00 | 2,91 | 9,97 | AT2G05160.1 \| Symbols: \| CCCH-type zinc fingerfamily protein with RNA-binding domain \| |
| Eucgr.I00574.2 | 13,15 | 1,29 | 2,31 | 2,03 | 11,55 | AT2G22620.1 \| Symbols: \| Rhamnogalacturonate lyase family protein \| chr2:9604902-9610156 REVERSE LENGTH=677 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.H03420.1 | 59,57 | 1,15 | 1,08 | 1,40 | 23,29 | AT3G51895.1 \| Symbols: SULTR3;1, AST12 \| sulfate transporter 3;1 \| chr3:19251503-19255677 REVERSE LENGTH=658 |
| Eucgr.B03112.1 | 90,16 | 4,80 | 18,07 | 34,72 | 60,93 | AT1G13635.2 \| Symbols: \| DNA glycosylase superfamily protein \| chr1:4674248-4675784 FORWARD LENGTH=311 |
| Eucgr.D01901.1 | 0,59 | 11,36 | 5,67 | 3,21 | 1,34 | AT5G59220.1 \| Symbols: HAI1 \| highly ABA-induced PP2C gene 1 \| chr5:23894672-23896497 REVERSE LENGTH=413 |
| Eucgr.D01065.1 | 5,47 | 0,67 | 0,56 | 1,04 | 3,52 | AT1G08930.2 \| Symbols: ERD6 \| Major facilitator superfamily protein \| chr1:2873604-2876979 FORWARD LENGTH=496 |
| Eucgr.A01383.1 | 0,43 | 8,83 | 7,37 | 5,16 | 0,99 | AT4G12680.1 \| Symbols: \| unknown protein; |
| Eucgr.K00892.1 | 1,68 | 0,00 | 0,02 | 0,02 | 0,77 | AT1G18010.1 \| Symbols: \| Major facilitator superfamily protein \| chr1:6199980-6201359 FORWARD LENGTH=459 |
| Eucgr.E00800.1 | 24,98 | 2,16 | 4,34 | 7,41 | 38,51 | AT2G46150.1 \| Symbols: \| Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family \| |
| Eucgr.B00458.1 | 92,46 | 9,79 | 21,72 | 35,60 | 60,49 | AT1G74690.1 \| Symbols: IQD31 \| IQ-domain 31 \| chr1:28061498-28063924 REVERSE LENGTH=587 |
| Eucgr.H01946.1 | 2,08 | 8,74 | 16,45 | 8,26 | 4,46 | AT3G50380.1 \| Symbols: \| Protein of unknown function (DUF1162) \| chr3:18686527-18700533 REVERSE LENGTH=3072 |
| Eucgr.K03248.1 | 6,20 | 185,16 | 141,68 | 125,30 | 13,51 | AT2G28400.1 \| Symbols: \| Protein of unknown function, DUF584 \| chr2:12148513-12149001 REVERSE LENGTH=162 |
| Eucgr.G02119.1 | 120,61 | 17,32 | 38,68 | 69,41 | 90,39 | AT1G14870.1 \| Symbols: PCR2 \| PLANT CADMIUM RESISTANCE 2 \| chr1:5128591-5129458 REVERSE LENGTH=152 |
| Eucgr.K00177.1 | 2,04 | 0,00 | 0,04 | 0,05 | 0,95 | AT1G65680.1 \| Symbols: ATEXPB2, EXPB2, ATHEXP BETA 1.4 \| expansin B2 \| |
| Eucgr.J01893.1 | 23,61 | 0,43 | 0,97 | 1,32 | 13,26 | AT2G30010.1 \| Symbols: TBL45 \| TRICHOME BIREFRINGENCE-LIKE 45 \| chr2:12805833-12809226 FORWARD LENGTH=398 |
| Eucgr.J00309.1 | 2,26 | 0,04 | 0,16 | 0,49 | 1,74 | AT3G03770.2 \| Symbols: \| Leucine-rich repeat protein kinase family protein \| chr3:945303-948436 REVERSE LENGTH=802 |
| Eucgr.E00644.1 | 2,51 | 0,05 | 0,08 | 0,06 | 1,45 | AT3G05170.1 \| Symbols: \| Phosphoglycerate mutase family protein \| chr3:1466738-1468219 FORWARD LENGTH=316 |
| Eucgr.J02976.1 | 1,02 | 0,06 | 0,03 | 0,10 | 0,50 | AT1G79890.1 \| Symbols: \| RAD3-like DNA-binding helicase protein \| chr1:30048655-30052203 FORWARD LENGTH=882 |
| Eucgr.D01294.1 | 10,82 | 1,01 | 1,54 | 1,66 | 7,36 | AT1G11545.1 \| Symbols: XTH8 \| xyloglucan endotransglucosylase/hydrolase 8 \| chr1:3878689-3880286 REVERSE LENGTH=305 |
| Eucgr.B01744.1 | 0,34 | 0,00 | 0,02 | 0,13 | 0,18 | AT5G54160.1 \| Symbols: ATOMT1, OMT1 \| O-methyltransferase 1 \| chr5:21982075-21984167 FORWARD LENGTH=363 |
| Eucgr.A02802.1 | 0,30 | 11,17 | 20,62 | 25,92 | 0,14 | No hits found |

| | | | | | | |
|---|---|---|---|---|---|---|
| Eucgr.A02803.1 | 0,02 | 2,72 | 2,87 | 3,18 | 0,00 | No hits found |
| Eucgr.I01808.1 | 0,03 | 1,35 | 1,33 | 0,98 | 0,00 | AT1G23740.1 \| Symbols: \| Oxidoreductase, zinc-binding dehydrogenase family protein \| |
| Eucgr.J00290.1 | 85,69 | 14,15 | 29,81 | 56,15 | 76,26 | AT5G04840.1 \| Symbols: \| bZIP protein \| chr5:1406005-1407648 FORWARD LENGTH=307 |
| Eucgr.J00838.1 | 0,06 | 0,80 | 0,40 | 0,31 | 0,13 | AT1G23030.1 \| Symbols: \| ARM repeat superfamily protein \| chr1:8156745-8158842 FORWARD LENGTH=612 |
| Eucgr.L00241.1 | 0,02 | 8,29 | 5,04 | 1,18 | 0,00 | AT1G56600.1 \| Symbols: AtGolS2, GolS2 \| galactinol synthase 2 \| chr1:21207620-21209291 FORWARD LENGTH=335 |
| Eucgr.F02332.1 | 7,23 | 19,30 | 17,84 | 15,66 | 10,47 | AT3G49180.1 \| Symbols: RID3 \| Transducin/WD40 repeat-like superfamily protein \| |
| Eucgr.H05077.1 | 39,05 | 7,29 | 16,20 | 30,22 | 32,75 | AT3G05270.2 \| Symbols: \| Plant protein of unknown function (DUF869) \| chr3:1500803-1502926 REVERSE LENGTH=615 |
| Eucgr.C00212.1 | 27,23 | 0,59 | 0,67 | 0,98 | 14,51 | AT4G30410.1 \| Symbols: \| sequence-specific DNA binding transcription factors \| |
| Eucgr.F00650.1 | 42,22 | 3,35 | 5,96 | 9,14 | 32,11 | AT5G55230.1 \| Symbols: ATMAP65-1, MAP65-1 \| microtubule-associated proteins 65-1 \| |
| Eucgr.C04173.1 | 39,88 | 12,41 | 10,96 | 16,18 | 35,36 | AT4G17486.1 \| Symbols: \| PPPDE putative thiol peptidase family protein \| chr4:9749992-9751201 REVERSE LENGTH=224 |
| Eucgr.G02236.1 | 7,69 | 21,24 | 21,64 | 19,84 | 11,07 | AT1G49540.1 \| Symbols: ELP2, AtELP2 \| elongator protein 2 \| chr1:18333767-18337382 REVERSE LENGTH=838 |
| Eucgr.A01426.1 | 1,11 | 16,49 | 10,30 | 8,79 | 2,09 | No hits found |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.H04616.1 | 8,31 | 0,40 | 0,52 | 0,64 | 5,00 | AT1G67320.2 \| Symbols: \| DNA primase, large subunit family \| chr1:25205520-25208966 REVERSE LENGTH=454 |
| Eucgr.L01040.1 | 25,93 | 131,16 | 128,06 | 85,19 | 43,84 | AT2G12400.1 \| Symbols: \| unknown protein; |
| Eucgr.J00129.2 | 5,26 | 0,38 | 0,37 | 0,99 | 3,07 | AT3G56290.1 \| Symbols: \| unknown protein; |
