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LUDYMILA BRANDÃO MOTTA

Genotipagem por sequenciamento para identificação de SNPs e associação com características agronômicas em *Coffea canephora*

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Tese apresentada à Universidade Federal do Espírito Santo, como parte das exigências do Programa de Pós-Graduação em Produção Vegetal, para obtenção do título de Doutora em Produção Vegetal.

Orientadora: Prof. Drª Taís Criastina Bastos Soares. Coorientadores: Drª. Maria Amélia Gava Ferrão, Dr. Alan Carvalho Andrade, Prof. Dr. Cosme Damião Cruz.

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À minha família por todo apoio, por ter me ensinado a lutar e persistir em meus objetivos.

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"Pensávamos que o nosso futuro estava nas estrelas,

hoje acreditamos que está nos nossos genes”

James Watson

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MOTTA, Ludymila Brandão Motta, Universidade Federal do Espírito Santo. Fevereiro de 2016. **Genotipagem por sequenciamento para identificação de SNPs e associação com características agronômicas em** *Coffea canephora*. Orientadora: Prof. Dr^{a}. Taís Cristina Bastos Soares. Coorientadores: Dr. Alan Carvalho Andrade, Prof. Dr. Cosme Damião Cruz, e Dr^{a}. Maria Amélia Gava Ferrão

RESUMO

A genotipagem por sequenciamento (GBS) é capaz de identificar e genotipar milhares de polimorfismos do tipo SNPs de forma simultânea. Objetiva-se contribuir para o melhoramento genético do cafeeiro Conilon através da caracterização da ocorrência de SNPs no genoma de *Coffea canephora* e de associações destes com características de interesse agronômico. Os145 indivíduos de duas famílias de irmãos completos (clones 109x120/120x109 e 76x48) do programa de melhoramento do Instituto Capixaba de Pesquisa, Assistência Técnica e Extensão Rural (Incaper)foram fenotipados e os DNAs foram multiplexados em sequenciador Ilumina na Universidade de Cornell. Detectaram-se 91.105 SNPs antes de aplicar os parâmetros de filtragem, sendo que após os filtros houve redução de 64%. Ampla distribuição dos SNPs foi encontrada, sendo que foram detectados em média 1330 SNPs gênicos e 2955 intergênicos, por pseudocromossomo. Verificou-se que o padrão de distribuição dos SNPs nas regiões do genoma difere. A menor ocorrência de SNPs detectada em regiões gênicas é esperada como consequência da pressão de seleção, que limita as alterações de aminoácidos nas sequências proteicas. Os estudos de associação permitiram encontrar 18 SNPs associados a características fenotípicas de *Coffea canephora* (S2_9329731, S2_4579518, S2_41329025, S2_17821870, S2_20934616, S3_23227842, S4_22978689, S5_10964474, S6_9949547, S7_13991105, S7_13991086, S7_13991077, S9_4618814, S9_18527411, S10_24840747, S11_30063996, S11_23828233). Localizam-se em regiões intergênicas 33% dos SNPs, sendo que os demais se distribuem em região de íntrons, éxons e 3'UTR. Os SNPs em região codificadora são responsáveis por alterações não sinônimas em 82% das ocorrências. Os resultados encontrados são importantes para a cafeicultura e podem contribuir para a seleção assistida por marcadores.

Palavras-chave: cafeeiro, sequenciamento, SNP, genotipagem, estudos de associação.

MOTTA, Ludymila Brandão Motta, Universidade Federal do Espírito Santo**.** February, 2016. **Genotyping by sequencing to identify SNPs and association with agronomic traits in Coffea canephora.** Advisor: Prof. Drª. Taís Cristina Bastos Soares. Co-advisors: Dr. Alan Carvalho Andrade, Prof. Dr. Cosme Damião Cruz, and Dr. Maria Amélia Gava Ferrão**.**

ABSTRACT

Genotyping by sequencing (GBS) is able to identify and genotype thousands of SNP simultaneously. This work aims to contribute to the genetic improvement of Robusta coffee characterizing the occurrence of SNPs in canephora genome and studying the associations with SNPs and important agronomic traits. Individuals from two full-sib families of the Incaper breeding program were phenotyped and the DNAs were multiplexed at Illumina sequencing at Cornell University. 91,105 SNPs were detected before applying the filtering parameters, and after the filters the number was reduced 64%. Wide distribution of SNPs was found and we detected on average of 1330 genic SNPs and 2955 intergenic SNPs by pseudo-chromosome.The distribution pattern of SNPs changes in different regions of the genome. The lowest occurrence of SNPs detected in gene regions is expected as a result of selection pressure, which limits the amino acid changes in protein sequences. The association studies allowed to find 18 SNPs associated with phenotypic characteristics of *Coffea canephora* ((S2_9329731, S2_4579518, S2_41329025, S2_17821870, S2_20934616, S3_23227842, S4_22978689, S5_10964474, S6_9949547, S7_13991105, S7_13991086, S7_13991077, S9_4618814, S9_18527411, S10_24840747, S11_30063996, S11_23828233)). 33% of the SNPs are located in inter-genic regions, and the remaining distributed in introns, exons and 3'UTR. SNPs in coding region are responsible for non-synonymous changes in 82% of cases. The results are important for the coffee and can contribute to marker-assisted selection.

Keywords: coffee, sequencing, SNP, genotyping, association studies.

LISTA DE SIGLAS E ABREVIAÇÕES

3’UTR – região 3’ não traduzida

AFLP - Polimorfismos de comprimento de fragmentos amplificados

Ch - Pseudocromossomo

EMMA - Eficiente modelo misto de associação

EST - Etiqueta de sequência expressa

FEM - Fazenda Experimental de Marilândia

GBS - Genotipagem por Sequenciamento

GWASs - Estudos de associação de genoma

GWS - Seleção Genômica Ampla

InDels - Inserções e deleções

Kb – Quilobase, 1.000 pares de base

MAF - Frequência alélica mínima

MAS - Seleção assistida por marcadores

Mb – Megabase, 1.000.000 pares de base

MLG - Modelo Linear Geral

MLM - Modelo Linear Misto

NGS - Sequenciamento de Nova Geração

Pb - Pares de bases

PCR - Reação em cadeia da polimerase

PIC - Conteúdo de informação polimórfica

RAPD - Polimorfismos de DNA amplificado ao acaso

RELM – Máxima verossimilhança restrita

RFLP - Polimorfismos de Tamanho de Fragmentos de Restrição

SNP - Polimorfismo de Nucleotídeo Único

SSR - Sequências Simples Repetidas

TALE - Transcription activator–like effector

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INTRODUÇÃO GERAL

Coffea canephora é a segunda espécie do gênero mais cultivada no mundo, e o Espírito Santo se destaca como o maior produtor brasileiro desta espécie, designada no Estado como café Conilon. A intensa parceria de órgãos governamentais como o Incaper, a Embrapa Café, Secretaria de Estado da Agricultura*,* Abastecimento, Aquicultura e Pesca, e Universidades auxilia a identificar áreas prioritárias para o programa de pesquisa em café, programar pesquisas e adotar práticas que visam disponibilizar soluções para o agronegócio do café Conilon. Pesquisas moleculares e biométricas contribuem de forma significativa no estudo das características de interesse para o setor da cafeicultura, facilitando as análises de genotipagem em larga escala.

As inovações tecnológicas de sequenciamento de DNA em larga escala em desenvolvimento associadas às ferramentas de genética quantitativa apresentam grande potencial para predizer marcadores moleculares de interesse agronômico. O desenvolvimento de métodos de genotipagem de nova geração (NGS) tornou os polimorfismos de nucleotídeo simples (SNPs) altamente utilizados como marcadores genéticos (KUMAR; BANKS; CLOUTIER, 2012).

Os SNPs são geralmente de natureza bialélica, devido serem originados de uma mutação pontual no genoma. Para que ocorra a fixação das mutações, forças evolutivas como seleção natural, deriva gênica e fluxo gênico devem atuar na população modulando as variações. Para que um terceiro alelo ocorra, é necessário uma segunda mutação em outro indivíduo, distinta da primeira na mesma posição no genoma, levando à geração de um SNP trialélico na população, o que possui baixa probabilidade de ocorrer. As frequências alélicas são diferentes, uma vez que os alelos que contribuem positivamente para a sobrevivência e reprodução da espécie possuem maior frequência. A fixação desses alelos ocorrerá se as mutações forem transmitidas para as gerações futuras e se mantiverem em frequência na população (Darwin, 1859; Brown, 2002).

A genotipagem por sequenciamento (GBS) é um método que explora o potencial das tecnologias de nova geração (NGS) e são capazes de identificar SNPs e, simultaneamente, genotipar indivíduos. A GBS apresenta diversas aplicações, que incluem a identificação de cultivares, construção de mapas genéticos, análise da diversidade genética, detecção de associações genótipo x fenótipo e seleção assistida por marcadores (ELSHIRE et al., 2011).

Este trabalho objetivou caracterizar a ocorrência de marcadores moleculares SNPs no genoma de *Coffea canephora* utilizando a genotipagem por sequenciamento em dois cruzamentos de café Conilon do programa de melhoramento do Incaper; estudar a associação fenotípica e genotípica de características de interesse na cafeicultura.

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REVISÃO BIBLIOGRÁFICA

O tópico I da revisão bibliográfica aborda os avanços alcançados nas pesquisas de cafeeiros comerciais e perspectivas futuras. No tópico II, aspectos da técnica de genotipagem por sequenciamento são apresentados.

I - Estado da arte e perspectivas das pesquisas em *Coffea arabica* e *Coffea canephora* na era da genômica[1]

O conjunto cromossômico de *Coffea arabica* é composto por 44 cromossomos (2n = 4x), o dobro do número de cromossomos de *Coffea canephora*, e das demais espécies de *Coffea* (Krug e Mendes, 1940; Bouharmount, 1959; Kammacher e Capot, 1972; Charrier, 1978). *C. arabica* é uma espécie alotetraploide originada da hibridação natural de *C. canephora* (progenitor masculino) e *C. eugenioides* (progenitor feminino) (LASHERMES et al., 1999).

O cultivo de *C. arabica* e *C. canephora* faz da cafeicultura uma importante atividade econômica, com representativa produção na América, África e Ásia (FAO, 2003, CONAB, 2014).

1. Pesquisas em *Coffea* na Era da Genômica

A disponibilização de informações genômicas é de fundamental importância para que a produção agrícola continue a aumentar face à crescente população humana e das mudanças climáticas, e para reduzir o impacto ambiental das atividades agrícolas (MORREL et al., 2012).

Os primeiros dados de marcadores de DNA no cafeeiro foram obtidos utilizando Polimorfismos de Tamanho de Fragmentos de Restrição – RFLP, e permitiu a construção do primeiro mapa de ligação (PAILLARD et al., 1996). Estes foram utilizados por um curto período devido **à** grande quantidade de DNA requerida por tais marcadores, e à menor informatividade.

Durante os anos 90, com o desenvolvimento da PCR surgiu um grande número de marcadores moleculares para avaliar a diversidade genética a espécie, construir

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[1] Capítulo publicado no livro “Tópicos Especiais em Produção Vegetal V”, PPGPV, cap.5 p.119-136, 2015.

mapas genéticos e identificar QTLs, como os Polimorfismos de DNA amplificado ao acaso - RAPD e os Polimorfismos de comprimento de fragmentos amplificados - AFLP. Um grande salto foi conseguido com o avanço das técnicas de Sequências Simples Repetidas - SSR e Polimorfismo de Nucleotídeo Único - SNP. Nos últimos anos, um grande avanço tem ocorrido com as metodologias de Sequenciamento de Nova Geração (NGS) (WILLIAMS et al., 1990; VOS et al., 1995; LITT e LUTY, 1989; BROOKES, 1999; KOCHKO et al., 2010).

O enorme esforço técnico de pesquisas com marcadores moleculares e processos de sequenciamento de DNA ficou denominado como a Era da Genômica (RAMALHO e LAMBERT, 2004).

O sequenciamento de um genoma trata-se de desvendar as sequências de nucleotídeos do DNA de uma espécie. A primeira planta a ser sequenciada, *Arabidopsis thaliana,* levou aproximadamente 10 anos para ter o primeiro rascunho de seu genoma apresentado (*Arabidopsis* GENOME INITIATIVE, 2000). Com a utilização d**a** segunda e terceira gerações de sequenciadores (*e.g.* 454, da Roche; SOLiD, da Applied Biosystems; *Genome Analyzer IIe,* da Illumina) e poderosos programas de bioinformática e modelagem computacional, os genomas podem ser sequenciados, montados e relacionados a características fenotípicas específicas de cada genótipo em poucas semanas (NEPOMUCENO et al., 2012).

O genoma de *C. canephora* é bastante extenso, apresentando aproximadamente 710 Mb (NOIROT et al. 2003), e como *C. arabica* é tetrapl**o**ide, este valor é ainda maior para esta espécie. O tamanho do genoma da espécie modelo vegetal *Arabdopsis thaliana* que teve todo genoma sequenciado de forma pioneira é estimado em 125 Mb (*Arabidopsis* GENOME INITIATIVE, 2000). Portanto, esta grande diferença de tamanho, torna maior a complexidade e, consequentemente, o alto custo para sequenciar o genoma inteiro do cafeeiro um fator limitante quando o Projeto Genoma Café brasileiro foi proposto no ano de 2002.

Para reduzir gastos com o sequenciamento de genomas, uma estratégia que vem sendo bastante utilizada é o sequenciamento apenas do genoma estrutural (*Expressed Sequence Tags* - EST) (RAMALHO e LAMBERT 2004). Esta estratégia foi a adotada pelo Projeto Genoma Café brasileiro.

1.1 Sequenciamento do genoma do cafeeiro

ESTs são sequências produzidas a partir de clones de cDNA. Estes clones de cDNA são geralmente organizados em grandes bibliotecas que fornecem um retrato da expressão dos genes em um tecido específico ou em um órgão, em diferentes estádios de desenvolvimento e sob diferentes condições ambientais.

Diferentes grupos de pesquisa têm produzido amplos conjuntos de sequências EST em *Coffea*. No entanto, o número de ESTs disponíveis publicamente permanece baixo porque a maioria dessas sequências é de propriedade privada. Algumas instituições decidiram manter seus próprios recursos confidenciais por um tempo (O Projeto Genoma Café Brasileiro, CENICAFÉ– https://alanine.cenargen.embrapa.br/cafEST), enquanto outros (Nestlé, Institut de recherche pour le développement -IRD - http://www.sgn.cornell.edu/content/coffee.pl) o tornaram livremente disponíveis.

O Projeto Genoma Café Brasileiro gerou 130.792, 12.381 e 10.566 sequências EST de *C. arabica*, *C. canephora* e *C. racemosa*, respectivamente, reunidos em 33.000 unigenes (VIEIRA et al., 2006). O grupo de pesquisa CENICAFÉ produziu 32.961 ESTs de *C. arabica* cv. Caturra, originados dos tecidos de folhas, frutos e flores, montados em 10.799 unigenes (MONTOYA e VUONG, 2006).

Os estudos de desenvolvimento de sequências EST em *C. canephora* têm sido conduzidos por diferentes grupos de pesquisa. No IRD francês, 10.420 ESTs (montados em 5534 unigenes potenciais) foram produzidos a partir de bibliotecas de cDNA de *C. canephora* obtidas de frutos e folhas (PONCET et al., 2006). Incluindo os 47.000 ESTs, representando 13.175 unigenes, publicado pela Nestlé e da Universidade de Cornell (LIN et al., 2005), um total de 55.694 sequências estão atualmente disponíveis, compreendendo o principal recurso público para a comunidade científica. A partir de duas cultivares de *C. arabica* (Catuai vermelho e Bourbon vermelho), 1587 ESTs foram produzidos para desenvolver um microarray de cDNA contendo 1.506 ESTs de folhas e raízes embrionárias (De Nardi et al., 2006).

O GenBank oferece acesso a 187.715 ESTs de *C. arabica,* 70.407 ESTs de *C. canephora*, e *C. racemosa* com 10.838 ESTs (agosto, 2014). Este tipo de informação também é possível de se obter no banco de dados de EST da Universidade de Cornell (http://www.sgn.cornell.edu/content/coffee.pl), que disponibilizou, em parceria com a Nestlé cerca de 47.000 ESTs provenientes de cinco bibliotecas cDNA de *C. canephora* organizados por tipo de tecido (LIN et al., 2005). Após o agrupamento e montagem das sequências, 13.175 unigenes foram identificados e usados para análise comparativa com os repertórios de genes de *Arabidopsis* e de tomate (*Solanum lycopersicum*). Na comparação computacional realizada, observou-se maior conservação das sequências entre *C. canephora* e tomate (ambos do clado Euasterid) do que entre *C. canephora* e Arabidopsis (clado Eurosid). Este número considerável de sequências representa um recurso valioso para estabelecer um catálogo exaustivo de genes para o gênero *Coffea*. No entanto, na ausência de softwares robustos de previsão de genes específicos para *Coffea*, recomenda-se que sejam realizados com algoritmos de previsão treinados com os genes de Eurosids (GUYOT et al., 2009).

O projeto de sequenciamento do genoma completo de *Coffea* só iniciou em 2010. Objetivou-se sequenciar 700 milhões de pares de bases (Mb), utlilizando-se tecnologias de sequenciamento de nova geração associadas a informações já disponíveis para o gênero, como de marcadores moleculares, bancos de sequências parciais e mapas genéticos (BERTRAND, 2010). Pretendia-se, inicialmente, sequenciar um exemplar de *C. canephora*, uma vez que a espécie possui genoma dipl**o**ide, o que o torna menos complexo do que o tetrap**o**ide *C. arabica*. Os resultados obtidos para *C. canephora*, um dos ancestrais de *C. arabica,* irão facilitar o subsequente sequenciamento dessa espécie tetrapl**o**ide. As sequências encontradas serão uma importante ferramenta na localização e identificação de genes controladores de caracteres de interesse agronômico. Portanto, será possível desenvolver marcadores moleculares para selecionar variedades que apresentem tais características que permitam um incremento na qualidade da bebida, na sustentabilidade e na viabilidade econômica para a cultura (BERTRAND, 2010).

O sequenciamento completo do genoma do café (*Coffea canephora*) foi publicado na revista Science no dia 5 de setembro de 2014 (DENOEUD et al., 2014). Este projeto foi fruto de um consórcio internacional composto por 11 países – Brasil, França, Itália, Canadá, Alemanha, China, Espanha, Indonésia, Austrália, Índia e Estados Unidos. Os inéditos resultados encontrados possibilitarão prever o desenvolvimento de algumas características de interesse agronômico e acelerar o melhoramento genético do cafeeiro de características relacionadas à produtividade, à precocidade, à tolerância a estresses climáticos e à resistência a doenças, por exemplo. O estudo comprovou, a partir de uma comparação entre os genomas do café, chá e cacau, que o surgimento da biossíntese de cafeína ocorreu independente e não oriunda de um ancestral comum, como se acreditava. Por enquanto, o banco de dados resultante do sequenciamento estrutural do café está na França, mas a ideia é trazê-lo para o Brasil, a exemplo do que foi gerado pelo genoma funcional, que desde 2004, está à disposição das instituições de pesquisa do Brasil e do exterior. Com o genoma de *C. canephora* sequenciado, se iniciam as buscas pelo sequenciamento completo de *C. arabica* (INFOCAFÉ, 2014).

1.2 Diversidade genética e DNA *fingerprint*

Ao longo do tempo os descritores morfológicos utilizados em espécies inseridas em programas de melhoramento genético se tornarão insuficientes para discriminar novas cultivares. Uma estratégia alternativa é a utilização de marcadores moleculares com a finalidade de identificação genética, o que é denominado *DNA fingerprint*. Esta técnica apresenta como principais vantagens em relação à fenotipagem: i) a análise do genótipo sem interferências do ambiente; ii) o alto polimorfismo presente no material genético; iii) o baixo custo da genotipagem; iv) o curto tempo requerido para as análises moleculares (RAMALHO e LAMBERT, 2004).

Marcadores de DNA já foram utilizados com a finalidade de i) estimar a diversidade genética e distinguir variedades crioulas de genótipos de populações naturais (TESFAYE et al., 2013); ii) auxiliar na determinação da origem geográfica no processo de rastreabilidade dos produtos alimentares no momento das transações comerciais; iii) caracterização de germoplasma e análise da diversidade genética (LASHERMES et al 1996, ANTHONY et al 2002, STEIGER et al 2002),

A variação de DNA nuclear no café foi avaliado por meio de marcadores moleculares como RFLP, RAPD (LASHERMES et al, 1999; DINIZ et al, 2005; ANTHONY et al, 2002, SILVEIRA et al, 2003), AFLP (STEIGER, et al, 2002; ANTHONY et al, 2002) e SSR (COMBES et al, 2000; ANTHONY et al, 2002; MONCADA e MCCOUTH 2004; MALUF et al, 2005; PONCET et al, 2006; AGGARWAL et al, 2007; SILVESTRINI et al, 2007, VIEIRA et al, 2010, FERRÃO et al., 2014), em que foi demonstrado que a variação genética no gênero *Coffea* é baixa, especialmente entre variedades cultivadas de *C. arabica*.

Os dados de *fingerprinting* já disponíveis para *C. canephora* e *C. arabica* podem ser usados para construir uma base de dados de DNA de referência que auxilie na identificação molecular de variedades, como já foi sugerido (AGGARWAL et al, 2004; HENDRE et al, 2008; VIEIRA et al, 2010).

Diversos marcadores moleculares estão disponíveis para estabelecer a origem das variedades de café para fins científicos, mas não t**ê**m sido utlilizados e validados para fins comerciais. Com o avanço da ciência forense na área alimentíc**i**a, metodologias de análise de DNA começaram a ser requerid**a**s para avaliar grãos de café verdes ou torrados, dos grupos Ar**á**bica, Robusta ou em blends. Este tipo de informação pode ser aplicado para verificar possíveis contaminações, permitir a rastreabilidade, e verificar a autenticidade do produto (TORNICASA et al., 2010). A pesquisa sobre café neste campo ainda é incipiente. Destacam-se a utilização de métodos baseados em PCR-RFLP (SPANIOLAS et al., 2006) e PCR em tempo real (TORNICASA et al., 2010).

1.3 Cafeeiro geneticamente modificado

Os transgênicos normalmente apresentam ganhos de função, enquanto o método convencional em muitas vezes ocorre perda de função, uma vez que muitos alelos importantes são recessivos. Isto occorre uma vez que no melhoramento clássico milhares de genes são manipulados simultaneamente, enquanto nos transgênicos trata-se de um ou poucos genes (GEPTS, 2002).

Os principais objetivos do uso da técnica de engenharia genética no cafeeiro são desenvolver novas cultivares tolerantes a estresses bióticos e abióticos, como pragas, doenças, herbicidas, seca, geada, além de materiais com alta qualidade da bebida e baixos teores de cafeína.

Os estudos do transcriptoma do cafeeiro, a disponibilidade de muitas ESTs de *C. canephora* e *C. arabica*, e o desenvolvimento de bibliotecas genômicas abriram novas possibilidades na área de genômica funcional de café. Isto vai ajudar no direcionamento da inserção da característica de interesse, utilizando várias ferramentas de transformação, com o aumento de probabilidade de sucesso e **a** redução dos custos (MISHRA e SLATER, 2012).

Cafeeiros geneticamente modificados foram obtidos por diferentes grupos de pesquisa do mundo, destacando-se o Brasil (ex. ALBUQUERQUE et al., 2009), Índia(ex. KUMAR et al., 2006) e França (ex. RIBAS et al., 2011). Apesar dos avanços significativos nos últimos anos, a transformação do café ainda não é um procedimento de rotina nos programas de melhoramento. Mishra e Slater (2012) fizeram uma revisão detalhada sobre transformação genética no cafeeiro.

1.4 Técnicas de edição do genoma

Abordagens das genéticas evolutiva e quantitativa podem ser utilizadas para identificar a localização genômica e o efeito de locos de importância agronômica. No entanto, a validação dos efeitos genéticos e o uso de alelos individuais em programas de melhoramento de plantas demandam alto investimento de tempo e dinheiro (BERNARDO, 2008). Espera-se que a seleção genômica acelere a introgressão de alelos múltiplos favoráveis em populações reprodutoras. Em programa de introgressão assistida por marcadores, grandes segmentos cromossômicos são introduzidos, o que limita o uso de retrocruzamentos para testar o efeito genético de alelos individuais, e aumenta o risco de que uma introgressão de variação indesejada esteja associada (MORREL et al., 2012).

Tecnologias direcionadas de edição de genomas podem proporcionar oportunidades interessantes para alterar nucleotídeos individuais e pequenas regiões de genes nativos. O recente desenvolvimento destas tecnologias de edições específicas de genoma, como as nucleases de dedos de zinco (WEINTHAL et al., 2010) e nucleases TALE (transcription activator–like effector) (BOGDANOVE e VOYTAS, 2011) oferecem um grande potencial para resolver os problemas mencionados anteriormente. Essas tecnologias fazem uso de nucleases de sequências específicas que clivam os locos alvos, permitindo a criação de pequenas inserções e deleções (indels), a inserção de segmentos de DNA ou mesmo a substituição de alelos individuais. É até possível conseguir substituir sequências que causam mutações deletérias em linhagens elites (CHARLESWORTH e WILLIS, 2009). Ambos os métodos de nucleases de dedos de zinco e nucleases TALE têm sido aplicados com sucesso para culturas vegetais, e seus impactos esperados para o melhoramento de plantas são enormes (SHUKLA et al., 2009; Morbitzer et al., 2010).

Uma vez que os ciclos de melhoramento do cafeeiro são longos, recomenda-se que estudos nesta área comecem a ser desenvolvidos. As técnicas de edição de genoma podem vir a contribuir na obtenção de características específicas com maior eficácia e rapidez, e menor custo.

1.5 Mapeamento genético

A maioria dos mapas genéticos interespecíficos de café foi construída para identificar QTLs envolvidos em características contrastantes existentes em várias espécies selvagens. Mapas genéticos de *C. canephora* e cruzamentos interespecíficos estão disponíveis (PAILLARD et al, 1996; KY et al, 2000; LASHERMES et al, 2001; HERRERA et al, 2002, AKAFFOU et al., 2003; COULIBALY et al, 2003; LEFEBVRE-PAUTIGNY et al., 2010, dentre outros). Essas informações disponíveis para *C. canephora* são importantes para que um mapa consenso seja criado para espécies de *Coffea*.

Mapas genéticos para *C. arabica* são mais escassos devido a algumas razões, como a complexidade de um genoma tetrapl**o**ide, o alto nível de homozigose e o pequeno número de polimorfismos (PEARL et al 2004; DE OLIVEIRA, 2007).

1.6 Seleção Assistida por Marcadores e Seleção Genômica Ampla

A seleção assistida por marcadores é a correlação genética entre a marca e os genes envolvidos no controle dos caracteres expressos (RAMALHO e LAMBERT, 2004). A técnica pode ser utilizada em duas vertentes: i) para acelerar a recuperação de alelos de interesse; ou ii) auxiliar na eliminação de alelos indesejáveis aos programas de melhoramento, que estão ligados a locos de interesse (HOSPITAL e CHARCOSSET, 1997).

O desenvolvimento de genotipagem ‘high-throughput’ levou a uma mudança nas análises de mapeamento de QTLs para estudos tradicionais de associação. A nova proposta, ao invés de focar em duas linhagens parentais contrastantes fenotipicamente, permite que no mapeamento associativo seja avaliada a correlação entre fenótipo e genótipo em conjuntos de indivíduos não aparentados. Com isto, amostra-se uma diversidade genética bem maior, resultante de muito mais eventos de recombinação, além de evitar as gerações de cruzamentos demorados que são necessárias para o mapeamento de QTLs (MYLES et al., 2009).

Marcadores genéticos de alta densidade estão sendo utilizados em estudos de associação de genoma (GWASs) e também podem ser explorados para seleção genômica (MORREL et al., 2012). A seleção genômica ampla é uma forma de seleção assistida por marcadores, em que um conjunto de dados moleculares é usado para fazer previsões fenotípicas (MEUWISSEN et al, 2001; HEFFNER et al, 2009). Seleção genômica e GWASs podem usar os mesmos dados genotípicos e fenotípicos. O que difere, principalmente é que os modelos de seleção genômica enfatizam a identificação de polimorfismos individuais controladores de características complexas por uma predição dos valores fenotípicos, que são baseados em um conjunto de dados de treinamento. Como os GWASs, a aplicação da seleção genômica estava sendo limitada pelo custo e pela disponibilidade de dados densos de marcadores do genoma. No entanto, com o surgimento de metodologias de genotipagem em larga escala as informações moleculares passaram a apresentar baixo custo e tempo reduzido (ANDOLFATTO et al., 2011; ELSHIRE et al., 2011).

Hoje, a eficiência da seleção genômica está muito abaixo da meta sugerida na proposta inicial. A precisão está limitada, principalmente, pela ineficiência na predição do fenótipo. Apesar destes problemas, os métodos atuais de seleção genômica mostram-se de 2-3 vezes mais rápidos do que pelo ciclo de reprodução tradicional. Espera-se que a seleção genômica revolucione a reprodução na próxima década (MORREL et al., 2012).

O grande potencial apresentado pela Seleção Genômica Ampla (Genome-Wide Selection – GWS) tem estimulado alguns grupos de pesquisa cafeeira a investir esforços na utilização da técnica para auxiliar na predição de genótipos de interesse com grande eficácia e prazos bem mais curtos. Ressalta-se que o laboratório de Bioquímica e Biologia Molecular do CCA-UFES está inserido em um projeto de GWS para *C. canephora,* em parceria com o Incaper e Embrapa Café.

1.7 Bancos de dados do Cafeeiro disponíveis na web

Nome	**Descrição**
The CENICAFE coffee databases – Colombia	Banco de Dados de 32.000 ESTs de *C. arabica* e *C. liberica*. Disponível em: http://bioinformatics.cenicafe.org/ Cristancho et al. (2006)
TropGENE DB CIRAD – France	Biblioteca com 55.296 BACs e 253 marcadores SSR de *C. canephora* Disponível em: http://tropgenedb.cirad.fr/tropgene/JSP/interface.jsp?module=COFFEE Leroy et al. (2005); Ruiz et al. (2004)
Ccmb coffee database – India	Banco de dados de caracterização molecular do germoplasma café disponível na Índia.Disponível em: http://www.ccmb.res.in/coffeegermplasm/index.htm (Em construção)
The Brazilian Coffee Genome EST Project CBP&D-Café – Brasil	130.792, 12.381 e 10.566 sequ**ê**ncias de C. arabica, C. canephora e C. racemosa, respectivamente, (37 bibliotecas de cDNA). Disponível em: http://www.lge.ibi.unicamp.br/cafe/ Vieira et al. (2006)
Coffee DNA -University of Trieste, Italy	Banco de dados com 13,686 ESTs, 266 Microsatellites, 43 retrotransposon. Disponível em: http://www.coffeedna.net/
MoccaDB – IRD, France	Informações de marcadores RFLP, EST-SSR, SSR, SNP (to date, 638 markers) de aproximadamente 38 espécies de Rubiaceae. Disponível em: http://moccadb.mpl.ird.fr/ Plechakova et al. (2009)
The SOL Genomics Network (SGN) Cornell University – USA	Informações genômicas da família Solanaceae e da família relacionada no clade Euasterid. Apresenta 47.000 ESTs de café (*C. canephora* var robusta) divulgados pela Universidade de Cornell e Nestlé S.A. Disponível em: http://sgn.cornell.edu/ Mueller et al. (2005)

Tabela modificada e traduzida de Kochko et al., 2010.

2. Fenotipagem

Os estudos moleculares no melhoramento de plantas precisam estar associados à caracterização fenotípica. As culturas vegetais podem ser propagadas por clonagem e mantidas como linhas puras. Isso torna possível sequenciar um genótipo apenas uma vez, porém fenotipá-lo ao longo do tempo e em ambientes diferentes (NORDBORG et al., 2008).

Portanto, é necessário obter as informações em campo com a maior precisão experimental possível. As plantas obtidas por métodos biotecnológicos apresentam as mesmas necessidades de serem avaliadas intensivamente em campo para verificar se irão expressar as características desejadas. Portanto, a fenotipagem continua sendo de extrema importância para se avançar na caracterização e avaliação de materiais genéticos vegetais. A necessidade de grande quantidade de informações fenotípicas faz com que a importância da biometria na Era da Genômica seja ainda maior do que no passado (RAMALHO e LAMBERT, 2004).

3. Perspectivas futuras

As projeções divulgadas sobre o enorme crescimento populacional e a respeito dos impactos das mudanças climáticas globais evidenciam a necessidade da agricultura se desenvolver a passos largos para que seja possível suprir as demandas geradas por tais eventos.

Os bancos de informações genéticas que já estão disponíveis precisam ser analisados criticamente para que seja possível avançar nas avaliações com as novas tecnologias que estão surgindo, mas também é preciso aprender com as informações que já estão disponíveis na literatura. E para isto, é necessário buscar as várias informações geradas por diferentes grupos de pesquisas e integrá-las.

A compreensão dos mecanismos genéticos e o conhecimento da diversidade disponível permitirão obter germoplasmas de cafeeiros mais produtivos, tolerantes a estresses bióticos e abióticos, com maior qualidade de bebida e importância nutricional. As pesquisas multidisciplinares possuem o potencial de proporcionar um incremento significativo nos programas de melhoramento do cafeeiro, seja via engenharia genética, seleção genômica ampla assistida por marcadores, edição de genomas, dentre outras metodologias. As técnicas moleculares precisam estar associadas com análises fenotípicas que gerem informações em volume e qualidade comparável com as informações genômicas que já se encontram disponíveis. Para lidar com este vultoso conjunto de informações precisa-se avançar, paralelamente, no desenvolvimento de softwares e na formação de profissionais na área de bioinformática.

4. Referências

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II – Genotipagem por sequenciamento: uma abordagem para estudos em culturas vegetais

1. Plataformas de sequenciamento

O advento do sequenciamento de nova geração (NGS) promoveu grandes avanços nas áreas de genômica e transcriptômica (METZKER, 2010; BARBAZUK & SCHNABLE, 2011). As plataformas NGS trabalham em quatro etapas principais, sendo: 1ª) redução da complexidade do genoma em estudo, 2ª) Amplificação dos fragmentos (PCR), 3ª) Sequenciamento dos produtos de PCR, e 4ª) Análises dos dados (bioinformática). Três plataformas de NGS comercialmente disponíveis e bastante utilizadas são as 454 FLX da Roche, a Solexa da Illumina, e a SOLiD da Applied Biosystems .

Os polimorfismos de nucleotídeo único (SNPs) vêm sendo muito utilizados como marcadores moleculares em estudos genéticos vegetais na última década. As informações obtidas com o sequenciamento de diversos organismos revelam que os SNPs e InDels estão presentes em abundância nos genomas de várias espécies, inclusive de plantas (VIGNAL et al., 2002; HAYASHI et al., 2004). A possibilidade de automação em plataformas de sequenciamento possibilita, com essa grande quantidade de marcadores moleculares disponíveis, que seja possível realizar a construção de mapas genéticos saturados, estudos de pedigree, distância genética, mapeamento fino de regiões específicas e estudos de associação com características fenotípicas (MAMMADOV et al., 2012; YANG et al., 2013; VIGNAL et al., 2002). Na literatura há grande disponibilidade de revisões e estudos de SNPs e InDels em plantas (GUPTA et al., 2001; RAFALSKI et al., 2002; HEESACKER et al., 2008; GANAL et al., 2009; DURAN et al., 2009; HOLLISTER et al., 2009; AMAR et al., 2011; GANAL et al., 2011; MAMMADOV et al., 2012; EMANUELLI et al., 2013).

Um SNP é originado por uma mutação pontual no genoma, que substitui um nucleotídeo por outro. As mutações em células reprodutivas de um indivíduo são herdadas pela progênie e após algumas gerações o SNP pode se estabelecer na população. Apesar de ser possível a ocorrência de qualquer um dos quatro nucleotídeos, comumente os SNPs são bialélicos devido à maneira que são originados e distribuídos entre os indivíduos da população (BROWN, 2002).

Diversas metodologias de detecção de SNPs por sequenciamento estão disponíveis, com metodologias do tipo: a) CRoPS (*Complexity Redution of polymorphic Sequencings*) – baseia-se no sequenciamento de fragmentos de marcadores AFLP (VAN ORSOUW et al., 2007); b) Sequenciamento completo do genoma (HILLIER et al., 2008); c) RAD-Seq (*Restriction-site Associated DNA Sequencing)* – sequenciamento com alta cobertura do genoma (BAIRD et al., 2008); d) Sequenciamento de exoma - sequenciamento das regiões codificadoras (éxons) do genoma (NG et al., 2009); e) Sequenciamento de DNA metilado (*methylated DNA sequencing*) – avaliação dos perfis de metilação, que diferenciam-se de acordo com os tipos celulares, tecidos, fase do desenvolvimento e condições fisiológicas dos organismos (BRUNNER et al., 2009); f) GBS (*Genotyping by Sequencing*) – sistema simples e altamente multiplex, que utiliza bibliotecas genômicas e sequenciamento de nova geração - plataforma Illumina (ELSHIRE et al., 2011).

Algumas dessas metodologias baseadas em NGS combinam a descoberta de polimorfismo e genotipagem em um único passo (BAIRD et al., 2008; HUANG et al., 2009; ELSHIRE et al., 2011). Ou seja, não se definem *a priori* quais os SNPs serão genotipados ao longo do genoma. Os SNPs são detectados e genotipados nos indivíduos, e depois se selecionam quais deles serão usados nas análises com base em um conjunto de critérios de filtragem.

As NGS permitem o sequenciamento de DNA em larga escala, de forma mais rápida e com custo reduzido (Tabela 1). Dentre as técnicas disponíveis, nesta revisão aprofundar-se-á as discussões na metodologia de Genotipagem por Sequenciamento (GBS) desenvolvida por Elshire et al. (2011), na Universidade de Cornell (EUA).

Tabela 1. Utilização de Sequenciamento de Nova geração para estudos em plantas

Análise	**Espécie**	**Referência**
Identificação de marcadores moleculares (SNPs)	Arroz (*Oriza sativa*)	Wang et al., 2011
	Gramínea *(Aegilops tauschii)*	You et al., 2011
	Cevada e trigo	Poland et al., 2012ª
	Algodão (*Populus trichocarpa*)	Geraldes et al., 2011
Melhoramento genético, Estudos de associação (GWAS) e Seleção genômica	Trigo (*Triticum*)	Poland et al., 2012b
	Pinheiros (*Pinus contorta*, *Picea glauca)*	Chen et al., 2013
	Milho (*Zea mays*)	Ogugo et al., 2014
	Feijão	Hart e Griffiths, 2015
Mapeamento de genes/QTL, mapa de ligação	Milho (*Zea mays*) e Cevada (*Hordeum vulgare*)	Elshire et al., 2011
	Arroz (*Oryza sativa*)	Spindel et al., 2013
	Framboesa (*Rubus idaeus*)	Ward et al. 2013
Diversidade molecular, genética de populações e estudos filogenéticos	Cevada (*Hordeum vulgare*)	Fu, 2012
	Gramínea ‘Switchgrass’	Lu et al., 2012
	Batata (*Solanum tuberosum*)	Uitdewilligen et al., 2013
	Ciperáceas do gênero *Carex*	Escudero et al., 2014

2.1 Genotipagem por Sequenciamento (GBS)

A genotipagem por sequenciamento (GBS) foi desenvolvida no laboratório Buckler da Universidade de Cornell, por Rob Elshire. Trata-se de um sistema simples e altamente multiplex, para a construção de bibliotecas para a plataforma de sequenciamento de nova geração Illumina.

O GBS é capaz de identificar centenas de milhares de polimorfismos do tipo SNPs e InDels, para utilização em análises genéticas (Figura 1) (CORNELL, 2015; ELSHIRE et al., 2011). Ao contrário dos métodos tradicionais, no GBS, a descoberta de marcadores e a genotipagem são feitas de forma simultânea. Por isso, uma inovação da técnica é que pode ser aplicada tanto a organismos modelos, que já possuem sequências referência de alta qualidade de referência do genoma, mas também para espécies com ausência de informações genômicas preexistentes (DAVEY et al., 2011; POLAND e RIFE, 2012).

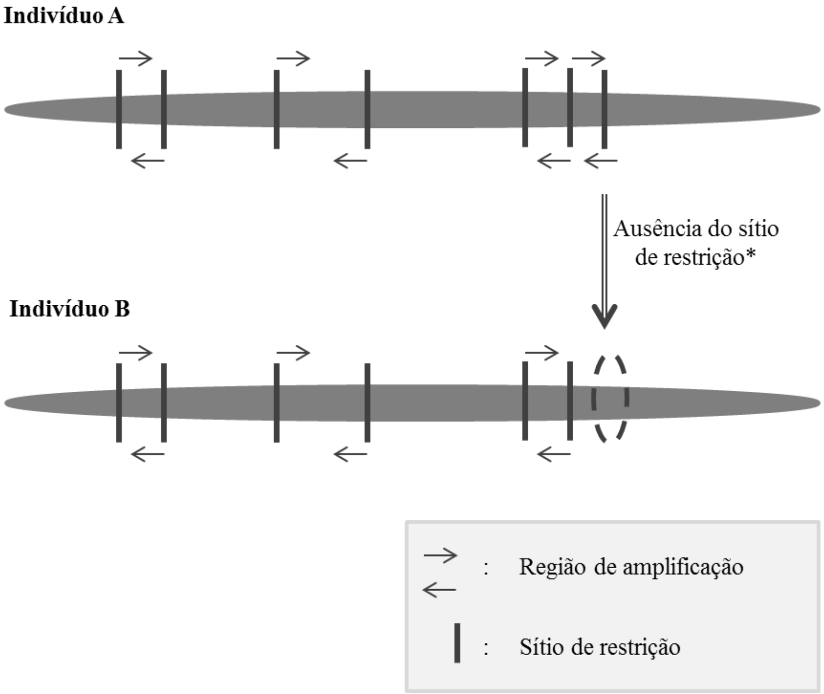

Figura 1. Representação de segmento cromossômico em dois indivíduos para ilustrar a essência da técnica de GBS *A perda do sítio de restrição pode ser ocasionada pela substituição de um nucleotídeo (SNP), ou pela perda/adição de um nucleotídeo (*InDels*).

As principais vantagens da GBS são: menor mão de oba, não há necessidade de fracionamento dos fragmentos de DNA por tamanho, utiliza menos etapas de PCR e purificação, reduzindo bastante o custo do *barcoding*. A técnica emprega a utilização de enzimas de restrição com a finalidade de reduzir a complexidade do genoma e evitar a fração que contenha sequências repetitivas do genoma (CORNELL, 2015). As vantagens e desvantagens da técnica encontram-se resumidas na Figura 2.

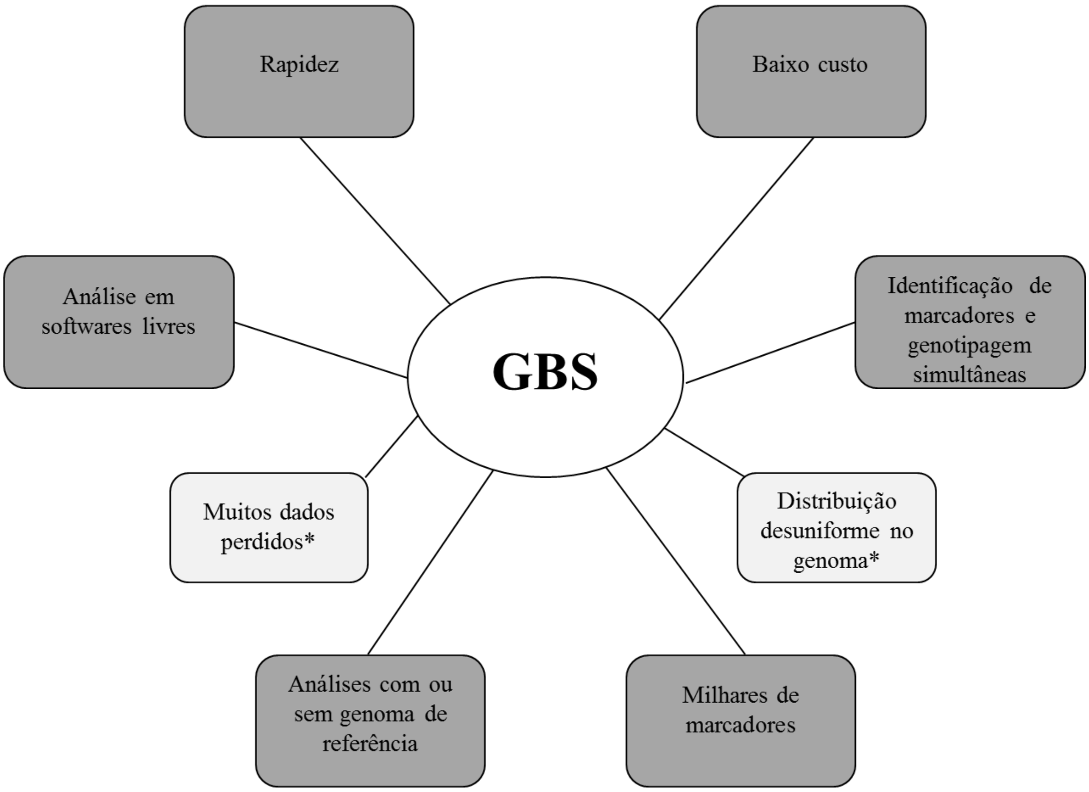

Figura 2. Características da Genotipagem por Sequenciamento (GBS)

*A presença de dados perdidos e a distribuição desuniforme no genoma são as desvantagens da técnica de GBS, mas podem ser contornadas utilizando-se algumas metodologias que serão apresentadas.

A tecnologia de GBS tem sido utilizada para sequenciamento de transcritos, perfis de expressão gênica, sequenciamento e ressequenciamento de genomas com a finalidade de obtenção de um número elevado de polimorfismos de nucleotídeo único (SNPs). Com isso, é possível explorar a diversidade dentro de cada espécie, construir mapas e realizar estudos de genética de associação (GWAS) (METZKER, 2010). A metodologia possibilita a seleção genômica sem a necessidade de ter que desenvolver nenhuma ferramenta molecular prévia, ou determinar a estrutura de uma população sem o conhecimento prévio do genoma ou da diversidade nas espécies (CRONN et al., 2008; HUANG et al., 2009; HUANG et al., 2010; METZKER, 2010).

A metodologia de GBS já foi utilizada em vegetais para: Identificação de SNPs (MARDIS, 2008; FUTSCHIK e SCHLOTTERER, 2010; YOU et al., 2011; WANG et al., 2011); Diversidade molecular, genética de populações e estudos filogenéticos (FU, 2012; LU et al., 2012); Mapeamento de genes/QTLs, Estudos de associação (BAIRD et al., 2008; ELSHIRE et al., 2011; POLAND et al., 2012a); Caracterização de germoplasma (FU et al., 2014; HAHN et al., 2014); Melhoramento genético, Seleção Genômica (POLAND et al., 2012b).

A metodologia proposta por Elshire et al., 2011, ilustrada na Figura 3, envolve uma sequência de oito etapas, ilustradas a seguir:

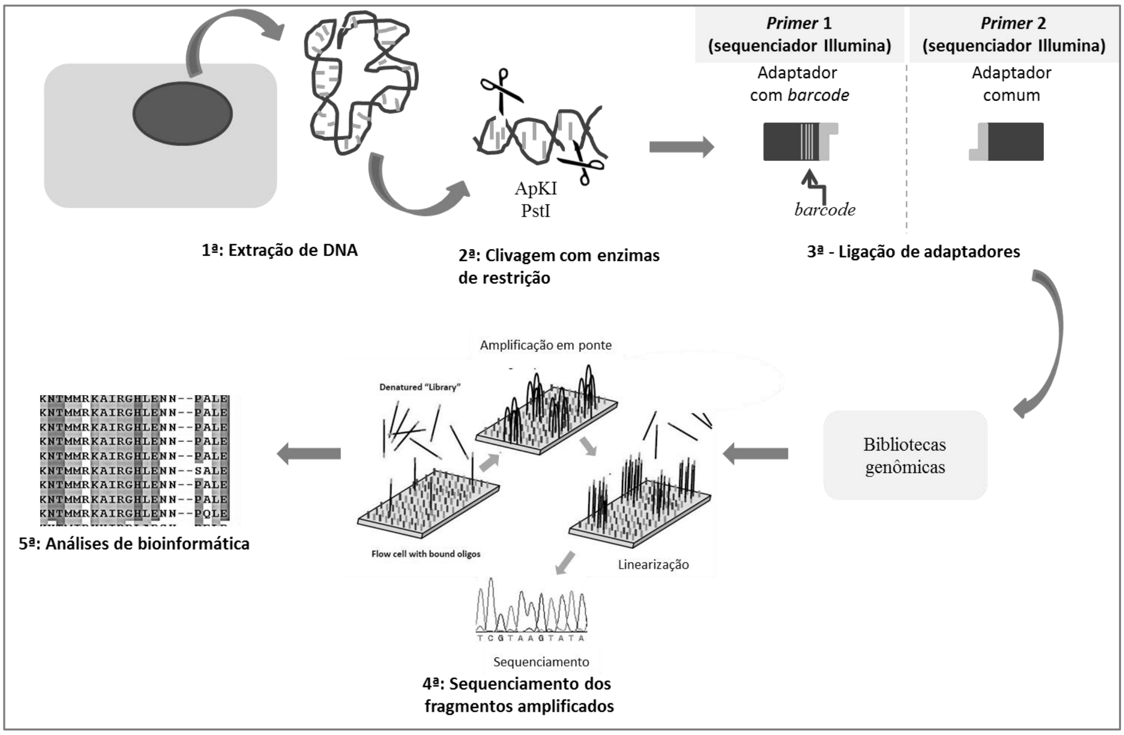

Figura 3. Principais etapas da Genotipagem por sequenciamento (GBS).

1) A extração de DNA para a técnica de GBS deve ser realizada com Kits comerciais. São selecionadas as amostras que atendem à exigência da metodologia, ou seja, DNAs livres de contaminantes, RNA e simbiontes e, de preferência, com menos de 5% de DNA organelar. Cada reação utiliza 100 ng de DNA de alta qualidade e elevado peso molecular;

2) A enzima de restrição ideal para ser utilizada depende da cobertura necessária para cada experimento, e das sequências repetitivas presentes no genoma. A ApeKI é considerada uma enzima de corte frequente, ao contrário das PstI e EcoT22I, que são de corte raro. Dessa forma, as duas últimas enzimas produzem menos fragmentos diferentes do que a primeira, resultando em uma biblioteca de menor tamanho. Para espécies em que a técnica do GBS ainda não foi aplicada, normalmente testam-se as três enzimas no genoma do organismo de estudo. A enzima selecionada para prosseguir com as análises será aquela que

gerar a biblioteca de fragmentos menos complexa, ou seja, que apresentar menos fragmentos com regiões repetitivas;

3) Às extreminades dos fragmentos clivados são ligadas a adaptadores com *barcode* e adaptadores sem barcode, ou comuns. O *barcode* trata-se de uma sequência de DNA específica que serve para identificar cada genótipo em ensaios multiplex;

4) Após a etapa de ligação de adaptadores, realiza-se uma PCR com todas as amostras misturadas. Os *primers* utilizados na reação são complementares tanto às sequências dos adaptadores, quanto aos oligonucleotídeos da plataforma de sequenciamento, em que os fragmentos ficarão aderidos;

5) Sequenciamento do DNA - produtos da PCR são purificados e, em seguida, avalia-se o tamanho dos fragmentos amplificados. Ressalta-se que apenas os fragmentos ligados a um adaptador com *barcode* em uma extremidade, e um adaptador comum na extremidade oposta serão sequenciados. Isto acontece uma vez que fragmentos que não seguem esta composição não são amplificados em ponte (*bridge PCR*) de maneira eficiente. Além disso, fragmentos grandes (> 1Kpb) também não são amplificados visto que o tamanho interfere na formação das pontes;

6) Após o sequenciamento iniciam-se as análises de bioinformática para a detecção de SNPs utilizando softwares específicos. A prospecção dos marcadores nas sequências brutas geradas pelo sequenciamento envolve várias etapas computacionais. Os fragmentos são agrupados pelos *barcodes* e, posteriormente, alinhados de acordo com um genoma de referência, ou considerando-se as próprias sequências (Figura 4);

7) Uma vez detectados os SNPs, os mesmos devem ser filtrados considerando-se os dados perdidos, os parâmetros de frequência alélica mínima (mAF) e a cobertura do sequenciamento. Após a filtragem, gera-se um arquivo com a chamada dos SNPs (*SNP calling*) nos formatos hapmap e/ou VCF, que serão analisados de acordo com os objetivos de cada estudo (GLAUBITZ et al. 2014). Apesar da aplicação desses parâmetros reduzirem muito a quantidade dos SNPs iniciais, eles devem ser utilizados para adequar os dados às características biológicas da população em estudo e, portanto, aumentar a confiabilidade dos

polimorfismos detectados. Mas, ainda com o filtro, milhares de marcadores continuam disponíveis para as análises posteriores;

8) Os *pipelines* para as análises de GBS podem ser realizados no *software* TASSEL. Análises como a de filtragem dos marcadores, estudos de associações de características, mapeamento associativo utilizando-se Modelo Linear Geral (MLG) e Modelo Linear Misto (MLM), padrões evolutivos, estrutura de populações e desequilíbrio de ligação podem ser realizadas neste *software*. Uma característica importante do Tassel é a capacidade de considerar para as análises tanto marcadores SNPs quanto InDels, uma vez que este último tipo de polimorfismo, apesar da grande importância, em muitos casos são desconsiderados das análises (BRADBURY et al., 2007).

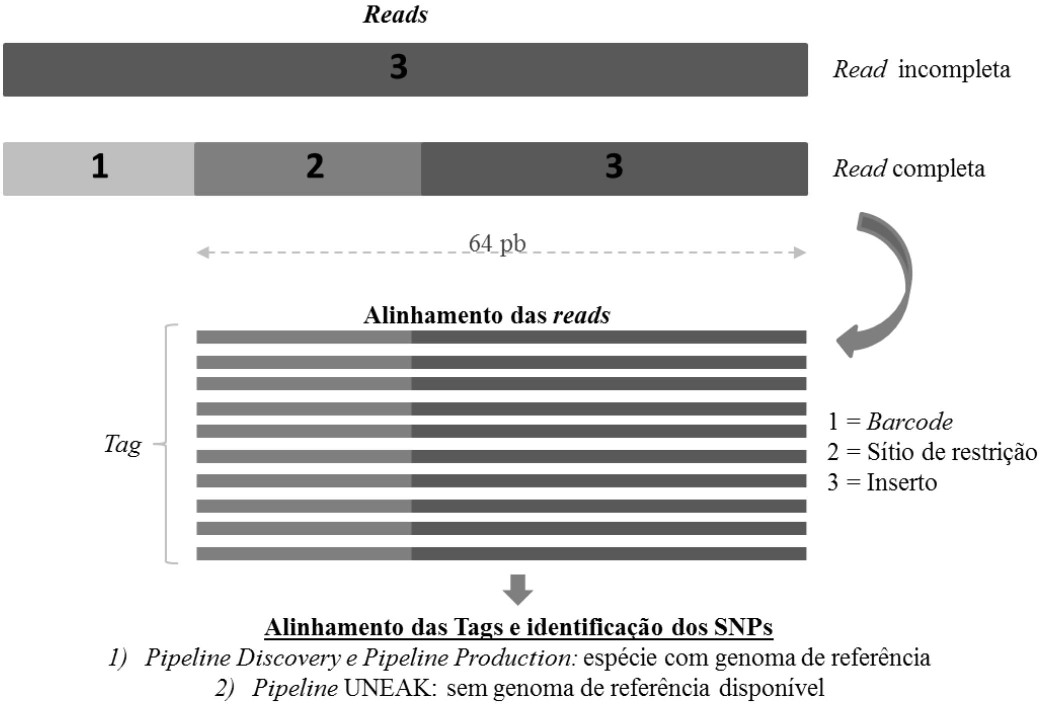

Figura 4. Resumo das etapas de obtenção do SNP call.

Uma questão recorrente é sobre qual a quantidade de SNPs que serão identificados nas amostras. É importante salientar que não existe um padrão, cada experimento possui o potencial de gerar um número diferente de SNPs, que normalmente são alguns milhares. Essa quantidade é influenciada por fatores como o tamanho do genoma a ser avaliado, a heterozigose esperada, a enzima de restrição utilizada, o quanto as amostras em estudo refletem a diversidade genética da espécie, e se existe um genoma de referência (Figura 5). Destaca-se que apenas a possibilidade de alinhamento com um genoma de referência pode aumentar em três a quatro vezes a quantidade de SNPs encontrada.

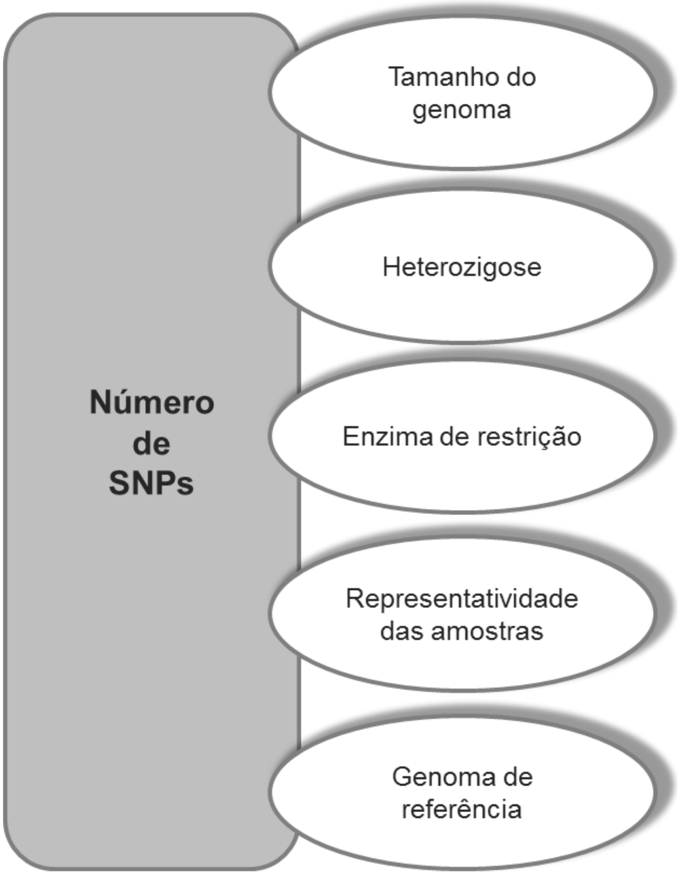

Figura 5. Fatores que influenciam na quantidade de SNPs encontrados (*SNP call*).

A grande quantidade de dados perdidos é o principal problema do GBS, que se deve a fatores técnicos ou biológicos. O fator técnico relaciona-se à deficiência na amostragem do genoma, principalmente em espécies com genomas extensos. Já o fator biológico ocorre pela existência de regiões genômicas ou sítios de clivagem de polimorfismos não compartilhados entre os genótipos. A imputação de dados é uma metodologia em que os dados faltantes são substituídos por valores estimados, sendo muito utilizada para resolver a questão dos dados perdidos. Na literatura várias metodologias de imputação estão disponíveis, sendo que as características de cada estudo devem ser consideradas para fazer a escolha da fórmula de imputação mais adequada (GLAUBITZ et al., 2014; MARCHINI e HOWIE, 2010).

Sequenciar a mesma biblioteca várias vezes, ou usar menor quantidade de amostras diferentes por reações multiplex, também são alternativas possíveis para reduzir a quantidade de dados perdidos, mas que elevam o custo da GBS. Como resultado, obtém-se maior quantidade de dados por amostra de uma mesma sequência (maior profundidade), o que reduz a porcentagem de dados perdidos (GLAUBITZ et al., 2014; MARCHINI e HOWIE, 2010).

Avanços significativos foram observados nos estudos genômicos na última década com o surgimento das tecnologias de sequenciamento de nova geração (NGS). A redução do tempo de análise e dos custos de genotipagem conseguidos pelo GBS, e o desenvolvimento de poderosas ferramentas de bioinformática, apontam para um aumento abrupto na eficiência dos programas de melhoramento vegetal. Com esse cenário, vislumbra-se a possibilidade de conseguir atender às demandas de aumento de produção mundial de alimentos, em consonância com o aumento da qualidade dos produtos agrícolas. Essas novas tecnologias são fundamentais inclusive para se avançar com os estudos genômicos em espécies vegetais poliploides, em que as análises genômicas tradicionais enfrentam grandes dificuldades.

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CAPÍTULO I – Prospecção de SNPs no genoma de *Coffea canephora*

1. Introdução

Coffea canephora possui 2n=2x=22 cromossomos. A espécie é originária de uma ampla região quente, úmida e de baixa altitude, que se estende da Costa oeste à região central do continente africano, predominantemente nas regiões ocidental, centro-tropical e subtropical do continente (CARVALHO et al., 1946; BERTHAUD, 1986).

O sequenciamento completo do genoma de *Coffea canephora* foi realizado por um grupo de pesquisadores participantes de um consórcio internacional composto por 11 países (DENOEUD et al., 2014). A utilização destes inéditos resultados permitirá acelerar o melhoramento genético do cafeeiro de características relacionadas à produtividade, precocidade, tolerância a estresses climáticos e resistência a doenças, dentre outras.

Importantes variações fenotípicas podem ser proporcionadas por variações alélicas herdáveis, como os polimorfismos de nucleotídeos simples (SNPs). O desenvolvimento de metodologias de sequenciamento *high throughput* tornaram os SNPs altamente atrativos como marcadores genéticos (PARIASKA-TANAKA et al., 2015; PATEL et al., 2015; WINFIELD et al., 2015).

O polimorfismo gerado pelos marcadores SNPs corresponde a uma única mudança de base na sequência de DNA, ou seja, em indivíduos da mesma espécie é possível encontrar dois nucleotídeos diferentes para uma mesma posição no genoma. Para que uma mutação aleatória não seja erroneamente considerada um SNP, apenas são considerados como marcadores genéticos, os alelos com frequência igual ou maior do que 1% (BROOKES, 1999).

A Genotipagem por Sequenciamento (GBS) é um sistema de construção de bibliotecas para sequenciamento de nova geração capaz de identificar centenas de milhares de polimorfismos do tipo SNPs, para utilização em análises genéticas (CORNELL, 2015; ELSHIRE et al., 2011). Ao contrário dos métodos tradicionais, no GBS, a descoberta de marcadores e a genotipagem são feitas de forma simultânea. Por isso, uma inovação da técnica é a possibilidade de ser aplicada tanto a organismos modelos, que já possuem genoma de referência, mas também para espécies com ausência de informações genômicas (DAVEY et al., 2011; POLAND e RIFE, 2012). Objetivou-se prospectar SNPs e caracterizar a ocorrência no genoma de *Coffea canephora*.

2.0 Material e métodos

2.1 Descrição dos cruzamentos

Famílias de irmãos completos oriundas de cruzamentos controlados entre clones de *C. canephora*, oriundos do Programa de Melhoramento do Incaper, foram conduzidos na Fazenda Experimental de Marilândia (FEM), localizada na região Noroeste do Estado do Espírito Santo.

As progênies dos cruzamentos entre os clones 76x48 (67 progênies) e o cruzamento entre os clones 109x120 (55 progênies) / 120x109 (19 progênies) foram levadas a campo em Agosto de 2008 e Maio de 2009, respectivamente. Os progenitores dos cruzamentos são clones de café Conilon com características de interesse para a cafeicultura, sendo: I) clone 48: clone de conilon, de porte médio a alto, grãos grandes, maturação média, suscetível à ferrugem e à seca; II) 76: clone com características de Conilon, porte médio, vigoroso, maturação média, mediamente resistente a ferrugem e tolerante à seca; III) clone 109: clone com características de Conilon, porte médio, maturaçao média, suscetivel à ferrugem e à seca; IV) 120: clones de café Conilon de porte médio, maturação média, suscetível à ferrugem, vigoroso e tolerante à seca.

Utilizou-se espaçamento de 3,0 x 1,0 m, sem implantação de sistema de irrigação, e tratos culturais conforme a recomendação para a cultura (Ferrão et al., 2007).

2.2 Extração de DNA

Utilizaram-se folhas jovens e completamente expandidas, de cada indivíduo dos cruzamentos, coletadas na Fazenda Experimental de Marilândia

(Incaper). A extração de DNA foi realizada no Laboratório de Biologia Molecular e Bioquímica do Centro de Ciências Agrárias, Alegre-ES. O tecido foliar foi pulverizado em presença de nitrogênio líquido, e para extração de DNA usou-se o DNeasy Plant mini Kit (Qiagen, Valencia, CA), de acordo com instruções do fabricante. A caracterização da quantidade e qualidade das amostras de DNA foram verificadas em NanoDrop 2000 (Thermo Fisher Scientific, Waltham, MA, EUA) e visualizada em gel de agarose a 1%. Para atender à exigência da metodologia, foram obtidas amostras de DNA livres de contaminantes, RNA e simbiontes e, de preferência, com menos de 5% de DNA organelar. Para cada reação utilizou-se 100 ng de DNA de alta qualidade e elevado peso molecular. Os DNAs foram pipetados em placas de PCR e enviados para a Universidade de Cornell – EUA (Institute of Biotechnology) para proceder a Genotipagem por Sequenciamento.

2.3 Genotipagem por sequenciamento (GBS)

A GBS é uma técnica que utiliza enzimas de restrição para amostrar o genoma e detectar marcadores moleculares SNP nos fragmentos gerados. Neste estudo, adotou-se um protocolo de GBS descrito por Elshire et al 2011. As 145 amostras de DNA foram multiplexadas em sequenciador Ilumina na Universidade de Cornell.

O DNA foi digerido com a enzima de restrição ApeKI, enzima de corte frequente que permitiu gerar uma biblioteca de fragmentos menos complexa para *C. canephora*, ou seja, que possuia menos fragmentos com regiões repetitivas. Às extreminades dos fragmentos clivados foram ligados um adaptador com *barcode* e um adaptador sem *barcode* (comum). O *barcode* trata-se de uma sequência de DNA específica que serve para identificar cada genótipo em ensaios multiplex.

Após a etapa de ligação de adaptadores, realizou-se uma PCR com todas as amostras misturadas, sendo que os *primers* utilizados na reação são complementares tanto às sequências dos adaptadores, quanto aos oligonucleotidios da plataforma de sequenciamento, em que os fragmentos ficam aderidos. Apenas os fragmentos ligados a um adaptador com *barcode* em uma extremidade, e um adaptador comum na extremidade oposta são sequenciados. Isto acontece uma vez que fragmentos que não seguem esta composição não são amplificados em ponte (*bridge PCR*) de maneira eficiente. Além disso, fragmentos grandes (> 1Kpb) também não são amplificados visto que o tamanho interfere na formação das pontes.

2.4 Análises estatísticas

Uma vez realizado o sequenciamento, procedeu-se com as análises de bioinformática, e cáculos de PIC, MAF, dissimilaridade e heterozigosidade no software Tassel versões 3.0 e 5.2.14 e IGV 2.3.

A prospecção dos marcadores nas sequências brutas geradas pelo sequenciamento envolveu várias etapas computacionais. Os fragmentos foram agrupados pelos *barcodes* e, posteriormente, alinhados de acordo com o genoma de referência de *Coffea canephora,* publicado em 2014 (DENOEUD et al., 2014).

O comando computacional para a chamada de SNPs (SNP *call)* proposto por Glaubitz et al., 2014 foi implementado para alinhar as várias sequências (*tags*) dos mesmos locais físicos do genoma de *C. canephora* através das amostras individuais. A saída de dados foi gerada por cromossomo, em arquivo de formato HapMap (.hmp.txt).

Uma vez detectados os SNPs, realizou-se uma filtragem considerando-se os dados perdidos, os parâmetros de frequência alélica mínima (MAF) e a cobertura do sequenciamento. Após a filtragem, arquivos com a SNP *call* nos formatos *hapmap* foram analisados.

As sequências dos *barcodes* foram removidas dos dados brutos das sequências obtidas pela plataforma Illumina. As sequências remanescentes foram então clivadas ou preenchidas com adeninas (“A”) na extremidade 3’ para atingirem o tamanho de 64 pb.

A tabela de genótipos resultantes foi então filtrada usando os parâmetros de Cobertura mínima local, Frequência máxima do menor alelo, Taxa mínima de cobertura e Frequência mínima do menor alelo (Tabela 1).

Tabela 1. Parâmetros utilizados para a filtragem dos SNPs de cruzamentos entre clones de Conilon do Programa de Melhoramento Genético do Incaper

Plugin	Opção	Valor	Descrição
GBSHapMapFiltersPlugin	mnSCov	0.8	Cobertura mínima local
GBSHapMapFiltersPlugin	mxMAF	1	Frequência máxima do menor alelo
GBSHapMapFiltersPlugin	mnTCov	0.1	Taxa mínima de cobertura
GBSHapMapFiltersPlugin	mnMAF	0.01	Frequência mínima do menor alelo

A fim de estimar a distribuição de SNPs gênicos e intergênicos nas famílias de irmãos completos de café Conilon, o conjunto de SNPs obtidos pela GBS foram comparados com o genoma do cafeeiro (pseudocromossomos 1 ao 11) disponibilizado pelo Projeto Genoma Café (DENOEUD et al., 2014), acessadas em http://www.coffee-genome.org, em agosto de 2015 (DEREEPER et al., 2015), com auxílio do software Geneious (versão 2.3).

3.0 Resultados e Discussão

Os detalhes da GBS em relação à quantidade de leituras de sequenciamento e a sequência dos *barcodes* utilizadas em cada indivíduo estão disponíveis na Tabela 2. Em média, foram feitas 2.177.528 leituras de *barcodes*/indivíduos.

Esses valores foram satisfatórios para dar prosseguimento às análises em todos os indivíduos, com excessão do número 93 (109x120R81), que foi excluído das análises pelo baixo número de leituras apresentadas (4.857).

No total, 91.105 SNPs foram detectados nos pseudocromossomos (Ch), sendo que após aplicar os parâmetros de filtragem, esse valor diminuiu em 64%, obtendo-se 32.620 SNPs (Figura 1).

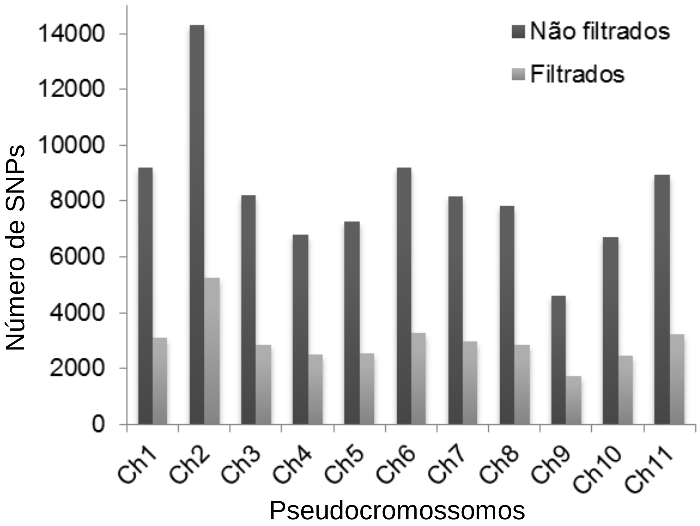

Figura 1. Número de *loci* com SNPs detectados nos cruzamentos 109x120/120x109 e 76x48 do programa de melhoramento do Incaper, antes e depois de aplicar os parâmetros de filtragem.

Tabela 2. Descrição das sequências dos *barcodes* e do número de leituras realizadas nos parentais e progênies dos cruzamentos dos genótipos 109x120/120x109 e 76x48 do programa de melhoramento de *C. canephora* do Incaper.

	Indivíduos	***Barcode***	**Número de leituras***
1)	109x120 R10	GATT	2379223
2)	109x120 R19	ACCGT	1802878
3)	109x120 R29	CGTCA	3204335
4)	109x120 R39	TCGCA	3548593
5)	109x120 R47	CGCAT	1743424
6)	109x120 R55	TCATAGT	1697939
7)	109x120 R64	TTACGAT	2066371
8)	109x120 R73	GGCTAGA	2882783
9)	109x120 R89	ACAAGAGT	2388567
10)	120x109 R6	GAACATGA	2774672
11)	109x120 R1	AGCATT	2061718
12)	109x120 R10	CTCCGA	1881319
13)	109x120 R21	TTGGCA	3107184
14)	109x120 R30	CCACGT	1854342
15)	109x120 R40	GATGTC	1746850
16)	109x120 R48	TGTTAC	1291871
17)	109x120 R56	CAGTTA	2532047
18)	109x120 R65	GCCTAT	1634604
19)	109x120 R74	AGTGGC	1670482
20)	109x120 R82	TGACCT	2267871
21)	P109	TTGCAC	1946723
22)	120x109 R6	CTAGCT	1870140
23)	109x120 R3	AATCGTT	1755119
24)	109x120 R12	CTATGGA	3190454
25)	109x120 R22	TACGGTA	2689053
26)	109x120 R31	ACTATGT	2184622
27)	109x120 R41	CGTGAAT	1626326
28)	109x120 R49	TTGCAGA	2958094
29)	109x120 R57	AACTTGT	1945358
30)	109x120 R66	TGACGTA	2107436
31)	109x120 R75	GCTATAA	1984226
32)	109x120 R83	ATCGTAT	1540930
33)	P120	TACTGAT	1880969
34)	120x109 R7	CTTGAGA	2470191
35)	109x120 R4	TCAAGTT	1730727
36)	109x120 R13	GATCATA	1607495
37)	109x120 R23	GCATTGA	3324178
38)	109x120 R32	CAGGTAT	1315432
39)	109x120 R42	TGCAATA	2225000
40)	109x120 R50	ATATCGT	1856852
41)	109x120 R59	AGTCTAT	1929973
42)	109x120 R67	GTCTGAA	2473963
43)	109x120 R76	ATCAGTT	1604339
44)	109x120 R84	CAGTTGA	2436267
45)	120x109 R1	TGTGCAA	2500281
46)	120x109 R8	CGACAGT	2141080
47)	109x120 R5	ACGTGTA	2509106
48)	109x120 R14	GATGCAT	1531793
49)	109x120 R25	CTAATGT	2085726
50)	109x120 R34	GTCGATA	2109255
51)	109x120 R43	TATACGT	1773041
52)	109x120 R51	GCGTAAT	1777271
53)	109x120 R60	AGCGTTA	2507154
54)	109x120 R68	ATCCGGA	2039130
55)	109x120 R77	TCAGTAT	1479080
56)	109x120 R85	CAATGTT	1923389
57)	120x109 R2	GTTACGA	2908022
58)	120x109 R9	TGCATAT	1516849
59)	109x120 R6	CAAGAAGT	2086548
60)	109x120 R14	GTCATGGT	2886302
61)	109x120 R26	AACAGTGA	2279891
62)	109x120 R35	GTGCAAGA	3395431
63)	109x120 R44	CAATAGGA	3461102
64)	109x120 R52	TGCAGTGT	1448003
65)	109x120 R61	AGGCTAGA	2255420
66)	109x120 R69	CTAGTGGT	1663179
67)	109x120 R79	GCTAGTGT	1480047
68)	109x120 R86	AGTTGGCA	2913177
69)	120x109 R3	TCGCAAGT	1859444
70)	120x109 R10	CGATGTGT	2727099
71)	109x120 R7	AACGTAGA	3307254
72)	109x120 R15	CTCACGGA	2148931
73)	109x120 R27	TAGCGTGT	1630942
74)	109x120 R37	ACGTAAGA	2525690
75)	109x120 R45	CGTATGGT	2188752
76)	109x120 R53	GTACGTGT	1608013
77)	109x120 R62	TTCGAAGA	2615192
78)	109x120 R70	AATACGGA	2061546
79)	109x120 R78	TGACTGGT	2312099
80)	109x120 R87	GCGGATGT	1847925
81)	120x109 R4	CATTGAGA	995933
82)	120x109 R11	GTAACAGA	2470441
83)	109x120 R9	AGCTTGGT	2487636
84)	109x120 R17	ACAGATGA	1646418
85)	109x120 R28	CAGTTGGT	2001522
86)	109x120 R38	TGCAAGAA	3114127
87)	109x120 R46	ACTCGAGA	3178403
88)	109x120 R54	GGAGCTGT	1956270
89)	109x120 R63	CTGAGTGT	1428392
90)	109x120 R72	GATCAGAA	3344774
91)	109x120 R80	TGCATAGA	2946171
92)	109x120 R88	GAACGAAT	1987315
93)	109x120 R81	ACAATGGA	4857
94)	120x109 R12	CGCCGCAT	1668374

Continua...

Continuação Tabela 2...