| Eucgr.H00366.1 | 108,13 | 13,22 | 11,41 | 12,49 | 62,24 | AT1G06040.1 \| Symbols: STO \| B-box zinc finger family protein \| chr1:1828662-1829659 REVERSE LENGTH=248 |
| Eucgr.D00408.2 | 0,38 | 0,00 | 0,00 | 0,01 | 0,25 | AT5G45650.1 \| Symbols: \| subtilase family protein \| chr5:18513520-18518790 REVERSE LENGTH=791 |
| Eucgr.J01434.1 | 6,83 | 0,06 | 0,19 | 0,44 | 3,55 | No hits found |
| Eucgr.I02455.1 | 14,29 | 1,86 | 1,93 | 2,06 | 10,28 | AT5G66750.1 \| Symbols: DDM1, CHR01, CHR1, CHA1, SOM4, SOM1, ATDDM1 \| chromatin remodeling 1 |
| Eucgr.B03245.1 | 6,37 | 33,40 | 31,78 | 22,98 | 10,70 | AT5G14420.2 \| Symbols: RGLG2 \| RING domain ligase2 \| chr5:4648355-4650563 REVERSE LENGTH=468 |
| Eucgr.I02090.1 | 11,49 | 0,17 | 2,19 | 3,07 | 6,60 | AT3G30530.1 \| Symbols: ATBZIP42, bZIP42 \| basic leucine-zipper 42 \| chr3:12139512-12140033 FORWARD LENGTH=173 |
| Eucgr.F04356.1 | 16,92 | 0,00 | 0,14 | 0,24 | 11,14 | AT1G44760.1 \| Symbols: \| Adenine nucleotide alpha hydrolases-like superfamily protein \| |
| Eucgr.G03317.1 | 4,73 | 0,06 | 0,06 | 0,07 | 2,77 | AT5G12470.1 \| Symbols: \| Protein of unknown function (DUF3411) \| chr5:4044950-4047290 REVERSE LENGTH=386 |
| Eucgr.E02667.1 | 78,18 | 13,06 | 25,76 | 45,74 | 59,90 | AT2G33990.1 \| Symbols: iqd9 \| IQ-domain 9 \| chr2:14360502-14361630 REVERSE LENGTH=263 |
| Eucgr.A01039.1 | 0,89 | 0,00 | 0,03 | 0,04 | 0,53 | AT5G48170.1 \| Symbols: SLY2 \| F-box family protein \| chr5:19532729-19533202 REVERSE LENGTH=157 |
| Eucgr.J02254.1 | 4,42 | 0,71 | 0,43 | 0,46 | 2,51 | AT5G14490.1 \| Symbols: anac085, NAC085 \| NAC domain containing protein 85 \| |
| Eucgr.A00996.1 | 15,85 | 0,99 | 1,76 | 2,42 | 11,61 | AT4G01680.3 \| Symbols: MYB55 \| myb domain protein 55 \| chr4:716401-717415 REVERSE LENGTH=241 |
| Eucgr.A02890.1 | 0,23 | 8,26 | 4,84 | 2,03 | 0,16 | AT5G23950.1 \| Symbols: \| Calcium-dependent lipid-binding (CaLB domain) family protein \| |
| Eucgr.B01827.1 | 5,07 | 0,16 | 0,81 | 1,35 | 3,68 | AT4G01680.3 \| Symbols: MYB55 \| myb domain protein 55 \| chr4:716401-717415 REVERSE LENGTH=241 |

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|---|---|---|---|---|---|---|
| Eucgr.I00052.1 | 5,17 | 0,77 | 0,64 | 0,49 | 8,13 | AT5G08720.1 \| Symbols: \| unknown protein |
| Eucgr.A01373.1 | 2,40 | 16,15 | 18,85 | 18,13 | 4,53 | No hits found |
| Eucgr.D01123.1 | 8,79 | 0,10 | 0,30 | 0,31 | 4,77 | AT3G17350.1 \| Symbols: \| unknown protein; |
| Eucgr.J01758.2 | 14,12 | 1,01 | 0,70 | 1,08 | 9,09 | AT1G55480.1 \| Symbols: ZKT \| protein containing PDZ domain, a K-box domain, and a TPR region \| |
| Eucgr.I00229.1 | 2,36 | 0,08 | 0,08 | 0,16 | 1,34 | No hits found |
| Eucgr.G01772.1 | 67,33 | 1,02 | 3,12 | 4,42 | 40,59 | AT4G38660.1 \| Symbols: \| Pathogenesis-related thaumatin superfamily protein \| |
| Eucgr.D02287.1 | 5,85 | 0,12 | 0,42 | 0,64 | 4,19 | AT1G63650.3 \| Symbols: EGL3 \| basic helix-loop-helix (bHLH) DNA-binding superfamily protein \| |
| Eucgr.F04348.1 | 7,69 | 2,28 | 2,27 | 2,42 | 6,21 | AT1G77580.2 \| Symbols: \| Plant protein of unknown function (DUF869) \| chr1:29144191-29146793 REVERSE LENGTH=779 |
| Eucgr.D00536.1 | 9,72 | 0,76 | 1,09 | 1,87 | 7,05 | AT5G45920.1 \| Symbols: \| SGNH hydrolase-type esterase superfamily protein \| |
| Eucgr.D02360.1 | 7,94 | 0,05 | 0,02 | 0,16 | 3,87 | AT5G53200.1 \| Symbols: TRY \| Homeodomain-like superfamily protein \| chr5:21582913-21583960 FORWARD LENGTH=106 |
| Eucgr.K01100.1 | 0,20 | 27,44 | 17,99 | 3,77 | 0,43 | AT2G42560.1 \| Symbols: \| late embryogenesis abundant domain-containing protein / LEA domain-containing protein \| |
| Eucgr.D02070.1 | 1,27 | 25,95 | 13,55 | 4,74 | 0,68 | AT4G25200.1 \| Symbols: ATHSP23.6-MITO, HSP23.6-MITO \| mitochondrion-localized small heat shock protein 23.6 \| |
| Eucgr.E02892.1 | 0,77 | 0,03 | 0,07 | 0,29 | 0,52 | AT1G17020.1 \| Symbols: SRG1, ATSRG1 \| senescence-related gene 1 \| chr1:5820258-5821741 FORWARD LENGTH=358 |
| Eucgr.F02333.1 | 1,19 | 0,04 | 0,08 | 0,37 | 0,78 | No hits found |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.I01048.1 | 7,39 | 0,30 | 0,43 | 0,43 | 5,01 | AT1G70210.1 \| Symbols: CYCD1;1, ATCYCD1;1 \| CYCLIN D1;1 \| chr1:26440015-26441980 FORWARD LENGTH=339 |
| Eucgr.J02034.1 | 2,07 | 17,67 | 20,57 | 28,18 | 1,51 | No hits found |
| Eucgr.B02872.1 | 4,92 | 0,56 | 1,01 | 1,32 | 3,73 | AT1G15170.1 \| Symbols: \| MATE efflux family protein \| chr1:5220690-5222756 FORWARD LENGTH=481 |
| Eucgr.E03358.1 | 24,39 | 4,93 | 8,11 | 10,91 | 20,70 | AT1G61100.1 \| Symbols: \| disease resistance protein (TIR class), putative \| chr1:22508831-22512122 REVERSE LENGTH=808 |
| Eucgr.K02268.1 | 30,11 | 103,55 | 90,24 | 79,91 | 43,26 | No hits found |
| Eucgr.L01175.1 | 0,63 | 0,04 | 0,06 | 0,25 | 0,44 | AT5G63020.1 \| Symbols: \| Disease resistance protein (CC-NBS-LRR class) family \| |
| Eucgr.J02694.1 | 1,36 | 0,04 | 0,02 | 0,14 | 0,72 | AT5G51260.1 \| Symbols: \| HAD superfamily, subfamily IIIB acid phosphatase \| |
| Eucgr.F00357.1 | 57,27 | 1,46 | 2,05 | 2,82 | 35,06 | AT4G08950.1 \| Symbols: EXO \| Phosphate-responsive 1 family protein \| chr4:5740378-5741322 FORWARD LENGTH=314 |
| Eucgr.K00384.1 | 9,00 | 0,28 | 0,64 | 0,99 | 6,32 | AT4G00990.1 \| Symbols: \| Transcription factor jumonji (jmjC) domain-containing protein \| |
| Eucgr.E02931.1 | 0,11 | 5,24 | 1,25 | 0,63 | 0,26 | AT1G16770.1 \| Symbols: \| unknown protein; |
| Eucgr.J01057.1 | 28,85 | 0,98 | 0,40 | 0,82 | 18,36 | AT3G07510.2 \| Symbols: \| unknown protein; |