	Indivíduos	***Barcode***	**Número de leituras***
95)	120x109 R5	TTGGCGGA	2799908
96)	120x109 R20	GATT	2266598
97)	76x48L7 R2	ACCGT	1891121
98)	76x48L7 R9	CGTCA	4965582
99)	76x48L7 R17	TCGCA	3879713
100)	76x48L7 R24	CGCAT	2142078
101)	76x48L7 R32	TCATAGT	1762894
102)	76x48L15 R3	TTACGAT	2599488
103)	76x48L15 R12	GGCTAGA	2798799
104)	76x48L15 R21	ACAATGGA	2604162
105)	76x48L15 R29	ACAAGAGT	1850453
106)	76x48L15 R38	GAACATGA	2311132
107)	120x109 R12	AGCATT	2376887
108)	120x109 R21	CTCCGA	5730007
109)	76x48L7 R3	TTGGCA	3048793
110)	76x48L7 R10	CCACGT	1671515
111)	76x48L7 R18	GATGTC	1340888
112)	76x48L7 R25	TGTTAC	1464376
113)	76x48L7 R33	CAGTTA	3036680
114)	76x48L15 R4	GCCTAT	2072755
115)	76x48L15 R13	AGTGGC	1403141
116)	76x48L15 R22	TGACCT	1815921
117)	76x48L15 R31	TTGCAC	1851948
118)	76x48L15 R40	CTAGCT	2055028
119)	120x109 R13	AATCGTT	1564074
120)	120x109 R22	CTATGGA	2377927
121)	76x48L7 R4	TACGGTA	2532293
122)	76x48L7 R11	ACTATGT	1620260
123)	76x48L7 R19	CGTGAAT	1694222
124)	76x48L7 R26	TTGCAGA	2897714
125)	76x48L7 R34	AACTTGT	1707362
126)	76x48L15 R5	TGACGTA	2004436
127)	76x48L15 R14	GCTATAA	2010935
128)	76x48L15 R23	ATCGTAT	1635666
129)	76x48L15 R32	TACTGAT	1471484
130)	76x48L15 R41	CTTGAGA	2960736
131)	120x109 R14	TCAAGTT	1730141
132)	120x109 R22	GATCATA	2107230
133)	76x48L7 R5	GCATTGA	2826344
134)	76x48L7 R12	CAGGTAT	1168376
135)	76x48L7 R20	TGCAATA	2137827
136)	76x48L7 R27	ATATCGT	1211214
137)	76x48L7 R35	AGTCTAT	1502426
138)	76x48L15 R6	GTCTGAA	2872783
139)	76x48L15 R15	ATCAGTT	1565169
140)	76x48L15 R24	CAGTTGA	2127942
141)	76x48L15 R33	TGTGCAA	2445391
142)	76x48L15 R43	CGACAGT	1450855
143)	120x109 R16	ACGTGTA	2631374
144)	120x109 R24	GATGCAT	1814174
145)	76x48L7 R6	CTAATGT	2083440
146)	76x48L7 R13	GTCGATA	2482707
147)	76x48L7 R20	TATACGT	2162984
148)	76x48L7 R28	GCGTAAT	1667791
149)	76x48L7 R36	AGCGTTA	2520826
150)	76x48L15 R7	ATCCGGA	2089560
151)	76x48L15 R16	TCAGTAT	1530783
152)	76x48L15 R25	CAATGTT	1915054
153)	76x48L15 R34	GTTACGA	2833603
154)	76x48L15 R44	TGCATAT	1905096
155)	120x109 R17	CAAGAAGT	2455316
156)	120x109 R25	GTCATGGT	2337341
157)	76x48L7 R7	AACAGTGA	2265079
158)	76x48L7 R14	GTGCAAGA	2438819
159)	76x48L7 R21	CAATAGGA	2504943
160)	76x48L7 R29	TGCAGTGT	1517361
161)	76x48L7 R37	AGGCTAGA	2398080
162)	76x48L15 R8	CTAGTGGT	1683284
163)	76x48L15 R17	GCTAGTGT	1517229
164)	76x48L15 R26	AGTTGGCA	2930149
165)	76x48L15 R35	TCGCAAGT	2076083
166)	76x48L15 R46	CGATGTGT	1481944
167)	120x109 R18	AACGTAGA	2235399
168)	76x48L7 R1	CTCACGGA	2494401
169)	76x48L7 R8	TAGCGTGT	1698911
170)	76x48L7 R15	ACGTAAGA	2138669
171)	76x48L7 R22	CGTATGGT	1796154
172)	76x48L7 R30	GTACGTGT	1184704
173)	76x48L7 R38	TTCGAAGA	1865458
174)	76x48L15 R9	AATACGGA	2342310
175)	76x48L15 R19	TGACTGGT	2584136
176)	76x48L15 R27	GCGGATGT	2030349
177)	76x48L15 R36	CATTGAGA	2616252
178)	P48	GTAACAGA	2213085
179)	120x109 R19	AGCTTGGT	2788276
180)	76x48L7 R2	ACAGATGA	2845447
181)	76x48L7 R9	CAGTTGGT	1907229
182)	76x48L7 R16	TGCAAGAA	2403386
183)	76x48L7 R23	ACTCGAGA	3139997
184)	76x48L7 R31	GGAGCTGT	1625042
185)	76x48L15 R2	CTGAGTGT	1613260
186)	76x48L15 R10	GATCAGAA	2993486
187)	76x48L15 R20	TGCATAGA	2204476
188)	76x48L15 R28	GAACGAAT	1692851
189)	76x48L15 R37	TTGGCGGA	1852360
190)	P76	CGCCGCAT	1525607

Os 32.620 SNPs detectados após a filtragem, para os 145 indivíduos de *C. canephora*, foram utilizados para as análises posteriores (Figura 2). Todos esses *loci* apresentaram polimorfismo pelo critério que o alelo mais comum de cada *locus* apresenta frequência menor que 99% (COLE, 2003), sendo que 86% possui heterozigose até 0,5. O valor médio de MAF foi de 0,199, heterozigosidade média de 0,499, dissimilaridade genética média de 0,253, e PIC médio de 0,2. Os loci moderadamente informativos apresentam 0,25<PIC<0,5 e os pouco informativos possuem PIC< 0,25 (BOTSTEIN et al., 1980). Os marcadores SNPs não possuem alta informatividade devido à característica bialélica desse tipo de marcador, no entanto, essa perda de informatividade é compensada pela abundância de polimorfismos detectados pelas tecnologias de NGS.

Tabela 3. Parâmetros genéticos de 32.620 SNPs em 145 indivíduos de cruzamentos de clones de Conilon do programa de melhoramento do Incaper. *MAF - Frequência do menor alelo; **PIC - Conteúdo de Informação Polimórfica

Parâmetro genético	média	amplitude
Dissimilaridade	0,253	0,183 – 0,339
MAF*	0,199	0,01 – 0,5
Heterozigosidade	0,499	0 - 1
PIC**	0,2	0,020 - 0,375

A técnica de GBS é conhecida por reduzir a complexidade do genoma e fazer uma boa amostragem (ELSHIRE et al., 2011). Ampla distribuição de SNPs foi verificada em *C. canephora* (Figura 3), o que representa uma vantagem para a associação com características fenotípicas.

Figura 2. Localização dos SNPs prospectados nos cruzamentos entre clones 109x120/120x109 e 76x48 de *C. canephora*, do programa de melhoramento genético do Incaper. As barras escuras representam áreas dos pseudocromossomos (Ch) em que foram identificados SNPs

Em média, foram detectados 1.330 SNPs gênicos e 2.965 intergênicos por pseudocromossomo (Figura 4). Maior proporção de SNPs em região intergênica foi detectada nos Ch1, Ch3, Ch4, Ch5, Ch6, Ch8, Ch9 e Ch11. O Ch10 apresentou quantidades semelhantes de SNPs gênicos e inter-gênicos, enquanto nos Ch2 e Ch7 o número de SNPs gênicos foi superior.

Os SNPs em região gênica possuem maior probabilidade de afetarem funções biológicas, e a ocorrência destes variou bastante entre os pseudocromossomos, de acordo com a relação que segue: 133 (Ch1) < 747 (Ch9) < 1195 (Ch4) < 1219 (Ch10) < 1237 (Ch5) < 1291 (Ch3) < 1330 (Ch8) < 1410 (Ch11) < 1595 (Ch6) < 1630 (Ch7) < 2849 (Ch2).

Em sequências codificantes de proteínas as mutações sem sentido causam terminação antecipada da tradução, o que pode acarretar em modificações funcionais. Já as mutações com perda de sentido normalmente proporcionam efeitos mais deletérios (ZHAO et al., 2003). A reduzida densidade de SNPs em regiões gênicas pode ser atribuída aos efeitos da seleção natural para limitar as alterações de aminoácidos nas sequências das proteínas.

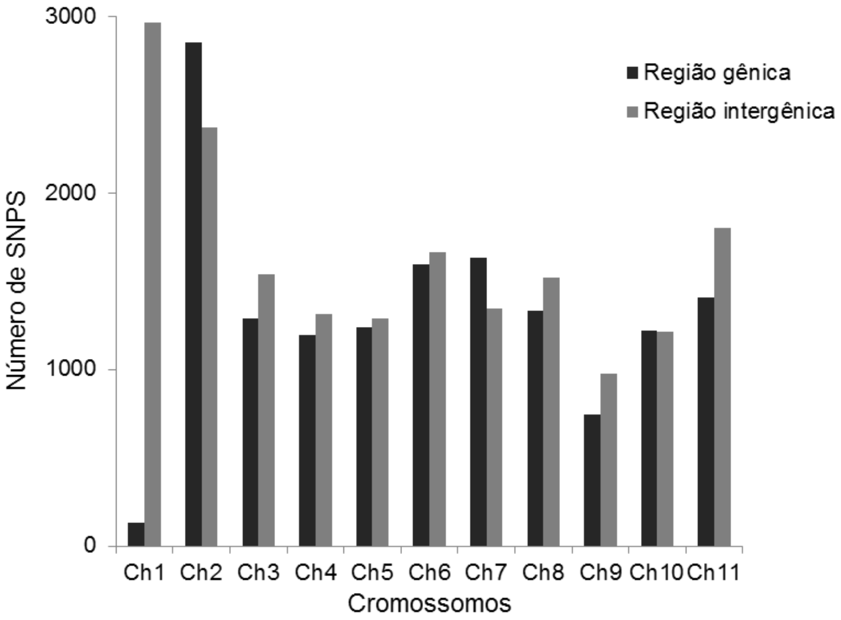

Figura 3. Caracterização dos SNPs quanto à região nos pseudocromossomos (Ch), de populações de *C.canephora* do Incaper.

A relação entre número total de SNPs e o tamanho dos pseudocromossomos é positiva (coeficiente de correlação = 0,98), conforme esperado. Ou seja, o Ch9, que é o menor pseudocromossomo de *C. canephora* (22.352.177 Mb), apresentou a menor quantidade de SNPs. Já o Ch2, o maior do genoma do Conilon (54.522.928 Mb), apresentou o maior número de SNPs (Figura 5). Essa relação tende a se manter quando comparamos separadamente os SNPs de regiões gênicas e intergênicas com o tamanho dos pseudocromossomos, à excessão do Ch1.

No Ch1, ao contrário dos demais, a relação não se mantém. Apesar de ser o segundo maior pseudocromossomo, detectaram-se o menor número de SNPs gênicos, contrastando bastante dos demais pseudocromossomos em relação à proporção de SNPs gênicos e intergênicos. Essa informação está suportada pelo ‘Coffee Genome Hub’, que apresenta que no cromossomo 1 de *C. canephora*, o número de SNPs por gene, detectados por *RNASeq*, é inferior aos demais cromossomos do genoma (DEREEPER et al., 2015).

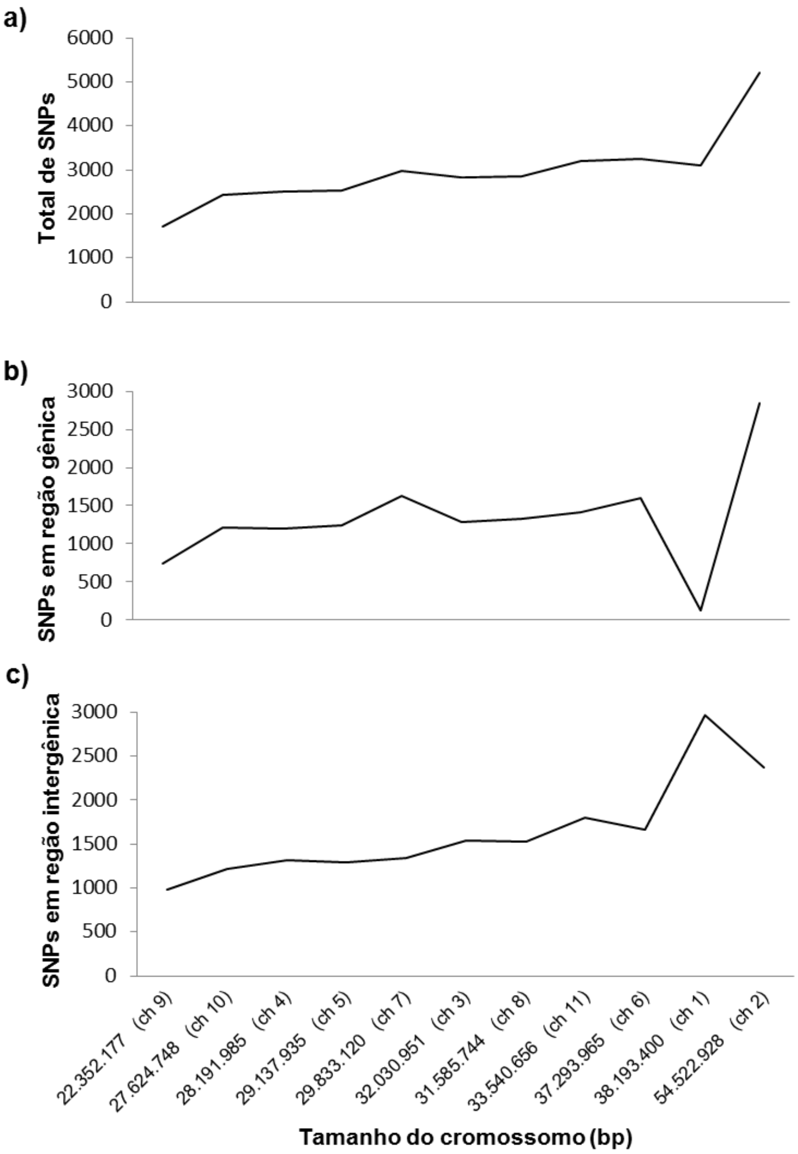

Figura 4. Relação entre a quantidade de SNPs e o tamanho dos pseudocromossomos (Ch): a) número total de SNPs; b) Número de SNPs em região gênica; c) Número de SNPs em região intergênica.

Observa-se que dentre os *loci* amostrados 73% estão em homozigose (Figura 6). Ressalta-se que os 11 pseudocromossomos de *C. canephora* apresentam grande semelhança na configuração alélica (desvio padrão médio = 0,005), considerando-se todos os loci amostrados: AA (21,084%); TT (20,6291%); CC (16,0511%); GG (15,9898%); AG (8,23257%); CT (8,1342%); AT (2,82919%); AC (2,52592%); GT (2,36159%); CG (2,16292%).

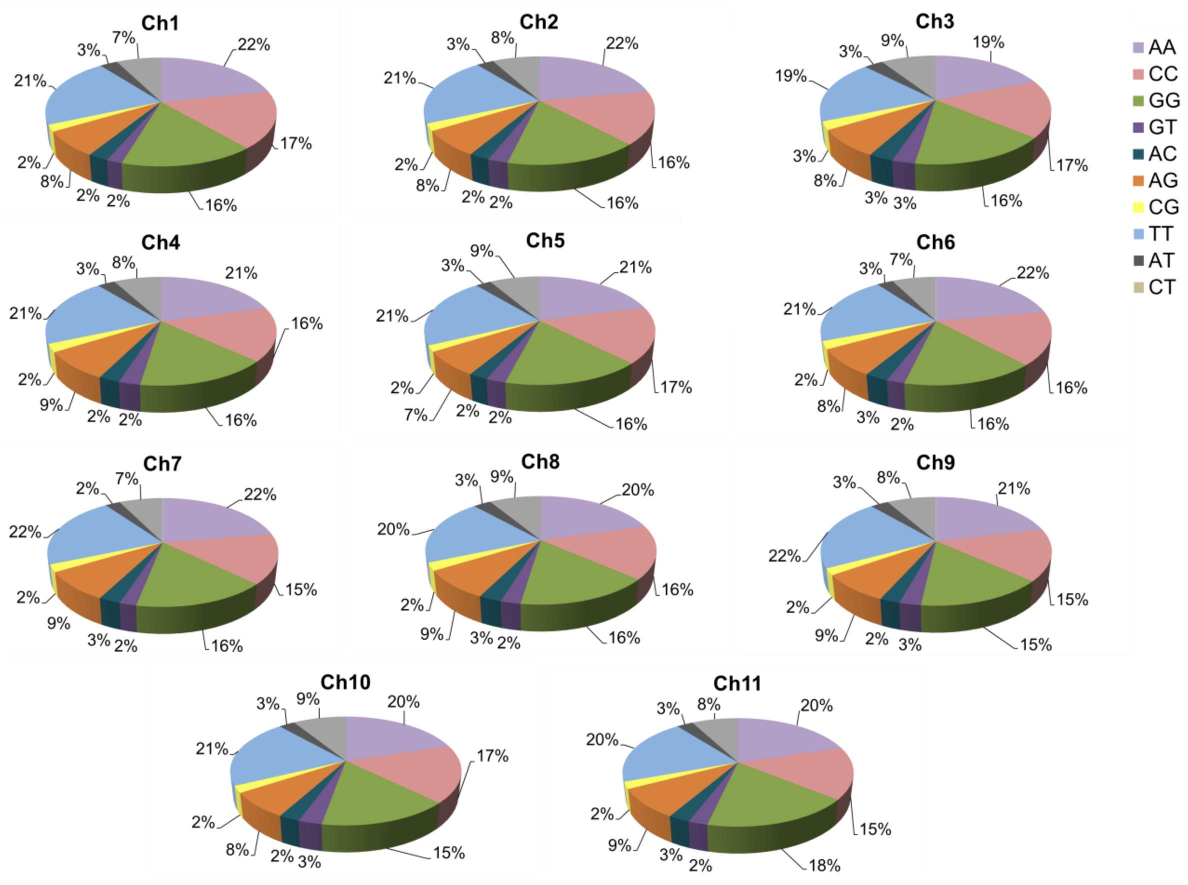

Figura 5. Configuração alélica, para cada pseudocromossomo (Ch), dos *loci* de *C. canephora* avaliados em populações de melhoramento do Incaper.

A densidade de SNPs nos pseudocromossomos (SNPs/100 kb) é, respectivamente do Ch 1 ao 11: 8,11; 9,58; 8,84; 8,89; 8,66; 8,73; 9,97; 9,02; 7,70; 8,80; 9,57, o que corresponde, em média, a um SNP a cada 11,24 kb. Considerando-se que existe, em média, um SNP a cada 100-300bp nos genomas de plantas (EDWARDS et al., 2007), ou um SNP a cada 3,3 kb de *Arabidopsis* (ARABIDOPSIS GENOME INIATIVE, 2000), o número de SNPs encontrados foi extremamente baixo. No entanto, ressalta-se que os indivíduos estudados pertencem a duas famílias de irmãos completos, o que explica tal resultado. Além disso, no presente estudo foram considerados os pseudocromossomos 1 a 11, sendo que as sequências sobre as quais não há informação sobre a localização no genoma (pseudocromossomo 0) foram excluídas das análises. Todos os SNPs encontrados em regiões gênicas foram identificados e poderão auxiliar em trabalhos posteriores (Tabela Suplementar 2).

Destaca-se que um número muito maior de SNPs será encontrado em análises com uma ampla gama de genótipos, que representem a diversidade de germoplasma da espécie *C. canephora*.

4.0 Conclusões

Verificou-se que o padrão de distribuição dos SNPs nas regiões do genoma difere. A menor ocorrência de SNPs detectada em regiões gênicas é esperada como consequência da pressão de seleção, que limita as alterações de aminoácidos nas sequências protéicas. Em suma, as análises dos resultados obtidos pela Genotipagem por Sequenciamento proporcionaram uma visão geral sobre a distribuição e densidade de SNPs em regiões gênicas e intergênicas do genoma de *C. canephora*, sendo que:

- Detectaram-se 91.105 SNPs antes de aplicar os parâmetros de filtragem. Após os filtros o número de SNPs ficou em 32.620, o que representa uma redução de 64%;
- O menor pseudocromossomo (Ch9) apresenta o menor número de SNPs, enquanto o maior pseudocromossomo (Ch2) é o que apresenta SNPs em maior quantidade;
- 73% dos *loci* amostrados estão em homozigose e os 11 pseudocromossomos apresentam grande semelhança na configuração alélica;
- A frequência média do menor alelo foi de 0,199, e a dissimilaridade média dos 145 indivíduos foi de 0,253, com intervalo de 0,183 a 0,399;
- Ampla distribuição dos SNPs foi encontrada, sendo que foram detectados em média 1330 SNPs gênicos e 2955 intergênicos, por pseudocromossomo.

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CAPÍTULO II - Associação de SNPs com características agronômicas de *Coffea canephora*

1. Introdução

O cafeeiro é uma das culturas mais importantes socialmente, cultivada em mais de 70 países, destes, o Brasil, Vietnã, Indonésia, Colômbia e Índia se destacam na produção desta *commodity*. A cultura é conduzida em sua maioria por pequenos produtores, cuja cafeicultura tem proporcionado melhorias na qualidade de vida (FAO, 2015).

Genótipos de café Conilon são bastante distintos com relação a uma série de características de interesse devido à reprodução alógama com presença de autoincompatibilidade gametofítica (FONSECA, 1999; CONAGIN & MENDES, 1961). A ampla variabilidade genética constitui-se importante fonte de matéria-prima para a seleção de genótipos de interesse e definição de estratégias no melhoramento genético da espécie (FONSECA, 1999).

A produção de café Conilon está sujeita a oscilações decorrentes da bienalidade e dos fatores climáticos. Períodos de seca podem prejudicar o desenvolvimento do cafeeiro, a floração, a formação de grãos e, consequentemente, a produção e qualidade final do produto (DAMATTA et al., 2010).

Os fatores bióticos também podem causar grandes prejuízos nas lavouras de Conilon, dentre eles estão o bicho mineiro (*Leucoptera coffeella* Guérin-Mèneville & Perrottet), a cercosporiose (*Cercospora coffeicola* Berk et Cook), a mancha manteigosa (*Colletotrichum gloeosporioides* Penz. - sin. *C. coffeanum*), e a ferrugem (*Hemileia vastratrix* Berk et Br.) (POZZA et al., 2010).

O estudo das características de interesse agronômico como, por exemplo, dos estresses citados acima e a associação destas características com marcadores moleculares está cada vez mais contribuindo para o melhoramento do cafeeiro, e de muitas outras espécies vegetais.

A possibilidade de automação em plataformas de sequenciamento possibilita que, com essa grande quantidade de marcadores moleculares disponíveis, seja possível realizar a construção de mapas genéticos saturados, estudos de pedigree, distância genética, mapeamento fino de regiões específicas e estudos de associação com características fenotípicas (MAMMADOV et al., 2012; YANG et al., 2013).

A análise de associação via modelos mistos lineares (*Mixed Linear Models - MLM*), possibilita encontrar no genoma a posição de uma região envolvida no controle de um fenótipo, e o respectivo efeito genético (BRADBURY et al., 2007). Os MLM são um dos métodos mais eficazes em análises de associação já descritos (YU et al., 2006).

Desta forma, caracterizar progênies oriundas de cruzamentos de clones elites de Conilon é importante para identificar indivíduos com as características agronômicas de interesse que podem ser utilizados como fonte de germoplasma para o melhoramento da espécie. Objetiva-se identificar SNPs associados a características de produção e tolerância a estresses bióticos e abióticos, em duas famílias de irmãos completos.

Material e métodos

2.1. Descrição dos cruzamentos

As progênies dos cruzamentos entre clones 76x48 (67 progênies) e o cruzamento entre clones 109x120 (55 progênies) / 120x109 (19 progênies) foram levadas a campo em Agosto de 2008 e Maio de 2009, respectivamente, na Fazenda Experimental de Marilândia (Incaper), localizada na região Noroeste do Estado do Espírito Santo.

Os progenitores dos cruzamentos são clones de café Conilon com características de interesse para a cafeicultura, sendo: I) clone 48: clone de conilon, de porte médio a alto, grãos grandes, maturação média, suscetível à ferrugem e à seca; II) 76: clone com características de Conilon, porte médio, vigoroso, maturação média, mediamente resistente **à** ferrugem e tolerante à seca; III) clone 109: clone com características de Conilon, porte médio, maturaçao média, suscetivel à ferrugem e à seca; IV) 120: clones de café Conilon de porte médio, maturação média, suscetível à ferrugem, vigoroso e tolerante à seca.

Utilizou-se espaçamento de 3,0 x 1,0 m, sem implantação de sistema de irrigação, e tratos culturais conforme a recomendação para a cultura (FERRÃO et al., 2007). As famílias de irmãos completos, que possuem genes de tolerância à seca, foram avaliadas sem repetição, e são oriundas de cruzamentos controlados entre clones de *C. canephora*, provenientes do programa de melhoramento genético do Incaper.

2.2. Cararacterização fenotípica

Os indivíduos foram fenotipados em 2013 apenas para tolerância à seca, e em 2014 para produção por planta (Kg), relação peso de café coco e beneficiado, e por escalas de notas para as características encontradas na Tabela 1.

Tabela 1. Escala de valores atribuídos na avaliação das características fenotípicas.

Característica	Avaliação
Uniformidade de maturação	1 - Pelo menos 90% dos frutos maduros 2 - Frutos 50% maduros e 50% verde 3 - Menos de 50% de frutos maduros, com a presença de secos a verdes
Tempo de maturação	1 - Super Precoce 2 - Precoce 3 - Médio 4 - Tardio 5 - Super Tardio
Ferrugem	1 - Sem sintomas visíveis 3 - Algumas folhas com poucas pústulas 5 - Folhas com infecção moderada, sem desfolha 7 - Folhas com infecção alta, pústulas abundantes e desfolha 9 - Sintomas muito severos, com grande desfolhas
Mancha de cercóspora	1 - Sem sintomas visíveis 3 - Presença de poucas lesões 5 - Lesões nas folhas e presença moderada nos frutos 7 - Presença de muitas lesões nas folhas e frutos 9 - Sintomas muito severos nas folhas, frutos e ramos
Incidência de bicho mineiro	1- Sem sintomas visíveis 3- Algumas folhas com poucas minas 5- Folhas moderadamente minadas, sem desfolha 7- Folhas muitas minas com ocorrência de desfolha 9- Sintomas muito severos com grandes desfolhas
Vigor	1 - Muito Fraco 3 - Fraco 5 - Intermediário 7 - Vigoroso 9 - Muito Vigoroso
Grau de inclinação	1- Ereto (1 – 35%) 2- Semi Ereto (36 – 50%) 3- Inclinado (51 – 100%)
Porte	1- Baixo 2- Médio 3- Alto

Tamanho do fruto	7 - Muito Graúdo 6- Graúdo 5- Entre graúdo e médio 4 - Médio 3- Entre médio e pequeno 2 - Pequeno 1 - Super Pequeno
Tolerância à seca	1 - Tolerante a seca 2 - Mediamente Tolerante 3 - Não Tolerante

2.3 Extração de DNA

Folhas jovens e completamente expandidas foram coletadas para a extração de DNA no Laboratório de Biologia Molecular e Bioquímica do Centro de Ciências Agrárias, Alegre-ES. Utilizou-se o kit da Qiagen DNeasy Plant para a obtenção de DNA com características qualitativas e quantitativas exigidas para a metodologia de sequenciamento. Os DNAs foram pipetados em placas de PCR e enviados para a Universidade de Cornell (EUA) para **proceder ao** sequenciamento pela metodologia de genotipagem por sequenciamento (GBS), conforme descrito no capítulo anterior.

2.4. Análises estatísticas

2.4.1 Análises de bioinformática

As análises de bioinformática dos resultados de sequenciamento realizado na Universidade de Cornell foram realizadas no software Tassel versões 3.0 e 5.2.14, considerando-se o genoma de referência de *Coffea canephora,* publicado em 2014 (DENOEUD et al., 2014). Realizaram-se a SNP *Call* proposta por Glaubitz et al., 2014, e a filtragem dos dados utilizando os parâmetros discutidos na Tabela 1 do capítulo anterior.

2.4.2 Análises via modelos mistos

Os modelos lineares mistos (MLM) utilizam efeitos fixos e aleatórios. A presença dos efeitos aleatórios no modelo possibilit**a** a incorporação das relações entre os indivíduos analisados. Quando os marcadores genéticos utilizados na construção da matriz de *Kinship* (K) são usados em conjunto com a estrutura da população (Q), o “K+Q” melhora o poder da estatística de associação do que quando apenas comparado com “Q” (YU et al., 2006). A notação da matriz de MLM é descrita por Henderson (1975):

$$y = X\beta + Zu + e,$$

em que: **y**= vetor de observações; **β**= vetor desconhecido que possui os efeitos fixos, incluindo o marcador genético e a estrutura da população (Q); **u**=vetor desconhecido dos efeitos genéticos aditivos aleatórios para múltiplos QTL por indivíduo/linha; **X** e **Z** são as matrizes conhecidas; **e**= vetor de resíduos. Assume-se que os vetores **u** e **e** possuem distribuição normal com média zero e variância (Var):

$$Var\left(\frac{u}{e}\right) = \begin{pmatrix} G & 0 \\ 0 & R \end{pmatrix},$$

onde G= $ó_a^2$K com $ó_a^2$ como variância genética aditiva e K como matriz de "kinship". A homogen**ei**dade de variância é assumida para matriz residual com R= I $ó_e^2$, onde $ó_e^2$ é a variência residual. Da variância total, a proporção da variância genética é definid**a** como herdabilidade (h^2):

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_e^2}$$

A esti**m**ativa de $ó_a^2$ foi via Máxima verossemelhança restrita (RELM) e a estimativa de $ó_e^2$ foi via algoritimo de Eficiente Modelo misto de Associação (EMMA), conforme Kang et al. (2008).

O quadro de leitura foi verificado no software Geneious e as modificações na tradução foram avaliadas no Seqbuilder (DNASTAR Inc., Madison, WI, USA).

3.0 Resultados e Discussão

O sequenciamento permitiu a identificação de 32.620 marcadores SNPs distribuídos nos 11 cromossomos de *C. canephora* (Figura 1).

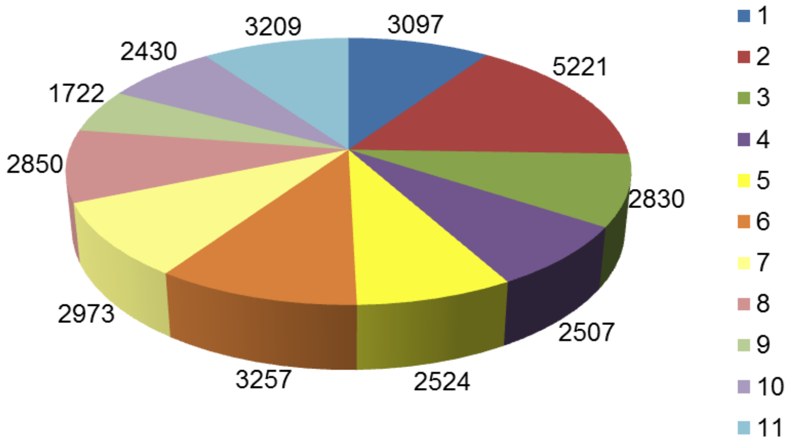


Figura1. Quantidade de SNPs identificados nos 11 pseudocromossomos dos indivíduos de *C. canephora*, cruzamentos 109x120 e 76x48.

Nos estudos de associação para características agronômicas dos cruzamentos 109x120 e 76x48 oriundos do Programa de Melhoramento do Cafeeiro do Incaper, dos 32.620 SNPs, 18 SNPs foram associados a características fenotípicas.

Dentre os 18 SNPs significativos, oito foram associados a porte da planta, três à tolerância à seca, quatro à cercosporiose, dois à relação peso de café coco e beneficiado e um à uniformidade de maturação. A posição nos pseudocromossomos, dos SNPs, significativos está representada nas figuras 2 e 3.

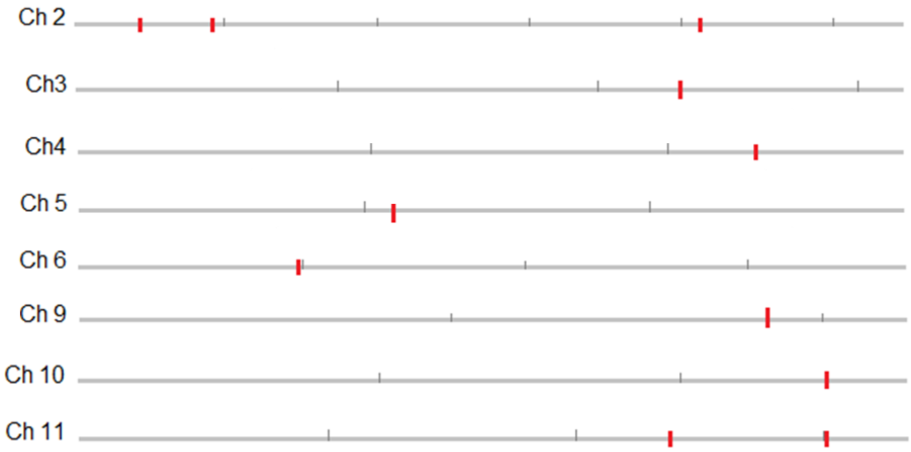


Figura 2. Localização dos SNPs significativos nos clones 109x120 e progênies. As linhas na horizontal representam os cromossomos, os traços em vermelho indicam as posições em que foram identificados SNPs associados a características fenotípicas. Os traços em cinza marcam cada 10mb. *Os SNPs

representados foram associados, respectivamente às características: Ch2= cercosporiose, relação peso de café coco e beneficiado e cercosporiose; Ch3= tolerância à seca; Ch4= porte; Ch5= cercosporiose; Ch6= relação peso de café coco e beneficiado; Ch9= tolerância à seca; Ch10= tolerância à seca; Ch11= cercosporiose e porte.

Figura 3. Localização dos SNPs significativos nos clones 76x48 e progênies. As linhas na horizontal representam os cromossomos, os traços em vermelho indicam as posições em que foram identificados SNPs associados a características fenotípicas. Os traços em cinza marcam cada 10mb. *Os SNPs representados foram associados, respectivamente às características: Ch2= ambos associados a porte; Ch7= os três SNPs associados a porte; Ch9= uniformidade de maturação; Ch11= porte.

A associação dos SNPs foi verificada em gráficos (*Manhattan plots*), cujo eixo Y apresenta os valores de $-\log_{10}$(Pvalor) e o eixo X consiste na identificação dos 11 pseudocromossomos do cafeeiro. A linha horizontal indica o limite negativo $-\log_{10}$(Pvalor) do menor valor significativo estatisticamente, pelo teste de Bonferroni (<0,05) (Figuras 4 a 9).

Os SNPs significativos foram classificados de acordo com o tipo de variação do nucleotídeo: transição purina-purina (A/G) ou pirimidina-pirimidina (C/T) ou transversões purina-pirimidina (C/A ou A/C; C/G ou G/C; T/A ou A/T; T/G ou G/T); e caracterizados quanto a característica fenotípica associada, posição no cromossomo, alelo de referência e alelo variante (Tabela 5). Dos 18 SNPs encontrados, dez foram transições (55,5%), sendo 27,78% transições purina-purina e 27,78% transições pirimidina-pirimidina. A razão transição/transversão foi de 1,25, sendo que as frequências de transversões foram de 5,56% A/C; 5,56% C/G; 16,7% A/T, 16,7% G/T.

Os SNPs foram caracterizados quanto ao pseudocromossomo e à região que estão presentes (gênica/intergênica) com auxílio do software Geneious 9.0.2. As identificações do gene em que os SNPs estão presentes, ou daqueles genes que estão adjacentes, foram verificadas (Tabela 2).

Tabela 2. Caracterização dos SNPs associados a características fenotípicas de cruzamentos de *C. canephora,*Incaper

Cromossomo	Posição	Cruzamento	Alelo de maior frequência (% de indivíduos)	Alelo de menor frequência (% de indivíduos)	Indivíduos indeterminados (%)	Característica Associada
Ch11	21239032	76x48	C (81,16)	A (4,35) 2,9 heterozigotos 1,45 homozigotos	14,49	Porte
	23828233	109x120	T (30,26)	A (69,74) 65,79 heterozigotos 3,95 homozigotos	0	Cercosporiose
	30063996	109x120	G (13,16)	A (86,84) 71,39 heterozigotos 15,44 homozigotos	0	Porte
Ch 10	24840747	109x120	A (97,37)	G (2,63) heterozigotos	0	Tolerância à seca
Ch 9	18527411	109x120	G (85,53)	A (2,63) heterozigotos	11,84	Tolerância à seca
	4618814	76x48	T (88,4)	G (4,35) heterozigotos	7,25	Uniformidade de Maturação

Continua...

Continuação Tabela 2...

Cromossomo	Posição	Cruzamento	Alelo de maior frequência (% de indivíduos)	Alelo de menor frequência (% de indivíduos)	Indivíduos indeterminados (%)	Característica Associada
Ch 7	13991077	76x48	C (66,67)	G (24,64) 21,74 heterozigotos 2,9 homozigotos	8,69	Porte
	13991086	76x48	G (66,67)	T (24,64) 21,74 heterozigotos 2,9 homozigotos	8,69	Porte
	13991105	76x48	C (66,67)	T (24,64) 21,74 heterozigotos 2,9 homozigotos	8,69	Porte
Ch 6	9949547	109x120	C (14,47)	T (85,53) 82,9 heterozigotos 2,63 homozigotos	0	Coco x beneficiado
Ch 5	10964474	109x120	A (93,42)	G(3,95) heterozigotos	2,63	Cercosporiose
Ch 4	22978689	109x120	T (80,26)	A (5,27) 3,95 heterozigotos 1,32 homozigoto	14,47	Porte

Continua...

Continuação Tabela 2...

Cromossomo	Posição	Cruzamento	Alelo de maior frequência (% de indivíduos)	Alelo de menor frequência (% de indivíduos)	Indivíduos indeterminados (%)	Característica Associada
Ch 3	23227842	109x120	G (96,05)	A (2,63) heterozigotos	1,32	Tolerância à seca
Ch2	17821870	76x48	T (60,87)	C (39,13) 36,23 heterozigotos 2,9 homozigotos	0	Porte
	20934616	76x48	C (94,20)	T (5,8) heterozigotos	0	Porte
	4579518	109x120	T (94,74)	C (2,63) heterozigotos	2,63	Cercosporiose
	9329731	109x120	T (86,84)	G (3,95) 2,63 heterozigotos 1,32 homozigoto	9,21	Coco x beneficiado
	41329025	109x120	T (96,05)	A (2,63) Heterozigotos	1,32	Cercosporiose

Tabela 3. SNPs associados a genes avaliados em população de melhoramento de *C. canephora* do Incaper

SNP	Ch	Posição	Região
			Cruzamento 109x120
Porte			
S4_22978689	4	22978689	intergênica (Putativa Proteína homóloga à proteína triptofano periódica 1~ PWP1 (posição: 22,809,726 -> 22,805,506) / Putativo domínio CCCH dedo de Zinco contendo a proteína 48~ ZFWD1 (posição: 23,076,108 -> 23,073,145))
S11_30063996	11	30063996	gênica (proteina a HVA22 ~ HVA22A (posição: 30,062,023 -> 30,065,283))
Tolerância à seca			
S10_24840747	10	24840747	gênica (Proteína da superfamíliaThioredoxina ~ unknown_gene (posição: 24,840,870 -> 24,831,385))
S9_18527411	9	18527411	intergênica (Homólogo ao gene da enzima Fosfo-N-acetilmuramoil-pentapeptídeo transferase ~ ATTRANS (posição: 18,401,932 -> 18,388,328) / Putativa proteína de ligação com RNA~ Larp7 (posição: 18,702,439 -> 18,694,830))
S3_23227842	3	23227842	gênica (Provável proteína serina/treonina-quinase GCN2~ GCN2 (posição: 23,226,884 -> 23,251,482))
Cercosporiose			
S2_41329025	2	41329025	intergênica (Fototropina-2~ PHOT2 (posição: 41,304,374 -> 41,320,603) / GTPase npa3~ xab1 (posição: 41,420,011 -> 41,423,621))
S2_4579518	2	4579518	gênica (Putativo Cation/H(+) antiporter 3~ CHX3 (posição: 4,577,969 -> 4,581,457))

continua…

…continuação Tabela 2

SNP	Ch	Posição	Região
			Cruzamento 109x120
Cercosporiose			
S11_23828233	11	23828233	gênica (Putativa proteína da família das repetições de Anqurinas~ At5g02620) (posição:)
S5_10964474	5	10964474	integênica (Repetição do Pentatricopeptídeo contendo a proteína At4g26680 , mitocondrial~ At4g26680~ complete (10,961,327 -> 10,958,486) / Proteína hipotética~ gene desconhecido (posição: 10,966,667 -> 10,964,575))
Relação peso de café coco e beneficiado			
S6_9949547	6	9949547	gênica (Proteína hipotética~At4g00755) (posição:)
S2_9329731	2	9329731	gênica (Proteína 2 ligadora de RNA de dupla fita ~ DRB2 (posição: 9,334,629 -> 9,329,915))
			Cruzamento 76 x 48
Uniformidade de maturação			
S9_4618814	9	4618814	gênica (Proteína ligadora de GTP ERG (posição: 4,619,086 -> 4,614,496))

continua…

…continuação Tabela 2

SNP	Ch	Posição	Região
			Cruzamento 76x48
S- porte maior valor			
S2_17821870	2	17821870	intergênica (Putativa proteína 10 da família Glicosil hidrolase ~ gene desconhecido~ fragmento (posição: 17,820,494 -> 17,819,898) / Putativa relação com ciclina~ gene desconhecido (posição: 17,825,934 -> 17,821,904)
S2_20934616	2	20934616	intergênica Putativa GTPase Der~ módulos (posição:20,925,432 -> 20,933,572) / NAC domain containing protein 35~ ANAC094 (posição: 20,942,844 -> 20,940,221)
S11_21239032	11	21239032	gênica (Proteína 7 associada a microtúbulos de 65-kDa ~ MAP65-7 (posição: 21,242,561 -> 21,236,663))
S7_13991077	7	13991077	gênica (Putativa proteína de resistência à doença RGA4 (posição: 13,993,130 -> 13,988,434))
S7_13991086	7	13991086	gênica (Putativa proteína de resistência à doença RGA4 (posição: 13,993,130 -> 13,988,434))
S7_13991105	7	13991105	gênica (Putativa proteína de resistência à doença RGA4 (posição: 13,993,130 -> 13,988,434))

Para o cruzamento 109x120 foi encontrado um SNP em uma região de íntrons no pseudocromossomo 4, o qual foi associado à porte da planta. Os SNPs em regiões não codificadoras podem alterar a afinidade da enzima RNA-polimerase no início da transcrição ou estar em desequilíbrio de ligação com mutações causais (ANDERSSON, 2013). Outro SNP associado a porte foi encontrado no pseudocromossomo11, localizado no gene codificador da proteína HVA22A (Figura 4). Uma vez que essa proteína tem a síntese induzida por ABA em condições de estresses abióticos, como estresses hídrico, térmico e salino (CHEN et al., 2002; PRABU et al., 2011; DONG et al., 2014), o desenvolvimento de um maior porte pode estar associado a uma melhor capacidade de a planta tolerar os estresses.

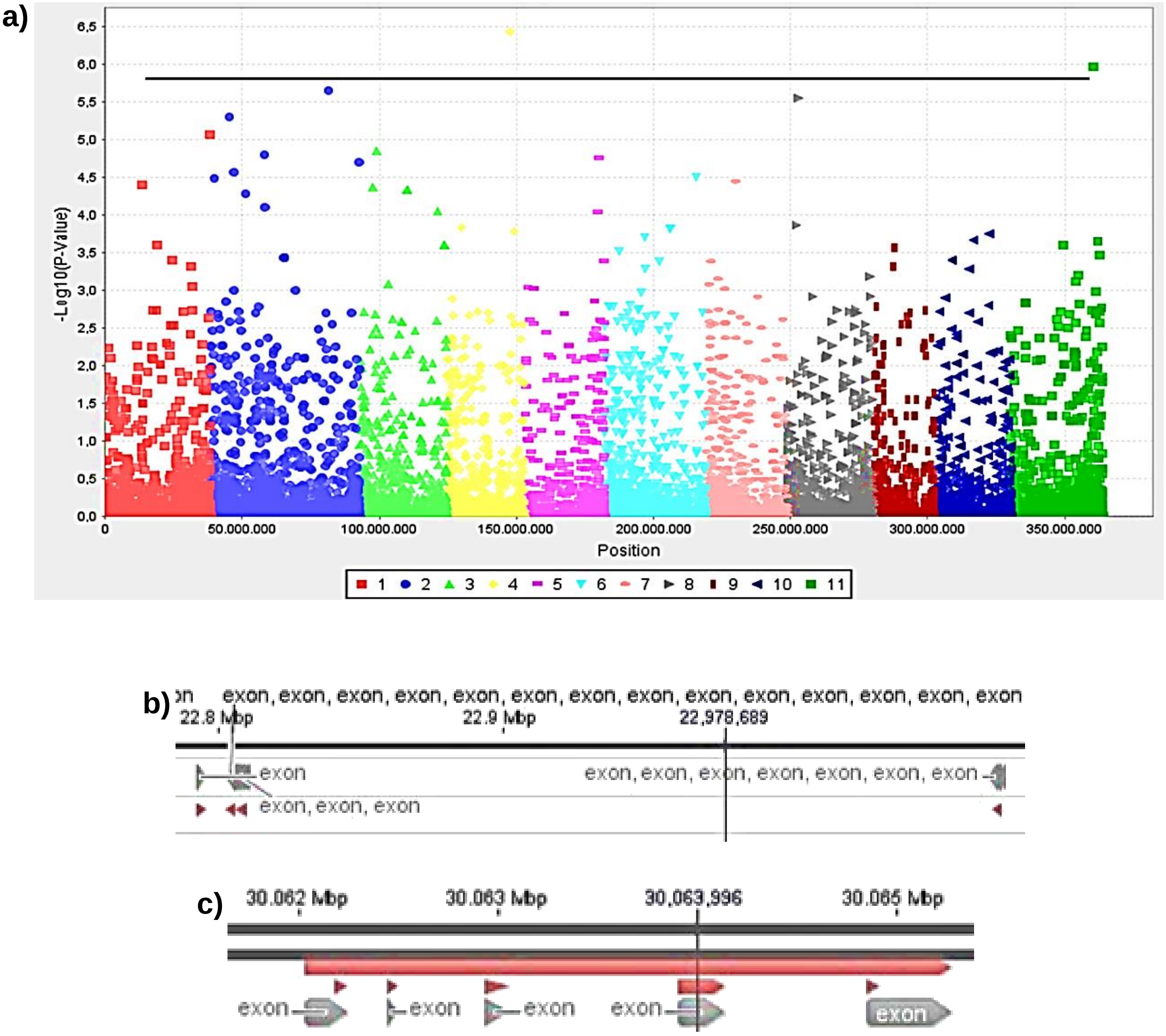
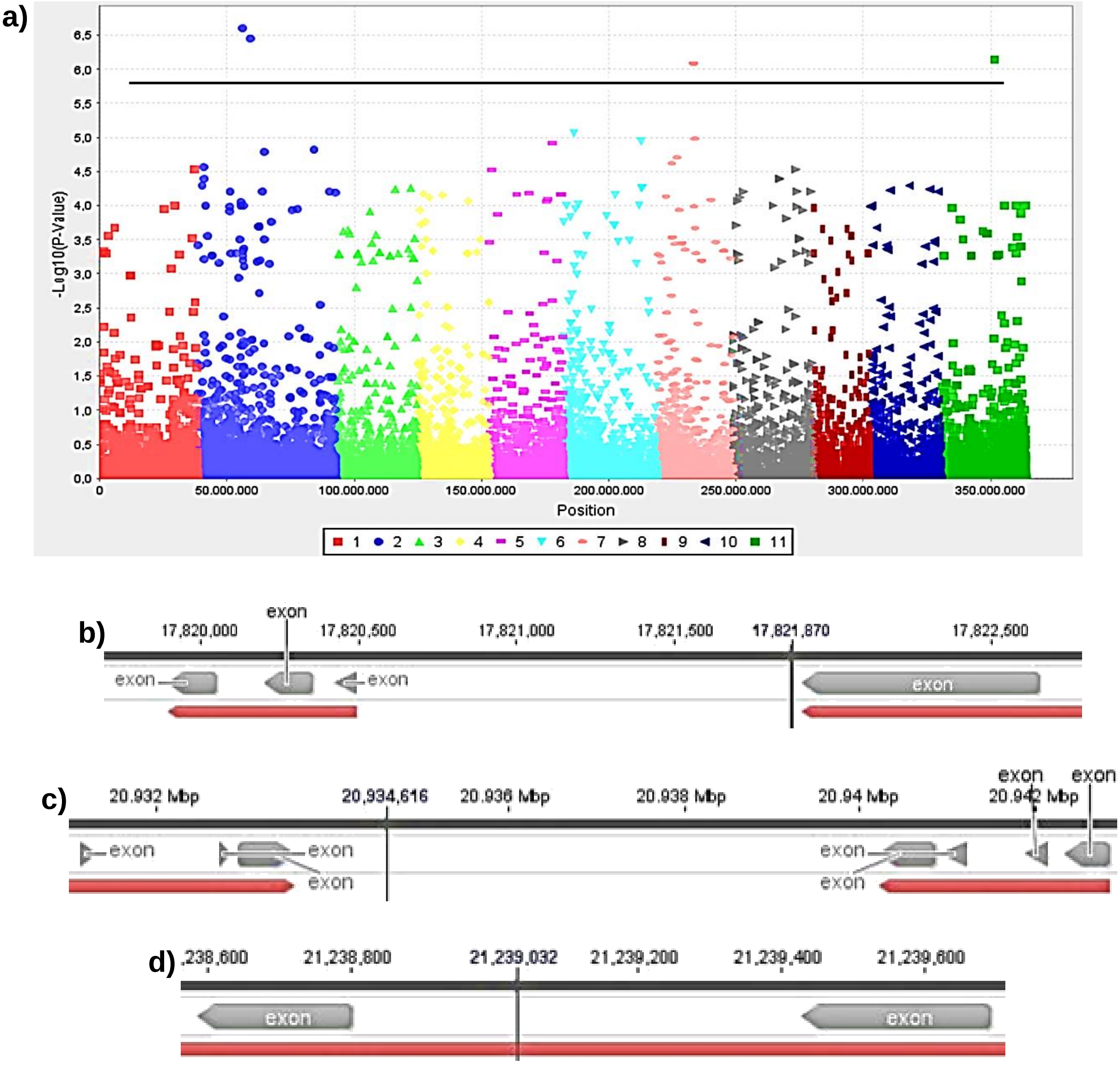


Figura 4. a) *Manhattan plot* do estudo de associação de SNPs com a característica ‘porte’ no cruzamento dos clones de Conilon 109x120. Os números de 1 a 11 se referem aos pseudocromossomos de *C. canephora.* * -Log$_{10}$(P-value)= -Log$_{10}$(1,532E-06)=5,814. **b)** Posição do SNP entre os genes ‘Putative Periodic

tryptophan protein 1 homolog~ PWP1’ e ‘Putative Zinc finger CCCH domain-containing protein 48~ ZFWD1’ do pseudocromossomo 4 de *C. canephora.* **c)** Posição do SNP no gene ‘HVA22-like protein a~ HVA22A’ do pseudocromossomo 11 de *C. canephora.*

No cruzamento 76x48 seis SNPs foram associados a porte da planta, sendo dois presentes em região intergênica, um SNP em íntron e três SNPs em éxons (Figura 5). Todos SNPs que estão em região codificadora estão localizados no gene ‘Putative disease resistance protein RGA4’, portanto, o maior porte de planta pode estar sendo influenciado pela capacidade de a planta tolerar doenças.



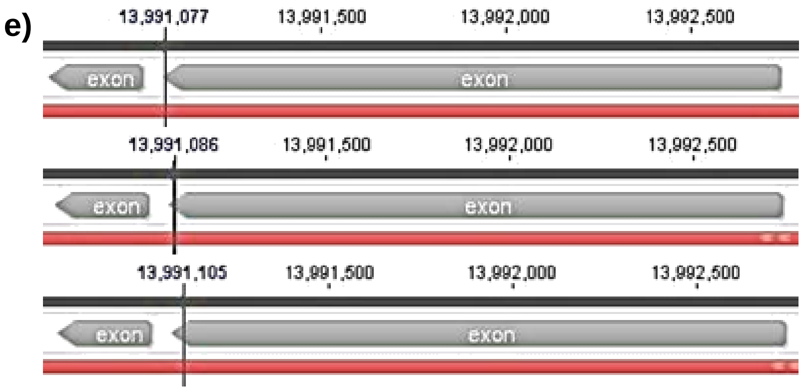


Figura 5. a) *Manhattan plot* do estudo de associação de SNPs com a característica ‘porte da planta’ no cruzamento dos clones de Conilon 76x48. Os números de 1 a 11 se referem aos pseudocromossomos de *C. canephora.* * -Log$_{10}$(P-value)= -Log$_{10}$(1,532E-06)=5,814. **b)** Posição do SNP entre os genes ‘Putative Glycosyl hydrolase family 10 protein~ unknown_gene’ e ‘Putative cyclin-related~ unknown_gene’ do pseudocromossomo 2 de *C. canephora.* **c)** Posição do SNP entre os genes S2_20934616 intergênica Putative GTPase Der~ der’ (posição:20,925,432 -> 20,933,572) / NAC domain containing protein 35~ ANAC094’ (posição: 20,942,844 -> 20,940,221) do pseudocromossomo 2 de *C. canephora.* **d)** Posição do SNP no gene ‘65-kDa microtubule-associated protein 7~ MAP65-7’ do pseudocromossomo 11 de *C. canephora.* **e)** Posição de três SNPs no gene ‘Putative disease resistance protein RGA4’ do pseudocromossomo 7 de *C. canephora*.

Quatro SNPs foram associados à cercosporiose, no cruzamento 109x120, sendo que dois localizam-se em regiões intergênicas dos Chs 2 e 5 e outros SNPs localizam-se em regiões codificadoras dos Chs 2 e 11 (Figura 6).

O SNP no gene ‘putative cation/H(+) antiporter 3~CHX3’, Ch 2, foi associado à incidência de cercosporiose. A abertura de canais de Ca^{2+} pode ser estimulada por luz vermelha, gravidade, toque, frio, hormônios, estresse salino, e por ataque fúngico. A presença de um desses estímulos ativa as vias de transdução de sinal (BUSH et al., 1995). O SNP no gene ‘putative ankirin repeat family protein ~At5g02620’, detectado no Ch 11 também foi associado à incidência de cercosporiose. As ‘ankirin repeats’ estão presentes em inúmeras proteínas, e trata-se de repetições de aproximadamente 33 aminoácidos que formam estruturas secundárias e terciárias, e servem como domínios de interação proteína-proteína (MICHAELY; BENNETT, 1992; SEDGWICK; SMERDON, 1999). A ação de genes com este tipo de repetições já foi reportada em *Arabidopsis* para a sinalização de transdução e de toxinas, e características relacionadas à resistência sistêmica adquirida a patógenos e ao metabolismo antioxidativo (SEDGWICK; SMERDON, 1999; YAN et al., 2002).

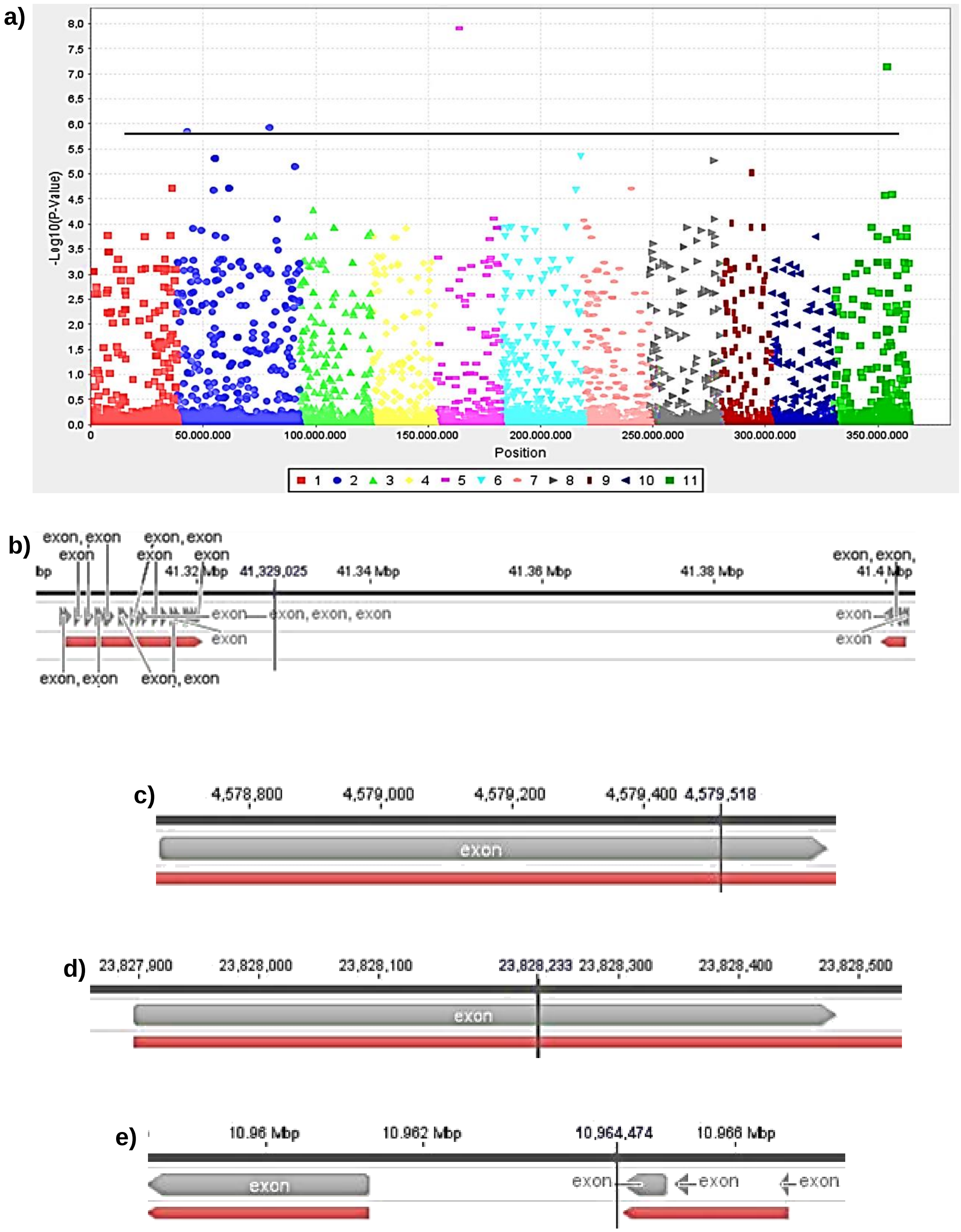
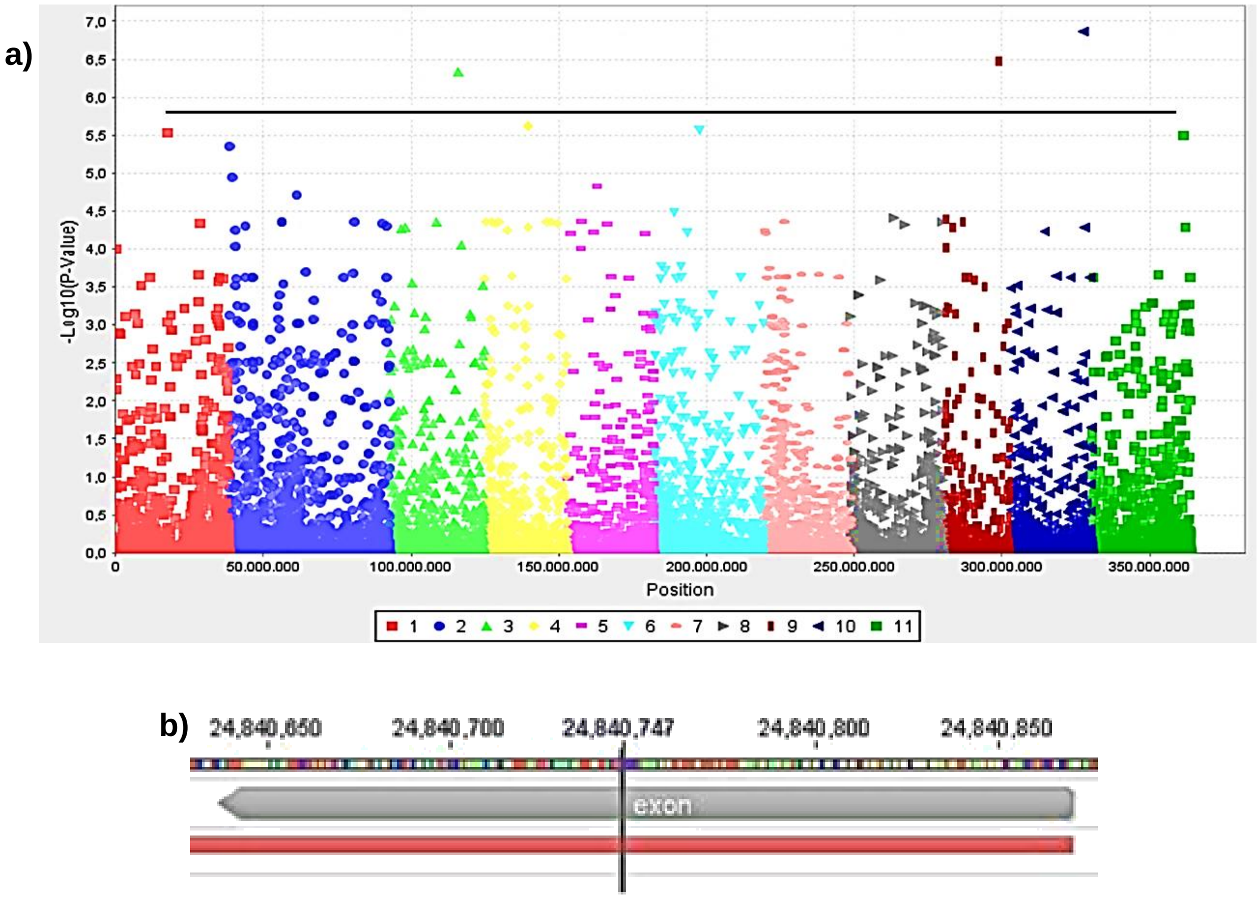


Figura 6. a) *Manhattan plot* do estudo de associação de SNPs com a característica ‘cercosporiose’ no cruzamento dos clones de Conilon 109x120. Os números de 1 a 11 se referem aos pseudocromossomos de *C. canephora.* * -Log$_{10}$(P-value)= -

Log$_{10}$(1,532E-06)=5,814. **b)** Posição do SNP entre os genes ‘Phototropin-2~ PHOT2’ e ‘GTPase npa3~ xab1’ do pseudocromossomo 2 de *C. canephora.* **c)** Posição do SNP no gene ‘Putative Cation/H(+) antiporter 3~ CHX3’ do pseudocromossomo 2 de *C. canephora.* **d)** Posição do SNP no gene ‘Putative Ankyrin repeat family protein~ At5g02620’ do pseudocromossomo 11 de *C. canephora.* **e)** Posição do SNP entre os genes ‘Pentatricopeptide repeat-containing protein At4g26680, mitochondrial~ At4g26680’ e ‘Hypothetical protein~ unknown_gene’ do pseudocromossomo 5 de *C. canephora.*

Um SNP em região intergênica do Ch 9 e dois em regiões codificadoras foram associados à tolerância à seca (Figura 7). O gene ‘Serine/threonine-protein kinase~GCN2’ está relacionado ao acúmulo de aminoácidos, e **à** tolerância a estresses térmico e osmótico (ZHANG et al.,2003; TERRY et al., 2015). O gene ‘Thiredoxinn superfamily protein’ também foi associado **a** essa característica. Tiorredoxinas são pequenas proteínas (cerca de 12 kDa) cuja diversidade encontrada em *A*. *thaliana*, de pelo menos 20 genes, é representativa para as plantas superiores. Participam da regulação do ambiente redox da célula e estão envolvidas na tolerância a estresses abióticos (MEYER et al., 2002).



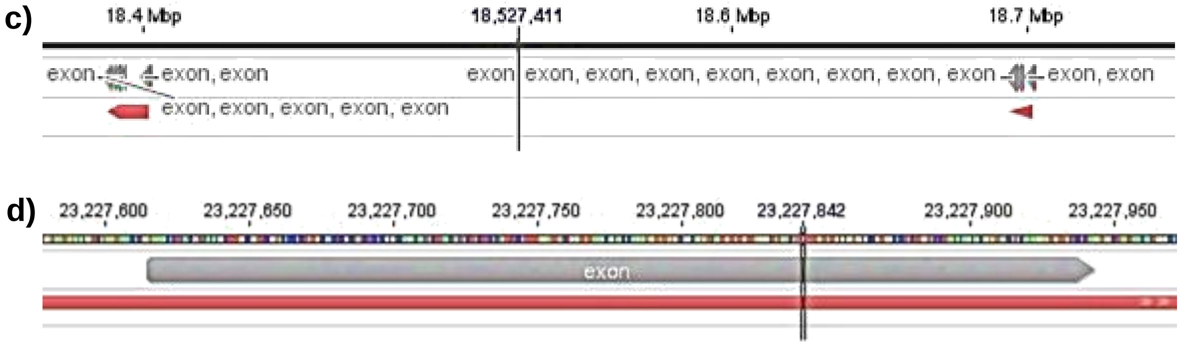
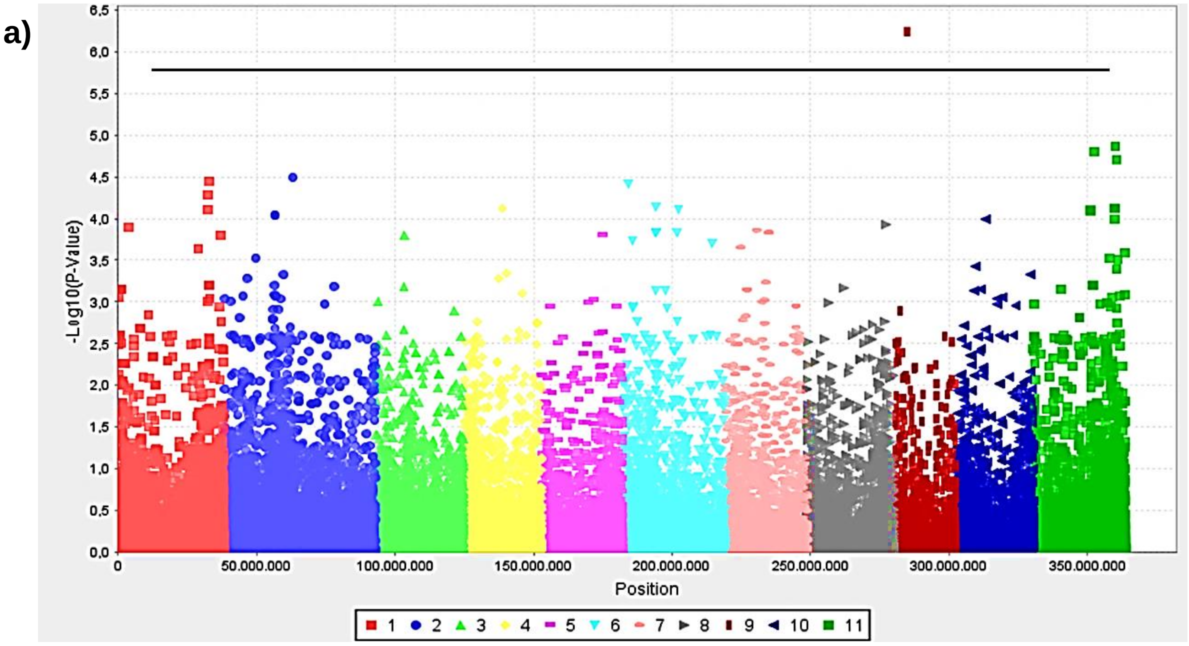


Figura 7. a) *Manhattan plot* do estudo de associação de SNPs com a característica 'tolerância à seca' no cruzamento dos clones de Conilon 109x120. Os números de 1 a 11 se referem aos pseudocromossomos de *C. canephora.* * $-\text{Log}_{10}$(P-value)= $-\text{Log}_{10}$(1,532E-06)=5,814. **b)** Posição do SNP no gene 'Thioredoxin superfamily protein~ unknown_gene' do pseudocromossomo 10 de *C. canephora.* **c)** Posição do SNP entre os genes 'Phospho-N-acetylmuramoyl-pentapeptide-transferase homolog~ ATTRANS' e 'Putative RNA-binding protein~ Larp7' do pseudocromossomo 9 de *C. canephora.* **d)** Posição do SNP no gene 'Probable serine/threonine-protein kinase GCN2' do pseudocromossomo 3 de *C. canephora.*

O SNP no gene 'GTP-binding protein ERG' foi associado à uniformidade de maturação (Figura 8). Genes da família GTP-binding podem ser estimulados pelo etileno, estão relacionados à sinalização celular, e já tiveram a função relacionada ao amadurecimento de frutos em outras espécies (ZAINAL et al., 1996; LU et al., 2001; MOSHKOV et al., 2003).



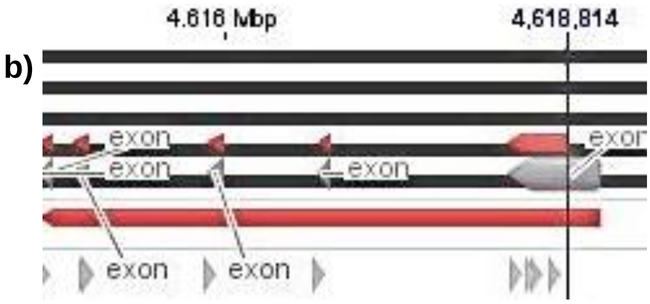
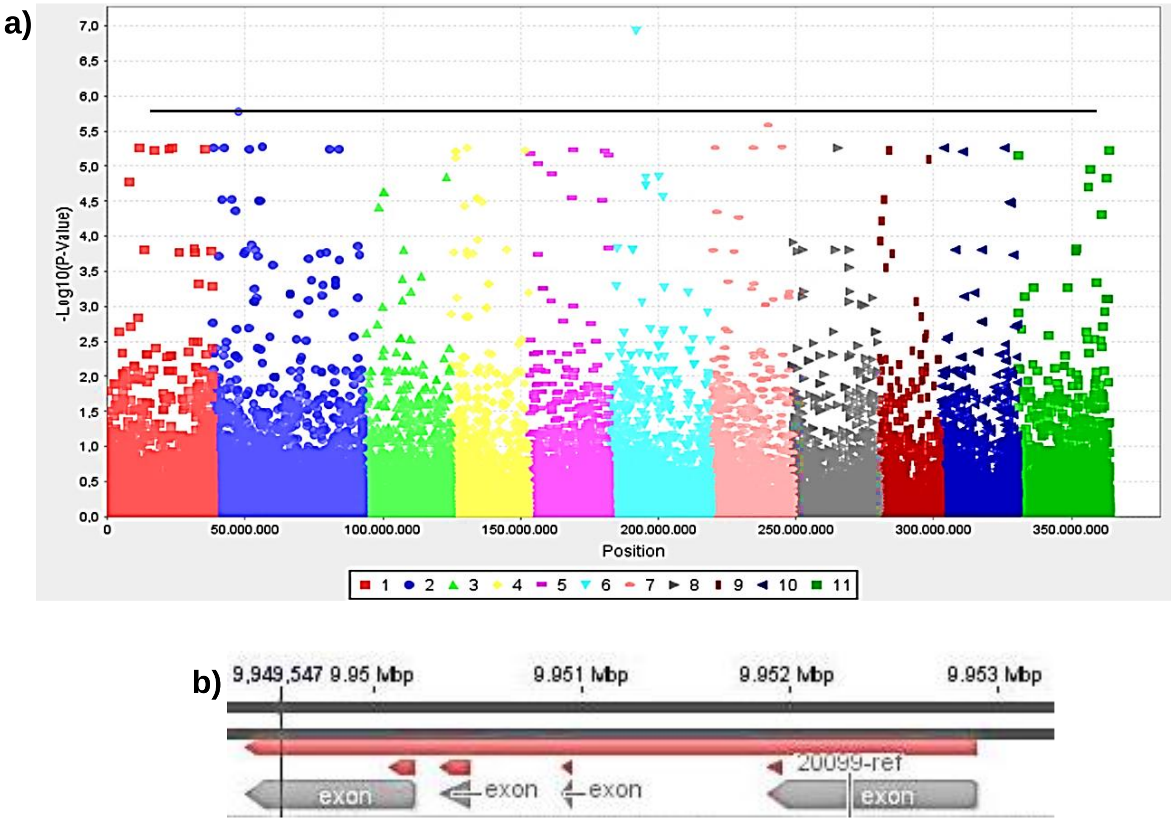


Figura 8. a) *Manhattan plot* do estudo de associação de SNPs com a característica 'uniformidade de maturação' no cruzamento dos clones de Conilon 76x48. Os números de 1 a 11 se referem aos pseudocromossomos de *C. canephora.* * – Log_{10}(P-value)= $-\text{Log}_{10}$(1,532E-06)=5,814. **b)** Posição do SNP no gene 'GTP-binding protein ERG' do pseudocromossomo 9 de *C. canephora*.

No cruzamento 109x120 dois SNPs em região codificante foram associados à 'relação peso de café coco e beneficiado' (Figura 9). Um SNPs está localizado em um gene cuja proteína não está caracterizada e o outro está presente no gene ' Double-stranded RNA-binding protein 2~ DRB2', cujo produto Interage de forma seletiva e não covalente com moléculas de RNA de dupla-fita. Tal proteína está relacionada à produção de micro-RNAs e a processos de silenciamento gênico (EAMENS et al., 2012).



c)

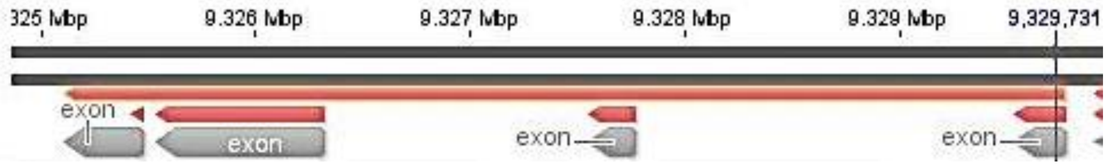


Figura 9. a) *Manhattan plot* do estudo de associação de SNPs com a característica 'relação peso de café coco e beneficiado' no cruzamento dos clones de Conilon 109x120. Os números de 1 a 11 se referem aos pseudocromossomos de *C. canephora.* * –Log_{10}(P-value)= –Log_{10}(1,532E-06)=5,814. **b)** Posição do SNP no gene 'Hypotetical protein~At4g00755~missing_ functional_ completness' do pseudocromossomo 6 de *C. canephora.* **c)** Posição do SNP no gene 'Double-stranded RNA-binding protein 2~ DRB2' do pseudocromossomo 2 de *C. canephora.*

A frequência de SNPs é heterogênea ao longo do genoma, diferindo entre região codificadora e região não codificadora, entre sequências gênicas, ou mesmo dentro de genes (éxon/intron). Em geral, os SNPs são menos abundantes em regiões codificadoras do que em outras regiões (FLADUNG e BUSCHBOM, 2009).

Os íntrons e regiões UTRs têm importante papel na regulação da expressão gênica de eucariotos (MIGNONE et al., 2002). Os íntrons podem apresentar *enhancers* e promotores alternativos, possibilitando a formação de diferentes proteínas a partir de um mesmo gene (ROSE, 2008). As regiões UTR também podem alterar o padrão de expressão em nível pós-transcricional, uma vez que interagem com proteínas RNA-binding e atuam como importante elemento na regulação em nível de RNA (SWEENEY et al., 1996).

Conforme esperado, dos 32.620 SNPs, 45% localizam-se em genes, mas a proporção de SNPs em regiões codificantes é ainda menor, uma vez que os SNPs gênicos estão distribuídos tanto em regiões codificantes, quanto em regulatórias e não codificantes. Dos 18 SNPs associados a características fenotípicas, 7 estão em íntrons, 1 em região 3'UTR e 10 em éxons.

As mudanças na codificação de aminoácidos foram classificadas em mutações sinônimas e não-sinônimas (MARTIN, 2015). Para isto, o quadro de leitura foi definido através de um alinhamento com genoma de *C. canephora* e, em seguida, os códons contendo os SNPs associados foram isolados e os aminoácidos foram traduzidos *in silico*. Dos SNPs situados em região codificadora do gene, nove são mutações não sinônimas (Tabela 4).

Tabela 4. SNPs gênicos em regiões de éxons, em populações de *C. canephora* do Incaper.

Posição	**Referência**		**SNP**	
	Códon	**Aminoácido**	**Códon**	**Aminoácido**
S2_9329731	G**T**T	Asparagina (N)	G**G**T	Prolina (P)
S2_4579518	G**T**G	Valina (V)	G**C**G	Alanina (A)
S3_23227842	AA**G**	Lisina (K)	AA**A**	Lisina (K)*
S6_9949547	TG**G**	- (3’UTR)	TC**C** TG**T**	- (3’UTR)
S7_13991105	T**C**C	Glicina (G)	T**T**C	Arginina (R)
S7_13991086	**T**TG	Glutamina (Q)	G**G**T	Prolina (P)
S7_13991077	**C**CT	Arginina (R)	**G**CT	Alanina (A)
S9_4618814	**T**AT	Isoleucina (I)	**G**AT	Serina (S)
S10_24840747	AA**A**	Fenilalanina (F)	AA**G**	Prolina (P)
S11_30063996	G**A**C	Ácido aspártico (D)	G**G**C	Alanina (A)
S11_23828233	**C**GG	Arginina (R)	**A**GG **T**GG	Arginina (R)* Glicina (G)

*mutação sinônima

SNPs não-sinônimos em regiões codificantes e SNPs em regiões regulatórias tendem a apresentar as maiores modificações no fenótipo (RAMENSKY; BORK; SUNYAEV, 2002). Os SNPs sinônimos são aqueles que têm efeito pequeno na expressão gênica, entretanto, tanto os SNP sinônimos quanto os não sinônimos são de grande importância como marcadores genéticos (CHEN et al., 2007). As mudanças não-sinônimas também podem determinar o fenótipo alternativo e mostrar grande associação com uma característica e dessa forma poderá ser de grande importância para a seleção assistida por marcadores (MAS) ou para o isolamento do gene (MARTIN, 2015). Grandes efeitos no fenótipo foram proporcionados tanto por SNPs intergênicos e gênicos, tanto em regiões 3’UTR, de éxons e de íntrons (Tabela 8).

Tabela 5. Caracterização dos SNPs de *C. canephora* quanto à localização, ao tipo de mutação e ao efeito no fenótipo.

Característica	Alelo	Cromossomo	Posição do SNP	Região	Alteração na tradução	Número de indivíduos
Cruzamento 109x120 / 120x109						
Porte	A T W	4	22978689	Intergênica	-	1 60 3
Porte	A G R	11	30063996	Éxon	não-sinônima	3 38 26
Tolerância à seca	A R	10	24840747	Éxon	não-sinônima	72 2
Tolerância à seca	G R	9	18527411	intergênica	-	63 2
Tolerância à seca	G R	3	23227842	Éxon	sinônima	71 2
Cercosporiose	T W	2	41329025	intergênica	-	71 2
Cercosporiose	T Y	2	4579518	Éxon	não-sinônima	70 2
Cercosporiose	A T W	11	23828233	Éxon	sinônima e não-sinônima	3 23 48
Cercosporiose	A R	5	10964474	intergênica	-	69 3
Relação peso de café coco e beneficiado	C T Y	6	9949547	3’UTR	-	10 2 61
Relação peso de café coco e beneficiado	G T K	2	9329731	Éxon	não-sinônima	1 64 2

Característica	Alelo	Cromossomo	Posição do SNP	Região	Alteração na tradução	Número de indivíduos
Cruzamento 76x48						
Uniformidade de maturação	T K	9	4618814	éxon	não-sinônima	59 3
Porte	C T Y	2	17821870	intergênica	-	2 41 24
Porte	C Y	2	20934616	intergênica	-	63 4
Porte	A C M	11	21239032	íntron	-	1 55 2
Porte	C G S	7	13991077	éxon	não-sinônima	44 2 15
Porte	G T K	7	13991086	éxon	não-sinônima	44 2 15
Porte	C T Y	7	13991105	éxon	não-sinônima	44 2 15

4.0 Conclusões

Os estudos de associação permitiram encontrar 18 SNPs associados a características fenotípicas de *Coffea canephora*: S2_9329731, S2_4579518, S2_41329025, S2_17821870, S2_20934616, S3_23227842, S4_22978689, S5_10964474, S6_9949547, S7_13991105, S7_13991086, S7_13991077, S9_4618814, S9_18527411, S10_24840747, S11_30063996, S11_23828233. Desses, 33% localizam-se em regiões intergênicas, e os demais se distribuem em região de íntrons, éxons e 3'UTR. Os SNPs encontrados em regiões codificadoras são responsáveis por alterações não sinônimas em 82% das ocorrências. Os resultados encontrados são importantes para a cafeicultura e podem contribuir para a seleção assistida por marcadores.

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CONSIDERAÇÕES FINAIS

A metodologia de GBS possibilitou a identificação de mais de 30.000 SNPs em famílias de irmãos completos de *C. canephora*, com a média de um SNP a cada 11,24kb do genoma. Verificou-se que o padrão de distribuição dos SNPs nas regiões do genoma difere, sendo a menor ocorrência em regiões gênicas. O menor pseudocromossomo (Ch9) apresenta o menor número de SNPs, enquanto o maior pseudocromossomo (Ch2) é o que apresenta SNPs em maior quantidade.

Constatou-se homozigose para 73% dos *loci* amostrados e a média de 1330 SNPs gênicos e 2965 intergênicos por pseudocromossomo. A frequência média do menor alelo foi de 0,199, e a dissimilaridade média dos 145 indivíduos foi de 0,253, com intervalo de 0,183 a 0,399. Ampla distribuição dos SNPs foi encontrada, sendo que foram detectados em média 1330 SNPs gênicos e 2955 intergênicos, por pseudocromossomo.

Os estudos de associação permitiram encontrar 18 SNPs associados a características fenotípicas de *Coffea canephora*: S2_9329731, S2_4579518, S2_41329025, S2_17821870, S2_20934616, S3_23227842, S4_22978689, S5_10964474, S6_9949547, S7_13991105, S7_13991086, S7_13991077, S9_4618814, S9_18527411, S10_24840747, S11_30063996, S11_23828233. Desses, 33% localizam-se em regiões intergênicas, e os demais se distribuem em região de íntrons, éxons e 3'UTR.

A caracterização e distribuição desses SNPs associados a características de interesse para a cafeicultura são promissores para acelerar o processo de melhoramento dos cruzamentos estudados. Os resultados encontrados poderão servir como fonte de informações para a identificação de SNPs em genes controladores de inúmeras características de interesse. Enfatiza-se a importância de estudos que concentrem esforços em análises fenotípicas que possam dissecar melhor cada característica separadamente, o que possibilitará a associação de outros parâmetros com mais SNPs já prospectados.

Material Suplementar

Tabela Suplementar 1. SNPs gênicos identificados em cruzamentos do programa de melhoramento genético de *C. canephora* do Incaper

Ch	Posição	Gene	Ch	Posição	Gene
1	12437001	GCT-(Mediator of RNA polymerase II transcription subunit 13 homolog)	6	41249001	unknown_gene-(unknown protein)
1	12431001	gene desconhecido-(Protein of Unknown Function (DUF239))	6	41247001	SCPL29-(Serine carboxypeptidase-like 29)
1	12418001	At4g08850-(Putative Probable LRR receptor-like serine/threonine-protein kinase At4g08850)	6	41242001	RPOT3-(DNA-directed RNA polymerase 3, chloroplastic)
1	12417001	CYP716B2-(Putative Cytoome P450)	6	41219001	Os06g0520600-(Eukaryotic initiation factor iso-4F subunit p82-34)
1	12415001	gene desconhecido-(protein containing PDZ domain, a K-box domain, and a TPR region)	6	30911001	SCPL24-(Serine carboxypeptidase 24)
1	11037001	RGA3-(Putative disease resistance protein RGA3)	6	30883001	PCMP-E99-(Putative Pentatricopeptide repeat-containing protein At4g04370)
1	11081001	TUBA3-(Tubulin alpha-3 chain)	6	30858001	ABCI1-(ABC transporter I family member 1)
1	38004001	At5g16730-(WEB family protein At5g16730, chloroplastic)	6	30846001	YKT61-(VAMP-like protein YKT61)
1	12434001	gene desconhecido-(Protein of unknown function (DUF1639))	6	30836001	fam108c1-(Putative Abhydrolase domain-containing protein FAM108C1)
1	12424001	PCMP-H69-(Pentatricopeptide repeat-containing protein At1g56690, mitochondrial)	6	30829001	CHIA-(Putative Acidic mammalian chitinase)
1	12422001	gene desconhecido-(Hypothetical protein)	6	30805001	C18orf8-(InterPro DOMAIN/s: Colon cancer-associated Mic1-like (InterPro:IPR009755)
1	12412001	At5g56460-(Probable receptor-like protein kinase At5g56460)	6	30803001	ZFP6-(Putative zinc finger protein 8)
1	12403001	Prkcsh-(calmodulin-binding protein)	6	30792001	At2g41970-(Probable protein kinase At2g41970)
1	11031001	RGA3-(Putative disease resistance protein RGA3)	6	30786001	ahsa-(Putative Activator of 90 kDa heat shock protein ATPase homolog)
1	11053001	PTC52-(Protochlorophyllide-dependent translocon component 52, chloroplastic)	6	30779001	Rnf185-(RING/U-box superfamily protein)
1	11072001	gene desconhecido-(Hypothetical protein)	6	30774001	unknown_gene-(Putative Cysteine/Histidine-rich C1 domain family protein)
1	11076001	midA-(Putative Protein midA, mitochondrial)	6	30745001	unknown_gene-(unknown protein)
1	11077001	Ipo5-(Putative Importin-5)	6	30742001	unknown_gene-(Emsy N Terminus (ENT)/ plant Tudor-like domains-containing protein)
1	38008001	gene desconhecido-(Hypothetical protein)	6	30733001	Rbp6-(Putative uncharacterized protein)
1	38000001	PCMP-E48-(Pentatricopeptide repeat-containing protein At2g21090)	6	30728001	At1g50180-(Putative disease resistance protein At1g50180)
1	37999001	cki2-(Putative Casein kinase I isoform alpha)	6	30712001	PGIP-(Putative Polygalacturonase inhibitor)
1	37986001	PHB2-(Prohibitin-2)	6	30708001	CYP93A1-(Cytoome P450 93A1)
1	37926001	At1g16930-(Putative F-box/FBD/LRR-repeat protein At1g16930)	6	30693001	PCMP-H85-(unknown protein)
1	12416001	CYP716B2-(Cytoome P450 716B2)	6	30682001	NEK6-(Serine/threonine-protein kinase Nek6)
1	12402001	At5g27430-(Signal peptidase complex subunit 3B)	6	30672001	TT1-(C2H2-type zinc finger family protein)
1	12401001	gene desconhecido-(antitermination NusB domain-containing protein)	6	30656001	PURA-(Adenylosuccinate synthetase, chloroplastic)
1	38005001	yqeH-(Putative Uncharacterized protein yqeH)	6	30653001	unknown_gene-(Putative uncharacterized protein)
1	37923001	gene desconhecido-(Hypothetical protein)	6	4122001	At2g41820-(Leucine-rich repeat receptor-like tyrosine-protein kinase At2g41820)
1	12414001	CPN60B2-(RuBisCO large subunit-binding protein subunit beta, chloroplastic)	6	4125001	efr3b-(Uncharacterized protein)
1	5542001	RGA3-(Putative disease resistance protein RGA3)	6	4130001	CYSEP-(Vignain)
1	11073001	gene desconhecido-(Hypothetical protein)	6	4131001	SAP16-(Zinc finger AN1 and C2H2 domain-containing stress-associated protein 16)
1	11080001	gene desconhecido-(Putative Plant protein 1589 of unknown function)	6	4142001	CPK8-(Calcium-dependent protein kinase 8)
1	37996001	NLP6-(Putative Protein NLP2)	6	4143001	unknown_gene-(Putative uncharacterized protein)
1	12435001	gene desconhecido-(arabinogalactan protein 14)	6	4144001	typA-(GTP-binding protein TypA/BipA homolog)
1	12421001	lysS-(Lysine--tRNA ligase)	6	4149001	NFYA9-(Transcription factor)
1	12410001	BCKDHB-(2-oxoisovalerate dehydrogenase subunit beta, mitochondrial)	6	4156001	PCMP-H52-(Putative pentatricopeptide repeat-containing protein At5g52630)
1	12407001	gene desconhecido-(unknown protein -Blast hits to 531 plant proteins, source: NCBI BLink)	6	12649001	PXM16-(Zinc-metallopeptidase, peroxisomal)
1	11044001	gene desconhecido-(Hypothetical protein)	6	12652001	unknown_gene-(Protein of unknown function (DUF288))
1	37952001	PCMP-H92-(Putative Pentatricopeptide repeat-containing protein At5g16860)	6	12662001	At4g08850-(Putative Probable LRR receptor-like serine/threonine-protein kinase At4g08850)
1	37936001	ACA8-(Hypothetical protein)	6	36350001	FIP2-(FH protein interacting protein FIP2)

1	12418001	At4g08850-(Putative Probable LRR receptor-like serine/threonine-protein kinase At4g08850)	6	36360001	unknown_gene-(Putative Multi antimicrobial extrusion protein MatE)
1	12432001	CAPN3-(calpain-type cysteine protease family)	6	36374001	purB-(Adenylosuccinate lyase)
1	12399001	gene desconhecido-(Putative uncharacterized protein)	6	36380001	unknown_gene-(BEST match: proline-rich family protein (TAIR:AT3G09000.1)
2	19782001	CYS6-(Hypothetical protein)	6	40344001	RRP12-(Putative ARM repeat superfamily protein)
2	19786001	GTG1-(Hypothetical protein)	6	40347001	At1g79540-(Pentatricopeptide repeat-containing protein At1g79540)
2	19787001	gene desconhecido-(Putative RING/FYVE/PHD zinc finger superfamily protein)	6	40348001	ABCA1-(ABC transporter A family member 1)
2	19789001	gene desconhecido-(Hypothetical protein)	6	40357001	AGL15-(Agamous-like MADS-box protein AGL15)
2	19799001	REF6-(Transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein)	6	40379001	At2g41620-(Uncharacterized protein At2g41620)
2	19813001	ARF1-(ADP-ribosylation factor)	6	40382001	unknown_gene-(Putative Calcium ATPase)
2	19815001	Stk36-(Protein kinase family protein with ARM repeat domain)	6	40385001	ACA4-(Calcium-transporting ATPase 4, plasma membrane-type)
2	19832001	XRN4-(5'-3' exoribonuclease 4)	6	40427001	unknown_gene-(Transmembrane proteins 14C)
2	19833001	XRN4-(Hypothetical protein)	6	40430001	At3g10140-(DNA repair protein recA homolog 2, mitochondrial)
2	19837001	tmem120-(Putative Transmembrane protein 120 homolog)	6	40450001	ARP-(Apurinic endonuclease-redox protein)
2	19871001	FHT-(Putative Flavanone 3-dioxygenase)	6	40463001	Pigq-(Putative N-acetylglucosaminyl transferase component family protein / Gpi1 family protein)
2	19883001	gene desconhecido-(plastid transcriptionally active 15)	6	40478001	At5g04060-(Probable methyltransferase PMT7)
2	19884001	gene desconhecido-(Putative uncharacterized protein)	6	40479001	NPR5-(Regulatory protein NPR5)
2	19890001	gene desconhecido-(CTC-interacting domain 12)	6	40482001	GLDH-(L-galactono-1,4-lactone dehydrogenase, mitochondrial)
2	19906001	CRK-(CDPK-related protein kinase)	6	40485001	PCMP-H61-(Putative Pentatricopeptide repeat-containing protein At5g66520)
2	19913001	GYP7-(Ypt/Rab-GAP domain of gyp1p superfamily protein)	6	28928001	ncapd2-(Putative Condensin complex subunit 1)
2	19916001	gene desconhecido-(Hypothetical protein)	6	28933001	SS1-(Putative Strictosidine synthase 1)
2	19917001	YSL3-(Metal-nicotianamine transporter YSL3)	6	28954001	HSR201-(Benzyl alcohol O-benzoyltransferase)
2	19923001	MFSD5-(Putative Major facilitator superfamily domain-containing protein 5)	6	28970001	unknown_gene-(unknown protein)
2	19936001	gene desconhecido-(3'-5' CDSuclease domain-containing protein)	6	28979001	unknown_gene-(Transcription factor IIIC, subunit 5)
2	19945001	BIP5-(Luminal-binding protein 5)	6	28995001	hisS-(Putative Histidine--tRNA ligase)
2	19950001	Kpnb1-(Putative Importin subunit beta-1)	6	28996001	TGA21-(TGACG-sequence-specific DNA-binding protein TGA-2.1)
2	19967001	gene desconhecido-(Putative Ribonuclease P protein subunit P38-related)	6	29029001	unknown_gene-(Putative uncharacterized protein)
2	19974001	IQD1-(Putative IQ-domain 21)	6	22860001	CAMK1-(Calcium/calmodulin-dependent serine/threonine-protein kinase 1)
2	19977001	KDM3A-(Putative Chloroplast DNA-binding protein PD3)	6	22886001	At5g05130-(Putative SWI/SNF-related matrix-associated actin-dependent regulator of omatin subfamily A member 3-like 1)
2	19978001	gene desconhecido-(Hypothetical protein)	6	22889001	At3g03300-(Putative Endoribonuclease Dicer homolog 2)
2	19989001	PME34-(Probable pectinesterase/pectinesterase inhibitor 34)	6	22907001	At5g03905-(Hypothetical protein)
2	19994001	ATX4-(Histone-lysine N-methyltransferase ATX4)	6	22929001	TGA1B-(TGACG-sequence-specific DNA-binding protein TGA-1B (Fragment))
2	19997001	SFT2D2-(Putative Vesicle transport protein SFT2B)	6	22935001	At1g68570-(Probable nitrite transporter At1g68570)
2	20018001	At5g53180-(Polypyrimidine tract-binding protein homolog 1)	6	22969001	CYP98A3-(Cytoome P450 98A3)
2	20019001	gene desconhecido-(unknown protein)	6	23000001	E2FE-(E2F transcription factor-like E2FE)
2	20025001	gene desconhecido-(Folylpolyglutamate synthetase family protein)	6	23007001	kdgA-(KDPG and KHG aldolase)
2	20028001	AGP20-(Arabinogalactan peptide 20)	6	23010001	HAT22-(Predicted protein)
2	20040001	myoD-(myosin heavy chain-related)	6	15851001	BC1L6-(Putative COBRA-like protein 1)
2	20041001	At4g23740-(Probable inactive receptor kinase At4g23740)	6	15841001	CYP80B2-(Putative (S)-N-methylcoclaurine 3'-hydroxylase isozyme 2)
2	20050001	PCMP-H77-(Putative pentatricopeptide repeat-containing protein At3g49142)	6	6446001	mettl21a-(Putative methyltransferase family protein)
2	20056001	PKP2-(Plastidial pyruvate kinase 2)	6	18124001	DPE2-(4-alpha-glucanotransferase DPE2)
2	20064001	At5g52880-(Putative F-box protein At5g52880)	6	18132001	unknown_gene-(Putative hydroxyproline-rich glycoprotein family protein)
2	20067001	Trappc1-(Putative Trafficking protein particle complex subunit 1)	6	1553001	CBR1-(NADH-cytoome b5 reductase 1)
2	20075001	gene desconhecido-(Tic22-like family protein)	6	1548001	unknown_gene-(protein folding, protein transport; chloroplast
2	20085001	gene desconhecido-(Putative Copper transport protein family)	6	1545001	VAR3-(Putative Zinc finger protein VAR3, chloroplastic)
2	20099001	At5g24010-(Probable receptor-like protein kinase At5g24010)	6	15578001	CXE1-(Putative Probable carboxylesterase 1)

2	20103001	yjcL-(Putative Uncharacterized membrane protein yjcL)	6	15599001	unknown_gene-(Putative uncharacterized protein)
2	20113001	TT12-(Putative Protein TRANSPARENT TESTA 12)	6	15620001	RIE1-(Putative E3 ubiquitin protein ligase RIE1)
2	20114001	FIB2-(rRNA 2'-O-methyltransferase fibrillarin 1)	6	17162001	HKT2-(Putative Cation transporter HKT2)
2	20133001	gene desconhecido-(Putative C2H2-like zinc finger protein)	6	17166001	R1B-12-(Putative late blight resistance protein homolog R1B-12)
2	20135001	At3g49055-(Putative Uncharacterized protein At3g49055)	6	11690001	MTX2-(Putative Metaxin-2)
2	20139001	P4HA1-(Putative Oxoglutarate/iron-dependent oxygenase)	6	40679001	UBC22-(Ubiquitin-conjugating enzyme E2 22)
2	20140001	gene desconhecido-(alpha/beta-Hydrolases superfamily protein)	6	40668001	ASD1-(Alpha-L-arabinofuranosidase 1)
2	20150001	Notum-(Pectinacetylesterase family protein)	6	40659001	fabG-(Short-chain type dehydrogenase/reductase)
2	20153001	polr3c-(Putative RNA polymerase III subunit RPC82 family protein)	6	40653001	cct8-(T-complex protein 1 subunit theta)
2	20154001	gene desconhecido-(PAR1 protein)	6	40649001	YTHDF2-(Hypothetical protein)
2	20155001	4CLL10-(4-coumarate--CoA ligase-like 10)	6	40615001	SODCC.2-(Superoxide dismutase [Cu-Zn] 2)
2	20156001	TUBB1-(Tubulin beta-1 chain)	6	40609001	TUBA3-(Tubulin alpha-3 chain)
2	20159001	CPIJ013394-(Arabidopsis thaliana protein of unknown function (DUF821))	6	40604001	HPT2-(Homogentisate phytyltransferase 2, chloroplastic)
2	20160001	CPIJ013394-(Putative O-glucosyltransferase rumi homolog)	6	40603001	unknown_gene-(calmodulin-binding family protein)
2	20161001	CPIJ013394-(Putative O-glucosyltransferase rumi homolog)	6	40600001	rsbQ-(Putative Sigma factor sigB regulation protein rsbQ)
2	20163001	POGLUT1-(Putative Protein O-glucosyltransferase 1)	6	40590001	ATXR4-(Histone-lysine N-methyltransferase ATXR4)
2	20165001	POGLUT1-(Putative Protein O-glucosyltransferase 1)	6	40586001	FAR2-(Fatty acyl-CoA reductase 2)
2	20167001	HIPP26-(Putative Heavy metal-associated isoprenylated plant protein 26)	6	40585001	SPAC823.11-(Putative Dihydrosphingosine 1-phosphate phosphatase C823.11)
2	20172001	At3g61260-(Remorin)	6	40584001	SMC2-1-(Structural maintenance of omosomes protein 2-1)
2	20176001	PCMP-E27-(Putative Pentatricopeptide repeat-containing protein At3g29230)	6	40576001	AHA8-(ATPase 8, plasma membrane-type)
2	20185001	MSBP2-(Membrane steroid-binding protein 2)	6	40563001	Os04g0609600-(Probable protein phosphatase 2C 44)
2	20202001	gene desconhecido-(Hypothetical protein)	6	40558001	unknown_gene-(Putative uncharacterized protein)
2	20203001	ANL2-(Homeobox-leucine zipper protein ANTHOCYANINLESS 2)	6	40552001	OCT7-(Organic cation/carnitine transporter 7)
2	20221001	SEU-(SEUSS-like 3)	6	40535001	SPL12-(Putative uncharacterized protein)
2	20222001	Slc47a2-(Putative Multidrug and toxin extrusion protein 2)	6	40527001	HT1-(Protein kinase superfamily protein)
2	20225001	Trabd-(TraB family protein)	6	23167001	unknown_gene-(InterPro DOMAIN/s: GOLD (InterPro:IPR009038)
2	20227001	DREB1D-(Dehydration-responsive element-binding protein 1D)	6	23170001	MLO8-(MLO-like protein 8)
2	20228001	pgap3-(Putative Post-GPI attachment to proteins factor 3)	6	23193001	unknown_gene-(Predicted protein (Fragment))
2	20232001	CPK29-(phosphoenolpyruvate carboxylase-related kinase 1)	6	23194001	At1g06840-(Probable LRR receptor-like serine/threonine-protein kinase At1g06840)
2	20237001	gene desconhecido-(peptidoglycan-binding LysM domain-containing protein)	6	23230001	PUB16-(U-box domain-containing protein 16)
2	20257001	BHLH36-(Putative Transcription factor bHLH36)	6	23231001	CIPK14-(CBL-interacting serine/threonine-protein kinase 14)
2	20265001	FUC1-(Alpha-L-fucosidase 1)	6	23236001	At2g38370-(Putative WEB family protein At2g38370)
2	20270001	KEA5-(K(+) efflux antiporter 5)	6	23279001	DTX44-(MATE efflux family protein 2, chloroplastic)
2	20271001	RAR1-(Cysteine and histidine-rich domain-containing protein RAR1)	6	23296001	unknown_gene-(unknown protein; chloroplast)
2	20290001	MAP65-3-(65-kDa microtubule-associated protein 3)	6	23323001	CHLG-(Chlorophyll synthase, chloroplastic)
2	20291001	gene desconhecido-(Putative uncharacterized protein)	6	23326001	unknown_gene-(Plant protein of unknown function (DUF828))
2	20297001	gene desconhecido-(Putative Protein of unknown function (DUF1442))	6	23333001	Stxbp5-(Putative transducin family protein / WD-40 repeat family protein)
2	20308001	PHR2-(DNA photolyases;DNA photolyases)	6	23341001	APL-(Predicted protein)
2	20327001	BAG7-(Putative BAG family molecular chaperone regulator 7)	6	23400001	RNGTT-(Putative mRNA-capping enzyme)
2	20334001	At3g47420-(Putative glycerol-3-phosphate transporter 1)	6	23419001	unknown_gene-(plastid transcriptionally active 13)
2	20353001	gene desconhecido-(Putative Predicted protein)	6	23465001	ATG1-(Protein kinase superfamily protein)
2	20360001	BBP-(splicing factor-related)	6	23468001	UPP-(Uracil phosphoribosyltransferase)
2	20372001	HEX6-(Hexose carrier protein HEX6)	6	23477001	HERC1-(Putative Probable E3 ubiquitin-protein ligase HERC1)
2	20374001	HEX6-(Hexose carrier protein HEX6)	6	23489001	unknown_gene-(Tetratricopeptide repeat (TPR)-like superfamily protein)
2	20375001	At5g61530-(Uncharacterized Rho GTPase-activating protein At5g61530)	6	23513001	sll1290-(Putative Uncharacterized ribonuclease sll1290)
2	20378001	DER1.2-(Derlin-1.2)	6	23520001	Ubr2-(Putative proteolysis 6)

2	20387001	At3g06530-(Putative Uncharacterized protein At3g06530)	6	23532001	unknown_gene-(unknown protein)
2	20403001	RABD2A-(Ras-related protein RABD2a)	6	23533001	unknown_gene-(Putative unknown protein)
2	20419001	gene desconhecido-(Hypothetical protein)	6	23549001	unknown_gene-(Hypothetical protein)
2	38995001	SPBC543.02c-(Putative Tetratricopeptide repeat (TPR)-like superfamily protein)	6	23552001	AGD7-(ADP-ribosylation factor GTPase-activating protein AGD7)
2	39013001	At5g58300-(Probable inactive receptor kinase At5g58300)	6	23581001	AFC1-(Serine/threonine-protein kinase AFC1)
2	39016001	ATPK2-(Serine/threonine-protein kinase AtPK2/AtPK19)	6	23608001	unknown_gene-(Putative Ribosomal protein S24e family protein)
2	39024001	Shprh-(Putative E3 ubiquitin-protein ligase SHPRH)	6	23629001	ADK-(Adenylate kinase, chloroplastic)
2	39029001	STR7-(Rhodanese-like domain-containing protein 7)	6	23647001	PCMP-E86-(Pentatricopeptide repeat-containing protein At3g53360, mitochondrial)
2	39036001	PCMP-E26-(Pentatricopeptide repeat-containing protein At2g40720)	6	23656001	unknown_gene-(unknown protein)
2	39037001	gpsA-(Putative Glycerol-3-phosphate dehydrogenase [NAD(P)+])	6	23674001	SYP71-(Syntaxin-71)
2	39043001	PUB62-(Putative uncharacterized protein)	6	23678001	DNAJC3-(Putative DnaJ homolog subfamily C member 3)
2	39044001	gene desconhecido-(Putative uncharacterized protein)	6	23703001	MOM1-(Hypothetical protein)
2	39048001	ATL72-(RING-H2 finger protein ATL72)	6	23723001	CDC48-(Cell division cycle protein 48 homolog)
2	39064001	gene desconhecido-(TLC ATP/ADP transporter)	6	23749001	Os04g0560200-(Thioredoxin-like 3-3)
2	39078001	At2g40460-(Probable peptide/nitrate transporter At2g40460)	6	42946001	unknown_gene-(Putative Transducin/WD40 repeat-like superfamily protein)
2	39103001	CHX3-(Putative Cation/H(+) antiporter 3)	6	42959001	NEC3-(Putative Bifunctional monodehydroascorbate reductase and carbonic anhydrase nectarin-3)
2	39118001	DREB2C-(Putative Dehydration-responsive element-binding protein 2C)	6	42967001	RABC2A-(Ras-related protein RABC2a)
2	39125001	RH18-(DEAD-box ATP-dependent RNA helicase 18)	6	42971001	EXPA9-(Expansin-A9)
2	39135001	At2g40280-(Probable methyltransferase PMT23)	6	43015001	At5g03820-(GDSL esterase/lipase At5g03820)
2	39139001	mad3-(Mad3/BUB1 homology region 1)	6	43016001	UPL7-(E3 ubiquitin-protein ligase UPL7)
2	39144001	PUB13-(Putative U-box domain-containing protein 13)	6	43041001	unknown_gene-(Putative Protein of unknown function (DUF668))
2	39149001	ABI4-(Putative Ethylene-responsive transcription factor ABI4)	6	43056001	HDT1-(Histone deacetylase HDT1)
2	39151001	CHC1-(Clathrin heavy chain 1)	6	43067001	HSFA3-(Putative Heat stress transcription factor A-3)
2	39155001	APC1-(Anaphase-promoting complex subunit 1)	6	43075001	unknown_gene-(Plant protein of unknown function (DUF868))
2	39189001	PLC2-(Phosphoinositide phospholipase C 2)	6	43083001	unknown_gene-(unknown protein)
2	39208001	gene desconhecido-(BEST Arabidopsis thaliana protein match is: proline-rich family protein	6	43106001	unknown_gene-(Putative Transducin/WD40 repeat-like superfamily protein)
2	39224001	LAX2-(Auxin transporter-like protein 2)	6	43108001	CYP94A1-(Putative Cytoome P450 94A1)
2	39233001	PIP1-2-(Aquaporin PIP1-2)	6	43164001	ABCB29-(ABC transporter B family member 29, chloroplastic)
2	39238001	gene desconhecido-(Putative Fasciclin-like arabinogalactan family protein)	6	31412001	At2g36090-(Putative Probable F-box protein At1g60180)
2	39242001	gene desconhecido-(Putative Calcium-dependent lipid-binding (CaLB domain) family protein)	6	31383001	Imp4-(U3 small nucleolar ribonucleoprotein protein IMP4)
2	39252001	At3g55800-(Sedoheptulose-1,7-bisphosphatase, chloroplastic)	6	31361001	PUB24-(Putative E3 ubiquitin-protein ligase PUB24)
2	39255001	At2g39910-(Uncharacterized protein At2g39910)	6	31264001	KNAT3-(Homeobox protein knotted-1-like 3)
2	39257001	PCNA-(Proliferating cell nuclear antigen large form)	6	31261001	unknown_gene-(unknown protein)
2	39268001	MYB44-(Putative myb domain protein 1)	6	31209001	UBP22-(Putative Ubiquitin carboxyl-terminal hydrolase 22)
2	29975001	C22orf13-(Putative Uncharacterized protein C22orf13 homolog)	6	31208001	TOC90-(Translocase of chloroplast 90, chloroplastic)
2	29965001	DAR2-(Protein DA1-related 2)	6	31197001	SPS-(Probable sucrose-phosphate synthase)
2	29963001	TOPP4-(Serine/threonine-protein phosphatase PP1 isozyme 4)	6	31193001	MYB4-(Putative myb domain protein 15)
2	29956001	FPGS1-(Folylpolyglutamate synthase)	6	31182001	unknown_gene-(Putative BSD domain-containing protein)
2	29937001	gene desconhecido-(Protein of unknown function (DUF604))	6	31168001	TBC1D15-(Putative TBC1 domain family member 15)
2	29935001	ESC-(AT-hook protein of GA feedback 2)	6	31156001	BCB-(Putative Stellacyanin)
2	29918001	SDIR1-(E3 ubiquitin-protein ligase SDIR1)	6	31151001	At2g27500-(Putative Glucan endo-1,3-beta-glucosidase 14)
2	29916001	gene desconhecido-(ROTUNDIFOLIA like 8)	6	31150001	At4g02530-(Thylakoid lumenal 16.5 kDa protein, chloroplastic)
2	29912001	ARP5-(Actin-related protein 5)	6	31139001	EBF1-(EIN3-binding F-box protein 1)
2	29910001	rlmE-(Putative Ribosomal RNA large subunit methyltransferase E)	6	31136001	rpmJ-(50S ribosomal protein L36)
2	29899001	AP3BA-(AP3-complex subunit beta-A)	6	31134001	PLD1-(Phospholipase D alpha 1)
2	29896001	gene desconhecido-(unknown protein)	6	31094001	At1g55270-(F-box/kelch-repeat protein At1g55270)
2	29887001	gene desconhecido-(Protein of unknown function (DUF506))	6	31080001	PID2-(Protein kinase PINOID 2)
2	29878001	AC58-(Actin)	6	41896001	unknown_gene-(Hypothetical protein)

2	29874001	PIMP1-(CASP-like protein PIMP1)	6	41783001	DDB_G0283291-(Putative 1-aminocyclopropane-1-carboxylate oxidase)
2	29863001	gene desconhecido-(Putative membrane lipoprotein)	6	41759001	vps15-(Putative Phosphoinositide 3-kinase regulatory subunit 4)
2	29857001	UBC7-(Ubiquitin-conjugating enzyme E2 7)	6	41718001	SYNC1-(Asparagine--tRNA ligase, cytoplasmic 1)
2	29801001	TIP1-3-(Aquaporin TIP1-3)	6	41715001	pqqL-(Insulinase (Peptidase family M16) protein)
2	29800001	THE1-(Receptor-like protein kinase THESEUS 1)	6	41710001	At4g29420-(F-box/LRR-repeat protein At4g29420)
2	29782001	gene desconhecido-(Hypothetical protein)	6	41663001	unknown_gene-(Hypothetical protein)
2	29773001	PRPF3-(Pre-mRNA-splicing factor 3)	6	41611001	TS1-(Threonine synthase 1, chloroplastic)
2	29765001	gene desconhecido-(Putative uncharacterized protein)	6	41610001	myoJ-(Myosin family protein with Dil domain)
2	29763001	RBCMT-(SET domain-containing protein)	6	41579001	At1g04910-(O-fucosyltransferase family protein)
2	29761001	maea-(Putative Macrophage erythroblast attacher)	6	41523001	unknown_gene-(Putative uncharacterized protein)
2	29741001	Rbm42-(Putative uncharacterized protein)	6	41504001	TIF3K1-(Eukaryotic translation initiation factor 3 subunit K)
2	29717001	ARA12-(Putative Subtilisin-like protease)	6	41503001	Fig4-(Phosphoinositide phosphatase family protein)
2	29714001	ERF1B-(Putative Ethylene-responsive transcription factor 1B)	6	41499001	SPAPJ696.02-(RING/FYVE/PHD-type zinc finger family protein)
2	29712001	gene desconhecido-(Hypothetical protein)	6	41493001	At1g51965-(Pentatricopeptide repeat-containing protein At1g51965, mitochondrial)
2	29697001	PURKE-(Phosphoribosylaminoimidazole carboxylase, chloroplastic (Fragment))	6	41470001	PIN2-(Auxin efflux carrier component 2)
2	29689001	GEX1-(Protein GAMETE EXPRESSED 1)	6	41428001	Ssx2ip-(Putative Afadin- and alpha-actinin-binding protein)
2	29679001	gene desconhecido-(Mitochondrial glycoprotein family protein)	6	41393001	BIO3-BIO1-(Bifunctional dethiobiotin synthetase/7,8-diamino-pelargonic acid aminotransferase, mitochondrial)
2	29677001	gene desconhecido-(unknown protein)	6	41392001	Fggy-(Putative FGGY carbohydrate kinase domain-containing protein)
2	29663001	gene desconhecido-(Putative bZIP protein)	6	41379001	SPAC977.11-(Putative UPF0695 membrane protein C977.11/PB8B6.06c)
2	29662001	Chmp5-(Putative Charged multivesicular body protein 5)	6	41359001	Os07g0190000-(Probable 1-deoxy-D-xylulose-5-phosphate synthase 2, chloroplastic)
2	29660001	At2g26230-(Uricase)	6	41334001	unknown_gene-(Putative Predicted protein)
2	29656001	MIOX1-(Inositol oxygenase 1)	6	41311001	unknown_gene-(Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region)
2	29650001	ERF1-3-(Eukaryotic peptide chain release factor subunit 1-3)	6	41287001	TAF13-(TBP-associated factor 13)
2	29644001	CAT6-(Cationic amino acid transporter 6, chloroplastic)	6	41254001	CG5315-(Putative ADIPOR-like receptor CG5315)
2	29634001	At2g25100-(Ribonuclease H2 subunit A)	6	41250001	RPL35-(50S ribosomal protein L35)
2	29627001	At2g16710-(Iron-sulfur assembly protein IscA-like 1, mitochondrial)	6	30915001	unknown_gene-(unknown protein)
2	29624001	gene desconhecido-(Putative unknown protein; LOCATED IN: chloroplast	6	30908001	At2g25060-(Putative Early nodulin-like protein 1)
2	29622001	purH-(Bifunctional purine biosynthesis protein PurH)	6	30907001	APO2-(APO protein 2, chloroplastic)
2	29620001	At3g10080-(Germin-like protein subfamily 3 member 2)	6	30899001	unknown_gene-(Hypothetical protein)
2	29619001	gene desconhecido-(TRICHOME BIREFRINGENCE-LIKE 36)	6	30879001	At3g27820-(Probable monodehydroascorbate reductase, cytoplasmic isoform 2)
2	29614001	Mvd-(Diphosphomevalonate decarboxylase)	6	30867001	GAPN-(NADP-dependent glyceraldehyde-3-phosphate dehydrogenase)
2	29612001	slc10a7-(Sodium Bile acid symporter family)	6	30860001	unknown_gene-(Hypothetical protein)
2	29600001	HIATL1-(Putative Major facilitator superfamily protein)	6	30819001	CHI3L1-(Putative Chitinase-3-like protein 1)
2	29587001	gene desconhecido-(Putative Enhancer of polycomb-like transcription factor protein)	6	30773001	unknown_gene-(zinc ion binding)
2	29572001	gene desconhecido-(Putative unknown protein)	6	30767001	At4g08850-(Putative Probable LRR receptor-like serine/threonine-protein kinase At4g08850)
2	29563001	gene desconhecido-(Hypothetical protein)	6	30765001	unknown_gene-(unknown protein)
2	29560001	gene desconhecido-(Hypothetical protein)	6	30760001	unknown_gene-(Putative Chaperone DnaJ-domain superfamily protein)
2	29548001	DME-(Putative uncharacterized protein)	6	30754001	PAP13-(Probable plastid-lipid-associated protein 13, chloroplastic)
2	29540001	gene desconhecido-(Putative Pyruvate kinase, cytosolic isozyme)	6	30749001	Os02g0194200-(Zinc finger CCCH domain-containing protein 14)
2	29531001	Ext2-(glycosyltransferase family protein 47)	6	30746001	SWR1-(SNF2 domain-containing protein / helicase domain-containing protein)
2	29510001	4CLL7-(Putative 4-coumarate--CoA ligase-like 7)	6	30735001	mettl16-(methyltransferases)
2	29505001	SKU5-(Putative Monocopper oxidase-like protein SKU5)	6	30720001	TGA21-(Transcription factor HBP-1b(c38))
2	29504001	SKS2-(Putative Monocopper oxidase-like protein SKS2)	6	30679001	unknown_gene-(Hypothetical protein)
2	29488001	gene desconhecido-(ACT-like superfamily protein)	6	30674001	ctpA-(Putative Carboxyl-terminal-processing protease)
2	29472001	SDP6-(Glycerol-3-phosphate dehydrogenase SDP6, mitochondrial)	6	30655001	Ighmbp2-(Putative DNA-binding protein SMUBP-2)
2	29457001	DDB_G0284757-(Cysteine proteinases superfamily protein)	6	30649001	unknown_gene-(Putative Cysteine/Histidine-rich C1 domain family protein)

2	29452001	At1g47710-(Putative Serpin-ZX)	6	4128001	SEN102-(Thiol protease SEN102)
2	29446001	URB1-(Putative CONTAINS InterPro DOMAIN/s: Ribosome 60S biogenesis N-terminal	6	4129001	CYSEP-(Putative Vignain)
2	29442001	THT4-(Putative Tyramine N-feruloyltransferase 4/11)	6	4153001	At2g41900-(Zinc finger CCCH domain-containing protein 30)
2	29441001	ELF6-(Putative Probable lysine-specific demethylase ELF6)	6	12657001	unknown_gene-(dolichol-phosphate mannosyltransferase-related)
2	29438001	PAL6-(Phenylalanine ammonia-lyase)	6	36352001	RF_0381-(Putative ankyrin repeat protein RF_0381)
2	29427001	algC-(Putative Phosphomannomutase/phosphoglucomutase)	6	36365001	unknown_gene-(Putative embryo defective 2759)
2	29425001	ermp1-(Zn-dependent exopeptidases superfamily protein)	6	36366001	unknown_gene-(Hypothetical protein)
2	29423001	dcp2-(decapping 2)	6	36386001	ACA8-(Calcium-transporting ATPase 8, plasma membrane-type)
2	29415001	GTE6-(Transcription factor GTE6)	6	36391001	DDB_G0289943-(unknown protein; mitochondrion)
2	29413001	Txlna-(CONTAINS InterPro DOMAIN/s: Taxilin	6	40371001	ZOG1-(Zeatin O-glucosyltransferase)
2	29410001	At3g52260-(RNA pseudourine synthase 5)	6	40380001	unknown_gene-(Putative Mitochondrial glycoprotein family protein)
2	29400001	VPS28-2-(Vacuolar protein sorting-associated protein 28 homolog 2)	6	40403001	PCMP-H42-(Putative Pentatricopeptide repeat-containing protein At4g13650)
2	29399001	PCF11-(Putative PCF11P-similar protein 4)	6	40413001	gpsA-(6-phosphogluconate dehydrogenase family protein)
2	29385001	THI1-2-(Thiamine thiazole synthase 2, chloroplastic)	6	40435001	GNS1-(Glucan endo-1,3-beta-glucosidase, acidic isoform PR-Q')
2	29381001	At4g27130-(Protein translation factor SUI1 homolog 1)	6	28904001	DDB_G0268948-(Putative methyltransferase DDB_G0268948)
2	29379001	gene desconhecido-(Putative tyrosyl-DNA phosphodiesterase-related)	6	28907001	unknown_gene-(Predicted protein)
2	29378001	CG7872-(Putative DnaJ homolog subfamily C member 25 homolog)	6	28908001	DDB_G0268948-(Putative methyltransferase DDB_G0268948)
2	29372001	gene desconhecido-(Protein of unknown function (DUF1218))	6	28957001	nol10-(embryo sac development arrest 7)
2	29370001	gene desconhecido-(Putative Protein of unknown function (DUF1218))	6	28987001	unknown_gene-(Hypothetical protein)
2	29357001	DYT1-(Putative Transcription factor DYSFUNCTIONAL TAPETUM 1)	6	29007001	unknown_gene-(Putative 3-hydroxyacyl-CoA dehydratase 1)
2	29349001	PUB8-(U-box domain-containing protein 8)	6	29012001	At2g33200-(Putative F-box protein At2g33200)
2	29338001	SD11-(G-type lectin S-receptor-like serine/threonine-protein kinase SD1-1)	6	22862001	unknown_gene-(Putative basic helix-loop-helix (bHLH) DNA-binding superfamily protein)
2	29333001	At1g61480-(Putative G-type lectin S-receptor-like serine/threonine-protein kinase At1g61480)	6	22869001	At3g12360-(Putative Ankyrin repeat-containing protein At3g12360)
2	29322001	HHT1-(Putative Hydroxycinnamoyl-Coenzyme A shikimate/quinate hydroxycinnamoyltransferase)	6	22884001	unknown_gene-(Major facilitator superfamily protein)
2	29308001	gene desconhecido-(Major facilitator superfamily protein)	6	22904001	unknown_gene-(G2/mitotic-specific cyclin-1)
2	29297001	At4g05090-(Putative PAP-specific phosphatase, mitochondrial)	6	22930001	PPD6-(PsbP domain-containing protein 6, chloroplastic)
2	29291001	PUB4-(ARM repeat superfamily protein)	6	22936001	At1g68570-(Probable nitrite transporter At1g68570)
2	29288001	NDH2-(NAD(P)H dehydrogenase B3)	6	23023001	HAL3A-(Phosphopantothenoylcysteine decarboxylase)
2	29280001	Wrap53-(Putative Telomerase Cajal body protein 1)	6	23041001	CEP1-(KDEL-tailed cysteine endopeptidase CEP1)
2	29274001	gene desconhecido-(Calmodulin-binding protein)	6	15872001	LIG4-(DNA ligase 4)
2	29271001	Os07g0563300-(Putative B3 domain-containing protein Os07g0563300)	6	15861001	unknown_gene-(Putative uncharacterized protein)
2	29263001	TP53I3-(Putative Quinone oxidoreductase PIG3)	6	15830001	unknown_gene-(zinc ion binding)
2	29250001	gene desconhecido-(Protein of unknown function (DUF707))	6	34097001	PER44-(Peroxidase 44)
2	29247001	PCMP-H24-(Putative Pentatricopeptide repeat-containing protein At4g02750)	6	34094001	MYB44-(Putative Predicted protein)
2	29244001	gene desconhecido-(Hypothetical protein)	6	18153001	At3g12390-(Nascent polypeptide-associated complex subunit alpha-like protein)
2	29243001	DDB_G0279265-(UPF0559 protein)	6	3216001	CNOT3-(transcription regulator NOT2/NOT3/NOT5 family protein)
2	29229001	gene desconhecido-(Polyphenol oxidase, chloroplastic)	6	8011001	pnp-(Putative Polyribonucleotide nucleotidyltransferase)
2	29213001	NQR-(NADPH:quinone oxidoreductase)	6	15553001	unknown_gene-(Protein of unknown function (DUF630 and DUF632))
2	29207001	CPL1-(RNA polymerase II C-terminal domain phosphatase-like 1)	6	17149001	CYP83B1-(Putative Cytoome P450 83B1)
2	29182001	gene desconhecido-(Hypothetical protein)	6	17161001	C1-(Replication-associated protein)
2	29173001	LOL2-(Protein LOL2)	6	17181001	unknown_gene-(Hypothetical protein)
2	29172001	RPB2-(DNA-directed RNA polymerase II subunit RPB2)	6	17204001	plaa2-(Putative Exopolygalacturonase (Fragment))
2	29138001	Smg7-(Putative Telomerase activating protein Est1)	6	12876001	GT6-(UDP-glucose flavonoid 3-O-glucosyltransferase 6)
2	29124001	Slc25a29-(Putative Mitochondrial carnitine/acylcarnitine carrier protein CACL)	6	40678001	unknown_gene-(Protein kinase superfamily protein)
2	29110001	NSL1-(MACPF domain-containing protein NSL1)	6	40676001	SIP2-1-(Probable aquaporin SIP2-1)
2	29099001	gene desconhecido-(unknown protein)	6	40663001	unknown_gene-(unknown protein)
2	29082001	HSL1-(Receptor-like protein kinase HSL1)	6	40641001	dnaJ-(Chaperone DnaJ-domain superfamily protein)

2	29053001	gene desconhecido-(vascular plant one zinc finger protein)	6	40598001	PDCD11-(Putative Protein RRP5 homolog)
2	13832001	ERF091-(Putative Ethylene-responsive transcription factor ERF091)	6	40595001	At2g44130-(Putative F-box/kelch-repeat protein At1g15670)
2	13833001	At5g45960-(GDSL esterase/lipase At5g45960)	6	40583001	RH37-(DEAD-box ATP-dependent RNA helicase 37)
2	13840001	ATPAF1-(LOCATED IN: mitochondrion, chloroplast)	6	40571001	unknown_gene-(FAD-dependent oxidoreductase family protein)
2	13846001	DHX35-(Probable ATP-dependent RNA helicase DHX35)	6	23199001	unknown_gene-(Putative uncharacterized protein)
2	13850001	NUDT15-(Nudix hydrolase 15, mitochondrial)	6	23208001	unknown_gene-(Hypothetical protein)
2	13861001	HEX6-(Hexose carrier protein HEX6)	6	23217001	Os07g0679700-(Putative B3 domain-containing protein Os07g0679700)
2	13864001	At1g28570-(Putative GDSL esterase/lipase At1g28570)	6	23308001	BAG4-(Putative BAG family molecular chaperone regulator 4)
2	13867001	At1g28600-(Putative uncharacterized protein)	6	23324001	AMPD-(AMP deaminase)
2	13871001	At1g28590-(GDSL esterase/lipase At1g28590)	6	23340001	SRG1-(Putative Protein SRG1)
2	13887001	CYSEP-(Vignain)	6	23382001	mgtA-(Putative GDP-mannose-dependent alpha-mannosyltransferase)
2	13893001	yabD-(Putative Uncharacterized deoxyribonuclease YabD)	6	23397001	ANTR3-(Probable anion transporter 3, chloroplastic)
2	13905001	BHLH30-(DNA binding protein, putative)	6	23409001	CBLL1-(RING/U-box superfamily protein)
2	13923001	SCAR1-(Putative Protein SCAR1)	6	23425001	LAC7-(Laccase-7)
2	13930001	gene desconhecido-(Protein of unknown function (DUF640))	6	23469001	P5CS-(Delta-1-pyrroline-5-carboxylate synthase)
2	13931001	gene desconhecido-(Putative sequence-specific DNA binding transcription factors)	6	23483001	unknown_gene-(Protein of unknown function (DUF604))
2	13935001	PEX7-(Peroxisome biogenesis protein 7)	6	23488001	unknown_gene-(Putative uncharacterized protein)
2	13943001	CDC48-(Cell division cycle protein 48 homolog)	6	23511001	ORP3A-(Oxysterol-binding protein-related protein 3A)
2	13950001	gene desconhecido-(transcription factor-related)	6	23514001	EXPA4-(Expansin-A4)
2	13961001	NAT2-(Nucleobase-ascorbate transporter 2)	6	23534001	XBAT31-(Putative E3 ubiquitin-protein ligase XBAT31)
2	13966001	GSO1-(Putative LRR receptor-like serine/threonine-protein kinase GSO1)	6	23545001	unknown_gene-(unknown protein;: mitochondrion)
2	13977001	EFR-(Putative LRR receptor-like serine/threonine-protein kinase EFR)	6	23613001	At3g19950-(RING/U-box superfamily protein)
2	14008001	gene desconhecido-(Putative unknown protein)	6	23639001	Mcm8-(Putative DNA replication licensing factor MCM8)
2	14010001	RABA1C-(Ras-related protein RABA1c)	6	23665001	unknown_gene-(Putative uncharacterized protein)
2	14012001	gene desconhecido-(NAD(P)-binding Rossmann-fold superfamily protein)	6	23679001	FLA11-(Fasciclin-like AGP 11)
2	14015001	ADT6-(Arogenate dehydratase/prephenate dehydratase 6, chloroplastic)	6	23746001	unknown_gene-(Putative 5'-AMP-activated protein kinase-related)
2	14025001	ubtd1-(Ubiquitin domain-containing protein 1)	6	43025001	unknown_gene-(Sulfite exporter TauE/SafE family protein)
2	14058001	RKF1-(Probable LRR receptor-like serine/threonine-protein kinase RFK1)	6	43065001	unknown_gene-(Putative uncharacterized protein)
2	14071001	At1g53430-(Putative Probable LRR receptor-like serine/threonine-protein kinase At1g53430)	6	43069001	PCF11-(Putative ENTH/VHS family protein)
2	14075001	NRT1.2-(Putative Nitrate transporter 1.2)	6	43080001	ERF024-(Ethylene-responsive transcription factor ERF024)
2	14106001	UPL3-(E3 ubiquitin-protein ligase UPL3)	6	43081001	At3g47200-(Putative UPF0481 protein At3g47200)
2	14108001	APX3-(L-ascorbate peroxidase 3, peroxisomal)	6	43105001	XSP1-(Xylem serine proteinase 1)
2	14125001	GRP2B-(Glycine-rich protein 2b)	6	43112001	At5g03610-(GDSL esterase/lipase At5g03610)
2	14128001	TOC132-(Hypothetical protein)	6	43130001	ABI5-(Putative Protein ABSCISIC ACID-INSENSITIVE 5)
2	14135001	gene desconhecido-(Putative Pollen Ole e 1 allergen and extensin family protein)	6	43136001	v1g226592-(Putative Probable cytosolic iron-sulfur protein assembly protein)
2	14155001	MTN1-(5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 1)	6	43170001	gacA-(Rho GTPase activating protein with PAK-box/P21-Rho-binding domain)
2	14161001	gene desconhecido-(Calcium-binding EF-hand family protein)	6	43176001	unknown_gene-(unknown protein)
2	14162001	HVA22G-(Putative HVA22-like protein g)	6	31382001	unknown_gene-(Hypothetical protein)
2	14188001	Ufd1l-(ubiquitin fusion degradation 1)	6	31349001	NFYA2-(Putative Nuclear transcription factor Y subunit A-2)
2	14193001	CIB22-(NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9)	6	31283001	A1CF-(Hypothetical protein)
2	14195001	gene desconhecido-(Hypothetical protein)	6	31281001	DBR4-(Putative Predicted protein)
2	14197001	FBA2-(Probable fructose-bisphosphate aldolase 2, chloroplastic)	6	31221001	SRG1-(Putative Protein SRG1)
2	14205001	DTX46-(MATE efflux family protein 4, chloroplastic)	6	31201001	PDF2.2-(Defensin-like protein)
2	14213001	gene desconhecido-(Hypothetical protein)	6	31192001	meaf6-(InterPro DOMAIN/s: Histone H4 acetyltransferase, NuA4 complex, Eaf6 (InterPro:IPR015418); vacuole)
2	14227001	BLH6-(Putative BEL1-like homeodomain protein 6)	6	31147001	unknown_gene-(Putative nucleoporin-related)
2	14230001	At4g39110-(Probable receptor-like protein kinase At4g39110)	6	31103001	BT1-(Protein brittle-1, chloroplastic/amyloplastic)
2	14235001	IMPL2-(Bifunctional phosphatase IMPL2, chloroplastic)	6	31100001	unknown_gene-(Hypothetical protein)
2	14246001	AGPS1-(Glucose-1-phosphate adenylyltransferase large subunit 1 (Fragment))	6	31074001	At3g12390-(Nascent polypeptide-associated complex subunit alpha-like protein)

2	14250001	At1g75280-(Isoflavone reductase homolog)	6	41871001	tilS-(Putative Adenine nucleotide alpha hydrolases-like superfamily protein)
2	14257001	gene desconhecido-(Adenine nucleotide alpha hydrolases-like superfamily protein)	6	41853001	AIM1-(Peroxisomal fatty acid beta-oxidation multifunctional protein AIM1)
2	14277001	At1g01500-(Putative Uncharacterized protein At1g01500)	6	41851001	lin-54-(Tesmin/TSO1-like CXC domain-containing protein)
2	14309001	PCMP-E92-(Putative pentatricopeptide repeat-containing protein At3g18840)	6	41842001	At1g52190-(Probable peptide transporter At1g52190)
2	14310001	HVA22K-(HVA22-like protein k)	6	41837001	IAA27-(Auxin-responsive protein IAA27)
2	14312001	At4g17486-(PPPDE putative thiol peptidase family protein)	6	41808001	DREB3-(Dehydration-responsive element-binding protein 3)
2	14324001	TT12-(Putative Protein TRANSPARENT TESTA 12)	6	41804001	unknown_gene-(Protein of unknown function (DUF810))
2	14326001	gene desconhecido-(Putative MATE efflux family protein)	6	41803001	Stt3a-(Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A)
2	14327001	ISPH-(4-hydroxy-3-methylbut-2-enyl diphosphate reductase, chloroplastic)	6	41766001	HXK2-(Hexokinase-2)
2	14331001	ARI1-(Probable E3 ubiquitin-protein ligase ARI1)	6	41755001	unknown_gene-(Putative oxidative stress 3)
2	14344001	ATL65-(Putative RING-H2 finger protein ATL65)	6	41727001	At4g29190-(Zinc finger CCCH domain-containing protein 49)
2	14345001	LACS2-(Long chain acyl-CoA synthetase 2)	6	41629001	CRTL-E-1-(Lycopene epsilon cyclase, chloroplastic)
2	14357001	gene desconhecido-(Family of unknown function (DUF716))	6	41612001	wdr61-(Putative WD repeat-containing protein 61)
2	14369001	PEX4-(Hypothetical protein)	6	41585001	med20-(Putative mediator of RNA polymerase II transcription subunit 20)
2	14373001	FHT-(Putative Naringenin,2-oxoglutarate 3-dioxygenase (Fragment))	6	41554001	At4g00755-(Hypothetical protein)
2	14377001	Kif15-(Putative phragmoplast orienting kinesin 2)	6	41452001	PMA4-(Plasma membrane ATPase 4)
2	14381001	Cstf3-(Putative Cleavage stimulation factor subunit 3)	6	41403001	VIT_11s0052g01140-(CASP-like protein 3)
2	14390001	ARR1-(Putative myb-like transcription factor family protein)	6	41381001	UFGT-(Kaempferol 3-O-beta-D-galactosyltransferase)
2	14397001	ARMC6-(Putative Armadillo repeat-containing protein 6)	6	41367001	XYLA-(Xylose isomerase)
2	14398001	gene desconhecido-(Cupredoxin superfamily protein)	6	41290001	hddc2-(Putative HD domain-containing protein 2)
2	14400001	CRK-(CDPK-related protein kinase)	6	41267001	unknown_gene-(Putative uncharacterized protein)
2	14414001	PREP1-(Presequence protease 1, chloroplastic/mitochondrial)	6	41227001	Os04g0179200-(Momilactone A synthase)
2	14422001	ATG2-(Putative autophagy 2)	6	30884001	UBP23-(Putative Ubiquitin carboxyl-terminal hydrolase)
2	14426001	CML1-(Calmodulin-like protein 1)	6	30876001	FH13-(Hypothetical protein)
2	14428001	At2g14440-(Putative leucine-rich repeat receptor-like serine/threonine-protein kinase At2g14440)	6	30862001	unknown_gene-(Hypothetical protein)
2	14434001	gene desconhecido-(Hypothetical protein)	6	30850001	GPDL3-(Putative Probable glycerophosphoryl diester phosphodiesterase 3)
2	14438001	Trmt11-(Putative tRNA (guanine(10)-N2)-methyltransferase homolog)	6	30789001	unknown_gene-(Hypothetical protein)
2	14441001	gene desconhecido-(Putative uncharacterized protein)	6	30781001	unknown_gene-(Plant protein of unknown function (DUF828))
2	14443001	ABF3-(Putative ABSCISIC ACID-INSENSITIVE 5-like protein 6)	6	30748001	fabI-(Enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic)
2	14453001	PUB25-(U-box domain-containing protein 25)	6	30744001	unknown_gene-(Putative DNA-binding bromodomain-containing protein)
2	14473001	At4g06744-(Uncharacterized protein At4g06744)	6	30743001	unknown_gene-(alpha/beta-Hydrolases superfamily protein)
2	14476001	gene desconhecido-(Hypothetical protein)	6	30698001	At1g66830-(Putative Probable inactive leucine-rich repeat receptor-like protein kinase At1g66830)
2	14486001	At4g34220-(Receptor protein kinase-like protein At4g34220)	6	12648001	PXM16-(Zinc-metallopeptidase, peroxisomal)
2	14487001	TIC21-(Protein TIC 21, chloroplastic)	6	40415001	INO80-(DNA helicase INO80)
2	14494001	GT2-(Limonoid UDP-glucosyltransferase)	6	40477001	PCMP-H27-(Putative Pentatricopeptide repeat-containing protein At4g35130, chloroplastic)
2	14497001	MTK-(Methylthioribose kinase)	6	40486001	PROC-(Pyrroline-5-carboxylate reductase)
2	14499001	REV1-(DNA repair protein REV1)	6	28905001	DDB_G0268948-(Putative methyltransferase DDB_G0268948)
2	14512001	PRH-(Uncharacterized protein)	6	29018001	FLS2-(Putative LRR receptor-like serine/threonine-protein kinase FLS2)
2	14523001	gene desconhecido-(SWIB/MDM2 domain superfamily protein)	6	29040001	unknown_gene-(Hypothetical protein)
2	14533001	SERK1-(Somatic embryogenesis receptor kinase 1)	6	22859001	unknown_gene-(unknown protein)
2	14540001	ERV1-(FAD-linked sulfhydryl oxidase ERV1)	6	22903001	unknown_gene-(plectin-related)
2	14541001	HDAC6-(Histone deacetylase hda2, putative)	6	22986001	unknown_gene-(C2H2-like zinc finger protein)
2	14544001	gene desconhecido-(Family of unknown function (DUF566))	6	15832001	At5g40670-(Cystinosin homolog)
2	14546001	LBD39-(LOB domain-containing protein, putative)	6	34072001	TR1-(Tropinone reductase homolog)
2	14547001	NPY2-(BTB/POZ domain-containing protein NPY2)	6	17148001	RPP3A-(Putative uncharacterized protein)

2	14556001	BXL5-(Probable beta-D-xylosidase 5)	6	40684001	SCL9-(Scarecrow-like protein 9)
2	14571001	TRB1-(Telomere repeat-binding factor 1)	6	40661001	PCMP-H42-(Putative Pentatricopeptide repeat-containing protein At4g13650)
2	14614001	AAP6-(Amino acid permease 6)	6	40650001	CSNK1D-(Protein kinase family protein)
2	14616001	PKP1-(Pyruvate kinase isozyme A, chloroplastic)	6	40636001	unknown_gene-(FMN binding)
2	14627001	aspS-(Aspartate--tRNA ligase)	6	40630001	unknown_gene-(unknown protein)
2	14631001	gene desconhecido-(Protein of unknown function (DUF1005))	6	40608001	RAP2-11-(Putative Ethylene-responsive transcription factor RAP2-11)
2	14636001	PR1B1-(Pathogenesis-related leaf protein 6)	6	40593001	unknown_gene-(Protein of unknown function (DUF620))
2	14644001	gene desconhecido-(Pathogenesis-related protein 1A)	6	40553001	OCT7-(Putative Organic cation/carnitine transporter 7)
2	14645001	At3g49720-(Uncharacterized protein At3g49720)	6	40551001	unknown_gene-(unknown protein; pollen exine formation)
2	14651001	PIP-(Proline iminopeptidase)	6	23182001	unknown_gene-(Auxin efflux carrier family protein)
2	14653001	MDHG-(Malate dehydrogenase, glyoxysomal)	6	23201001	FER-(Receptor-like protein kinase FERONIA)
2	14655001	BHLH25-(Putative uncharacterized protein)	6	23239001	PNC1-(Cationic peroxidase 1)
2	14665001	rmnd5a-(Putative Protein RMD5 homolog A)	6	23303001	Kpnb1-(Putative Importin subunit beta-1)
2	14667001	gene desconhecido-(Plant protein of unknown function (DUF828))	6	23385001	DCR-(Putative BAHD acyltransferase DCR)
2	14669001	FAAH-(Fatty acid amide hydrolase)	6	23395001	At3g09070-(Putative UPF0503 protein At3g09070, chloroplastic)
2	14675001	pol5-(DNA polymerase V family)	6	23527001	NOTUM-(Pectinacetylesterase family protein)
2	14676001	HSP1-(Heat shock 70 kDa protein, mitochondrial)	6	23557001	TIF3A1-(Eukaryotic translation initiation factor 3 subunit A)
2	14690001	LECRK91-(Putative L-type lectin-domain containing receptor kinase IX.1)	6	23602001	RS2Z32-(Serine/arginine-rich splicing factor RS2Z32)
2	14698001	DRP3A-(Dynamin-related protein 3A)	6	23637001	UPL4-(E3 ubiquitin-protein ligase UPL4)
2	14702001	gene desconhecido-(MED32)	6	23657001	unknown_gene-(Putative uncharacterized protein)
2	14709001	FBP-(Putative Fructose-1,6-bisphosphatase, chloroplastic)	6	23687001	VATG-(Putative V-type proton ATPase subunit G)
2	14722001	CA1-(beta carbonic anhydrase 5)	6	23698001	unknown_gene-(29 kDa ribonucleoprotein A, chloroplastic)
2	14734001	BHLH143-(Putative Transcription factor bHLH143)	6	43034001	waaA-(Putative 3-deoxy-D-manno-octulosonic-acid transferase)
2	14739001	PEPKR2-(Serine/threonine-protein kinase PEPKR2)	6	43154001	unknown_gene-(Thioredoxin family protein)
2	14751001	ACT-(Putative Vinorine synthase)	6	31409001	unknown_gene-(LETM1-like protein)
2	14760001	At1g16830-(Putative pentatricopeptide repeat-containing protein At1g16830)	6	31401001	At3g19330-(Putative UPF0496 protein At3g19330)
2	14765001	ABCG11-(ABC transporter G family member 11)	6	31353001	TRAPPC8-(Putative Trafficking protein particle complex subunit 8)
2	14778001	dnaJ-(Chaperone protein DnaJ)	6	31348001	ssb2-(Putative Replication factor A protein 2)
2	14796001	AOMI-(Alternative oxidase, mitochondrial)	6	31225001	At5g34940-(Heparanase-like protein 3)
2	14797001	PAA1-(Putative Copper-transporting ATPase PAA1, chloroplastic)	6	41938001	HHT1-(Putative Omega-hydroxypalmitate O-feruloyl transferase)
2	14800001	SRSF2-(Hypothetical protein)	6	41937001	DNAJC13-(Putative DnaJ homolog subfamily C member 13)
2	14802001	gene desconhecido-(Putative CD2-binding protein-related)	6	41834001	tsf-(Elongation factor Ts)
2	14809001	trpH-(Putative Protein trpH)	6	41690001	unknown_gene-(Putative effector of transcription2)
2	14811001	PNC2-(Cationic peroxidase 2)	6	41633001	DWA1-(WD repeat-containing protein DWA1)
2	14815001	gene desconhecido-(LOCATED IN: plasma membrane)	6	41525001	ARF19-(Auxin response factor)
2	14834001	Zfp36l1-(Putative uncharacterized protein)	6	41478001	GG18702-(Putative Predicted protein)
2	14842001	At2g32230-(Pentatricopeptide repeat-containing protein At2g32230, mitochondrial)	6	41417001	bcsl1b-(P-loop containing nucleoside triphosphate hydrolases superfamily protein)
2	14844001	psd3-(Putative uncharacterized protein)	6	30780001	HAT14-(Homeobox-leucine zipper protein HAT14)
2	14845001	At1g03050-(Putative clathrin assembly protein At1g03050)	6	12653001	bchH-(Putative Magnesium-chelatase subunit H)
2	14857001	gene desconhecido-(Putative Auxin-induced protein 5NG4)	6	40329001	At4g08850-(Putative Probable LRR receptor-like serine/threonine-protein kinase At4g08850)
2	14891001	MSI1-(Histone-binding protein RBBP4)	6	40434001	GN1-(Glucan endo-1,3-beta-glucosidase, acidic isoform PR-Q')
2	14913001	gene desconhecido-(Protein of unknown function (DUF3411))	6	40496001	VTE4-(Probable tocopherol O-methyltransferase, chloroplastic)
2	14915001	gluP-(Putative RHOMBOID-like protein 10)	6	28920001	At1g12700-(Putative pentatricopeptide repeat-containing protein At1g12700, mitochondrial)
2	14917001	At1g10780-(F-box protein At1g10780)	6	28935001	Nanp-(Putative N-acylneuraminate-9-phosphatase)
2	14920001	AKR2-(Ankyrin repeat domain-containing protein 2)	6	22896001	unknown_gene-(Putative omatin remodeling 42)
2	14934001	PCMP-H77-(Putative pentatricopeptide repeat-containing protein At3g49142)	6	22973001	unknown_gene-(Hypothetical protein)
2	14944001	At1g11050-(Probable receptor-like protein kinase At1g11050)	6	40607001	RPS5-(40S ribosomal protein S5 (Fragment))
2	14954001	rnf170-(Putative RING finger protein 170)	6	23245001	Stam2-(Hypothetical protein)
2	14964001	MRS2-4-(Magnesium transporter MRS2-4)	6	23441001	unknown_gene-(CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP022260

2	14976001	DDB_G0284253-(Putative Protein EI24 homolog)
2	14977001	NIPA2-(Magnesium transporter NIPA2)
2	14980001	gene desconhecido-(Putative unknown protein)
2	14991001	ATL24-(Putative RING-H2 finger protein ATL10)
2	15005001	BAM1-(Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM1)
2	15035001	Gba2-(Putative Non-lysosomal glucosylceramidase)
2	15041001	gene desconhecido-(Protein of unknown function (DUF707))
2	15051001	SERP2049-(NAD(P)-binding Rossmann-fold superfamily protein)
2	15067001	At3g07870-(Putative F-box protein At3g07870)
2	15082001	AL6-(PHD finger protein ALFIN-LIKE 6)
2	15088001	gene desconhecido-(Polyketide cyclase/dehydrase and lipid transport superfamily protein)
2	15091001	At5g49770-(Putative Probable leucine-rich repeat receptor-like protein kinase At5g49770)
2	15097001	At3g60800-(Probable S-acyltransferase At3g60800)
2	15098001	gene desconhecido-(BEST match: Calcium-binding EF-hand family protein)
2	15112001	GAE3-(UDP-glucuronate 4-epimerase 3)
2	15123001	NRT1.5-(Nitrate transporter 1.5)
2	15134001	PECS-2.1-(Pectinesterase 2)
2	15140001	ARG7-(Putative Auxin-induced protein X10A)
2	2339001	FMOGS-OX5-(Flavin-containing monooxygenase FMO GS-OX5)
2	2335001	gene desconhecido-(PLATZ transcription factor family protein)
2	28894001	RABB1B-(Ras-related protein RABB1b)
2	28885001	SPX3-(SPX domain-containing protein 3)
2	28871001	SPL8-(Putative Squamosa promoter-binding-like protein 8)
2	28867001	gene desconhecido-(unknown protein)
2	28858001	CYCU2-2-(Cyclin-U2-2)
2	28855001	EXPB15-(Putative Expansin-B15)
2	28846001	CCD7-(Carotenoid cleavage dioxygenase 7, chloroplastic)
2	28841001	gene desconhecido-(alpha/beta-Hydrolases superfamily protein)
2	28835001	gene desconhecido-(Phosphoglycerate mutase family protein)
2	28831001	Pcbp4-(Putative Poly(rC)-binding protein 4)
2	28822001	DSP8-(Putative dual specificity protein phosphatase DSP8)
2	28779001	ALG12-(Putative GPI mannosyltransferase)
2	28772001	CYCU4-1-(Cyclin-U4-1)
2	28745001	gene desconhecido-(Hypothetical protein)
2	28742001	EIF4G-(Putative uncharacterized protein)
2	28733001	At2g44660-(Probable dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase)
2	28724001	gene desconhecido-(Hypothetical protein)
2	28717001	RABH1B-(Ras-related protein RABH1b)
2	28716001	PUP11-(Probable purine permease 11)
2	28697001	WAX2-(Putative Protein WAX2)
2	28696001	WAX2-(Putative Protein WAX2)
2	28689001	ABCC9-(ABC transporter C family member 9)
2	28670001	At4g35230-(Probable serine/threonine-protein kinase At4g35230)
2	28656001	PUB23-(Putative E3 ubiquitin-protein ligase PUB23)
2	28652001	TTL-(Uric acid degradation bifunctional protein TTL)
2	28649001	gene desconhecido-(Putative uncharacterized protein)
2	28647001	ESC-(Predicted AT-hook DNA-binding family protein)
		(InterPro:IPR016802))
6	23578001	DAPF-(Diaminopimelate epimerase, chloroplastic)
6	23716001	At5g15080-(Protein kinase superfamily protein)
6	23747001	unknown_gene-(unknown protein; chloroplast)
6	42988001	Chd4-(Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain)
6	43117001	SLC35F1-(Putative Solute carrier family 35 member F1)
6	31325001	unknown_gene-(unknown protein)
6	31312001	DLD-(D-lactate dehydrogenase [cytoome], mitochondrial)
6	31288001	ibtk-(Putative RCC1 and BTB domain-containing protein 2)
6	31126001	AMY1.4-(Putative Alpha-amylase isozyme 3E)
6	41917001	PAB2-(Hypothetical protein)
6	41789001	RDR5-(Putative Probable RNA-dependent RNA polymerase 5)
6	41764001	Slc47a1-(Putative Multidrug and toxin extrusion protein 1)
6	41698001	unknown_gene-(unknown protein)
6	41680001	unknown_gene-(tetraspanin2)
6	41634001	unknown_gene-(Eukaryotic initiation factor 4A-8)
6	41563001	ARA12-(Subtilisin-like protease)
6	41509001	EMB8-(Putative Embryogenesis-associated protein EMB8)
6	30835001	unknown_gene-(Calcineurin-like metallo-phosphoesterase superfamily protein)
6	40398001	At4g08850-(Putative Probable LRR receptor-like serine/threonine-protein kinase At4g08850)
6	29034001	At4g27190-(Putative uncharacterized protein)
6	15560001	HMA2-(Cadmium/zinc-transporting ATPase HMA2)
6	23304001	ETO1-(Ethylene-overproduction protein 1)
6	23315001	BHLH140-(Transcription factor bHLH140)
6	23381001	FLU-(Predicted protein (Fragment))
6	23440001	COPT6-(Putative Copper transporter 6)
6	23586001	unknown_gene-(Putative uncharacterized protein)
6	23643001	unknown_gene-(alpha/beta-Hydrolases superfamily protein)
6	23734001	ManS-(Mannan synthase 1)
6	31394001	RCJMB04_2g19-(Putative UPF0554 protein C2orf43 homolog)
6	31152001	BCB-(Putative Umecyanin)
6	41932001	unknown_gene-(Plant protein of unknown function (DUF936))
6	41231001	Cbei_0202-(Putative Uncharacterized protein Cbei_0202)
6	30798001	CCR4-2-(Carbon catabolite repressor protein 4 homolog 2)
6	30660001	F8H-(exostosin family protein)
6	40338001	DTWD2-(Putative DTW domain-containing protein)
6	28924001	At3g22470-(Putative Pentatricopeptide repeat-containing protein At3g22470, mitochondrial)
6	23003001	unknown_gene-(Hypothetical protein)
6	40667001	RIE1-(Putative Zinc finger, C3HC4 type (RING finger) family protein)
6	40545001	KCS15-(3-ketoacyl-CoA synthase 15)
6	23361001	At5g58770-(Dehydrodolichyl diphosphate synthase 2)
6	31088001	At5g20080-(NADH-cytoome b5 reductase-like protein)
6	41753001	At5g56590-(Glucan endo-1,3-beta-glucosidase 13)
6	41437001	CHY1-(3-hydroxyisobutyryl-CoA hydrolase 1)
6	41408001	4CL1-(4-coumarate--CoA ligase 1)
6	41339001	unknown_gene-(Putative uncharacterized protein)
6	30842001	unknown_gene-(Hypothetical protein)
6	40372001	ZOG1-(Zeatin O-glucosyltransferase)