| Eucgr.H00037.1 | 1,32 | 0,02 | 0,10 | 0,09 | 0,83 | AT2G01120.1 \| Symbols: ORC4, ATORC4 \| origin recognition complex subunit 4 \| |
| Eucgr.H04541.2 | 31,01 | 2,69 | 7,10 | 13,17 | 24,12 | AT1G28570.1 \| Symbols: \| SGNH hydrolase-type esterase superfamily protein \| |
| Eucgr.G02885.1 | 137,27 | 2,76 | 9,13 | 23,45 | 108,13 | AT1G09070.1 \| Symbols: SRC2, (AT)SRC2 \| soybean gene regulated by cold-2 \| chr1:2927767-2928741 FORWARD LENGTH=324 |
| Eucgr.F02583.1 | 5,14 | 31,22 | 29,00 | 22,63 | 3,68 | AT1G22640.1 \| Symbols: ATMYB3, MYB3 \| myb domain protein 3 \| chr1:8006289-8007219 FORWARD LENGTH=257 |

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|---|---|---|---|---|---|---|
| Eucgr.B00225.1 | 0,00 | 0,17 | 0,21 | 0,08 | 0,00 | AT5G50170.1 \| Symbols: \| C2 calcium/lipid-binding and GRAM domain containing protein \| |
| Eucgr.E00198.1 | 0,02 | 3,23 | 2,24 | 0,60 | 0,00 | AT2G45760.1 \| Symbols: BAP2, BAL \| BON association protein 2 \| chr2:18847125-18847748 REVERSE LENGTH=207 |
| Eucgr.L02067.1 | 0,02 | 1,90 | 1,51 | 0,18 | 0,00 | No hits found |
| Eucgr.F02697.1 | 0,02 | 1,22 | 1,11 | 0,65 | 0,00 | No hits found |
| Eucgr.K00891.1 | 0,60 | 0,02 | 0,02 | 0,01 | 0,36 | AT1G18010.1 \| Symbols: \| Major facilitator superfamily protein \| chr1:6199980-6201359 FORWARD LENGTH=459 |
| Eucgr.G03224.1 | 4,84 | 19,98 | 15,95 | 17,07 | 7,02 | AT3G06730.1 \| Symbols: TRX P, TRX z \| Thioredoxin z \| chr3:2124276-2125845 FORWARD LENGTH=183 |
| Eucgr.D00314.1 | 9,08 | 0,82 | 0,89 | 1,04 | 6,04 | AT5G49010.1 \| Symbols: SLD5 \| DNA replication protein-related \| chr5:19866464-19868074 FORWARD LENGTH=220 |
| Eucgr.E03993.2 | 0,09 | 1,57 | 1,73 | 3,13 | 0,10 | AT4G04330.1 \| Symbols: \| Chaperonin-like RbcX protein \| chr4:2116700-2118563 REVERSE LENGTH=174 |
| Eucgr.I02808.1 | 37,46 | 7,02 | 12,32 | 24,06 | 32,73 | AT2G31930.1 \| Symbols: \| unknown protein; |
| Eucgr.G00660.1 | 6,11 | 15,46 | 16,90 | 15,98 | 8,68 | AT3G26410.1 \| Symbols: TRM11, AtTRM11 \| methyltransferases;nucleic acid binding \| |
| Eucgr.E04327.1 | 11,72 | 0,18 | 0,28 | 0,41 | 7,85 | AT5G44680.1 \| Symbols: \| DNA glycosylase superfamily protein \| chr5:18024461-18025893 REVERSE LENGTH=353 |
| Eucgr.C01374.1 | 3,70 | 0,00 | 0,39 | 0,75 | 6,50 | AT5G52600.1 \| Symbols: AtMYB82, MYB82 \| myb domain protein 82 \| chr5:21343197-21343968 REVERSE LENGTH=201 |
| Eucgr.A02016.1 | 9,94 | 0,13 | 0,85 | 1,93 | 6,84 | AT4G18260.1 \| Symbols: \| Cytochrome b561/ferric reductase transmembrane protein family |
| Eucgr.G02426.1 | 11,24 | 0,16 | 0,50 | 1,03 | 7,23 | AT1G69080.1 \| Symbols: \| Adenine nucleotide alpha hydrolases-like superfamily protein |
| Eucgr.I00735.1 | 53,06 | 0,45 | 0,88 | 0,65 | 36,95 | AT2G39540.1 \| Symbols: \| Gibberellin-regulated family protein \| chr2:16500866-16501241 FORWARD LENGTH=87 |
| Eucgr.J00725.1 | 0,11 | 6,36 | 3,63 | 1,74 | 0,11 | No hits found |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.E01052.1 | 22,26 | 0,53 | 1,73 | 3,34 | 16,27 | AT1G64690.1 \| Symbols: BLT \| branchless trichome \| chr1:24038069-24038890 FORWARD LENGTH=273 |
| Eucgr.K00441.1 | 1,79 | 0,04 | 0,25 | 0,41 | 1,19 | AT5G38280.1 \| Symbols: PR5K \| PR5-like receptor kinase \| chr5:15293325-15295838 REVERSE LENGTH=665 |
| Eucgr.B03158.1 | 0,20 | 3,04 | 2,65 | 1,65 | 0,42 | No hits found |
| Eucgr.G02486.1 | 0,39 | 3,91 | 2,48 | 1,76 | 0,71 | AT1G69490.1 \| Symbols: NAP, ANAC029, ATNAP \| NAC-like, activated by AP3/PI \| |
| Eucgr.F02085.1 | 19,98 | 0,09 | 0,55 | 1,20 | 12,89 | AT1G75590.1 \| Symbols: \| SAUR-like auxin-responsive protein family \| chr1:28383250-28383714 REVERSE LENGTH=154 |
| Eucgr.G02347.5 | 17,99 | 2,45 | 2,54 | 3,97 | 12,90 | AT1G68830.1 \| Symbols: STN7 \| STT7 homolog STN7 \| chr1:25872654-25875473 REVERSE LENGTH=562 |
| Eucgr.I02161.1 | 10,99 | 1,54 | 2,13 | 5,30 | 9,49 | AT3G14280.1 \| Symbols: \| unknown protein; |
| Eucgr.D01725.1 | 1,95 | 0,18 | 0,19 | 0,16 | 1,40 | AT5G41850.1 \| Symbols: \| alpha/beta-Hydrolases superfamily protein \| chr5:16756698-16757791 REVERSE LENGTH=224 |
| Eucgr.H02963.1 | 70,93 | 3,44 | 2,65 | 3,31 | 47,81 | AT2G05620.1 \| Symbols: PGR5 \| proton gradient regulation 5 \| chr2:2081204-2081687 REVERSE LENGTH=133 |
| Eucgr.C00105.1 | 29,83 | 7,01 | 7,08 | 11,79 | 24,54 | AT4G29930.1 \| Symbols: \| basic helix-loop-helix (bHLH) DNA-binding superfamily protein |
| Eucgr.H04382.1 | 22,55 | 1,11 | 3,43 | 4,89 | 18,19 | AT3G04810.2 \| Symbols: ATNEK2, NEK2 \| NIMA-related kinase 2 \| chr3:1318096-1321101 FORWARD LENGTH=606 |
| Eucgr.C00725.1 | 13,96 | 0,00 | 0,16 | 0,35 | 8,81 | AT3G13540.1 \| Symbols: ATMYB5, MYB5 \| myb domain protein 5 \| chr3:4420239-4421443 FORWARD LENGTH=249 |
| Eucgr.C02807.1 | 4,74 | 0,08 | 0,54 | 2,81 | 8,18 | AT3G15680.1 \| Symbols: \| Ran BP2/NZF zinc finger-like superfamily protein \| chr3:5315437-5316048 FORWARD LENGTH=164 |

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|---|---|---|---|---|---|---|
| Eucgr.I01248.1 | 14,63 | 3,98 | 4,37 | 5,55 | 12,42 | AT4G36750.1 \| Symbols: \| Quinone reductase family protein \| chr4:17324642-17326215 FORWARD LENGTH=273 |
| Eucgr.F02320.1 | 101,08 | 0,80 | 3,34 | 5,57 | 85,41 | AT1G46480.1 \| Symbols: WOX4 \| WUSCHEL related homeobox 4 \| chr1:17236903-17237953 REVERSE LENGTH=251 |
| Eucgr.B03435.1 | 2,43 | 0,05 | 0,21 | 0,36 | 1,77 | AT1G26840.1 \| Symbols: ORC6, ATORC6 \| origin recognition complex protein 6 \| |