2	28641001	PCMP-H48-(Pentatricopeptide repeat-containing protein At4g37380, chloroplastic)	6	12875001	GT6-(UDP-glucose flavonoid 3-O-glucosyltransferase 6)
2	28640001	SCAI-(Putative Protein SCAI)	6	23426001	MYB44-(Putative myb domain protein 1)
2	28638001	gene desconhecido-(unknown protein; LOCATED IN: plasma membrane)	6	23645001	IQD1-(Putative Protein IQ-DOMAIN 1)
2	28612001	SKIP25-(Putative F-box/kelch-repeat protein SKIP25)	6	41926001	NUDT20-(Nudix hydrolase 20, chloroplastic)
2	24977001	HEX1-(Putative Beta-hexosaminidase)	6	30838001	unknown_gene-(Protein of unknown function (DUF1068))
2	24988001	At1g27950-(Putative Uncharacterized GPI-anchored protein At1g27950)	6	28964001	GLU1-(Ferredoxin-dependent glutamate synthase 1, chloroplastic)
2	24993001	bcsl1b-(Putative P-loop containing nucleoside triphosphate hydrolases superfamily protein)	6	15579001	ACT7-(Putative uncharacterized protein)
2	25006001	gene desconhecido-(Hypothetical protein)	6	40651001	YTHDF2-(Putative evolutionarily conserved C-terminal region 2)
2	25028001	gene desconhecido-(Putative DNA-binding bromodomain-containing protein)	6	22977001	NCS1-(S-norcoclaurine synthase 1)
2	25036001	BGLU13-(Vicianin hydrolase (Fragment))	6	41335001	ATL56-(Putative uncharacterized protein)
2	25037001	BGLU17-(Putative Beta-glucosidase 17)	6	40336001	CTU2-(Cytoplasmic tRNA 2-thiolation protein 2)
2	25059001	cysG-(urophorphyrin methylase 1)	6	40340001	VLN2-(Villin-2)
2	25075001	cluA-(Putative Protein KIAA0664 homolog)	6	31160001	WDR11-(Transducin family protein / WD-40 repeat family protein)
2	25082001	BHLH130-(Putative Transcription factor bHLH122)	6	30806001	kif11-(P-loop containing nucleoside triphosphate hydrolases superfamily protein)
2	25086001	DRT100-(DNA-damage-repair/toleration protein DRT100)	6	23259001	IREG2-(Solute carrier family 40 member 2)
2	25091001	LSM7-(U6 snRNA-associated Sm-like protein LSm7)	6	31245001	At3g02645-(Putative UPF0481 protein At3g02645)
2	25121001	gene desconhecido-(BEST Arabidopsis thaliana protein match is: arabinogalactan protein 23	6	40580001	AHA8-(ATPase 8, plasma membrane-type)
2	25133001	ANT-(ADP,ATP carrier protein, mitochondrial)	6	18123001	DPE2-(4-alpha-glucanotransferase DPE2)
2	25156001	NQR-(NADPH:quinone oxidoreductase)	7	19065001	CCDC101-(Putative SAGA-associated factor 29 homolog)
2	25160001	RGA1-(Putative disease resistance protein RGA1)	7	19083001	9612-(Pectate lyase)
2	25164001	ULT2-(Putative Protein ULTRAPETALA 2)	7	19087001	At3g46610-(Pentatricopeptide repeat-containing protein At3g46610)
2	25167001	NFYA1-(Putative Nuclear transcription factor Y subunit A-1)	7	19103001	unknown_gene-(unknown protein; endomembrane system)
2	25179001	FKBP42-(Peptidyl-prolyl cis-trans isomerase FKBP42)	7	19107001	BST1-(hydrolases, acting on ester bonds)
2	25186001	BHLH120-(Putative Transcription factor bHLH118)	7	19113001	G6PDH-(Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform)
2	25193001	TT12-(Putative Protein TRANSPARENT TESTA 12)	7	19115001	GT-1-(Trihelix transcription factor GT-1)
2	25195001	CYP71D55-(Premnaspirodiene oxygenase)	7	19120001	unknown_gene-(Mitochondrial ribosomal protein L37)
2	25197001	Scyl2-(Hypothetical protein)	7	19121001	mib1-(Ankyrin repeat family protein)
2	9421001	SNRNP200-(U5 small nuclear ribonucleoprotein 200 kDa helicase)	7	19126001	GTE8-(Transcription factor GTE8)
2	9426001	At2g36240-(Putative Pentatricopeptide repeat-containing protein At2g36240)	7	19131001	unknown_gene-(unknown protein)
2	9447001	RPPL1-(Putative disease resistance RPP13-like protein 1)	7	19134001	TPLATE-(Protein TPLATE)
2	18166001	GFPT2-(Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 2)	7	19142001	unknown_gene-(molecular_function unknown; plasma membrane)
2	18176001	At3g52030-(F-box/WD-40 repeat-containing protein At3g52030)	7	19145001	unknown_gene-(Putative uncharacterized protein)
2	18182001	cluA-(Tetratricopeptide repeat (TPR)-like superfamily protein)	7	19150001	pc1998-(Putative Uncharacterized RNA methyltransferase pc1998)
2	18201001	METTL13-(S-adenosyl-L-methionine-dependent methyltransferases superfamily protein)	7	19158001	SOX-(Sulfite oxidase)
2	11528001	NAGLU-(Putative Alpha-N-acetylglucosaminidase)	7	19163001	TOM20-(Mitochondrial import receptor subunit TOM20)
2	11530001	DFR-(Putative Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase)	7	19176001	unknown_gene-(Hypothetical protein)
2	11531001	DFR-(Putative Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase)	7	19179001	unknown_gene-(Protein of unknown function (DUF 3339))
2	11532001	DFR-(Putative Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase)	7	19185001	TCP20-(Transcription factor TCP20)
2	11538001	DFR-(Putative Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase)	7	19188001	RPRD1B-(Putative Regulation of nuclear pre-mRNA domain-containing protein 1A)
2	10443001	gene desconhecido-(Endosomal targeting BRO1-like domain-containing protein)	7	19192001	PBS1-(Serine/threonine-protein kinase PBS1)
2	18364001	ACT-(Putative Vinorine synthase)	7	19215001	unknown_gene-(MALE GAMETOPHYTE DEFECTIVE 2)
2	18394001	SCL3-(Scarecrow-like protein 3)	7	19218001	RNF10-(RING/U-box superfamily protein)
2	38966001	IQD14-(Putative IQ-domain 11)	7	19223001	unknown_gene-(Hypothetical protein)
2	38967001	EXOSC7-(Putative Exosome complex component RRP42)	7	19225001	unknown_gene-(Cytoome b-c1 complex subunit Rieske, mitochondrial)
2	38972001	gene desconhecido-(Hypothetical protein)	7	19226001	unknown_gene-(cofactor assembly of complex C)
2	6393001	gene desconhecido-(Putative uncharacterized protein)	7	19228001	unknown_gene-(unknown protein)

2	18313001	PME42-(Pectinesterase-3, putative)
2	18315001	gene desconhecido-(Hypothetical protein)
2	23788001	gene desconhecido-(Hypothetical protein)
2	23801001	At4g02290-(Endoglucanase 17)
2	23816001	HB2-(Non-symbiotic hemoglobin 2)
2	23832001	ZIFL1-(Protein ZINC INDUCED FACILITATOR-LIKE 1)
2	23841001	gene desconhecido-(Hypothetical protein)
2	23846001	gene desconhecido-(FAD/NAD(P)-binding oxidoreductase family protein)
2	23864001	PCBP1-(Putative Poly(rC)-binding protein 1)
2	27615001	At1g54570-(Acyltransferase-like protein At1g54570, chloroplastic)
2	27593001	wdr48-(Putative WD repeat-containing protein 48)
2	27586001	SDE3-(Probable RNA helicase SDE3)
2	27580001	CDC27B-(Cell division cycle protein 27 homolog B)
2	27569001	XRN4-(5'-3' exoribonuclease 4)
2	27522001	gene desconhecido-(unknown protein; LOCATED IN: chloroplast)
2	27519001	gene desconhecido-(Putative Protein of unknown function (DUF506))
2	27514001	gene desconhecido-(Hypothetical protein)
2	27465001	GSO1-(Putative LRR receptor-like serine/threonine-protein kinase GSO1)
2	27461001	PNG1-(Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase)
2	18907001	GYRA-(DNA gyrase subunit A, chloroplastic/mitochondrial)
2	18914001	TFT10-(14-3-3 protein 10)
2	12955001	tif225-(Putative Probable translation initiation factor eIF-2B subunit epsilon)
2	12960001	gene desconhecido-(Protein of unknown function, transmembrane-40)
2	12969001	gene desconhecido-(Putative DnaJ protein-like protein)
2	12983001	gene desconhecido-(Hypothetical protein)
2	1220001	GSH2-(Glutathione synthetase, chloroplastic)
2	1213001	gene desconhecido-(Hypothetical protein)
2	1208001	At1g54790-(GDSL esterase/lipase At1g54790)
2	16699001	gene desconhecido-(unknown protein; LOCATED IN: chloroplast)
2	16700001	At3g04970-(Probable S-acyltransferase At3g04970)
2	16719001	Dnajb12-(Putative DNAJ heat shock N-terminal domain-containing protein)
2	16739001	R1B-17-(Putative NB-ARC domain-containing disease resistance protein)
2	15337001	HSP70-11-(Putative Heat shock protein 70)
2	15362001	vmp1-(SNARE associated Golgi protein family)
2	15368001	EBM-(Mannosylglycoprotein endo-beta-mannosidase)
2	15372001	gene desconhecido-(Putative Homeodomain-like superfamily protein)
2	15377001	CYCP3-1-(Predicted protein)
2	15378001	GEM1-(Putative Mitochondrial Rho GTPase 1)
2	15379001	ANT1-(Putative Peroxisomal adenine nucleotide transporter 1)
2	15405001	CCX5-(Cation/calcium exchanger 5)
2	15406001	ARA12-(Putative Subtilisin-like protease)
2	15422001	CDC48C-(Cell division control protein 48 homolog C)
2	8632001	RBP47B'-(Polyadenylate-binding protein RBP47B')
2	8636001	gene desconhecido-(Putative alpha/beta-Hydrolases superfamily protein)
2	8637001	PPD2-(Predicted protein (Fragment))
2	8648001	gene desconhecido-(Hypothetical protein)
2	8651001	gene desconhecido-(unknown protein)
7	19234001	NORK-(Putative Nodulation receptor kinase)
7	19237001	LWD1-(WD repeat-containing protein LWD1)
7	39321001	unknown_gene-(Hypothetical protein)
7	39336001	AIM32-(Putative Altered inheritance of mitochondria protein 32)
7	39358001	At3g27700-(Putative Zinc finger CCCH domain-containing protein 41)
7	39395001	fray2-(Protein kinase superfamily protein)
7	39404001	nphp3-(Tetratricopeptide repeat (TPR)-like superfamily protein)
7	39409001	FTB-(Protein farnesyltransferase subunit beta)
7	39418001	HT1-(Putative Serine/threonine-protein kinase HT1)
7	39444001	DEGP9-(Protease Do-like 9)
7	39451001	Mb2253c-(Polynucleotidyl transferase, ribonuclease H-like superfamily protein)
7	39452001	unknown_gene-(Putative Heavy metal transport/detoxification superfamily protein)
7	39455001	mcd4-(Putative GPI ethanolamine phosphate transferase 1)
7	39456001	unknown_gene-(Putative senescence-associated gene 101)
7	39478001	MAN2A1-(Putative Alpha-mannosidase 2)
7	39479001	Sec13-(Protein SEC13 homolog)
7	39484001	SNL2-(Paired amphipathic helix protein Sin3-like 2)
7	39491001	At1g27190-(Probable inactive receptor kinase At1g27190)
7	39493001	unknown_gene-(Hypothetical protein)
7	39509001	AHA4-(ATPase 4, plasma membrane-type)
7	39517001	LAT59-(Probable pectate lyase P59)
7	39533001	IQD31-(Putative Protein IQ-DOMAIN 31)
7	39548001	ABCB19-(ABC transporter B family member 19)
7	39558001	DEGP8-(Protease Do-like 8, chloroplastic)
7	39571001	AVT1-(Putative Vacuolar amino acid transporter 1)
7	39578001	DOF5.2-(Putative Dof zinc finger protein DOF5.2)
7	39612001	KIN10-(SNF1-related protein kinase catalytic subunit alpha KIN10)
7	39617001	At1g54610-(Protein kinase superfamily protein)
7	39634001	unknown_gene-(Hypothetical protein)
7	39639001	unknown_gene-(Putative uncharacterized protein)
7	39660001	RBM47-(Putative uncharacterized protein)
7	39667001	unknown_gene-(Putative uncharacterized protein)
7	39668001	AMYC2-(Alpha-amylase isozyme 2A)
7	39675001	unknown_gene-(Putative hydroxyproline-rich glycoprotein family protein)
7	39684001	TCP13-(Putative uncharacterized protein)
7	39686001	unknown_gene-(unknown protein)
7	39691001	SP1L2-(Protein SPIRAL1-like 2)
7	39694001	OsABCB25-(ABC transporter B family member 25)
7	39698001	Slc25a44-(Putative Solute carrier family 25 member 44)
7	39700001	SEP2-(Developmental protein SEPALLATA 2)
7	39702001	Herc4-(Putative Probable E3 ubiquitin-protein ligase HERC4)
7	39704001	unknown_gene-(Putative DSBA oxidoreductase)
7	39717001	fam108c1-(Abhydrolase domain-containing protein FAM108C1)
7	39719001	RPOT2-(DNA-directed RNA polymerase 2, chloroplastic/mitochondrial)
7	39720001	SLC4A1AP-(SMAD/FHA domain-containing protein)
7	39722001	FRYL-(ARM repeat superfamily protein)
7	39725001	PCMP-E90-(Pentatricopeptide repeat-containing protein At3g02330)

2	8659001	SRP-(Stress-related protein)	7	39726001	unknown_gene-(Hypothetical protein)
2	652001	LSM4-(Probable U6 snRNA-associated Sm-like protein LSm4)	7	39737001	unknown_gene-(unknown protein)
2	670001	gene desconhecido-(INVOLVED IN: response to oxidative stress)	7	39745001	SAMDC-(S-adenosylmethionine decarboxylase proenzyme)
2	680001	PME22-(Putative pectinesterase/pectinesterase inhibitor 22)	7	39756001	unknown_gene-(Putative TRICHOME BIREFRINGENCE-LIKE 19)
2	684001	At1g12775-(Putative Pentatricopeptide repeat-containing protein At1g12775, mitochondrial)	7	39758001	DFR-(Putative NAD(P)-binding Rossmann-fold superfamily protein)
2	697001	gene desconhecido-(pale cress protein (PAC))	7	39766001	CYB561B-(Probable transmembrane ascorbate ferrireductase 2)
2	721001	GATL6-(Probable galacturonosyltransferase-like 6)	7	39783001	YOL092W-(Putative Uncharacterized membrane protein YOL092W)
2	11800001	CKI1-(Putative Histidine kinase CKI1)	7	39795001	BLH2-(BEL1-like homeodomain protein 2)
2	11821001	Rpap3-(Putative RNA polymerase II-associated protein 3)	7	39807001	unknown_gene-(cold-regulated 413-plasma membrane 2)
2	12344001	CSP41B-(Chloroplast stem-loop binding protein of 41 kDa b, chloroplastic)	7	39808001	At5g66560-(BTB/POZ domain-containing protein At5g66560)
2	42877001	STR6-(Rhodanese-like domain-containing protein 6)	7	39820001	VRN1-(Putative B3 domain-containing transcription factor VRN1)
2	42870001	gene desconhecido-(Putative agenet domain-containing protein)	7	39841001	CYP76B1-(7-ethoxycoumarin O-deethylase)
2	42867001	PCMP-E64-(Putative pentatricopeptide repeat-containing protein At1g56570)	7	39845001	Bp10-(L-ascorbate oxidase homolog)
2	42864001	gene desconhecido-(Putative Galactinol synthase)	7	39854001	LBD36-(LOB domain-containing protein 36)
2	42862001	MIMI_R707-(Putative Uncharacterized protein R707)	7	39867001	unknown_gene-(Transducin/WD40 repeat-like superfamily protein)
2	42860001	GUX3-(Putative Uncharacterized protein R707)	7	39899001	unknown_gene-(Putative alpha/beta-Hydrolases superfamily protein)
2	42846001	At1g09420-(Glucose-6-phosphate 1-dehydrogenase 4, chloroplastic)	7	39916001	AP2-(Putative uncharacterized protein)
2	42834001	ABCG31-(Putative ABC transporter G family member 31)	7	39919001	ERF008-(Ethylene-responsive transcription factor ERF008)
2	42821001	ACLA-2-(ATP-citrate synthase alpha chain protein 2)	7	39935001	WRKY7-(Putative Probable WRKY transcription factor 7)
2	42808001	PDR3-(Pleiotropic drug resistance protein 3)	7	39936001	IRX14H-(Probable beta-1,4-xylosyltransferase IRX14H)
2	42805001	PDR3-(Pleiotropic drug resistance protein 3)	7	39949001	At4g37250-(Probable LRR receptor-like serine/threonine-protein kinase At4g37250)
2	42802001	PDR3-(Pleiotropic drug resistance protein 3)	7	39956001	Morf4l1-(Putative Mortality factor 4-like protein 1)
2	42781001	Os05g0567100-(Aspartic proteinase oryzasin-1)	7	39963001	DTXL1-(Putative MATE efflux family protein 5)
2	42764001	HOMT1-(Caffeic acid 3-O-methyltransferase 1)	7	39971001	unknown_gene-(Putative TRICHOME BIREFRINGENCE-LIKE 21)
2	42762001	MYB86-(Putative myb domain protein 61)	7	40002001	unknown_gene-(Hypothetical protein)
2	3934001	ESYT2-(Calcium-dependent lipid-binding (CaLB domain) family protein)	7	40021001	unknown_gene-(Acetamidase/Formamidase family protein)
2	3932001	gene desconhecido-(Copper ion binding protein, putative)	7	40030001	At1g11820-(Putative Glucan endo-1,3-beta-glucosidase 1)
2	3928001	CYP76C4-(Cytoome P450 76C4)	7	40050001	DG1-(Uncharacterized protein)
2	3920001	gene desconhecido-(Ubiquitin-protein ligase, putative)	7	40053001	FRO1-(NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial)
2	3914001	ANKZF1-(zinc finger protein-related)	7	40054001	argA-(Putative Amino-acid acetyltransferase)
2	3911001	gene desconhecido-(Putative SMAD/FHA domain-containing protein)	7	40058001	CG5315-(heptahelical protein 4)
2	3906001	CML10-(Putative Probable calcium-binding protein CML10)	7	40063001	GT6-(Glycosyltransferase 6)
2	3902001	At1g01970-(Pentatricopeptide repeat-containing protein At1g01970)	7	40065001	GT6-(Glycosyltransferase 6)
2	3901001	gene desconhecido-(Hypothetical protein)	7	40074001	PP2A10-(Putative Protein PHLOEM PROTEIN 2-LIKE A10)
2	3889001	KU80-(ATP-dependent DNA helicase 2 subunit KU80)	7	40103001	PRCP-(Putative Lysosomal Pro-X carboxypeptidase)
2	3888001	FKBP43-(Hypothetical protein)	7	40107001	EPFL2-(Putative uncharacterized protein)
2	3885001	GSTZ2-(Glutathione S-transferase zeta class)	7	40161001	unknown_gene-(unknown protein; mitochondrion)
2	3883001	GSTZ1-(Glutathione S-transferase zeta class)	7	40171001	At5g57670-(Protein kinase superfamily protein)
2	3873001	MLO13-(MLO-like protein 13)	7	40178001	DEGP7-(Protease Do-like 7)
2	3870001	gene desconhecido-(Transducin/WD40 repeat-like superfamily protein)	7	40184001	At1g66480-(Uncharacterized protein At1g66480)
2	3864001	At4g38150-(Tetratricopeptide repeat (TPR)-like superfamily protein)	7	40186001	unknown_gene-(Putative uncharacterized protein)
2	3863001	RH3-(DEAD-box ATP-dependent RNA helicase 3, chloroplastic)	7	40187001	PK-(Pyridoxal kinase)
2	3861001	TMEM184A-(Protein of unknown function (DUF300))	7	40211001	DDB_G0271682-(Putative Integrin-linked protein kinase family)
2	3854001	PHYA1-(Phytoome A1)	7	40231001	zgc:66014-(HEAT repeat-containing protein)
2	28049001	FRK1-(Fructokinase-1)	7	40265001	unknown_gene-(unknown protein; plasma membrane)
2	28048001	SOC1-(MADS-box protein SOC1)	7	40268001	unknown_gene-(alpha/beta-Hydrolases superfamily protein)
2	28041001	Atxn10-(Putative Ataxin-10)	7	40280001	ATR3-(NADPH-dependent diflavin oxidoreductase ATR3)

2	28035001	gene desconhecido-(Putative peptidoglycan-binding LysM domain-containing protein)	7	40287001	At1g25520-(GDT1-like protein 4)
2	28031001	RBCMT-(SET domain-containing protein)	7	40296001	unknown_gene-(Putative uncharacterized protein)
2	28014001	PUB3-(ARM repeat superfamily protein)	7	40302001	ddost-(Putative Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit)
2	28009001	At4g00755-(F-box protein At4g00755)	7	40304001	unknown_gene-(Major facilitator superfamily protein)
2	27985001	gene desconhecido-(NAD-dependent malic enzyme 59 kDa isoform, mitochondrial)	7	40307001	GT5-(Putative Anthocyanidin 3-O-glucosyltransferase 5)
2	27980001	SDR1-((+)-neomenthol dehydrogenase)	7	40316001	AMP2-2-(Putative RmlC-like cupins superfamily protein)
2	27969001	PMM-(Phosphomannomutase)	7	40317001	At4g16580-(Probable protein phosphatase 2C 80)
2	27967001	At4g00590-(Probable isoaspartyl peptidase/L-asparaginase 4)	7	37261001	PLT6-(Probable polyol transporter 6)
2	27964001	Cct8-(Putative T-complex protein 1 subunit theta)	7	37259001	unknown_gene-(Protein of unknown function (DUF620))
2	27952001	CAC3-(Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha, chloroplastic)	7	37250001	PERK5-(Proline-rich receptor-like protein kinase PERK5)
2	27940001	ESC-(AT hook motif DNA-binding family protein)	7	37239001	SCL4-(Scarecrow-like protein 4)
2	27928001	RPL36B-(60S ribosomal protein L36-2)	7	37231001	SPCC23B6.04c-(Putative Phosphatidylinositol transfer protein PDR16)
2	27918001	gene desconhecido-(Hypothetical protein)	7	37222001	At1g75220-(Sugar transporter ERD6-like 6)
2	27905001	PIP1-3-(Aquaporin PIP1-3)	7	37217001	atad3-a-(Putative ATPase family AAA domain-containing protein 3-A)
2	27901001	CYP86A2-(Cytoome P450 86A2)	7	37214001	PUB5-(Putative U-box domain-containing protein 5)
2	27898001	gene desconhecido-(Putative unknown protein)	7	37197001	GAMMACA1-(Gamma carbonic anhydrase 1, mitochondrial)
2	27891001	UBC5-(Ubiquitin-conjugating enzyme E2 5)	7	37194001	PCMP-E38-(Pentatricopeptide repeat-containing protein At5g66500, mitochondrial)
2	27880001	TMEM8B-(transmembrane protein-related)	7	37182001	CYP707A7-(Putative Abscisic acid 8'-hydroxylase 3)
2	27872001	Kiaa1432-(Putative Protein RIC1 homolog)	7	37175001	RPP13L4-(Disease resistance RPP13-like protein 4)
2	27871001	FRO2-(Ferric reduction oxidase 2)	7	37169001	unknown_gene-(InterPro DOMAIN/s: Ubiquitin-conjugating enzyme E2C-binding protein (InterPro:IPR019193)
2	27817001	agtA-(Nucleotide-diphospho-sugar transferase family protein)	7	37164001	unknown_gene-(UDP-Glycosyltransferase superfamily protein)
2	27803001	POB1-(BTB/POZ domain-containing protein POB1)	7	37161001	PER72-(Peroxidase 72)
2	27772001	JAR1-(Jasmonic acid-amido synthetase JAR1)	7	37145001	MORC3-(compromised recognition of TCV 1)
2	27762001	DFRA-(Putative Dihydroflavonol-4-reductase)	7	37136001	ALDH3F1-(Aldehyde dehydrogenase family 3 member F1)
2	27750001	gene desconhecido-(alpha/beta-Hydrolases superfamily protein)	7	37133001	Mcrs1-(Putative uncharacterized protein)
2	27744001	LACS4-(Long chain acyl-CoA synthetase 4)	7	37129001	At1g35710-(Putative Probable leucine-rich repeat receptor-like protein kinase At1g35710)
2	27739001	RMF-(Probable F-box protein At3g61730)	7	37127001	GATA5-(Putative GATA transcription factor 5)
2	27730001	cluA-(Tetratricopeptide repeat (TPR)-like superfamily protein)	7	37122001	unknown_gene-(Putative uncharacterized protein)
2	27708001	ERF023-(AP2/ERF domain-containing transcription factor)	7	37109001	kif11-(Putative ATP binding microtubule motor family protein)
2	27703001	RPP1A-(60S acidic ribosomal protein P1-2)	7	37105001	NAC007-(NAC domain-containing protein 7)
2	27697001	gene desconhecido-(Putative unknown protein)	7	37101001	BPC6-(Putative Protein BASIC PENTACYSTEINE6)
2	27687001	gene desconhecido-(NC domain-containing protein-related)	7	37066001	At1g75040-(Pathogenesis-related protein 5)
2	27684001	WNK4-(Serine/threonine-protein kinase WNK8)	7	37061001	unknown_gene-(Major facilitator superfamily protein)
2	27680001	RSP31-(Arginine/serine-rich-splicing factor RSP31)	7	37057001	MLO4-(Putative MLO-like protein 4)
2	27679001	LCA1-(Calcium-transporting ATPase, endoplasmic reticulum-type)	7	37056001	MBP1-(26S proteasome non-ATPase regulatory subunit 4)
2	27645001	KCS1-(3-ketoacyl-CoA synthase 1)	7	37055001	MAN2B1-(Putative Lysosomal alpha-mannosidase)
2	27642001	NAC043-(NAC domain-containing protein 43)	7	37054001	RPS24B-(40S ribosomal protein S24-2)
2	27638001	Vps8-(transducin family protein / WD-40 repeat family protein)	7	37050001	unknown_gene-(unknown protein)
2	27626001	gene desconhecido-(Putative SAUR-like auxin-responsive protein family)	7	37045001	unknown_gene-(unknown protein)
2	19777001	yakA-(Putative Serine/threonine-protein kinase ppk15)	7	37034001	At3g51320-(Putative Pentatricopeptide repeat-containing protein At3g51320)
2	19778001	rpoD-(Putative RNA polymerase sigma-B factor)	7	37006001	AMT3-1-(Ammonium transporter 3 member 1)
2	19779001	gene desconhecido-(unknown protein)	7	37001001	unknown_gene-(NAD(P)H dehydrogenase (quinone)s)
2	19810001	syvn1-(RING/U-box superfamily protein)	7	36978001	SAT2-(Probable serine acetyltransferase 2)
2	19817001	gene desconhecido-(Hypothetical protein)	7	36975001	unknown_gene-(unknown protein)
2	19835001	gene desconhecido-(unknown protein;LOCATED IN: chloroplast)	7	36962001	At4g35600-(Probable serine/threonine-protein kinase Cx32, chloroplastic)
2	19860001	NAC078-(Putative NAC 014)	7	36945001	unknown_gene-(unknown protein)
2	19862001	gene desconhecido-(Heavy metal transport/detoxification superfamily protein)	7	36929001	unknown_gene-(unknown protein)
2	19879001	APRR5-(Putative Two-component response regulator-like APRR5)	7	36928001	MLO-H1-(MLO protein homolog 1)

2	19912001	OsI_031067-(Probable 6-phosphogluconolactonase 4, chloroplastic)
2	19926001	nbas-(unknown)
2	19944001	ACBP2-(Acyl-CoA-binding domain-containing protein 2)
2	19980001	clpX-(ATP-dependent Clp protease ATP-binding subunit ClpX)
2	19983001	EMB1796-(Pentatricopeptide repeat-containing protein At3g49240)
2	19999001	GLT1-(Glutamate synthase [NADH], amyloplastic)
2	20001001	ATL21A-(Putative RING-H2 finger protein ATL21A)
2	20004001	SPMS-(Spermine synthase)
2	20008001	CNGC1-(Cyclic nucleotide-gated ion channel 1)
2	20014001	TPP2-(Probable trehalose-phosphate phosphatase 2)
2	20024001	SPCH-(Transcription factor SPEECHLESS)
2	20032001	PDV1-(Putative Plastid division protein PDV1)
2	20043001	gene desconhecido-(Ubiquitin-associated/translation elongation factor EF1B protein)
2	20047001	ABCC10-(ABC transporter C family member 10)
2	20051001	SE2-(Acidic endochitinase SE2)
2	20063001	SPAST-(P-loop containing nucleoside triphosphate hydrolases superfamily protein)
2	20086001	ASG4-(Transcription factor ASG4)
2	20102001	yjcL-(Putative uncharacterized protein)
2	20104001	gene desconhecido-(Putative uncharacterized protein)
2	20122001	ANP1-(Protein kinase superfamily protein)
2	20138001	GA4-(Putative Gibberellin 3-beta-dioxygenase 1)
2	20145001	gene desconhecido
2	20148001	CPSF100-(Cleavage and polyadenylation specificity factor subunit 2)
2	20149001	Sppl3-(Putative Signal peptide peptidase-like 3)
2	20184001	At3g48880-(F-box/LRR-repeat protein At3g48880)
2	20186001	MBD13-(Putative uncharacterized protein)
2	20190001	gene desconhecido-(Putative uncharacterized protein)
2	20209001	IQD31-(Putative IQ-domain 22)
2	20213001	Polr2f-(RNA polymerase Rpb6)
2	20235001	ZFWD1-(Zinc finger CCCH domain-containing protein 48)
2	20267001	RH7-(DEAD-box ATP-dependent RNA helicase 7)
2	20283001	gene desconhecido-(Predicted protein)
2	20293001	FKBP53-(Peptidyl-prolyl cis-trans isomerase FKBP15-3)
2	20311001	PYR6-(Adenylate kinase)
2	20317001	PME3-(Putative 21 kDa protein)
2	20322001	INV*DC4-(Beta-fructofuranosidase, soluble isoenzyme I)
2	20332001	RIN2-(E3 ubiquitin protein ligase RIN2)
2	20335001	HSP22-(Heat shock 22 kDa protein, mitochondrial)
2	20354001	TDR-(Leucine-rich repeat receptor-like protein kinase TDR)
2	20371001	HEX6-(Hexose carrier protein HEX6)
2	20391001	PFK4-(6-phosphofructokinase 4, chloroplastic)
2	20396001	ERF2-(Ethylene-responsive transcription factor 2)
2	38996001	gene desconhecido-(Putative uncharacterized protein)
2	38999001	CYP734A1-(Putative Cytoome P450 734A1)
2	39030001	WRKY70-(Putative WRKY1)
2	39032001	WRKY55-(WRKY transcription factor 55)
2	39070001	gene desconhecido-(Haloacid dehalogenase-like hydrolase (HAD) superfamily protein)
2	39109001	BEST Arabidopsis thaliana protein match is: DCD
7	36923001	MSSP2-(Monosaccharide-sensing protein 2)
7	36919001	Slc25a3-(Putative Phosphate carrier protein, mitochondrial)
7	36907001	HMGR-(3-hydroxy-3-methylglutaryl-coenzyme A reductase)
7	36882001	At2g17695-(UPF0548 protein At2g17695)
7	36878001	Taz-(Phospholipid/glycerol acyltransferase family protein)
7	36877001	ARF8-(Auxin response factor 8)
7	36875001	unknown_gene-(unknown protein; endomembrane system)
7	36872001	unknown_gene-(NC domain-containing protein-related)
7	36814001	At3g01520-(Putative Universal stress protein A-like protein)
7	36805001	COX11-(Cytoome c oxidase assembly protein ctaG)
7	36801001	KAN1-(Putative Transcription repressor KAN1)
7	36800001	nmd3-(Putative 60S ribosomal export protein NMD3)
7	36754001	RKL1-(Probable inactive receptor kinase At1g48480)
7	36748001	unknown_gene-(Hypothetical protein)
7	36740001	folD-(Putative Bifunctional protein FolD)
7	36739001	At5g37690-(GDSL esterase/lipase At5g37690)
7	36736001	unknown_gene-(alpha/beta-Hydrolases superfamily protein)
7	36735001	Refbp2-(Putative RNA-binding (RRM/RBD/RNP motifs) family protein)
7	36723001	unknown_gene-(Protein of unknown function DUF2359, transmembrane)
7	36713001	rhiE-(Rhamnogalacturonate lyase family protein)
7	36701001	CAD-(Probable mannitol dehydrogenase)
7	36699001	CAD-(Probable mannitol dehydrogenase)
7	36697001	GEDH1-(Geraniol dehydrogenase 1)
7	36696001	ELP4-(Elongator complex protein 4)
7	36683001	At4g18375-(Putative KH domain-containing protein At4g18375)
7	36669001	RBK1-(Receptor-like cytosolic serine/threonine-protein kinase RBK1)
7	36658001	unknown_gene-(Putative uncharacterized protein)
7	36650001	unknown_gene-(Hypothetical protein)
7	36639001	yvyE-(Putative IMPACT family member HI_0722)
7	36634001	unknown_gene-(unknown protein)
7	36631001	CYCD2-1-(Putative Cyclin-D2-1)
7	36624001	GEM-(GLABRA2 expression modulator)
7	36596001	ATHB-6-(Putative Homeobox-leucine zipper protein ATHB-16)
7	36584001	Snapc3-(snRNA activating complex family protein)
7	36583001	At1g65010-(Putative Predicted protein)
7	36578001	SAPK2-(Serine/threonine-protein kinase SAPK2)
7	36563001	unknown_gene-(Predicted protein)
7	36559001	cbbY-(Putative Protein CbbY)
7	36516001	CMTA3-(Putative Calmodulin-binding transcription activator 3)
7	36513001	CDKC-1-(Cyclin-dependent kinase C-1)
7	36497001	unknown_gene-(unknown protein)
7	36492001	ABCC1-(ABC transporter D family member 1)
7	36486001	TTL3-(Putative TPR repeat-containing thioredoxin TTL1)
7	36462001	SULTR2;1-(Sulfate transporter 2.1)
7	36460001	PAT-(Bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase)
7	36455001	AAO-(L-ascorbate oxidase)
7	36454001	MADS29-(Putative AGAMOUS-like 104)
7	36430001	unknown_gene-(Hypothetical protein)

		(Development and Cell Death) domain protein			
2	39115001	IMK2-(Probably inactive leucine-rich repeat receptor-like protein kinase IMK2)	7	36426001	TGA1A-(TGACG-sequence-specific DNA-binding protein TGA-1A)
2	39120001	okr-(Putative uncharacterized protein)	7	36419001	PCMP-H41-(Pentatricopeptide repeat-containing protein At2g22070)
2	39153001	At2g30020-(Probable protein phosphatase 2C 25)	7	36418001	Ggt1-(Putative Gamma-glutamyltranspeptidase 1)
2	39194001	DYAD-(Hypothetical protein)	7	37634001	CYP71A26-(Putative Cytoome P450 71A26)
2	9484001	UGT85A2-(Putative UDP-glycosyltransferase 85A2)	7	37632001	CYP71B10-(Putative Cytoome P450 71B10)
2	29946001	BPM3-(BTB/POZ and MATH domain-containing protein 3)	7	37625001	CYP71A1-(Cytoome P450 71A1)
2	29943001	Papd4-(Nucleotidyltransferase family protein)	7	37612001	RKP-(E3 ubiquitin-protein ligase RKP)
2	29924001	Os11g0706600-(Thaumatin-like protein)	7	37603001	CYP81D1-(Putative Cytoome P450 81D1)
2	29923001	APUM1-(Pumilio homolog 1)	7	37592001	otud6b-(Putative OTU domain-containing protein 6B)
2	29917001	FKBP20-1-(Peptidyl-prolyl cis-trans isomerase FKBP20-1)	7	37582001	At2g21940-(Shikimate kinase, chloroplastic)
2	29902001	gene desconhecido-(XH/XS domain-containing protein)	7	37578001	unknown_gene-(unknown protein; plasma membrane)
2	29890001	TPIP1-(Triosephosphate isomerase, cytosolic)	7	37568001	unknown_gene-(Hypothetical protein)
2	29870001	DOF3.6-(Putative Dof zinc finger protein DOF3.6)	7	37566001	WRKY51-(Probable WRKY transcription factor 51)
2	29854001	gene desconhecido-(Putative SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein)	7	37541001	TKI1-(Putative uncharacterized protein)
2	29845001	metG-(Methionine--tRNA ligase)	7	37535001	unknown_gene-(Hypothetical protein)
2	29838001	gene desconhecido-(unknown protein)	7	37532001	UBP27-(Ubiquitin carboxyl-terminal hydrolase 27)
2	29825001	RABE1C-(Ras-related protein RABE1c)	7	37462001	unknown_gene-(Hypothetical protein)
2	29804001	gar2-(Putative phragmoplastin interacting protein 1)	7	37451001	R1A-6-(Putative late blight resistance protein homolog R1A-6)
2	29788001	MTP5-(Metal tolerance protein 5)	7	37448001	unknown_gene-(Hypothetical protein)
2	29784001	DHAR2-(Glutathione S-transferase DHAR2)	7	37440001	PAP7-(Probable plastid-lipid-associated protein 7, chloroplastic)
2	29762001	RS2Z32-(Serine/arginine-rich splicing factor RS2Z32)	7	37436001	ACT7-(Actin-7)
2	29755001	gene desconhecido-(unknown protein)	7	37435001	UBP26-(Ubiquitin carboxyl-terminal hydrolase 26)
2	29739001	JMJ14-(Transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein)	7	37434001	ATL78-(RING-H2 finger protein ATL78)
2	29724001	CYP87A3-(Putative Cytoome P450 87A3)	7	18835001	SPAC3H5.08c-(Putative Transducin/WD40 repeat-like superfamily protein)
2	29722001	PPCK2-(Phosphoenolpyruvate carboxylase kinase 2)	7	18830001	unknown_gene-(Putative Ankyrin repeat family protein)
2	29710001	gene desconhecido-(unknown protein)	7	18816001	unknown_gene-(Putative Protein of unknown function (DUF506))
2	29680001	gene desconhecido-(Putative uncharacterized protein)	7	18797001	unknown_gene-(TRICHOME BIREFRINGENCE-LIKE 7)
2	29613001	gene desconhecido-(alpha/beta-Hydrolases superfamily protein)	7	18792001	ADH1-(Alcohol dehydrogenase 1)
2	29604001	NIFU4-(NFU1 iron-sulfur cluster scaffold homolog, mitochondrial)	7	18791001	CYP716B2-(Putative Cytoome P450 716B2)
2	29594001	gene desconhecido-(IQ calmodulin-binding motif family protein)	7	18783001	ADH1-(Alcohol dehydrogenase 1)
2	29584001	PDR2-(Pleiotropic drug resistance protein 2)	7	18779001	csd-(Putative uncharacterized protein)
2	29583001	gene desconhecido-(Putative uncharacterized protein)	7	18777001	GLU10-(Putative Endoglucanase 7)
2	29554001	FER-(Putative Receptor-like protein kinase FERONIA)	7	18769001	unknown_gene-(Hypothetical protein)
2	29546001	CSLA9-(Glucomannan 4-beta-mannosyltransferase 9)	7	18744001	CHLI-(Magnesium-chelatase subunit chlI, chloroplastic)
2	29541001	gene desconhecido-(Putative uncharacterized protein)	7	18743001	ABCI10-(ABC transporter I family member 10, chloroplastic)
2	29525001	gene desconhecido-(UDP-Glycosyltransferase superfamily protein)	7	18741001	At5g09310-(Putative uncharacterized protein)
2	29516001	gene desconhecido-(Protein of unknown function (DUF1997))	7	18734001	GA2-(Ent-kaur-16-ene synthase, chloroplastic)
2	29512001	At4g30220-(Probable small nuclear ribonucleoprotein F)	7	18724001	SAL1-(SAL1 phosphatase)
2	29474001	ARK1-(Armadillo repeat-containing kinesin-like protein 1)	7	18721001	Bckdha-(Putative uncharacterized protein)
2	29473001	rluB-(Putative Ribosomal large subunit pseudouridine synthase B)	7	18698001	ABCG5-(Hypothetical protein)
2	29450001	dnlz-(Zim17-type zinc finger protein)	7	18696001	PCMP-E76-(Pentatricopeptide repeat-containing protein At2g13600)
2	29445001	Es2-(Putative Protein DGCR14 homolog)	7	18687001	NFYB7-(Nuclear transcription factor Y subunit B-7)
2	29439001	gene desconhecido-(Transketolase, chloroplastic)	7	18684001	HDA19-(Histone deacetylase 19)
2	29436001	sll0103-(Putative Uncharacterized protein sll0103)	7	18644001	SRP19-(Signal recognition particle 19 kDa protein)
2	29429001	GATA9-(Putative GATA transcription factor 9)	7	18631001	CHLREDRAFT_111274-(Putative Ribosome biogenesis

					protein BOP1 homolog)
2	29428001	ARF18-(Auxin response factor 18)	7	18629001	CHLREDRAFT_111274-(Ribosome biogenesis protein BOP1 homolog)
2	29409001	ncor1-(Putative Duplicated homeodomain-like superfamily protein)	7	18617001	TOP3A-(Putative DNA topoisomerase 3-alpha)
2	29392001	PME18-(Pectinesterase/pectinesterase inhibitor 18)	7	18616001	nat9-(N-acetyltransferase 9-like protein)
2	29377001	CRK25-(Putative Cysteine-rich receptor-like protein kinase 25)	7	18603001	Herc4-(Putative Probable E3 ubiquitin-protein ligase HERC4)
2	29376001	gene desconhecido-(Sulfite exporter TauE/SafE family protein)	7	18599001	SRT2-(NAD-dependent protein deacetylase SRT2)
2	29303001	Xab2-(Pre-mRNA-splicing factor SYF1)	7	18591001	CPZ-(Ribonuclease Z, chloroplastic)
2	29301001	KDM3A-(Putative Transcription factor jumonji (jmjC) domain-containing protein)	7	18565001	At1g71060-(Pentatricopeptide repeat-containing protein At1g71060, mitochondrial)
2	29292001	STC-(Sugar carrier protein C)	7	18540001	HCF164-(Thioredoxin-like protein HCF164, chloroplastic)
2	29284001	Hnrnpul1-(Putative uncharacterized protein)	7	33853001	R1B-12-(Late blight resistance protein, putative)
2	29241001	YSL1-(Metal-nicotianamine transporter YSL1)	7	33856001	unknown_gene-(InterPro DOMAIN/s: Putative harbinger transposase-derived nuclease (InterPro:IPR006912))
2	29223001	SF3B2-(Putative Splicing factor 3B subunit 2)	7	33883001	NEC3-(Bifunctional monodehydroascorbate reductase and carbonic anhydrase nectarin-3)
2	29204001	gene desconhecido-(sensitive to freezing 6)	7	33890001	unknown_gene-(Putative smr (Small MutS Related) domain-containing protein)
2	29188001	gene desconhecido-(Putative uncharacterized protein)	7	33893001	ECA4-(Calcium-transporting ATPase 4, endoplasmic reticulum-type)
2	29162001	LOX3.1-(Linoleate 13S-lipoxygenase 3-1, chloroplastic)	7	33940001	KDM3B-(Putative Transcription factor jumonji (jmjC) domain-containing protein)
2	29087001	TPT-(Triose phosphate/phosphate translocator, chloroplastic)	7	16982001	unknown_gene-(Putative SAGA-associated factor 29)
2	29081001	ACR4-(Putative Serine/threonine-protein kinase-like protein ACR4)	7	15716001	unknown_gene-(Eukaryotic initiation factor 4A-9)
2	29079001	At1g28590-(GDSL esterase/lipase At1g28590)	7	15720001	unknown_gene-(Hypothetical protein)
2	29062001	MLO6-(Putative MLO-like protein 6)	7	7209001	ARA12-(Putative Subtilisin-like protease)
2	29054001	SPBC1703.11-(Putative OPA3-like protein)	7	27317001	TFIP11-(Putative uncharacterized protein)
2	13826001	WOX8-(Putative WUSCHEL-related homeobox 8)	7	27260001	trpB2-(Tryptophan synthase beta chain 2)
2	13858001	At4g20830-(Putative Reticuline oxidase-like protein)	7	27253001	CHFR-(RING/U-box superfamily protein)
2	13862001	PCMP-E34-(Pentatricopeptide repeat-containing protein At1g28690, mitochondrial)	7	27251001	RPL21-(50S ribosomal protein L21, chloroplastic)
2	13876001	gene desconhecido-(unknown protein)	7	27217001	MSRA5-(Putative uncharacterized protein)
2	13883001	gene desconhecido-(TRICHOME BIREFRINGENCE-LIKE 38)	7	11160001	At3g12260-(NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6)
2	13892001	gene desconhecido-(Hypothetical protein)	7	11162001	FRS5-(Putative Far-red impaired responsive (FAR1) family protein)
2	13906001	gene desconhecido-(Hypothetical protein)	7	11165001	RGA3-(Putative disease resistance protein RGA3)
2	13941001	RD21A-(Putative Cysteine proteinase RD21a)	7	16945001	WRI1-(Hypothetical protein)
2	13951001	gene desconhecido-(Putative delay of germination 1)	7	16966001	unknown_gene-(Mitochondrial transcription termination factor family protein)
2	13996001	CESA8-(Cellulose synthase A catalytic subunit 8 [UDP-forming])	7	19068001	unknown_gene-(Putative Surfeit locus protein 2 (SURF2))
2	14026001	dnaX-(Putative AAA-type ATPase family protein)	7	19071001	RGLG2-(E3 ubiquitin-protein ligase RGLG2)
2	14032001	gene desconhecido-(unknown protein)	7	19084001	CIA2-(Putative CCT motif family protein)
2	14064001	gene desconhecido-(Hypothetical protein)	7	19100001	unknown_gene-(Putative CONTAINS InterPro DOMAIN/s: EF-Hand 1, calcium-binding site (InterPro:IPR018247))
2	14065001	At1g53430-(Putative Probable LRR receptor-like serine/threonine-protein kinase At1g53430)	7	19112001	ASPSCR1-(plant UBX domain-containing protein 1)
2	14085001	drkD-(Integrin-linked protein kinase family)	7	19146001	LIP2-(Triacylglycerol lipase 2)
2	14121001	At1g18250-(Thaumatin-like protein)	7	19160001	unknown_gene-(Peptidase family M48 family protein)
2	14123001	TL1-(Thaumatin-like protein 1a)	7	19167001	unknown_gene-(unknown protein)
2	14140001	NUP188-(Putative Protein of unknown function (DUF3414))	7	19191001	unknown_gene-(unknown protein)
2	14145001	BHLH121-(Putative uncharacterized protein)	7	19207001	unknown_gene-(Hypothetical protein)
2	14150001	gene desconhecido-(Putative CONTAINS InterPro DOMAIN/s: Nucleolar 27S pre-rRNA processing, Urb2/Npa2)	7	19220001	MAN2B1-(Putative Lysosomal alpha-mannosidase)
2	14163001	At4g34830/At4g34820-(Putative Pentatricopeptide repeat-containing protein At4g34830, chloroplastic)	7	19221001	unknown_gene-(unknown protein; endomembrane system)
2	14183001	BPC4-(Protein BASIC PENTACYSTEINE4)	7	39353001	LOB-(LOB domain-containing protein 25)
2	14187001	SPE2-(Arginine decarboxylase)	7	39355001	wdr82-b-(Putative WD repeat-containing protein 82-B)
2	14223001	BGAL3-(Beta-galactosidase 3)	7	39356001	unknown_gene-(Putative ARM repeat superfamily protein)
2	14247001	At2g16365-(Putative uncharacterized protein)	7	39360001	unknown_gene-(Putative Protein of unknown function (DUF1421))
2	14259001	BHLH63-(Putative Transcription factor bHLH63)	7	39371001	IDH1-(Isocitrate dehydrogenase [NADP], chloroplastic (Fragment))
2	14263001	ephx3-(Putative Epoxide hydrolase 3)	7	39423001	ATL47-(Uncharacterized protein)

2	14288001	SWI3D-(Putative SWI/SNF complex subunit SWI3D)	7	39437001	At2g26730-(Putative Probable inactive receptor kinase At2g26730)
2	14299001	CLPP6-(ATP-dependent Clp protease proteolytic subunit 6, chloroplastic)	7	39466001	Os08g0360100-(CRM family member 2)
2	14313001	ALTA7-(Minor allergen Alt a 7)	7	39494001	ylbH-(Putative rRNA methyltransferase ylbH)
2	14329001	TIC62-(Protein TIC 62, chloroplastic)	7	39498001	Xylt1-(Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein)
2	14339001	gene desconhecido-(Cysteine/Histidine-rich C1 domain family protein)	7	39531001	RCOM_0855130-(Translation factor GUF1 homolog, mitochondrial)
2	14349001	CYP74A2-(Allene oxide synthase)	7	39534001	qheDH-(Putative uncharacterized protein)
2	14399001	SCNM1-(Putative Sodium channel modifier 1)	7	39542001	ATHB-20-(Homeobox-leucine zipper protein ATHB-20)
2	14416001	KRP7-(Putative uncharacterized protein)	7	39565001	HB29-(homeobox protein 34)
2	14429001	gene desconhecido-(Hypothetical protein)	7	39585001	unknown_gene-(Polypyrimidine tract binding protein, putative)
2	14431001	CYPRO4-(Protein CYPRO4)	7	39586001	PTB-(Hypothetical protein)
2	14435001	LAG2-(LAG1 longevity assurance homolog 2)	7	39607001	VTI13-(Vesicle transport v-SNARE 13)
2	14442001	gene desconhecido-(Protein of unknown function (DUF1685))	7	39611001	RAP2-11-(Putative uncharacterized protein)
2	14462001	FPP7-(Putative Filament-like plant protein 7)	7	39630001	PUB1-(Probable ubiquitin conjugation factor E4)
2	14472001	gene desconhecido-(Protein of unknown function (DUF579))	7	39643001	Nipbl-(PHD finger family protein)
2	14488001	Cdc123-(Putative Cell division cycle protein 123 homolog)	7	39681001	unknown_gene-(Hypothetical protein)
2	14506001	At4g34260-(Alpha-L-fucosidase 2)	7	39688001	unknown_gene-(Predicted protein (Fragment))
2	14528001	At4g33920-(Probable protein phosphatase 2C 63)	7	39708001	BIG-(Auxin transport protein BIG)
2	14555001	gene desconhecido-(Putative Plant protein of unknown function (DUF936))	7	39712001	At1g04910-(O-fucosyltransferase family protein)
2	14635001	PR1B1-(Basic form of pathogenesis-related protein 1)	7	39741001	At5g14450-(GDSL esterase/lipase At5g14450)
2	14638001	gene desconhecido-(Pathogenesis-related protein 1B)	7	39754001	unknown_gene-(Putative TRICHOME BIREFRINGENCE-LIKE 19)
2	14652001	IKU2-(Receptor-like protein kinase HAIKU2)	7	39755001	eng1-(Putative Endo-1,3(4)-beta-glucanase 1)
2	14658001	PPA1-(Soluble inorganic pyrophosphatase 1, chloroplastic)	7	39760001	ICMEL2-(Probable isoprenylcysteine alpha-carbonyl methylesterase ICMEL2)
2	14659001	PPA1-(Soluble inorganic pyrophosphatase 1, chloroplastic)	7	39774001	At2g01390/At2g01380-(Pentatricopeptide repeat-containing protein At2g01390)
2	14696001	gene desconhecido-(Cox19-like CHCH family protein)	7	39790001	DAR1-(Protein DA1-related 1)
2	14711001	EX1-(Protein EXECUTER 1, chloroplastic)	7	39797001	At3g50780-(BTB/POZ domain-containing protein At3g50780)
2	14738001	gene desconhecido-(unknown protein)	7	39811001	unknown_gene-(homolog of Synechocystis YCF37)
2	14750001	gene desconhecido-(Putative uncharacterized protein)	7	39829001	CDCA7L-(Putative Zinc-finger domain of monoamine-oxidase A repressor R1)
2	14768001	UGT85A3-(UDP-glycosyltransferase 85A3)	7	39843001	DOF5.3-(Zinc finger protein, putative)
2	14784001	gene desconhecido-(unknown protein; LOCATED IN: endomembrane system)	7	39847001	PCMP-H5-(Pentatricopeptide repeat-containing protein At4g37170)
2	14792001	gene desconhecido-(tobamovirus multiplication 1)	7	39852001	spp27-(Putative Upstream activation factor subunit spp27)
2	14812001	PNC2-(Cationic peroxidase 2)	7	39856001	unknown_gene-(Putative mitogen-activated protein kinase kinase kinase 5)
2	14831001	Xyl2-(Beta-xylosidase/alpha-L-arabinofuranosidase 2)	7	39859001	PER10-(Peroxidase 10)
2	14833001	WRKY19-(Probable WRKY transcription factor 19)	7	39887001	HSF24-(Heat shock factor protein HSF24)
2	14847001	PER43-(Peroxidase 43)	7	39893001	ABA2-(Zeaxanthin epoxidase, chloroplastic)
2	14862001	TULP8-(Tubby-like F-box protein 8)	7	39894001	unknown_gene-(Putative Remorin family protein)
2	14910001	At1g18250-(Putative Thaumatin-like protein)	7	39924001	At5g67200-(Probable inactive receptor kinase At5g67200)
2	14912001	DDB_G0272012-(Putative Elongation of fatty acids protein 1)	7	39948001	MAPRE3-(Putative Microtubule-associated protein RP/EB family member 3)
2	14958001	TM9SF3-(Transmembrane 9 superfamily member 3)	7	39954001	HMA1-(Probable cadmium/zinc-transporting ATPase HMA1, chloroplastic)
2	14963001	gene desconhecido-(Hypothetical protein)	7	39978001	GH3.1-(Probable indole-3-acetic acid-amido synthetase GH3.1)
2	14979001	NIFU2-(NifU-like protein 3, chloroplastic)	7	39981001	PUB4-(U-box domain-containing protein 4)
2	14984001	gene desconhecido-(Ubiquitin carboxyl-terminal hydrolase family protein)	7	39982001	ABCF4-(ABC transporter F family member 4)
2	14987001	DMI1-(Ion channel DMI1)	7	39985001	unknown_gene-(Arabinogalactan)
2	15000001	truA-(Putative tRNA pseudouridine synthase A)	7	40035001	ncapg2-(Putative ARM repeat superfamily protein)
2	15013001	HSP70-(Stromal 70 kDa heat shock-related protein, chloroplastic)	7	40040001	At3g49900-(Putative BTB/POZ domain-containing protein At3g49900)
2	15015001	PUR2-(Phosphoribosylamine--glycine ligase, chloroplastic)	7	40068001	unknown_gene-(Putative uncharacterized protein)
2	15020001	CRTISO-(Putative Prolycopene isomerase, chloroplastic)	7	40081001	RPL23A-(Putative 60S ribosomal protein L23a)
2	15031001	At1g54610-(Protein kinase superfamily protein)	7	40119001	BAM1-(Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM1)
2	15034001	CC-1-(Cytoome c)	7	40130001	Os06g0160700-(Hypothetical protein)

2	15052001	gene desconhecido-(Hypothetical protein)
2	15055001	SKIV2L2-(Superkiller viralicidic activity 2-like 2)
2	15074001	gene desconhecido-(Hypothetical protein)
2	15079001	dnaX-(AAA-type ATPase family protein)
2	15090001	At5g49770-(Probable leucine-rich repeat receptor-like protein kinase At5g49770)
2	15108001	gene desconhecido-(Hypothetical protein)
2	15131001	Tbcd-(Putative Tubulin-specific chaperone D)
2	28890001	cdsA-(Putative Phosphatidate cytidylyltransferase)
2	28886001	gene desconhecido-(unknown protein)
2	28834001	GAM1-(myb-like HTH transcriptional regulator family protein)
2	28833001	gene desconhecido-(Hypothetical protein)
2	28797001	CSN7-(COP9 signalosome complex subunit 7)
2	28782001	gene desconhecido-(Nucleoside diphosphate kinase B)
2	28764001	RPS7-(40S ribosomal protein S7)
2	28758001	At2g01680-(Putative Ankyrin repeat family protein)
2	28726001	gene desconhecido-(GroES-like family protein)
2	28721001	MTACP1-(Acyl carrier protein 1, mitochondrial)
2	28711001	gene desconhecido-(NAD-dependent malic enzyme 62 kDa isoform, mitochondrial)
2	28708001	DRP1E-(Dynamin-related protein 1E)
2	28706001	TM_1254-(Putative Phosphorylated carbohydrates phosphatase TM_1254)
2	28702001	PYR6-(UMP/CMP kinase)
2	28688001	rpmA-(50S ribosomal protein L27)
2	28687001	ndufaf3-(Putative NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3)
2	28657001	rbgA-(Putative Ribosome biogenesis GTPase A)
2	28625001	BHLH91-(Putative uncharacterized protein)
2	28620001	gene desconhecido-(unknown protein)
2	24946001	LHP1-(Putative omo domain protein LHP1)
2	24968001	gene desconhecido-(Protein of Unknown Function (DUF239))
2	24974001	FLOT1-(Flotillin-like protein 1)
2	25024001	gene desconhecido-(Putative proline-rich family protein)
2	25067001	At5g42850-(Thioredoxin-like protein Clot)
2	25068001	SYN3-(Putative Sister omatid cohesion 1 protein 3)
2	25074001	ATJ1-(Putative Chaperone protein dnaJ 1, mitochondrial)
2	25134001	BB-(E3 ubiquitin ligase BIG BROTHER)
2	25149001	At5g13450-(ATP synthase subunit O, mitochondrial)
2	25150001	MYB46-(Putative myb domain protein 83)
2	25154001	At2g41900-(Zinc finger CCCH domain-containing protein 30)
2	25162001	CESA3-(Cellulose synthase A catalytic subunit 3 [UDP-forming])
2	25170001	CNR6-(Cell number regulator 6)
2	25194001	At3g08650-(Putative zinc transporter At3g08650)
2	18168001	gene desconhecido-(unknown protein)
2	4504001	gene desconhecido-(Uncharacterized protein)
2	18357001	RPPL1-(Putative disease resistance protein At3g14460)
2	18398001	PVS1-(Putative Vetispiradiene synthase 1)
2	10173001	ARP2-(Actin-related protein 2)
2	38920001	RPPL1-(Putative disease resistance protein At3g14460)
2	23793001	At5g28840-(Putative UDP-XYL synthase 5)
2	23843001	gene desconhecido-(Putative unknown protein; LOCATED IN: chloroplast)
7	40157001	unknown_gene-(Serine hydroxymethyltransferase, mitochondrial)
7	40176001	unknown_gene-(Putative ARM repeat superfamily protein)
7	40180001	unknown_gene-(Hypothetical protein)
7	40197001	Eaf-(RNA polymerase II transcription elongation factor)
7	40204001	EIF5-(Eukaryotic translation initiation factor 5)
7	40212001	At5g37990-(Putative Probable S-adenosylmethionine-dependent methyltransferase At5g37990)
7	40262001	unknown_gene-(unknown protein)
7	40267001	mpi-(Putative Probable mannose-6-phosphate isomerase)
7	40300001	GGPS1-(Geranylgeranyl pyrophosphate synthase, chloroplastic)
7	40324001	SF3B4-(RNA-binding (RRM/RBD/RNP motifs) family protein)
7	37258001	unknown_gene-(Protein of unknown function (DUF1195))
7	37233001	unknown_gene-(Putative uncharacterized protein)
7	37207001	YMR099C-(Putative glucose-6-phosphate 1-epimerase)
7	37203001	yugF-(Putative Uncharacterized hydrolase yugF)
7	37157001	EPHX2-(Putative Epoxide hydrolase 2)
7	37139001	GRXS6-(Monothiol glutaredoxin-S6)
7	37099001	Syncrip-(RNA binding protein, putative)
7	37097001	MUR1-(GDP-mannose 4,6 dehydratase 2)
7	37093001	PIN1-(Peptidyl-prolyl cis-trans isomerase Pin1)
7	37080001	AN3-(Naringenin,2-oxoglutarate 3-dioxygenase (Fragment))
7	37003001	IQD31-(IQ-domain 20)
7	36976001	GRIP-(Protein GRIP)
7	36973001	CYCB2-3-(G2/mitotic-specific cyclin-1)
7	36890001	DGAT2-(Diacylglycerol O-acyltransferase 2)
7	36850001	unknown_gene-(Putative unknown protein)
7	36849001	MAA3-(Putative P-loop containing nucleoside triphosphate hydrolases superfamily protein)
7	36834001	HERC1-(Putative Probable E3 ubiquitin-protein ligase HERC1)
7	36828001	LHY-(Putative At5g37260 (Fragment))
7	36817001	GAD-(Glutamate decarboxylase)
7	36810001	phg1b-(Putative phagocytic receptor 1b)
7	36802001	unknown_gene-(unknown protein)
7	36799001	CRK3-(Putative Cysteine-rich receptor-like protein kinase 3)
7	36777001	MMD1-(PHD finger protein MALE MEIOCYTE DEATH 1)
7	36775001	SKOR-(Potassium channel SKOR)
7	36763001	KLC3-(Tetratricopeptide repeat (TPR)-like superfamily protein)
7	36761001	NCAPG-(ARM repeat superfamily protein)
7	36742001	At1g66250-(Glucan endo-1,3-beta-glucosidase 2)
7	36726001	unknown_gene-(NTA15 protein)
7	36709001	GEDH1-(Geraniol dehydrogenase 1)
7	36688001	ALDH6B2-(Putative uncharacterized protein)
7	36665001	PUB50-(Putative U-box domain-containing protein 50)
7	36654001	At1g04910-(Putative DUF246 domain-containing protein At1g04910)
7	36643001	unknown_gene-(Putative hydroxyproline-rich glycoprotein family protein)
7	36627001	PFK5-(6-phosphofructokinase 5, chloroplastic)
7	36621001	TT12-(Putative Protein TRANSPARENT TESTA 12)
7	36602001	At4g01020-(Putative uncharacterized protein At4g01020, chloroplastic)
7	36600001	SODIT1-(Putative 2-oxoglutarate/malate translocator, chloroplastic)
7	36581001	TFT6-(14-3-3-like protein 16R)

2	23845001	At4g27290-(Putative G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290)	7	36573001	PER17-(Peroxidase 17)
2	23875001	gluA-(Putative Lysosomal beta glucosidase)	7	36478001	unknown_gene-(Putative Protein of unknown function (DUF630 and DUF632))
2	27611001	At1g54570-(Acyltransferase-like protein At1g54570, chloroplastic)	7	36472001	gpmA-(2,3-bisphosphoglycerate-dependent phosphoglycerate mutase)
2	27596001	sf3b1-(Splicing factor 3B subunit 1)	7	36443001	unknown_gene-(unknown protein)
2	27589001	gene desconhecido-(CONTAINS InterPro DOMAIN/s: SEC-C motif)	7	36439001	BHLH25-(Hypothetical protein)
2	27565001	ACT-(Putative Vinorine synthase)	7	37608001	CXE6-(Putative Probable carboxylesterase 6)
2	27543001	gene desconhecido-(Hypothetical protein)	7	37595001	GRXS6-(Hypothetical protein)
2	27484001	SPBC1A4.09-(Putative pseudouridine synthase C1A4.09)	7	37580001	drg1-(Developmentally-regulated GTP-binding protein 1)
2	27482001	At5g28300-(Putative Duplicated homeodomain-like superfamily protein)	7	37564001	ISCA-(Iron-sulfur assembly protein IscA, chloroplastic)
2	27480001	NEK2-(Serine/threonine-protein kinase Nek2)	7	37563001	BRI1-(Putative Protein BRASSINOSTEROID INSENSITIVE 1)
2	27468001	UGT83A1-(Putative UDP-glycosyltransferase 83A1)	7	37560001	At1g10490-(UPF0202 protein At1g10490)
2	12961001	gene desconhecido-(Putative unknown protein)	7	37555001	THG1L-(Putative Probable tRNA(His) guanylyltransferase)
2	1245001	GATA26-(Putative GATA transcription factor 26)	7	37546001	DDB_G0268328-(unknown protein)
2	1236001	At1g54730-(Sugar transporter ERD6-like 5)	7	37480001	unknown_gene-(Hypothetical protein)
2	1225001	DDB_G0282801-(unknown protein)+C1367	7	8838001	unknown_gene-(Putative endonuclease or glycosyl hydrolase)
2	16690001	PIGA-(UDP-Glycosyltransferase superfamily protein)	7	18823001	unknown_gene-(Hypothetical protein)
2	16708001	gene desconhecido-(unknown protein; LOCATED IN: nucleolus)	7	18821001	unknown_gene-(Putative Ankyrin repeat family protein)
2	16746001	GLIP5-(Putative GDSL esterase/lipase 5)	7	18765001	unknown_gene-(Serine protease inhibitor, potato inhibitor I-type family protein)
2	15338001	BIP5-(Luminal-binding protein 5)	7	18762001	NAC078-(Putative Nam-like protein 2)
2	15350001	CYCH1-1-(Cyclin-H1-1)	7	18753001	CALS5-(Callose synthase 5)
2	15354001	CUL1-(Putative Cullin-1)	7	18736001	RABC1-(Ras-related protein RABC1)
2	15358001	Rev3l-(recovery protein 3)	7	18731001	unknown_gene-(Hypothetical protein)
2	635001	BHLH25-(Predicted protein (Fragment))	7	18633001	unknown_gene-(unknown protein)
2	644001	BHLH25-(DNA binding protein, putative)	7	18589001	unknown_gene-(RING/FYVE/PHD zinc finger superfamily protein)
2	646001	CLPR3-(ATP-dependent Clp protease proteolytic subunit-related protein 3, chloroplastic)	7	18581001	OEP80-(Outer envelope protein 80, chloroplastic)
2	651001	At3g05520-(F-actin-capping protein subunit alpha)	7	18561001	FPP3-(Putative Filament-like plant protein 3)
2	653001	Hgsnat-(Putative Heparan-alpha-glucosaminide N-acetyltransferase)	7	18541001	XDH1-(Xanthine dehydrogenase 1)
2	656001	gene desconhecido-(Putative RING/U-box superfamily protein)	7	18537001	der-(GTPase Der)
2	681001	FBL3-(Putative F-box/LRR-repeat protein 3)	7	33886001	At5g08430-(Putative Zinc finger CCCH domain-containing protein 19)
2	730001	gene desconhecido-(Putative uncharacterized protein)	7	33888001	MET1B-(DNA (cytosine-5)-methyltransferase 1B)
2	11804001	At1g56345-(RNA pseudourine synthase 1)	7	33905001	CYP72A1-(Putative Cytoome P450 734A1)
2	11814001	gene desconhecido-(unknown protein; LOCATED IN: endomembrane system)	7	33925001	unknown_gene-(Hypothetical protein)
2	42890001	gene desconhecido-(Hypothetical protein)	7	16979001	unknown_gene-(Putative uncharacterized protein)
2	42888001	PCMP-H61-(Putative Pentatricopeptide repeat-containing protein At5g66520)	7	16993001	SWI3A-(Putative SWI/SNF complex subunit SWI3A)
2	42863001	GUX1-(Putative UDP-glucuronate:xylan alpha-glucuronosyltransferase 1)	7	27231001	At3g11710-(Lysine--tRNA ligase)
2	42851001	ARF1-(ADP-ribosylation factor 1)	7	16948001	unknown_gene-(Putative nodulin MtN21 /EamA-like transporter family protein)
2	42827001	ASK3-(Shaggy-related protein kinase gamma)	7	19066001	MIMI_L728-(Uncharacterised conserved protein UCP015417, vWA)
2	42809001	PDR3-(Pleiotropic drug resistance protein 3)	7	19102001	unknown_gene-(Putative Predicted protein)
2	42796001	At1g11820-(Hydrolase, hydrolyzing O-glycosyl compounds, putative)	7	19140001	PPXII-(Protoporphyrinogen oxidase, mitochondrial)
2	42795001	gene desconhecido-(unknown protein)	7	19161001	POT1B-(Putative Protection of telomeres protein 1b)
2	42780001	Gpatch8-(D111/G-patch domain-containing protein)	7	19213001	AK1-(Aspartokinase 1, chloroplastic)
2	3926001	lvsC-(WD-40 repeat family protein / beige-related)	7	39333001	PCMP-E87-(Putative pentatricopeptide repeat-containing protein At3g01580)
2	3921001	Fignl1-(AAA-type ATPase family protein)	7	39340001	Pom210-(embryo defective 3012)
2	3907001	ESC-(AT-hook motif nuclear-localized protein 22)	7	39370001	pnp-(Putative Polyribonucleotide nucleotidyltransferase)
2	3882001	GSTZ1-(Glutathione S-transferase zeta class)	7	39384001	RPL12-(50S ribosomal protein L12, chloroplastic)
2	3879001	KOR-(Endoglucanase 25)	7	39389001	unknown_gene-(RNA-binding (RRM/RBD/RNP motifs) family protein)
2	28042001	PLDBETA1-(Phospholipase D beta 1)	7	39457001	PER63-(Peroxidase 63)
2	28029001	UTR4-(UDP-galactose/UDP-glucose transporter 4)	7	39490001	unknown_gene-(Putative uncharacterized protein)

2	28007001	At4g00750-(Probable methyltransferase PMT15)	7	39505001	ytfP-(Oxidoreductase, putative)
2	27998001	ANL2-(Homeobox-leucine zipper protein ANTHOCYANINLESS 2)	7	39624001	Plut_0637-(Protein of unknown function (DUF179))
2	27994001	At4g11680-(E3 ubiquitin-protein ligase At4g11680)	7	39627001	At5g39410-(Probable mitochondrial saccharopine dehydrogenase-like oxidoreductase At5g39410)
2	27962001	gene desconhecido-(Hypothetical protein)	7	39633001	CNGC2-(Cyclic nucleotide-gated ion channel 2)
2	27932001	TNNI3K-(Putative Serine/threonine-protein kinase TNNI3K)	7	39655001	PCMP-E16-(Pentatricopeptide repeat-containing protein At5g39350)
2	27917001	med12-(RNA polymerase II transcription mediators)	7	39658001	CLPB3-(Chaperone protein ClpB3, chloroplastic)
2	27870001	FRO2-(Ferric reduction oxidase 2)	7	39664001	UGT83A1-(UDP-glycosyltransferase 83A1)
2	27867001	FACE1-(CAAX prenyl protease 1 homolog)	7	39674001	SCPL25-(Serine carboxypeptidase-like 25)
2	27865001	At1g01540-(Probable serine/threonine-protein kinase At1g01540)	7	39706001	unknown_gene-(unknown protein)
2	27861001	gene desconhecido-(Putative unknown protein)	7	39747001	ftsH-(Cell division protease ftsH, putative)
2	27841001	pli1-(Hypothetical protein)	7	39750001	unknown_gene-(Putative tetraspanin3)
2	27836001	trs20-(Transport protein particle 20 kDa subunit)	7	39773001	Os03g0199100-(UPF0496 protein 1)
2	27812001	BAG6-(Hypothetical protein)	7	39818001	DDB_G0277179-(Protein of unknown function, DUF647)
2	27788001	UBC28-(Ubiquitin-conjugating enzyme E2 28)	7	39823001	ptrB-(Putative Protease 2)
2	27778001	SPA1-(Putative Protein SUPPRESSOR OF PHYA-105 1)	7	39876001	MAP1D-(Methionine aminopeptidase 1D, chloroplastic/mitochondrial)
2	27756001	STR4-(Rhodanese-like domain-containing protein 4, chloroplastic)	7	39878001	KRP3-(Putative uncharacterized protein)
2	27755001	chid1-(Putative Chitinase domain-containing protein 1)	7	39901001	unknown_gene-(Putative uncharacterized protein)
2	27729001	gene desconhecido-(Putative Tetratricopeptide repeat (TPR)-like superfamily protein)	7	39912001	CLF-(Histone-lysine N-methyltransferase CLF)
2	27714001	ASPG1-(Putative Protein ASPARTIC PROTEASE IN GUARD CELL 1)	7	39980001	NRAMP3-(Metal transporter Nramp3)
2	27675001	gene desconhecido-(unknown protein; LOCATED IN: chloroplast, chloroplast inner membrane, chloroplast envelope)	7	39984001	unknown_gene-(Hypothetical protein)
2	27643001	IQD14-(IQ-domain 18)	7	39988001	TTC13-(Putative Tetratricopeptide repeat protein 13)
2	27635001	gene desconhecido-(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	7	39999001	ARA12-(Subtilisin-like protease)
2	19775001	IGHMBP2-(Putative DNA-binding protein SMUBP-2)	7	40008001	CKA1-(Casein kinase II subunit alpha)
2	19784001	ALATS-(Alanine--tRNA ligase)	7	40010001	At5g67385-(BTB/POZ domain-containing protein At5g67385)
2	19800001	PTRH2-(Peptidyl-tRNA hydrolase II (PTH2) family protein)	7	40044001	PUB49-(Peptidyl-prolyl cis-trans isomerase-like 2)
2	19846001	TL1-(Putative Thaumatin-like protein 1a)	7	40046001	unknown_gene-(Arabinanase/levansucrase/invertase)
2	19856001	At1g18010-(UNC93-like protein 2)	7	40059001	GT7-(Putative glycosyltransferase 7)
2	20180001	MSH3-(DNA mismatch repair protein Msh3)	7	40086001	AYR1-(Putative NADPH-dependent 1-acyldihydroxyacetone phosphate reductase)
2	20263001	ARA12-(Subtilisin-like protease)	7	40090001	RH16-(DEAD-box ATP-dependent RNA helicase 16)
2	20264001	KCS5-(Putative 3-ketoacyl-CoA synthase 5)	7	40098001	ACS3-(1-aminocyclopropane-1-carboxylate synthase 3)
2	20289001	gene desconhecido-(TRICHOME BIREFRINGENCE-LIKE 18)	7	40108001	unknown_gene-(Hypothetical protein)
2	20315001	gene desconhecido-(Putative 21 kDa protein)	7	40173001	DRB4-(Putative uncharacterized protein)
2	20346001	NOS1-(Nitric oxide synthase 1)	7	40230001	PMI2-(Putative Protein PLASTID MOVEMENT IMPAIRED 2)
2	20358001	gene desconhecido-(Putative RNA polymerase III RPC4)	7	40242001	At1g18390-(Probable serine/threonine-protein kinase At1g18390)
2	20389001	zgc:110256-(Putative UPF0451 protein C17orf61 homolog)	7	40249001	At1g67000-(Hypothetical protein)
2	38998001	gene desconhecido-(Transducin/WD40 repeat-like superfamily protein)	7	40272001	unknown_gene-(abscisic acid (aba)-deficient 4)
2	39067001	AZG1-(Adenine/guanine permease AZG1)	7	40306001	BEH2-(BES1/BZR1 homolog protein 2)
2	39075001	LBD13-(Putative uncharacterized protein)	7	37240001	SDH1-1-(Succinate dehydrogenase [ubiquinone] flavoprotein subunit 1, mitochondrial)
2	39099001	gene desconhecido-(Putative uncharacterized protein)	7	37229001	RPL6-(60S ribosomal protein L6, mitochondrial)
2	39130001	mipp1-(histidine acid phosphatase family protein)	7	37199001	Rfc3-(Putative Replication factor C subunit 3)
2	39229001	HSPRO2-(Nematode resistance protein-like HSPRO2)	7	37189001	PCMP-E43-(Putative pentatricopeptide repeat-containing protein At3g47840)
2	39243001	mcfQ-(Putative Mitochondrial substrate carrier family protein Q)	7	37158001	Slc25a32-(Putative Mitochondrial folate transporter/carrier)
2	39256001	SF3-(Putative Pollen-specific protein SF3)	7	37107001	At4g36180-(Probable LRR receptor-like serine/threonine-protein kinase At4g36180)
2	29960001	NEDD1-(Transducin/WD40 repeat-like superfamily protein)	7	37089001	unknown_gene-(2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein)
2	29898001	gene desconhecido-(Protein of unknown function, DUF547)	7	37071001	unknown_gene-(armadillo repeat only 2)
2	29869001	HSP70-(Heat shock cognate 70 kDa protein)	7	37046001	unknown_gene-(Protein of unknown function (DUF630) ;Protein of unknown function (DUF632))

2	29836001	gene desconhecido-(CONTAINS InterPro DOMAIN/s: Putative zinc-finger domain)	7	37031001	FD-(Putative Protein FD)
2	29832001	PCMP-E33-(Putative Pentatricopeptide repeat-containing protein At2g39620)	7	37030001	LARP1-(Putative winged-helix DNA-binding transcription factor family protein)
2	29796001	xt-(Putative Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein)	7	37004001	HT1-(ACT-like protein tyrosine kinase family protein)
2	29792001	At1g31860-(Histidine biosynthesis bifunctional protein hisIE, chloroplastic)	7	36970001	Ubqln1-(Putative Ubiquilin-1)
2	29664001	CS3-(Probable caffeine synthase 3)	7	36959001	Rep-(Putative Rab proteins geranylgeranyltransferase component A)
2	29601001	gene desconhecido-(Putative Major facilitator superfamily protein)	7	36954001	unknown_gene-(unknown protein; endomembrane system)
2	29557001	At5g39000-(Putative receptor-like protein kinase At5g39000)	7	36655001	MSL2-(Mechanosensitive ion channel protein 2, chloroplastic)
2	29543001	Mtm1-(Putative Myotubularin)	7	36652001	CRK42-(Cysteine-rich receptor-like protein kinase 42)
2	29529001	utp7-(Putative Probable U3 small nucleolar RNA-associated protein 7)	7	36451001	At5g10080-(Aspartic proteinase-like protein 1)
2	29526001	DSP4-(Phosphoglucan phosphatase DSP4, chloroplastic)	7	37556001	At1g74260-(Probable phosphoribosylformylglycinamidine synthase, chloroplastic/mitochondrial)
2	29483001	SCPL49-(Serine carboxypeptidase-like 49)	7	37525001	ERF114-(DNA binding protein, putative)
2	29454001	WBC30-(Putative white-brown complex homolog protein 30)	7	37524001	RNR1-(Ribonucleoside-diphosphate reductase large subunit)
2	29453001	ABCG28-(ABC transporter G family member 28)	7	37437001	carA-(Carbamoyl-phosphate synthase small chain)
2	29421001	DRB2-(Double-stranded RNA-binding protein 2)	7	18874001	CPI1-(Cycloeucalenol cycloisomerase)
2	29373001	PSBQ2-(Oxygen-evolving enhancer protein 3-2, chloroplastic)	7	18869001	TOC159-(Translocase of chloroplast 159, chloroplastic)
2	29310001	At4g19050-(Putative disease resistance protein At4g19050)	7	18849001	TSK-(Putative Protein TONSOKU)
2	29275001	APC4-(Anaphase-promoting complex subunit 4)	7	18839001	R1A-6-(Putative late blight resistance protein homolog R1B-17)
2	29251001	SCAMP1-(Putative secretory carrier-associated membrane protein 1)	7	18729001	unknown_gene-(Putative Auxin-induced protein 5NG4)
2	29123001	DEG15-(Glyoxysomal processing protease, glyoxysomal)	7	18689001	unknown_gene-(unknown protein)
2	29118001	FES1-(Putative Zinc finger CCCH domain-containing protein 27)	7	18635001	At1g10890-(Putative Uncharacterized protein At1g10890)
2	29088001	gene desconhecido-(Putative homeobox-1)	7	18569001	unknown_gene-(unknown protein)
2	29061001	ARF2-(Auxin response factor 2)	7	18545001	ARP7-(Actin-related protein 7)
2	13902001	HNRNPA1-(Putative uncharacterized protein)	7	33916001	At1g23740-(Quinone oxidoreductase-like protein At1g23740, chloroplastic)
2	13989001	gene desconhecido-(Putative uncharacterized protein)	7	16992001	C9orf41-(S-adenosyl-L-methionine-dependent methyltransferases superfamily protein)
2	13997001	Wdr53-(Putative WD repeat-containing protein 53)	7	27240001	ORTH2-(E3 ubiquitin-protein ligase ORTHRUS 2)
2	14046001	NIP1-1-(Aquaporin NIP1-1)	7	27235001	FLCY-(Farnesylcysteine lyase)
2	14076001	At1g62200-(Hypothetical protein)	7	27221001	snrpd3-(Small nuclear ribonucleoprotein Sm D3)
2	14092001	At1g29670-(Putative GDSL esterase/lipase At1g29670)	7	16965001	unknown_gene-(Hypothetical protein)
2	14110001	PAD1-(Proteasome subunit alpha type-7-B)	7	19119001	phbA-(Prohibitin-1, mitochondrial)
2	14281001	Cap2-(Putative Adenylyl cyclase-associated protein 2)	7	19151001	CLC-B-(Chloride channel protein CLC-b)
2	14304001	gene desconhecido-(Putative hydroxyproline-rich glycoprotein family protein)	7	19172001	PER55-(Peroxidase 55)
2	14308001	yeiI-(pfkB-like carbohydrate kinase family protein)	7	19202001	POPTRDRAFT_752786-(Putative CASP-like protein POPTRDRAFT_752786)
2	14334001	gene desconhecido-(Putative Protein of unknown function, DUF547)	7	19222001	SUVH4-(Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH4)
2	14355001	Smg1-(Putative uncharacterized protein)	7	39342001	Gpaa1-(Putative Glycosylphosphatidylinositol anchor attachment 1 protein)
2	14395001	CYP40-(Peptidyl-prolyl cis-trans isomerase CYP40)	7	39361001	RFS-(Galactinol--sucrose galactosyltransferase)
2	14413001	CXE7-(Probable carboxylesterase 7)	7	39375001	unknown_gene-(unknown protein)
2	14444001	park7-(Putative Protein DJ-1)	7	39442001	unknown_gene-(Putative Auxin-induced protein 5NG4)
2	14452001	At5g67130-(PI-PLC X domain-containing protein At5g67130)	7	39454001	GASA14-(Putative Gibberellin regulated protein)
2	14478001	gene desconhecido-(Hypothetical protein)	7	39650001	ZAT4-(Putative uncharacterized protein)
2	14482001	gene desconhecido-(stress enhanced protein 1)	7	39690001	At1g33990-(Putative Probable esterase At1g33990)
2	14483001	gene desconhecido-(sodium:hydrogen antiporter 1)	7	39705001	At3g02290-(E3 ubiquitin-protein ligase At3g02290)
2	14529001	MIMI_L728-(Putative Uncharacterised conserved protein UCP015417, vWA)	7	39780001	Rnf185-(RING/U-box superfamily protein)
2	14552001	CBG06644-(RING/U-box superfamily protein)	7	39787001	At5g15080-(Putative protein kinase family protein / peptidoglycan-binding LysM domain-containing protein)
2	14559001	rlmN-(Putative Ribosomal RNA large subunit methyltransferase N)	7	39831001	DOF3.4-(Putative Dof zinc finger protein DOF3.4)
2	14650001	gene desconhecido-(Putative unknown protein)	7	39851001	SRK2I-(Serine/threonine-protein kinase SRK2I)
2	14692001	gene desconhecido-(Putative DUF593-containing protein)	7	39917001	CBSX1-(Putative Uncharacterized protein MJ1426)

2	14816001	fabZ-((3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase)	7	40138001	IAA9-(Auxin-responsive protein IAA9)
2	14983001	EMB8-(Putative Embryogenesis-associated protein EMB8)	7	40155001	prlC-(Putative Oligopeptidase A)
2	14993001	Os06g0170500-(Zinc finger CCCH domain-containing protein 40)	7	40213001	ATPB-(ATP synthase subunit beta, mitochondrial)
2	15001001	gene desconhecido-(Putative Predicted protein)	7	40221001	DTXL3-(Putative MATE efflux family protein 7)
2	15007001	gene desconhecido-(unknown protein)	7	40247001	fam108b1-(Putative Abhydrolase domain-containing protein FAM108B1)
2	15012001	gene desconhecido-(Putative uncharacterized protein)	7	40253001	At5g16180-(Chloroplastic group IIA intron splicing facilitator CRS1, chloroplastic)
2	15048001	gene desconhecido-(CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF482, Acyl-CoA N-acyltransferase)	7	40282001	Heatr5b-(HEAT repeat-containing protein)
2	15064001	CAND1-(Cullin-associated NEDD8-dissociated protein 1)	7	40309001	AMPP-(Putative Probable Xaa-Pro aminopeptidase P)
2	15089001	gene desconhecido-(Putative S-adenosyl-L-methionine-dependent methyltransferases superfamily protein)	7	37247001	DDM1-(ATP-dependent DNA helicase DDM1)
2	15094001	TBL2-(Putative Uncharacterized WD repeat-containing protein all2124)	7	37209001	TULP5-(Tubby-like F-box protein 5)
2	28870001	SPL7-(Putative uncharacterized protein)	7	37196001	At4g12780-(Putative uncharacterized protein)
2	28830001	AATF-(rRNA processing protein-related)	7	37188001	unknown_gene-(Phosphatidic acid phosphatase (PAP2) family protein)
2	28808001	gene desconhecido-(unknown protein; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0565)	7	37114001	EDA2-(Probable serine protease EDA2)
2	28752001	At1g28695-(Uncharacterized protein At1g28695)	7	37102001	unknown_gene-(Histone H1)
2	28749001	gene desconhecido-(Putative uncharacterized protein)	7	37083001	TRRAP-(Putative Transformation/transcription domain-associated protein)
2	28712001	gene desconhecido-(Putative unknown protein; LOCATED IN: plasma membrane)	7	37078001	CPK28-(Calcium-dependent protein kinase 28)
2	28691001	PRS5-(Ribose-phosphate pyrophosphokinase 5, chloroplastic)	7	37012001	Dnajc2-(Putative DnaJ homolog subfamily C member 2)
2	28680001	COX10-(Protoheme IX farnesyltransferase, mitochondrial)	7	36862001	KDM3B-(Putative Uncharacterized protein)
2	24945001	rpoD-(Putative RNA polymerase sigma factor rpoD)	7	36512001	Slc25a24-(Putative Calcium-binding mitochondrial carrier protein SCaMC-1)
2	24957001	PCMP-H35-(Putative pentatricopeptide repeat-containing protein At5g09950)	7	37627001	CYP84A1-(Cytoome P450 84A1)
2	24986001	NPP5-(Serine/threonine-protein phosphatase PP2A-5 catalytic subunit)	7	37621001	LEP-(Putative Ethylene-responsive transcription factor LEP)
2	25061001	gene desconhecido-(Hypothetical protein)	7	37616001	sll1770-(Putative Uncharacterized protein sll1770)
2	25078001	gene desconhecido-(Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein)	7	37575001	Polr2d-(Putative DNA-directed RNA polymerase II subunit RPB4)
2	25087001	GR1-(Putative Protein gamma response 1)	7	37499001	RGA4-(Putative disease resistance protein RGA4)
2	25094001	At5g08430-(Uncharacterized protein At5g08430)	7	37428001	ULK3-(Putative Serine/threonine-protein kinase ULK3)
2	25211001	Smt1-1-(Cycloartenol-C-24-methyltransferase 1)	7	18829001	unknown_gene-(Putative Ankyrin repeat family protein)
2	9437001	rpoD-(Putative RNA polymerase sigma factor rpoD)	7	18764001	unknown_gene-(Putative ankyrin repeat containing protein, identical)
2	18169001	DDB_G0274487-(Plasma-membrane choline transporter family protein)	7	16991001	At4g24290-(MACPF domain-containing protein At4g24290)
2	4484001	gene desconhecido-(unknown protein; LOCATED IN: chloroplast)	7	16998001	PECS-2.1-(Putative Pectinesterase 2)
2	4499001	TAF9-(TATA binding protein associated factor 21kDa subunit)	7	27264001	EXOSC8-(Putative Exosome complex component RRP43)
2	18358001	TOPBP1-(transcription coactivators)	7	19247001	Tnpo3-(ARM repeat superfamily protein)
2	18393001	gene desconhecido-(Hypothetical protein)	7	39354001	At3g01570-(Oleosin 5)
2	10174001	SKIP5-(F-box protein SKIP5)	7	39369001	CRK42-(Cysteine-rich receptor-like protein kinase 42)
2	38925001	gene desconhecido-(unknown protein)	7	39377001	RH46-(ATP-dependent RNA helicase-like protein DB10)
2	38944001	RPPL1-(Putative disease resistance RPP13-like protein 1)	7	39408001	At2g36330-(CASP-like protein At2g36330)
2	6395001	ytcJ-(Putative amidohydrolase ytcJ)	7	39462001	unknown_gene-(Putative uncharacterized protein)
2	23754001	At5g43530-(Hypothetical protein)	7	39486001	ABCB15-(ABC transporter B family member 15)
2	23805001	gene desconhecido-(Hypothetical protein)	7	39629001	trmH-(Putative tRNA (guanosine(18)-2'-O)-methyltransferase)
2	27581001	CTR1-(Protein kinase superfamily protein)	7	39695001	FER-(Putative Receptor-like protein kinase FERONIA)
2	12953001	HST1-(Protein HASTY 1)	7	39825001	FLACCA-(Pyridoxal phosphate (PLP)-dependent transferases superfamily protein)
2	16697001	gene desconhecido-(Putative unknown protein; LOCATED IN: endomembrane system)	7	39896001	unknown_gene-(Putative alpha/beta-Hydrolases superfamily protein)
2	15326001	gene desconhecido-(Putative uncharacterized protein)	7	40031001	FH6-(Formin-like protein 6)
2	15366001	AMPP-(Putative Probable Xaa-Pro aminopeptidase P)	7	40045001	SHR-(Protein SHORT-ROOT)
2	15390001	CAB1R-(Chlorophyll a-b binding protein 1, chloroplastic)	7	40067001	unknown_gene-(Hypothetical protein)

2	15402001	gene desconhecido-(HSP20-like chaperones superfamily protein)	7	40245001	msrA-(Putative Peptide methionine sulfoxide reductase MsrA)
2	645001	BHLH25-(Putative Transcription factor bHLH18)	7	40298001	AOC4-(Allene oxide cyclase 4, chloroplastic)
2	647001	gene desconhecido-(unknown protein)	7	37219001	At4g24660-(Putative ZF-HD homeobox protein At4g24660)
2	682001	gene desconhecido-(Protein of unknown function (DUF1399))	7	36657001	At4g38062-(Putative Uncharacterized protein At4g38062)
2	11790001	Zmat2-(Zinc finger matrin-type protein 2)	7	36504001	At5g65000-(CMP-sialic acid transporter 5)
2	11798001	lpdA-(Dihydrolipoyl dehydrogenase)	7	36503001	Os06g0265000-(Asparagine synthetase [glutamine-hydrolyzing])
2	11802001	AVP1-(Pyrophosphate-energized vacuolar membrane proton pump)	7	37591001	unknown_gene-(unknown protein; chloroplast)
2	11822001	gene desconhecido-(Putative HIT zinc finger ;PAPA-1-like conserved region)	7	37430001	NAGK-(Acetylglutamate kinase, chloroplastic)
2	42782001	gene desconhecido-(unknown protein)	7	37424001	RLK1-(Putative G-type lectin S-receptor-like serine/threonine-protein kinase RLK1)
2	42773001	PIF3-(Putative Transcription factor PIF3)	7	18872001	RLK1-(Putative G-type lectin S-receptor-like serine/threonine-protein kinase RLK1)
2	42772001	gene desconhecido-(Hypothetical protein)	7	18796001	Chaf1b-(Putative omatin assembly factor 1 subunit B)
2	42761001	Notum-(Pectinacetylesterase family protein)	7	18775001	unknown_gene-(Membrane fusion protein Use1)
2	3935001	At2g45590-(Receptor-like serine/threonine-protein kinase At2g45590)	7	27243001	At5g66980-(Putative B3 domain-containing protein At5g66980)
2	3927001	CYP76C2-(Cytoome P450 76C2)	7	19214001	unknown_gene-(unknown protein)
2	3916001	gene desconhecido-(Putative uncharacterized protein)	7	39507001	PPIP5K1-(Putative Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 1)
2	3895001	gene desconhecido-(Putative AT-hook motif nuclear-localized protein 1)	7	39555001	THADA-(unknown protein; InterPro DOMAIN/s: Protein of unknown function DUF2428, death-receptor-like (InterPro:IPR019442))
2	28045001	XSP1-(Xylem serine proteinase 1)	7	39618001	WRKY4-(Putative Probable WRKY transcription factor 4)
2	28032001	ptges2-(Putative Prostaglandin E synthase 2)	7	39759001	unknown_gene-(unknown protein; membrane; InterPro DOMAIN/s: Uncharacterised protein family UPF0121 (InterPro:IPR005344)
2	27948001	MYB39-(myb domain protein 17)	7	39764001	HAC1-(Putative Histone H3-K56 acetyltransferase, RTT109)
2	27931001	gene desconhecido-(Putative unknown protein)	7	40134001	DUS2L-(tRNA-dihydrouridine(20) synthase [NAD(P)+]-like)
2	27892001	BRM-(ATP-dependent helicase BRM)	7	40191001	fmt-(Putative Methionyl-tRNA formyltransferase)
2	27844001	MRPL46-(decoy)	7	40259001	At5g16150-(Plastidic glucose transporter 4)
2	27818001	ABIL1-(Protein ABIL1)	7	36912001	MORC3-(Zinc finger protein, putative)
2	27724001	DRP1A-(Dynamin-related protein 5A)	7	36770001	EMB1467-(NADH dehydrogenase [ubiquinone] iron-sulfur protein 1, mitochondrial)
2	27656001	At4g00840-(Probable S-acyltransferase At4g00840)	7	36700001	CAD-(Probable mannitol dehydrogenase)
2	27631001	LHY-(Putative Protein LHY)	7	37489001	CYP75B1-(Putative Flavonoid 3'-monooxygenase)
2	19805001	Smg9-(Putative Protein SMG9)	7	18566001	NDC1-(NADH dehydrogenase C1, chloroplastic/mitochondrial)
2	19819001	cdc20-(Anaphase-promoting complex subunit cdc20)	7	33933001	unknown_gene-(unknown protein; endomembrane system; InterPRO DOMAIN/s: Protein of unknown function DUF1365 (InterPro:IPR010775))
2	19898001	Gpr107-(Putative Protein GPR108)	7	16983001	VITISV_013255-(Hypothetical protein)
2	20022001	rpoD-(sigma factor E)	7	16984001	VITISV_013255-(Translation factor GUF1 homolog, chloroplastic)
2	20226001	ERF025-(Putative Ethylene-responsive transcription factor ERF027)	7	39322001	unknown_gene-(Putative Predicted protein)
2	20318001	PME33-(Probable pectinesterase/pectinesterase inhibitor 33)	7	39652001	EMB2076-(Pentatricopeptide repeat-containing protein At3g29290)
2	39040001	At3g28040-(Putative Probably inactive leucine-rich repeat receptor-like protein kinase At3g28040)	7	39832001	unknown_gene-(hydroxyproline-rich glycoprotein family protein)
2	39116001	SNX2A-(Sorting nexin 2A)	7	39915001	OTUD3-(SEC-C motif-containing protein / OTU-like cysteine protease family protein)
2	39143001	gene desconhecido-(UDP-glucose pyrophosphorylase 3)	7	40006001	ACBP3-(Hypothetical protein)
2	39164001	gene desconhecido-(Putative 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein)	7	40137001	unknown_gene-(Putative Zinc finger (C3HC4-type RING finger) family protein)
2	39198001	CYP89A9-(Putative Cytoome P450 89A9)	7	36449001	unknown_gene-(binding)
2	39205001	CYP90A1-(Cytoome P450 90A1)	7	18822001	unknown_gene-(Putative Ankyrin repeat family protein)
2	29972001	gene desconhecido-(Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein)	7	18679001	At2g23200-(Putative Probable receptor-like protein kinase At2g23200)
2	29921001	RING1-(Putative E3 ubiquitin-protein ligase RING1)	7	39401001	unknown_gene-(unknown protein; INVOLVED IN: N-terminal protein myristoylation)
2	29871001	PIMP1-(CASP-like protein PIMP1)	7	40100001	BCAT5-(Branched-chain-amino-acid aminotransferase 5, chloroplastic)
2	29834001	ELP1-(Elongator complex protein 1)	7	40142001	BXL6-(Probable beta-D-xylosidase 6)
2	29805001	gene desconhecido-(Putative Protein of unknown function DUF966)	7	40214001	LIG1-(DNA LIGASE 6)
2	29791001	MKP1-(Putative Protein-tyrosine-phosphatase MKP1)	7	36995001	At3g51390-(Probable S-acyltransferase At3g51390)

2	29781001	gene desconhecido-(Putative Disease resistance-responsive (dirigent-like protein) family protein)	7	8836001	CAD9-(Probable cinnamyl alcohol dehydrogenase 9)
2	29760001	gene desconhecido-(Putative unknown protein)	7	15727001	R1B-12-(Putative late blight resistance protein homolog R1B-12)
2	29748001	ptar1-(Putative Protein prenylyltransferase superfamily protein)	7	40258001	unknown_gene-(unknown protein)
2	29676001	nt5c3-(Putative Cytosolic 5'-nucleotidase 3)	7	40283001	CCT6A-(T-complex protein 1 subunit zeta)
2	29607001	RCOM_1506700-(Probable aspartyl aminopeptidase)	7	37202001	At1g75280-(Isoflavone reductase homolog)
2	29592001	gene desconhecido-(alkaline/neutral invertase)	7	36846001	pfpI-(Putative Intracellular protease 1)
2	29544001	gene desconhecido-(Putative uncharacterized protein)	7	37630001	CYP84A1-(Putative Cytoome P450 84A1)
2	29487001	At2g21430-(Cysteine proteinase 15A)	7	37482001	R1B-16-(Putative late blight resistance protein homolog R1B-16)
2	29469001	PUB14-(U-box domain-containing protein 14)	7	19186001	GAI1-(GRAS family transcription factor)
2	29434001	RPN1-(Putative Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1)	7	39602001	CGS1-(Putative Cystathionine beta-lyase)
2	29432001	gene desconhecido-(Pleckstrin homology (PH) and lipid-binding START domains-containing protein)	7	36662001	SKIP34-(Putative uncharacterized protein)
2	29419001	At2g18220-(Putative Noc2p family)	7	18828001	unknown_gene-(Putative Ankyrin repeat family protein)
2	29411001	gene desconhecido-(unknown protein)	7	18562001	TCP7-(Transcription factor TCP7)
2	29334001	At1g61370-(Putative G-type lectin S-receptor-like serine/threonine-protein kinase At1g61370)	7	19067001	At5g14450-(GDSL esterase/lipase At5g14450)
2	29264001	Os03g0255100-(Beta-galactosidase 6)	7	39475001	MTP12-(Metal tolerance protein 12)
2	29222001	PLT4-(Probable polyol transporter 4)	7	39925001	unknown_gene-(Protein of unknown function (DUF579))
2	29185001	gene desconhecido-(Putative Predicted protein)	7	40189001	unknown_gene-(unknown protein; INVOLVED IN: response to salt stress.)
2	29091001	glpV-(Glycogen phosphorylase 1)	7	37142001	unknown_gene-(Putative Lateral root primordium (LRP) protein-related)
2	13886001	HPA-(Histidinol-phosphate aminotransferase, chloroplastic)	7	40318001	MGP-(C2H2-like zinc finger protein)
2	13959001	At2g24230-(Putative Probable LRR receptor-like serine/threonine-protein kinase At2g24230)	7	15725001	C2orf29-(unknown protein; InterPro DOMAIN/s: Protein of unknown function DUF2363 (InterPro:IPR019312))
2	14117001	gene desconhecido-(Major facilitator superfamily protein)	7	37509001	NAGK-(Hypothetical protein)
2	14119001	xynF1-(Putative Probable endo-1,4-beta-xylanase C)	7	37450001	YOR059C-(Hydrolase-like protein family)
2	14202001	At2g16485/At2g16480/At2g16470-(Putative Zinc finger CCCH domain-containing protein 19)	8	5557001	pds5b-b-(BEST match: Tudor/PWWP/MBT superfamily protein (TAIR:AT1G15940.1); cytosol, chloroplast)
2	14243001	gene desconhecido-(Putative unknown protein)	8	5559001	CLPB4-(Chaperone protein ClpB4, mitochondrial)
2	14251001	At1g75280-(Isoflavone reductase homolog P3)	8	5563001	At2g39795-(Mitochondrial glycoprotein family protein)
2	14285001	At4g34450-(Coatomer subunit gamma)	8	5564001	At4g17486-(Putative Desumoylating isopeptidase 2)
2	14300001	NUS1-(Putative Undecaprenyl pyrophosphate synthetase family protein)	8	5569001	unknown_gene-(Hypothetical protein)
2	14318001	At4g34320-(UPF0496 protein At4g34320)	8	5570001	unknown_gene-(unknown protein)
2	14408001	RBP47-(Polyadenylate-binding protein RBP47)	8	5577001	KNAT3-(Homeobox protein knotted-1-like 3)
2	14469001	CBSX2-(CBS domain-containing protein CBSX1, chloroplastic)	8	5578001	unknown_gene-(Hypothetical protein)
2	14475001	pteN-(PTEN 2)	8	5587001	unknown_gene-(unknown protein; plasma membrane)
2	14558001	gene desconhecido-(Putative Uncharacterized protein)	8	5588001	unknown_gene-(serine-rich protein-related)
2	14606001	Prpf40a-(Putative pre-mRNA-processing protein 40A)	8	5591001	micu1-(Putative Calcium uptake protein 1, mitochondrial)
2	14656001	ARA2-(Putative D-arabinose 1-dehydrogenase)	8	38534001	TPR1-(Topless-related protein 1)
2	15010001	At5g05010-(Coatomer subunit delta)	8	38529001	At5g34940-(Heparanase-like protein 3)
2	15118001	gene desconhecido-(Transketolase, chloroplastic)	8	38528001	cysS-(Cysteine--tRNA ligase)
2	28837001	ERF034-(Putative uncharacterized protein)	8	38509001	APT2-(Adenine phosphoribosyltransferase 2)
2	28690001	gene desconhecido-(DnaJ/Hsp40 cysteine-rich domain superfamily protein)	8	38507001	unknown_gene-(Putative Myosin heavy chain-related protein)
2	28671001	NRT1.5-(Nitrate transporter 1.5)	8	38506001	KEG-(Protein kinase superfamily protein)
2	28631001	At5g35930-(Putative acyl-activating enzyme 19)	8	38503001	unknown_gene-(Putative Ubiquitin-like superfamily protein)
2	28621001	CHIB1-(Acidic endochitinase)	8	38495001	At2g25430-(Putative clathrin assembly protein At2g25430)
2	24958001	myoJ-(myosin-like protein XIF)	8	38486001	unknown_gene-(Putative uncharacterized protein)
2	24972001	LTP8-(Non-specific lipid-transfer protein 8)	8	38484001	EBF1-(EIN3-binding F-box protein 1)
2	25022001	HAT14-(Hypothetical protein)	8	38478001	PLD1-(Phospholipase D alpha 1)
2	25095001	At5g08430-(Putative Uncharacterized protein At5g08430)	8	38468001	RDR6-(RNA-dependent RNA polymerase 6)
2	25220001	STR1-(Putative Strictosidine synthase)	8	38452001	BT1-(Protein brittle-1, chloroplastic/amyloplastic)
2	9443001	PDX1-(Probable pyridoxal biosynthesis protein PDX1)	8	38451001	At2g34160-(Uncharacterized protein At2g34160)

2	11529001	NLE1-(Notchless protein homolog)	8	38447001	unknown_gene-(Putative overexpressor of cationic peroxidase 3)
2	18351001	SPAC869.01-(Putative amidase C869.01)	8	38445001	unknown_gene-(unknown protein)
2	38914001	RPPL1-(Putative disease resistance protein At3g14460)	8	38431001	ERECTA-(LRR receptor-like serine/threonine-protein kinase ERECTA)
2	18320001	POP1-(Putative ribonuclease Ps)	8	38429001	unknown_gene-(YGGT family protein)
2	27621001	At1g54610-(Probable serine/threonine-protein kinase At1g54610)	8	38427001	rhp7-(InterPro DOMAIN/s: Leucine-rich repeat, cysteine-containing subtype (InterPro:IPR006553); BEST match: RNI-like superfamily protein (TAIR:AT5G21900.1)
2	27594001	At1g54570-(Esterase/lipase/thioesterase family protein)	8	38424001	FBL15-(F-box/LRR-repeat protein 15)
2	27471001	At3g04780-(PITH domain-containing protein At3g04780)	8	38423001	FBL15-(F-box/LRR-repeat protein 15)
2	8643001	gene desconhecido-(Hypothetical protein)	8	38420001	gyaR-(Putative Glyoxylate reductase)
2	11789001	PDIL2-2-(Probable protein disulfide-isomerase A6)	8	38414001	GT-2-(Hypothetical protein)
2	11828001	BHLH52-(Putative Transcription factor bHLH52)	8	38409001	unknown_gene-(Putative uncharacterized protein)
2	42849001	gene desconhecido-(Putative Auxin-induced protein 5NG4)	8	38408001	PEX10-(Peroxisome biogenesis factor 10)
2	3903001	ARFGEF2-(Putative Brefeldin A-inhibited guanine nucleotide-exchange protein 2)	8	38405001	unknown_gene-(photosystem II subunit X)
2	28044001	ARA12-(Putative Subtilisin-like protease)	8	38400001	unknown_gene-(Putative uncharacterized protein ORF40)
2	27958001	Cct8-(Putative T-complex protein 1 subunit theta)	8	38393001	SLC25A44-(Putative Solute carrier family 25 member 44)
2	27956001	KEA2-(K(+) efflux antiporter 2, chloroplastic)	8	38388001	At3g12360-(Putative Ankyrin repeat-containing protein At3g12360)
2	27929001	Acot8-(Putative Acyl-coenzyme A thioesterase 8)	8	38382001	PCMP-E91-(Pentatricopeptide repeat-containing protein At3g16610)
2	27926001	BAM7-(Beta-amylase 7)	8	38379001	okr-(Putative omatin remodeling 31)
2	27805001	At5g41620-(Putative Uncharacterized protein At5g41620)	8	38376001	NPSN11-(Novel plant SNARE 11)
2	19802001	F8H-(Putative Probable glucuronosyltransferase GUT1)	8	38348001	RPM1-(Putative Disease resistance protein RPM1)
2	19807001	At1g33260-(Probable receptor-like protein kinase At1g33260)	8	38342001	Tbl3-(Putative Transducin beta-like protein 3)
2	19824001	gene desconhecido-(rubredoxin family protein)	8	38341001	SCRM-(Transcription factor ICE1)
2	19838001	gene desconhecido-(Hypothetical protein)	8	38337001	PUP9-(Putative Predicted protein)
2	20357001	gene desconhecido-(Putative Uncharacterised conserved protein (UCP012943))	8	38331001	DRP1E-(Dynamin-related protein 1E)
2	20368001	qor-(Putative Quinone oxidoreductase)	8	37665001	RPM1-(Putative Disease resistance protein RPM1)
2	29969001	XSP1-(Cucumisin)	8	37669001	At4g18030-(Probable methyltransferase PMT14)
2	29967001	mcfB-(Putative Mitochondrial substrate carrier family protein B)	8	37673001	IP5P2-(Type I inositol 1,4,5-trisphosphate 5-phosphatase 2)
2	29823001	ogdh-(2-oxoglutarate dehydrogenase, mitochondrial)	8	37676001	NCS1-(Putative S-norcoclaurine synthase 1)
2	29795001	gene desconhecido-(Putative Protein of unknown function (DUF674))	8	37681001	At1g50180-(Putative disease resistance protein At1g50180)
2	29771001	ABCG1-(ABC transporter G family member 1)	8	37715001	At5g46580-(Pentatricopeptide repeat-containing protein At5g46580, chloroplastic)
2	29766001	leng8-(SAC3/GANP/Nin1/mts3/eIF-3 p25 family)	8	37725001	LOL1-(Protein LOL1)
2	29753001	ANKRD13B-(Ankyrin repeat family protein)	8	37731001	unknown_gene-(Putative uncharacterized protein)
2	29464001	AVT1-(Transmembrane amino acid transporter family protein)	8	37743001	CXE1-(Putative Carboxylesterase 1)
2	29340001	SD18-(Putative Receptor-like serine/threonine-protein kinase SD1-8)	8	37744001	CXE1-(Putative Carboxylesterase 1)
2	13820001	PDAP1-(CONTAINS InterPro DOMAIN/s: Casein kinase substrate, phosphoprotein PP28)	8	37754001	CXE1-(Carboxylesterase 1)
2	13836001	gene desconhecido-(Putative negative regulator of systemic acquired resistance (SNI1))	8	37771001	RAP1-(Transcription factor MYC2)
2	13918001	At3g03300-(Putative Endoribonuclease Dicer homolog 2)	8	37773001	AGD8-(Putative uncharacterized protein)
2	13920001	gene desconhecido-(Putative B-block binding subunit of TFIIIC)	8	37792001	RBP31-(RNA-binding (RRM/RBD/RNP motifs) family protein)
2	14467001	PAB2-(Polyadenylate-binding protein 2)	8	37801001	At1g32360-(Zinc finger CCCH domain-containing protein 12)
2	14550001	CLPR1-(ATP-dependent Clp protease proteolytic subunit-related protein 1, chloroplastic)	8	37808001	unknown_gene-(Putative Tetratricopeptide repeat (TPR)-like superfamily protein)
2	14570001	gene desconhecido-(Putative myosin heavy chain-related)	8	37815001	MYB28-(Putative myb domain protein 9)
2	14708001	GT4-(Putative UDP-rhamnose:rhamnosyltransferase 1)	8	37832001	Rf1-(Putative Protein Rf1, mitochondrial)
2	14904001	PAP4-(Probable plastid-lipid-associated protein 4, chloroplastic)	8	37840001	unknown_gene-(INVOLVED IN: GPI anchor biosynthetic process; LOCATED IN: endoplasmic reticulum membrane; InterPro DOMAIN/s: PIG-X/PBN1 (InterPro:IPR013233))
2	14905001	Pnpla2-(Putative Patatin-like phospholipase domain-containing protein 4)	8	10789001	REF6-(Transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein)
2	15083001	der-(Putative GTPase Der)	8	10779001	ROC3-(Homeobox-leucine zipper protein ROC3)
2	15122001	osgepl1-(Putative Probable tRNA	8	10775001	CML17-(Probable calcium-binding protein CML17)

		threonylcarbamoyladenosine biosynthesis protein osgepl1)			
2	28864001	gene desconhecido-(Uncharacterised conserved protein UCP022280)	8	34133001	CSLD3-(Cellulose synthase-like protein D3)
2	28863001	cnot1-(Putative CCR4-NOT transcription complex subunit 1)	8	34135001	XTH30-(Probable xyloglucan endotransglucosylase/hydrolase protein 30)
2	28794001	gene desconhecido-(Protein of unknown function (DUF630 and DUF632))	8	34146001	RPM1-(Putative Disease resistance protein RPM1)
2	28748001	CYP734A1-(Putative Cytoome P450 734A1)	8	34184001	RPM1-(Putative NBS-LRR type disease resistance protein)
2	24953001	UGP-(Putative UTP--glucose-1-phosphate uridylyltransferase)	8	34244001	PCMP-E28-(Putative Pentatricopeptide repeat-containing protein At2g22410, mitochondrial)
2	4493001	rpsI-(30S ribosomal protein S9)	8	34255001	At1g75280-(Isoflavone reductase homolog)
2	38949001	Ino80c-(CONTAINS InterPro DOMAIN/s: YL1 nuclear, C-terminal)	8	15626001	PIP1-2-(Putative Probable aquaporin PIP1-2)
2	23856001	gene desconhecido-(Putative uncharacterized protein)	8	15632001	RAP2-12-(Putative Ethylene-responsive transcription factor RAP2-12)
2	18928001	ALA1-(Phospholipid-transporting ATPase 1)	8	15663001	RING1-(Putative uncharacterized protein)
2	15363001	At1g55000-(F-box protein At1g55000)	8	42450001	unknown_gene-(Plant protein of unknown function (DUF946))
2	15384001	At5g27470-(Serine--tRNA ligase)	8	42442001	Rpa1-(Putative Replication protein A 70 kDa DNA-binding subunit)
2	15399001	gene desconhecido-(Putative uncharacterized protein)	8	24281001	FH14-(Hypothetical protein)
2	13095001	LOX1.5-(Hypothetical protein)	8	24306001	Ganab-(heteroglycan glucosidase 1)
2	42878001	gene desconhecido-(Putative uncharacterized protein)	8	24347001	COG6-(Putative Conserved oligomeric Golgi complex subunit 6)
2	42755001	gene desconhecido-(Hypothetical protein)	8	24381001	ABCE2-(ABC transporter E family member 2)
2	28019001	ATL59-(Putative uncharacterized protein)	8	24404001	lsm14b-a-(Putative decapping 5-like)
2	27947001	At3g61260-(Uncharacterized protein At3g61260)	8	40971001	AHK5-(Histidine kinase 5)
2	27934001	ribD-(Putative Riboflavin biosynthesis protein RibD)	8	36046001	CNGC14-(Probable cyclic nucleotide-gated ion channel 14)
2	19796001	gene desconhecido-(Protein kinase superfamily protein)	8	36047001	CSLC5-(Probable xyloglucan glycosyltransferase 5)
2	20030001	SLC25A39-(Putative Solute carrier family 25 member 39)	8	5866001	ASPG2-(Putative Protein ASPARTIC PROTEASE IN GUARD CELL 2)
2	20215001	BB-(Putative uncharacterized protein)	8	5441001	HEMB-(Delta-aminolevulinic acid dehydratase, chloroplastic)
2	20277001	gene desconhecido-(Hypothetical protein)	8	25229001	N-(Putative TMV resistance protein N)
2	20313001	PECS-1.1-(21 kDa protein)	8	25230001	N-(Putative TMV resistance protein N)
2	20314001	gene desconhecido-(Hypothetical protein)	8	25284001	PVS1-(Putative Vetispiradiene synthase 1)
2	20379001	PUB35-(U-box domain-containing protein 35)	8	25298001	pat2-k3-(Hypothetical protein)
2	39132001	MCA1-(Putative Protein MID1-COMPLEMENTING ACTIVITY 1)	8	25313001	unknown_gene-(Putative uncharacterized protein)
2	29530001	PHF1-(SEC12-like protein 1)	8	25327001	At5g44450-(Alpha N-terminal protein methyltransferase 1)
2	29336001	SD18-(Receptor-like serine/threonine-protein kinase SD1-8)	8	25338001	PCMP-H88-(Putative Pentatricopeptide repeat-containing protein At5g06540)
2	13919001	At3g03300-(Endoribonuclease Dicer homolog 2)	8	25341001	PCMP-E22-(Putative Pentatricopeptide repeat-containing protein At2g02750)
2	13968001	At3g47570-(Putative Probable LRR receptor-like serine/threonine-protein kinase At3g47570)	8	25348001	U2SURP-(RNA recognition motif (RRM)-containing protein)
2	14607001	gene desconhecido-(ethylene-dependent gravitropism-deficient and yellow-green-like 3)	8	25372001	ACT-(Putative Vinorine synthase)
2	14620001	TOR-(Serine/threonine-protein kinase TOR)	8	25374001	CYP71D55-(Premnaspirodiene oxygenase)
2	14881001	RPL3-(60S ribosomal protein L3)	8	25388001	UBP22-(Ubiquitin carboxyl-terminal hydrolase 22)
2	14901001	ATG26-(UDP-Glycosyltransferase superfamily protein)	8	25406001	MGD1-(Monogalactosyldiacylglycerol synthase, chloroplastic)
2	28757001	At3g12360-(Putative Ankyrin repeat-containing protein At3g12360)	8	11880001	WRKY40-(Putative Probable WRKY transcription factor 40)
2	9434001	A-(Putative Dihydroflavonol-4-reductase)	8	11892001	RPL5-(60S ribosomal protein L5)
2	9440001	Smc5-(Putative Structural maintenance of omosomes protein 5)	8	11895001	CM1-(Chorismate mutase, chloroplastic)
2	42803001	PDR3-(Pleiotropic drug resistance protein 3)	8	13079001	unknown_gene-(Putative uncharacterized protein)
2	28050001	MADS6-(MADS-box transcription factor 6)	8	7242001	unknown_gene-(Putative Enhancer of polycomb-like transcription factor protein)
2	28040001	TCP19-(Putative Transcription factor TCP19)	8	7234001	DNAJB4-(Putative DnaJ homolog subfamily B member 4)
2	27924001	BAM2-(Beta-amylase 2, chloroplastic)	8	7233001	PHF3-(Putative SPOC domain / Transcription elongation factor S-II protein)
2	20287001	CPSF160-(Cleavage and polyadenylation specificity factor subunit 1)	8	7230001	CYCA2-1-(Cyclin-A2-1)
2	20386001	gene desconhecido-(ubiquinol-cytoome C chaperone family protein)	8	9039001	RD22-(Dehydration-responsive protein RD22)
2	39159001	At2g44540-(Endoglucanase 12)	8	9041001	POLQ-(helicases;ATP-dependent helicases;nucleic acid binding;ATP binding;DNA-directed DNA polymerases;DNA binding)
2	29936001	At2g44920-(Putative uncharacterized protein)	8	9060001	unknown_gene-(unknown protein)
2	29925001	gene desconhecido-(Putative hAT transposon superfamily)	8	9063001	unknown_gene-(BEST match: DDT domain superfamily (TAIR:AT1G18950.1)

2	29723001	PGSIP6-(Putative glucuronosyltransferase PGSIP6)	8	9068001	At3g47570-(Putative Probable LRR receptor-like serine/threonine-protein kinase At3g47570)
2	29699001	gene desconhecido-(SSXT family protein)	8	17212001	RD22-(Putative BURP domain-containing protein 5)
2	29671001	DNAJ1-(DnaJ protein homolog)	8	17234001	BETAA-AD-(Beta-adaptin-like protein A)
2	14883001	gene desconhecido-(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	8	17247001	ADHIII-(Putative Alcohol dehydrogenase class-3)
2	15062001	smndc1-(Putative Survival of motor neuron-related-splicing factor 30)	8	17253001	unknown_gene-(unknown protein)
2	28876001	MDH-(Malate dehydrogenase, cytoplasmic)	8	17254001	At5g57850-(Branched-chain-amino-acid aminotransferase-like protein 3, chloroplastic)
2	28859001	UNE10-(Putative Transcription factor UNE10)	8	17256001	PEX4-(Protein PEROXIN-4)
2	28820001	FKBP20-2-(Peptidyl-prolyl cis-trans isomerase FKBP20-2, chloroplastic)	8	17260001	unknown_gene-(alpha/beta-Hydrolases superfamily protein)
2	28792001	GRAMD1C-(Putative GRAM domain family protein)	8	17262001	unknown_gene-(Hypothetical protein)
2	24948001	RGA3-(Putative disease resistance protein RGA3)	8	17272001	At3g16180-(Probable peptide/nitrate transporter At3g16180)
2	27547001	guaD-(Guanine deaminase)	8	17294001	unknown_gene-(Putative Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region)
2	27499001	ZDS-(Zeta-carotene desaturase, chloroplastic/omoplastic)	8	26886001	RRP46-(Exosome complex CDSuclease RRP46 homolog)
2	16703001	CYCL1-1-(Cyclin-L1-1)	8	26898001	CCAMK-(Calcium and calcium/calmodulin-dependent serine/threonine-protein kinase)
2	3937001	CXE8-(Probable carboxylesterase 8)	8	26905001	PER5-(Lignin-forming anionic peroxidase)
2	3886001	ANT18-(Putative Dihydroflavonol-4-reductase)	8	26914001	unknown_gene-(Hypothetical protein)
2	3866001	gene desconhecido-(Putative Uncharacterized protein)	8	26915001	PTRH2-(Putative Peptidyl-tRNA hydrolase 2, mitochondrial)
2	19808001	At5g17010-(D-xylose-proton symporter-like 2)	8	26917001	GATA12-(GATA transcription factor 12)
2	20312001	PCMP-E53-(Pentatricopeptide repeat-containing protein At4g25270, chloroplastic)	8	26921001	At2g25790-(Probably inactive leucine-rich repeat receptor-like protein kinase At2g25790)
2	29532001	PDPK2-(3-phosphoinositide-dependent protein kinase 2)	8	26943001	AHP4-(Histidine-containing phosphotransfer protein 4)
2	29515001	HIS2B-(Histone H2B)	8	26944001	CDC2A-(Cell division control protein 2 homolog A)
2	29508001	NAC078-(Putative NAC domain-containing protein 78)	8	26964001	unknown_gene-(BEST match: glycine-rich protein (TAIR:AT4G32920.3)
2	29497001	gene desconhecido-(Hypothetical protein)	8	26976001	PCMP-E6-(Pentatricopeptide repeat-containing protein At4g22760)
2	14028001	PUB17-(U-box domain-containing protein 17)	8	26989001	PXL1-(Putative Leucine-rich repeat receptor-like protein kinase PXL1)
2	14082001	fdxB-(2Fe-2S ferredoxin)	8	26999001	unknown_gene-(InterPro DOMAIN/s: Phosphorylated adapter RNA export protein, RNA-binding domain (InterPro:IPR019385)
2	14305001	PI4KALPHA1-(Phosphatidylinositol 4-kinase alpha)	8	27000001	At5g36250-(Putative Probable protein phosphatase 2C 74)
2	14554001	VSR3-(Vacuolar-sorting receptor 3)	8	27021001	HDA2-(Histone deacetylase 2)
2	28847001	Nup62-(Putative Nucleoporin, Nsp1-like, C-terminal)	8	27025001	RTE1-(Protein REVERSION-TO-ETHYLENE SENSITIVITY1)
2	24966001	SPBC776.05-(Putative Uncharacterized membrane protein C776.05)	8	27035001	unknown_gene-(Hypothetical protein)
2	38973001	CHLP-(Geranylgeranyl diphosphate reductase, chloroplastic)	8	27036001	unknown_gene-(Putative Predicted protein)
2	11098001	MGP-(Putative uncharacterized protein)	8	27039001	At1g68400-(Putative Probable leucine-rich repeat receptor-like protein kinase At1g68400)
2	16725001	gene desconhecido-(Hypothetical protein)	8	27044001	SQD1-(UDP-sulfoquinovose synthase, chloroplastic)
2	27665001	At1g16860-(Putative Uncharacterized membrane protein At1g16860)	8	27051001	CWINV1-(Beta-fructofuranosidase, insoluble isoenzyme CWINV1)
2	20243001	gene desconhecido-(2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein)	8	27054001	CWINV1-(Beta-fructofuranosidase, insoluble isoenzyme CWINV1)
2	29562001	gene desconhecido-(Hypothetical protein)	8	27061001	TBXAS1-(Putative Thromboxane-A synthase)
2	9438001	NIR1-(Ferredoxin--nitrite reductase, chloroplastic)	8	27096001	unknown_gene-(unknown protein)
2	18199001	AGL15-(Agamous-like MADS-box protein AGL15)	8	27117001	unknown_gene-(Putative uncharacterized protein)
2	39077001	GSVIVT00023967001-(Peroxidase 4)	8	27119001	unknown_gene-(peptidyl-prolyl cis-trans isomerases)
2	29948001	WAKL20-(Wall-associated receptor kinase-like 20)	8	27130001	unknown_gene-(Putative uncharacterized protein)
2	14562001	gene desconhecido-(Predicted protein)	8	27143001	EXLB1-(Expansin-like B1)
2	14981001	dhx29-(RNA helicase family protein)	8	27147001	BI-1-(Bax inhibitor 1)
2	18332001	ROMT-15-(Putative Tricin synthase 1)	8	27162001	ABA2-(Putative Zeaxanthin epoxidase, chloroplastic)
2	27576001	mon2-(Putative Protein MON2 homolog)	8	27164001	RABD2A-(Ras-related protein RABD2a)
2	19990001	At4g10955-(Putative GDSL esterase/lipase At4g10955)	8	27172001	At1g14450-(NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3-B)
2	25008001	CALS2-(Callose synthase 2)	8	27177001	RNF168-(Putative zinc finger (C3HC4-type RING finger) family protein)
2	27966001	folD-(Bifunctional protein FolD)	8	30561001	UCHL3-(Ubiquitin carboxyl-terminal hydrolase isozyme L3)
2	19895001	gene desconhecido-(Putative uncharacterized protein)	8	30557001	OLE16-(Oleosin)

2	14391001	Larp7-(Putative RNA-binding protein)	8	30555001	ERF5-(Putative Ethylene-responsive transcription factor 5)
2	16741001	GLIP2-(GDSL esterase/lipase 2)	8	30543001	At5g47360-(Putative Pentatricopeptide repeat-containing protein At5g47360)
2	11801001	CRT1-(Calreticulin)	8	30518001	ERF034-(Ethylene-responsive transcription factor ERF039)
2	29742001	xpo4-(Putative Exportin-4)	8	30504001	unknown_gene-(Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region)
2	14464001	MARCH6-(Putative E3 ubiquitin-protein ligase MARCH6)	8	30495001	PCMP-E103-(Putative pentatricopeptide repeat-containing protein At5g47460)
2	29798001	ABCB6-(ABC transporter B family member 6)	8	30470001	sec14-(Putative Sec14 cytosolic factor)
2	14974001	TCP8-(Putative Transcription factor TCP8)	8	30456001	unknown_gene-(Hypothetical protein)
3	25571001	gene desconhecido-(unknown protein)	8	30446001	SCL6-(Hairy meristem)
3	25573001	Os05g0567100-(Aspartic proteinase oryzasin-1)	8	30445001	SDD1-(Putative Subtilisin-like protease SDD1)
3	25578001	gene desconhecido-(Putative uncharacterized protein)	8	30437001	At4g00165-(Hypothetical protein)
3	25587001	PERK9-(Putative uncharacterized protein)	8	30430001	At4g00165-(14 kDa proline-rich protein DC2.15)
3	25590001	gene desconhecido-(hAT dimerisation domain-containing protein)	8	30429001	At4g00165-(14 kDa proline-rich protein DC2.15)
3	25591001	fcf2-(Fcf2 pre-rRNA processing protein)	8	30427001	ORP2A-(Oxysterol-binding protein-related protein 2A)
3	25592001	Pdk-(Putative [Pyruvate dehydrogenase [lipoamide]] kinase, mitochondrial)	8	30423001	APT1-(Adenine phosphoribosyltransferase 1, chloroplastic)
3	25598001	PTI1-(Pto-interacting protein 1)	8	30422001	unknown_gene-(Putative uncharacterized protein)
3	25600001	EMB2750-(Pentatricopeptide repeat-containing protein At3g06430, chloroplastic)	8	30409001	INVA-(Acid beta-fructofuranosidase)
3	25604001	IvsG-(protein serine/threonine kinases;protein tyrosine kinases;ATP binding;protein kinases)	8	30393001	C8orf38-(Putative UPF0551 protein C8orf38 homolog, mitochondrial)
3	25605001	METTL13-(Putative Methyltransferase-like protein 13)	8	30391001	STI-(Heat shock protein STI)
3	25606001	gene desconhecido-(Hypothetical protein)	8	30383001	ODO1-(Protein ODORANT1)
3	25607001	KIF15-(Putative phragmoplast orienting kinesin 1)	8	30369001	SPG21-(Putative Maspardin)
3	25609001	gene desconhecido-(unknown protein)	8	30364001	unknown_gene-(Predicted protein)
3	25618001	gene desconhecido-(unknown protein)	8	30360001	PHR1-(Deoxyribodipyrimidine photo-lyase)
3	25622001	B3GALT16-(Putative Probable beta-1,3-galactosyltransferase 16)	8	30356001	At3g47570-(Putative Probable LRR receptor-like serine/threonine-protein kinase At3g47570)
3	25632001	SFR2-(Beta-glucosidase-like SFR2, chloroplastic)	8	30353001	At4g22758-(Putative Uncharacterized protein At4g22758)
3	25640001	gene desconhecido-(Predicted protein)	8	30352001	unknown_gene-(Predicted protein (Fragment))
3	25651001	FCA-(Putative uncharacterized protein)	8	30349001	CLPR2-(ATP-dependent Clp protease proteolytic subunit-related protein 2, chloroplastic)
3	25665001	UBC23-(Probable ubiquitin-conjugating enzyme E2 23)	8	30322001	NUDT14-(Nudix hydrolase 14, chloroplastic)
3	25673001	PHYB-(Phytoome B)	8	30317001	SDD1-(Putative Subtilisin-like protease SDD1)
3	25692001	UBC32-(Ubiquitin-conjugating enzyme E2 32)	8	30316001	unknown_gene-(Putative uncharacterized protein)
3	25703001	smek1-(binding)	8	30313001	BHLH120-(Putative Transcription factor bHLH118)
3	25714001	gene desconhecido-(Putative uncharacterized protein)	8	30311001	ANT17-(Leucoanthocyanidin dioxygenase)
3	25716001	AMSH3-(AMSH-like ubiquitin thioesterase 3)	8	30309001	EXPA18-(Expansin-A18)
3	25718001	MYB12-(Putative R2R3-MYB transcriptional factor)	8	30306001	unknown_gene-(non-yellowing 1)
3	25719001	gene desconhecido-(Putative unknown protein)	8	30292001	HTH-(Protein HOTHEAD)
3	25729001	ARR2-(Two-component response regulator ARR2)	8	30283001	unknown_gene-(unknown protein)
3	25761001	plaa2-(Putative Exopolygalacturonase (Fragment))	8	30279001	STC-(Sugar carrier protein C)
3	25764001	Acad10-(Putative Acyl-CoA dehydrogenase family member 10)	8	30276001	BAG3-(BAG family molecular chaperone regulator 3)
3	25767001	PME28-(Putative pectinesterase/pectinesterase inhibitor 28)	8	30273001	SEU-(Putative uncharacterized protein)
3	25779001	Slc47a1-(Putative Multidrug and toxin extrusion protein 1)	8	30263001	unknown_gene-(Putative IQ-domain 22)
3	25782001	gene desconhecido-(Putative Protein of unknown function (DUF581))	8	30260001	Rfc2-(Replication factor C subunit 2)
3	25784001	Fanci-(Putative unknown protein)	8	30259001	unknown_gene-(Putative Protein of unknown function (DUF810))
3	25808001	Kif2c-(P-loop containing nucleoside triphosphate hydrolases superfamily protein)	8	30256001	Os02g0636300-(DEAD-box ATP-dependent RNA helicase 47A)
3	25815001	gene desconhecido-(Putative BEST Arabidopsis thaliana protein)	8	30254001	At1g12780-(UDP-glucose 4-epimerase 1)
3	25828001	gene desconhecido-(ralf-like 33)	8	30243001	tfa2-(Putative Transcription initiation factor IIE subunit beta)
3	25837001	gene desconhecido-(unknown protein)	8	30238001	RH33-(Putative DEAD-box ATP-dependent RNA helicase 33)
3	25847001	obg-(Putative GTPase obg)	8	30215001	srr-(Putative Probable serine racemase)
3	25850001	PPP2R3C-(Putative Serine/threonine-protein phosphatase 2A regulatory subunit B'' subunit gamma)	8	30213001	HMA5-(Putative copper-transporting ATPase HMA5)
3	25863001	Rchy1-(Putative RING finger and CHY zinc	8	30211001	GSTT1-(Glutathione S-transferase T1)

		finger domain-containing protein 1)			
3	25878001	At1g54610-(Probable serine/threonine-protein kinase At1g54610)	8	30203001	KAM1-(Exostosin family protein)
3	25879001	gene desconhecido-(Hypothetical protein)	8	30195001	At5g41260-(Probable serine/threonine-protein kinase At5g41260)
3	25892001	SOD1-(Superoxide dismutase [Cu-Zn])	8	35379001	unknown_gene-(Putative Protein of unknown function (DUF3527))
3	25901001	PER24-(Peroxidase 24)	8	35389001	guaA-(GMP synthase [glutamine-hydrolyzing])
3	25914001	Dcaf11-(LEC14B homolog)	8	35391001	murE-(Putative UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase)
3	25933001	gene desconhecido-(Putative Predicted protein)	8	35399001	CYP86A2-(Cytoome P450 86A2)
3	25941001	RF298-(Putative E3 ubiquitin-protein ligase RF298)	8	35403001	At5g41330-(BTB/POZ domain-containing protein At5g41330)
3	25946001	MCM3AP-(Putative SAC3/GANP/Nin1/mts3/eIF-3 p25 family)	8	35413001	At3g02290-(Putative RING/U-box superfamily protein)
3	25948001	SAMDC-(Putative S-adenosylmethionine decarboxylase proenzyme)	8	35419001	SPAC25G10.01-(Arginine/serine-rich-splicing factor, putative)
3	25950001	AP5M1-(clathrin adaptor complexes medium subunit family protein)	8	35422001	XPB1-(DNA repair helicase XPB1)
3	25952001	FBL4-(F-box/LRR-repeat protein 4)	8	35425001	unknown_gene-(PLAC8 family protein)
3	25955001	gene desconhecido-(Putative Predicted protein)	8	35432001	GC6-(Golgin candidate 6)
3	25976001	Cmbl-(Putative Carboxymethylenebutenolidase homolog)	8	35446001	unknown_gene-(from the Czech 'roh' meaning 'corner')
3	25977001	RNR2A-(Ribonucleoside-diphosphate reductase small chain A)	8	35460001	ZMIZ2-(Putative uncharacterized protein)
3	25978001	gene desconhecido-(REF4-related 1)	8	35464001	EMB2744-(Pentatricopeptide repeat-containing protein At5g39680)
3	26019001	SLC25A17-(Putative Peroxisomal membrane protein PMP34)	8	35465001	RBOHA-(Respiratory burst oxidase homolog protein A)
3	26023001	D2Wsu81e-(Uncharacterized protein C9orf114 homolog)	8	35484001	WRKY19-(Probable WRKY transcription factor 19)
3	26025001	RANGAP2-(RAN GTPase-activating protein 2)	8	35494001	At5g41620-(Putative Uncharacterized protein At5g41620)
3	26039001	CYCT1-1-(Putative uncharacterized protein)	8	35495001	unknown_gene-(Putative uncharacterized protein)
3	26041001	LACS7-(Long chain acyl-CoA synthetase 7, peroxisomal)	8	35497001	POB1-(BTB/POZ domain-containing protein POB1)
3	26050001	LOX5-(Linoleate 9S-lipoxygenase 5, chloroplastic)	8	35501001	infB-(Putative Translation initiation factor IF-2, mitochondrial)
3	26052001	psaD-(Photosystem I reaction center subunit II, chloroplastic)	8	35502001	VATE-(V-type proton ATPase subunit E)
3	26055001	Vps39-(Putative Vam6/Vps39-like protein)	8	35506001	YMR099C-(Putative glucose-6-phosphate 1-epimerase)
3	26068001	rsc5-(Sec14p-like phosphatidylinositol transfer family protein)	8	35516001	SPA2-(Putative Protein SPA1-RELATED 2)
3	26071001	surE-(Putative 5'-nucleotidase surE)	8	35520001	unknown_gene-(Putative myosin heavy chain-related)
3	26074001	Chd3-(Putative Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein)	8	35521001	unknown_gene-(Putative COP1-interactive protein 1)
3	26076001	gene desconhecido-(photosystem II 11 kDa protein-related)	8	35528001	LHT1-(Putative Lysine histidine transporter 1)
3	26077001	RPS18A-(40S ribosomal protein S18)	8	35529001	unknown_gene-(Avr9/Cf-9 rapidly elicited protein 194)
3	26078001	gene desconhecido (BEST match : XS domain-containing protein / XS zinc finger domain-containing protein-related)	8	35543001	Prim1-(Putative DNA primase small subunit)
3	26081001	FD3-(Putative Ferredoxin-1)	8	35564001	NDK4-(Nucleoside diphosphate kinase IV, chloroplastic/mitochondrial)
3	26091001	gene desconhecido-(Putative Protein of unknown function (DUF1423))	8	35566001	unknown_gene-(unknown protein)
3	26104001	CDC73-(Putative Parafibromin)	8	35568001	At4g10960-(UDP-glucose 4-epimerase GEPI48)
3	26105001	At2g13820-(Putative Non-specific lipid-transfer protein-like protein At2g13820)	8	35575001	CBL7-(Calcineurin B-like protein 7)
3	26109001	SDE3-(Probable RNA helicase SDE3)	8	35583001	unknown_gene-(Hypothetical protein)
3	26131001	gene desconhecido-(Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region)	8	35589001	KAS1-(3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplastic)
3	26134001	gene desconhecido-(RNA polymerase II, Rpb4, core protein)	8	35594001	RPS6-(30S ribosomal protein S6 alpha, chloroplastic)
3	26145001	TSJT1-(Putative Stem-specific protein TSJT1)	8	35595001	RPN12A-(26S proteasome non-ATPase regulatory subunit RPN12A)
3	26156001	ACA12-(Calcium-transporting ATPase 12, plasma membrane-type)	8	35596001	ABIL3-(Putative Protein ABIL3)
3	26164001	gene desconhecido-(37 kDa inner envelope membrane protein, chloroplastic)	8	35598001	unknown_gene-(Putative uncharacterized protein)
3	26171001	gene desconhecido-(Protein of unknown function (DUF506))	8	35601001	NLP7-(Protein NLP7)
3	26196001	At1g06800-(Phospholipase A1-Igamma1, chloroplastic)	8	35607001	BIP5-(Luminal-binding protein 5)
3	26211001	CRS1-(Putative Chloroplastic group IIA intron splicing facilitator CRS1, chloroplastic)	8	35609001	ABCF3-(ABC transporter F family member 3)
3	26214001	At2g30620-(Hypothetical protein)	8	35613001	TIC32-(Putative Short-chain dehydrogenase TIC 32, chloroplastic)
3	26220001	ACA12-(Putative Calcium-transporting ATPase 12, plasma membrane-type)	8	35643001	GYP7-(Ypt/Rab-GAP domain of gyp1p superfamily protein)

3	26226001	At1g62910-(Putative Pentatricopeptide repeat-containing protein At1g62910)	8	35645001	EMB8-(Embryogenesis-associated protein EMB8)
3	26238001	CSLG1-(Putative Cellulose synthase-like protein G1)	8	35653001	BHLH14-(Putative Transcription factor bHLH14)
3	26242001	CSLG3-(Putative Cellulose synthase-like protein G3)	8	35654001	unknown_gene-(alpha/beta-Hydrolases superfamily protein)
3	26259001	At5g43530-(DNA repair helicase rad5,16, putative)	8	35666001	NAC043-(Putative NAC domain-containing protein 12)
3	26270001	ACO3-(1-aminocyclopropane-1-carboxylate oxidase homolog)	8	35678001	unknown_gene-(Polyketide cyclase/dehydrase and lipid transport superfamily protein)
3	26273001	D4H-(Deacetoxyvindoline 4-hydroxylase)	8	35681001	PPA-(Soluble inorganic pyrophosphatase)
3	26275001	D4H-(Deacetoxyvindoline 4-hydroxylase)	8	35703001	unknown_gene-(Hypothetical protein)
3	26281001	At1g06620-(1-aminocyclopropane-1-carboxylate oxidase homolog 1)	8	35705001	HEATR6-(Putative ARM repeat superfamily protein)
3	26286001	BHLH104-(Transcription factor bHLH34)	8	5581001	unknown_gene-(unknown protein;plasma membrane)
3	26308001	meaf6-(CONTAINS InterPro DOMAIN/s: Histone H4 acetyltransferase, NuA4 complex, Eaf6 (InterPro:IPR015418))	8	38527001	B3GALT10-(Probable beta-1,3-galactosyltransferase 10)
3	26316001	LEGB-(Putative 11S globulin subunit beta)	8	38526001	At4g32130-(UPF0480 protein At4g32130)
3	26324001	gene desconhecido-(Protein of unknown function (DUF640))	8	38521001	At5g25310-(Probable glycosyltransferase At5g25310)
3	26329001	PCMP-H32-(Putative pentatricopeptide repeat-containing protein At3g23330)	8	38454001	CjBAp12-(Putative EG45-like domain containing protein 2)
3	26332001	gene desconhecido-(Putative COP1-interacting protein-related)	8	38401001	NIT2-(Omega-amidase NIT2)
3	26345001	ATK1-(P-loop containing nucleoside triphosphate hydrolases superfamily protein)	8	38359001	RPM1-(Putative Disease resistance protein RPM1)
3	26350001	PHO1-(Phosphate transporter PHO1)	8	38343001	Tbl3-(Putative Transducin beta-like protein 3)
3	26363001	U2af50-(Putative Splicing factor U2AF 50 kDa subunit)	8	38330001	TM_1254-(Putative Phosphorylated carbohydrates phosphatase TM_1254)
3	26413001	SUVR2-(Hypothetical protein)	8	37693001	At1g50180-(Putative Nbs-lrr resistance protein)
3	26414001	gene desconhecido-(Putative Protein of unknown function (DUF3527))	8	37713001	PLL1-(Protein phosphatase 2C 29)
3	26424001	gene desconhecido-(unknown protein)	8	37720001	MIP1-(MND1-interacting protein 1)
3	26436001	mutS-(MUTL protein homolog 1)	8	37740001	unknown_gene-(unknown protein; chloroplast)
3	26493001	YOR131C-(Haloacid dehalogenase-like hydrolase (HAD) superfamily protein)	8	37746001	CXE20-(Putative Probable carboxylesterase 120)
3	26534001	HCAR-(7-hydroxymethyl chlorophyll a reductase, chloroplastic)	8	37805001	unknown_gene-(InterPro DOMAIN/s: ATPase, vacuolar ER assembly factor, Vma12 (InterPro:IPR021013)
3	26540001	CPN60-2-(Chaperonin CPN60-2, mitochondrial)	8	37817001	MYB39-(Putative Transcription factor MYB39)
3	26541001	ING1-(PHD finger protein ING1)	8	37829001	TPS5-(Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 5)
3	26561001	gene desconhecido-(Hypothetical protein)	8	37841001	SYP22-(Syntaxin-22)
3	26570001	CTR1-(Putative uncharacterized protein)	8	10772001	unknown_gene-(unknown protein; mitochondrion)
3	26596001	VAMP726-(Putative vesicle-associated membrane protein 726)	8	34137001	unknown_gene-(Protein of unknown function (DUF760))
3	26597001	chtf18-(Putative P-loop containing nucleoside triphosphate hydrolases superfamily protein)	8	34160001	At1g68310-(MIP18 family protein At1g68310)
3	26613001	Gba2-(Beta-glucosidase, GBA2 type family protein)	8	34176001	GPA2-(Putative Guanine nucleotide-binding protein alpha-2 subunit)
3	26615001	At3g24170-(Glutathione reductase, chloroplastic (Fragment))	8	34215001	TPR1-(Topless-related protein 1)
3	26616001	LTI65-(Putative Predicted protein)	8	34258001	unknown_gene-(ENHANCED DISEASE RESISTANCE 2)
3	26640001	PME29-(Probable pectinesterase 29)	8	15657001	RPM1-(Putative Disease resistance protein RPM1)
3	26644001	LECRKS2-(Receptor like protein kinase S.2)	8	42478001	VIT_01s0010g01180-(Anamorsin homolog)
3	33163001	HMGB15-(Putative High mobility group B protein 10)	8	42434001	At1g31850-(Probable methyltransferase PMT20)
3	33171001	PAP15-(Purple acid phosphatase 15)	8	24284001	dur3-1-(Putative Probable urea active transporter 1)
3	33185001	TBC1D13-(Putative TBC1 domain family member 13)	8	24300001	AOX1-(Alternative oxidase 1, mitochondrial)
3	33200001	At4g13780-(Probable methionine--tRNA ligase)	8	24415001	Rbbp5-(Putative Retinoblastoma-binding protein 5)
3	33202001	SPS2-(Probable sucrose-phosphate synthase 2)	8	40940001	unknown_gene-(glutamine dumper 2)
3	33203001	METTL13-(Putative Methyltransferase-like protein 13)	8	40935001	COL4-(Zinc finger protein CONSTANS-LIKE 4)
3	33204001	RIN4-(Putative RPM1-interacting protein 4)	8	36031001	UGT74F2-(Putative UDP-glycosyltransferase 74F2)
3	33262001	gene desconhecido-(Putative unknown protein)	8	36040001	unknown_gene-(InterPro DOMAIN/s: Prefoldin (InterPro:IPR009053)
3	33271001	gene desconhecido-(Hypothetical protein)	8	5816001	DCL3A-(Endoribonuclease Dicer homolog 3a)
3	33275001	RGA3-(Putative NBS resistance protein (Fragment))	8	25276001	At4g15080-(Probable S-acyltransferase At4g15080)
3	33276001	RGA1-(Putative disease resistance protein RGA1)	8	25333001	unknown_gene-(Sas10/Utp3/C1D family)
3	42714001	EMB2217-(Pentatricopeptide repeat-containing protein At1g79490, mitochondrial)	8	25381001	unknown_gene-(Major facilitator superfamily protein)
3	42703001	XTH16-(Probable xyloglucan endotransglucosylase/hydrolase protein 16)	8	11870001	ERF017-(Putative Ethylene-responsive transcription factor ERF017)

3	30927001	gene desconhecido-(Hypothetical protein)	8	11878001	FBX13-(F-box only protein 13)
3	30957001	OsI_15387-(Probable aldo-keto reductase 2)	8	13073001	TIFY8-(Putative uncharacterized protein)
3	30962001	Os04g0338000-(Probable aldo-keto reductase 2)	8	7243001	AGD14-(Putative ArfGap/RecO-like zinc finger domain-containing protein)
3	30971001	Os04g0338000-(Probable aldo-keto reductase 2)	8	7241001	REM15.15-(Putative B3 domain-containing protein REM15)
3	30975001	At1g60690-(Probable aldo-keto reductase 3)	8	9051001	unknown_gene-(Putative Protein of unknown function (DUF630 and DUF632))
3	31037001	SPAC644.07-(Putative cytoome BC1 synthesis)	8	9056001	Os10g0490500-(Putative ripening-related protein 5)
3	31071001	SPPL2B-(Putative Signal peptide peptidase-like 2B)	8	17241001	LHP1-(La protein 1)
3	7798001	UGT73C5-(UDP-glycosyltransferase 73C5)	8	17244001	Os01g0234100-(Putative B3 domain-containing protein Os01g0234100)
3	7799001	DDB_G0269860-(Putative Probable importin-7 homolog)	8	17255001	Tom1l2-(ENTH/VHS/GAT family protein)
3	42005001	HM13-(Putative Minor histocompatibility antigen H13)	8	17265001	PUB26-(Putative ARM repeat superfamily protein)
3	42010001	At4g27190-(Putative Disease resistance protein At4g27190)	8	17274001	At1g52190-(Putative Probable peptide transporter At1g52190)
3	42059001	ASHR2-(Histone-lysine N-methyltransferase ASHR2)	8	17283001	At1g52190-(Probable peptide transporter At1g52190)
3	42086001	At3g49140-(Putative Pentatricopeptide repeat (PPR) superfamily protein)	8	26884001	At3g02645-(Putative UPF0481 protein At3g02645)
3	42090001	At4g09550-(Mitotic-spindle organizing protein 1B)	8	26936001	cki2-(Protein kinase family protein)
3	43195001	RGA3-(Putative disease resistance protein RGA3)	8	26942001	trpS-(Tryptophan--tRNA ligase)
3	43235001	gene desconhecido-(ARM repeat superfamily protein)	8	26968001	EPSIN1-(Clathrin interactor EPSIN 1)
3	15300001	RING1A-(Putative E3 ubiquitin-protein ligase RING1a)	8	26980001	At3g47570-(Putative Probable LRR receptor-like serine/threonine-protein kinase At3g47570)
3	15297001	FPA-(Putative Flowering time control protein FPA)	8	27008001	At5g11770-(NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial)
3	15295001	3BETAHSD/D3-(3beta-hydroxysteroid-dehydrogenase/decarboxylase isoform 3)	8	27011001	ATH1-(Putative uncharacterized protein)
3	15283001	ZIP5-(Zinc transporter 5)	8	27028001	ycf36-(Putative Uncharacterized protein ycf36)
3	15241001	SHR-(Protein SHORT-ROOT)	8	27037001	PCMP-H27-(Pentatricopeptide repeat-containing protein At4g35130, chloroplastic)
3	15231001	gene desconhecido-(Putative uncharacterized protein)	8	27082001	CWC27-(Putative Peptidyl-prolyl cis-trans isomerase CWC27 homolog)
3	15229001	At3g25440-(RNA-binding CRS1 / YhbY (CRM) domain protein)	8	27098001	NSUN5-(Putative methyltransferase NSUN5)
3	15227001	ULK4-(Protein kinase family protein with ARM repeat domain)	8	27123001	UVH1-(DNA repair endonuclease UVH1)
3	15223001	gene desconhecido-(Chitinase 2)	8	27129001	RLP12-(Putative Receptor-like protein 12)
3	15202001	gene desconhecido-(unknown protein)	8	27138001	CLPR4-(ATP-dependent Clp protease proteolytic subunit-related protein 4, chloroplastic)
3	15184001	RGA3-(Putative disease resistance protein RGA3)	8	27142001	EXLB1-(Expansin-like B1)
3	30642001	At2g30105-(LRR repeats and ubiquitin-like domain-containing protein At2g30105)	8	27152001	At4g17550-(Putative glycerol-3-phosphate transporter 4)
3	30639001	gene desconhecido-(Putative Predicted protein)	8	27188001	unknown_gene-(unknown protein)
3	30623001	gene desconhecido-(Hypothetical protein)	8	12605001	unknown_gene-(BEST match: 3'-5' CDSuclease domain-containing protein / K homology domain-containing protein / KH domain-containing protein (TAIR:AT2G25910.2))
3	30621001	At2g02240-(Putative F-box protein At2g02240)	8	30556001	ERF2-(Ethylene-responsive transcription factor 2)
3	30613001	gemin2-(Putative Gem-associated protein 2)	8	30515001	At5g03795-(Putative Probable glycosyltransferase At5g25310)
3	30608001	gene desconhecido-(sequence-specific DNA binding transcription factors)	8	30509001	MSH4-(Putative MutS protein homolog 4)
3	30599001	ASHH1-(Histone-lysine N-methyltransferase ASHH1)	8	30502001	unknown_gene-(Putative Protein of unknown function, DUF547)
3	30598001	ATPC-(ATP synthase subunit gamma, mitochondrial)	8	30464001	HSP14.7-(Putative 14.7 kDa heat shock protein)
3	30596001	Cgl1970-(Putative ribonuclease J Rv2752c)	8	30419001	At1g62620-(Flavin-containing monooxygenase FMO GS-OX-like 3)
3	30594001	VPS45-(Vacuolar protein sorting-associated protein 45 homolog)	8	30381001	unknown_gene-(Putative copper ion binding)
3	18978001	At1g34300-(G-type lectin S-receptor-like serine/threonine-protein kinase At1g34300)	8	30377001	CYP75B2-(Putative Flavonoid 3'-monooxygenase)
3	31705001	LECRK41-(L-type lectin-domain containing receptor kinase IV.1)	8	30374001	At1g62810-(Primary amine oxidase)
3	31712001	gene desconhecido-(Putative XH/XS domain-containing protein)	8	30344001	At4g12060-(Clp protease-related protein At4g12060, chloroplastic)
3	31722001	CHI4-(Endochitinase PR4)	8	30337001	sll0608-(Ycf49-like protein)
3	31767001	MED21-(Mediator of RNA polymerase II transcription subunit 21)	8	30296001	HMGS-(Hydroxymethylglutaryl-CoA synthase)
3	31786001	SPBC4B4.04-(Putative Eukaryotic translation initiation factor 2A)	8	30274001	RRP36-(Putative Ribosomal RNA processing protein 36 homolog)
3	31815001	gene desconhecido-(Basic endochitinase)	8	30265001	VIP2-(Probable NOT transcription complex subunit VIP2 (Fragment))

3	31820001	gene desconhecido-(Acyl-[acyl-carrier-protein] desaturase, chloroplastic)	8	30253001	MYB3R-1-(Hypothetical protein)
3	26651001	FAM136A-(Eukaryotic protein of unknown function (DUF842))	8	30249001	tlp-(Thaumatin-like protein)
3	26662001	CASTOR-(Ion channel CASTOR)	8	35466001	unknown_gene-(Putative Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)
3	26744001	gene desconhecido-(Protein of unknown function (DUF177))	8	35475001	SPAST-(P-loop containing nucleoside triphosphate hydrolases superfamily protein)
3	26747001	gene desconhecido-(Putative uncharacterized protein)	8	35532001	seh1l-(Putative Nucleoporin seh1)
3	26756001	snrnp35-(RNA-binding (RRM/RBD/RNP motifs) family protein)	8	35552001	OXA1-(Mitochondrial inner membrane protein OXA1)
3	26809001	ilvH-(Acetolactate synthase small subunit)	8	35567001	unknown_gene-(Pentatricopeptide repeat (PPR) superfamily protein)
3	26813001	P2-(NADP-dependent alkenal double bond reductase P2)	8	35611001	unknown_gene-(Hypothetical protein)
3	26850001	P2-(NADP-dependent alkenal double bond reductase P2)	8	35616001	MYB5-(Putative TT2 like MYB transcriptoin factor)
3	26852001	P1-(NADP-dependent alkenal double bond reductase P1)	8	35636001	unknown_gene-(unknown protein; chloroplast)
3	26876001	At2g43860-(Polygalacturonase)	8	35641001	YSL3-(Metal-nicotianamine transporter YSL3)
3	1649001	SKIP35-(F-box/ankyrin repeat protein SKIP35)	8	35651001	ATHB-7-(Putative uncharacterized protein)
3	1677001	At2g43860-(Polygalacturonase)	8	35658001	unknown_gene-(unknown protein)
3	2095001	RROP1-(Nucleoside-triphosphatase)	8	35700001	unknown_gene-(Hypothetical protein)
3	25580001	nt5c2-(Putative Cytosolic purine 5'-nucleotidase)	8	5561001	PKL-(CHD3-type omatin-remodeling factor PICKLE)
3	25581001	truA1-(Putative tRNA pseudouridine synthase A 1)	8	5566001	ERF003-(Ethylene-responsive transcription factor ERF003)
3	25601001	SAMS2-(S-adenosylmethionine synthase 2)	8	5568001	At1g80640-(Probable receptor-like protein kinase At1g80640)
3	25615001	mcfJ-(Putative Mitochondrial substrate carrier family protein J)	8	5579001	ncdn-(neurochondrin family protein)
3	25619001	Vps13c-(calcium-dependent lipid-binding family protein)	8	5584001	FLOT1-(Flotillin-like protein 1)
3	25629001	Nemf-(Putative Nuclear export mediator factor Nemf)	8	38505001	RPM1-(Putative uncharacterized protein)
3	25630001	UPL6-(E3 ubiquitin-protein ligase UPL6)	8	38453001	CjBAp12-(Putative EG45-like domain containing protein)
3	25638001	CASD1-(O-acetyltransferase family protein)	8	38430001	PAA2-(Copper-transporting ATPase PAA2, chloroplastic)
3	25662001	gene desconhecido-(Putative Ca2+-binding protein 1)	8	38347001	unknown_gene-(unknown protein; endomembrane system)
3	25680001	PI206-(Putative Disease resistance-responsive (dirigent-like protein) family protein)	8	38340001	SEC10-(Exocyst complex component 5)
3	25683001	gene desconhecido-(Putative uncharacterized protein)	8	37671001	APRR2-(Two-component response regulator-like APRR2)
3	25689001	ALDH22A1-(Aldehyde dehydrogenase 22A1)	8	37712001	unknown_gene-(ubiquitin family protein)
3	25699001	gene desconhecido-(Hypothetical protein)	8	37762001	PYR1-(Abscisic acid receptor PYR1)
3	25740001	PRUA1-(Putative Major allergen Pru av 1)	8	37772001	AGD8-(Probable ADP-ribosylation factor GTPase-activating protein AGD8)
3	25745001	gene desconhecido-(Putative Chaperone DnaJ-domain superfamily protein)	8	37797001	BHLH96-(Putative Transcription factor bHLH94)
3	25755001	PLDP1-(Phospholipase D p1)	8	37830001	Rbm34-(Putative RNA-binding (RRM/RBD/RNP motifs) family protein)
3	25777001	Dbt-(Putative Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial)	8	34129001	unknown_gene-(Glycerol-3-phosphate acyltransferase, chloroplastic)
3	25822001	CARM1-(Probable histone-arginine methyltransferase CARM1)	8	34138001	GBF1-(Putative Transcription factor HBP-1a)
3	25840001	gene desconhecido-(Putative uncharacterized protein)	8	34185001	RCOM_1206790-(Putative CASP-like protein RCOM_1206790)
3	25869001	VIT_05s0020g01820-(CASP-like protein VIT_05s0020g01820)	8	34211001	unknown_gene-(Putative uncharacterized protein)
3	25904001	TKT2-(Probable 1-deoxy-D-xylulose-5-phosphate synthase, chloroplastic)	8	34217001	RGA1-(Putative disease resistance protein RGA1)
3	25931001	RBK2-(Protein kinase family protein)	8	34247001	CMT2-(DNA (cytosine-5)-methyltransferase CMT2)
3	25935001	gene desconhecido-(DUF679 domain membrane protein 2)	8	34260001	tmem45b-(Putative Transmembrane protein 45B)
3	25939001	gene desconhecido-(tRNA/rRNA methyltransferase (SpoU) family protein)	8	15652001	unknown_gene-(Protein of unknown function (DUF1350))
3	25961001	Eif2s3y-(Eukaryotic translation initiation factor 2 subunit 3, Y-linked)	8	42509001	HD3A-(Protein HEADING DATE 3A)
3	25970001	gene desconhecido-(ARM repeat superfamily protein)	8	42505001	UBP12-(Putative TRAF-like family protein)
3	25997001	BG-(Putative Basic 7S globulin)	8	42491001	At4g19050-(Putative disease resistance protein At4g19050)
3	26004001	NFYC9-(Nuclear transcription factor Y subunit C-9)	8	42459001	RF_0381-(Putative ankyrin repeat protein RF_0381)
3	26005001	VIT_05s0020g02800-(ATP-dependent (S)-NAD(P)H-hydrate dehydratase)	8	42451001	unknown_gene-(unknown protein)
3	26010001	KDSR-(Putative 3-ketodihydrosphingosine reductase)	8	24309001	DDB_G0277179-(Protein of unknown function, DUF647)
3	26020001	ANP3-(Mitogen-activated protein kinase kinase kinase 3)	8	24385001	unknown_gene-(xyloglucanase 113)