| Eucgr.K02194.1 | 3,98 | 19,91 | 15,22 | 16,23 | 5,89 | AT5G50930.1 \| Symbols: \| Histone superfamily protein \| chr5:20722069-20724317 FORWARD LENGTH=242 |
| Eucgr.A02563.1 | 12,92 | 1,21 | 1,83 | 3,51 | 10,92 | AT5G01420.1 \| Symbols: \| Glutaredoxin family protein \| chr5:174886-176091 REVERSE LENGTH=401 |
| Eucgr.H01076.1 | 34,40 | 91,65 | 87,28 | 88,04 | 48,24 | AT3G06760.1 \| Symbols: \| Drought-responsive family protein \| chr3:2132971-2134355 FORWARD LENGTH=224 |
| Eucgr.J01082.1 | 42,67 | 2,92 | 7,55 | 12,94 | 33,44 | AT5G03250.1 \| Symbols: \| Phototropic-responsive NPH3 family protein \| chr5:774591-776855 FORWARD LENGTH=592 |
| Eucgr.I00762.1 | 6,66 | 0,81 | 1,22 | 1,77 | 5,56 | AT5G67280.1 \| Symbols: RLK \| receptor-like kinase \| chr5:26842430-26845126 REVERSE LENGTH=751 |
| Eucgr.K00929.1 | 17,01 | 1,98 | 2,92 | 3,77 | 14,14 | AT4G28220.1 \| Symbols: NDB1 \| NAD(P)H dehydrogenase B1 \| chr4:13993078-13995651 FORWARD LENGTH=571 |
| Eucgr.H04081.1 | 78,04 | 0,92 | 1,14 | 1,64 | 49,01 | No hits found |
| Eucgr.K02470.1 | 0,61 | 19,17 | 10,27 | 4,78 | 0,98 | AT3G47600.1 \| Symbols: MYB94, ATMYBCP70, ATMYB94 \| myb domain protein 94 \| |
| Eucgr.J01901.1 | 66,36 | 6,44 | 19,72 | 43,79 | 54,74 | AT3G51780.1 \| Symbols: ATBAG4, BAG4 \| BCL-2-associated athanogene 4 \| chr3:19207029-19208178 REVERSE LENGTH=269 |
| Eucgr.B03203.1 | 0,04 | 1,66 | 1,03 | 0,34 | 0,06 | AT1G69480.1 \| Symbols: \| EXS (ERD1/XPR1/SYG1) family protein \| chr1:26114187-26117479 REVERSE LENGTH=777 |
| Eucgr.G02011.1 | 0,00 | 0,59 | 0,34 | 0,09 | 0,00 | AT4G13420.1 \| Symbols: HAK5, ATHAK5 \| high affinity K+ transporter 5 \| chr4:7797038-7802174 REVERSE LENGTH=785 |
| Eucgr.A00205.1 | 0,00 | 4,14 | 2,98 | 0,70 | 0,00 | AT3G62560.1 \| Symbols: \| Ras-related small GTP-binding family protein \| chr3:23137539-23138880 FORWARD LENGTH=193 |
| Eucgr.F02242.1 | 0,00 | 7,53 | 3,96 | 0,98 | 0,00 | AT1G27461.1 \| Symbols: \| unknown protein; |
| Eucgr.K00224.1 | 0,00 | 0,47 | 0,27 | 0,19 | 0,00 | AT4G23030.1 \| Symbols: \| MATE efflux family protein \| chr4:12072857-12074365 FORWARD LENGTH=502 |
| Eucgr.F01607.1 | 0,00 | 1,71 | 1,16 | 0,04 | 0,00 | AT1G75490.1 \| Symbols: \| Integrase-type DNA-binding superfamily protein \| |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.L03185.1 | 0,00 | 5,78 | 2,76 | 1,18 | 0,00 | AT1G56600.1 \| Symbols: AtGolS2, GolS2 \| galactinol synthase 2 \| chr1:21207620-21209291 FORWARD LENGTH=335 |
| Eucgr.A01560.1 | 0,00 | 1,45 | 2,30 | 1,08 | 0,00 | AT3G10020.2 \| Symbols: \| unknown protein; |
| Eucgr.B01991.1 | 0,00 | 15,76 | 9,07 | 3,42 | 0,00 | AT1G54860.1 \| Symbols: \| Glycoprotein membrane precursor GPI-anchored \| chr1:20457522-20458434 REVERSE LENGTH=200 |
| Eucgr.G00593.1 | 0,00 | 0,57 | 0,11 | 0,00 | 0,00 | AT3G14690.1 \| Symbols: CYP72A15 \| cytochrome P450, family 72, subfamily A, polypeptide 15 \| |
| Eucgr.B01792.1 | 0,00 | 2,16 | 0,51 | 0,00 | 0,00 | AT1G56600.1 \| Symbols: AtGolS2, GolS2 \| galactinol synthase 2 \| chr1:21207620-21209291 FORWARD LENGTH=335 |
| Eucgr.E02621.1 | 0,00 | 4,20 | 2,55 | 0,21 | 0,00 | AT2G18540.1 \| Symbols: \| RmlC-like cupins superfamily protein \| chr2:8042382-8045008 REVERSE LENGTH=707 |
| Eucgr.C00859.1 | 0,00 | 1,60 | 0,83 | 0,28 | 0,00 | AT5G49690.1 \| Symbols: \| UDP-Glycosyltransferase superfamily protein \| chr5:20189968-20191350 REVERSE LENGTH=460 |
| Eucgr.I02269.1 | 0,00 | 9,89 | 1,64 | 0,00 | 0,00 | AT3G12500.1 \| Symbols: ATHCHIB, PR3, PR-3, CHI-B, B-CHI, HCHIB \| basic chitinase \| |
| Eucgr.J00396.1 | 0,00 | 1,28 | 0,82 | 0,48 | 0,00 | AT1G08170.1 \| Symbols: \| Histone superfamily protein \| chr1:2562941-2563672 REVERSE LENGTH=243 |
| Eucgr.F02406.1 | 0,00 | 0,59 | 0,17 | 0,06 | 0,00 | AT4G31940.1 \| Symbols: CYP82C4 \| cytochrome P450, family 82, subfamily C, polypeptide 4 \| |
| Eucgr.E02381.1 | 583,82 | 14,25 | 21,98 | 52,95 | 210,10 | AT2G34430.1 \| Symbols: LHB1B1, LHCB1.4 \| light-harvesting chlorophyll-protein complex II subunit B1 \| |

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|---|---|---|---|---|---|---|
| Eucgr.K03437.1 | 12,80 | 0,59 | 0,65 | 0,65 | 9,94 | No hits found |
| Eucgr.A01301.1 | 9,53 | 21,38 | 24,00 | 24,64 | 12,97 | AT5G11240.1 \| Symbols: \| transducin family protein / WD-40 repeat family protein \| |
| Eucgr.H04316.1 | 101,04 | 26,20 | 35,12 | 40,53 | 84,26 | AT1G54460.1 \| Symbols: \| TPX2 (targeting protein for Xklp2) protein family \| chr1:20340907-20342900 REVERSE LENGTH=338 |
| Eucgr.F04176.1 | 7,68 | 37,72 | 32,00 | 34,90 | 11,57 | AT1G71697.1 \| Symbols: ATCK1, CK, CK1 \| choline kinase 1 \| chr1:26971537-26973177 FORWARD LENGTH=346 |
| Eucgr.K01523.1 | 2,70 | 10,18 | 10,24 | 12,48 | 2,06 | AT5G35220.1 \| Symbols: EGY1 \| Peptidase M50 family protein \| chr5:13484606-13487546 REVERSE LENGTH=548 |
| Eucgr.F03689.1 | 42,16 | 9,06 | 13,58 | 12,25 | 55,76 | AT5G55730.2 \| Symbols: FLA1 \| FASCICLIN-like arabinogalactan 1 \| chr5:22558375-22560392 REVERSE LENGTH=424 |
| Eucgr.K00027.1 | 0,31 | 0,00 | 0,00 | 0,10 | 0,22 | AT4G18250.1 \| Symbols: \| receptor serine/threonine kinase, putative \| chr4:10087343-10091963 REVERSE LENGTH=853 |
| Eucgr.J02152.1 | 0,53 | 0,00 | 0,01 | 0,02 | 0,39 | AT5G40030.1 \| Symbols: \| Protein kinase superfamily protein \| chr5:16026227-16028283 FORWARD LENGTH=499 |
| Eucgr.I01028.1 | 25,13 | 0,20 | 0,32 | 0,07 | 29,67 | AT2G23690.1 \| Symbols: \| unknown protein; |