3	26024001	SNF2-(Putative Probable global transcription activator SNF2L2)	8	24399001	At1g31730-(AP-4 complex subunit epsilon)
3	26139001	Dym-(Putative Dymeclin)	8	40951001	unknown_gene-(Putative RING/U-box superfamily protein)
3	26173001	At5g28840-(GDP-mannose 3,5-epimerase)	8	36024001	Exoc7-(exocyst subunit exo70 family protein G1)
3	26246001	EIN4-(Protein EIN4)	8	11890001	FH18-(Formin-like protein 18)
3	26261001	ARP9-(Actin-related protein 9)	8	7264001	CYP72A1-(Putative Cytoome P450)
3	26306001	At1g50180-(Putative disease resistance protein At1g50180)	8	9054001	yjbI-(hemoglobin 3)
3	26349001	FAO1-(Long-chain-alcohol oxidase FAO1)	8	17242001	MYB3R-1-(Putative Myb-related protein 3R-1)
3	26355001	GTE1-(Transcription factor GTE1)	8	17297001	At3g02645-(Putative UPF0481 protein At3g02645)
3	26370001	PTR3-A-(Peptide transporter PTR3-A)	8	26897001	FBXL2-(Putative F-box/LRR-repeat protein 2)
3	26375001	gene desconhecido-(Putative unknown protein)	8	26947001	AAP8-(Amino acid permease 8)
3	26390001	RPL23A-(60S ribosomal protein L23)	8	26956001	PFK7-(6-phosphofructokinase 7)
3	26419001	TOM22-2-(Putative Mitochondrial import receptor subunit TOM22 homolog 1)	8	27010001	SF21-(Pollen-specific protein SF21)
3	26431001	gene desconhecido-(Putative Tetratricopeptide repeat (TPR)-like superfamily protein)	8	27015001	At3g47200-(Putative UPF0481 protein At3g47200)
3	26444001	gene desconhecido-(Putative unknown protein)	8	27034001	ZIP4-(Zinc transporter 4, chloroplastic)
3	26446001	gene desconhecido-(unknown protein)	8	27062001	IQD1-(IQ-domain 6)
3	26489001	gene desconhecido-(Major facilitator superfamily protein)	8	27113001	At4g17616-(Putative Pentatricopeptide repeat-containing protein At4g17616)
3	26501001	AMT1-1-(Ammonium transporter 1 member 1)	8	27122001	Mb2253c-(Putative RNase H family protein)
3	26548001	CTR1-(Putative Serine/threonine-protein kinase CTR1)	8	27135001	SDD1-(tRNA/rRNA methyltransferase (SpoU) family protein)
3	26554001	RHD3-(Putative Protein ROOT HAIR DEFECTIVE 3 homolog 1)	8	27158001	unknown_gene-(Hypothetical protein)
3	26560001	gene desconhecido-(Putative unknown protein)	8	30554001	LHA1-(Plasma membrane ATPase 1)
3	26563001	RCH2-(Receptor-like protein kinase 2)	8	30516001	C1-(unknown protein; endomembrane system)
3	26568001	PAP23-(Purple acid phosphatase 23)	8	30461001	wrbA-(Flavoprotein WrbA)
3	26574001	PED1-(3-ketoacyl-CoA thiolase 2, peroxisomal)	8	30448001	unknown_gene-(unknown protein)
3	26591001	gene desconhecido-(Putative uncharacterized protein)	8	30388001	PME3-(Putative 21 kDa protein)
3	26595001	pigl-(Putative Probable N-acetylglucosaminyl-phosphatidylinositol de-N-acetylase)	8	30321001	CCS-(Putative Copper chaperone for superoxide dismutase)
3	26603001	PP2B11-(Putative F-box protein PP2-B11)	8	30284001	UTR4-(UDP-galactose/UDP-glucose transporter 4)
3	26642001	APL-(Homeodomain-like superfamily protein)	8	30264001	CTR1-(Putative PAS domain-containing protein tyrosine kinase family protein)
3	26645001	gene desconhecido-(Putative uncharacterized protein)	8	30216001	NOB1-(InterPro DOMAIN/s: Nin one binding (NOB1) Zn-ribbon like (InterPro:IPR014881), D-site 20S pre-rRNA nuclease (InterPro:IPR017117))
3	33219001	At3g47200-(Putative UPF0481 protein At3g47200)	8	30198001	ESC-(Putative AT hook motif DNA-binding family protein)
3	33229001	gene desconhecido-(Hypothetical protein)	8	30196001	rbr-2-(Putative transcription factor jumonji (jmjC) domain-containing protein)
3	33235001	gene desconhecido-(Lactoylglutathione lyase / glyoxalase I family protein)	8	30193001	GSH1-(Glutamate--cysteine ligase, chloroplastic)
3	33237001	gene desconhecido (BEST match: RNA-directed DNA polymerase (reverse transcriptase)-related family protein)	8	35390001	unknown_gene-(Putative Protein of unknown function (DUF3741))
3	33267001	WEX-(Putative Werner Syndrome-like CDSuclease)	8	35404001	At1g76660-(Putative hydroxyproline-rich glycoprotein family protein)
3	33269001	shmt1-(Serine hydroxymethyltransferase 1)	8	35450001	ISPF-(2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, chloroplastic)
3	42710001	SEC23-(Putative Protein transport protein SEC23)	8	35468001	unknown_gene-(Putative Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)
3	42706001	gene desconhecido-(Putative Uncharacterized protein)	8	35511001	AGP20-(Arabinogalactan peptide 20)
3	42701001	gene desconhecido-(Putative Uncharacterized protein)	8	35539001	unknown_gene-(Putative uncharacterized protein)
3	42697001	UGT75D1-(Putative UDP-glycosyltransferase 75D1)	8	35612001	TRE1-(Trehalase)
3	42681001	RGA3-(Putative disease resistance protein RGA3)	8	35617001	unknown_gene-(Hypothetical protein)
3	42680001	A6-(Probable glucan endo-1,3-beta-glucosidase A6)	8	35684001	NGA1-(B3 domain-containing protein Os03g0120900)
3	42679001	A6-(Probable glucan endo-1,3-beta-glucosidase A6)	8	35693001	NUP98-(Putative Nuclear pore complex protein Nup98-Nup96)
3	30952001	RABA5C-(Ras-related protein RABA5c)	8	5583001	ATX2-(Putative uncharacterized protein)
3	30954001	RPS1-(Putative 30S ribosomal protein S1)	8	38432001	myoJ-(myosin, putative)
3	30978001	OsI_15387-(Probable aldo-keto reductase 2)	8	38392001	At5g02620-(Putative Ankyrin repeat-containing protein At5g02620)
3	30980001	OsI_15387-(Probable aldo-keto reductase 2)	8	38355001	RPM1-(Putative Disease resistance protein RPM1)
3	30999001	GWD3-(Phosphoglucan, water dikinase, chloroplastic)	8	38346001	Mettl21d-(Putative uncharacterized protein)
3	41999001	3BETAHSD/D2-(3beta-hydroxysteroid-dehydrogenase/decarboxylase isoform 2)	8	37702001	NRT1.5-(Nitrate transporter 1.5)

3	42003001	ttc27-(Putative Tetratricopeptide repeat protein 27 homolog)	8	37728001	unknown_gene-(Putative Late embryogenesis abundant protein, group 1 protein)
3	42020001	BMS1-(Putative Ribosome biogenesis protein bms1)	8	37789001	unknown_gene-(PLATZ transcription factor family protein)
3	42046001	H6H-(Putative uncharacterized protein)	8	34199001	4CLL6-(4-coumarate--CoA ligase-like 6)
3	42050001	DAPB2-(Dihydrodipicolinate reductase 2, chloroplastic)	8	34261001	cdc20-(Putative Anaphase-promoting complex subunit cdc20)
3	19338001	G6PD-(Glucose-6-phosphate 1-dehydrogenase, chloroplastic)	8	15640001	unknown_gene-(Protein of unknown function (DUF1350))
3	19342001	gene desconhecido-(Putative unknown protein)	8	42506001	UGAT-(Putative Cyanidin-3-O-glucoside 2-O-glucuronosyltransferase)
3	19377001	At2g17140-(Putative Pentatricopeptide repeat-containing protein At2g17140)	8	42493001	unknown_gene-(Putative Cysteine/Histidine-rich C1 domain family protein)
3	43206001	RGA3-(Putative disease resistance protein RGA3)	8	42462001	unknown_gene-(Putative Cysteine/Histidine-rich C1 domain family protein)
3	15192001	CYP704C1-(Putative Cytoome P450 704C1)	8	42460001	VIT_01s0010g01180-(Anamorsin homolog)
3	30644001	At2g30105-(LRR repeats and ubiquitin-like domain-containing protein At2g30105)	8	7027001	TPR4-(Putative Topless-related protein 4)
3	30617001	rplO-(50S ribosomal protein L15)	8	24378001	CPIJ013394-(Putative O-glucosyltransferase rumi homolog)
3	31766001	SPBC3B8.09-(Putative Uncharacterized protein C3B8.09)	8	7240001	unknown_gene-(embryo defective 2410)
3	31774001	RGA4-(Putative disease resistance protein RGA4)	8	7228001	COMT1-(Caffeic acid 3-O-methyltransferase)
3	31780001	RPS2-(Putative Probable disease resistance protein At4g27220)	8	17226001	BURP3-(Putative BURP domain-containing protein 5)
3	31782001	BG-(Putative Basic 7S globulin 2)	8	26899001	unknown_gene-(Protein of unknown function (DUF810))
3	31806001	PTR3-A-(Peptide transporter PTR3-A)	8	26994001	unknown_gene-(Hypothetical protein)
3	31811001	IQD14-(Putative Protein IQ-DOMAIN 14)	8	27030001	GDCSP-(Glycine dehydrogenase [decarboxylating], mitochondrial)
3	31813001	CHIT3-(Basic endochitinase)	8	27101001	ANK2-(Putative Ankyrin-2)
3	26667001	At3g25440-(Putative uncharacterized protein)	8	30540001	SDD1-(Putative Subtilisin-like protease SDD1)
3	26670001	At1g48120-(Aminotransferase-like, plant mobile domain family protein)	8	30539001	ARA12-(Putative Subtilisin-like protease)
3	26765001	AIM25-(Putative uncharacterized protein)	8	30406001	At1g12250-(Thylakoid lumenal protein At1g12250, chloroplastic)
3	26767001	UGT74E2-(Putative UDP-glycosyltransferase 74E2)	8	30384001	ST13-(Putative Hsc70-interacting protein)
3	26773001	UGT74E2-(Putative UDP-glycosyltransferase 74E2)	8	30376001	CYP76C1-(Putative Cytoome P450 76C1)
3	26776001	CYP71A2-(Cytoome P450 71A2)	8	30367001	CAF17-(Putative transferase CAF17, mitochondrial)
3	26787001	LETM1-(LETM1-like protein)	8	30307001	FZR2-(Protein FIZZY-RELATED 2)
3	26795001	Nolc1-(Predicted protein)	8	30247001	tlp-(Thaumatin-like protein)
3	26796001	At4g20830-(Putative Reticuline oxidase-like protein)	8	30244001	unknown_gene-(Hypothetical protein)
3	26812001	SKIP24-(F-box protein SKIP24)	8	30228001	At3g61260-(Remorin)
3	26825001	RGA2-(Putative Disease resistance protein RGA2)	8	35530001	AS-(Hydroquinone glucosyltransferase)
3	26851001	P2-(NADP-dependent alkenal double bond reductase P2)	8	35531001	AS-(Putative Hydroquinone glucosyltransferase)
3	1653001	URH2-(Probable uridine nucleosidase 2)	8	35549001	Os01g0656200-(Putative highly ABA-induced PP2C gene 2)
3	2114001	APS1-(Putative Glucose-1-phosphate adenylyltransferase small subunit, chloroplastic/amyloplastic)	8	35591001	CSLG3-(Cellulose synthase-like protein G3)
3	2103001	Os06g0508700-(Hypothetical protein)	8	35624001	faf2-b-(Putative FAS-associated factor 2-B)
3	25582001	APO1-(APO protein 1, chloroplastic)	8	35663001	PAP27-(Probable inactive purple acid phosphatase 27)
3	25602001	gene desconhecido-(Hypothetical protein)	8	35670001	At1g32780-(Alcohol dehydrogenase-like 3)
3	25624001	LPD1-(Dihydrolipoyl dehydrogenase 1, mitochondrial)	8	5573001	unknown_gene-(unknown protein)
3	25690001	gene desconhecido-(Adenine nucleotide alpha hydrolases-like superfamily protein)	8	38504001	ATPG-(ATP synthase subunit b', chloroplastic)
3	25744001	APUM24-(Pumilio homolog 24)	8	38363001	LON2-(Lon protease homolog 2, peroxisomal)
3	25773001	fahd1-(Acylpyruvase FAHD1, mitochondrial)	8	37708001	DAT-(Putative Deacetylvindoline O-acetyltransferase)
3	25803001	Ncapd3-(binding)	8	37733001	unknown_gene-(AT hook motif DNA-binding family protein)
3	25813001	Gmcl1-(BTB/POZ domain-containing protein)	8	37825001	RLP12-(Putative Receptor-like protein 12)
3	25875001	DRB2-(Putative uncharacterized protein)	8	34209001	SPAC2G11.09-(ERD (early-responsive to dehydration stress) family protein)
3	26047001	TIC-(Putative Protein TIME FOR COFFEE)	8	34213001	unknown_gene-(Ribosomal protein L35)
3	26065001	HSP70-8-(Heat shock 70 kDa protein 8)	8	42439001	unknown_gene-(unknown protein)
3	26087001	gene desconhecido-(Late embryogenesis abundant protein D-34)	8	24338001	unknown_gene-(Major facilitator superfamily protein)
3	26115001	SUPV3L1-(Putative ATP-dependent RNA helicase SUPV3L1, mitochondrial)	8	24354001	unknown_gene-(Family of unknown function (DUF716))
3	26132001	At4g15470-(Putative BI1-like protein)	8	25342001	At1g14390-(Probable LRR receptor-like serine/threonine-protein kinase At1g14390)
3	26260001	gene desconhecido-(3-hydroxyacyl-CoA	8	25370001	PHS1-(Putative Beta-phellandrene synthase (neryl-

		dehydratase 1)			diphosphate-cyclizing), chloroplastic)
3	26272001	At1g06620-(1-aminocyclopropane-1-carboxylate oxidase homolog 1)	8	25412001	At3g27220-(Kelch repeat-containing protein At3g27220)
3	26298001	Trip4-(RNA-binding ASCH domain protein)	8	11874001	unknown_gene-(Putative hydroxyproline-rich glycoprotein family protein)
3	26335001	gene desconhecido-(Hypothetical protein)	8	17291001	At1g52190-(Probable peptide transporter At1g52190)
3	26362001	RPL28-(50S ribosomal protein L28, chloroplastic)	8	26887001	At5g03795-(Putative Exostosin family protein)
3	26392001	At1g59780-(Putative disease resistance protein At1g59780)	8	26916001	unknown_gene-(unknown protein; chloroplast)
3	26429001	nxt3-(Putative G3BP-like protein)	8	26948001	RLK5-(Putative Receptor-like protein kinase 5)
3	26453001	gene desconhecido-(AWPM-19-like family protein)	8	27009001	unknown_gene-(unknown protein)
3	26544001	gene desconhecido-(Disease resistance-responsive (dirigent-like protein) family protein)	8	27087001	clp1-(Putative Protein CLP1 homolog)
3	26584001	Ankrd13b-(Ankyrin repeat family protein)	8	27128001	OSCPNY2-(Beta-Amyrin Synthase 2)
3	26598001	CSLD1-(Cellulose synthase-like protein D1)	8	27175001	GSO1-(Putative LRR receptor-like serine/threonine-protein kinase GSO1)
3	26599001	At2g02240-(Putative F-box protein At2g02240)	8	30535001	unknown_gene-(Hypothetical protein)
3	26629001	gene desconhecido-(Uncharacterized protein)	8	30320001	ARA12-(Putative Subtilisin-like protease)
3	33170001	At5g61130-(Carbohydrate-binding X8 domain superfamily protein)	8	30319001	ARA12-(Putative Subtilisin-like protease)
3	33220001	PCYT1B-(phosphorylcholine cytidylyltransferase)	8	30252001	tlp-(Thaumatin-like protein)
3	33225001	R1B-14-(Hypothetical protein)	8	35569001	At4g10955-(GDSL esterase/lipase At4g10955)
3	33236001	hexb2-(Putative Beta-hexosaminidase subunit B2)	8	37696001	PRS2-(Ribose-phosphate pyrophosphokinase 2, chloroplastic)
3	33258001	HHT1-(Putative HXXXD-type acyl-transferase family protein)	8	37821001	C1-(Putative uncharacterized protein)
3	42727001	CYC02-(Putative CYC02 protein)	8	34186001	At4g15970-(Uncharacterized protein At4g15970)
3	42724001	gene desconhecido-(Hypothetical protein)	8	34188001	Os07g0301200-(DEAD-box ATP-dependent RNA helicase 5)
3	42716001	FKBP65-(Peptidyl-prolyl cis-trans isomerase FKBP65)	8	34198001	ywbG-(membrane protein, putative)
3	42686001	UGT75D1-(Putative UDP-glycosyltransferase 75D1)	8	34207001	SPAC2G11.09-(early-responsive to dehydration stress protein (ERD4))
3	30959001	OsI_15387-(Probable aldo-keto reductase 2)	8	42457001	unknown_gene-(Hypothetical protein)
3	31023001	CYP76C3-(Putative Cytoome P450 76C3)	8	26961001	GATC-(Glutamyl-tRNA(Gln) amidotransferase subunit C, chloroplastic/mitochondrial)
3	31055001	R1B-17-(Putative late blight resistance protein homolog R1B-17)	8	27170001	Os02g0512300-(RNA pseudourine synthase 7)
3	42079001	ASNSD1-(Putative Asparagine synthetase domain-containing protein 1)	8	30512001	Rbbp6-(DWNN domain, a CCHC-type zinc finger)
3	42085001	Dml-(Putative 2,3-dimethylmalate lyase)	8	30372001	GAE3-(UDP-glucuronate 4-epimerase 3)
3	45001	SLC35F1-(Putative Solute carrier family 35 member F1)	8	5567001	ASP5-(Aspartate aminotransferase, chloroplastic)
3	43215001	TBC1D22B-(Putative GTPase-activating protein gyp1)	8	34191001	CYP76C4-(Putative Cytoome P450 76C4)
3	15267001	SKIP16-(F-box protein SKIP16)	8	15641001	unknown_gene-(Putative Protein of unknown function (DUF1350))
3	15216001	INT4-(Sugar transporter, putative)	8	24371001	NUDT3-(Nudix hydrolase 3)
3	15172001	RGA3-(Putative disease resistance protein RGA3)	8	36050001	FLA3-(Putative Fasciclin-like arabinogalactan protein 5)
3	15166001	RGA4-(Putative Cc-nbs-lrr resistance protein)	8	7259001	DDB_G0276689-(unknown protein)
3	30564001	BIO2-(Biotin synthase)	8	7253001	Rchy1-(Putative RING finger and CHY zinc finger domain-containing protein 1)
3	18949001	EFR-(Putative LRR receptor-like serine/threonine-protein kinase EFR)	8	30500001	unknown_gene-(Putative uncharacterized protein)
3	18960001	At1g06710-(Pentatricopeptide repeat-containing protein At1g06710, mitochondrial)	8	30363001	unknown_gene-(unknown protein; chloroplast)
3	31706001	LECRK41-(L-type lectin-domain containing receptor kinase IV.1)	8	30288001	CPK4-(phosphoenolpyruvate carboxylase-related kinase 1)
3	31721001	CHI4-(Endochitinase PR4)	8	30261001	RPL24-(60S ribosomal protein L24-1)
3	31735001	At4g27190-(Hypothetical protein)	8	30204001	MCTP2-(C2 calcium/lipid-binding plant phosphoribosyltransferase family protein)
3	31736001	gene desconhecido-(Hypothetical protein)	8	5574001	ALF4-(Putative Aberrant root formation protein 4)
3	26692001	R1B-17-(Putative NB-ARC domain-containing disease resistance protein)	8	38353001	RPM1-(Putative Disease resistance protein RPM1)
3	26820001	RGA4-(Putative disease resistance protein RGA4)	8	27133001	ylbA-(Putative Uncharacterized protein ylbA)
3	26875001	At2g43860-(Polygalacturonase)	8	30297001	XSP1-(Putative Xylem serine proteinase 1)
3	1663001	gene desconhecido-(unknown protein)	8	37668001	unknown_gene-(Putative CONTAINS InterPro DOMAIN/s: Inner nuclear membrane protein MAN1 (InterPro:IPR018996))
3	1667001	HOL3-(Probable thiol methyltransferase 2)	8	37822001	At4g09580-(Uncharacterized membrane protein At4g09580)
3	1668001	5PTASE12-(Type I inositol 1,4,5-trisphosphate 5-phosphatase 12)	8	10792001	unknown_gene-(shikimate kinase like 2)

3	1673001	PCMP-E94-(Putative Pentatricopeptide repeat-containing protein At3g20730)	8	15665001	unknown_gene-(pigment defective 320)
3	2122001	CSLD5-(Cellulose synthase-like protein D5)	8	24339001	unknown_gene-(Putative uncharacterized protein)
3	2115001	PARG1-(Poly(ADP-ribose) glycohydrolase 1)	8	30354001	unknown_gene-(Hypothetical protein)
3	2112001	gene desconhecido-(RAP)	8	30341001	ARK3-(Armadillo repeat-containing kinesin-like protein 3)
3	25623001	At3g62260-(Probable protein phosphatase 2C 49)	8	26940001	ME1-(NADP-dependent malic enzyme)
3	25671001	CTR1-(PAS domain-containing protein tyrosine kinase family protein)	8	38391001	At3g12360-(Putative Ankyrin repeat-containing protein At2g01680)
3	25702001	OEP162-(Outer envelope pore protein 16-2, chloroplastic)	8	38369001	vps13A-(pleckstrin homology (PH) domain-containing protein)
3	25709001	AAE7-(Acetate/butyrate--CoA ligase AAE7, peroxisomal)	8	27104001	caskin2-(Putative Ankyrin-3)
3	25710001	BXL1-(Beta-D-xylosidase 1)	8	37837001	HSF8-(Heat shock factor protein HSF8)
3	25834001	alaS-(Putative Alanine--tRNA ligase)	8	5575001	TRAPPC9-(TRS120)
3	25861001	gene desconhecido-(alpha/beta-Hydrolases superfamily protein)	8	42492001	At5g67130-(Hypothetical protein)
3	25893001	EMB3004-(Bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase, chloroplastic)	8	38345001	UPF1-(Regulator of nonsense transcripts 1 homolog)
3	25940001	PPD-(Pyruvate, phosphate dikinase, chloroplastic)	9	17988001	PFK2-(6-phosphofructokinase 2)
3	26175001	gene desconhecido-(ARM repeat superfamily protein)	9	17980001	At5g47800-(BTB/POZ domain-containing protein At5g47800)
3	26208001	CDS1-(Phosphatidate cytidylyltransferase)	9	17977001	FPS1-(Farnesyl pyrophosphate synthase 1)
3	26218001	Stard7-(Polyketide cyclase/dehydrase and lipid transport superfamily protein)	9	17975001	pho2-(Putative 4-nitrophenylphosphatase)
3	26258001	At5g43530-(Putative SWI/SNF-related matrix-associated actin-dependent regulator of omatin subfamily A member 3-like 3)	9	17973001	unknown_gene-(Mitochondrial transcription termination factor family protein)
3	26529001	gene desconhecido-(Putative unknown protein; INVOLVED IN: N-terminal protein myristoylation)	9	17966001	ALKBH3-(Putative Alpha-ketoglutarate-dependent dioxygenase alkB homolog 2)
3	26636001	At2g32720-(Cytoome b5, seed isoform)	9	17955001	OPT3-(Oligopeptide transporter 3)
3	33183001	PCMP-H64-(Putative Pentatricopeptide repeat-containing protein At1g04840)	9	17931001	unknown_gene-(Putative agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein)
3	33213001	At3g47200-(Putative UPF0481 protein At3g47200)	9	17930001	ADA2B-(Transcriptional adapter ADA2b)
3	33291001	At4g08850-(Probable LRR receptor-like serine/threonine-protein kinase At4g08850)	9	17922001	PVIP-(OBERON-like protein)
3	42677001	AAE16-(Probable acyl-activating enzyme 16, chloroplastic)	9	17917001	dazap1-(RNA-binding (RRM/RBD/RNP motifs) family protein)
3	5524001	Srrm2-(Putative mRNA splicing factor, Cwf21)	9	17913001	PUB4-(ARM repeat superfamily protein)
3	31029001	ACT-(Putative Vinorine synthase)	9	17901001	CPR30-(Putative F-box protein CPR30)
3	31064001	gene desconhecido-(Putative Uncharacterized protein C3orf26 homolog)	9	17891001	GDI1-(Rho GDP-dissociation inhibitor 1)
3	7797001	KU70-(ATP-dependent DNA helicase 2 subunit KU70)	9	17866001	Ehd1-(EPS15 homology domain 2)
3	41994001	At3g28040-(Probably inactive leucine-rich repeat receptor-like protein kinase At3g28040)	9	17862001	unknown_gene-(Protein of unknown function (DUF3537))
3	43231001	At3g46870-(Putative uncharacterized protein)	9	17860001	COP1-(E3 ubiquitin-protein ligase COP1)
3	15195001	At5g65560-(Putative Pentatricopeptide repeat-containing protein At5g65560)	9	17834001	SRF8-(Protein STRUBBELIG-RECEPTOR FAMILY 8)
3	15161001	gene desconhecido-(Hypothetical protein)	9	17827001	KDM3B-(Transcription factor jumonji (jmjC) domain-containing protein)
3	18954001	PCMP-E10-(Pentatricopeptide repeat-containing protein At1g62260, mitochondrial)	9	17824001	unknown_gene-(Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein)
3	26665001	SPAC1093.03-(sacI homology domain-containing protein / WW domain-containing protein)	9	17808001	unknown_gene-(B-cell receptor-associated 31-like)
3	26775001	At1g05350-(Ubiquitin-like modifier-activating enzyme 5)	9	17799001	Utp6-(Putative U3 small nucleolar RNA-associated protein 6 homolog)
3	26843001	gene desconhecido-(Putative transducin family protein / WD-40 repeat family protein)	9	17797001	At1g14600-(DNA binding protein, putative)
3	1642001	RGA4-(Putative disease resistance protein RGA4)	9	17787001	ankrd13c-a-(Ankyrin repeat family protein)
3	1669001	At5g02620-(Ankyrin repeat-containing protein At5g02620)	9	17776001	At4g04670-(tRNA wybutosine-synthesizing protein 2/3/4)
3	1675001	RTNLB11-(Reticulon-like protein B11)	9	17774001	PER42-(Peroxidase 42)
3	1678001	At2g43860-(Polygalacturonase)	9	17772001	CPK2-(Calcium-dependent protein kinase)
3	2107001	MLO1-(MLO-like protein 1)	9	17765001	TT12-(Protein TRANSPARENT TESTA 12)
3	25670001	gene desconhecido-(DNA-binding enhancer protein-related)	9	17755001	ASPM-(Putative Abnormal spindle-like microcephaly-associated protein homolog)
3	25728001	COBL7-(COBRA-like protein 7)	9	17750001	unknown_gene-(Hypothetical protein)
3	25853001	APC7-(Anaphase-promoting complex subunit 7)	9	17745001	PNPLA8-(phospholipases;galactolipases)
3	25895001	gene desconhecido-(Putative DNAJ heat shock N-terminal domain-containing protein)	9	17744001	ADAL-(Putative Adenosine deaminase-like protein)
3	25993001	gene desconhecido-(Hypothetical protein)	9	17742001	CYP77A3-(Putative Cytoome P450 77A3)

3	26415001	PUB72-(U-box domain-containing protein 72)	9	17740001	BGLU45-(Putative Beta-glucosidase 45)
3	33191001	gene desconhecido-(Putative Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein)	9	17739001	unknown_gene-(plastid transcriptionally active 14)
3	33231001	BGAL9-(Beta-galactosidase 9)	9	17735001	CAB6A-(Chlorophyll a-b binding protein 6A, chloroplastic)
3	33253001	gene desconhecido-(Hypothetical protein)	9	17727001	unknown_gene-(Putative Patatin group A-3)
3	33268001	RAD50-(DNA repair protein RAD50)	9	17713001	unknown_gene-(Putative BEST Arabidopsis thaliana protein match is: myosin heavy chain-related (TAIR:AT2G34730.1))
3	30943001	KIF15-(phragmoplast-associated kinesin-related protein, putative)	9	17703001	unknown_gene-(Hypothetical protein)
3	31032001	Os04g0338000-(Probable aldo-keto reductase 2)	9	17684001	SPAC22A12.08c-(Putative Uncharacterized CDP-alcohol phosphatidyltransferase class-I family protein C22A12.08c)
3	42014001	TRANK1-(Putative P-loop containing nucleoside triphosphate hydrolases superfamily protein)	9	17677001	UPF2-(Putative Nonsense-mediated mRNA decay protein 2)
3	31784001	gene desconhecido-(mitochondrial ribosomal protein L51/S25/CI-B8 family protein)	9	17649001	ATM-(Putative Tudor/PWWP/MBT superfamily protein)
3	26661001	gene desconhecido-(unknown protein)	9	17642001	At1g11330-(G-type lectin S-receptor-like serine/threonine-protein kinase At1g11330)
3	26785001	UGT74E1-(Putative UDP-glycosyltransferase 74E1)	9	17632001	LBD1-(Hypothetical protein)
3	26792001	At5g49770-(Probable leucine-rich repeat receptor-like protein kinase At5g49770)	9	17624001	IQD1-(Putative Protein IQ-DOMAIN 1)
3	1650001	CLC-E-(Chloride channel protein CLC-e)	9	17612001	PEX16-(Peroxisome biogenesis protein 16)
3	1676001	At2g43860-(Polygalacturonase)	9	17596001	EXOSC1-(Putative Exosome complex component CSL4)
3	2116001	tyrS-(Tyrosine--tRNA ligase)	9	17592001	unknown_gene-(Protein of Unknown Function (DUF239))
3	2104001	MAP2B-(Methionine aminopeptidase 2)	9	17588001	At5g33370-(GDSL esterase/lipase At5g33370)
3	26216001	gene desconhecido-(Putative uncharacterized protein)	9	17585001	DREB2D-(Putative Dehydration-responsive element-binding protein 2D)
3	26530001	myoJ-(myosin XI B)	9	17583001	PUB9-(U-box domain-containing protein 9)
3	26537001	gene desconhecido-(Putative uncharacterized protein)	9	17578001	At5g48740-(Serine-threonine protein kinase, plant-type, putative)
3	42683001	RGA4-(Putative disease resistance protein RGA4)	9	17550001	unknown_gene-(Putative uncharacterized protein)
3	30979001	OsI_15387-(Probable aldo-keto reductase 2)	9	17548001	TGD3-(Protein TRIGALACTOSYLDIACYLGLYCEROL 3, chloroplastic)
3	42074001	LARS-(Leucine--tRNA ligase, cytoplasmic)	9	17542001	unknown_gene-(Ubiquitin carboxyl-terminal hydrolase family protein)
3	15218001	RNS2-(Ribonuclease 2)	9	17540001	unknown_gene-(Protein of unknown function (DUF707))
3	31731001	dph2-(Putative Diphthamide biosynthesis protein 2)	9	17523001	unknown_gene-(zinc finger (C2H2 type) family protein)
3	31763001	RGA1-(Putative disease resistance protein RGA1)	9	17508001	PPC6-1-(Probable protein phosphatase 2C 33)
3	31831001	gene desconhecido-(Hypothetical protein)	9	17498001	TIC20-II-(Protein TIC 20-II, chloroplastic)
3	26705001	gene desconhecido-(Putative Protein of unknown function (DUF594))	9	17497001	TIC20-II-(Putative Protein TIC 20-II, chloroplastic)
3	26726001	UGT71C2-(Putative UDP-glycosyltransferase 71C4)	9	17490001	LUC7L-(LUC7 related protein)
3	26793001	DDB_G0284757-(Cysteine proteinases superfamily protein)	9	17476001	LCAT3-(Phospholipase A(1) LCAT3)
3	25705001	lpdA-(Dihydrolipoyl dehydrogenase)	9	17475001	BBM2-(Putative AP2-like ethylene-responsive transcription factor BBM2)
3	25958001	gene desconhecido-(Hypothetical protein)	9	17469001	At2g43240-(CMP-sialic acid transporter 2)
3	26160001	ACA13-(Putative calcium-transporting ATPase 13, plasma membrane-type)	9	17463001	unknown_gene-(unknown protein)
3	26535001	gene desconhecido-(Putative uncharacterized protein)	9	17457001	BGLU42-(Beta-glucosidase 42)
3	42722001	CYC02-(Putative CYC02 protein)	9	17450001	Tubgcp2-(Putative Gamma-tubulin complex component 2)
3	42019001	At3g58180-(Deoxyhypusine hydroxylase)	9	17449001	unknown_gene-(Hypothetical protein)
3	37001	PIGO-(Alkaline-phosphatase-like family protein)	9	17441001	LBD6-(LOB domain-containing protein 6)
3	15190001	At1g61900-(Putative Uncharacterized GPI-anchored protein At1g61900)	9	17439001	DEGP10-(Protease Do-like 10, mitochondrial)
3	26786001	UGT74E1-(Putative UDP-glycosyltransferase 74E1)	9	17434001	unknown_gene-(Putative RING/U-box superfamily protein)
3	26847001	EMB976-(Putative Pentatricopeptide repeat-containing protein At5g27270)	9	17431001	VPS27-(Putative uncharacterized protein)
3	25708001	CMTA5-(Calmodulin-binding transcription activator 5)	9	17418001	unknown_gene-(Hypothetical protein)
3	25862001	gene desconhecido-(Hypothetical protein)	9	17416001	GLCAK1-(Glucuronokinase 1)
3	26159001	ACA13-(Putative calcium-transporting ATPase 13, plasma membrane-type)	9	17413001	TAF11-(TBP-associated factor 11B)
3	26545001	thiM-(Putative Hydroxyethylthiazole kinase)	9	17383001	ANTR5-(Probable anion transporter 5)
3	26547001	At4g13590-(GDT1-like protein 2, chloroplastic)	9	17382001	TGD2-(Protein TRIGALACTOSYLDIACYLGLYCEROL 2, chloroplastic)
3	26646001	gene desconhecido-(Putative uncharacterized protein)	9	7062001	hormad1-(DNA-binding HORMA family protein)
3	30935001	SEC-(Probable UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SEC)	9	7067001	PCMP-H81-(Pentatricopeptide repeat-containing protein At3g57430, chloroplastic)

3	30632001	GCN2-(Probable serine/threonine-protein kinase GCN2)
3	1655001	larp7-(Putative RNA-binding protein)
3	15179001	RGA4-(Putative disease resistance protein RGA4)
3	18959001	UBXN4-(Putative Ubiquitin-like superfamily protein)
3	26734001	RPPL1-(Putative disease resistance protein RGA4)
3	26780001	CYP71A4-(Cytoome P450 71A4)
3	26829001	RGA3-(Putative disease resistance protein RGA3)
3	1651001	SKIP35-(F-box/ankyrin repeat protein SKIP35)
3	1660001	ITPK4-(Inositol-tetrakisphosphate 1-kinase 4)
3	33278001	RGA1-(Putative disease resistance protein RGA1)
3	2094001	Dock8-(guanyl-nucleotide exchange factors;GTPase binding;GTP binding)
3	25757001	RAP2-3-(Putative Ethylene-responsive transcription factor RAP2-3)
3	42011001	Z-ISO-(15-cis-zeta-carotene isomerase, chloroplastic)
3	25810001	ABCC14-(ABC transporter C family member 14)
3	26684001	R1B-17-(Putative late blight resistance protein homolog R1B-17)
3	30976001	R1B-17-(Putative Disease resistance protein (CC-NBS-LRR class) family)
3	31072001	UGT92A1-(Putative UDP-glycosyltransferase 92A1)
3	15146001	RGA3-(Putative disease resistance protein RGA3)
3	30940001	R1B-14-(Putative Disease resistance protein (CC-NBS-LRR class) family)
4	21597001	gene desconhecido-(Putative SAUR-like auxin-responsive protein family)
4	21603001	APUM5-(Putative Pumilio homolog 5)
4	21610001	SRF5-(Protein STRUBBELIG-RECEPTOR FAMILY 5)
4	21614001	AVPL2-(Pyrophosphate-energized membrane proton pump 3)
4	21616001	gene desconhecido-(unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1754))
4	21617001	DWF5-(7-dehydrocholesterol reductase)
4	21618001	gene desconhecido-(Hypothetical protein)
4	21637001	ACA9-(Calcium-transporting ATPase 9, plasma membrane-type)
4	21642001	gene desconhecido-(proton gradient regulation 7)
4	21669001	PSYR1-(Tyrosine-sulfated glycopeptide receptor 1)
4	21670001	SPAC630.12-(Putative Uncharacterized protein C630.12)
4	21674001	AHA10-(ATPase 10, plasma membrane-type)
4	21692001	MPE3-(Pectinesterase 3)
4	21697001	ALAAT2-(Alanine aminotransferase 2, mitochondrial)
4	21722001	gene desconhecido-(Putative sequence-specific DNA binding transcription factors)
4	21724001	gene desconhecido-(BEST Arabidopsis thaliana protein match is: COP1-interacting protein-related)
4	21726001	ABCB19-(Putative ABC transporter B family member 19)
4	21735001	gene desconhecido-(Putative CONTAINS InterPro DOMAIN/s: Spt20 family)
4	21736001	NUP107-(FUNCTIONS IN: molecular_function unknown; LOCATED IN: nuclear pore))
4	21750001	DDB_G0292028-(inter-alpha-trypsin inhibitor heavy chain-related)
4	21765001	PSD-(Exportin-T)
4	21791001	RPS3C-(40S ribosomal protein S3-3)
4	21798001	gene desconhecido-(Putative Kinase-related protein of unknown function (DUF1296))
4	21799001	BRXL2-(Protein Brevis radix-like 2)
4	21824001	At1g54220-(Dihydrolipoyllysine-residue acetyltransferase component 3 of pyruvate
9	7101001	ZNF207-(zinc finger (C2H2 type) family protein)
9	7121001	QRT3-(Polygalacturonase QRT3)
9	7127001	RAN1-(Copper-transporting ATPase RAN1)
9	13392001	BAH1-(E3 ubiquitin-protein ligase BAH1)
9	13393001	unknown_gene-(InterPro DOMAIN/s: Ribosome biogenesis protein Nop16 (InterPro:IPR019002))
9	33416001	At4g35850-(Pentatricopeptide repeat-containing protein At4g35850, mitochondrial)
9	33412001	SNRPB-(Small nuclear ribonucleoprotein-associated protein B')
9	33405001	POT11-(Potassium transporter 11)
9	33381001	At3g12360-(Putative Ankyrin repeat family protein)
9	33361001	At3g46870-(Putative Pentatricopeptide repeat-containing protein At1g62350)
9	33360001	At4g19890-(Pentatricopeptide repeat-containing protein At4g19890)
9	33339001	BGLU24-(Furcatin hydrolase)
9	11293001	zpr1-(Putative Zinc finger protein ZPR1 homolog)
9	11295001	CYP75B1-(Putative Flavonoid 3'-monooxygenase)
9	5120001	At5g45160-(Protein ROOT HAIR DEFECTIVE 3 homolog 2)
9	5141001	unknown_gene-(Putative SBP (S-ribonuclease binding protein) family protein)
9	36326001	EMB2279-(Putative uncharacterized protein)
9	36324001	MUR4-(UDP-arabinose 4-epimerase 1)
9	36323001	unknown_gene-(Hypothetical protein)
9	36308001	ARA12-(Putative Subtilisin-like protease)
9	36291001	unknown_gene-(Hypothetical protein)
9	36283001	Vps54-(Putative Vacuolar protein sorting-associated protein 54)
9	36281001	PRUNE-(Predicted protein)
9	36272001	4-(Putative DNA primase/helicase)
9	36247001	unknown_gene-(Putative maternal effect embryo arrest 22)
9	36226001	C19orf6-(molecular_function unknown)
9	3770001	OLA1-(Obg-like ATPase 1)
9	3777001	Mgll-(Putative Monoglyceride lipase)
9	3806001	DRT111-(DNA-damage-repair/toleration protein DRT111, chloroplastic)
9	20782001	unknown_gene-(Putative Protein of unknown function (DUF2921))
9	20786001	unknown_gene-(Putative Heavy metal transport/detoxification superfamily protein)
9	20791001	At1g30440-(BTB/POZ domain-containing protein At1g30440)
9	20809001	ABCC2-(ABC transporter C family member 2)
9	20830001	Taf5-(Putative Transcription initiation factor TFIID subunit 5)
9	20849001	B3GALT20-(Probable beta-1,3-galactosyltransferase 20)
9	20862001	unknown_gene-(Plant protein of unknown function (DUF828))
9	23157001	CHX15-(Putative Cation/H(+) antiporter 15)
9	23146001	unknown_gene-(InterPro DOMAIN/s: Protein of unknown function DUF1084 (InterPro:IPR009457); BEST match: tobamovirus multiplication 1 (TAIR:AT4G21790.1)
9	23115001	glgA-(Putative Glycogen synthase)
9	23108001	PUP10-(Putative Probable purine permease 10)
9	23089001	CASD1-(Putative CAS1 domain-containing protein 1)
9	4079001	DHRSX-(Putative Dehydrogenase/reductase SDR family member on omosome X)
9	4081001	unknown_gene-(Magnesium transporter CorA-like family protein)
9	4082001	CDC20-(Hypothetical protein)

		dehydrogenase complex, mitochondrial)			
4	21830001	COPZ2-(Coatomer subunit zeta-2)	9	4102001	unknown_gene-(unknown protein)
4	21840001	surE-(Survival protein SurE-like phosphatase/nucleotidase)	9	6973001	unknown_gene-(Putative Mavicyanin)
4	21844001	Hrb27C-(Putative RNA-binding protein Musashi homolog 2)	9	6972001	syf2-(Putative Pre-mRNA-splicing factor syf2)
4	21846001	Nap1l1-(nucleosome assembly protein 1;2)	9	5755001	PIP2-7-(Aquaporin PIP2-7)
4	21858001	ALE2-(Receptor-like serine/threonine-protein kinase ALE2)	9	41101001	ARA12-(Putative Subtilisin-like protease)
4	21860001	RHD3-(Protein ROOT HAIR DEFECTIVE 3)	9	41083001	unknown_gene-(Basic-leucine zipper (bZIP) transcription factor family protein)
4	21866001	gene desconhecido-(Putative unknown protein; LOCATED IN: mitochondrion, plastid)	9	41071001	Os06g0717800-(Probable protein phosphatase 2C 60)
4	21873001	PLDEPSILON-(Phospholipase D epsilon)	9	41066001	unknown_gene-(Protein of unknown function (DUF3353))
4	21878001	ABCC8-(ABC transporter C family member 8)	9	41063001	VHA-B2-(V-type proton ATPase subunit B 1)
4	21884001	At3g24230-(Probable pectate lyase 9)	9	41060001	Dnajc17-(Putative DnaJ homolog subfamily C member 17)
4	21890001	chmp1-(Putative Charged multivesicular body protein 1)	9	41050001	At2g17033-(Pentatricopeptide repeat-containing protein At2g17033)
4	21892001	gene desconhecido-(Hypothetical protein)	9	41045001	FBL10-(F-box/LRR-repeat protein 10)
4	21894001	At1g51745-(Putative Uncharacterized protein At1g51745)	9	41043001	DDB_G0289893-(Putative Coiled-coil domain-containing protein 124 homolog)
4	21906001	gene desconhecido-(Plant protein of unknown function (DUF868))	9	41037001	AATL1-(Lysine histidine transporter-like 8)
4	21912001	pabpc1-b-(Putative Polyadenylate-binding protein 1-B)	9	41031001	ANAC094-(NAC domain containing protein 36)
4	21920001	IQD31-(IQ-domain 26)	9	41025001	ycf39-(Hypothetical protein)
4	21926001	At3g21360-(Clavaminate synthase-like protein At3g21360)	9	41013001	PCMP-H44-(Pentatricopeptide repeat-containing protein At2g03880, mitochondrial)
4	21968001	Ascc1-(Predicted eukaryotic LigT)	9	41002001	At4g35600-(Probable serine/threonine-protein kinase Cx32, chloroplastic)
4	21973001	gene desconhecido-(BEST match: Vacuolar sorting protein 9 (VPS9) domain); chloroplast)	9	40986001	ARID3-(AT-rich interactive domain-containing protein 3)
4	21982001	At1g79820-(Probable plastidic glucose transporter 3)	9	18001001	unknown_gene-(Putative uncharacterized protein)
4	21990001	GL2-(Homeobox-leucine zipper protein GLABRA 2)	9	17997001	unknown_gene-(Phosphoglycerate mutase family protein)
4	22010001	RPL37A-(60S ribosomal protein L37-1)	9	17994001	unknown_gene-(alpha/beta-Hydrolases superfamily protein)
4	22015001	kif6-(ATP binding microtubule motor family protein)	9	17979001	Ppp1r8-(SMAD/FHA domain-containing protein)
4	22016001	PDX12-(Probable pyridoxal biosynthesis protein PDX1.2)	9	17964001	PDS5B-(binding)
4	22025001	gene desconhecido-(Putative uncharacterized protein)	9	17963001	trm10-(Putative tRNA (guanine(9)-N1)-methyltransferase)
4	22027001	METTL22-(Putative Methyltransferase-like protein 22)	9	17954001	OPT3-(Oligopeptide transporter 3)
4	22030001	21D7-(Probable 26S proteasome non-ATPase regulatory subunit 3)	9	17946001	unknown_gene-(Hypothetical protein)
4	22032001	gene desconhecido (Protein of unknown function DUF630)	9	17926001	Narfl-(Putative Cytosolic Fe-S cluster assembly factor NARFL)
4	22033001	RHN1-(Ras-related protein RHN1)	9	17906001	IMP3-(Inositol monophosphatase 3)
4	22042001	gene desconhecido-(Putative Protein of unknown function DUF581)	9	17881001	unknown_gene-(Putative Mavicyanin)
4	22048001	RGPD4-(Putative NUP50 (Nucleoporin 50 kDa) protein)	9	17865001	RIN4-(Putative RPM1-interacting protein 4)
4	22055001	Naa15-(Putative N-alpha-acetyltransferase 15, NatA auxiliary subunit)	9	17849001	PFP-BETA-(Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta)
4	22057001	IAA16-(Putative Auxin-responsive protein IAA16)	9	17842001	H1-(Homeodomain protein ARBORKNOX1)
4	22062001	CYCA2-1-(Cyclin-A2-1)	9	17786001	unknown_gene-(Predicted protein)
4	22065001	At1g80330-(Putative Gibberellin 3-beta-dioxygenase 4)	9	17783001	SS3-(Soluble starch synthase 3, chloroplastic/amyloplastic)
4	22092001	gene desconhecido-(alpha/beta-Hydrolases superfamily protein)	9	17778001	unknown_gene-(Putative Homeodomain-like superfamily protein)
4	22105001	gene desconhecido-(Protein of unknown function, DUF642)	9	17730001	CS1-(Chorismate synthase 2, chloroplastic)
4	22113001	PWP2-(Putative Periodic tryptophan protein 2 homolog)	9	17723001	VATG-(V-type proton ATPase subunit G)
4	22114001	GRXS15-(Monothiol glutaredoxin-S15, mitochondrial)	9	17717001	PDIL1-3-(Protein disulfide isomerase-like 1-3)
4	22118001	brcc3-(Putative Lys-63-specific deubiquitinase BRCC36)	9	17695001	pgsA-(Putative CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase)
4	22125001	At5g15710-(Ubiquitin-protein ligase, putative)	9	17687001	NFIA_083260-(Putative Leukotriene A-4 hydrolase homolog)
4	22137001	At2g34160-(Uncharacterized protein At2g34160)	9	17680001	PCMP-H87-(Pentatricopeptide repeat-containing protein At3g24000, mitochondrial)
4	22138001	At1g04910-(Putative DUF246 domain-containing protein At1g04910)	9	17646001	At1g11330-(G-type lectin S-receptor-like serine/threonine-protein kinase At1g11330)
4	22140001	At1g52620-(Putative Pentatricopeptide repeat-containing protein At1g52620)	9	17639001	unknown_gene-(Hypothetical protein)
4	22143001	SEC11C-(Signal peptidase complex catalytic subunit SEC11C)	9	17623001	APL-(Putative Homeodomain-like superfamily protein)

4	22146001	gene desconhecido-(SNARE-like superfamily protein)	9	17611001	rad54l2-(P-loop containing nucleoside triphosphate hydrolases superfamily protein)
4	22149001	gene desconhecido-(Putative unknown protein; LOCATED IN: endomembrane system)	9	17599001	AMT1-2-(Ammonium transporter 1 member 2)
4	22161001	AHP6-(Histidine-containing phosphotransfer protein 6)	9	17591001	GCN1L1-(Putative Translational activator GCN1)
4	22164001	gene desconhecido-(phosphatidic acid phosphatase-related / PAP2-related)	9	17572001	unknown_gene-(Putative uncharacterized protein)
4	22167001	TPR4-(Topless-related protein 4)	9	17567001	CYP97A3-(Protein LUTEIN DEFICIENT 5, chloroplastic)
4	22170001	gene desconhecido-(Putative uncharacterized protein)	9	17555001	unknown_gene-(Protein of unknown function (DUF616))
4	22174001	gene desconhecido-(Putative uncharacterized protein)	9	17552001	unknown_gene-(Predicted protein)
4	22184001	gene desconhecido-(alpha/beta-Hydrolases superfamily protein)	9	17546001	CBSX6-(CBS domain-containing protein CBSX6)
4	22185001	mutM-(Putative Formamidopyrimidine-DNA glycosylase)	9	17451001	VHA-H-(V-type proton ATPase subunit H)
4	22202001	ABA2-(Xanthoxin dehydrogenase)	9	17442001	FRA3-(Type II inositol 1,4,5-trisphosphate 5-phosphatase FRA3)
4	22224001	At1g80640-(Probable receptor-like protein kinase At1g80640)	9	17440001	unknown_gene-(Putative uncharacterized protein)
4	22239001	NIP6-1-(Aquaporin NIP6-1)	9	17420001	Mbtps2-(Putative Peptidase M50 family protein)
4	22259001	ABCC13-(ABC transporter C family member 13)	9	17408001	Os01g0233000-(plasma-membrane associated cation-binding protein 1)
4	22265001	MRS2-1-(Magnesium transporter MRS2-1)	9	17376001	RROP1-(Apyrase)
4	22272001	HSP70-(Heat shock 70 kDa protein)	9	7053001	RPM1-(Putative Disease resistance protein RPM1)
4	22279001	gene desconhecido-(unknown protein)	9	7056001	VSR7-(Vacuolar-sorting receptor 7)
4	22284001	At1g16060-(AP2-like ethylene-responsive transcription factor At1g16060)	9	7073001	Cstf2-(Putative cleavage stimulating factor 64)
4	22285001	TULP8-(Tubby-like protein 8)	9	7084001	Tamm41-(Putative Mitochondrial translocator assembly and maintenance protein 41 homolog)
4	22295001	WAX2-(Protein WAX2)	9	7124001	TIF3C1-(Eukaryotic translation initiation factor 3 subunit C)
4	22302001	gene desconhecido-(Predicted protein)	9	7129001	At2g35010-(Putative Thioredoxin O1, mitochondrial)
4	22313001	FRI-(Putative Inactive protein FRIGIDA)	9	13390001	BGLU11-(Beta-glucosidase 11)
4	22314001	At1g09760-(U2 small nuclear ribonucleoprotein A')	9	33409001	PKL-(omatin remodeling 4)
4	22315001	CLPD-(Chaperone protein ClpD, chloroplastic)	9	33403001	unknown_gene-(unknown protein)
4	22325001	SND1-(Putative Staphylococcal nuclease domain-containing protein 1)	9	33389001	WAKL1-(Putative Wall-associated receptor kinase-like 6)
4	22359001	gene desconhecido-(Histone superfamily protein)	9	33380001	GT3-(Putative UDP-glucose flavonoid 3-O-glucosyltransferase 3)
4	22372001	pqqL-(Insulinase (Peptidase family M16) family protein)	9	33375001	NAP1-(Protein NAP1)
4	22385001	DDB_G0272282-(Protein kinase superfamily protein)	9	33365001	At3g47570-(Putative Probable LRR receptor-like serine/threonine-protein kinase At3g47570)
4	22390001	SURF1-(Surfeit locus protein 1)	9	11300001	SIRK-(Putative Senescence-induced receptor-like serine/threonine-protein kinase)
4	22403001	SEL1L2-(Putative Protein sel-1 homolog 2)	9	5136001	AGO2-(Putative Protein argonaute 2)
4	22412001	AGD11-(Putative Probable ADP-ribosylation factor GTPase-activating protein AGD11)	9	36309001	At2g01290-(Putative Probable ribose-5-phosphate isomerase)
4	22425001	FKBP17-2-(Peptidyl-prolyl cis-trans isomerase FKBP17-3, chloroplastic)	9	36287001	Os06g0675700-(Alpha-glucosidase)
4	22429001	CTR1-(Hypothetical protein)	9	36234001	Os02g0491600-(Putative germin-like protein 2-1)
4	22430001	CTR1-(protein tyrosine kinase family protein)	9	20833001	BRCA1-(Putative Protein BREAST CANCER SUSCEPTIBILITY 1 homolog)
4	22438001	DRB4-(Putative uncharacterized protein)	9	20856001	unknown_gene-(Remorin family protein)
4	22441001	PCMP-H24-(Pentatricopeptide repeat-containing protein At4g02750)	9	23067001	BOU-(Mitochondrial carnitine/acylcarnitine carrier-like protein)
4	22449001	wdpA-(Putative 66 kDa stress protein)	9	23066001	PSP-(Phosphoserine phosphatase, chloroplastic)
4	22459001	Gspt1-(Translation elongation factor EF1A/initiation factor IF2gamma family protein)	9	23058001	SPCPB16A4.05c-(Uncharacterized urease accessory protein ureG-like)
4	22482001	gene desconhecido-(Uncharacterised conserved protein UCP031088, alpha/beta hydrolase)	9	754001	FLS2-(LRR receptor-like serine/threonine-protein kinase FLS2)
4	22489001	ykfB-(Putative L-Ala-D/L-Glu epimerase)	9	4077001	ctpA-(Putative Carboxyl-terminal-processing protease)
4	22492001	kif4-(ATP binding microtubule motor family protein)	9	4080001	unknown_gene-(Putative Kinase-related protein of unknown function (DUF1296))
4	22500001	gene desconhecido-(Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein)	9	4085001	MCA0497-(Putative pterin-4-alpha-carbinolamine dehydratase)
4	22501001	DELTA-ADR-(AP-3 complex subunit delta)	9	41090001	ARA12-(Putative Subtilisin-like protease)
4	22514001	NAC100-(NAC domain containing protein 58)	9	41082001	unknown_gene-(high-affinity nickel-transport family protein)
4	22522001	COL16-(Putative Zinc finger protein CONSTANS-LIKE 16)	9	41080001	SKP1A-(SKP1-like protein 1A)
4	22544001	ASPG1-(Putative Protein ASPARTIC PROTEASE IN GUARD CELL 1)	9	41056001	unknown_gene-(Hypothetical protein)
4	22572001	FAM116A-(Putative Protein FAM116A)	9	41053001	unknown_gene-(Hypothetical protein)
4	22590001	Eif2b4-(Putative Translation initiation factor eIF-	9	41047001	MSL8-(Putative Mechanosensitive ion channel protein 8)

		2B subunit delta)			
4	22600001	At2g25060-(Putative Early nodulin-like protein 1)	9	41044001	ROPGEF1-(Rop guanine nucleotide exchange factor 1)
4	22606001	GPATCH1-(SWAP (Suppressor-of-White-APricot)/surp domain-containing protein)	9	41035001	POPTRDRAFT_821063-(Probable alanine--tRNA ligase, chloroplastic)
4	22618001	AAE17-(Probable acyl-activating enzyme 17, peroxisomal)	9	41019001	IDH1-(Isocitrate dehydrogenase [NAD] regulatory subunit 1, mitochondrial)
4	22621001	gene desconhecido-(Putative tetraspanin11)	9	41011001	Acy1-(Putative Aminoacylase-1)
4	22631001	udkC-(Putative Uridine-cytidine kinase C)	9	41005001	At1g08570-(Thioredoxin-like 1-1, chloroplastic)
4	22635001	Os02g0581300-(ASC1-like protein 1)	9	41004001	GAUT3-(Probable galacturonosyltransferase 3)
4	22638001	sppA-(signal peptide peptidase)	9	40994001	CPK4-(Calcium-dependent protein kinase 4)
4	22639001	gene desconhecido-(Hypothetical protein)	9	17986001	At4g31140-(Glucan endo-1,3-beta-glucosidase 5)
4	22648001	gene desconhecido-(Hypothetical protein)	9	17944001	P67-(Pentatricopeptide repeat-containing protein At4g16390, chloroplastic)
4	22649001	RING1-(Putative RING/U-box superfamily protein)	9	17903001	TDT-(Tonoplast dicarboxylate transporter)
4	22666001	UGT89B1-(Putative UDP-glycosyltransferase 89B1)	9	17879001	Acer3-(Putative Alkaline ceramidase 3)
4	22672001	BIM1-(Putative Transcription factor BIM1)	9	17657001	unknown_gene-(Putative unknown protein)
4	22678001	gene desconhecido-(Putative uncharacterized protein)	9	17647001	At1g11330-(G-type lectin S-receptor-like serine/threonine-protein kinase At1g11330)
4	22681001	At2g18110-(Elongation factor 1-delta)	9	17584001	unknown_gene-(Putative uncharacterized protein)
4	22690001	SD25-(Putative G-type lectin S-receptor-like serine/threonine-protein kinase SD2-5)	9	17551001	unknown_gene-(unknown protein)
4	22692001	ASP-(Miraculin)	9	17549001	unknown_gene-(Haloacid dehalogenase-like hydrolase (HAD) superfamily protein)
4	22705001	CDP1-(Plastid division protein CDP1, chloroplastic)	9	17532001	At5g36290-(GDT1-like protein 3)
4	22738001	At1g11330-(Putative Cysteine-rich receptor-like protein kinase 25)	9	17529001	Cwc22-(Putative Pre-mRNA-splicing factor CWC22 homolog)
4	22739001	SD17-(Putative Receptor-like serine/threonine-protein kinase SD1-7)	9	17515001	GSVIVT00037159001-(Peroxidase 5)
4	22747001	STR8-(Rhodanese-like domain-containing protein 8, chloroplastic)	9	17502001	At1g65240-(Aspartic proteinase-like protein 2)
4	22753001	gene desconhecido-(CONTAINS InterPro DOMAIN/s: Nucleoporin protein Ndc1-Nup)	9	17486001	At5g40400-(Pentatricopeptide repeat-containing protein At5g40400)
4	22756001	CYP716B2-(Putative Cytoome P450 716B2)	9	17462001	HTATSF1-(RNA binding (RRM/RBD/RNP motifs) family protein)
4	22765001	POLR3B-(DNA-directed RNA polymerase III subunit RPC2)	9	17453001	unknown_gene-(Haloacid dehalogenase-like hydrolase (HAD) superfamily protein)
4	22768001	gene desconhecido-(unknown protein)	9	17415001	unknown_gene-(Putative Protein of unknown function (DUF1639))
4	22769001	NAC74-(NAC domain containing protein 57)	9	17404001	unknown_gene-(C4916nucleus-encoded thylakoid protein)
4	22770001	HDG11-(Homeobox-leucine zipper protein HDG11)	9	17400001	RPK2-(Putative LRR receptor-like serine/threonine-protein kinase RPK2)
4	22775001	CNGC20-(Probable cyclic nucleotide-gated ion channel 20, chloroplastic)	9	7094001	ERG-(GTP-binding protein ERG)
4	22778001	gene desconhecido-(unknown protein;chloroplast)	9	33349001	petJ-(Cytoome c6, chloroplastic)
4	22802001	CALM1-(Calmodulin)	9	5108001	pds5b-b-(Putative uncharacterized protein)
4	22806001	At4g01400-(Pentatricopeptide repeat-containing protein At4g01400, mitochondrial)	9	36221001	WAK5-(Putative Wall-associated receptor kinase 5)
4	22816001	gene desconhecido-(Putative Cysteine/Histidine-rich C1 domain family protein)	9	36216001	ERI2-(Putative uncharacterized protein)
4	22823001	preA-(pyrimidine 1)	9	3775001	nagk-(Putative N-acetyl-D-glucosamine kinase)
4	22836001	gene desconhecido-(ARM repeat superfamily protein)	9	3776001	WAP-(Putative WPP domain-associated protein (Fragment))
4	22849001	gene desconhecido-(Hypothetical protein)	9	17129001	ATTRANS-(Phospho-N-acetylmuramoyl-pentapeptide-transferase homolog)
4	42548001	GTE11-(Transcription factor GTE11)	9	6976001	trappc2l-(Putative Trafficking protein particle complex subunit 2-like protein)
4	42556001	gene desconhecido-(Nucleic acid-binding, OB-fold-like protein)	9	41110001	SRG1-(Protein SRG1)
4	42557001	LHT1-(Lysine histidine transporter 1)	9	41103001	EXO1-(CDSuclease 1)
4	42569001	gene desconhecido-(Putative Predicted protein)	9	41084001	PERK11-(Putative Protein kinase protein with adenine nucleotide alpha hydrolases-like domain)
4	42574001	At4g24820-(Probable 26S proteasome non-ATPase regulatory subunit 6)	9	41034001	EXLA1-(Expansin-like A1)
4	42576001	gene desconhecido-(unknown protein;mitochondrion)	9	40996001	MSSP2-(Monosaccharide-sensing protein 2)
4	42589001	gene desconhecido-(Hypothetical protein)	9	40993001	unknown_gene-(Putative uncharacterized protein)
4	42600001	AZG2-(Adenine/guanine permease AZG2)	9	17992001	unknown_gene-(Putative Senescence-associated protein)
4	42602001	gene desconhecido-(RING/U-box superfamily protein)	9	17968001	At1g12150-(Putative WEB family protein At1g12150)
4	42632001	PDCD4-(Putative Programmed cell death protein 4)	9	17965001	AGD11-(Putative Probable ADP-ribosylation factor GTPase-activating protein AGD11)
4	42638001	EMB1006-(Pentatricopeptide repeat-containing protein At5g50280, chloroplastic)	9	17962001	NFYB6-(Leafy cotyledon 1-like protein)

4	42639001	At3g48380-(Probable Ufm1-specific protease)	9	17882001	RAP74-(Transcription initiation factor IIF subunit alpha)
4	42647001	At1g67000-(Putative Probable receptor-like protein kinase At1g67000)	9	17878001	unknown_gene-(Putative Protein of unknown function (DUF506))
4	42664001	SOBIR1-(Leucine-rich repeat receptor-like serine/threonine/tyrosine-protein kinase SOBIR1)	9	17820001	unknown_gene-(Putative Stigma-specific Stig1 family protein)
4	37271001	RFS2-(Probable galactinol--sucrose galactosyltransferase 2)	9	17712001	Mgll-(Putative Monoglyceride lipase)
4	37279001	trpD-(Putative Anthranilate phosphoribosyltransferase)	9	17678001	PHT1-11-(Inorganic phosphate transporter 1-11)
4	37280001	Iars-(Isoleucine--tRNA ligase, cytoplasmic)	9	17645001	At1g11330-(G-type lectin S-receptor-like serine/threonine-protein kinase At1g11330)
4	37281001	STR11-(Rhodanese-like domain-containing protein 11, chloroplastic)	9	17579001	VDE1-(Violaxanthin de-epoxidase, chloroplastic)
4	37290001	At1g74260-(Probable phosphoribosylformylglycinamidine synthase, chloroplastic/mitochondrial)	9	17481001	MEE12-(Putative TATA box-binding protein-associated factor RNA polymerase I subunit B)
4	37303001	AFC2-(Serine/threonine-protein kinase AFC2)	9	17480001	At3g03300-(Endoribonuclease Dicer homolog 2)
4	37333001	At3g48250-(Putative Pentatricopeptide repeat-containing protein At3g48250, chloroplastic)	9	17461001	mnmA-(Putative tRNA-specific 2-thiouridylase MnmA)
4	37349001	NBR1-(Putative ubiquitin-associated (UBA)/TS-N domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein)	9	17445001	ilvH-(Acetolactate synthase small subunit)
4	37371001	gene desconhecido-(Putative Octicosapeptide/Phox/Bem1p family protein)	9	17419001	arcB-(Putative Actin-related protein 2/3 complex subunit 2)
4	37383001	HDA6-(Histone deacetylase 6)	9	33422001	CCT3-(T-complex protein 1 subunit gamma)
4	37393001	gene desconhecido-(Putative Predicted protein)	9	11289001	VAMP722-(Vesicle-associated membrane protein 722)
4	37398001	TAR2-(Tryptophan aminotransferase-related protein 2)	9	36257001	At4g20830-(Reticuline oxidase-like protein)
4	5256001	plekhm3-(Putative Phox (PX) domain-containing protein)	9	3774001	At1g30570-(Probable receptor-like protein kinase At1g30570)
4	5314001	gene desconhecido-(Putative Disease resistance-responsive (dirigent-like protein) family protein)	9	20744001	Ppp6r3-(SIT4 phosphatase-associated family protein)
4	5318001	CDC48-(Cell division cycle protein 48 homolog)	9	20854001	At1g13570-(Putative F-box/FBD/LRR-repeat protein At1g13570)
4	3254001	CNGC16-(Probable cyclic nucleotide-gated ion channel 16)	9	23073001	RPPL1-(Putative Ankyrin repeat family protein)
4	3257001	ALDH2B4-(Putative aldehyde dehydrogenase 2C4)	9	41099001	TP53I3-(Putative Quinone oxidoreductase PIG3)
4	3271001	ATL1-(Putative RING-H2 finger protein ATL1)	9	17749001	PPR336-(Pentatricopeptide repeat-containing protein At1g61870, mitochondrial)
4	11361001	RAC3-(Rac-like GTP-binding protein 3)	9	17736001	sll0005-(Putative Uncharacterized protein slr1919)
4	11363001	gene desconhecido-(Putative BAH domain ;TFIIS helical bundle-like domain)	9	17715001	Mgll-(Putative Monoglyceride lipase)
4	11367001	gene desconhecido (Putative unknown protein)	9	17689001	At2g37250-(Probable adenylate kinase 1, chloroplastic)
4	11374001	SF3-(Pollen-specific protein SF3)	9	17633001	LBD1-(Hypothetical protein)
4	18886001	UGT83A1-(Putative UDP-glycosyltransferase 83A1)	9	17577001	unknown_gene-(Predicted protein)
4	18891001	gene desconhecido-(BEST match: dentin sialophosphoprotein-related)	9	17458001	AAE14-(2-succinylbenzoate--CoA ligase, chloroplastic/peroxisomal)
4	18904001	CYP75B2-(Flavonoid 3'-monooxygenase)	9	17424001	CPX-(Coproporphyrinogen-III oxidase, chloroplastic)
4	18302001	gene desconhecido-(Putative Adenine nucleotide alpha hydrolases-like superfamily protein)	9	7065001	topA-(Putative DNA topoisomerase 1)
4	18298001	gene desconhecido-(Putative Uncharacterized protein)	9	33420001	ARA12-(Putative Subtilisin-like protease)
4	18290001	gene desconhecido-(Putative Calmodulin binding protein-like)	9	33386001	WAKL9-(Hypothetical protein)
4	18261001	pdxH-(Pyridoxine/pyridoxamine 5'-phosphate oxidase)	9	33341001	IMPL1-(Phosphatase IMPL1, chloroplastic)
4	18260001	ALDH10A8-(Betaine aldehyde dehydrogenase 1, chloroplastic)	9	33334001	At2g22425-(Probable signal peptidase complex subunit 1)
4	35881001	At4g35600-(Putative Probable serine/threonine-protein kinase Cx32, chloroplastic)	9	11294001	unknown_gene-(BEST Arabidopsis thaliana protein match is: exocyst complex component 84B
4	35886001	At4g35600-(Putative Probable serine/threonine-protein kinase Cx32, chloroplastic)	9	3767001	KCS21-(3-ketoacyl-CoA synthase 21)
4	35887001	EX1-(Putative Protein EXECUTER 1, chloroplastic)	9	3778001	GSTU15-(Glutathione S-transferase U15)
4	35910001	PPT1-(4-hydroxybenzoate polyprenyltransferase, mitochondrial)	9	20779001	CAT1-(Cationic amino acid transporter 1)
4	35912001	RPP8-(Putative Disease resistance protein RPP8)	9	41065001	crtQ-(Putative uncharacterized protein)
4	35943001	ATM-(Putative Serine/threonine-protein kinase ATM)	9	41057001	B'ETA-(Putative Serine/threonine protein phosphatase 2A 59 kDa regulatory subunit B' eta isoform)
4	35955001	At5g62930-(GDSL esterase/lipase At5g62930)	9	41048001	ATR-(Serine/threonine-protein kinase ATR)
4	35961001	PPT2-(Phosphoenolpyruvate/phosphate translocator 2, chloroplastic)	9	41038001	AATL1-(Putative Lysine histidine transporter-like 8)
4	35962001	At1g50180-(Putative Probable disease resistance RPP8-like protein 2)	9	40992001	At4g35335-(CMP-sialic acid transporter 4)

4	4359001	At3g47570-(Putative Probable LRR receptor-like serine/threonine-protein kinase At3g47570)
4	40725001	LECRK41-(L-type lectin-domain containing receptor kinase IV.1)
4	40728001	LinJ25.1380-(Excinuclease ABC, C subunit, N-terminal)
4	40767001	DCTPP1-(dCTP pyrophosphatase 1)
4	40773001	gene desconhecido-(mitochondrial proton-transporting ATP synthase complex assembly)
4	40776001	At5g22810-(GDSL esterase/lipase At5g22810)
4	4733001	DHX16-(Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16)
4	4745001	ARID2-(BEST match: ELM2 domain-containing protein)
4	2602001	PCMP-H38-(Putative Pentatricopeptide repeat-containing protein At5g48910)
4	42312001	Ado-(Putative 2-aminoethanethiol dioxygenase)
4	42322001	gene desconhecido-(C2 calcium/lipid-binding plant phosphoribosyltransferase family protein)
4	42327001	gene desconhecido-(Protein of unknown function (DUF1118))
4	42331001	At5g47150-(Putative uncharacterized protein)
4	42334001	gene desconhecido-(Integral membrane HPP family protein)
4	42350001	At5g62680-(Probable peptide/nitrate transporter At5g62680)
4	42367001	LBD27-(LOB domain-containing protein, putative)
4	42368001	ABCC3-(ABC transporter C family member 3)
4	42372001	At1g74750-(Pentatricopeptide repeat-containing protein At1g74750)
4	42385001	SPAC2F3.16-(Putative RING finger and CHY zinc finger domain-containing protein 1)
4	42389001	HIPL1-(HIPL1 protein)
4	42395001	Os03g0694000-(Putative Germin-like protein 3-6)
4	42399001	Tnpo3-(Putative Transportin-3)
4	42413001	ints3-(embryo defective 2739)
4	42418001	FH8-(Putative alpha/beta-Hydrolases superfamily protein)
4	35712001	DDB_G0278493-(Probable adenylate kinase isoenzyme 6)
4	35737001	GGM13-(Putative uncharacterized protein)
4	35757001	VIT_19s0014g04930-((-)-germacrene D synthase)
4	35758001	VIT_19s0014g04930-((-)-germacrene D synthase)
4	35773001	gene desconhecido-(alpha/beta-Hydrolases superfamily protein)
4	35787001	At1g26850-(Probable methyltransferase PMT2)
4	35789001	At4g35600-(Putative Probable serine/threonine-protein kinase Cx32, chloroplastic)
4	35796001	Set-(NAP1-related protein 2)
4	35806001	CDN1-(Putative uncharacterized protein)
4	35814001	HVA22A-(HVA22-like protein a)
4	35848001	SKIP11-(Hypothetical protein)
4	35857001	ABCA7-(ABC transporter A family member 7)
4	13574001	B3GALT19-(Probable beta-1,3-galactosyltransferase 19)
4	21605001	BT1-(Putative Solute carrier family 25 member 42)
4	21608001	gene desconhecido-(Polyketide cyclase/dehydrase and lipid transport superfamily protein)
4	21636001	MTPC4-(Metal tolerance protein (Fragment))
4	21640001	Nop2-(S-adenosyl-L-methionine-dependent methyltransferases superfamily protein)
4	21647001	exoc8-(exocyst complex component 84B)
4	21652001	INRPK1-(Receptor-like protein kinase)
4	21706001	ARID4-(AT-rich interactive domain-containing protein 4)
4	21708001	ARA12-(Subtilisin-like protease)
4	21718001	HSP17.4B-(17.4 kDa class III heat shock protein)
9	17641001	At1g11330-(G-type lectin S-receptor-like serine/threonine-protein kinase At1g11330)
9	17621001	unknown_gene-(Hypothetical protein)
9	17406001	PUP4-(Probable purine permease 4)
9	20800001	OXP1-(5-oxoprolinase)
9	6978001	Rbm39-(Putative Splicing factor, CC1-like)
9	41000001	unknown_gene-(EXORDIUM like 5)
9	17825001	leuS-(Leucine--tRNA ligase)
9	17690001	PRR73-(Two-component response regulator-like PRR73)
9	41100001	TP53I3-(Putative Quinone oxidoreductase PIG3)
9	41094001	At4g18975-(Pentatricopeptide repeat-containing protein At4g18975, chloroplastic)
9	17852001	unknown_gene-(Putative RING/U-box superfamily protein)
9	20787001	unknown_gene-(Putative Protein of unknown function (DUF2921))
9	40998001	DFR-(Putative Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase)
9	17873001	CNF02430-(Putative Acyl-protein thioesterase 1)
9	17761001	RBP45-(Putative uncharacterized protein)
9	17407001	MCM6-(Putative DNA replication licensing factor MCM6)
9	4105001	CASKIN1-(Putative Ankyrin repeat family protein)
9	5099001	At3g02645-(Putative UPF0481 protein At3g02645)
10	24436001	At1g79600-(Uncharacterized aarF domain-containing protein kinase At1g79600, chloroplastic)
10	24459001	BZIP60-(Putative BZIP transcription factor protein)
10	24474001	PPD3-(PsbP domain-containing protein 3, chloroplastic)
10	24476001	SDR42E1-(Putative Short-chain dehydrogenase/reductase family 42E member 1)
10	24487001	MLO5-(MLO-like protein 5)
10	24488001	At2g33640-(Probable S-acyltransferase At2g33640)
10	24491001	GAPB-(Glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic)
10	24499001	At5g42350-(F-box/kelch-repeat protein At5g42350)
10	24500001	PUB43-(U-box domain-containing protein 43)
10	24513001	CAT3-(Catalase)
10	24517001	unknown_gene-(Hypothetical protein)
10	24520001	At2g30600/At2g30610-(BTB/POZ domain-containing protein At2g30600)
10	24536001	At4g35230-(Probable serine/threonine-protein kinase At4g35230)
10	24537001	FTSH-(ATP-dependent zinc metalloprotease FTSH, chloroplastic)
10	24539001	unknown_gene-(Hypothetical protein)
10	24547001	ECPP44-(Phosphoprotein ECPP44)
10	24550001	unknown_gene-(unknown protein)
10	24555001	ROPGEF1-(Rop guanine nucleotide exchange factor 1)
10	24562001	ECH2-(Enoyl-CoA hydratase 2, peroxisomal)
10	24566001	MSL8-(Putative Mechanosensitive ion channel protein 8)
10	24575001	PLDDELTA-(Phospholipase D delta)
10	24576001	PLDDELTA-(Phospholipase D delta)
10	24577001	Hiatl1-(Putative Major facilitator superfamily protein)
10	24591001	unknown_gene-(Thioredoxin superfamily protein)
10	24594001	xlnD-(Putative 3-hydroxybenzoate 6-hydroxylase 1)
10	24600001	At1g20180-(Putative UPF0496 protein At1g20180)
10	24601001	CAD6-(Probable cinnamyl alcohol dehydrogenase 6)
10	24602001	Larp1-(Putative winged-helix DNA-binding transcription factor family protein)