| Eucgr.A02070.1 | 1,00 | 17,38 | 8,86 | 5,29 | 1,76 | AT3G04070.1 \| Symbols: anac047, NAC047 \| NAC domain containing protein 47 \| |
| Eucgr.K01575.1 | 0,71 | 0,08 | 0,04 | 0,11 | 0,52 | AT5G03960.1 \| Symbols: IQD12 \| IQ-domain 12 \| chr5:1068333-1069683 REVERSE LENGTH=403 |
| Eucgr.E03963.1 | 0,50 | 0,03 | 0,03 | 0,07 | 0,37 | AT1G61370.1 \| Symbols: \| S-locus lectin protein kinase family protein \| chr1:22642096-22645147 REVERSE LENGTH=814 |
| Eucgr.H01178.1 | 3,52 | 0,19 | 0,21 | 0,55 | 2,53 | AT1G02970.1 \| Symbols: WEE1, ATWEE1 \| WEE1 kinase homolog \| chr1:673408-676127 FORWARD LENGTH=500 |
| Eucgr.H04752.1 | 1,96 | 0,00 | 0,00 | 0,12 | 1,40 | AT5G10310.1 \| Symbols: \| unknown protein; |
| Eucgr.F01004.1 | 0,15 | 3,50 | 4,05 | 3,97 | 0,17 | No hits found |
| Eucgr.G01335.1 | 15,84 | 0,00 | 0,18 | 0,60 | 13,02 | AT2G15220.1 \| Symbols: \| Plant basic secretory protein (BSP) family protein \| chr2:6608689-6609366 FORWARD LENGTH=225 |
| Eucgr.K00375.1 | 4,48 | 0,16 | 0,16 | 0,39 | 3,38 | AT5G24270.2 \| Symbols: SOS3 \| Calcium-binding EF-hand family protein \| chr5:8238781-8240179 REVERSE LENGTH=222 |
| Eucgr.K02858.1 | 218,59 | 19,50 | 43,49 | 66,15 | 141,91 | AT3G48000.1 \| Symbols: ALDH2B4, ALDH2, ALDH2A \| aldehyde dehydrogenase 2B4 \| |
| Eucgr.J00814.1 | 0,86 | 39,56 | 39,35 | 42,76 | 0,63 | AT3G20810.1 \| Symbols: JMJD5 \| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein \| |
| Eucgr.H02790.1 | 3,07 | 0,05 | 0,22 | 0,28 | 2,33 | AT4G31980.1 \| Symbols: \| unknown protein; |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.B00400.3 | 49,34 | 23,50 | 19,02 | 18,39 | 42,32 | AT5G62670.1 \| Symbols: AHA11, HA11 \| H(+)-ATPase 11 \| chr5:25159495-25164957 FORWARD LENGTH=956 |
| Eucgr.H04727.1 | 2,46 | 0,12 | 0,11 | 0,24 | 1,87 | AT5G65400.1 \| Symbols: \| alpha/beta-Hydrolases superfamily protein \| chr5:26131448-26133062 FORWARD LENGTH=252 |
| Eucgr.L01215.1 | 0,52 | 0,03 | 0,02 | 0,04 | 0,40 | AT5G60900.1 \| Symbols: RLK1 \| receptor-like protein kinase 1 \| chr5:24498467-24501494 REVERSE LENGTH=748 |
| Eucgr.C00184.1 | 45,26 | 0,45 | 0,72 | 0,22 | 37,20 | AT4G25810.1 \| Symbols: XTR6, XTH23 \| xyloglucan endotransglycosylase 6 \| |
| Eucgr.B02604.1 | 1,57 | 0,16 | 0,20 | 0,33 | 1,32 | AT5G60900.1 \| Symbols: RLK1 \| receptor-like protein kinase 1 \| chr5:24498467-24501494 REVERSE LENGTH=748 |
| Eucgr.F02442.1 | 0,37 | 0,00 | 0,00 | 0,03 | 0,27 | AT1G78060.1 \| Symbols: \| Glycosyl hydrolase family protein \| chr1:29349796-29352868 REVERSE LENGTH=767 |
| Eucgr.G01033.1 | 4,60 | 0,00 | 0,64 | 1,92 | 3,56 | AT3G27890.1 \| Symbols: NQR \| NADPH:quinone oxidoreductase \| chr3:10350807-10351938 REVERSE LENGTH=196 |
| Eucgr.K01122.1 | 16,74 | 1,68 | 3,16 | 4,48 | 14,64 | AT2G42580.1 \| Symbols: TTL3, VIT \| tetratricopetide-repeat thioredoxin-like 3 |
| Eucgr.J03079.2 | 4,27 | 0,21 | 0,24 | 0,57 | 3,52 | AT1G52510.1 \| Symbols: \| alpha/beta-Hydrolases superfamily protein \| chr1:19563039-19565260 REVERSE LENGTH=380 |

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|---|---|---|---|---|---|---|
| Eucgr.J02006.1 | 0,69 | 0,03 | 0,03 | 0,00 | 1,06 | AT1G07440.1 \| Symbols: \| NAD(P)-binding Rossmann-fold superfamily protein \| chr1:2286436-2287665 REVERSE LENGTH=266 |
| Eucgr.K03116.2 | 21,97 | 1,81 | 0,90 | 0,98 | 20,94 | AT5G02230.2 \| Symbols: \| Haloacid dehalogenase-like hydrolase (HAD) superfamily protein \| |
| Eucgr.H04927.1 | 0,64 | 0,02 | 0,08 | 0,08 | 0,51 | AT5G60900.1 \| Symbols: RLK1 \| receptor-like protein kinase 1 \| chr5:24498467-24501494 REVERSE LENGTH=748 |
| Eucgr.C04145.1 | 0,36 | 0,02 | 0,06 | 0,10 | 0,29 | AT2G26910.1 \| Symbols: PDR4, ATPDR4 \| pleiotropic drug resistance 4 \| chr2:11481623-11487874 FORWARD LENGTH=1420 |
| Eucgr.J01268.1 | 4,76 | 0,04 | 0,38 | 0,46 | 4,09 | AT3G63530.2 \| Symbols: BB, BB2 \| RING/U-box superfamily protein \| chr3:23456407-23457787 REVERSE LENGTH=248 |
| Eucgr.F00223.1 | 2,30 | 63,00 | 63,86 | 76,36 | 2,12 | AT5G42900.2 \| Symbols: \| cold regulated gene 27 \| chr5:17198366-17199712 REVERSE LENGTH=246 |
| Eucgr.A00882.1 | 246,28 | 23,21 | 64,91 | 87,97 | 141,86 | AT1G79620.1 \| Symbols: \| Leucine-rich repeat protein kinase family protein \| chr1:29957633-29962174 REVERSE LENGTH=971 |
| Eucgr.C00960.1 | 24,76 | 1,91 | 4,06 | 5,27 | 21,47 | AT4G29240.1 \| Symbols: \| Leucine-rich repeat (LRR) family protein \| chr4:14418826-14420073 FORWARD LENGTH=415 |
| Eucgr.B02677.1 | 1,47 | 0,03 | 0,05 | 0,07 | 1,24 | AT1G14820.3 \| Symbols: \| Sec14p-like phosphatidylinositol transfer family protein \| |
| Eucgr.A01353.1 | 0,50 | 0,03 | 0,00 | 0,04 | 0,45 | AT4G08850.1 \| Symbols: \| Leucine-rich repeat receptor-like protein kinase family protein \| |
| Eucgr.I00190.2 | 27,64 | 1,25 | 1,27 | 1,92 | 23,73 | AT2G13610.1 \| Symbols: \| ABC-2 type transporter family protein \| chr2:5673827-5675776 REVERSE LENGTH=649 |
| Eucgr.G00960.1 | 14,22 | 0,68 | 1,32 | 2,31 | 12,29 | AT5G64330.1 \| Symbols: NPH3, RPT3, JK218 \| Phototropic-responsive NPH3 family protein \| |
| Eucgr.J02113.1 | 25,87 | 3,02 | 5,53 | 8,49 | 22,64 | AT2G28550.3 \| Symbols: RAP2.7 \| related to AP2.7 \| chr2:12226168-12228251 REVERSE LENGTH=464 |
| Eucgr.E03919.1 | 0,57 | 25,27 | 9,68 | 0,90 | 0,82 | AT5G47550.1 \| Symbols: \| Cystatin/monellin superfamily protein \| chr5:19286596-19286964 REVERSE LENGTH=122 |
| Eucgr.E02995.1 | 4,23 | 21,74 | 21,81 | 19,90 | 5,59 | No hits found |
| Eucgr.J02625.1 | 6,60 | 0,33 | 0,53 | 0,75 | 5,93 | AT5G11000.1 \| Symbols: \| Plant protein of unknown function (DUF868) \| chr5:3479166-3480335 REVERSE LENGTH=389 |
| Eucgr.B03632.1 | 2,65 | 13,13 | 15,32 | 17,69 | 3,48 | AT2G34860.2 \| Symbols: EDA3 \| DnaJ/Hsp40 cysteine-rich domain superfamily protein \| |
| Eucgr.B02605.1 | 0,48 | 0,02 | 0,09 | 0,10 | 0,40 | AT5G60900.1 \| Symbols: RLK1 \| receptor-like protein kinase 1 \| chr5:24498467-24501494 REVERSE LENGTH=748 |
| Eucgr.C03960.1 | 1,22 | 0,04 | 0,31 | 0,52 | 1,02 | AT3G24430.1 \| Symbols: HCF101 \| ATP binding \| chr3:8868731-8872154 REVERSE LENGTH=532 |
| Eucgr.C02507.1 | 1,32 | 7,47 | 6,07 | 6,63 | 1,84 | AT4G30720.1 \| Symbols: \| FAD/NAD(P)-binding oxidoreductase family protein \| |
| Eucgr.K00883.2 | 607,60 | 16,06 | 29,74 | 37,61 | 288,85 | AT4G03210.1 \| Symbols: XTH9 \| xyloglucan endotransglucosylase/hydrolase 9 \| |
| Eucgr.K02468.1 | 66,99 | 551,20 | 399,69 | 392,53 | 97,85 | AT1G18800.1 \| Symbols: NRP2 \| NAP1-related protein 2 \| chr1:6481466-6483463 REVERSE LENGTH=256 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.B02479.5 | 8,67 | 34,19 | 31,92 | 29,91 | 11,70 | AT3G45300.1 \| Symbols: IVD, ATIVD, IVDH \| isovaleryl-CoA-dehydrogenase \| chr3:16621659-16624848 REVERSE LENGTH=409 |
| Eucgr.C02516.1 | 1,62 | 0,13 | 0,00 | 0,08 | 1,40 | AT4G30845.1 \| Symbols: \| unknown protein; |
| Eucgr.F02642.1 | 0,27 | 0,00 | 0,02 | 0,04 | 0,23 | AT5G09360.1 \| Symbols: LAC14 \| laccase 14 \| chr5:2906426-2908658 REVERSE LENGTH=569 |
| Eucgr.A01352.1 | 0,57 | 0,03 | 0,02 | 0,01 | 0,60 | AT4G08850.1 \| Symbols: \| Leucine-rich repeat receptor-like protein kinase family protein \| |
| Eucgr.A01447.2 | 14,35 | 4,98 | 5,05 | 8,17 | 13,76 | AT4G27800.1 \| Symbols: TAP38, PPH1 \| thylakoid-associated phosphatase 38 \| |
| Eucgr.D00397.1 | 0,52 | 0,06 | 0,04 | 0,06 | 0,44 | AT5G45470.1 \| Symbols: \| Protein of unknown function (DUF594) \| chr5:18422164-18424764 REVERSE LENGTH=866 |
| Eucgr.B03360.1 | 12,37 | 0,93 | 1,94 | 2,24 | 11,59 | AT1G70230.1 \| Symbols: TBL27 \| TRICHOME BIREFRINGENCE-LIKE 27 \| chr1:26450389-26451724 FORWARD LENGTH=416 |

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|---|---|---|---|---|---|---|
| Eucgr.G03419.1 | 1,67 | 0,10 | 0,21 | 0,20 | 1,46 | AT2G31900.1 \| Symbols: XIF, ATXIF, ATMYO5 \| myosin-like protein XIF \| chr2:13560760-13569623 REVERSE LENGTH=1556 |
| Eucgr.H01685.1 | 60,58 | 12,89 | 16,34 | 18,83 | 50,93 | AT4G02630.1 \| Symbols: \| Protein kinase superfamily protein \| chr4:1151683-1153161 FORWARD LENGTH=492 |
| Eucgr.I00651.1 | 23,67 | 74,34 | 61,77 | 52,40 | 30,88 | AT5G65720.1 \| Symbols: ATNIFS1, NIFS1, NFS1, ATNFS1 \| nitrogen fixation S (NIFS)-like 1 \| |
| Eucgr.K02098.1 | 1,29 | 0,00 | 0,22 | 0,47 | 1,85 | AT4G12970.1 \| Symbols: STOMAGEN, EPFL9 \| stomagen \| chr4:7586244-7586798 REVERSE LENGTH=102 |
| Eucgr.K02948.1 | 2,31 | 0,10 | 0,03 | 0,31 | 2,14 | AT3G51660.1 \| Symbols: \| Tautomerase/MIF superfamily protein \| chr3:19164229-19165076 REVERSE LENGTH=112 |
| Eucgr.F02749.1 | 0,61 | 53,80 | 22,67 | 6,72 | 0,82 | AT1G21460.1 \| Symbols: SWEET1, AtSWEET1 \| Nodulin MtN3 family protein \| chr1:7512030-7513281 REVERSE LENGTH=247 |
| Eucgr.C02594.1 | 28,57 | 4,87 | 4,63 | 5,60 | 25,81 | AT2G24270.4 \| Symbols: ALDH11A3 \| aldehyde dehydrogenase 11A3 \| chr2:10327109-10329601 REVERSE LENGTH=503 |
| Eucgr.H00494.1 | 6,14 | 20,25 | 26,24 | 27,22 | 7,22 | AT5G26570.1 \| Symbols: PWD, OK1, ATGWD3 \| catalytics;carbohydrate kinases;phosphoglucan, water dikinases \| |
| Eucgr.A01640.1 | 4,07 | 0,08 | 0,22 | 0,57 | 3,60 | AT4G20990.1 \| Symbols: ATACA4, ACA4 \| alpha carbonic anhydrase 4 \| chr4:11219772-11221126 FORWARD LENGTH=267 |
| Eucgr.L01886.1 | 0,66 | 20,69 | 7,89 | 2,80 | 0,82 | AT5G51440.1 \| Symbols: \| HSP20-like chaperones superfamily protein \| chr5:20891242-20892013 FORWARD LENGTH=210 |
| Eucgr.B02634.1 | 32,97 | 2,94 | 6,54 | 9,05 | 31,72 | AT1G14630.1 \| Symbols: \| unknown protein; |
| Eucgr.H02330.1 | 22,76 | 4,23 | 3,01 | 3,00 | 20,90 | AT4G37730.1 \| Symbols: AtbZIP7, bZIP7 \| basic leucine-zipper 7 \| chr4:17723800-17724717 FORWARD LENGTH=305 |
| Eucgr.F00464.1 | 28,18 | 85,70 | 85,04 | 82,49 | 36,89 | AT1G09960.1 \| Symbols: SUT4, ATSUT4, SUC4, ATSUC4 \| sucrose transporter 4 \| |
| Eucgr.L00920.1 | 0,57 | 0,03 | 0,01 | 0,04 | 0,56 | AT3G49340.1 \| Symbols: \| Cysteine proteinases superfamily protein \| chr3:18293347-18294577 REVERSE LENGTH=341 |
| Eucgr.L02477.1 | 3,59 | 0,66 | 0,34 | 0,83 | 5,03 | AT2G31900.1 \| Symbols: XIF, ATXIF, ATMYO5 \| myosin-like protein XIF \| chr2:13560760-13569623 REVERSE LENGTH=1556 |
| Eucgr.K00240.1 | 0,61 | 15,71 | 20,30 | 32,17 | 0,72 | No hits found |
| Eucgr.B02498.1 | 113,87 | 14,29 | 40,05 | 58,07 | 104,95 | AT2G28410.1 \| Symbols: \| unknown protein; |
| Eucgr.J00254.2 | 102,60 | 8,85 | 18,16 | 28,91 | 87,50 | AT5G05830.1 \| Symbols: \| RING/FYVE/PHD zinc finger superfamily protein \| chr5:1755910-1756825 FORWARD LENGTH=204 |
| Eucgr.C00760.1 | 6,07 | 0,20 | 0,60 | 1,33 | 7,75 | AT5G20860.1 \| Symbols: \| Plant invertase/pectin methylesterase inhibitor superfamily \| |
| Eucgr.K01270.1 | 13,04 | 0,28 | 0,23 | 0,37 | 15,01 | AT2G40435.1 \| Symbols: \| unknown protein |
| Eucgr.I02212.1 | 0,39 | 4,15 | 7,02 | 12,24 | 0,39 | AT2G17480.1 \| Symbols: MLO8, ATMLO8 \| Seven transmembrane MLO family protein \| chr2:7590559-7593768 REVERSE LENGTH=593 |
| Eucgr.K02666.1 | 11,07 | 56,40 | 52,31 | 43,86 | 10,44 | AT5G50860.1 \| Symbols: \| Protein kinase superfamily protein \| chr5:20693778-20696983 REVERSE LENGTH=580 |