4	21727001	gene desconhecido-(Plant protein of unknown function (DUF936))	10	24612001	ptges2-(Glutathione S-transferase family protein)
4	21734001	GLO3-(Peroxisomal (S)-2-hydroxy-acid oxidase GLO3)	10	24619001	CLV1-(Receptor protein kinase CLAVATA1)
4	21738001	TIAL1-(RNA-binding (RRM/RBD/RNP motifs) family protein)	10	24629001	At1g18250-(Thaumatin-like protein)
4	21743001	Exoc7-(exocyst subunit exo70 family protein D1)	10	24650001	unknown_gene-(Hypothetical protein)
4	21755001	gene desconhecido-(Putative exocyst subunit exo70 family protein D3)	10	24664001	E2FC-(Putative Uncharacterized protein)
4	21803001	AL5-(PHD finger protein ALFIN-LIKE 5)	10	24670001	Os09g0533900-(Endoglucanase 24)
4	21815001	gene desconhecido-(Putative uncharacterized protein)	10	24681001	unknown_gene-(DNA-directed RNA polymerases)
4	21847001	CWINV1-(Beta-fructofuranosidase, insoluble isoenzyme CWINV1)	10	24688001	IQD32-(Putative Protein IQ-DOMAIN 32)
4	21859001	HTH-(Protein HOTHEAD)	10	24690001	RF2b-(Putative Basic-leucine zipper (bZIP) transcription factor family protein)
4	21864001	BGAL1-(Beta-galactosidase)	10	24703001	ARC6-(Protein ACCUMULATION AND REPLICATION OF CHLOROPLASTS 6, chloroplastic)
4	21886001	gene desconhecido-(Putative uncharacterized protein)	10	24713001	Mcrs1-(Putative Forkhead-associated (FHA) domain-containing protein)
4	21889001	gdh-(Putative NADP-specific glutamate dehydrogenase)	10	24718001	At1g62020-(Coatomer subunit alpha-1)
4	21925001	PERK8-(Putative proline-rich receptor-like protein kinase PERK11)	10	24719001	unknown_gene-(Putative SHI-related sequence 5)
4	21928001	mms19-(Putative ARM repeat superfamily protein)	10	24723001	unknown_gene-(Auxin-induced protein 5NG4)
4	21932001	MODA-(NADP-dependent malic enzyme, chloroplastic)	10	24734001	BGAL3-(Beta-galactosidase 3)
4	21940001	hhp1-(Protein kinase family protein)	10	24744001	hflX-(Putative GTPase HflX)
4	21953001	CPN60B1-(RuBisCO large subunit-binding protein subunit beta, chloroplastic)	10	24754001	BHLH110-(Putative Transcription factor bHLH110)
4	21958001	gene desconhecido-(unknown protein)	10	24779001	At1g19525-(Pentatricopeptide repeat-containing protein At1g19525)
4	21969001	alr3466-(Putative Uncharacterized WD repeat-containing protein alr3466)	10	24781001	At4g24660-(Putative ZF-HD homeobox protein At4g24660)
4	21979001	AAE13-(Malonate--CoA ligase)	10	24821001	unknown_gene-(Protein of unknown function (DUF620))
4	21985001	GC5-(Golgin candidate 5)	10	24827001	CSN4-(COP9 signalosome complex subunit 4)
4	22018001	gene desconhecido-(sequence-specific DNA binding transcription factors)	10	24832001	MGP-(C2H2-like zinc finger protein)
4	22045001	SULTR3;4-(Probable sulfate transporter 3.4)	10	24838001	At4g16580-(Probable protein phosphatase 2C 55)
4	22050001	gene desconhecido-(Putative CASC3/Barentsz eIF4AIII binding)	10	24839001	unknown_gene-(Nucleotide-diphospho-sugar transferase family protein)
4	22068001	20ox1-(Putative Flavonol synthase/flavanone 3-hydroxylase)	10	24851001	guaA-(Putative DNA-3-methyladenine glycosylase 1)
4	22081001	gene desconhecido (unknown protein)	10	24853001	RCE1-(NEDD8-conjugating enzyme Ubc12)
4	22159001	BCB-(Putative Umecyanin)	10	24854001	GGPS1-(Geranylgeranyl pyrophosphate synthase, chloroplastic)
4	22173001	dnaJ-(Chaperone protein DnaJ)	10	24863001	unknown_gene-(Hypothetical protein)
4	22187001	cluA-(Tetratricopeptide repeat (TPR)-like superfamily protein)	10	24874001	At1g47510-(Type I inositol 1,4,5-trisphosphate 5-phosphatase 11)
4	22199001	TPL-(Protein TOPLESS)	10	24903001	ABA3-(Pyridoxal phosphate (PLP)-dependent transferases superfamily protein)
4	22263001	At1g80880-(Predicted protein)	10	24905001	PEX3-(Pollen-specific leucine-rich repeat extensin-like protein 4)
4	22273001	At2g24130-(Putative leucine-rich repeat receptor-like serine/threonine-protein kinase At2g24130)	10	24919001	At4g33300-(Probable disease resistance protein At4g33300)
4	22291001	PR2-(Glucan endo-1,3-beta-glucosidase, acidic isoform GI9)	10	24922001	MEKK1-(Putative uncharacterized protein)
4	22318001	RBOHC-(Respiratory burst oxidase homolog protein C)	10	24923001	TUBGCP5-(Spc97 / Spc98 family of spindle pole body (SBP) component)
4	22341001	gene desconhecido (unknown protein)	10	34996001	unknown_gene-(Protein of unknown function, DUF547)
4	22352001	gene desconhecido-(Protein Transporter, Pam16)	10	34991001	UROS-(Uroporphyrinogen-III synthase, chloroplastic)
4	22383001	RKL1-(Probable inactive receptor kinase At1g48480)	10	34987001	unknown_gene-(Calcineurin-like metallo-phosphoesterase superfamily protein)
4	22414001	PIN1-(Auxin efflux carrier component 1)	10	34986001	ZAT3-(Zinc finger protein ZAT3)
4	22419001	WOX1-(Putative WUSCHEL-related homeobox 1)	10	34985001	unknown_gene-(P-loop containing nucleoside triphosphate hydrolases superfamily protein)
4	22420001	At1g18250-(Thaumatin-like protein)	10	34980001	DCL-(Protein DCL, chloroplastic)
4	22443001	At4g28100-(Putative Uncharacterized GPI-anchored protein At4g28100)	10	34977001	trc-(Serine/threonine-protein kinase tricorner)
4	22490001	gene desconhecido-(Probable non-specific lipid-transfer protein AKCS9)	10	34956001	BKI1-(Putative BRI1 kinase inhibitor 1)
4	22495001	At1g67000-(Putative Probable receptor-like protein kinase At1g67000)	10	34955001	At1g47380-(Probable protein phosphatase 2C 12)
4	22497001	At1g67000-(Putative Probable receptor-like protein kinase At1g67000)	10	34950001	unknown_gene-(unknown protein)
4	22503001	SPAC2F3.16-(Putative RING finger and CHY zinc finger domain-containing protein 1)	10	34946001	unknown_gene-(unknown protein)

4	22541001	CASP-(Protein CASP)	10	34930001	HO2-(Probable inactive heme oxygenase 2, chloroplastic)
4	22574001	gene desconhecido-(Transmembrane Fragile-X-F-associated protein)	10	34924001	WDR18-(Putative WD repeat-containing protein 18)
4	22591001	gene desconhecido-(BED zinc finger ;hAT family dimerisation domain)	10	34923001	HSFB4-(Heat stress transcription factor B-4)
4	22599001	ccmH-(Putative Cytoome c-type biogenesis protein CcmH)	10	34915001	ARA12-(Putative Subtilisin-like protease)
4	22680001	DOF5.4-(Putative Dof zinc finger protein DOF5.4)	10	34913001	SPT-(Putative uncharacterized protein)
4	22751001	At1g78910-(RNA pseudourine synthase 3, mitochondrial)	10	34901001	unknown_gene-(C2H2-like zinc finger protein)
4	22754001	FLS2-(Putative LRR receptor-like serine/threonine-protein kinase FLS2)	10	34900001	unknown_gene-(SPla/RYanodine receptor (SPRY) domain-containing protein)
4	22755001	gene desconhecido (unknown protein)	10	34889001	Os04g0650000-(Oryzain alpha chain)
4	22759001	RAB15-(Predicted protein)	10	34879001	At3g16150-(Probable isoaspartyl peptidase/L-asparaginase 2)
4	22780001	DNAJC19-(Chaperone DnaJ-domain superfamily protein)	10	34858001	Cirh1a-(Putative Cirhin)
4	22784001	C14orf102-(Putative UPF0614 protein C14orf102)	10	34854001	SCPL9-(Serine carboxypeptidase-like 9)
4	22812001	ssu72-(RNA polymerase II subunit A C-terminal domain phosphatase SSU72)	10	34852001	FKBP62-(Peptidyl-prolyl cis-trans isomerase FKBP62)
4	22813001	gene desconhecido (unknown protein)	10	34851001	unknown_gene-(Putative Uncharacterised conserved protein UCP031279)
4	22830001	BHLH137-(Putative uncharacterized protein)	10	34847001	PK1-(Putative receptor protein kinase ZmPK1)
4	22837001	VIT_17s0000g00560-(CASP-like protein VIT_17s0000g00560)	10	34833001	CYP81E1-(Putative Isoflavone 2'-hydroxylase)
4	22841001	Msed_1424-(Putative Succinate-semialdehyde dehydrogenase (acetylating))	10	34807001	CYP81E1-(Putative Isoflavone 2'-hydroxylase)
4	22842001	gene desconhecido-(Putative Surfeit locus protein 6)	10	34804001	APUM12-(Putative Predicted protein)
4	22844001	Hnrnpab-(Putative RNA-binding (RRM/RBD/RNP motifs) family protein)	10	34802001	unknown_gene-(Protein of unknown function (DUF620))
4	22845001	gene desconhecido (unknown protein)	10	34801001	unknown_gene-(Putative F-BOX WITH WD-40 2)
4	94001	gene desconhecido (unknown protein)	10	34798001	SPCC757.02c-(NAD(P)-binding Rossmann-fold superfamily protein)
4	95001	Os10g0113100-(Putative Probable NAD(P)H-dependent oxidoreductase 2)	10	34793001	rmt2-(Putative Arginine N-methyltransferase 2)
4	10619001	gene desconhecido-(Protein of unknown function (DUF1218))	10	34789001	unknown_gene-(Putative TBP-associated factor 4)
4	42526001	Dnajb12-(Putative DNAJ heat shock N-terminal domain-containing protein)	10	34786001	unknown_gene-(Putative uncharacterized protein)
4	42535001	CBSCBSPB5-(CBS domain-containing protein CBSCBSPB5)	10	34778001	unknown_gene-(Putative nucleic acid binding)
4	42541001	Fignl1-(Putative ATPase family AAA domain-containing protein 1)	10	34739001	unknown_gene-(Uncharacterized protein)
4	42563001	AAO3-(Abscisic-aldehyde oxidase)	10	34737001	unknown_gene-(BEST match: FBD, F-box and Leucine Rich Repeat domains containing protein (TAIR:AT1G22000.1); vacuole)
4	42585001	Telo2-(embryo defective 2423)	10	34733001	unknown_gene-(Hypothetical protein)
4	42599001	Klhdc4-(Putative Kelch domain-containing protein 4)	10	34728001	unknown_gene-(Hypothetical protein)
4	42622001	REF6-(Lysine-specific demethylase REF6)	10	34726001	ATL76-(Putative RING/U-box superfamily protein)
4	42655001	tipD-(Putative Autophagy-related protein 16-1)	10	34723001	RHA2A-(Putative Predicted protein)
4	42656001	AGO4A-(Protein argonaute 4A)	10	34715001	PPCS2-(Phosphopantothenate--cysteine ligase 2)
4	42661001	gene desconhecido (unknown protein)	10	34711001	unknown_gene-(Putative Mitochondrial transcription termination factor family protein)
4	37310001	gene desconhecido-(Putative uncharacterized protein)	10	34677001	At1g71810-(Uncharacterized aarF domain-containing protein kinase At1g71810, chloroplastic)
4	37348001	PCMP-H32-(Putative Pentatricopeptide repeat-containing protein At2g22070)	10	34638001	At4g40080-(Putative clathrin assembly protein At4g40080)
4	37375001	gene desconhecido-(Putative Adenine nucleotide alpha hydrolases-like superfamily protein)	10	34624001	ATHB-16-(Putative Homeobox-leucine zipper protein ATHB-16)
4	37379001	maoII-(Putative Copper methylamine oxidase)	10	34614001	unknown_gene-(Putative VQ motif-containing protein)
4	37380001	gene desconhecido-(Putative armadillo repeat only 4)	10	34609001	PUP3-(Putative Purine permease 3)
4	37385001	XTH15-(Probable xyloglucan endotransglucosylase/hydrolase protein 15)	10	34607001	SHKA-(Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic)
4	5247001	At1g58390-(Putative Probable disease resistance protein At1g58390)	10	34603001	unknown_gene-(Phosphate-responsive 1 family protein)
4	5261001	gene desconhecido-(Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein)	10	34585001	UGT85A2-(UDP-glycosyltransferase 85A2)
4	5319001	At4g26540-(Probable LRR receptor-like serine/threonine-protein kinase At4g26540)	10	34583001	At1g06840-(Probable LRR receptor-like serine/threonine-protein kinase At1g06840)
4	5324001	FIP37-(FKBP12-interacting protein of 37 kDa, putative)	10	34565001	MBD8-(Putative uncharacterized protein)
4	3261001	UGT90A1-(Putative UDP-glycosyltransferase 90A1)	10	34564001	APRL4-(5'-adenylylsulfate reductase-like 4)
4	11359001	NAGLU-(Putative Alpha-N-acetylglucosaminidase)	10	34551001	mcfB-(Putative Calcium-binding mitochondrial carrier protein SCaMC-1)

4	12383001	TPP2-(Hypothetical protein)	10	34540001	ANN1-(Annexin D1)
4	35888001	At2g36330-(CASP-like protein At2g36330)	10	34539001	APUM7-(Putative uncharacterized protein)
4	35950001	At4g32180-(Pantothenate kinase 2)	10	34538001	unknown_gene-(unknown protein)
4	35951001	At4g32180-(Pantothenate kinase 2)	10	34533001	unknown_gene-(Putative uncharacterized protein)
4	1605001	At3g17611-(Uncharacterized protein At3g17611)	10	34532001	TTL3-(Putative Tetratricopeptide repeat (TPR)-like superfamily protein)
4	4336001	FH20-(Hypothetical protein)	10	34529001	unknown_gene-(Putative Mitochondrial transcription termination factor family protein)
4	4361001	ARR2-(Putative Two-component response regulator ARR2)	10	34514001	SEN1-(P-loop containing nucleoside triphosphate hydrolases superfamily protein)
4	40729001	At3g51990-(Serine/threonine-protein kinase-like protein At3g51990)	10	34491001	ANT-(Putative uncharacterized protein)
4	40771001	gene desconhecido-(Putative uncharacterized protein)	10	34482001	unknown_gene-(Chaperone DnaJ-domain superfamily protein)
4	10525001	VTI13-(Vesicle transport v-SNARE 13)	10	34477001	RAX3-(Putative uncharacterized protein)
4	10526001	APRR1-(Two-component response regulator-like APRR1)	10	34476001	BCAT2-(Branched-chain-amino-acid aminotransferase 2, chloroplastic)
4	2594001	FT1-(Galactoside 2-alpha-L-fucosyltransferase)	10	34461001	unknown_gene-(Protein of unknown function (DUF1005))
4	42317001	Ylpm1-(Putative uncharacterized protein)	10	34457001	At4g18375-(Putative KH domain-containing protein At4g18375)
4	42320001	gene desconhecido-(Putative Uncharacterized protein)	10	34452001	XYLB-(Xylulose kinase)
4	42352001	At5g62680-(Probable peptide/nitrate transporter At5g62680)	10	34444001	SHKA-(Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic)
4	42355001	At1g18880-(Probable peptide/nitrate transporter At1g18880)	10	34431001	At1g27530-(Ubiquitin-fold modifier-conjugating enzyme 1)
4	42382001	OTP43-(Pentatricopeptide repeat-containing protein At1g74900, mitochondrial)	10	34420001	CIPK8-(CBL-interacting serine/threonine-protein kinase 8)
4	42383001	APC8-(Anaphase-promoting complex subunit 8)	10	34413001	At1g09900-(Pentatricopeptide repeat-containing protein At1g09900)
4	42405001	fam135b-(Putative serine esterase family protein)	10	34404001	XAF1-(TRAF-type zinc finger-related)
4	35735001	VIT_19s0014g04930-((-)-germacrene D synthase)	10	34392001	At1g47710-(Putative Serpin-ZX)
4	35826001	gene desconhecido-(Putative Pectinesterase)	10	34379001	NGDN-(Putative Neuroguidin)
4	35849001	TUBA-(Tubulin alpha chain)	10	34376001	crtp1-(CRT (chloroquine-resistance transporter)-like transporter 2)
4	21599001	gene desconhecido-(Tetratricopeptide repeat (TPR)-like superfamily protein)	10	34364001	AKHSDH2-(Bifunctional aspartokinase/homoserine dehydrogenase, chloroplastic (Fragment))
4	21613001	AVPL1-(Pyrophosphate-energized membrane proton pump 2)	10	34360001	unknown_gene-(Putative Protein of unknown function (DUF1442))
4	21649001	PCMP-H66-(Putative Pentatricopeptide repeat-containing protein At4g32450, mitochondrial)	10	34332001	MT4A-(Metallothionein-like protein 4A)
4	21676001	gene desconhecido-(alpha/beta-Hydrolases superfamily protein)	10	34331001	unknown_gene-(Metallothionein-like protein 1)
4	21711001	GLIP5-(GDSL esterase/lipase 5)	10	34325001	unknown_gene-(Putative Ankyrin repeat family protein)
4	21754001	DAGLA-(Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3)	10	34291001	At1g54610-(Protein kinase superfamily protein)
4	21776001	NSP1-(Nodulation-signaling pathway 1 protein)	10	34270001	unknown_gene-(unknown protein; chloroplast)
4	21821001	PUB34-(Putative Protein kinase protein with adenine nucleotide alpha hydrolases-like domain)	10	31562001	OPR11-(Putative 12-oxophytodienoate reductase 11)
4	21883001	DOF1.7-(Putative uncharacterized protein)	10	31553001	Os02g0220500-(Elongation factor 1-gamma 2)
4	21913001	CHUP1-(Putative actin binding protein family)	10	31550001	AGL11-(Agamous-like MADS-box protein AGL11)
4	21929001	PAF1-(Putative uncharacterized protein)	10	31549001	PP2A3-(Putative Protein AIG1)
4	21930001	AHP4-(Histidine-containing phosphotransfer protein 4)	10	31546001	PP2A3-(Putative protein PHLOEM PROTEIN 2-LIKE A3)
4	21935001	PDR12-(Pleiotropic drug resistance protein 12)	10	31543001	LECRK91-(Putative uncharacterized protein)
4	22002001	gene desconhecido-(Sulfite exporter TauE/SafE family protein)	10	31534001	RH42-(DEAD-box ATP-dependent RNA helicase 42)
4	22101001	strap-(Serine-threonine kinase receptor-associated protein)	10	31512001	PATL5-(Patellin 1)
4	22198001	Fbxl14-(Putative F-box/LRR-repeat protein 14)	10	31509001	At1g72125-(Putative Probable peptide/nitrate transporter At1g72125)
4	22221001	gene desconhecido (unknown protein)	10	31508001	At1g22540-(Putative Probable peptide/nitrate transporter At1g22540)
4	22228001	Nup98-(Putative Nuclear pore complex protein Nup98-Nup96)	10	31506001	At1g72125-(Hypothetical protein)
4	22235001	RPL7A-(60S ribosomal protein L7-1)	10	31482001	At1g22540-(Probable peptide/nitrate transporter At1g22540)
4	22349001	FL-(Floricaula/leafy homolog)	10	31478001	At1g22570-(Predicted protein)
4	22355001	ERF114-(Hypothetical protein)	10	31467001	BHLH80-(Transcription factor bHLH80)
4	22421001	At3g18020-(Pentatricopeptide repeat-containing protein At3g18020)	10	31430001	At1g04910-(Putative DUF246 domain-containing protein At1g04910)
4	22450001	BGLU44-(Beta-glucosidase 44)	10	10114001	RPS24B-(40S ribosomal protein S24-2)
4	22508001	AMSH1-(AMSH-like ubiquitin thioesterase 1)	10	7963001	unknown_gene-(unknown protein; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0220 (InterPro:IPR007919)

4	22538001	Dennd4b-(Putative Vegetative incompatibility protein HET-E-1)	10	36003001	HLCS-(Putative Biotin--protein ligase)
4	22589001	gene desconhecido-(Hypothetical protein)	10	36010001	At1g04910-(O-fucosyltransferase family protein)
4	22598001	ZC3HC1-(Putative C3HC zinc finger-like)	10	19391001	unknown_gene-(unknown protein;plasma membrane)
4	22617001	CAS-(Calcium sensing receptor, chloroplastic)	10	19393001	ARA12-(Protease-associated PA; Proteinase inhibitor I9, subtilisin propeptide)
4	22732001	RKS1-(G-type lectin S-receptor-like serine/threonine-protein kinase RKS1)	10	16624001	P4ha1-(Putative Prolyl 4-hydroxylase subunit alpha-1)
4	22783001	At2g38640-(Protein LURP-one-related 8)	10	16644001	unknown_gene-(Putative Auxin-induced protein 5NG4)
4	22791001	RCOM_1206790-(Putative CASP-like protein RCOM_1206790)	10	16652001	RING1-(Putative E3 ubiquitin-protein ligase RING1)
4	22799001	At4g24660-(Putative ZF-HD homeobox protein At4g24660)	10	16656001	ybdL-(Putative Methionine aminotransferase)
4	42543001	gene desconhecido-(Malate synthase, glyoxysomal)	10	16661001	unknown_gene-(unknown protein)
4	42546001	gene desconhecido (unknown protein)	10	16684001	ACT-(Putative Vinorine synthase)
4	42570001	NDPK2-(Nucleoside diphosphate kinase 2, chloroplastic)	10	18481001	R1A-6-(Putative late blight resistance protein homolog R1A-6)
4	42603001	NUP155-(Putative Nuclear pore complex protein Nup155)	10	13656001	unknown_gene-(Putative uncharacterized protein)
4	42607001	CALS10-(Callose synthase 10)	10	1434001	R1A-(Putative Late blight resistance protein R1-A)
4	37361001	RPP8-(Putative Disease resistance protein RPP8)	10	31844001	PDS5A-(Putative Sister omatid cohesion protein PDS5 homolog A)
4	5249001	gene desconhecido (unknown protein)	10	31862001	LACS9-(Long chain acyl-CoA synthetase 9, chloroplastic)
4	5253001	gene desconhecido (unknown protein)	10	31874001	VIT_11s0016g04350-(tRNA (guanine(37)-N1)-methyltransferase 2)
4	5260001	AMS-(Putative Transcription factor ABORTED MICROSPORES)	10	31883001	At1g77540-(Acetyltransferase At1g77540)
4	5264001	PAT1-(Anthranilate phosphoribosyltransferase, chloroplastic)	10	31886001	ILL6-(IAA-amino acid hydrolase ILR1-like 6)
4	5269001	gene desconhecido (unknown protein)	10	31888001	TGA21-(BEST match: transcription factor-related (TAIR:AT4G18650.1)
4	5296001	MOS1-(Putative uncharacterized protein)	10	31889001	PDI-(Protein disulfide-isomerase)
4	5298001	gene desconhecido-(Hypothetical protein)	10	31897001	TIM9-(Mitochondrial import inner membrane translocase subunit Tim9)
4	5320001	gene desconhecido-(Putative CONTAINS InterPro DOMAIN/s: Kinetochore-Ndc80 complex, subunit Spc25 (InterPro:IPR013255)	10	31929001	Ogg1-(Putative N-glycosylase/DNA lyase)
4	3262001	GA4-(Gibberellin 3-beta-dioxygenase 1)	10	31930001	SWI3C-(SWI/SNF complex subunit SWI3C)
4	11357001	DEGP9-(Protease Do-like 9)	10	31935001	IF2CP-(Hypothetical protein)
4	11375001	gene desconhecido (unknown protein)	10	31975001	unknown_gene-(Hypothetical protein)
4	18301001	ER-ANT1-(ADP,ATP carrier protein ER-ANT1)	10	31983001	GSA-(Glutamate-1-semialdehyde 2,1-aminomutase, chloroplastic)
4	35868001	SWEET5-(Bidirectional sugar transporter SWEET5)	10	31993001	NADK2-(NAD kinase 2, chloroplastic)
4	35914001	NPHP3-(Tetratricopeptide repeat (TPR)-like superfamily protein)	10	31995001	DEFH21-(MADS-box protein defh21)
4	35922001	DXR-(1-deoxy-D-xylulose 5-phosphate reductoisomerase, chloroplastic)	10	31997001	PQBP1-(WW domain-containing protein)
4	4341001	RLP12-(Putative Receptor-like protein 12)	10	32007001	RH21-(DEAD-box ATP-dependent RNA helicase 21)
4	40735001	RPPL1-(Putative disease resistance RPP13-like protein 1)	10	35362001	ADH1-(Alcohol dehydrogenase 2)
4	40777001	gene desconhecido-(Putative UPF0420 protein C16orf58 homolog)	10	35343001	SWEET1-(Bidirectional sugar transporter SWEET1)
4	2606001	APRR1-(Hypothetical protein)	10	35340001	SWEET1-(Bidirectional sugar transporter SWEET1)
4	42353001	At5g62680-(Probable peptide/nitrate transporter At5g62680)	10	35338001	SEU-(Transcriptional corepressor SEUSS)
4	42369001	CYCL-(Cytoome c1, heme protein, mitochondrial)	10	35333001	SCL1-(Scarecrow-like protein 1)
4	42386001	gene desconhecido-(Nodulin-like / Major Facilitator Superfamily protein)	10	35311001	At3g50280-(Putative Uncharacterized acetyltransferase At3g50280)
4	42398001	At5g11010-(Polynucleotide 5'-hydroxyl-kinase NOL9)	10	35299001	unknown_gene-(Hypothetical protein)
4	42400001	ATPK2-(Serine/threonine-protein kinase AtPK2/AtPK19)	10	35298001	RIOK1-(Putative Serine/threonine-protein kinase RIO1)
4	42406001	gene desconhecido-(Putative uncharacterized protein)	10	35285001	unknown_gene-(Hypothetical protein)
4	35709001	GAUT11-(Probable galacturonosyltransferase 11)	10	35266001	MBD9-(Putative RING/FYVE/PHD-type zinc finger family protein)
4	35748001	gene desconhecido-(Biotin/lipoate A/B protein ligase family)	10	35255001	PEX1-(Peroxisome biogenesis protein 1)
4	35842001	At1g74510-(F-box/kelch-repeat protein At1g74510)	10	35239001	unknown_gene-(plastid transcriptionally active 6)
4	35854001	VPS29-(Vacuolar protein sorting-associated protein 29)	10	35231001	SINAT4-(Hypothetical protein)
4	13575001	bcsl1b-(AAA-ATPase 1)	10	35223001	NAK-(Putative Probable serine/threonine-protein kinase NAK)
4	21632001	gene desconhecido-(Pyridoxamine 5'-phosphate oxidase family protein)	10	2161001	TIF3I1-(Eukaryotic translation initiation factor 3 subunit I)
4	21699001	gene desconhecido-(Putative Remorin family protein)	10	11992001	unknown_gene-(nucleotide binding;nucleic acid binding)

4	21701001	FAB1-(phosphatidylinositol-4-phosphate 5-kinase family protein)	10	11999001	PUB28-(Putative U-box domain-containing protein 28)
4	21813001	gene desconhecido-(Putative NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3)	10	12009001	DOF1.2-(Putative Dof zinc finger protein DOF3.5)
4	21842001	GLYR1-(Putative oxidoreductase GLYR1)	10	12011001	RCH1-(LRR receptor-like serine/threonine-protein kinase RCH1)
4	21897001	ILL4-(IAA-amino acid hydrolase ILR1-like 4)	10	12035001	GUX3-(Putative UDP-glucuronate:xylan alpha-glucuronosyltransferase 3)
4	21942001	gene desconhecido (unknown protein)	10	6178001	GBF4-(G-box-binding factor 4)
4	22061001	GLYK-(D-glycerate 3-kinase, chloroplastic)	10	6180001	atg26-(UDP-Glycosyltransferase superfamily protein)
4	22087001	AATP1-(Plastidic ATP/ADP-transporter)	10	33590001	unknown_gene-(Putative uncharacterized protein)
4	22136001	gene desconhecido-(Lactoylglutathione lyase / glyoxalase I family protein)	10	33655001	ASR2-(Abscisic stress-ripening protein 3)
4	22177001	ZBED4-(BED zinc finger ;hAT family dimerisation domain)	10	33678001	At4g24630-(Probable S-acyltransferase At4g24630)
4	22223001	gene desconhecido-(Hypothetical protein)	10	33690001	UDP-GALT2-(UDP-galactose transporter 2)
4	22245001	DFR-(Putative Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase)	10	33704001	TAR4-(Tryptophan aminotransferase-related protein 4)
4	22309001	4CL1-(4-coumarate--CoA ligase 1)	10	33707001	TAR4-(Putative Tryptophan aminotransferase-related protein 4)
4	22357001	BON1-(Protein BONZAI 1)	10	33710001	TAR4-(Tryptophan aminotransferase-related protein 4)
4	22409001	TOC64-(Translocon at the outer membrane of chloroplasts 64)	10	33718001	PUP3-(Putative Purine permease 3)
4	22424001	GC2-(Putative Golgin candidate 2)	10	33719001	PUP3-(Purine permease 3)
4	22542001	At1g18440-(Putative Chloroplastic group IIB intron splicing facilitator CRS2, chloroplastic)	10	33725001	unknown_gene-(Hypothetical protein)
4	22685001	HRQ1-(Putative Uncharacterized ATP-dependent helicase yprA)	10	33730001	PEPKR2-(Serine/threonine-protein kinase PEPKR2)
4	22750001	OCT1-(Organic cation/carnitine transporter 1)	10	33731001	unknown_gene-(Putative unknown protein)
4	42515001	NAC029-(Putative NAC domain-containing protein 68)	10	33732001	At4g14600-(Bet1-like protein At4g14600)
4	42627001	rrp45-(Putative Exosome complex component rrp45)	10	33745001	unknown_gene-(Hypothetical protein)
4	42671001	RBP31-(28 kDa ribonucleoprotein, chloroplastic)	10	33759001	pgi-(Glucose-6-phosphate isomerase)
4	37308001	NRT3.1-(High-affinity nitrate transporter 3.1)	10	33769001	unknown_gene-(BEST match: methyltransferases (TAIR:AT5G01710.1)
4	37362001	At5g50170-(C2 and GRAM domain-containing protein At5g50170)	10	33770001	At1g05910-(ATPase family AAA domain-containing protein At1g05910)
4	37368001	ALDH2C4-(Aldehyde dehydrogenase family 2 member C4)	10	33771001	nep1-(Putative Protein ASPARTIC PROTEASE IN GUARD CELL 1)
4	5259001	mpp10-(Putative U3 small nucleolar ribonucleoprotein protein mpp10)	10	33778001	AP4M1-(Putative AP-4 complex subunit mu-1)
4	5279001	RH50-(DEAD-box ATP-dependent RNA helicase 50)	10	33796001	unknown_gene-(Putative uncharacterized protein)
4	18274001	At4g03230-(G-type lectin S-receptor-like serine/threonine-protein kinase At4g03230)	10	33798001	ATR1-(NADPH--cytoome P450 reductase)
4	35924001	RPP8L3-(Putative Disease resistance RPP8-like protein 3)	10	33812001	slp1-(Putative Galactose-binding protein)
4	4355001	GSO1-(Putative LRR receptor-like serine/threonine-protein kinase GSO1)	10	33816001	SPS4-(Probable sucrose-phosphate synthase 4)
4	42392001	dlcB-(Dynein light chain LC6, flagellar outer arm)	10	33825001	unknown_gene-(Why2 protein)
4	42403001	PTAC2-(Putative Pentatricopeptide repeat-containing protein At1g74850, chloroplastic)	10	33826001	At1g33440-(Probable peptide/nitrate transporter At1g33440)
4	35725001	ValCS-(Putative Pinene synthase)	10	33835001	xlnD-(Putative 3-hydroxybenzoate 6-hydroxylase 1)
4	35743001	SOT5-(Putative Cytosolic sulfotransferase 5)	10	33839001	unknown_gene-(glycine-rich protein)
4	35776001	gene desconhecido-(Late embryogenesis abundant protein D-34)	10	33845001	clpX-(ATP-dependent Clp protease)
4	35816001	HERC1-(Putative Probable E3 ubiquitin-protein ligase HERC1)	10	33850001	unknown_gene-(CONTAINS InterPro DOMAIN/s: WW-domain-binding protein (InterPro:IPR018826); cytosol, plasma membrane)
4	21761001	RGA4-(Putative disease resistance protein RGA4)	10	11263001	GH3.17-(Indole-3-acetic acid-amido synthetase GH3.17)
4	21891001	At1g73020-(Anoctamin-like protein At1g73020)	10	13406001	At1g71691-(GDSL esterase/lipase At1g71691)
4	21937001	ABCG35-(ABC transporter G family member 35)	10	13408001	SMU1-(WD40 repeat-containing protein SMU1)
4	22084001	gene desconhecido-(Hypothetical protein)	10	13410001	unknown_gene-(unknown protein; endomembrane system)
4	22190001	AVP1-(Pyrophosphate-energized vacuolar membrane proton pump)	10	24471001	RBM38-(RNA-binding (RRM/RBD/RNP motifs) family protein)
4	22387001	TDX-(TPR repeat-containing thioredoxin TDX)	10	24494001	GLR3.3-(Glutamate receptor 3.3)
4	22582001	Taf2-(TBP-associated factor 2)	10	24510001	NPC1-(Putative Niemann-Pick C1 protein)
4	22693001	SD25-(Putative G-type lectin S-receptor-like serine/threonine-protein kinase SD2-5)	10	24524001	unknown_gene-(Zn-dependent exopeptidases superfamily protein)
4	22818001	MKK5-(Putative Mitogen-activated protein kinase kinase 5)	10	24526001	tsr1-(Putative Pre-rRNA-processing protein TSR1 homolog)
4	22847001	PDH2-(Pyruvate dehydrogenase E1 component subunit beta, mitochondrial)	10	24531001	unknown_gene-(unknown protein)
4	42554001	ABCB21-(Putative ABC transporter B family member 21)	10	24541001	unknown_gene-(Putative Arabidopsis protein of unknown function (DUF241))

4	42568001	ACT-(Putative Vinorine synthase)	10	24552001	SKIP23-(Putative F-box protein SKIP23)
4	42577001	plcC-(non-specific phospholipase C6)	10	24615001	ABCB13-(ABC transporter B family member 13)
4	42669001	PCM-(Protein-L-isoaspartate O-methyltransferase)	10	24644001	CERBERUS-(Putative E3 ubiquitin-protein ligase LIN-1)
4	37403001	gene desconhecido-(Hypothetical protein)	10	24656001	unknown_gene-(Putative uncharacterized protein)
4	37407001	At3g06240-(Putative F-box/kelch-repeat protein At3g06240)	10	24706001	CENPE-(Putative ATP binding microtubule motor family protein)
4	5286001	gene desconhecido-(Putative uncharacterized protein)	10	24707001	At1g05150-(Uncharacterized TPR repeat-containing protein At1g05150)
4	5291001	Mospd2-(Putative Motile sperm domain-containing protein 2)	10	24720001	vatM-(Putative Vacuolar proton translocating ATPase 100 kDa subunit)
4	5325001	gene desconhecido-(Putative D111/G-patch domain-containing protein)	10	24721001	RD19A-(Cysteine proteinase 15A)
4	35729001	VIT_19s0014g04930-((-)-germacrene D synthase)	10	24737001	UBC16-(Probable ubiquitin-conjugating enzyme E2 16)
4	21961001	ELAC2-(Putative Zinc phosphodiesterase ELAC protein 2)	10	24739001	CKX5-(Cytokinin dehydrogenase 5)
4	21972001	IAA27-(Auxin-responsive protein IAA27)	10	24742001	BLH7-(Putative uncharacterized protein)
4	21975001	rutB-(Putative Peroxyureidoacrylate/ureidoacrylate amidohydrolase RutB)	10	24753001	CYCT1-3-(Putative Cyclin-T1-3)
4	22043001	MFP1-1-(MAR-binding filament-like protein 1-1)	10	24776001	TULP5-(Tubby-like F-box protein 5)
4	22317001	gene desconhecido-(Putative forkhead-associated domain-containing protein / FHA domain-containing protein)	10	24808001	unknown_gene-(Putative uncharacterized protein)
4	22493001	TTC7B-(tetratricopeptide repeat (TPR)-containing protein)	10	24816001	Gigyf2-(Putative GYF domain-containing protein)
4	22664001	wdhd1-(Putative WD repeat and HMG-box DNA-binding protein 1)	10	24842001	DDB_G0271664-(Putative SPX and EXS domain-containing protein 5)
4	22735001	CRK10-(Cysteine-rich receptor-like protein kinase 10)	10	24864001	RMA1H1-(Putative E3 ubiquitin-protein ligase RMA1H1)
4	42643001	dnaX-(Replication factor C / DNA polymerase III gamma-tau subunit, putative)	10	24879001	ARI1-(Probable E3 ubiquitin-protein ligase ARI1)
4	37415001	HAT22-(homeobox from Arabidopsis thaliana)	10	24884001	unknown_gene-(unknown protein; chloroplast envelope)
4	2609001	PCMP-H74-(Pentatricopeptide repeat-containing protein At1g25360)	10	24893001	PERK9-(Putative Protein kinase protein with adenine nucleotide alpha hydrolases-like domain)
4	42388001	gene desconhecido-(Epstein-Barr nuclear antigen, putative)	10	24899001	tmem147-(unknown protein; InterPro DOMAIN/s: Protein of unknown function DUF2053, membrane (InterPro:IPR019164))
4	35859001	ABCA2-(ABC transporter A family member 2)	10	34989001	unknown_gene-(Hypothetical protein)
4	21691001	PMEU1-(Pectinesterase/pectinesterase inhibitor U1)	10	34984001	SQP1,1-(Squalene monooxygenase)
4	21763001	At1g72540-(Putative receptor-like protein kinase At1g72540)	10	34965001	WEB1-(Protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1)
4	22453001	ARCA-(Guanine nucleotide-binding protein subunit beta-like protein)	10	34874001	MYB44-(Putative Transcription factor MYB44)
4	22498001	gene desconhecido-(Calmodulin binding protein-like)	10	34845001	unknown_gene-(Hypothetical protein)
4	10617001	gene desconhecido-(DNA binding;ATP binding)	10	34809001	CYP81E1-(Putative Isoflavone 2'-hydroxylase)
4	37404001	At1g67000-(Putative Probable receptor-like protein kinase At1g67000)	10	34808001	NRAMP2-(Metal transporter Nramp2)
4	35934001	gene desconhecido-(Putative Protein of unknown function (DUF1645))	10	34785001	unknown_gene-(Putative Family of unknown function (DUF566))
4	42365001	PPT1-(4-hydroxybenzoate polyprenyltransferase, mitochondrial)	10	34765001	TTC7A-(no pollen germination related 1)
4	42374001	Usp54-(Ubiquitin carboxyl-terminal hydrolase-related protein)	10	34693001	ERF086-(DNA binding protein, putative)
4	35731001	VIT_19s0014g04930-((-)-germacrene D synthase)	10	34690001	TT10-(Laccase-15)
4	21619001	gene desconhecido-(mediator subunit 8)	10	34683001	CYP78A4-(Cytoome P450 78A4)
4	21960001	gene desconhecido-(Putative uncharacterized protein)	10	34649001	At1g34110-(Probable LRR receptor-like serine/threonine-protein kinase At1g34110)
4	42588001	XSP1-(Cucumisin)	10	34630001	unknown_gene-(Hypothetical protein)
4	2596001	RPE-(Ribulose-phosphate 3-epimerase, chloroplastic (Fragment))	10	34629001	ISA3-(Isoamylase 3, chloroplastic)
4	37367001	PR1B1-(Pathogenesis-related leaf protein 6)	10	34627001	Fam91a1-(Putative Protein FAM91A1)
4	37412001	RPP8-(Putative Disease resistance protein RPP8)	10	34605001	unknown_gene-(Phosphate-responsive 1 family protein)
4	5301001	impdh-(Inosine-5'-monophosphate dehydrogenase)	10	34548001	CCR4-1-(Putative Carbon catabolite repressor protein 4 homolog 2)
4	11351001	IPMSA-(2-isopropylmalate synthase A)	10	34504001	unknown_gene-(CW7)
4	5293001	Tatdn1-(Putative deoxyribonuclease TATDN1)	10	34496001	unknown_gene-(Putative growth-regulating factor 1)
4	37410001	At3g06240-(Putative F-box/kelch-repeat protein At3g06240)	10	34470001	unknown_gene-(Putative glycosyl hydrolase family 10 protein / carbohydrate-binding domain-containing protein)
4	42408001	TOR1-(Putative Microtubule-associated protein TORTIFOLIA1)	10	34456001	AAP6-(Amino acid permease 6)
5	17008001	SCR-(GRAS family transcription factor)	10	34447001	Os01g0639100-(DEAD-box ATP-dependent RNA helicase 2)
5	17033001	UGT82A1-(Putative UDP-glycosyltransferase	10	34442001	rnf217-(Putative RING/U-box superfamily protein)

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5	17042001	unknown_gene-(Topoisomerase II-associated protein PAT1)	10	34430001	PCKA-(Phosphoenolpyruvate carboxykinase [ATP])
5	17046001	GLR2.7-(Putative Glutamate receptor 2.7)	10	34371001	unknown_gene-(glyoxal oxidase-related protein)
5	17057001	PIF4-(Putative Transcription factor PIF4)	10	34368001	At1g07160-(Putative Probable protein phosphatase 2C 74)
5	17061001	pat2-k1-(Putative Patatin group A-3)	10	34340001	PCMP-H42-(Putative Pentatricopeptide repeat-containing protein At4g13650)
5	17089001	PCMP-E15-(Pentatricopeptide repeat-containing protein At2g35030, mitochondrial)	10	31540001	At1g33990-(Probable esterase At1g33990)
5	17090001	CYP87A3-(Putative Cytoome P450 87A3)	10	31496001	At5g39110-(Germin-like protein subfamily 1 member 14)
5	17094001	CYP82A3-(Cytoome P450 82A3)	10	31464001	Tmem205-(Putative Late embryogenesis abundant protein (LEA) family protein)
5	17100001	unknown_gene-(Putative RING/U-box superfamily protein)	10	31439001	ARI2-(Probable E3 ubiquitin-protein ligase ARI2)
5	17104001	unknown_gene-(Ubiquitin carboxyl-terminal hydrolase family protein)	10	31437001	unknown_gene-(Putative Proteinase inhibitor I20, Pin2)
5	18202001	unknown_gene-(Putative uncharacterized protein)	10	35992001	ASHR1-(Histone-lysine N-methyltransferase ASHR1)
5	18223001	HPD-(4-hydroxyphenylpyruvate dioxygenase)	10	36008001	ESC-(Putative C2H2-like zinc finger protein)
5	18241001	mrpl19-(54S ribosomal protein L19, mitochondrial)	10	36016001	SD25-(Putative G-type lectin S-receptor-like serine/threonine-protein kinase SD2-5)
5	18256001	unknown_gene-(Protein of unknown function (DUF3531))	10	16666001	dis3l2-(Putative DIS3-like CDSuclease 2)
5	10972001	sll1770-(Putative Uncharacterized protein sll1770)	10	18465001	unknown_gene-(Hypothetical protein)
5	15751001	CYP82G1-(Cytoome P450 82G1)	10	18488001	TIC40-(Protein TIC 40, chloroplastic)
5	15755001	ASPG1-(Eukaryotic aspartyl protease family protein)	10	13665001	Kiaa1704-(DNAJ heat shock N-terminal domain-containing protein)
5	40838001	unknown_gene-(Major facilitator superfamily protein)	10	1430001	unknown_gene-(Putative Polynucleotide adenylyltransferase family protein)
5	40831001	unknown_gene-(Major facilitator superfamily protein)	10	31871001	At1g23740-(Quinone oxidoreductase-like protein At1g23740, chloroplastic)
5	40825001	COL9-(Zinc finger protein CONSTANS-LIKE 9)	10	31873001	unknown_gene-(TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein)
5	40820001	PUB4-(ARM repeat superfamily protein)	10	31875001	unknown_gene-(unknown protein; endomembrane system)
5	40815001	unknown_gene-(Putative uncharacterized protein)	10	31902001	CAO-(Putative Probable signal recognition particle 43 kDa protein, chloroplastic)
5	40814001	unknown_gene-(Putative Kinase-related protein of unknown function (DUF1296))	10	31908001	HCC1-(Putative Protein SCO1 homolog, mitochondrial)
5	18435001	At3g03773-(Uncharacterized protein At3g03773)	10	31910001	Rfc5-(Replication factor C subunit 5)
5	20990001	QNS1-(Glutamine-dependent NAD(+) synthetase)	10	31944001	ABCC9-(Putative ABC transporter C family member 9)
5	20892001	AGO16-(Protein argonaute 16)	10	31960001	CYCA1-1-(Cyclin-A1-1)
5	20879001	COP1-(E3 ubiquitin-protein ligase COP1)	10	35356001	PCMP-E29-(Putative Pentatricopeptide repeat-containing protein At3g21470)
5	33463001	taf6-(Putative Transcription initiation factor TFIID subunit 6)	10	35348001	UGAT-(Putative Cyanidin-3-O-glucoside 2-O-glucuronosyltransferase)
5	33466001	PUB4-(ARM repeat superfamily protein)	10	35322001	LDL2-(Lysine-specific histone demethylase 1 homolog 2)
5	33497001	NAT1-(Nucleobase-ascorbate transporter 1)	10	35319001	bkdA-(2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial)
5	33498001	unknown_gene-(Nodulin MtN21 /EamA-like transporter family protein)	10	35291001	unknown_gene-(unknown protein)
5	33501001	At1g05030-(Probable plastidic glucose transporter 1)	10	35271001	RPL15-(60S ribosomal protein L15-1)
5	33502001	At5g17580-(Putative BTB/POZ domain-containing protein At5g17580)	10	35251001	ndhM-(NAD(P)H-quinone oxidoreductase subunit M, chloroplastic)
5	33543001	PERK13-(chitin elicitor receptor kinase 1)	10	35250001	At1g21570-(Zinc finger CCCH domain-containing protein 7)
5	33548001	CG5931-(Putative U5 small nuclear ribonucleoprotein 200 kDa helicase)	10	35243001	ASHH2-(Putative Histone-lysine N-methyltransferase ASHH2)
5	33559001	RSN1-(ERD (early-responsive to dehydration stress) family protein)	10	35237001	At1g04910-(O-fucosyltransferase family protein)
5	17320001	unknown_gene-(Putative Cellulase (glycosyl hydrolase family 5) protein)	10	2158001	sap-49-(RNA-binding (RRM/RBD/RNP motifs) family protein)
5	31571001	EPHX2-(Putative Epoxide hydrolase 2)	10	12012001	unknown_gene-(Thioredoxin superfamily protein)
5	31577001	CYP71D55-(Premnaspirodiene oxygenase)	10	24445001	ttc37-(Tetratricopeptide repeat (TPR)-like superfamily protein)
5	31582001	CYP71D55-(Premnaspirodiene oxygenase)	10	12013001	Plekha8-(glycolipid transfer protein 2)
5	31588001	CYPRO1-(Cyprosin (Fragment))	10	33597001	RGLG2-(E3 ubiquitin-protein ligase RGLG2)
5	31589001	mkkA-(mitogen-activated protein kinase kinase kinase 18)	10	33614001	At3g61360-(Pentatricopeptide repeat-containing protein At3g61360)
5	31641001	unknown_gene-(Hypothetical protein)	10	33619001	FAM188A-(Putative Protein FAM188A)
5	31682001	R1B-14-(Putative NB-ARC domain-containing disease resistance protein)	10	33620001	unknown_gene-(Fructose-1,6-bisphosphatase, cytosolic)
5	31697001	RRP6-(Polynucleotidyl transferase, ribonuclease H fold protein with HRDC domain)	10	33622001	Lsm3-(U6 snRNA-associated Sm-like protein LSm3)
5	31700001	WDR74-(WD-repeat protein)	10	33662001	At4g08850-(Putative Probable LRR receptor-like serine/threonine-protein kinase At4g08850)
5	31703001	ACO2-(Aconitate hydratase 2, mitochondrial)	10	33670001	MTHFSD-(NagB/RpiA/CoA transferase-like superfamily protein)

5	7004001	PNAE-(Polyneuridine-aldehyde esterase)	10	33682001	PER12-(Peroxidase 12)
5	35007001	TT12-(Putative Protein TRANSPARENT TESTA 12)	10	33686001	unknown_gene-(one-helix protein 2)
5	35016001	TT12-(Putative Protein TRANSPARENT TESTA 12)	10	33695001	unknown_gene-(Hypothetical protein)
5	35039001	unknown_gene-(Isocitrate lyase)	10	33701001	GAI1-(Putative DELLA protein GAI1)
5	35054001	MJ1365-(TraB family protein)	10	33713001	DHRS12-(Putative Dehydrogenase/reductase SDR family member 12)
5	35056001	Os02g0161200-(Putative Zinc finger CCCH domain-containing protein 13)	10	33721001	At5g27460-(Pentatricopeptide repeat-containing protein At5g27460)
5	35059001	CYP71D11-(Putative Cytoome P450 71D11 (Fragment))	10	33724001	PUR7-(Phosphoribosylaminoimidazole-succinocarboxamide synthase, chloroplastic)
5	35070001	CYCU1-1-(Cyclin-U1-1)	10	33751001	CYCD4-1-(Cyclin-D4-1)
5	35084001	R1B-17-(Putative late blight resistance protein homolog R1B-17)	10	33760001	unknown_gene-(unknown protein)
5	35089001	MAE_39970-(Putative pterin-4-alpha-carbinolamine dehydratase)	10	33772001	At3g01520-(Putative Universal stress protein A-like protein)
5	35098001	gene desconhecido (unknown protein)	10	33775001	ESC-(Predicted AT-hook DNA-binding family protein)
5	35132001	At5g56420-(Putative F-box family protein)	10	33786001	SVP-(MADS-box protein SVP)
5	35151001	MYB4-(Predicted protein)	10	33791001	argH-(Argininosuccinate lyase)
5	35160001	GT6-(Putative UDP-glucose flavonoid 3-O-glucosyltransferase 6)	10	33803001	CEL3-(Endoglucanase 9)
5	35170001	GT6-(Putative UDP-glucose flavonoid 3-O-glucosyltransferase 6)	10	33814001	BBE1-(Putative Reticuline oxidase)
5	35172001	GT6-(Putative UDP-glucose flavonoid 3-O-glucosyltransferase 6)	10	33817001	unknown_gene-(unknown protein)
5	35177001	MYB4-(Putative myb domain protein 15)	10	33819001	unknown_gene-(PLC-like phosphodiesterases superfamily protein)
5	35210001	3MAT-(Putative Malonyl-coenzyme A:anthocyanin 3-O-glucoside-6''-O-malonyltransferase)	10	33832001	B3GALT8-(Probable beta-1,3-galactosyltransferase 8)
5	42093001	unknown_gene-(Wound-responsive family protein)	10	33840001	ycf45-(Putative Uncharacterized protein ycf45)
5	42097001	PVA42-(Vesicle-associated protein 4-2)	10	13398001	unknown_gene-(Putative uncharacterized protein)
5	42111001	NDE1-(NAD(P)H dehydrogenase B4)	10	24437001	mcfQ-(Putative Mitochondrial substrate carrier family protein Q)
5	42113001	NDH2-(Putative External alternative NADH-ubiquinone oxidoreductase, mitochondrial)	10	24439001	UDP-GALT2-(UDP-galactose transporter 2)
5	42119001	At4g20830-(Putative Reticuline oxidase-like protein)	10	24444001	unknown_gene-(Calcineurin-like metallo-phosphoesterase superfamily protein)
5	42132001	GAUT10-(Probable galacturonosyltransferase 10)	10	24447001	unknown_gene-(Cysteine/Histidine-rich C1 domain family protein)
5	42137001	FTCD-(Putative Formimidoyltransferase-cyclodeaminase)	10	24448001	SPL14-(Putative Squamosa promoter-binding-like protein 14)
5	42183001	At4g03415-(Probable protein phosphatase 2C 52)	10	24463001	unknown_gene-(Auxin efflux carrier family protein)
5	42199001	ERF053-(AP2/ERF domain-containing transcription factor)	10	24481001	unknown_gene-(plastid movement impaired1)
5	42210001	PLT4-(Probable polyol transporter 4)	10	24493001	At5g56590-(Putative Glucan endo-1,3-beta-glucosidase 13)
5	42228001	At2g20710-(Putative Pentatricopeptide repeat-containing protein At2g20710, mitochondrial)	10	24495001	bioF-(Hypothetical protein)
5	42230001	At2g20710-(Putative Pentatricopeptide repeat-containing protein At2g20710, mitochondrial)	10	24508001	At4g35600-(Probable serine/threonine-protein kinase Cx32, chloroplastic)
5	42242001	TPC1A-(Two pore calcium channel protein 1A)	10	24521001	SBE1-(1,4-alpha-glucan-branching enzyme)
5	42244001	UBC26-(Putative uncharacterized protein)	10	24532001	unknown_gene-(unknown protein; endomembrane system)
5	42279001	Bub1-(ATP binding;protein kinases;protein serine/threonine kinases)	10	24548001	Bag6-(Putative Ubiquitin-like superfamily protein)
5	16754001	TAT-(Tyrosine aminotransferase)	10	24584001	CPK29-(Calcium-dependent protein kinase 29)
5	16772001	At5g66631-(Pentatricopeptide repeat-containing protein At5g66631)	10	24604001	FD-(Putative Protein FD)
5	16783001	gene desconhecido (unknown protein)	10	24618001	CLV1-(Receptor protein kinase CLAVATA1)
5	16844001	GSO1-(Putative LRR receptor-like serine/threonine-protein kinase GSO1)	10	24636001	unknown_gene-(unknown protein; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0307 (InterPro:IPR006839)
5	16852001	unknown_gene-(ATP synthase protein I -related)	10	24647001	TUBB1-(Tubulin beta-1 chain)
5	16862001	CTR1-(Mitogen activated protein kinase kinase kinase-related)	10	24668001	At4g31790-(Probable diphthine synthase)
5	16873001	ASK6-(Shaggy-related protein kinase zeta)	10	24799001	unknown_gene-(Hypothetical protein)
5	16889001	unknown_gene-(Hypothetical protein)	10	24912001	unknown_gene-(Hypothetical protein)
5	16893001	Rnf115-(Putative RING/U-box superfamily protein)	10	24924001	At5g22670-(Putative F-box/FBD/LRR-repeat protein At5g22670)
5	16906001	CYP72A1-(Secologanin synthase)	10	24932001	dpf-6-(alpha/beta-Hydrolases superfamily protein)
5	16909001	CYP72A1-(Secologanin synthase)	10	34970001	At1g07700-(Putative uncharacterized protein)
5	16912001	CYP72A1-(Secologanin synthase)	10	34800001	TTC1-(ARM-repeat/Tetratricopeptide repeat (TPR)-like protein)
5	16915001	CYP72A1-(Secologanin synthase)	10	34722001	unknown_gene-(DNA-directed RNA polymerase II protein)

5	16934001	SD25-(Putative uncharacterized protein)	10	34717001	unknown_gene-(Chaperone DnaJ-domain superfamily protein)
5	2685001	At5g35370-(Putative G-type lectin S-receptor-like serine/threonine-protein kinase At5g35370)	10	34628001	unknown_gene-(Hypothetical protein)
5	2682001	unknown_gene-(Putative alpha-crystallin domain 32.1)	10	34562001	Abhd6-(Putative Monoacylglycerol lipase ABHD6)
5	2672001	At4g19050-(Putative disease resistance protein At4g19050)	10	34536001	At1g78140-(Uncharacterized methyltransferase At1g78140, chloroplastic)
5	2669001	GATA-(Glutamyl-tRNA(Gln) amidotransferase subunit A, chloroplastic/mitochondrial)	10	34474001	HAT22-(Homeobox-leucine zipper protein HAT22)
5	2665001	CSY2-(Citrate synthase, glyoxysomal)	10	34463001	At1g10030-(Ergosterol biosynthetic protein 28)
5	2662001	PAPP5-(Serine/threonine-protein phosphatase 5)	10	34441001	unknown_gene-(Mitochondrial ribosomal protein L37)
5	21589001	unknown_gene-(Hypothetical protein)	10	34422001	unknown_gene-(Phosphoglycerate mutase family protein)
5	21570001	ARA12-(Putative Subtilisin-like protease)	10	34396001	TFIIA-S-(Transcription initiation factor IIA subunit 2)
5	21567001	plaa2-(Putative Exopolygalacturonase (Fragment))	10	34387001	lvsC-(binding)
5	21566001	TPKC-(Hypothetical protein)	10	34326001	unknown_gene-(Putative Ankyrin repeat family protein)
5	21553001	CALS7-(Callose synthase 7)	10	34295001	unknown_gene-(Rieske (2Fe-2S) domain-containing protein)
5	21546001	vps16-(Putative Vacuolar protein sorting-associated protein 16 homolog)	10	34294001	ERF020-(Ethylene-responsive transcription factor ERF020)
5	21522001	CAB8-(Chlorophyll a-b binding protein 8, chloroplastic)	10	34285001	CYP82C4-(Putative Cytoome P450 82C4)
5	21493001	GLO1-(Peroxisomal (S)-2-hydroxy-acid oxidase)	10	34284001	CYP75B1-(Putative Flavonoid 3'-monooxygenase)
5	21492001	Alg1-(Putative Chitobiosyldiphosphodolichol beta-mannosyltransferase)	10	31532001	rnf170-(Putative RING finger protein 170)
5	21488001	NCED1-(9-cis-epoxycarotenoid dioxygenase NCED1, chloroplastic)	10	31521001	CMBL-(Putative Carboxymethylenebutenolidase homolog)
5	21485001	unknown_gene-(CTC-interacting domain 9)	10	31515001	unknown_gene-(Putative Protein of unknown function DUF543)
5	21483001	SIP5-(RING/U-box superfamily protein)	10	19384001	R1B-14-(Putative late blight resistance protein homolog R1B-14)
5	21436001	RPL18AA-(Putative 60S ribosomal protein L18a-1)	10	2512001	ORC3-(Putative origin recognition complex subunit 3)
5	21432001	SPS1-(Solanesyl diphosphate synthase 1)	10	31893001	APXT-(L-ascorbate peroxidase T, chloroplastic)
5	21431001	GLC1-(Carbohydrate-binding X8 domain superfamily protein)	10	31906001	kif11-(P-loop containing nucleoside triphosphate hydrolases superfamily protein)
5	21426001	rbsK-(Putative Ribokinase)	10	31948001	NRAMP5-(Metal transporter Nramp5)
5	21413001	SWEET2-(Bidirectional sugar transporter SWEET2)	10	35375001	SCPL42-(Serine carboxypeptidase-like 42)
5	21411001	RHM1-(Probable rhamnose biosynthetic enzyme 1)	10	35369001	unknown_gene-(Putative Auxin-induced protein 5NG4)
5	21401001	RPL13-(50S ribosomal protein L13, chloroplastic)	10	35352001	UGAT-(Putative Cyanidin-3-O-glucoside 2-O-glucuronosyltransferase)
5	21396001	unknown_gene-(TRICHOME BIREFRINGENCE-LIKE 41)	10	35229001	At1g65250-(Putative Probable inactive receptor-like protein kinase At1g65250)
5	21373001	At1g53330-(Putative pentatricopeptide repeat-containing protein At1g53330)	10	12012001	unknown_gene-(Thioredoxin superfamily protein)
5	21359001	Rab3gap2-(unknown protein)	10	12019001	unknown_gene-(Putative sequence-specific DNA binding transcription factors)
5	21356001	At3g14930-(Uroporphyrinogen decarboxylase 1, chloroplastic)	10	33621001	SEC5A-(Exocyst complex component 2)
5	21344001	murA-(Putative UDP-N-acetylglucosamine 1-carboxyvinyltransferase)	10	33660001	At4g08850-(Putative Probable LRR receptor-like serine/threonine-protein kinase At4g08850)
5	21337001	unknown_gene-(Putative Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein)	10	33698001	At4g08850-(Probable LRR receptor-like serine/threonine-protein kinase At4g08850)
5	21326001	unknown_gene-(Plant protein of unknown function (DUF828))	10	33717001	KCS4-(Putative 3-ketoacyl-CoA synthase 4)
5	21325001	IPT9-(tRNA dimethylallyltransferase 9)	10	13415001	OPR11-(Putative 12-oxophytodienoate reductase 11)
5	21313001	unknown_gene-(Putative uncharacterized protein)	10	24573001	unknown_gene-(Zim17-type zinc finger protein)
5	21311001	unknown_gene-(Putative sodium/calcium exchanger family protein / calcium-binding EF hand family protein)	10	24648001	unknown_gene-(Hypothetical protein)
5	21310001	GLR2.7-(Putative Glutamate receptor 2.7)	10	24689001	RCC2-(Putative Protein RCC2)
5	21304001	rexo4-(Polynucleotidyl transferase, ribonuclease H-like superfamily protein)	10	24728001	obg-(Putative uncharacterized protein)
5	21300001	RTN4IP1-(Putative Reticulon-4-interacting protein 1, mitochondrial)	10	24792001	nt5c2-(Putative Cytosolic purine 5'-nucleotidase)
5	21286001	At3g15140-(Uncharacterized CDSuclease domain-containing protein At3g15140)	10	34925001	unknown_gene-(alpha/beta-Hydrolases superfamily protein)
5	21285001	MMS21-(E3 SUMO-protein ligase MMS21)	10	34890001	WRKY7-(Putative Probable WRKY transcription factor 7)
5	21281001	At5g57850-(Branched-chain-amino-acid aminotransferase-like protein 3, chloroplastic)	10	34857001	ECA3-(Calcium-transporting ATPase 3, endoplasmic reticulum-type)
5	21278001	NAC098-(Protein CUP-SHAPED COTYLEDON 2)	10	34799001	SPCC757.02c-(NAD(P)-binding Rossmann-fold superfamily protein)
5	21264001	At3g15260-(Probable protein phosphatase 2C 39)	10	34523001	unknown_gene-(Hypothetical protein)
5	21247001	unknown_gene-(proton pump interactor 1)	10	34518001	RAP2-4-(Ethylene-responsive transcription factor RAP2-4)

5	21235001	NSF-(Vesicle-fusing ATPase)
5	21231001	PAPD5-(Nucleotidyltransferase family protein)
5	21222001	unknown_gene-(Hypothetical protein)
5	21220001	chtl-1-(Putative Choline transporter-like protein 1)
5	21205001	HERC2-(Putative Probable E3 ubiquitin-protein ligase HERC2)
5	21204001	CBSX5-(CBS domain-containing protein CBSX5)
5	21195001	unknown_gene-(Putative Predicted protein)
5	21174001	AHL-(PAP-specific phosphatase HAL2-like)
5	21156001	myoJ-(Putative Myosin-J heavy chain)
5	21152001	CNGC4-(Cyclic nucleotide-gated ion channel 4)
5	21151001	Cdlc2-(Dynein light chain LC6, flagellar outer arm)
5	21138001	unknown_gene-(Putative uncharacterized protein)
5	21133001	At4g27290-(G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290)
5	21118001	unknown_gene-(Putative Uncharacterised conserved protein (UCP012943))
5	21114001	GRP2-(RNA-binding (RRM/RBD/RNP motifs) family protein)
5	21098001	PSBQ2-(PsbQ-like 1)
5	21079001	GOS2-(Protein translation factor SUI1 homolog)
5	21077001	PME2.1-(Pectinesterase 2.1)
5	21076001	Os07g0103200-(DDRGK domain-containing protein 1)
5	21068001	Ap5z1-(unknown protein)
5	21065001	ERF118-(Hypothetical protein)
5	21055001	LTD-(Protein LHCP TRANSLOCATION DEFECT)
5	21052001	TOR1-(Microtubule-associated protein TORTIFOLIA1)
5	21035001	CPK2-(Calcium-dependent protein kinase isoform 2)
5	21028001	At5g41620-(unknown protein; chloroplast)
5	21021001	RH32-(DEAD-box ATP-dependent RNA helicase 32)
5	21018001	PAP18-(Purple acid phosphatase 18)
5	21014001	unknown_gene-(Hypothetical protein)
5	21013001	unknown_gene-(RNI-like superfamily protein)
5	21012001	Os08g0191100-(Putative aconitate hydratase, cytoplasmic)
5	21005001	B3GALT2-(Probable beta-1,3-galactosyltransferase 2)
5	20996001	lpxK-(Putative Tetraacyldisaccharide 4'-kinase)
5	38866001	YBL036C-(Putative Proline synthase co-transcribed bacterial homolog protein)
5	38865001	Prosc-(Proline synthase co-transcribed bacterial homolog protein)
5	38849001	At5g56590-(Putative Glucan endo-1,3-beta-glucosidase 13)
5	38848001	ERF3-(Ethylene-responsive transcription factor 3)
5	38835001	TIG-(Trigger factor-like protein TIG)
5	38821001	FTSZ1-(Cell division protein FtsZ)
5	38807001	At5g47540-(Putative MO25-like protein At5g47540)
5	38804001	RPS8-(Hypothetical protein)
5	38801001	KIF15-(Putative Kinesin motor family protein)
5	38797001	At1g64210-(Putative inactive receptor-like protein kinase At1g64210)
5	38791001	unknown_gene-(Putative Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A)
5	38781001	CYP71D10-(Cytoome P450 71D10)
5	38768001	TPK1-(Two-pore potassium channel 1)
5	38753001	unknown_gene-(Hypothetical protein)
5	38747001	unknown_gene-(Putative uncharacterized protein)

10	34385001	UGT91C1-(UDP-glycosyltransferase 91C1)
10	34334001	unknown_gene-(Predicted protein (Fragment))
10	34317001	unknown_gene-(Hypothetical protein)
10	34316001	unknown_gene-(Putative Ankyrin repeat-containing protein (Fragment))
10	31494001	VLN3-(Hypothetical protein)
10	31457001	R1B-16-(Putative late blight resistance protein homolog R1B-16)
10	31425001	WAK5-(Wall-associated receptor kinase 5)
10	31890001	unknown_gene-(Putative Protein of unknown function (DUF630 and DUF632))
10	31985001	SECA2-(Protein translocase subunit SECA2, chloroplastic)
10	35361001	PIN6-(Probable auxin efflux carrier component 6)
10	2159001	PCMP-H24-(Putative Pentatricopeptide repeat-containing protein At4g02750)
10	24445001	ttc37-(Tetratricopeptide repeat (TPR)-like superfamily protein)
10	33623001	GT-2-(Putative Trihelix transcription factor GT-2)
10	33645001	unknown_gene-(Sphingomyelin synthetase family protein)
10	33677001	ERF112-(Putative uncharacterized protein)
10	33728001	PUR7-(Phosphoribosylaminoimidazole-succinocarboxamide synthase, chloroplastic)
10	33815001	Eif2d-(Putative Eukaryotic translation initiation factor 2D)
10	24440001	unknown_gene-(Putative uncharacterized protein)
10	24473001	SWI3B-(SWI/SNF complex subunit SWI3B)
10	24519001	CYCB2-4-(Cyclin-B2-4)
10	24662001	unknown_gene-(C2H2-like zinc finger protein)
10	24858001	unknown_gene-(unknown protein)
10	24871001	DA1-(Protein DA1)
10	34958001	LPIN2-(Hypothetical protein)
10	34916001	ARA12-(Putative Subtilisin-like protease)
10	34914001	At1g01540-(Probable serine/threonine-protein kinase At1g01540)
10	34885001	unknown_gene-(Hypothetical protein)
10	34753001	ACC1-(Acetyl-CoA carboxylase 1)
10	34639001	TT12-(Putative Protein TRANSPARENT TESTA 12)
10	34545001	STP5-(Sugar transport protein 5)
10	34486001	CSLC12-(Probable xyloglucan glycosyltransferase 12)
10	34428001	HEMA1-(Glutamyl-tRNA reductase 1, chloroplastic)
10	31548001	PP2A3-(Putative Protein AIG1)
10	16649001	Acy1a-(Putative Aminoacylase-1A)
10	16665001	unknown_gene-(Putative uncharacterized protein)
10	1423001	ISA1-(Isoamylase 1, chloroplastic)
10	1425001	At4g19050-(Putative disease resistance protein At4g19050)
10	31959001	unknown_gene-(Putative Ubiquitin system component Cue protein)
10	31988001	SPCC584.13-(Putative Uncharacterized amino-acid permease C584.13)
10	33830001	rbm24-(RNA-binding (RRM/RBD/RNP motifs) family protein)
10	33837001	LHCB5-(Chlorophyll a-b binding protein CP26, chloroplastic)
10	24506001	At4g15970-(Nucleotide-diphospho-sugar transferase family protein)
10	24597001	PER64-(Peroxidase 64)
10	24649001	unknown_gene-(unknown protein)
10	24777001	unknown_gene-(Hypothetical protein)
10	24911001	TPP1-(Thylakoidal processing peptidase 1, chloroplastic)
10	34686001	LAC14-(Laccase-14)

5	38737001	At5g39865-(Glutaredoxin family protein)
5	38732001	At5g55860-(WEB family protein At5g55860)
5	38724001	OPT1-(Oligopeptide transporter 1)
5	38720001	TMEM230-(Eukaryotic protein of unknown function (DUF872))
5	38710001	unknown_gene-(Hypothetical protein)
5	38707001	At1g28600-(Putative GDSL esterase/lipase At1g28600)
5	38696001	ATK4-(kinesin-like protein 1)
5	38688001	At1g55760-(BTB/POZ domain-containing protein At1g55760)
5	38687001	DDI1-(Putative DNA damage-inducible protein 1)
5	38662001	LRE-(Putative GPI-anchored protein LORELEI)
5	38654001	WIP1-(Putative WPP domain-interacting protein 1)
5	38653001	unknown_gene-(P-loop containing nucleoside triphosphate hydrolases superfamily protein)
5	38651001	unknown_gene-(Putative uncharacterized protein)
5	38627001	At1g53430-(Probable LRR receptor-like serine/threonine-protein kinase At1g56130)
5	38613001	cyp13-(cyclophilin 59)
5	38604001	At2g26730-(Predicted protein)
5	38590001	unknown gene (Putative uncharacterized protein)
5	38588001	unknown gene (unknown protein;plasma membrane)
5	38573001	unknown gene (Phosphoglycerate kinase, cytosolic)
5	38572001	unknown gene (Phosphoglycerate kinase, cytosolic)
5	38564001	mrpl19-(54S ribosomal protein L19, mitochondrial)
5	38557001	unknown gene (molecular_function unknown; chloroplast, vacuole)
5	38556001	unknown_gene-(molecular_function unknown; chloroplast, vacuole)
5	38554001	GAPC-(Glyceraldehyde-3-phosphate dehydrogenase, cytosolic)
5	38551001	MTP10-(Metal tolerance protein 10)
5	38548001	CYCB3-1-(Putative cyclin-B3-1)
5	38541001	unknown_gene-(Putative uncharacterized protein)
5	17009001	CYP97B2-(Cytoome P450 97B2, chloroplastic)
5	17016001	GABA-TP3-(Gamma aminobutyrate transaminase 3, chloroplastic)
5	17073001	NRT1.8-(Putative ABC transporter B family member 2)
5	17091001	nagk-(Putative N-acetyl-D-glucosamine kinase)
5	17103001	Cyb5d2-(Putative Neuferricin)
5	17106001	At1g61700-(DNA-directed RNA polymerases I, II, and III subunit RPABC5)
5	13183001	Ythdc2-(Putative Probable ATP-dependent RNA helicase YTHDC2)
5	13184001	PCMP-E12-(Pentatricopeptide repeat-containing protein At4g16470)
5	18209001	NAC042-(NAC domain-containing protein 42)
5	18220001	unknown_gene-(Putative Protein of unknown function DUF506, plant)
5	18225001	HAL3A-(Phosphopantothenoylcysteine decarboxylase)
5	18227001	RPP0A-(60S acidic ribosomal protein P0-1)
5	15742001	VHA-C-(V-type proton ATPase subunit C)
5	15748001	unknown gene (unknown protein)
5	15754001	unknown gene (unknown protein)
5	7324001	unknown gene (unknown protein)
5	20927001	LIP2-(Triacylglycerol lipase 2)
5	20893001	At1g04990-(Putative Zinc finger CCCH domain-containing protein 3)
5	33505001	At2g32990-(Endoglucanase 11)
10	34567001	unknown_gene-(Putative Outer arm dynein light chain 1 protein)
10	34472001	xynC-(glycosyl hydrolase family 10 protein / carbohydrate-binding domain-containing protein)
10	31505001	At1g22540-(Probable peptide/nitrate transporter At1g22540)
10	31450001	Fig4-(Phosphoinositide phosphatase family protein)
10	10113001	At4g09580-(Uncharacterized membrane protein At4g09580)
10	32009001	unknown_gene-(Putative wound-responsive family protein)
10	12014001	KOR-(Putative Endoglucanase 25)
10	24489001	MLO-H1-(MLO protein homolog 1)
10	24913001	At1g27040-(Putative Probable peptide/nitrate transporter At1g27040)
10	24917001	At1g47710-(Serpin-ZX)
10	34712001	ATPD-(ATP synthase delta chain, chloroplastic)
10	34484001	unknown_gene-(DNA binding)
10	34310001	unknown_gene-(Putative Uncharacterized protein)
10	31972001	At5g62680-(Probable peptide/nitrate transporter At5g62680)
10	33754001	CUTA-(Protein CutA, chloroplastic)
10	33807001	PCMP-H24-(Putative Pentatricopeptide repeat-containing protein At4g02750)
10	24861001	At1g75040-(Pathogenesis-related protein 5)
10	34395001	UPL2-(E3 ubiquitin protein ligase upl2, putative)
10	34314001	unknown_gene-(Hypothetical protein)
10	31511001	At1g22540-(Putative Probable peptide/nitrate transporter At1g22540)
10	31976001	At4g32640-(Protein transport protein Sec24-like At4g32640)
10	35222001	At4g35600-(Putative Probable serine/threonine-protein kinase Cx32, chloroplastic)
10	11266001	Scyl2-(Protein kinase family protein with ARM repeat domain)
10	24445001	ttc37-(Tetratricopeptide repeat (TPR)-like superfamily protein)
10	34380001	unknown_gene-(Golgi-body localisation protein domain ;RNA pol II promoter Fmp27 protein domain)
10	4650001	GYRA-(DNA gyrase subunit A, chloroplastic/mitochondrial)
10	31925001	BBE1-(Putative Reticuline oxidase)
10	33647001	At1g76760-(Thioredoxin Y1, chloroplastic)
10	8276001	WAK2-(Putative Wall-associated receptor kinase 2)
10	35218001	PERK9-(Putative Probable protein kinase At2g41970)
10	35288001	SDD1-(Putative Subtilisin-like protease SDD1)
10	31911001	unknown_gene-(Armadillo/beta-catenin-like repeat ; C2 calcium/lipid-binding domain (CaLB) protein)
10	24696001	gnb1l-(Putative Guanine nucleotide-binding protein subunit beta-like protein 1 homolog)
10	33720001	ATJ1-(Chaperone protein dnaJ 1, mitochondrial)
11	10267001	unknown_gene-(Putative Protein of unknown function (DUF3755))
11	10269001	unknown_gene-(high chlorophyll fluorescence phenotype 173)
11	19436001	MSP1-(Putative Protein MSP1)
11	19446001	At3g19850-(BTB/POZ domain-containing protein At3g19850)
11	19451001	thrB-(Putative Homoserine kinase)
11	19481001	SE2-(Putative Acidic endochitinase)
11	7397001	SFC1-(Putative Succinate/fumarate mitochondrial transporter)
11	4225001	unknown_gene-(Hypothetical protein)
11	19687001	T10-(Putative Uncharacterized protein C22orf25 homolog)
11	19685001	T10-(Putative Ser/Thr-rich protein T10 in DGCR region)
11	19650001	PRUA1-(Major allergen Pru ar 1)
11	19643001	PRMT6-(Probable protein arginine N-methyltransferase 6)

5	33506001	NRT1.3-(Nitrate transporter 1.3)
5	33540001	PERK8-(chitin elicitor receptor kinase 1)
5	33551001	unknown_gene-(Hypothetical protein)
5	33578001	CRK25-(Putative Cysteine-rich receptor-like protein kinase 25)
5	17322001	DREB2D-(Dehydration-responsive element-binding protein 2G, putative)
5	31650001	rhp16-(Helicase protein with RING/U-box domain)
5	31660001	ADT1-(Putative uncharacterized protein)
5	35013001	TT12-(Putative Protein TRANSPARENT TESTA 12)
5	35018001	GLR3.7-(Glutamate receptor 3.7)
5	35027001	GPT2-(Glucose-6-phosphate/phosphate translocator 2, chloroplastic)
5	35028001	PDF2-(Putative Homeobox-leucine zipper protein PROTODERMAL FACTOR 2)
5	35045001	PER3-(Peroxidase 3)
5	35090001	R1B-14-(Putative late blight resistance protein homolog R1C-3)
5	35100001	ATXR3-(Probable histone-lysine N-methyltransferase ATXR3)
5	9863001	BMY1-(Putative Glycoside hydrolase, family 14)
5	42122001	At4g20830-(Putative Reticuline oxidase-like protein)
5	42166001	LIP1-(Lipoyl synthase, mitochondrial)
5	42202001	unknown_gene-(Acyl-CoA N-acyltransferases (NAT) superfamily protein)
5	42206001	Lancl2-(Putative LanC-like protein 2)
5	42215001	EPHX2-(Putative Epoxide hydrolase 2)
5	42240001	unknown_gene-(Protein of unknown function (DUF1421))
5	42281001	RING1A-(Putative uncharacterized protein)
5	42287001	At1g03790-(Zinc finger CCCH domain-containing protein 2)
5	16786001	phbB-(Prohibitin-2)
5	16806001	VIP1-(Basic-leucine zipper (bZIP) transcription factor family protein)
5	16812001	At3g58100-(Glucan endo-1,3-beta-glucosidase-like protein 1)
5	16818001	GTE4-(Transcription factor GTE4)
5	16828001	unknown_gene-(Predicted protein)
5	16847001	Gs1l-(Putative Probable pseudouridine-5'-monophosphatase)
5	16911001	CYP72A1-(Secologanin synthase)
5	2675001	unknown_gene-(Hypothetical protein)
5	2664001	COQ3-(Putative 3-demethylubiquinone-9 3-methyltransferase)
5	2655001	AG2-(Floral homeotic protein AGAMOUS)
5	21565001	unknown gene-(unknown protein; chloroplast)
5	21539001	ARA12-(Putative Subtilisin-like protease)
5	21525001	unknown gene (unknown protein)
5	21523001	EFTS-(Elongation factor Ts, mitochondrial)
5	21507001	OsI_021818-(Putative Protein kinase G11A)
5	21497001	At3g14410-(Probable sugar phosphate/phosphate translocator At3g14410)
5	21453001	UBP15-(Ubiquitin carboxyl-terminal hydrolase 15)
5	21422001	unknown gene (unknown protein)
5	21415001	unknown gene (unknown protein)
5	21409001	TPS1-(Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 1)
5	21402001	sll0875-(Putative Uncharacterized membrane protein sll0875)
5	21389001	LRR-RLK-(Probable leucine-rich repeat receptor-like serine/threonine-protein kinase At3g14840)
5	21379001	ubtd2-(Ubiquitin domain-containing protein 2)
11	19639001	SPBC23E6.02-(Putative SWI/SNF-related matrix-associated actin-dependent regulator of omatin subfamily A member 3-like 2)
11	19617001	At1g05600-(Pentatricopeptide repeat-containing protein At1g05600)
11	19612001	ASP1-(Putative Aspartic proteinase Asp1)
11	19589001	LUG-(Transcriptional corepressor LEUNIG)
11	19588001	LUG-(STYLOSA protein)
11	19564001	ABCG40-(ABC transporter G family member 40)
11	19547001	unknown_gene-(Putative uncharacterized protein)
11	19541001	unknown_gene-(Putative uncharacterized protein)
11	19536001	unknown_gene-(unknown protein; chloroplast)
11	19522001	CYP76C4-(Putative Cytoome P450 76C4)
11	19521001	unknown_gene-(Protein of unknown function, DUF642)
11	19505001	AMT3-1-(Ammonium transporter 3 member 1)
11	33032001	At1g50180-(Putative disease resistance protein At1g50180)
11	33016001	At3g47570-(Putative Probable LRR receptor-like serine/threonine-protein kinase At3g47570)
11	33009001	AG118-(Acetylornithine aminotransferase, mitochondrial)
11	33004001	AGD4-(ADP-ribosylation factor GTPase-activating protein AGD4)
11	33003001	unknown_gene-(Ubiquitin-protein ligase, putative)
11	18501001	R1B-17-(Putative late blight resistance protein homolog R1B-17)
11	25560001	RGA2-(Putative uncharacterized protein)
11	25534001	At3g07100-(Protein transport protein Sec24-like At3g07100)
11	25528001	FLOT1-(Flotillin-like protein 1)
11	25527001	FMOGS-OX3-(Putative Flavin-containing monooxygenase FMO GS-OX3)
11	25524001	PSKR-(Phytosulfokine receptor 1)
11	25520001	AAMP-(Putative Angio-associated migratory cell protein)
11	25514001	unknown_gene-(Putative hAT transposon superfamily protein)
11	25510001	RPP8L2-(Putative Probable disease resistance RPP8-like protein 2)
11	25506001	At1g50180-(Putative disease resistance protein At1g50180)
11	25448001	ARA1-(L-arabinokinase)
11	25446001	unknown_gene-(Remorin family protein)
11	25444001	unknown_gene-(tobamovirus multiplication protein 3)
11	25424001	MGP-(Putative indeterminate(ID)-domain 4)
11	40795001	UGT85A2-(Putative UDP-glycosyltransferase 85A2)
11	6460001	ANP1-(Mitogen-activated protein kinase kinase kinase ANP1)
11	6462001	GLR1.3-(Putative Glutamate receptor 1.3)
11	6464001	GUX4-(Putative UDP-glucuronate:xylan alpha-glucuronosyltransferase 4)
11	33952001	OR23-(F-box/kelch-repeat protein OR23)
11	33965001	MGLL-(Putative Monoglyceride lipase)
11	33981001	R1B-14-(Putative late blight resistance protein homolog R1B-14)
11	34012001	RSL1D1-(Putative Ribosomal L1 domain-containing protein 1)
11	1342001	P1-(Hypothetical protein)
11	4782001	BTAF1-(Putative TATA-binding protein-associated factor 172)
11	4785001	Pyroxd2-(Pyridine nucleotide-disulfide oxidoreductase domain-containing protein 2)
11	4819001	Os04g0179200-(Momilactone A synthase)
11	4824001	At1g09820-(Putative Pentatricopeptide repeat (PPR-like) superfamily protein)
11	42931001	R1A-6-(Putative NB-ARC domain-containing disease resistance protein)
11	20441001	PERK2-(Protein kinase superfamily protein)

5	21349001	TFIP11-(Putative Tuftelin-interacting protein 11)	11	20461001	RCOM_1506700-(Probable aspartyl aminopeptidase)
5	21330001	HNRNPA1-(Hypothetical protein)	11	20497001	phg1b-(Putative phagocytic receptor 1b)
5	21317001	TCP4-(Transcription factor TCP4)	11	20506001	Bm1_28435-(Putative Macrophage migration inhibitory factor homolog)
5	21307001	HGO-(Homogentisate 1,2-dioxygenase)	11	20509001	phg1b-(Putative phagocytic receptor 1b)
5	21305001	BBR-(Putative RING/U-box superfamily protein)	11	20517001	GSO1-(Putative LRR receptor-like serine/threonine-protein kinase GSO1)
5	21275001	RPS20-(30S ribosomal protein S20, chloroplastic)	11	20545001	modA-(Neutral alpha-glucosidase AB)
5	21237001	cox17-(cytoome c oxidase 17)	11	20557001	unknown_gene-(Putative hydroxyproline-rich glycoprotein family protein)
5	21178001	CYP37-(Peptidyl-prolyl cis-trans isomerase CYP37, chloroplastic)	11	20567001	unknown_gene-(CONTAINS InterPro DOMAIN/s: Mediator complex subunit Med27 (InterPro:IPR021627))
5	21176001	unknown_gene-(S-adenosyl-L-methionine-dependent methyltransferases superfamily protein)	11	20569001	CYB561C-(Putative Probable transmembrane ascorbate ferrireductase 3)
5	21169001	TMEM184A-(Putative Transmembrane protein 184A)	11	20588001	unknown_gene-(Putative Ankyrin-repeat containing protein)
5	21157001	MYO5B-(myosin 2)	11	20610001	DTX1-(MATE efflux family protein DTX1)
5	21132001	At4g27290-(G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290)	11	20617001	unknown_gene-(Putative Ankyrin repeat family protein)
5	21024001	PLSC-(1-acyl-sn-glycerol-3-phosphate acyltransferase)	11	20628001	unknown_gene-(Hypothetical protein)
5	21011001	unknown_gene-(NADH:ubiquinone oxidoreductase, 17.2kDa subunit)	11	20635001	TMK1-(Probable receptor protein kinase TMK1)
5	21006001	unknown_gene-(Geranyl geranyl pyrophosphate synthase, putative)	11	20641001	At1g03050-(Putative clathrin assembly protein At1g03050)
5	20993001	Msh5-(Putative MutS protein homolog 5)	11	20643001	BGLU18-(Beta-glucosidase 18)
5	38851001	At2g32990-(Endoglucanase 11)	11	20644001	BGLU18-(Beta-glucosidase 18)
5	38831001	IAMT1-(Indole-3-acetate O-methyltransferase 1)	11	20675001	R1B-14-(Putative late blight resistance protein homolog R1B-14)
5	38829001	At3g20280-(Putative RING/FYVE/PHD zinc finger superfamily protein)	11	20677001	unknown_gene-(RNA-binding (RRM/RBD/RNP motifs) family protein)
5	38819001	TOP1-(DNA topoisomerase 1)	11	20679001	CCZ1-(Protein of unknown function (DUF1712))
5	38809001	GPDL2-(Probable glycerophosphoryl diester phosphodiesterase 2)	11	20720001	At2g38100-(Putative peptide/nitrate transporter At2g38100)
5	38763001	DEK-(Putative DEK domain-containing omatin associated protein)	11	20722001	At2g38100-(Putative peptide/nitrate transporter At2g38100)
5	38762001	NFYB3-(Nuclear transcription factor Y subunit B)	11	20732001	RDR1-(RNA-dependent RNA polymerase 1)
5	38760001	unknown_gene-(RNA-binding (RRM/RBD/RNP motifs) family protein)	11	20733001	RDR1-(RNA-dependent RNA polymerase 1)
5	38751001	At4g27520-(Mavicyanin, putative)	11	20735001	RDR1-(RNA-dependent RNA polymerase 1)
5	38729001	AIM32-(Sucrase/ferredoxin-like family protein)	11	18114001	NUDT17-(Nudix hydrolase 17, mitochondrial)
5	38718001	EMB2731-(UPF0172 protein At5g55940)	11	18101001	PER4-(Lignin-forming anionic peroxidase)
5	38711001	FPS1-(Farnesyl pyrophosphate synthase 1)	11	18091001	GTF3A-(Putative transcription factor IIIA)
5	38709001	unknown_gene-(Putative WW domain-containing protein)	11	18071001	RIE1-(E3 ubiquitin protein ligase RIE1)
5	38685001	EDC4-(Transducin/WD40 repeat-like superfamily protein)	11	18065001	unknown_gene-(Hypothetical protein)
5	38678001	AAP7-(Probable amino acid permease 7)	11	18008001	YKL091C-(Putative CRAL-TRIO domain-containing protein YKL091C)
5	38655001	ZAT6-(Putative C2H2 type zinc finger transcription factor family)	11	18007001	TLP-(Pathogenesis-related protein R major form)
5	38645001	BRL1-(Serine/threonine-protein kinase BRI1-like 1)	11	32939001	At3g07870-(Putative F-box protein At3g07870)
5	38582001	RUB2-(Ubiquitin-NEDD8-like protein RUB2)	11	32935001	RKL1-(Putative Probable inactive receptor kinase At1g48480)
5	38546001	rlmI-(Putative Ribosomal RNA large subunit methyltransferase I)	11	32933001	UBXN6-(plant UBX domain-containing protein 2)
5	17022001	SCL23-(Scarecrow-like protein 23)	11	32923001	APL-(Putative Myb family transcription factor APL)
5	17052001	At3g47570-(Putative Probable LRR receptor-like serine/threonine-protein kinase At3g47570)	11	32921001	PCR2-(Protein PLANT CADMIUM RESISTANCE 2)
5	17101001	ergic3-(Putative Endoplasmic reticulum-Golgi intermediate compartment protein 3)	11	32909001	PECS-2.1-(Pectinesterase 2)
5	9664001	RGA3-(Putative disease resistance protein RGA3)	11	32902001	unknown_gene-(Hypothetical protein)
5	937001	NPR3-(Regulatory protein NPR3)	11	32891001	AGD13-(Putative Probable ADP-ribosylation factor GTPase-activating protein AGD13)
5	10968001	At5g47720-(Probable acetyl-CoA acetyltransferase, cytosolic 2)	11	32849001	SCPL50-(Serine carboxypeptidase-like 50)
5	20967001	At1g61900-(Hypothetical protein)	11	32830001	R1B-12-(Putative late blight resistance protein homolog R1B-12)
5	20944001	unknown_gene-(HIT-type Zinc finger family protein)	11	32825001	FAB1-(FORMS APLOID AND BINUCLEATE CELLS 1C)
5	20939001	unknown_gene-(Putative uncharacterized protein)	11	32823001	PUB10-(U-box domain-containing protein 10)
5	33515001	B'GAMMA-(Serine/threonine protein phosphatase 2A 59 kDa regulatory subunit B' gamma isoform)	11	32817001	HIPP26-(Putative Heavy metal-associated isoprenylated plant protein 26)
5	3013001	RFL1-(Putative Disease resistance protein	11	32803001	R1A-6-(Putative late blight resistance protein homolog

		RFL1)			R1A-6)
5	35087001	At4g27220-(Putative BED finger-nbs-lrr resistance protein)	11	32793001	unknown_gene-(RING/FYVE/PHD zinc finger superfamily protein)
5	35128001	RPP13L4-(Putative Disease resistance RPP13-like protein 4)	11	32782001	unknown_gene-(unknown protein)
5	35130001	PCMP-H43-(Pentatricopeptide repeat-containing protein At3g12770)	11	32777001	At5g37990-(Putative Probable S-adenosylmethionine-dependent methyltransferase At5g37990)
5	35135001	unknown_gene-(Hypothetical protein)	11	32757001	ORC4-(Putative Origin recognition complex subunit 4)
5	35176001	MYB4-(Putative Predicted protein)	11	32725001	RPP13-(Putative late blight resistance protein homolog R1A-6)
5	35208001	HSP70-4-(Heat shock 70 kDa protein 4)	11	32717001	unknown_gene-(Hypothetical protein)
5	35212001	DGKI-(diacylglycerol kinase 5)	11	32697001	LPP3-(Putative lipid phosphate phosphatase 3, chloroplastic)
5	42091001	unknown_gene-(Wound-responsive family protein)	11	32678001	unknown_gene-(Hypothetical protein)
5	42095001	unknown_gene-(Wound-responsive family protein)	11	32668001	At1g68400-(Probable leucine-rich repeat receptor-like protein kinase At1g68400)
5	42178001	PXMP2-(Putative Peroxisomal membrane protein 2)	11	32659001	ZFP6-(Putative Zinc finger protein 6)
5	42198001	unknown_gene-(Putative Predicted protein)	11	32650001	glnS-(Glutamine--tRNA ligase)
5	42253001	unknown_gene-(Putative Protein of unknown function (DUF506))	11	32644001	At3g01520-(Putative Universal stress protein A-like protein)
5	42283001	unknown_gene-(targeting protein for XKLP2)	11	32641001	ENDO2-(Endonuclease 2)
5	16755001	TAT-(Tyrosine aminotransferase)	11	32617001	LBD41-(LOB domain-containing protein 41)
5	16822001	SBP65-(Putative late embryogenesis abundant domain-containing protein / LEA domain-containing protein)	11	32574001	PAN-(Transcription factor PERIANTHIA)
5	16826001	NECAP2-(Putative Adaptin ear-binding coat-associated protein 2)	11	32572001	At1g25520-(GDT1-like protein 4)
5	2681001	unknown_gene-(Putative TRICHOME BIREFRINGENCE-LIKE 43)	11	32571001	At1g25530-(Lysine histidine transporter-like 6)
5	2660001	drkD-(Integrin-linked protein kinase family)	11	32570001	med25-(phytoome and flowering time regulatory protein (PFT1))
5	21530001	ARA12-(Putative Subtilisin-like protease)	11	32564001	AOC4-(Allene oxide cyclase 4, chloroplastic)
5	21496001	UBP25-(Putative Ubiquitin carboxyl-terminal hydrolase 25)	11	32553001	GCFC1-(GC-rich sequence DNA-binding factor-like protein)
5	21395001	unknown_gene-(Hypothetical protein)	11	32551001	unknown_gene-(Transmembrane Fragile-X-F-associated protein)
5	21381001	GGH-(Gamma-glutamyl hydrolase)	11	32515001	ICMEL1-(Probable isoprenylcysteine alpha-carbonyl methylesterase ICMEL1)
5	21374001	unknown_gene-(Plant protein of unknown function (DUF641))	11	32497001	SPCC4G3.17-(Putative HD domain-containing protein C4G3.17)
5	21361001	PNKP-(phosphoesterase)	11	32487001	unknown_gene-(Uncharacterized protein)
5	21257001	ALF5-(MATE efflux family protein ALF5)	11	32485001	captC-(Putative Uncharacterized CDP-alcohol phosphatidyltransferase class-I family protein 3)
5	21202001	TSJT1-(Putative Stem-specific protein TSJT1)	11	32479001	At1g13570-(Putative F-box/FBD/LRR-repeat protein At1g13570)
5	21191001	BGLU14-(Probable inactive beta-glucosidase 14)	11	32463001	PHYLLO-(Protein PHYLLO, chloroplastic)
5	21179001	PXMP2-(Putative Peroxisomal membrane protein 2)	11	32460001	PHYLLO-(Protein PHYLLO, chloroplastic)
5	21161001	unknown_gene-(Putative Protein of unknown function (DUF761))	11	32458001	MENB-(1,4-Dihydroxy-2-naphthoyl-CoA synthase, peroxisomal)
5	21104001	DFRA-(Putative Dihydroflavonol-4-reductase)	11	32450001	PUB42-(Putative U-box domain-containing protein 43)
5	20997001	BRPF3-(Putative DNA-binding bromodomain-containing protein)	11	32447001	TP02_0244-(Putative Heat shock protein 90)
5	38812001	FIM2-(Fimbrin-like protein 2)	11	32446001	UGT89A2-(UDP-glycosyltransferase 89A2)
5	38802001	unknown_gene-(Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein)	11	32442001	guaA-(Putative DNA-3-methyladenine glycosylase)
5	38796001	WNK11-(Probable serine/threonine-protein kinase WNK11)	11	32436001	unknown_gene-(Hypothetical protein)
5	38795001	FRI-(Putative FRIGIDA like 1)	11	32429001	GEK1-(D-aminoacyl-tRNA deacylase)
5	38705001	FKBP16-1-(Peptidyl-prolyl cis-trans isomerase FKBP16-1, chloroplastic)	11	32417001	unknown_gene-(Putative uncharacterized protein)
5	38698001	SBE3-(1,4-alpha-glucan-branching enzyme 3, chloroplastic/amyloplastic)	11	32413001	unknown_gene-(Putative uncharacterized protein)
5	38694001	UKL4-(Uridine kinase-like protein 4)	11	32410001	AP1-(Floral homeotic protein APETALA 1)
5	38673001	ODO1-(Putative uncharacterized protein)	11	32406001	SPL6-(Putative uncharacterized protein)
5	38641001	CSN6A-(COP9 signalosome complex subunit 6a)	11	32405001	DL-(Protein DROOPING LEAF)
5	38614001	unknown gene (unknown protein)	11	32395001	fol1-(Putative Folic acid synthesis protein fol1)
5	38559001	CTR1-(Uncharacterized protein)	11	32382001	unknown_gene-(Putative Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain)
5	38545001	ALIS3-(ALA-interacting subunit 3)	11	32362001	At1g26460-(Pentatricopeptide repeat-containing protein At1g26460, mitochondrial)
5	17050001	GSO2-(Putative LRR receptor-like serine/threonine-protein kinase GSO2)	11	32355001	kti12-(Putative Protein KTI12 homolog)

5	17081001	TT12-(Protein TRANSPARENT TESTA 12)
5	17088001	ARF6-(Auxin response factor 6)
5	13163001	SE2-(Acidic endochitinase)
5	934001	Taf7-(Putative Transcription initiation factor TFIID subunit 7)
5	18224001	COP10-(Constitutive photomorphogenesis protein 10)
5	18254001	unknown_gene-(Hypothetical protein)
5	40805001	GRXS15-(Monothiol glutaredoxin-S15, mitochondrial)
5	20969001	RFL1-(Putative Disease resistance protein RFL1)
5	3711001	RGA3-(Putative disease resistance protein RGA3)
5	35049001	unknown_gene-(Hypothetical protein)
5	35058001	At5g16420-(Pentatricopeptide repeat-containing protein At5g16420, mitochondrial)
5	35099001	BHLH117-(Putative Uncharacterized protein (Fragment))
5	9860001	FH5-(Putative Formin-like protein 3)
5	42125001	TMEM184C-(Protein of unknown function (DUF300))
5	42138001	FTCD-(Putative transferases;folic acid binding)
5	42201001	PLT4-(Probable polyol transporter 4)
5	16820001	HI_0077-(Putative Uncharacterized protein HI_0077)
5	16854001	PPCC-(Phosphoenolpyruvate carboxylase 2)
5	16892001	NIFU3-(NifU-like protein 3, chloroplastic)
5	16908001	CYP72A1-(Secologanin synthase)
5	21568001	unknown_gene-(Magnesium transporter CorA-like family protein)
5	21397001	unknown_gene-(TRICHOME BIREFRINGENCE-LIKE 41)
5	21377001	sec61a-(Protein transport protein Sec61 subunit alpha)
5	21336001	PARK7-(Putative Protein DJ-1)
5	21170001	unknown_gene-(Hypothetical protein)
5	21126001	BHLH123-(Putative Transcription factor bHLH123)
5	21092001	BCAS3-(Putative homolog of yeast autophagy 18 (ATG18) F)
5	21050001	PBS1-(Serine/threonine-protein kinase PBS1)
5	21007001	unknown_gene-(Putative Protein of unknown function, DUF584)
5	38854001	PYRB1-(Aspartate carbamoyltransferase 1, chloroplastic)
5	38813001	Nsd1-(ENHANCED DOWNY MILDEW 2)
5	38793001	WRKY20-(Probable WRKY transcription factor 20)
5	38786001	PUB4-(ARM repeat superfamily protein)
5	38745001	UPL1-(E3 ubiquitin-protein ligase UPL1)
5	38664001	sec14-(Putative Sec14 cytosolic factor)
5	38637001	At1g16220-(Probable protein phosphatase 2C 6)
5	38584001	noc3l-(binding)
5	38578001	unknown_gene-(ARM repeat superfamily protein)
5	17019001	unknown_gene-(response to cadmium ion; plasma membrane)
5	13180001	PGM1-(2,3-bisphosphoglycerate-independent phosphoglycerate mutase)
5	924001	OBE4-(Putative Protein of unknown function DUF1423, plant)
5	18431001	unknown_gene-(Hypothetical protein)
5	20978001	FLA7-(Fasciclin-like arabinogalactan protein 7)
5	20871001	EMG1-(Putative Ribosomal RNA small subunit methyltransferase NEP1)
5	17317001	CBF5-(Predicted protein (Fragment))
5	7006001	unknown_gene-(Hypothetical protein)
5	7009001	Bp10-(L-ascorbate oxidase homolog)
5	35010001	TDC-(Aromatic-L-amino-acid decarboxylase)
11	32354001	Cbwd1-(Putative COBW domain-containing protein 1)
11	32353001	BGLU40-(Beta-glucosidase 40)
11	32344001	SNAP30-(Putative SNAP25 homologous protein SNAP30)
11	32335001	unknown_gene-(Putative Remorin family protein)
11	32309001	At1g69420-(Probable S-acyltransferase At1g69420)
11	32304001	DDB_G0285389-(Putative Protein UXT homolog)
11	32296001	Psmd11-(26S proteasome non-ATPase regulatory subunit 11)
11	32273001	unknown_gene-(PsbQ-like 2)
11	32257001	MYB44-(Putative uncharacterized protein)
11	32255001	DOF5.2-(Putative Dof zinc finger protein DOF5.2)
11	32233001	RPL34-(60S ribosomal protein L34)
11	32231001	unknown_gene-(CAAX amino terminal protease family protein)
11	32220001	mog1-(Putative Probable ran guanine nucleotide release factor)
11	32215001	PCMP-E54-(Pentatricopeptide repeat-containing protein At1g26900, mitochondrial)
11	32211001	TIF-(Hypothetical protein)
11	32209001	RPS9C-(40S ribosomal protein S9-2)
11	32208001	unknown_gene-(unknown protein)
11	32206001	SKIP11-(F-box/kelch-repeat protein SKIP11)
11	32200001	SUC3-(Sucrose transport protein SUC3)
11	32190001	IQD31-(Putative Protein IQ-DOMAIN 31)
11	32187001	unknown_gene-(Putative Peptidase S10, serine carboxypeptidase)
11	32186001	unknown_gene-(ssDNA-binding transcriptional regulator)
11	32169001	HAT5-(Homeodomain leucine zipper protein HDZ2)
11	32166001	HERC1-(Putative Probable E3 ubiquitin-protein ligase HERC1)
11	32161001	Mb2253c-(Putative Polynucleotidyl transferase, ribonuclease H-like superfamily protein)
11	32152001	ttc38-(Putative Tetratricopeptide repeat protein 38)
11	32143001	B3GALT18-(Probable beta-1,3-galactosyltransferase 18)
11	32132001	ALA3-(Phospholipid-transporting ATPase 3)
11	32128001	N-(Putative TMV resistance protein N)
11	32121001	RCOM_0699480-(UPF0392 protein RCOM_0530710)
11	32118001	SNL3-(Paired amphipathic helix protein Sin3-like 3)
11	32109001	unknown_gene-(unknown protein; endomembrane system)
11	32093001	ILL2-(IAA-amino acid hydrolase ILR1-like 2)
11	32073001	unknown_gene-(unknown protein)
11	32065001	unknown_gene-(Putative Auxin-induced protein 5NG4)
11	32052001	POT6-(Potassium transporter 6)
11	32049001	unknown_gene-(Putative ankyrin repeat family protein)
11	32045001	Prpf31-(Putative U4/U6 small nuclear ribonucleoprotein Prp31)
11	32026001	unknown_gene-(Putative basic helix-loop-helix (bHLH) DNA-binding superfamily protein)
11	1041001	At5g13400-(Probable peptide/nitrate transporter At5g13400)
11	1038001	FKBP19-(Peptidyl-prolyl cis-trans isomerase)
11	1016001	CRN-(Inactive leucine-rich repeat receptor-like protein kinase CORYNE)
11	38024001	At1g60420-(Putative Probable nucleoredoxin 1)
11	38042001	DRM2-(DNA (cytosine-5)-methyltransferase DRM2)
11	38043001	unknown_gene-(SBP (S-ribonuclease binding protein) family protein)
11	38046001	CAF2-(CRS2-associated factor 2, chloroplastic)
11	38084001	TT12-(Putative Protein TRANSPARENT TESTA 12)
11	38085001	TT12-(Putative Protein TRANSPARENT TESTA 12)

5	35019001	GLR3.4-(Glutamate receptor 3.4)	11	38089001	ABCB26-(ABC transporter B family member 26, chloroplastic)
5	42139001	At4g27220-(Putative Probable disease resistance protein At4g27220)	11	38090001	unknown_gene-(Hypothetical protein)
5	42159001	RGA3-(Putative disease resistance protein RGA3)	11	38093001	unknown_gene-(Putative Octicosapeptide/Phox/Bem1p family protein)
5	42204001	EXPB3-(Expansin-B3)	11	38114001	At3g26430-(GDSL esterase/lipase At3g26430)
5	42205001	At2g20760-(Putative Clathrin light chain 1)	11	38115001	At5g14450-(Putative GDSL esterase/lipase At5g14450)
5	16794001	SPBC1703.11-(Putative Optic atrophy 3 protein homolog)	11	38122001	SPAC869.07c-(Putative Alpha-galactosidase)
5	16801001	typA-(elongation factor family protein)	11	38147001	unknown_gene-(Pyridoxal-5'-phosphate-dependent enzyme family protein)
5	16824001	unknown_gene-(unknown protein)	11	38148001	SDAD1-(Putative Protein SDA1 homolog)
5	16843001	PGAAIR-(Ketol-acid reductoisomerase, chloroplastic)	11	38156001	HERC2-(Putative E3 ubiquitin-protein ligase HERC2)
5	16856001	unknown_gene-(Putative sequence-specific DNA binding transcription factors)	11	38158001	ALB3L1-(ALBINO3-like protein 1, chloroplastic)
5	21519001	VIT_01s0010g01870-(CASP-like protein VIT_01s0010g01870)	11	38183001	B'ETA-(Serine/threonine protein phosphatase 2A 59 kDa regulatory subunit B' eta isoform)
5	21509001	ATK4-(Di-glucose binding protein with Kinesin motor domain)	11	38187001	GT-1-(Trihelix transcription factor GT-1)
5	21503001	unknown_gene-(Hypothetical protein)	11	38189001	ABCC3-(Putative ABC transporter C family member 3)
5	21388001	LRR-RLK-(Probable leucine-rich repeat receptor-like serine/threonine-protein kinase At3g14840)	11	38200001	unknown_gene-(unknown protein; plasma membrane)
5	21364001	TULP7-(Tubby-like F-box protein 7)	11	38201001	RECQL5-(ATP-dependent DNA helicase Q-like 5)
5	21242001	At1g54610-(Protein kinase superfamily protein)	11	38213001	URE1-(Urease)
5	38547001	At3g13560-(Predicted protein)	11	38237001	CTDSPL2-(Putative CTD small phosphatase-like protein 2)
5	13169001	SE2-(Acidic endochitinase)	11	38246001	At1g11780-(Alpha-ketoglutarate-dependent dioxygenase alkB)
5	18412001	At4g27190-(Putative Disease resistance protein At4g27190)	11	38252001	At1g67325-(RanBP2-type zinc finger protein At1g67325)
5	33518001	unknown_gene-(Lycopene beta/epsilon cyclase protein)	11	38264001	unknown_gene-(Protein of unknown function (DUF 3339))
5	17311001	trmB-(Putative tRNA (guanine-N(7)-)-methyltransferase)	11	38265001	unknown_gene-(unknown protein)
5	35173001	GT6-(Putative UDP-glucose flavonoid 3-O-glucosyltransferase 6)	11	38276001	WRKY75-(WRKY DNA binding protein)
5	9858001	R1A-6-(Putative late blight resistance protein homolog R1A-6)	11	38294001	unknown_gene-(Putative GYF domain-containing protein)
5	42164001	SRF3-(Protein STRUBBELIG-RECEPTOR FAMILY 3)	11	38316001	unknown_gene-(C5734unknown protein)
5	42200001	POR1-(Protochlorophyllide reductase, chloroplastic)	11	38319001	unknown_gene-(Putative Predicted protein)
5	42219001	At5g02620-(Putative Ankyrin repeat-containing protein At5g02620)	11	19421001	ALATS-(Alanine--tRNA ligase)
5	42269001	RGA2-(Putative Disease resistance protein RGA2)	11	19435001	YSL7-(Probable metal-nicotianamine transporter YSL7)
5	16891001	FTSH2-(ATP-dependent zinc metalloprotease FTSH 2, chloroplastic)	11	19440001	PME24-(Putative pectinesterase/pectinesterase inhibitor 24)
5	2673001	R1B-8-(Putative late blight resistance protein homolog R1B-8)	11	19442001	At5g64813-(Uncharacterized GTP-binding protein At5g64813)
5	21549001	unknown_gene-(Uncharacterized protein)	11	19472001	unknown_gene-(Pyruvate kinase, cytosolic isozyme)
5	21532001	unknown_gene-(Hypothetical protein)	11	19478001	unknown_gene-(Putative Acidic endochitinase)
5	21297001	unknown_gene-(Putative Predicted protein)	11	19488001	unknown_gene-(Hypothetical protein)
5	21189001	BGLU16-(Putative Beta-glucosidase 16)	11	4220001	PYRD-(Dihydroorotate dehydrogenase (quinone), mitochondrial)
5	21060001	DDL-(FHA domain-containing protein DDL)	11	19676001	FKBP17-1-(Peptidyl-prolyl cis-trans isomerase)
5	38681001	RFS1-(Probable galactinol--sucrose galactosyltransferase 1)	11	19652001	SDE3-(Hypothetical protein)
5	38640001	PEX5-(Peroxisome biogenesis protein 5)	11	19613001	unknown_gene-(Plant protein of unknown function (DUF639))
5	916001	unknown_gene-(Hypothetical protein)	11	19594001	Cct7-(T-complex protein 1 subunit eta)
5	18205001	unknown_gene-(Hypothetical protein)	11	19561001	PDR1-(Pleiotropic drug resistance protein 1)
5	33475001	unknown_gene-(unknown protein)	11	19542001	At3g47570-(Putative Probable LRR receptor-like serine/threonine-protein kinase At3g47570)
5	33577001	CRK10-(Putative Cysteine-rich receptor-like protein kinase 10)	11	19535001	CCR4-6-(Putative Carbon catabolite repressor protein 4 homolog 6)
5	17356001	lpxB-(Putative Lipid-A-disaccharide synthase)	11	19528001	AKT1-(Potassium channel AKT1)
5	16797001	ACX3-(Acyl-coenzyme A oxidase 3, peroxisomal)	11	19509001	At3g54980-(Putative Pentatricopeptide repeat-containing protein At3g54980, mitochondrial)
5	16827001	unknown_gene-(Putative uncharacterized protein OSJNBa0095J15.6)	11	19508001	TRDMT1-(Putative tRNA (cytosine(38)-C(5))-methyltransferase)
5	2668001	unknown_gene-(Putative Cysteine/Histidine-rich C1 domain family protein)	11	19496001	mip120-(Tso1, putative)
5	2645001	GEP4-(haloacid dehalogenase (HAD) superfamily protein)	11	33017001	NLP7-(Putative Uncharacterized protein)
5	13179001	wdr26-(Putative WD repeat-containing protein 26)	11	32997001	HCF136-(Photosystem II stability/assembly factor HCF136, chloroplastic)

5	18255001	Cmbl-(Putative Carboxymethylenebutenolidase homolog)
5	35096001	R1A-6-(Putative late blight resistance protein homolog R1A-3)
5	42273001	TUL1-(RING/U-box superfamily protein)
5	38571001	At1g56190-(Phosphoglycerate kinase, cytosolic)
5	38544001	ALDH5F1-(Succinate-semialdehyde dehydrogenase, mitochondrial)
5	2677001	arcA-(Putative Actin-related protein 2/3 complex subunit 1)
5	21587001	unknown_gene-(Putative Predicted protein)
5	21064001	At3g59230-(Putative F-box/LRR-repeat protein At3g59230)
5	38672001	Psme4-(Putative Proteasome activator complex subunit 4)
5	16884001	WRKY69-(Putative Probable WRKY transcription factor 69)
5	13173001	SE2-(Acidic endochitinase SE2)
5	38549001	unknown_gene-(Uncharacterized conserved protein (DUF2358))
5	42218001	At5g02620-(Putative Ankyrin repeat-containing protein At5g02620)
5	35095001	R1A-6-(Putative late blight resistance protein homolog R1A-6)
5	33541001	PERK1-(Putative Proline-rich receptor-like protein kinase PERK3)
5	794001	RGA1-(Putative disease resistance protein RGA1)
6	23165001	GAUT7-(Probable galacturonosyltransferase 7)
6	23178001	unknown_gene-(Putative Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)
6	23180001	At1g12150-(Putative WEB family protein At5g55860)
6	23181001	CML42-(Calcium-binding protein CML42)
6	23196001	NSI-(Acetyltransferase NSI)
6	23198001	At5g58300-(Probable inactive receptor kinase At5g58300)
6	23203001	unknown_gene-(Hypothetical protein)
6	23210001	ALA1-(Phospholipid-transporting ATPase 1)
6	23214001	unknown_gene-(Putative Transmembrane proteins 14C)
6	23219001	unknown_gene-(Hypothetical protein)
6	23220001	CAD1-(MACPF domain-containing protein CAD1)
6	23224001	DTXL1-(Putative MATE efflux family protein 5)
6	23232001	unknown_gene-(unknown protein)
6	23234001	PSAP-(Putative Predicted protein)
6	23255001	TS2-(Sex determination protein tasselseed-2)
6	23256001	SCAR2-(Hypothetical protein)
6	23272001	ints4-(Putative ARM repeat superfamily protein)
6	23280001	DTX44-(Hypothetical protein)
6	23306001	AMT3-1-(Ammonium transporter 3 member 1)
6	23322001	B19.3-(Late embryogenesis abundant protein B19.3)
6	23327001	GRXS16-(Monothiol glutaredoxin-S16, chloroplastic)
6	23329001	sacm1l-(SAC domain-containing protein 8)
6	23335001	At3g47300-(SelT-like protein)
6	23337001	GT-3A-(Trihelix transcription factor GT-3a)
6	23342001	AL1-(PHD finger protein ALFIN-LIKE 1)
6	23349001	unknown_gene-(Putative RING/U-box superfamily protein)
6	23354001	At5g01460-(LIMR family protein At5g01460)
6	23356001	unknown_gene-(S-adenosyl-L-methionine-dependent methyltransferases superfamily protein)
6	23360001	DDB_G0277179-(Protein of unknown function, DUF647)
6	23362001	unknown_gene-(RING/U-box superfamily protein)
11	32972001	At5g23160-(Putative Predicted protein)
11	25562001	TIPIN-(Putative zinc knuckle (CCHC-type) family protein)
11	25546001	GSO1-(Putative LRR receptor-like serine/threonine-protein kinase GSO1)
11	25522001	unknown_gene-(Putative Protein of unknown function, DUF599)
11	25436001	UBXN7-(UBX domain-containing protein)
11	25421001	Smarcad1-(SNF2 domain-containing protein / helicase domain-containing protein)
11	6465001	unknown_gene-(Plant protein 1589 of unknown function)
11	33974001	R1B-23-(Putative Disease resistance protein (CC-NBS-LRR class) family)
11	34018001	ccbl2-(Putative Kynurenine--oxoglutarate transaminase 3)
11	34037001	R1B-17-(Putative Disease resistance protein (CC-NBS-LRR class) family)
11	34046001	R1A-6-(Putative late blight resistance protein homolog R1A-6)
11	34048001	unknown_gene-(Hypothetical protein)
11	34051001	R1B-17-(Putative NB-ARC domain-containing disease resistance protein)
11	20426001	At1g14600-(Putative uncharacterized protein)
11	20452001	At4g27290-(G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290)
11	20459001	PTR2-(Peptide transporter PTR2)
11	20468001	HAK17-(Probable potassium transporter 17)
11	20474001	SD25-(G-type lectin S-receptor-like serine/threonine-protein kinase SD2-5)
11	20512001	XSP1-(Putative Cucumisin)
11	20521001	Os10g0113000-(NAD(P)H-dependent 6'-deoxychalcone synthase)
11	20533001	Os05g0446300-(Protein BUD31 homolog 2)
11	20542001	ABCB11-(ABC transporter B family member 11)
11	20546001	ABCB11-(ABC transporter B family member 11)
11	20605001	R1B-17-(Putative late blight resistance protein homolog R1B-17)
11	20659001	CHX20-(Cation/H(+) antiporter 20)
11	20672001	R1A-6-(Putative NB-ARC domain-containing disease resistance protein)
11	20694001	TPS6-(Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 6)
11	20695001	At1g14780-(MACPF domain-containing protein At1g14780)
11	20727001	R1A-(Putative Late blight resistance protein R1-A)
11	20734001	RDR1-(RNA-dependent RNA polymerase 1)
11	18075001	vac14-(ARM repeat superfamily protein)
11	18058001	MAP70.1-(Microtubule-associated protein 70-1)
11	18054001	GSO2-(Putative LRR receptor-like serine/threonine-protein kinase GSO2)
11	18048001	EXS-(Putative Leucine-rich repeat receptor protein kinase EXS)
11	18022001	At5g38100-(Putative Probable S-adenosylmethionine-dependent methyltransferase At5g38100)
11	32864001	At1g04910-(Putative DUF246 domain-containing protein At1g04910)
11	32856001	DMTF1-(Hypothetical protein)
11	32847001	SCPL50-(Uncharacterized protein)
11	32818001	unknown_gene-(Putative uncharacterized protein)
11	32812001	ABCG7-(ABC transporter G family member 7)
11	32795001	unknown_gene-(unknown protein; endomembrane system)
11	32754001	FATB1-(Putative fatA acyl-ACP thioesterase)
11	32751001	Dhx36-(DEA(D/H)-box RNA helicase family protein)
11	32676001	At1g18390-(Probable serine/threonine-protein kinase At1g18390)
11	32675001	mcfW-(Putative Mitochondrial substrate carrier family protein W)
11	32640001	unknown_gene-(unknown protein)

6	23366001	At1g53430-(Putative Probable LRR receptor-like serine/threonine-protein kinase At1g53420)	11	32609001	DFR-(Putative Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase)
6	23367001	CPL2-(RNA polymerase II C-terminal domain phosphatase-like 2)	11	32582001	PCR11-(Protein PLANT CADMIUM RESISTANCE 11)
6	23378001	At2g38100-(Putative peptide/nitrate transporter At2g38100)	11	32580001	At2g38100-(Putative peptide/nitrate transporter At2g38100)
6	23403001	DET2-(Probable steroid reductase DET2)	11	32569001	unknown_gene-(Putative Endosomal targeting BRO1-like domain-containing protein)
6	23408001	RTNLB12-(Reticulon-like protein B12)	11	32557001	STN7-(Serine/threonine-protein kinase STN7, chloroplastic)
6	23412001	C3orf32-(Putative Uncharacterized protein C3orf32)	11	32554001	NAC008-(NAC domain-containing protein 8)
6	23415001	FRK2-(Putative Fructokinase-2)	11	32538001	Lsm14b-(decapping 5)
6	23422001	Os03g0267300-(Fructose-1,6-bisphosphatase, chloroplastic)	11	32537001	At5g65770-(Putative nuclear matrix constituent protein-related)
6	23434001	unknown_gene-(Putative uncharacterized protein)	11	32456001	WIT2-(Putative WPP domain-interacting tail-anchored protein 2)
6	23446001	unknown_gene-(Putative Encodes a protein involved in salt tolerance, names SIS (Salt Induced Serine rich).)	11	32317001	RMD1-(Protein of unknown function (DUF155))
6	23454001	At2g37900-(Putative peptide/nitrate transporter At2g37900)	11	32314001	Bub3-(Putative Mitotic checkpoint protein BUB3)
6	23470001	At3g53850-(CASP-like protein At3g53850)	11	32283001	SLC25A27-(Putative Mitochondrial uncoupling protein 4)
6	23476001	LHW-(Putative Transcription factor LHW)	11	32239001	unknown_gene-(RING/FYVE/PHD zinc finger superfamily protein)
6	23478001	TR1-(Putative Tropinone reductase 1)	11	32218001	TCP14-(Putative BHLH (Fragment))
6	23492001	FES1-(Putative Hsp70 nucleotide exchange factor FES1)	11	32194001	mybl2-(myb domain protein 88)
6	23493001	unknown_gene-(unknown protein;s unknown; chloroplast)	11	32146001	HIPL1-(HIPL1 protein)
6	23498001	nep1-(Putative Aspartic proteinase nepenthesin-1)	11	32126001	PP2A2-(Serine/threonine-protein phosphatase PP2A-2 catalytic subunit)
6	23499001	LAC17-(Laccase-17)	11	32125001	unknown gene (unknown protein; endomembrane system)
6	23500001	LAC4-(Laccase-4)	11	32116001	At1g59900-(Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial)
6	23503001	LAC17-(Laccase-17)	11	32081001	At1g50920-(Nucleolar GTP-binding protein 1)
6	23507001	FTSH10-(ATP-dependent zinc metalloprotease FTSH 10, mitochondrial)	11	32055001	TPS10-(Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10)
6	23508001	SPAC24B11.05-(Haloacid dehalogenase-like hydrolase (HAD) superfamily protein)	11	32044001	ALDH2B7-(Aldehyde dehydrogenase family 2 member B7, mitochondrial)
6	23512001	rhbdf1-(RHOMBOID-like 1)	11	1046001	LEP-(Hypothetical protein)
6	23518001	AS1-(Transcription factor AS1)	11	1024001	SUVH4-(Hypothetical protein)
6	23522001	MYB3R-1-(myb domain protein 3r-5)	11	38037001	MENB-(1,4-Dihydroxy-2-naphthoyl-CoA synthase, peroxisomal)
6	23526001	PLL5-(Probable protein phosphatase 2C 4)	11	38078001	unknown_gene-(armadillo repeat only 4)
6	23528001	Alg10b-(Putative Dol-P-Glc:Glc(2)Man(9)GlcNAc(2)-PP-Dol alpha-1,2-glucosyltransferase)	11	38086001	TT12-(Putative Protein TRANSPARENT TESTA 12)
6	23536001	DOF2.4-(Putative Dof zinc finger protein DOF2.4)	11	38143001	Os02g0190300-(Putative multidrug resistance protein)
6	23544001	unknown_gene-(Hypothetical protein)	11	38163001	unknown_gene-(G-protein coupled receptors;GTPase activators)
6	23554001	TIC32-(Short-chain dehydrogenase TIC 32, chloroplastic)	11	38180001	CXE16-(Probable carboxylesterase 16)
6	23555001	At3g09470-(UNC93-like protein 3)	11	38191001	GAPC-(Glyceraldehyde-3-phosphate dehydrogenase, cytosolic)
6	23576001	CVP2-(Type I inositol 1,4,5-trisphosphate 5-phosphatase CVP2)	11	38194001	LHT1-(Lysine histidine transporter 1)
6	23593001	At3g12360-(Ankyrin repeat-containing protein At3g12360)	11	38209001	unknown_gene-(Protein of unknown function (DUF3537))
6	23594001	MAKR4-(Putative Probable membrane-associated kinase regulator 4)	11	38220001	SPAC644.07-(P-loop containing nucleoside triphosphate hydrolases superfamily protein)
6	23596001	LPIN2-(Putative uncharacterized protein)	11	38225001	At1g66830-(Putative Probable inactive leucine-rich repeat receptor-like protein kinase At1g66830)
6	23610001	nfrkb-(Hypothetical protein)	11	38227001	RPL17B-(60S ribosomal protein L17)
6	23614001	unknown_gene-(Putative Predicted protein)	11	38251001	At1g27950-(Putative Uncharacterized GPI-anchored protein At1g27950)
6	23616001	unknown_gene-(Putative uncharacterized protein)	11	19438001	Os04g0620700-(Hypothetical protein)
6	23621001	ASG4-(Transcription factor ASG4)	11	19448001	unknown_gene-(Putative Transducin/WD40 repeat-like superfamily protein)
6	23631001	WRKY44-(Putative WRKY transcription factor 44)	11	19466001	Os10g0493600-(Alpha-galactosidase)
6	23638001	HCF152-(Pentatricopeptide repeat-containing protein At3g09650, chloroplastic)	11	19630001	unknown_gene-(Putative uncharacterized protein)
6	23641001	ATM-(Hypothetical protein)	11	19530001	CLA1-(1-deoxy-D-xylulose-5-phosphate synthase 1, chloroplastic)
6	23646001	IRX9-(Probable beta-1,4-xylosyltransferase IRX9)	11	19512001	RAN3-(ras-related nuclear protein 4)
6	23650001	RH57-(DEAD-box ATP-dependent RNA helicase 57)	11	33038001	RDL6-(Putative Probable disease resistance protein RDL6)
6	23652001	Os01g0158000-(Importin subunit alpha-2)	11	25554001	unknown_gene-(glutaredoxin-related)

6	23658001	unknown_gene-(Putative Predicted protein)
6	23675001	NAC029-(Putative NAC domain-containing protein 29)
6	23692001	unknown_gene-(Putative uncharacterized protein)
6	23696001	ARF18-(Auxin response factor 18)
6	23702001	IDH5-(3-isopropylmalate dehydrogenase, chloroplastic)
6	23709001	unknown_gene-(Hypothetical protein)
6	23718001	TCP11-(TCP transcription factor 19)
6	23719001	rpoD-(RNApolymerase sigma-subunit F)
6	23726001	At1g56190-(Putative Phosphoglycerate kinase, cytosolic)
6	23738001	ABCB1-(ABC transporter B family member 1)
6	23742001	4CLL7-(4-coumarate--CoA ligase-like 7)
6	23743001	unknown_gene-(unknown protein; chloroplast)
6	42953001	unknown_gene-(Major facilitator superfamily protein)
6	42955001	unknown_gene-(unknown protein; chloroplast)
6	42957001	At3g53190-(Probable pectate lyase 12)
6	42960001	Rchy1-(Putative RING finger and CHY zinc finger domain-containing protein 1)
6	42968001	sf3a2-(Putative Splicing factor 3A subunit 2)
6	42974001	heatr7a-(Putative HEAT repeat-containing protein 7A homolog)
6	42977001	UGT73C4-(UDP-glycosyltransferase 73C4)
6	42992001	unknown_gene-(ATSMC2, putative)
6	42993001	CYP97C1-(Carotene epsilon-monooxygenase, chloroplastic)
6	43001001	VPS37-1-(Vacuolar protein-sorting-associated protein 37 homolog 1)
6	43004001	RH38-(DEAD-box ATP-dependent RNA helicase 38)
6	43007001	At2g36660-(Probable polyadenylate-binding protein At2g36660)
6	43010001	FKBP16-4-(Peptidyl-prolyl cis-trans isomerase FKBP16-4, chloroplastic)
6	43011001	CHUP1-(Putative uncharacterized protein)
6	43021001	At5g03795-(Probable glycosyltransferase At5g03795)
6	43024001	unknown_gene-(Putative Embryonic protein DC-8)
6	43031001	unknown_gene-(Putative Pyruvate kinase, cytosolic isozyme)
6	43039001	CYP76A2-(Putative Cytoome P450 76A2)
6	43047001	PRXIIE-(Peroxiredoxin-2E, chloroplastic)
6	43076001	FBA-(Fructose-bisphosphate aldolase, cytoplasmic isozyme)
6	43079001	GT-2-(Putative Trihelix transcription factor GT-2)
6	43087001	unknown_gene-(Putative growth-regulating factor 4)
6	43088001	SBE2.2-(1,4-alpha-glucan-branching enzyme 2-2, chloroplastic/amyloplastic)
6	43091001	unknown_gene-(Calcineurin-like metallo-phosphoesterase superfamily protein)
6	43093001	ABCG39-(ABC transporter G family member 39)
6	43094001	FBL11-(Putative BTB/POZ domain-containing protein FBL11)
6	43096001	MRE11-(Putative Double-strand break repair protein MRE11)
6	43099001	At4g24660-(homeobox protein 21)
6	43104001	unknown_gene-(IQ calmodulin-binding motif family protein)
6	43114001	URH1-(Uridine nucleosidase 1)
6	43116001	TAF12-(Putative uncharacterized protein)
6	43139001	At5g03905-(Iron-sulfur assembly protein IscA-like 2, mitochondrial)
6	43146001	HIS6-(1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase, chloroplastic)
6	43153001	APL-(Homeodomain-like superfamily protein)
11	25526001	FLOT1-(Flotillin-like protein 1)
11	25525001	AKR2-(Putative Ankyrin repeat-containing protein P16F5.05c)
11	25471001	UGT76E11-(Putative UDP-glycosyltransferase 76E11)
11	25462001	UGT76E1-(Putative UDP-glycosyltransferase 76E1)
11	25452001	At2g02160-(Putative Zinc finger CCCH domain-containing protein 32)
11	34004001	At3g12360-(Putative Ankyrin repeat family protein)
11	34035001	FAO1-(Long-chain-alcohol oxidase FAO1)
11	1337001	PUR5-(Phosphoribosylformylglycinamidine cyclo-ligase, chloroplastic/mitochondrial)
11	42936001	PME40-(Putative Pectinesterase 2)
11	42937001	PME40-(Probable pectinesterase/pectinesterase inhibitor 40)
11	20473001	ELC-(Protein ELC)
11	20538001	IAR1-(IAA-alanine resistance protein 1)
11	20551001	ANN5-(Annexin D5)
11	20554001	PAP8-(Putative Purple acid phosphatase 8)
11	20579001	At5g02620-(Putative ankyrin repeat containing protein, identical)
11	20678001	SDS-(Putative Cyclin-SDS)
11	20683001	Gulo-(D-arabinono-1,4-lactone oxidase family protein)
11	20687001	GULO-(D-arabinono-1,4-lactone oxidase family protein)
11	20690001	VIT1-(Vacuolar iron transporter 1)
11	18045001	At5g02620-(Putative Ankyrin repeat-containing protein At5g02620)
11	18042001	DRP1C-(Dynamin-related protein 1C)
11	18040001	R1B-12-(Hypothetical protein)
11	32940001	At5g02620-(Putative Ankyrin repeat-containing protein At5g02620)
11	32928001	med23-(CONTAINS InterPro DOMAIN/s: Mediator complex subunit Med23 (InterPro:IPR021629)
11	32862001	SULTR3;3-(Probable sulfate transporter 3.3)
11	32813001	XYLT1-(Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein)
11	32805001	COBL7-(COBRA-like protein 7)
11	32801001	GT6-(Putative UDP-glucose flavonoid 3-O-glucosyltransferase 6)
11	32776001	alxA-(Putative ALG-2 interacting protein X)
11	32774001	pKIWI502-(Fruit protein pKIWI502)
11	32761001	DTX1-(Putative MATE efflux family protein DTX1)
11	32748001	At1g22950-(Uncharacterized PKHD-type hydroxylase At1g22950)
11	32706001	At1g68200-(Putative Zinc finger CCCH domain-containing protein 15)
11	32696001	unknown_gene-(Putative Octicosapeptide/Phox/Bem1p family protein)
11	32664001	BX1-(Indole-3-glycerol phosphate lyase, chloroplastic)
11	32646001	unknown_gene-(unknown protein)
11	32594001	Prpf4b-(Protein kinase superfamily protein)
11	32567001	ARR19-(myb-like transcription factor family protein)
11	32547001	CCDC130-(Putative Coiled-coil domain-containing protein 130)
11	32513001	PHO1-H1-(Phosphate transporter PHO1 homolog 1)
11	32502001	ALA9-(Putative phospholipid-transporting ATPase 9)
11	32491001	Ipo9-(Putative Importin-9)
11	32482001	SAMDC-(S-adenosylmethionine decarboxylase proenzyme)
11	32477001	udkC-(Putative Uridine-cytidine kinase C)
11	32448001	RPOT1-TOM-(DNA-directed RNA polymerase 1B, mitochondrial)
11	32433001	16OMT-(Hypothetical protein)

6	43167001	FFC-(Signal recognition particle 54 kDa protein, chloroplastic)
6	43179001	INV1-(Beta-fructofuranosidase, insoluble isoenzyme 1)
6	43180001	INV1-(Beta-fructofuranosidase, insoluble isoenzyme 1)
6	43182001	INV1-(Beta-fructofuranosidase, insoluble isoenzyme 1)
6	31418001	SPY-(Probable UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SPINDLY)
6	31416001	RP120-(Putative Uncharacterized protein RP120)
6	31414001	At1g08370-(mRNA-decapping enzyme-like protein)
6	31405001	At5g06250-(Putative B3 domain-containing protein At3g11580)
6	31395001	unknown_gene-(Putative Ovate family protein)
6	31391001	E2FA-(Transcription factor E2FA)
6	31384001	CLPB1-(Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein)
6	31381001	SYP24-(Putative NDR1/HIN1-like 2)
6	31375001	unknown_gene-(Hypothetical protein)
6	31372001	At4g31480-(Coatomer subunit beta-1)
6	31360001	PUB22-(E3 ubiquitin-protein ligase PUB22)
6	31356001	DHX36-(Putative Probable ATP-dependent RNA helicase DHX36)
6	31345001	unknown_gene-(Hypothetical protein)
6	31328001	unknown_gene-(Putative Uncharacterized protein)
6	31309001	AMP1-(Probable glutamate carboxypeptidase 2)
6	31305001	At3g01520-(Putative Adenine nucleotide alpha hydrolases-like superfamily protein)
6	31290001	unknown_gene-(C2 calcium/lipid-binding plant phosphoribosyltransferase family protein)
6	31282001	Nom1-(Putative uncharacterized protein)
6	31280001	METE-(5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase)
6	31273001	STP7-(Sugar transport protein 7)
6	31270001	Tm9sf4-(Putative Transmembrane 9 superfamily member 4)
6	31263001	unknown_gene-(unknown protein)
6	31251001	unknown_gene-(chlororespiratory reduction 6)
6	31240001	micu1-(Putative Calcium uptake protein 1, mitochondrial)
6	31238001	Nub1-(ubiquitin-associated (UBA)/TS-N domain-containing protein)
6	31236001	Ttc1-(Octicosapeptide/Phox/Bem1p (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protein)
6	31219001	TYRAAT2-(Arogenate dehydrogenase 2, chloroplastic)
6	31202001	CBSCLC6-(Putative chloride channel-like protein CLC-g)
6	31199001	At4g00330-(calmodulin-binding receptor-like cytoplasmic kinase 3)
6	31159001	At3g15810-(Putative Protein LURP-one-related 12)
6	31153001	BCB-(Putative Umecyanin)
6	31144001	unknown_gene-(Putative Tetratricopeptide repeat (TPR)-like superfamily protein)
6	31130001	SPX2-(SPX domain-containing protein 2)
6	31128001	PER25-(Peroxidase 25)
6	31121001	unknown_gene-(InterPro DOMAIN/s: Methyltransferase FkbM (InterPro:IPR006342))
6	31120001	NUP205-(Protein of unknown function (DUF3414))
6	31104001	At2g37990-(Ribosome biogenesis regulatory protein homolog)
6	31083001	PCMP-H12-(Putative Pentatricopeptide repeat-containing protein At1g08070)
6	31081001	unknown_gene-(Early nodulin-93)
6	31077001	At4g17486-(Putative Desumoylating isopeptidase 2)
11	32422001	unknown_gene-(Putative Uncharacterized protein)
11	32412001	NOP14-(Putative Nucleolar protein 14)
11	32385001	CDC48B-(Cell division control protein 48 homolog B)
11	32323001	PCMP-E66-(Putative pentatricopeptide repeat-containing protein At1g69350, mitochondrial)
11	32280001	APC2-(Anaphase-promoting complex subunit 2)
11	32223001	DDB_G0276861-(Putative FAM203 family protein DDB_G0276861)
11	32217001	HVA22A-(HVA22-like protein a)
11	32177001	POR1-(Mitochondrial outer membrane protein porin of 36 kDa)
11	32170001	NRT1.2-(Nitrate transporter 1.2)
11	32138001	exoc8-(Vps51/Vps67 family (components of vesicular transport) protein)
11	32117001	ISE2-(DEAD-box ATP-dependent RNA helicase ISE2, chloroplastic)
11	32112001	unknown_gene-(Putative uncharacterized protein)
11	32053001	POT6-(Potassium transporter 6)
11	32028001	unknown_gene-(Plant protein of unknown function (DUF936))
11	38053001	KNAT6-(Homeobox protein knotted-1-like 6)
11	38125001	unknown_gene-(Putative sphere organelles protein-related)
11	38149001	ORP1D-(Oxysterol-binding protein-related protein 1D)
11	38196001	Pola2-(DNA polymerase alpha 2)
11	38199001	unknown_gene-(Putative Lojap-related protein)
11	38217001	unknown_gene-(plasma membrane; BEST match: nucleolar protein gar2-related
11	38314001	PDH2-(Pyruvate dehydrogenase E1 component subunit beta, mitochondrial)
11	38318001	COL15-(Putative uncharacterized protein)
11	19651001	SDE3-(Hypothetical protein)
11	19614001	GT4-(Putative UDP-rhamnose:rhamnosyltransferase 1)
11	19562001	PDR1-(Pleiotropic drug resistance protein 1)
11	33028001	unknown gene (BEST match: Polyketide cyclase / dehydrase and lipid transport protein)
11	25467001	UGT76E3-(Putative UDP-glycosyltransferase 76E3)
11	33957001	Taf12-(Transcription initiation factor TFIID subunit 12)
11	34009001	unknown_gene-(alpha/beta-Hydrolases superfamily protein)
11	34015001	RPP8-(Putative Disease resistance protein RPP8)
11	34025001	R1B-12-(Putative late blight resistance protein homolog R1B-12)
11	42929001	UCHL3-(Putative Ubiquitin carboxyl-terminal hydrolase isozyme L3)
11	20531001	At1g25240-(Putative clathrin assembly protein At1g25240)
11	18120001	CRRSP12-(Cysteine-rich repeat secretory protein 12)
11	18047001	RPL17B-(Hypothetical protein)
11	18020001	R1A-6-(Putative late blight resistance protein homolog R1A-6)
11	32913001	CEL1-(Endoglucanase 8)
11	32852001	unknown_gene-(Putative uncharacterized protein)
11	32814001	IGS1-(Isoeugenol synthase 1)
11	32763001	DTX1-(MATE efflux family protein DTX1)
11	32743001	CHIT3-(Acidic endochitinase)
11	32599001	pdhC-(Putative Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex)
11	32586001	PP2AA2-(Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform)
11	32560001	At2g14440-(Putative leucine-rich repeat receptor-like serine/threonine-protein kinase At2g14440)

6	31076001	LYPLA2-(Putative Acyl-protein thioesterase 2)	11	32444001	unknown_gene-(Hypothetical protein)
6	41983001	CYP734A1-(Cytoome P450 734A1)	11	32384001	unknown_gene-(Hypothetical protein)
6	41982001	RAN3-(GTP-binding nuclear protein Ran-3)	11	32372001	PAP1-(Probable inactive purple acid phosphatase 1)
6	41971001	strap-(Serine-threonine kinase receptor-associated protein)	11	32248001	RNALX-(Intracellular ribonuclease LX)
6	41968001	At3g10130-(SOUL heme-binding family protein)	11	32188001	CBSCBS2-(SNF1-related protein kinase regulatory subunit gamma-1-like)
6	41943001	TDRD3-(Putative Domain of unknown function (DUF1767))	11	32124001	mybJ-(Putative Transcription factor MYB1R1)
6	41941001	TMEM19-(Putative Transmembrane protein 19)	11	32120001	SP2L-(Putative ARM repeat superfamily protein)
6	41933001	unknown_gene-(copper ion binding)	11	32111001	FH8-(Putative Formin-like protein 8)
6	41927001	unknown_gene-(2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein)	11	32098001	unknown_gene-(Putative Sterile alpha motif (SAM) domain-containing protein)
6	41925001	At4g13360-(3-hydroxyisobutyryl-CoA hydrolase-like protein 3, mitochondrial)	11	38111001	unknown_gene-(chloroplast sensor kinase)
6	41911001	SERINC3-(Putative Serine incorporator 3)	11	38133001	GLE1-(Putative embryo defective 1745)
6	41909001	LRX4-(Predicted protein (Fragment))	11	38139001	unknown_gene-(Putative CONTAINS InterPro DOMAIN/s: Mediator complex subunit Med28 (InterPro:IPR021640); unknown protein)
6	41899001	ALDH2C4-(Aldehyde dehydrogenase family 2 member C4)	11	38161001	unknown_gene-(Hypothetical protein)
6	41892001	RHN1-(Ras-related protein RHN1)	11	38175001	ODO1-(myb domain protein 40)
6	41889001	DDB_G0289029-(Putative uncharacterized protein)	11	38198001	CLKR27-(3-oxoacyl-[acyl-carrier-protein] reductase, chloroplastic)
6	41879001	unknown_gene-(unknown protein; chloroplast)	11	38262001	CMTA4-(Calmodulin-binding transcription activator 4)
6	41872001	MBTPS1-(Membrane-bound transcription factor site-1 protease)	11	19456001	Wrnip1-(AAA-type ATPase family protein)
6	41857001	Os01g0760600-(Aspartate aminotransferase, cytoplasmic)	11	19567001	PDR1-(Pleiotropic drug resistance protein 1)
6	41856001	Os01g0760900-(Putative uncharacterized protein)	11	33046001	At1g58390-(Putative Probable disease resistance protein At1g58390)
6	41850001	unknown_gene-(Putative RNA-binding protein-related)	11	33025001	At1g65750-(Putative ribonuclease H protein At1g65750)
6	41849001	unknown_gene-(Hypothetical protein)	11	25431001	At4g15970-(Nucleotide-diphospho-sugar transferase family protein)
6	41846001	ARAC7-(Rac-like GTP-binding protein ARAC7)	11	25429001	ARC3-(Putative Protein ACCUMULATION AND REPLICATION OF CHLOROPLASTS 3)
6	41840001	BSPA-(Putative Bark storage protein A)	11	20478001	SD25-(G-type lectin S-receptor-like serine/threonine-protein kinase SD2-5)
6	41833001	unknown_gene-(unknown protein; chloroplast)	11	20490001	R1B-17-(Putative late blight resistance protein homolog R1B-17)
6	41832001	XTH26-(Probable xyloglucan endotransglucosylase/hydrolase protein 26)	11	20525001	BRL2-(Serine/threonine-protein kinase BRI1-like 2)
6	41828001	unknown_gene-(Hypothetical protein)	11	20682001	GULO-(D-arabinono-1,4-lactone oxidase family protein)
6	41822001	MC410-(Ninja-family protein mc410)	11	18060001	CPSF73-II-(Cleavage and polyadenylation specificity factor subunit 3-II)
6	41818001	STP14-(Sugar transport protein 14)	11	18055001	GSO1-(Putative LRR receptor-like serine/threonine-protein kinase GSO1)
6	41812001	unknown_gene-(Putative uncharacterized protein)	11	18005001	ARA12-(Putative Cucumisin)
6	41775001	unknown_gene-(Nucleotide-diphospho-sugar transferases superfamily protein)	11	8239001	At5g02620-(Putative Ankyrin repeat-containing protein At5g02620)
6	41756001	argS-(Putative Arginine--tRNA ligase)	11	32901001	unknown_gene-(ARM repeat superfamily protein)
6	41751001	DER1-(Derlin-1)	11	32828001	nadC-(Putative Probable nicotinate-nucleotide pyrophosphorylase [carboxylating])
6	41739001	MPP-(Mitochondrial-processing peptidase subunit alpha)	11	32820001	syc1174_c-(Uncharacterized lipoprotein syc1174_c)
6	41716001	RPL31-(60S ribosomal protein L31)	11	32759001	unknown gene (unknown protein)
6	41714001	unknown_gene-(Putative uncharacterized protein)	11	32665001	CG12375-(Putative Beta-lactamase-like protein 2)
6	41700001	PRMT1-(Probable protein arginine N-methyltransferase 1)	11	32663001	SPAC2F3.16-(Putative RING finger and CHY zinc finger domain-containing protein 1)
6	41697001	RPP8L3-(Putative Disease resistance RPP8-like protein 3)	11	32441001	At1g26270-(Probable phosphatidylinositol 4-kinase type 2-beta At1g26270)
6	41689001	PERK9-(Protein kinase protein with adenine nucleotide alpha hydrolases-like domain)	11	32129001	N-(Putative disease resistance protein At4g11170)
6	41688001	lpxA-(Putative Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase)	11	32056001	unknown_gene-(NHL domain-containing protein)
6	41685001	KEA4-(K(+) efflux antiporter 4)	11	32038001	MBD9-(Putative Methyl-CpG-binding domain-containing protein 9)
6	41678001	unknown_gene-(S-adenosyl-L-methionine-dependent methyltransferases superfamily protein)	11	32029001	rlmN-(Putative Ribosomal RNA large subunit methyltransferase N)
6	41676001	cdd-(Putative Cytidine deaminase)	11	19447001	RFS2-(Putative Probable galactinol--sucrose galactosyltransferase 2)
6	41670001	grwd1-(Putative Glutamate-rich WD repeat-containing protein 1)	11	19463001	At5g23430-(Katanin p80 WD40 repeat-containing subunit B1 homolog 1)
6	41661001	MSI4-(WD-40 repeat-containing protein MSI4)	11	19540001	unknown_gene-(Putative 6-hydroxynicotinate 3-monooxygenase)

6	41645001	rpsP-(Ribosomal protein S16 family protein)
6	41644001	EMB1789-(Putative uncharacterized protein)
6	41642001	HSFA2-(Heat shock factor)
6	41621001	unknown_gene-(unknown protein)
6	41616001	cpsf5-(Putative Cleavage and polyadenylation specificity factor subunit 5)
6	41615001	unknown_gene-(Ribosomal protein L18ae family)
6	41600001	MSL10-(Putative Mechanosensitive ion channel protein 10)
6	41583001	unknown_gene-(Putative uncharacterized protein)
6	41578001	ABP20-(Auxin-binding protein ABP20)
6	41566001	CYP-3-(Cysteine proteinase 3)
6	41562001	unknown_gene-(Predicted protein (Fragment))
6	41559001	unknown_gene-(Predicted protein)
6	41550001	RECQL3-(ATP-dependent DNA helicase Q-like 3)
6	41548001	POPTRDRAFT_832064-(Methylthioribose-1-phosphate isomerase)
6	41545001	unknown_gene-(Putative Ankyrin repeat family protein)
6	41541001	ITIH3-(inter-alpha-trypsin inhibitor heavy chain-related)
6	41540001	At1g71210-(Putative Pentatricopeptide repeat-containing protein At1g71210)
6	41537001	unknown_gene-(Putative Small nuclear ribonucleoprotein family protein)
6	41531001	GSVIVT00026920001-(Putative Probable polygalacturonase)
6	41516001	FMO1-(Probable flavin-containing monooxygenase 1)
6	41508001	PMEU1-(Putative Pectinesterase/pectinesterase inhibitor U1)
6	41505001	kif4-(ATP binding microtubule motor family protein)
6	41501001	GLIP5-(Putative GDSL esterase/lipase 5)
6	41496001	FAB1-(1-phosphatidylinositol-4-phosphate 5-kinases;zinc ion binding;1-phosphatidylinositol-3-phosphate 5-kinases)
6	41490001	VLN4-(Villin-4)
6	41481001	HAT14-(Putative Homeobox-leucine zipper protein HAT14)
6	41477001	GRXC4-(Glutaredoxin-C4)
6	41423001	KAS3B-(3-oxoacyl-[acyl-carrier-protein] synthase 3 B, chloroplastic)
6	41421001	unknown_gene-(unknown protein; plasma membrane, chloroplast)
6	41397001	XTH22-(Xyloglucan endotransglucosylase/hydrolase protein 22)
6	41394001	BIO3-BIO1-(Bifunctional dethiobiotin synthetase/7,8-diamino-pelargonic acid aminotransferase, mitochondrial)
6	41366001	MKK4-(Putative Mitogen-activated protein kinase kinase 4)
6	41354001	AAE-(Acetylajmalan esterase)
6	41350001	GLR2.2-(Putative Glutamate receptor 2.2)
6	41343001	SCY1-(Preprotein translocase subunit SCY1, chloroplastic)
6	41342001	CNGC17-(Probable cyclic nucleotide-gated ion channel 17)
6	41340001	unknown_gene-(unknown protein; chloroplast thylakoid membrane)
6	41331001	CjBAp12-(EG45-like domain containing protein)
6	41312001	PIGB-(Putative GPI mannosyltransferase 3)
6	41299001	COX6B-1-(Cytoome c oxidase subunit 6b-1)
6	41297001	unknown_gene-(unknown protein)
6	41283001	unknown_gene-(Putative Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)
6	41269001	Vps53-(Putative Vacuolar protein sorting-associated protein 53 homolog)
6	41255001	At1g16060-(AP2-like ethylene-responsive transcription factor At1g16060)
11	33041001	RPP8L2-(Putative Probable disease resistance RPP8-like protein 2)
11	25493001	ICR2-(Interactor of constitutive active ROPs 2, chloroplastic)
11	25478001	ACA12-(Calcium-transporting ATPase 12, plasma membrane-type)
11	25457001	PHT1-4-(Inorganic phosphate transporter 1-4)
11	6467001	unknown_gene-(Hypothetical protein)
11	1344001	unknown_gene-(Putative uncharacterized protein)
11	18004001	TLP-(Pathogenesis-related protein R major form)
11	32680001	At1g18390-(Putative Probable serine/threonine-protein kinase At1g18390)
11	32278001	Smyd3-(SET domain protein 35)
11	32122001	unknown_gene-(Hypothetical protein)
11	38025001	unknown_gene-(Senescence/dehydration-associated protein-related)
11	19572001	unknown_gene-(Hypothetical protein)
11	19538001	UGT85A3-(Putative UDP-glycosyltransferase 85A3)
11	25449001	Rep-(Putative Rab escort protein)
11	18076001	At3g12360-(Putative Ankyrin repeat-containing protein At3g12360)
11	32903001	At2g01600-(Putative clathrin assembly protein At2g01600)
11	32087001	Os09g0383400-(DEAD-box ATP-dependent RNA helicase 22)
11	32041001	PUB19-(Putative U-box domain-containing protein 19)
11	38083001	unknown_gene-(unknown protein; chloroplast)
11	7403001	POPTRDRAFT_831870-(Biotin carboxylase 1, chloroplastic)
11	19758001	CRK25-(Putative Cysteine-rich receptor-like protein kinase 25)
11	34000001	EMB1270-(Pentatricopeptide repeat-containing protein At3g18110, chloroplastic)
11	20425001	unknown_gene-(unknown protein)
11	32791001	unknown_gene-(Hypothetical protein)
11	32160001	AMPD-(AMP deaminase)
11	20477001	SD25-(G-type lectin S-receptor-like serine/threonine-protein kinase SD2-5)
11	20500001	phg1b-(Putative phagocytic receptor 1b)
11	20646001	R1B-14-(Putative late blight resistance protein homolog R1B-14)
11	18015001	ARR2-(Two-component response regulator ARR2)
11	32409001	CMB1-(MADS-box protein CMB1)
11	19454001	HAC12-(Histone acetyltransferase HAC12)
11	32469001	unknown_gene-(Hypothetical protein)
11	20540001	MAP65-7-(65-kDa microtubule-associated protein 7)
11	18117001	At5g59530-(1-aminocyclopropane-1-carboxylate oxidase homolog 11)
11	32779001	TTC5-(Putative Tetratricopeptide repeat protein 5)
11	38129001	unknown_gene-(Putative uncharacterized protein)
11	32267001	METTL7A-(Putative Methyltransferase-like protein 7A)
11	20519001	unknown gene (CONTAINS InterPro DOMAIN/s; unknown protein)
11	18068001	CPSF73-II-(Cleavage and polyadenylation specificity factor subunit 3-II)
11	38270001	SPL16-(Putative Squamosa promoter-binding-like protein 16)
11	20510001	RCH2-(Putative Receptor-like protein kinase 2)
11	20724001	R1A-(Putative Late blight resistance protein R1-A)
11	32970001	Sacs-(Putative Sacsin)
11	18085001	At5g02620-(Putative Ankyrin repeat family protein)

6	41253001	cluA-(Tetratricopeptide repeat (TPR)-like superfamily protein)	11	18081001	At3g12360-(Putative Ankyrin repeat-containing protein At3g12360)