| Eucgr.B03599.2 | 17,72 | 3,00 | 3,77 | 4,78 | 16,45 | No hits found |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.J00341.1 | 27,89 | 0,69 | 3,03 | 5,81 | 25,77 | No hits found |
| Eucgr.H01338.1 | 10,78 | 0,18 | 0,38 | 0,41 | 13,22 | AT3G05910.1 \| Symbols: \| Pectinacetylesterase family protein \| chr3:1764509-1767240 REVERSE LENGTH=415 |
| Eucgr.G01458.1 | 14,20 | 0,30 | 0,49 | 0,58 | 13,53 | AT5G42700.1 \| Symbols: \| AP2/B3-like transcriptional factor family protein \| |
| Eucgr.I00788.1 | 4,85 | 0,51 | 0,76 | 1,50 | 4,57 | AT5G67280.1 \| Symbols: RLK \| receptor-like kinase \| chr5:26842430-26845126 REVERSE LENGTH=751 |
| Eucgr.B03185.1 | 13,19 | 0,54 | 0,83 | 2,82 | 13,56 | AT2G03350.1 \| Symbols: \| Protein of unknown function, DUF538 \| chr2:1019733-1021071 REVERSE LENGTH=179 |
| Eucgr.G01214.1 | 2,95 | 0,21 | 0,45 | 0,67 | 2,72 | AT4G33820.1 \| Symbols: \| Glycosyl hydrolase superfamily protein \| chr4:16217010-16219515 REVERSE LENGTH=570 |

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|---|---|---|---|---|---|---|
| Eucgr.K02352.1 | 2,14 | 0,00 | 0,25 | 0,41 | 1,96 | AT1G05680.1 \| Symbols: UGT74E2 \| Uridine diphosphate glycosyltransferase 74E2 \| |
| Eucgr.H00801.5 | 7,59 | 38,25 | 42,75 | 37,11 | 8,29 | AT2G32700.6 \| Symbols: LUH \| LEUNIG_homolog \| chr2:13867235-13871844 FORWARD LENGTH=785 |
| Eucgr.K02353.1 | 2,12 | 0,05 | 0,15 | 0,36 | 2,06 | AT1G05680.1 \| Symbols: UGT74E2 \| Uridine diphosphate glycosyltransferase 74E2 \| |
| Eucgr.B02381.1 | 10,55 | 0,00 | 0,33 | 0,85 | 10,43 | No hits found |
| Eucgr.B03602.2 | 193,14 | 7,72 | 16,05 | 23,58 | 137,13 | AT3G13510.1 \| Symbols: \| Protein of Unknown Function (DUF239) \| chr3:4403776-4405741 FORWARD LENGTH=419 |
| Eucgr.K00961.1 | 1,99 | 25,38 | 20,89 | 15,29 | 1,94 | AT2G20880.1 \| Symbols: \| Integrase-type DNA-binding superfamily protein \| chr2:8986053-8987063 FORWARD LENGTH=336 |
| Eucgr.I01833.1 | 1,88 | 0,00 | 0,13 | 0,14 | 1,77 | AT3G28180.1 \| Symbols: ATCSLC04, CSLC04, ATCSLC4, CSLC4 \| Cellulose-synthase-like C4 \| |
| Eucgr.E01689.1 | 1,55 | 0,04 | 0,05 | 0,11 | 1,70 | AT5G08640.2 \| Symbols: FLS1 \| flavonol synthase 1 \| chr5:2804009-2805175 FORWARD LENGTH=336 |
| Eucgr.H02604.1 | 91,88 | 8,08 | 9,71 | 9,37 | 75,19 | AT2G30520.1 \| Symbols: RPT2 \| Phototropic-responsive NPH3 family protein \| |
| Eucgr.H02774.1 | 0,43 | 0,02 | 0,16 | 0,01 | 0,41 | AT3G07130.1 \| Symbols: ATPAP15, PAP15 \| purple acid phosphatase 15 \| chr3:2255763-2257981 REVERSE LENGTH=532 |
| Eucgr.A00492.1 | 10,69 | 0,31 | 1,97 | 3,86 | 10,28 | AT1G19330.2 \| Symbols: \| unknown protein |
| Eucgr.J01875.1 | 11,96 | 0,36 | 0,78 | 1,55 | 11,50 | AT2G30140.2 \| Symbols: \| UDP-Glycosyltransferase superfamily protein \| chr2:12872200-12873691 FORWARD LENGTH=454 |
| Eucgr.I01733.1 | 14,44 | 84,36 | 69,78 | 70,48 | 14,06 | AT3G27540.1 \| Symbols: \| beta-1,4-N-acetylglucosaminyltransferase family protein |
| Eucgr.H05065.1 | 0,32 | 0,04 | 0,02 | 0,01 | 0,34 | AT2G38290.1 \| Symbols: ATAMT2, AMT2;1, AMT2 \| ammonium transporter 2 \| |
| Eucgr.A02126.1 | 1369,19 | 134,99 | 259,54 | 284,25 | 467,15 | AT5G17920.2 \| Symbols: ATCIMS \| Cobalamin-independent synthase family protein \| |
| Eucgr.J00502.1 | 28,27 | 4,09 | 5,06 | 7,33 | 27,45 | AT3G44380.1 \| Symbols: \| Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family \| |
| Eucgr.B03026.1 | 1,02 | 4,48 | 4,62 | 3,74 | 1,32 | No hits found |
| Eucgr.C02733.1 | 12,63 | 67,36 | 80,38 | 96,78 | 15,27 | AT5G25280.2 \| Symbols: \| serine-rich protein-related \| chr5:8773882-8774544 FORWARD LENGTH=220 |
| Eucgr.C03707.1 | 6,11 | 1,45 | 1,73 | 2,28 | 5,86 | AT4G29310.1 \| Symbols: \| Protein of unknown function (DUF1005) \| chr4:14437892-14439609 REVERSE LENGTH=424 |
| Eucgr.F03859.2 | 33,36 | 101,32 | 71,97 | 78,01 | 40,09 | AT4G29850.1 \| Symbols: \| Eukaryotic protein of unknown function (DUF872) \| |
| Eucgr.D00477.1 | 3,33 | 0,37 | 0,12 | 0,22 | 4,20 | AT4G18740.1 \| Symbols: \| Rho termination factor \| chr4:10303543-10304479 REVERSE LENGTH=245 |
| Eucgr.B03753.1 | 12,70 | 1,38 | 2,68 | 6,03 | 12,37 | No hits found |
| Eucgr.I01191.1 | 5,14 | 1,11 | 0,77 | 0,65 | 6,35 | AT3G19000.1 \| Symbols: \| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein \| |
| Eucgr.D02033.1 | 50,03 | 7,66 | 9,50 | 11,64 | 51,25 | AT4G22570.1 \| Symbols: APT3 \| adenine phosphoribosyl transferase 3 \| chr4:11882310-11885250 REVERSE LENGTH=183 |
| Eucgr.G00854.1 | 8,35 | 31,91 | 33,46 | 32,78 | 10,10 | AT4G33510.1 \| Symbols: DHS2 \| 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase \| |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.A00534.1 | 14,19 | 54,90 | 54,03 | 46,35 | 17,02 | AT2G38280.2 \| Symbols: FAC1, ATAMPD \| AMP deaminase, putative / myoadenylate deaminase, putative \| |
| Eucgr.B02014.1 | 16,39 | 1,97 | 4,29 | 6,06 | 16,18 | AT1G54730.2 \| Symbols: \| Major facilitator superfamily protein \| chr1:20424471-20429978 FORWARD LENGTH=470 |
| Eucgr.D01737.1 | 1,62 | 13,99 | 12,83 | 9,19 | 1,70 | AT5G53110.1 \| Symbols: \| RING/U-box superfamily protein \| chr5:21529022-21533008 FORWARD LENGTH=382 |
| Eucgr.H01397.1 | 2,80 | 0,16 | 0,23 | 0,14 | 2,81 | AT4G12910.1 \| Symbols: scpl20 \| serine carboxypeptidase-like 20 \| chr4:7550576-7553051 REVERSE LENGTH=497 |

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|---|---|---|---|---|---|---|
| Eucgr.J02154.1 | 3,05 | 0,05 | 0,35 | 0,84 | 3,81 | No hits found |
| Eucgr.B00830.1 | 2,26 | 9,06 | 10,46 | 12,27 | 2,71 | AT1G73750.1 \| Symbols: \| Uncharacterised conserved protein UCP031088, alpha/beta hydrolase \| |
| Eucgr.F01551.1 | 25,89 | 4,48 | 6,22 | 7,93 | 27,99 | AT1G75130.1 \| Symbols: CYP721A1 \| cytochrome P450, family 721, subfamily A, polypeptide 1 \| |
| Eucgr.H00646.1 | 0,70 | 0,04 | 0,20 | 0,21 | 0,74 | AT5G64740.1 \| Symbols: CESA6, IXR2, E112, PRC1 \| cellulose synthase 6 \| chr5:25881555-25886333 FORWARD LENGTH=1084 |
| Eucgr.F02183.1 | 1716,98 | 105,00 | 291,10 | 447,72 | 519,92 | AT4G14960.2 \| Symbols: TUA6 \| Tubulin/FtsZ family protein \| chr4:8548769-8550319 REVERSE LENGTH=450 |
| Eucgr.K00551.3 | 9,90 | 2,75 | 1,74 | 0,95 | 10,13 | AT5G66460.1 \| Symbols: MAN7, AtMAN7 \| Glycosyl hydrolase superfamily protein \| |
| Eucgr.E00821.1 | 3,07 | 0,38 | 0,35 | 0,78 | 3,03 | AT4G24000.1 \| Symbols: ATCSLG2, CSLG2 \| cellulose synthase like G2 \| chr4:12462142-12465471 FORWARD LENGTH=722 |
| Eucgr.B02486.1 | 2814,83 | 239,55 | 537,13 | 845,92 | 821,98 | AT5G60490.1 \| Symbols: FLA12 \| FASCICLIN-like arabinogalactan-protein 12 \| chr5:24325916-24326665 REVERSE LENGTH=249 |
| Eucgr.I01189.1 | 27,02 | 7,50 | 8,61 | 10,57 | 31,80 | AT3G19000.1 \| Symbols: \| 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein \| |
| Eucgr.F04235.1 | 28,30 | 2,07 | 3,77 | 5,89 | 28,69 | AT1G21090.1 \| Symbols: \| Cupredoxin superfamily protein \| chr1:7384854-7386199 FORWARD LENGTH=242 |
| Eucgr.A01371.1 | 10,65 | 28,80 | 34,26 | 35,50 | 11,87 | AT3G07650.4 \| Symbols: COL9 \| CONSTANS-like 9 \| chr3:2442494-2443901 FORWARD LENGTH=372 |
| Eucgr.A01444.1 | 6,26 | 0,45 | 1,14 | 1,70 | 6,81 | AT5G24320.1 \| Symbols: \| Transducin/WD40 repeat-like superfamily protein \| chr5:8284858-8287651 REVERSE LENGTH=694 |
| Eucgr.B03946.1 | 7,30 | 0,88 | 1,40 | 1,96 | 8,05 | AT5G40240.2 \| Symbols: \| nodulin MtN21 /EamA-like transporter family protein \| |
| Eucgr.H00308.1 | 505,18 | 47,41 | 110,30 | 194,67 | 268,51 | AT3G59690.1 \| Symbols: IQD13 \| IQ-domain 13 \| chr3:22049572-22051479 FORWARD LENGTH=517 |
| Eucgr.D02037.1 | 10,34 | 42,33 | 30,56 | 18,36 | 12,06 | AT1G12110.1 \| Symbols: NRT1.1, CHL1-1, NRT1, B-1, ATNRT1, CHL1 \| nitrate transporter 1.1 \| |
| Eucgr.I02691.1 | 87,53 | 15,36 | 20,83 | 22,59 | 75,88 | AT5G64550.1 \| Symbols: \| loricrin-related \| chr5:25801794-25803698 REVERSE LENGTH=634 |
| Eucgr.C01809.1 | 29,77 | 9,97 | 10,66 | 15,35 | 31,65 | AT4G32570.1 \| Symbols: TIFY8 \| TIFY domain protein 8 \| chr4:15716433-15718702 REVERSE LENGTH=361 |
| Eucgr.J00751.1 | 12,23 | 1,25 | 2,83 | 4,05 | 13,42 | AT3G21070.2 \| Symbols: NADK1 \| NAD kinase 1 \| chr3:7380434-7383874 REVERSE LENGTH=524 |
| Eucgr.F01752.1 | 21,08 | 62,97 | 56,81 | 55,11 | 24,28 | AT4G35230.1 \| Symbols: BSK1 \| BR-signaling kinase 1 \| chr4:16755325-16758041 REVERSE LENGTH=512 |
| Eucgr.F03305.1 | 96,42 | 2,13 | 6,32 | 16,93 | 98,09 | No hits found |
| Eucgr.H00896.1 | 76,24 | 2,72 | 10,01 | 15,98 | 69,72 | AT2G47160.1 \| Symbols: BOR1 \| HCO3- transporter family \| chr2:19357740-19360787 REVERSE LENGTH=704 |
| Eucgr.F00581.1 | 5,38 | 23,68 | 22,14 | 20,45 | 5,64 | AT1G30755.1 \| Symbols: \| Protein of unknown function (DUF668) \| chr1:10905991-10908773 REVERSE LENGTH=615 |
| Eucgr.J00385.2 | 66,16 | 2,03 | 4,51 | 7,69 | 68,84 | AT5G22930.1 \| Symbols: \| Protein of unknown function (DUF1635) \| chr5:7668229-7669315 REVERSE LENGTH=238 |
| Eucgr.I01383.1 | 5,06 | 0,54 | 2,27 | 2,71 | 5,31 | AT4G34880.1 \| Symbols: \| Amidase family protein \| chr4:16615549-16617424 FORWARD LENGTH=466 |
| Eucgr.C00546.1 | 8,12 | 0,82 | 1,83 | 1,98 | 8,69 | AT5G11590.1 \| Symbols: TINY2 \| Integrase-type DNA-binding superfamily protein \| |
| Eucgr.J02264.2 | 8,00 | 20,31 | 19,28 | 21,47 | 8,49 | No hits found |
| Eucgr.H00495.1 | 144,56 | 1,81 | 5,52 | 12,64 | 176,15 | AT3G07880.1 \| Symbols: SCN1 \| Immunoglobulin E-set superfamily protein \| chr3:2514175-2515544 FORWARD LENGTH=240 |
| GENE ID | FPKM | | | | | Annotation |
| | CT | CH | NAR | CHSTOP | NARSTOP | TAIR |
| Eucgr.G03246.4 | 100,42 | 12,92 | 15,05 | 15,54 | 141,43 | AT3G54500.1 \| Symbols: \| unknown protein |
| Eucgr.J01177.3 | 8,06 | 1,76 | 2,79 | 3,96 | 8,69 | AT5G13500.3 \| Symbols: \| unknown protein; |

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|---|---|---|---|---|---|---|
| Eucgr.H05081.4 | 4,84 | 0,93 | 1,11 | 1,60 | 5,34 | AT4G34240.1 \| Symbols: ALDH3I1, ALDH3 \| aldehyde dehydrogenase 3I1 \| chr4:16389801-16392633 FORWARD LENGTH=550 |
| Eucgr.H02297.1 | 8,31 | 32,34 | 24,25 | 19,28 | 8,92 | No hits found |
| Eucgr.F02039.1 | 14,22 | 41,88 | 33,89 | 24,33 | 16,13 | AT5G55860.1 \| Symbols: \| Plant protein of unknown function (DUF827) \| chr5:22610146-22612166 FORWARD LENGTH=649 |
| Eucgr.D00506.1 | 257,68 | 0,26 | 2,84 | 6,70 | 239,70 | AT5G45890.1 \| Symbols: SAG12 \| senescence-associated gene 12 \| chr5:18613300-18614759 FORWARD LENGTH=346 |
| Eucgr.H04094.1 | 89,16 | 1,50 | 9,20 | 14,90 | 104,05 | AT3G62270.1 \| Symbols: \| HCO3- transporter family \| chr3:23042528-23045633 REVERSE LENGTH=703 |
| Eucgr.H02634.1 | 386,73 | 21,78 | 47,14 | 72,69 | 396,09 | AT3G23730.1 \| Symbols: XTH16 \| xyloglucan endotransglucosylase/hydrolase 16 \| |
| Eucgr.B00824.1 | 2280,86 | 132,19 | 233,56 | 407,73 | 1834,47 | AT3G18280.1 \| Symbols: \| Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein |