

ESTUDO DA AÇÃO DO ÁCIDO ABSCÍSICO E
FLURIDONA NA DIFERENCIAÇÃO DE EMBRIÕES
SOMÁTICOS DE CANA-DE-AÇÚCAR (*Saccharum*
spp. L.): EVIDÊNCIAS DO PERFIL PROTEÔMICO E
HORMONAL

LAÍS DOS SANTOS DA CONCEIÇÃO

UNIVERSIDADE ESTADUAL DO NORTE FLUMINENSE DARCY RIBEIRO

CAMPOS DOS GOYTACAZES – RIO DE JANEIRO

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LAÍS DOS SANTOS DA CONCEIÇÃO

Dissertação apresentada ao Centro de
Biotecnologia e Biotecnologia, da Universidade
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como parte das exigências para obtenção do
título de Mestre em Biotecnologia Vegetal.

Orientador: Prof. Dr. Vanildo Silveira

Coorientador: Prof. Dr. Vitor Batista Pinto

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Dissertação apresentada ao curso pós-graduação
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Resumo

A cana-de-açúcar (*Saccharum* spp.) é reconhecida como uma significativa opção para a produção de açúcar, bioenergia e biocombustíveis, sendo o Brasil o maior produtor mundial. O melhoramento genético dessa cultura é essencial para o aumento do rendimento agroindustrial da cadeia produtiva e estudos de embriogênese somática (ES) com a espécie têm se destacado como modelo para compreensão das bases moleculares da aquisição da competência embriogênica, potencializando as ferramentas biotecnológicas para regeneração de plantas geneticamente modificadas. A ES é regulada por diversos fatores, entre eles os fitohormônios. O ácido abscísico (ABA), é um fitohormônio fundamental na embriogênese, desempenhando um papel crucial para o acúmulo de reservas e sinalização no desenvolvimento embrionário. No entanto, os mecanismos moleculares associados em resposta ao ABA durante a diferenciação de embriões somáticos ainda são pouco explorados, representando uma lacuna de estudo para otimização do processo de propagação *in vitro* e regeneração de plantas. Dessa forma, estudos investigando a modulação dos níveis de ABA e da inibição da produção de ABA endógeno, se fazem necessários. O objetivo deste estudo foi investigar o papel do ABA na diferenciação da ES em cana-de-açúcar, por meio de análises proteômicas e fosfoproteômicas. Calos embriogênicos foram tratados com diferentes concentrações de ABA ou de fluridona (FDN, inibidor da biossíntese de ABA) durante o período de maturação. As concentrações de ABA que foram adicionadas não afetaram a diferenciação e desenvolvimento dos embriões somáticos, quando comparados com o controle, mas o ABA endógeno foi fundamental para a formação de embriões somáticos. A adição de 0,1 μM FDN apresentou menor formação de embriões somáticos, mas ainda não citotóxicos. Para investigar os mecanismos celulares dependentes do ABA, análises proteômicas e fosfoproteômicas comparativas foram realizadas entre calos tratados com 0,1 μM FDN e os sem adição de quaisquer reguladores durante o período da maturação. As análises proteômicas e fosfoproteômicas revelaram mecanismos distintos de regulação epigenética, sinalização de ABA e auxinas, metabolismo energético e modificação pós-traducionais de proteínas, revelando diversos processos biológicos dependentes do ABA. As proteínas relacionadas as respostas e transporte de auxinas, como a *Auxin transport*

protein BIG e ABC transporter B family member 19, e ainda seus envolvimento com as vias fotossintéticas, de respostas a luz e de antocianinas foram mais expressas no controle. Além disso, fosfoproteínas associadas com regulação epigenéticas foram identificadas, como a AGO1, *S-adenosyl-L-methionine-dependent (SAM)*, *CTR9-like* e *Lysine-specific demethylase JMJ25* em calos embriogênicos. Esses resultados demonstram o papel crucial do ABA na regulação da ES, além de ajudar a melhorar a compreensão das vias e proteínas-chave para o processo de diferenciação e desenvolvimento de embriões somáticos de cana-de-açúcar.

Palavras-chave: cana-de-açúcar, embriogênese somática, ácido abscísico, fosfoproteômica.

Abstract

Sugarcane (*Saccharum* spp.) is recognized as a significant option for the biofuel industry, due to its remarkable potential for generating ethanol and its derivatives. The genetic improvement of sugarcane is essential for increasing the agro-industrial yield of the production chain and studies of somatic embryogenesis (SE) with the species have stood out as a model for understanding the molecular bases of the acquisition of embryogenic competence, enhancing biotechnological tools for the regeneration of genetically modified plants. ES is regulated by various factors, including phytohormones. Absciscic acid (ABA) is a fundamental phytohormone in embryogenesis, playing a crucial role in the accumulation of reserves and embryonic development. However, the molecular mechanisms associated with the response to ABA during the differentiation of somatic embryos are still little explored, representing a study gap for optimizing the process of in vitro propagation and plant regeneration. Therefore, studies investigating the modulation of ABA levels and the inhibition of endogenous ABA production are necessary. The objective of this study was to investigate the role of ABA in the differentiation of somatic embryogenesis in sugarcane, using proteomic and phosphoproteomic analyses. Embryogenic calli (EC) were treated with different concentrations of ABA or fluridone (NDF, an inhibitor of ABA biosynthesis). The concentrations of ABA that were added did not affect the differentiation and development of somatic embryos when compared to the control, but

endogenous ABA was fundamental for the formation of somatic embryos. However, 0.1 μ M FDN showed lower values, but still not cytotoxic. To investigate ABA-dependent cellular mechanisms, comparative proteomic and phosphoproteomic analyses were performed between ECs treated with 0.1 μ M NDF and those without the addition of any regulators during the ripening period. The proteomic and phosphoproteomic analyses revealed distinct mechanisms of epigenetic regulation, ABA and auxin signaling, energy metabolism and post-translational modification of proteins, revealing diverse ABA-dependent biological processes. Proteins related to auxin responses and transport, such as Auxin transport protein BIG and ABC transporter B family member 19, and their involvement in the photosynthetic, light response and anthocyanin pathways were more expressed in the control. In addition, phosphoproteins associated with epigenetic regulation were identified, such as AGO1, S-adenosyl-L-methionine-dependent (SAM), CTR9-like and Lysine-specific demethylase JMJ25 in embryogenic callus. These results demonstrate the crucial role of ABA in the regulation of ES, and help to improve understanding of the key pathways and proteins involved in the differentiation and development of sugarcane somatic embryos.

Keywords: sugarcane, somatic embryogenesis, abscisic acid, phosphoproteomics.

1. Introdução

1.1 Aspectos gerais

A cana-de-açúcar (*Saccharum* spp.) é uma planta da família Poaceae, cultivada nas regiões tropicais e subtropicais (Iqbal et al., 2023), sendo considerada um exemplo de recurso agrícola renovável e utilizada em diferentes indústrias para produção de açúcar, biocombustível, fibra, fertilizante e diversos subprodutos (Salokhe, 2021).

O desenvolvimento de ferramentas biotecnológicas direcionadas a cana se faz necessário como estratégias para o melhoramento genético e desenvolvimento de novas cultivares mais produtivas (Suprasanna et al., 2011). Dessa forma, um dos grandes gargalos para a produção de plantas geneticamente modificadas é a falta de sistema de regeneração das plantas transformadas/editadas, onde abordagens de micropropagação são essenciais para melhorar características como produção de biomassa, desempenho agrônomo, tolerância a estresses bióticos e abióticos (Moraes et al., 2014). Assim, métodos de cultivo *in vitro* da cana-de-açúcar vem apresentando impactos positivos nas pesquisas e também no âmbito comercial para produção de plantas geneticamente modificadas e mudas em larga-escala (Suprasanna et al., 2011).

Dentre os métodos de cultivo *in vitro*, a embriogênese somática (ES) é análoga à embriogênese zigótica e consiste no processo em que uma única, ou um pequeno grupo de células somáticas, com competência embriogênica, sofrem reprogramação genética e se diferenciam em embriões somáticos com genótipo semelhante ao do explante (Fehér, 2019).

Diferentes biotecnologias são usadas para compreensão da regulação molecular da ES (Lakshmanan et al., 2005), por meio de estudos genômicos e transcriptômicos em espécies modelo, como *Arabidopsis*. Além disso, estudos proteômicos e fosfoproteômicos têm sido utilizados em várias espécies, inclusive cana-de-açúcar, para entender condições da aquisição da competência embriogênica e ainda na identificação de possíveis proteínas

relacionadas ao desenvolvimento embrionário somático (Almeida et al., 2020; Heringer et al., 2015, 2018; Xavier et al., 2022).

Proteínas relacionadas à sinalização do ácido abscísico foram encontradas, como por exemplo a quinase *OSK3*. Essa proteína fosforilada é importante na aquisição da competência embriogênica em cana-de-açúcar (Almeida et al., 2020).

Por outro lado, nenhum estudo sobre a fosforilação de proteínas se centrou nas respostas específicas do ABA durante a ES, um processo que permanece pouco estudado. O papel do ABA endógeno na modulação do perfil proteômico e do nível de fosforilação de proteínas associadas à embriogênese permanece desconhecido. Nesta pesquisa, investigamos a influência do ABA durante a diferenciação e desenvolvimento de embriões somáticos de cana-de-açúcar, mapeando sua associação com o acúmulo e regulação de fosfoproteínas cruciais que orquestram a progressão da morfogênese *in vitro*.

1.2 A cultura de cana-de-açúcar no Brasil

O Brasil se destaca como o maior produtor mundial, sendo responsável por mais de 40% da safra mundial (Salokhe, 2021). De acordo com o 3º Levantamento da Safra 2023/24, tem-se a estimativa de que a produção nacional deve crescer 10,9% em comparação ao ciclo anterior e chegar a 677,6 milhões de toneladas, sendo que em relação a produção de açúcar, estima-se que 46,88 milhões de toneladas sejam produzidos no período 2023/24, representando um incremento de 27,4% em relação à safra anterior (Companhia Nacional de Abastecimento, 2023).

O uso da biomassa de cana-de-açúcar para a geração de energia, tem um grande potencial de expansão e se consolida como um produto adicional do setor sucroenergético brasileiro (Seabra & Macedo, 2011). Assim, o setor sucroalcooleiro é um dos mais importantes para o agronegócio brasileiro, com grande destaque no cenário econômico devido ao potencial na produção de etanol e seus subprodutos, contribuindo efetivamente para uma matriz energética mais sustentável (Souza et al., 2019). No Brasil, a produção estimada de etanol para o período 2023/24 é de 34,05 bilhões de litros do biocombustível, sendo 27,99 bilhões de litros a partir da cana-de-açúcar,

significando um aumento em torno de 9,9% comparado com a safra anterior (Companhia Nacional de Abastecimento, 2023).

O melhoramento genético da cana-de-açúcar é essencial para o aumento do rendimento agroindustrial da cadeia produtiva (Cursi et al., 2022), no entanto é um processo dificultado devido à poliploidia e aneuploidia dos híbridos, já que a constituição genômica do híbrido tornou-se mais complexa do que sua espécie parental, apresentando entre 100-130 cromossomos (Souza et al., 2019). Esses híbridos são resultados dos cruzamentos interespecíficos entre *S. officinarum* ($2n= 80$) e *S. spontaneum* ($2n= 40 - 128$) (Arruda, 2012) com cerca de 5% de cromossomos recombinados entre esses dois progenitores (Souza et al., 2019). Dessa forma, fatores como a ploidia, ser uma espécie híbrida e o tamanho do genoma representam uma barreira para o sequenciamento.

No ano de 2018, diferentes trabalhos relataram o sequenciamento do genoma da cana-de-açúcar, como a utilização da cultivar R570, em que foi elaborado *in silico* um genoma de cana-de-açúcar contendo 382 milhões de bases, gerando um resultado de 25.316 proteínas preditas a partir de genes codificantes (Garsmeur et al., 2018). Além disso, o trabalho com *Saccharum spontaneum*, AP85-441, facilitou a montagem de 32 pseudo- cromossomos, contendo 35.525 genes (Zhang et al., 2018). No ano seguinte, pesquisadores da FAPESP publicaram a versão mais completa da sequência do genoma da cana-de-açúcar cultivar SP80-3280. Ao todo foram sequenciados 373.869 genes e regiões promotoras, correspondendo a 99,1% do genoma desta cultivar (Souza et al., 2019). A montagem desse genoma representa um avanço para obtenção de informações moleculares de cana-de- açúcar.

1.3 A embriogênese somática (ES) em plantas

A ES é análoga à embriogênese zigótica e consiste no processo em que uma única, ou um pequeno grupo de células somáticas, com competência embriogênica, sofrem reprogramação genética e se diferenciam em embriões somáticos com genótipo semelhante ao do explante (Fehér, 2019). Desta forma, a ES pode ser utilizada para produzir mudas de espécies de interesse

agronômico e livres de patógenos, além de regenerar plantas geneticamente modificadas (Passamani et al., 2018; Silveira et al., 2013).

Durante o processo de diferenciação celular na ES, o explante responde a estímulos endógenos e exógenos que desencadeiam respostas de sinalização, reprogramando a expressão gênica e assim adquirindo a característica de célula totipotente (Fehér et al., 2003). Esses estímulos podem ser dados por reguladores de crescimento vegetal (PGR) ou algum tipo de estresse (temperatura, luminosidade, estresse osmótico e outros), e ainda por meio de fatores de transcrição (TFs) está implicada na iniciação do calo (Fehér, 2015, 2023). Os sinais endógenos e exógenos podem ocasionar um estresse, gerando um conteúdo hormonal celular desequilibrado, levando à desdiferenciação em células competentes, seguida pela formação de embriões, seja na forma da embriogênese direta ou indireta (Fehér, 2015).

Uma fonte exógena que promove a competência embriogênica em células somáticas é a modificação do equilíbrio de auxinas nas células do explante (Fehér, 2015). A utilização do ácido 2,4-diclorofenoxiacético (2,4-D, molécula sintética com atividade de auxina) para induzir a ES promove respostas ao estresse, reprogramação da expressão genética, tradução de proteínas, respostas hormonais, regulação epigenética e modificações pós-traducionais durante o processo de diferenciação (Fehér, 2019). As diferenças fundamentais entre as diferentes vias embriogênicas residem principalmente na fase de iniciação e a ES possui uma grande variação a este respeito (Figura 1).

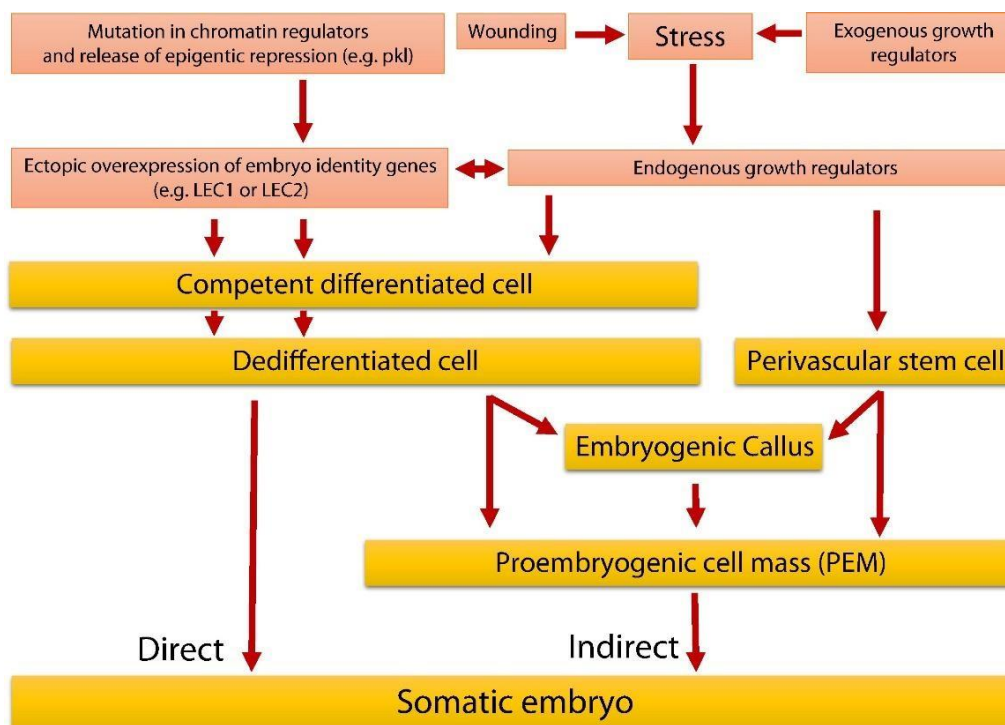


Figura 1. Caminhos que levam à formação de embriões somáticos. A ES pode ser iniciada de forma direta ou indireta. Os sinais endógenos ou exógenos levam à dediferenciação em células competentes, resultando na formação de embriões ou superproliferação de calos. Mutações em genes que reprimem o desenvolvimento embrionário em células vegetativas (PICKLE) ou a expressão ectópica de genes de identidade embriogênica (*WUSHEL (WUS)*, *LEAFY COTYLEDON 1 e 2 (LEC1)* ou (*LEC2*) podem resultar na diferenciação de embriões somáticos. Fonte: Fehér (2015).

Embora a presença da auxina seja fundamental para a indução de calos e a aquisição de capacidade embriogênica em diversas espécies, é preciso que haja a diminuição ou a sua remoção para o maior desenvolvimento e diferenciação dos embriões somáticos (Reis et al., 2016). Em cana-de-açúcar cv. SP80-3280, a retirada do 2,4-D do meio de cultura durante um pré-tratamento de 21 dias antes da etapa de maturação apresentou resultados positivos no rendimento de embriões somáticos em calos embriogênicos (Reis et al., 2021). No entanto, o cultivo em tempo prolongado com 2,4D acarreta em uma diminuição da competência embriogênica dos calos embriogênicos de cana-de-açúcar (Passamani et al., 2020).

Além disso, o balanço hormonal é fundamental nesse processo, os níveis endógenos de ABA parecem ser significativos para o início das culturas embriogênicas, especialmente em algumas monocotiledôneas (Bhaskaran e Smith, 1990). Experimentos com *Medicago* spp. ressaltam a importância do

ABA endógeno na regulação da ES (Kępczyńska & Kępczyński, 2023). Dessa forma, a ES foi observada em várias espécies, sendo usada por grupos de pesquisa, na busca da compreensão de bases bioquímicas, fisiológicas e moleculares da ES.

1.4 Regulação hormonal com ênfase no ABA durante a embriogênese somática

A importância do ABA endógeno no processo de ES e desenvolvimento dos embriões somáticos, além da expressão de fatores de transcrições relacionados ao ABA como o *ABI3*, demonstrou um papel central desse hormônio na promoção da competência embriogênica (Kikuchi et al., 2006). Neste sentido, a otimização no uso de reguladores de crescimento nos explantes cultivados *in vitro* é um fator crítico na indução da ES.

Hormônios vegetais como auxina e citocinina, são considerados os principais da divisão e diferenciação celular em plantas (Jiménez, 2005). As auxinas são reconhecidas por estimular respostas relacionadas ao crescimento e divisão celular e o uso do 2,4-D) tem sido mais aplicado devido a sua eficiência na indução da ES (Ikeda-Iwai et al., 2003; Pasternak et al., 2002; Reis et al., 2016). Além de induzir respostas semelhantes às da auxina, também foi observado aumentando os níveis de ácido indolacético (IAA) (Jiménez, 2005). O IAA regula a morfogênese das plantas por meio de gradientes de concentração específicos de tecidos obtidos pelos processos de transporte, biossíntese, conjugação e degradação de auxina (Su et al., 2009). Em *Arabidopsis thaliana*, os gradientes de concentração de IAA nos tecidos são importantes para a embriogênese (Simon & Petrášek, 2011). É válido ressaltar que as citocininas desempenham um papel crucial na fase inicial de divisão celular durante a ES, porém, sua importância diminui nos estágios posteriores do desenvolvimento e maturação embrionária (Fraga et al., 2016).

O ácido jasmônico (AJ) é um regulador que pode afetar a desdiferenciação de células somáticas, dados bioinformáticos sugerem que o metabolismo do AJ pode afetar a ES e ainda o nível em calos embriogênicos é maior do que em calos não embriogênicos (Elhiti et al., 2013). A inclusão do paclobutrazol, antagonista da giberelina, no meio de indução ou de diferenciação inibiu fortemente o crescimento de calos, bem como a indução e

produção de embriões somáticos de *Medicago sativa* L., dessa forma indicando que seus níveis endógenos são essenciais nesses processos (Ruduś et al., 2002).

O ABA comumente sintetizado em todas as plantas vasculares, e presente em musgos e algas (Rai et al., 2011) possui papel significativo na regulação de processos fisiológicos que ocorrem nas plantas e está envolvido em processos de regulação do crescimento, desenvolvimento e as respostas ao estresse vegetal (K. Chen et al., 2020). Além disso, também está associado à maturação do embrião, dormência das sementes, germinação, indução floral e respostas a estresses ambientais, como seca, salinidade, frio, ataque de patógenos e radiação UV (Finkelstein & Gibson, 2002).

Além disso, sabe-se que as vias de sinalização do ABA, juntamente com a ativação de genes em resposta ao estresse, desempenham um papel fundamental nas fases de desenvolvimento e maturação dos embriões somáticos (Gulzar et al., 2020), esses mecanismos regulam a produção e a acumulação de proteínas de reserva, como as proteínas *Late Embryogenesis Abundant* (LEA) (Linacero et al., 2001). Em cenoura, foi evidenciada a importância do ABA endógeno no processo de ES e a formação de embriões somáticos, além da expressão de *ABI3*, demonstrando o papel central desse hormônio na promoção da competência embriogênica (Kikuchi et al., 2006). Além disso, em estudos recentes sobre embriogênese *in vitro* em *Arabidopsis thaliana*, foi investigada a importância da síntese e sinalização do ABA e descobriu-se que os fatores de transcrição *INSENSÍVEL AO ÁCIDO ABSCÍSICO 3 (ABI3)* e *ABI4* desempenham um papel significativo na formação de embriões durante esse processo (B. Chen et al., 2021).

Além disso, entender os efeitos da biossíntese e inibição dos reguladores é de extrema importância para a otimização dos protocolos (Grzyb et al., 2018; Jiménez, 2005) (Figura 2).

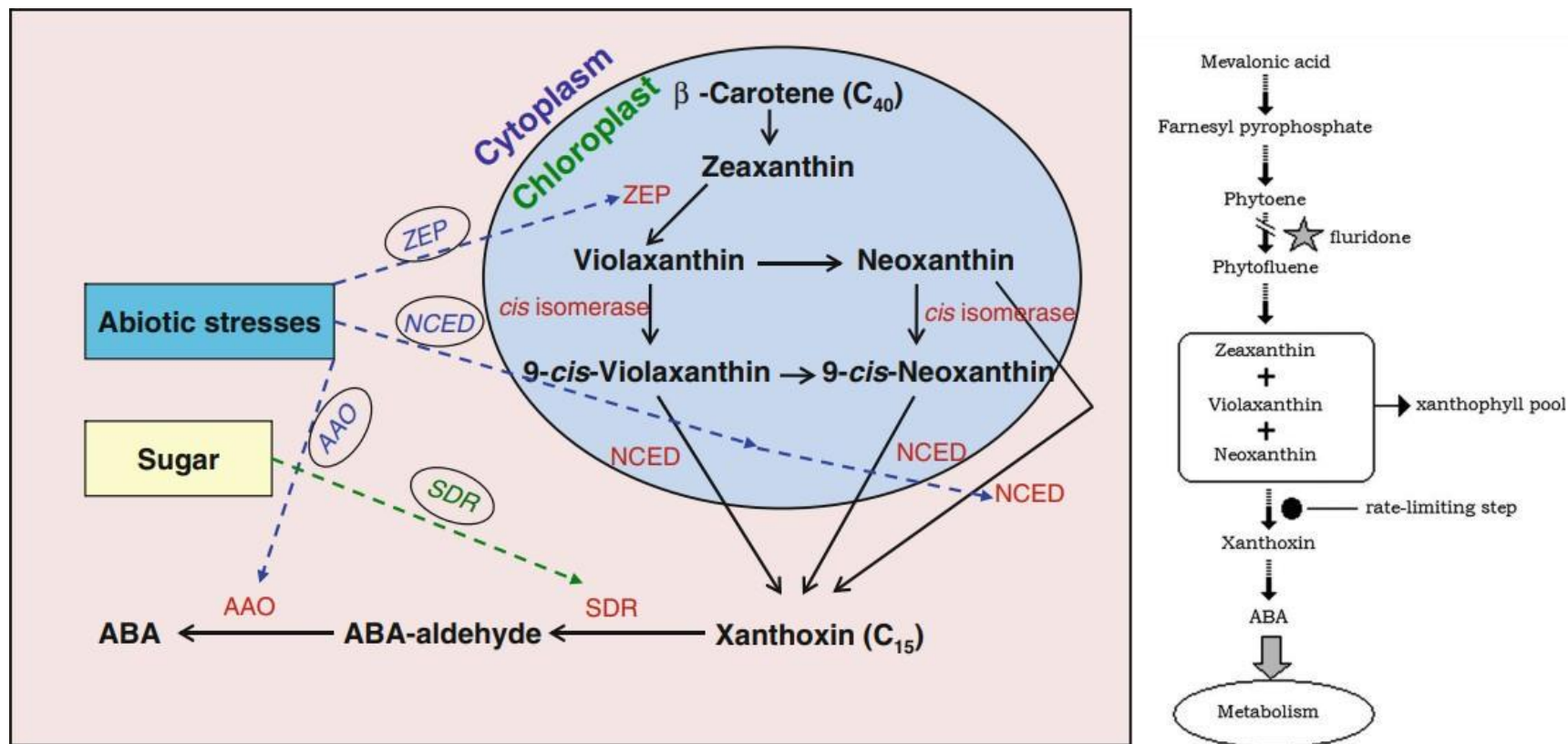


Figura 2. (A) Via de biossíntese do ABA | Em plantas, o ABA é sintetizado pela via dos carotenóides, chamada por via indireta onde seu início ocorre nos plastídios por meio da clivagem oxidativa de um 9-cis-epoxicarotenóide (C_{40}) para produzir xantoxina (C_{15}), seguido por uma conversão em duas etapas do intermediário xantoxina em ABA via ABA-aldeído no citoplasma. Na última etapa da via, o ABA-aldeído é oxidado a ABA por ABA-aldeído oxidase (AAO). Os genes ZEP, NCED e AAO, são regulados positivamente por estresses abióticos por meio da via de fosforilação dependente de cálcio, no entanto o SDR é regulado por açúcares Fonte: Rai et al., 2011 | **(B) Inibição do fitoeno em fitoflueno.** A fluridona é um herbicida inibidor de fitoeno que converte fitoeno em fitoflueno inibindo a biossíntese de precursores de carotenoides. Fonte: Ren et al., 2006

A fluridona (FDN) inibe a biossíntese de precursores de carotenoides (Figura 2B). A ausência de carotenoides na planta irá resultar no bloqueio da formação da membrana plastidial, ocorrendo uma alteração no acúmulo de pigmentos, resultando no branqueamento dos tecidos (Tanaka et al., 2008). Dessa forma, como os carotenoides são os principais precursores de ABA em plantas (GAMBLE & MULLET, 1986), a inibição da carotenogênese também deve impedir a biossíntese de ABA. Tratamentos com fluridona inibiu o acúmulo de carotenoides e de ABA em cevada (GAMBLE & MULLET, 1986) e em milho (Moore & Smith, 1984). Já foi demonstrado o papel da fluridona na inibição de ABA durante a ES de *Pennisetum purpureum* Schum (Rajasekaran et al., 1987), *Arabidopsis* (Su et al., 2013), cenoura (Kikuchi et al., 2006) e *Cyathea delgadii* (Grzyb et al., 2018). Assim, compreender o papel do ABA durante o processo da ES se faz necessário não só para entender os mecanismos moleculares que orquestram a resposta a esse hormônio, mas também para a otimização de protocolos de micropropagação de cana-de-açúcar.

1.5 A embriogênese somática na cana-de-açúcar

Métodos de cultivo *in vitro* da cana-de-açúcar apresentam impactos positivos nas pesquisas e também no âmbito comercial para produção de plantas geneticamente modificadas e mudas em larga-escala (Suprasanna et al., 2011). Tratando-se dessa espécie, a ES se destaca como uma técnica de melhora nos índices de sua produtividade através da produção de mudas saudáveis e regeneração de plantas geneticamente modificadas (Henringer et al., 2017). Ao longo da década de 80, diversos estudos envolvendo o desenvolvimento de embriões somáticos por meio de calos de cana-de-açúcar foram publicados (Ahloowalia & Maretzki, 1983; Ho & Vasil, 1983). Boa parte das descobertas foi possível devido a estudos genômicos em que foi mostrado que os genes que controlam a desdiferenciação e diferenciação das células vegetais estão envolvidos com a ES (Horstman et al., 2017).

A embriogênese somática em cana-de-açúcar compreende as fases de indução, multiplicação, pré-tratamento da maturação, maturação e conversão (Figura 3), no qual as células do explante passam por etapas de

desdiferenciação e aquisição de competência embriogênica (Almeida et al., 2022). Essa ferramenta representa uma alternativa à propagação convencional da cana-de-açúcar, e viabilizando protocolos de transformação genética e usada na produção de sementes sintéticas (Almeida et al., 2022).

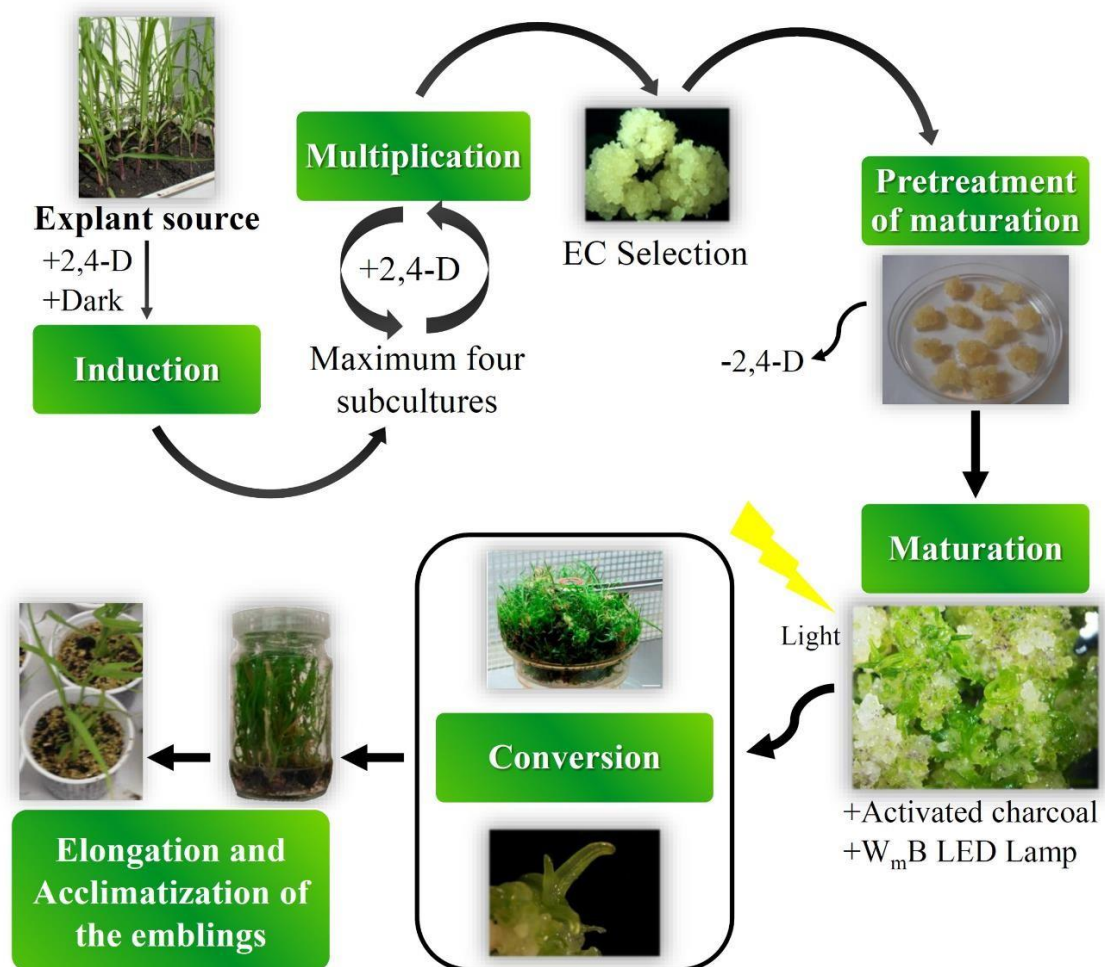


Figura 3. Fases da embriogênese somática na cana-de-açúcar. Fonte: Almeida et al., 2022

Protocolos eficientes e detalhados para a embriogênese somática podem ser aplicados para melhorar a produtividade das culturas e reduzir os custos do processo em cultivares de cana-de-açúcar (Almeida et al., 2022).

1.6 Regulação molecular da embriogênese somática

Por meio de abordagem proteômica *gel-free* possibilitou-se a identificação de proteínas envolvidas nas respostas a estresses, metabolismo proteico, transdução de sinais e processos de metabolismo de carboidratos durante a ES (Heringer et al., 2018). Trabalhos do nosso grupo pesquisa, identificaram proteínas diferencialmente acumuladas em etapas diversas da ES de cana-de-açúcar, incluindo as *proteínas 14-3-3*, *arabinogalactan*, *germin-like*, *heat shock protein (HSP)*, *IAA-amido sintase*, *late embryogenesis abundant proteins (LEAs)*, *peroxidase*, *catalase*, *6- fosfogluconato desidrogenase*, *histonas* e *proteínas ribossomais* (Heringer et al., 2015, 2017, 2018; Passamani et al., 2018; Reis et al., 2016). *HSP* e *LEAs* estão relacionadas ao estresse. Além disso, a identificação de proteínas P-H⁺-ATPase e H⁺-PPase em frações microsossomais de calos embriogênicos de cana-de-açúcar associaram o acúmulo e atividade de bombas de prótons à competência embriogênica dos calos (Passamani et al., 2018). Proteínas envolvidas no metabolismo de carboidratos, como *aldose 1-epimerase*, *aldolase*, *gliceraldeído-3-fosfato desidrogenase (GAPDH)*, *triosefosfato isomerase* e *sacarose sintase (SUS)*, desempenham papéis essenciais em diversos processos celulares durante a maturação dos embriões somáticos (Heringer et al., 2018). Proteínas como *dehydrogenase-like protein*, *desiccation-related protein-62 PCC13*, *callose synthase1 catalytic subunit* e *NOS-interacting protein* foram identificadas mais acumuladas em calos embriogênicos em comparação aos calos não-embriogênicos de cana-de-açúcar (Heringer et al., 2015).

O uso da proteômica permite identificar e quantificar proteínas, gerando resultados inovadores para melhorar o entendimento das bases fisiológicas e moleculares associadas à competência morfogênética celular durante a ES (Reis et al., 2016). Diversos fatores, incluindo hormônios vegetais, fatores de transcrição, modificações epigenéticas e regulação pos-traducional de proteínas, interagem em complexas redes de regulação da expressão gênica para coordenar os processos moleculares envolvidos na formação de embriões somáticos (Fehér, 2015).

O fator de transcrição *BABY BOOM (BBM)* ativa a rede de sinalização de genes do grupo de reguladores transcricionais *LAFL*, que é composto por fatores de transcrição conhecidos por *ABI3*, *FUSCA 3 (FUS3)*, *LEC1* e *LEC* (Horstman et al., 2017) para promover ainda mais o progresso da ES (Gaj et al., 2005), assim como *AGAMOUS-LIKE15 (AGL15)* (Zheng et al., 2016). Os genes *LAFL* são capazes de regular a biossíntese de ABA (Horstman et al., 2017). *BBM*, *LEC1* e *LEC2* desempenham papéis essenciais na totipotência das células vegetais, sendo pelo fato de que a expressão excessiva de qualquer um desses fatores de transcrição pode induzir a formação de embriões somáticos a partir de mudas de *Arabidopsis* sem a necessidade de reguladores de crescimento exógenos (Horstman et al., 2017). Em cana-de-açúcar, a expressão de *BBM* e *LEC* foi observada em calos embriogênicos, sugerindo que esses genes expressos desempenhavam um papel na regulação da ES da espécie (Maulidiya et al., 2020).

A proteína *SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE (SERK)* está envolvidas em processos de fosforilação, uma vez que são quinases e ainda atuam na regulação da expressão gênica durante o desenvolvimento embrionário e vegetativo das plantas (Hu et al., 2005). Esta regulação depende de alterações no acúmulo de hormônios, causando mudanças no estado da cromatina, e resultando na ativação de fatores de transcrição como *WUS*, *LEC* ou *BBM*, que são específicos de programas embriogênicos. O *FUS3* relacionado à fase de maturação durante o desenvolvimento da semente regula positivamente a biossíntese de ABA, (Curaba et al. 2004); Gazzarrini et al. 2004) além disso, o *FUS3* é considerado codificador de miRNA da transição de fase durante o desenvolvimento de sementes (Wang & Perry 2013).

Além da importância da transcrição dos genes na regulação da expressão gênica, os eventos de tradução e as modificações pós-traducionais das proteínas (PTMs) também são considerados fundamentais (Ramakrishnan et al., 2023), podendo incluir a fosforilação, metilação, ubiquitinação, acetilação, entre outras (Han et al., 2022).

A fosfoproteômica é um subcampo da proteômica que se concentra na identificação e quantificação das fosfoproteínas e

fosfopeptídeos em larga-escala, sendo essa uma das principais e mais estudada (Ajadi et al., 2020), em que é realizado a ligação de um grupo fosfato a um grupo hidroxila em resíduos de serina, tirosina ou treonina (Reinders & Sickmann, 2005) sendo mediado por um complexo de enzimas conhecidos como quinases (Ajadi et al., 2020).

A fosforilação é capaz de modular a estrutura e função das proteínas que podem ser fosforiladas, influenciando atividades enzimáticas, especificidades de substratos, determinando a localização e interações das proteínas, a formação de complexos e o processo de degradação (Reinders & Sickmann, 2005), e ainda identificar seus estados e sítios de fosforilação (Xavier et al., 2022).

Em trabalho recente na ES de cana-de-açúcar, foram identificadas proteínas fosforiladas envolvidas em respostas ao ABA associadas à tolerância ao estresse e à regulação da expressão gênica por meio do remodelamento da cromatina e do controle transcricional, como *OSK3*, *ABF1*, *LEAs* e *RD29Bs* (Almeida et al., 2020). A *quinase OSK3*, pertencente à família *SNRK1*, foi identificada como uma reguladora central da homeostase metabólica e da sinalização ABA em resposta a condições de estresse (Almeida et al., 2020). A presença de *OSK3* fosforilada sugere um papel crucial dessa quinase na aquisição da competência embriogênica em cana-de-açúcar (Almeida et al., 2020).

Estudos de fosfoproteômica na ES de cana-de-açúcar também revelaram que as proteínas fosforiladas relacionadas à multiplicação foram identificadas e associadas à regulação transcricional, destacando papéis específicos de *SNF1 quinase homóloga 10 (KIN10)*, *SEUSS (SEU)* e *LEUNIG_HOMOLOG (LUH)* (Xavier et al., 2022). Na fase de maturação, a regulação das proteínas do fotossistema e dos fatores de interação dos fitocromos sugeriu uma promoção do metabolismo bioenergético e da fixação de carbono (Xavier et al., 2022). Os resultados também apontaram *motifs* específicos durante a diferenciação do embrião somático, e as interações previstas entre proteínas indicaram novos participantes, tais como *proteína quinase 2 relacionada ao SNF1 (SnRK2)*, *fator de ligação de elementos*

responsivos ao ácido abscísico 2 (ABF2), KIN10 e TOPLESS (TPL), revelando dinâmicas reguladoras e novos atores no processo de ES (Xavier et al., 2022).

Dessa forma, essas interações evidenciam a complexidade da regulação dos fatores de transcrição, seus genes-alvo e o desenvolvimento da ES, fornecendo *insights* sobre os mecanismos moleculares que coordenam esse processo de desenvolvimento.

2. Objetivos

2.1 Geral

Identificar os mecanismos moleculares mediadas pelo ABA durante a embriogênese somática (ES) de cana-de-açúcar.

2.2 Específicos

- Analisar o perfil histomorfológico de calos embriogênicos em resposta à diferentes concentrações de ABA e fluridona exógenos;
- Quantificar o número de embriões somáticos após a aplicação de diferentes doses de ABA e fluridona em calos embriogênicos;
- Determinar o efeito da fluridona no acúmulo dos níveis endógenos de ABA, ácido 1-aminociclopropanocarboxílico (ACC), ácido 3-indoleacético (IAA); ácido jasmônico (JA) em calos embriogênicos de cana-de-açúcar;
- Identificar proteínas e fosfoproteínas diferencialmente acumuladas através da abordagem *shotgun label-free* em calos embriogênicos sob ação de fluridona;
- Identificar as interações proteína-proteína preditas na resposta molecular associada ao ABA durante a ES.

3. Material e métodos

3.1 Indução e multiplicação de calos embriogênicos

A cultivar de cana-de-açúcar SP-8032-80 foi utilizada para a indução de calos embriogênicos, seguindo os métodos descritos de acordo com (Passamani et al., 2018). Segmentos nodais de cana-de-açúcar foram cultivados em substrato comercial PlantMax (DDL Agroindústria, Paulínia, SP, Brasil) por 60 dias em casa de vegetação. As plantas jovens foram coletadas, as folhas maduras foram retiradas e os rolos foliares tiveram as extremidades

seladas com parafina e desinfetados em etanol 70% (Sigma-Aldrich, St. Louis, EUA) por 1 min, imersos em hipoclorito de sódio comercial Qboa® 50% (hipoclorito de sódio de 2 a 2,5%) por 30 min e, posteriormente, lavados três vezes com água autoclavada em capela de fluxo laminar. Os explantes foram seccionados transversalmente em fatias de 3 mm de espessura e cultivados em tubos de ensaio de vidro (150 × 25 mm) contendo 10 mL de meio de cultura MS (Murashige & Skoog) (Phytotechnology Lab, Overland Park, EUA) suplementado com 20 g L⁻¹ de sacarose, 2 g L⁻¹ de Phytigel® (Sigma-Aldrich) e 10 µM de 2,4-D (Sigma-Aldrich). O pH do meio de cultura foi ajustado para 5,8 antes da autoclavagem por 15 min a 121°C. Inicialmente, os explantes foram mantidos no escuro a 25 °C ± 1 °C por 45 dias (período de indução), para a formação de calos embriogênicos e não embriogênicos (Silveira et al., 2013). Apenas os calos embriogênicos foram transferidos para placas de Petri (90 × 15 mm) contendo 20 mL do mesmo meio de cultura de indução e subcultivados em intervalos de 21 dias para multiplicação seguindo as mesmas condições ambientais do período de indução.

3.2 Maturação de calos embriogênicos

Após a multiplicação, quatro calos de 250 mg/cada, foram transferidos para novas placas de Petri contendo 20 mL de meio MS suplementado com 30 g L⁻¹ de sacarose e 2 g L⁻¹ de Phytigel, com o pH do meio de cultura ajustado para 5,8 antes do processo de autoclavagem por 15 min a 121 °C (Passamani et al., 2018). Ao meio de cultura, foram adicionadas as concentrações de 1, 10, 50 e 100 µM de ácido abscísico (ABA; Sigma-Aldrich product number 8621) ou 0,1, 1 e 10 µM de fluridona (FDN; Sigma-Aldrich product number 455), além do controle (sem adição de ABA ou fluridona). O experimento foi mantido no escuro a 25 °C ± 1 °C por 21 dias (período de pré-maturação). Em seguida, os calos foram transferidos para um meio de cultura suplementado com 30 g L⁻¹ de sacarose e 2 g L⁻¹ de Phytigel e cultivados no escuro durante 7 dias, passando depois para um fotoperíodo de 16h estabelecido com lâmpadas GreenPower TLED 20-W WmB (Koninklijke Philips Electronics NV, Amsterdam, Holanda) a 55 µmol m⁻² s⁻¹, sob temperatura de 25 ± 1 °C, até 42 dias de cultivo (período de maturação). Ao início (EC0), 28º (EC28) e 42º (EC42) dias de maturação, foi realizada a análise morfológica dos calos e, no 42º dia foi realizada a

quantificação de embriões somáticos formados em cada tratamento.

O experimento foi conduzido em um esquema completamente randomizado com oito repetições biológicas, cada uma consistindo por uma placa de Petri. Os dados foram analisados por análise de variância (ANOVA) ($P < 0,05$) seguida pelo teste de Tukey a 5% de probabilidade usando o software R (R Core Team, 2014) e o pacote *easyanova* (Arnhold, 2013).

Com base nos resultados obtidos, foi dado prosseguimento com a quantificação de ABA endógeno nos tempos 0,14 e 28 dias de maturação, análise proteômica e fosfoproteômica apenas para 0,1 μM FDN e o controle nos tempos 0 e .

3.3 Quantificação de hormônios vegetais

Cinco réplicas biológicas (quatro calos/réplica) de cada tratamento foram maceradas em nitrogênio líquido e 300 mg foram homogeneizados com um tampão de extração contendo 80% de etanol e 1% de polivinilpirrolidona (Sigma-Aldrich). Posteriormente, as amostras foram sonicadas, seguidas de centrifugação a 16000 g, ambas a 4 °C durante 10 minutos. O sobrenadante foi recolhido e seco em Speed Vac a 45 °C durante 160 minutos até atingir aproximadamente 200 μL de volume. Em seguida, o volume de cada tubo foi ajustado com água Mili'Q para 500 μL utilizando uma balança. Posteriormente, foi adicionada, duas vezes, 1 mL de éter e misturado em vórtex, seguido de incubação em nitrogênio líquido durante 10 segundos, separando-se a fase orgânica da fase líquida. O éter (fase orgânica) foi completamente seco num Speed Vac a 45 °C e o pellet ressuspendido em 300 μL de água:metanol (proporção 90:10), e filtrado através de um filtro PVDF de 0,2 μm .

Os metabólitos foram separados por cromatografia líquida carregando 10 μL do extrato em coluna BEH C18 1,7 μm (2,1 μm $\times$ 50 mm) aquecida a 40 °C, com fluxo de 300 $\mu\text{L min}^{-1}$. O gradiente binário consistiu em água grau LC-MS + 0,01% de ácido fórmico e metanol de grau LC-MS + 0,01% de ácido fórmico como eluente. O gradiente de eluição foi iniciado com 10% de metanol e mantido durante dois minutos, aumentando linearmente para 90% durante quatro minutos, depois aumentando linearmente para 100% durante um minuto e reduzindo para 10% durante 50 segundos, mantido a 10% durante 70 segundos, totalizando nove minutos de corrida.

Utilizando uma fonte de ionização por Z-spray electrospray ionization (ESI) dupla de alto desempenho (Waters), o efluente do Acquity UPLC I-Class FTN (Waters) foi introduzido no espectrômetro de massa de quadrupolo triplo Xevo TQ-XS (Waters). Nebulização de gás nitrogénio pressurizado a 7 Bar, fluxo de dessolvatação de 1000 L h⁻¹ e fluxo no cone de 150 L h⁻¹. A temperatura do gás de dessolvatação foi de 650 °C, a temperatura da fonte de 150 °C e a tensão capilar de 3 kV. Para o funcionamento do duplo quadrupolo em tandem (MS/MS), utilizou-se argônio como gás de colisão, com uma pressão de 0,8 kgf cm² na célula de colisão. O espectrômetro foi operado no modo de monitorização de reações múltiplas (MRM), com a tensão do cone, a energia de colisão e a massa do precursor e do fragmento a depender do hormônio em estudo, e estão resumidas no Apêndice 1. Os espectros de massa foram adquiridos utilizando o software MassLynx v4.2 (Waters).

Os espectros metabolômicos foram integrados e as linhas suavizadas com médias entre dois pontos. As áreas dos picos de ABA, ACC, IAA e JA foram estimadas utilizando uma equação linear obtida a partir da área do pico de uma curva padrão em diferentes concentrações (0; 0,5; 1; 2; 4; 6; 8; 10; 25; 50; 75; 100; 150; e 200 pg) utilizando o software TargetLynx XS (Waters). As médias das cinco réplicas biológicas de cada tratamento foram comparadas pelo teste T para inferir uma diferença significativa entre as médias ao nível de 5% de probabilidade.

3.4 Extração e digestão de proteínas

Cinco réplicas biológicas (500 mg de matéria fresca por amostra) de calos do tratamento controlem e 0,1 µM FDN foram trituradas com auxílio de pistilo dentro de microtubos de 1,5 mL. Em seguida, 1 mL de tampão de extração, consistindo de uréia 7M, tiouréia 2M, Triton X-100 2% (v/v), ditiotreitól 1% (p/v) (DTT; GE Healthcare, Piscataway, EUA), e 10 µL de coquetel inibidor de Halt protease e fosfatase, livre de EDTA (Thermo Fisher Scientific, Waltham, EUA), foi adicionado a amostra. A concentração de proteínas foi estimada usando um kit Bradford (Laboratórios Bio-Rad, Hercules, EUA).

A digestão trípica foi realizada utilizando o método FASP (filter-aided sample preparation), como descrito anteriormente por Wiśniewski *et al.* (2009)

usando 3.200 µg de proteínas de cada réplica biológica. Cada réplica biológica foi dividida em oito alíquotas de 400 µg devido ao limite de carga da unidade filtrante na digestão trípica usando FASP e realizada de acordo com Almeida et al. (2020). Os peptídeos das oito alíquotas de cada réplica biológica foram combinados, secos a vácuo e ressuspensos em 800 µL de uma solução contendo acetonitrila 5% (v/v) (Thermo Fisher Scientific) e ácido fórmico 0,1% (v/v) em água de grau MS (Sigma-Aldrich). Em seguida, foram separadas alíquotas de 50 µL para análise proteômica e o todo o restante das amostras foi utilizado para realizar o enriquecimento de fosfopeptídeos. A concentração dos peptídeos foi estimada medindo A205 nm usando um espectrofotômetro NanoDrop 2000c (Thermo Fisher Scientific). Os peptídeos foram armazenados a -80 °C antes das análises.

3.5 Enriquecimento dos fosfopeptídeos

O kit de enriquecimento de fosfopeptídeos High-Select™ TiO₂ (Thermo Fisher Scientific) foi utilizado para enriquecer os fosfopeptídeos das amostras de peptídeos digeridas com tripsina. Os peptídeos digeridos de cada réplica biológica foram secos a vácuo e ressuspensos em 150 µL de solução B do kit de enriquecimento de fosfopeptídeos. Todas as etapas de enriquecimento foram realizadas de acordo com as instruções do fabricante. Após a eluição dos fosfopeptídeos, o eluido foi seco a vácuo e ressuspendido em 50 µL de uma solução contendo acetonitrila 5% (v/v) (Thermo Fisher Scientific) e ácido fórmico 0,1% (v/v) em água grau MS (Sigma-Aldrich). A concentração de fosfopeptídeos foi estimada através do espectrofotômetro NanoDrop 2000c (Thermo Fisher Scientific) a 205nm. Os fosfopeptídeos foram armazenados em ultrafreezer -80 °C até a realização das análises.

3.6 Análise proteômicas e fosfoproteômica *label-free*

Para a aquisição dos espectros de massas, 1,2 µg de fosfopeptídeos e 400ng de peptídeos de cada amostra foram transferidos para uma coluna descartável Evotip C18 trap (Evosep Biosystems, Dinamarca) de acordo com as instruções do fabricante (Krieger et al., 2019). Em resumo, as Evotips foram hidratadas com 2-propanol, equilibradas com ácido fórmico a 0,1% e, em seguida, submetidas a uma força centrífuga de 1200 g. Posteriormente, as

Evotips foram lavadas com ácido fórmico a 0,1% e, em seguida, 200 µL de ácido fórmico a 0,1% foram adicionados a cada ponta para evitar a secagem. Para a corrida, cada amostra foi carregada em ponteiras Evosep (Evosep Biosystems, Odense, Dinamarca) para separação com cromatografia de fase reversa de nanofluxo com um sistema Evosep One LC (Evosep Biosystems). A separação foi realizada com o método 30 SPD (duração do gradiente de 44 min) usando uma coluna Evosep de 15 cm × 150 µm (Evosep Biosystems) embalada com partículas ReproSil-Pur C18-AQ de 1,5 µm. A Evosep One foi acoplada a um espectrômetro de massa de mobilidade iônica timsTOF Pro 2 (Bruker, Billerica, MA, EUA) operado em aquisição dependente de dados - acumulação paralela - fragmentação serial (DDA PASEF) (Meier *et al.*, 2015; Meier *et al.*, 2018).

3.7 Análise de dados proteômicos e fosfoproteômicos

Tanto os espectros MS/MS proteômicos quanto os fosfoproteômicos foram pesquisados em relação ao banco de dados de proteínas gerado a partir do sequenciamento do haploide de *S. spontaneum*, AP85-441 (Zhang *et al.*, 2018) (versão do banco de dados: Disponível em: Ensembl plants - v20190103).

O processamento de dados de proteômica e fosfoproteômica e a pesquisa em banco de dados foram realizados usando o *software* MaxQuant v. 1.6.3.4 (Cox e Mann, 2008) como descrito por (Almeida *et al.*, 2020). A quantificação *label-free* das proteínas identificadas foi realizada utilizando *normalized label-free quantification (LFQ intensity)* com os algoritmos MaxLFQ (Cox *et al.*, 2014). Após o processamento dos dados, apenas as proteínas presentes em pelo menos três corridas ou ausentes em todas as réplicas biológicas (para as proteínas únicas foram consideradas para análise do acúmulo diferencial na comparação FDN/controle. Proteínas com resultados significativos do teste-t de Student (bicaudal; $P < 0,05$) foram consideradas diferencialmente acumuladas (DAPs) e valores de $\text{Log}_2 \text{ fold change}$ (FC) maiores que 0,585 caracterizaram proteínas up-acumuladas e menores que -0,585, proteínas down-acumuladas.

Apenas os fosfopeptídeos que apresentaram probabilidade de fosforilação $\geq 0,75$ foram considerados para as análises. Somente as fosfoproteínas contendo fosfopeptídeos modificados com fosfato e presente em pelo menos em três das réplicas biológicas ou ausentes em todas as réplicas biológicas (para proteínas únicas) foram consideradas para análise de regulação diferencial na comparação FDN/controle. Fosfoproteínas com resultados significativos do teste-t de Student (bicaudal; $P < 0,05$) foram consideradas diferentemente reguladas (DRPs).

A análise da anotação funcional de proteínas e fosfoproteínas foi efetuada utilizando o software OmicsBox (<https://www.biobam.com/omicsbox>) e UniProtKB (<https://www.uniprot.org>). As sequências de proteínas foram submetidas a uma pesquisa BLAST na base de dados não redundante de proteínas de plantas do NCBI (taxa: 33090, Viridiplantae).

As redes de interação proteína-proteína preditas para as DAPs foram construídas usando homólogos de arroz (*Oryza sativa*) em cana-de-açúcar que foram identificados por meio de uma pesquisa STRING seguida pela análise downstream utilizando o Cytoscape (v3.0.1) (Szklarczyk et al. 2020). As quinases, fatores de transcrição e reguladores transcricionais previstos entre DAPs e DRPs foram identificados usando o software iTAK (Zheng et al., 2016).

4. Resultados

4.1 Efeitos de diferentes concentrações de ABA e fluridona na diferenciação e desenvolvimento de embriões somáticos

Após o tratamento durante o período de pré-maturação, as culturas foram subcultivadas em meio de cultura de maturação por 42 dias sob luz para a diferenciação de embriões somáticos. As características morfológicas dos calos foram analisadas nos 0, 28º e 42º dias de incubação (Figura 4). No tempo zero não foram observados sinais de maturação de embriões somáticos (Figura 4A, D, G, J, M, P, S e V), todos os tratamentos apresentaram aspectos morfológicamente semelhantes, com calos embriogênicos (CE) em coloração amarelada e compactos. Após 28 dias de maturação, com a diferenciação dos embriões, foi possível observar o aparecimento de pontuações clorofiladas na superfície dos calos na condição controle e dos tratados com 1, 10, 50 e 100

μM de ABA, com estruturas embrionárias mais desenvolvidas (Figura 4 B, E, H, K e N). Por outro lado, os calos tratados com FDN apresentavam uma cor esbranquiçada e um aspeto gelatinoso (Figura 4 Q, T, W). Ao final do período de maturação, com 42 dias, foi possível observar a formação de embriões somáticos no controle e os tratados com 1 e 10 μM de ABA (Figura 4 C, F e I), enquanto que os tratados com 50 e 100 μM de ABA apresentaram uma quantidade menor, e regiões pigmentadas na superfície do calo (Figura 4 L e O). Nos calos que receberam tratamento com FDN, foi possível observar poucas estruturas embrionárias no tratamento com 0,1 μM (Figura 4 R) e nos demais tratamentos (1 e 10 μM de FDN), não foi possível observar embriões somáticos que provavelmente foi devido à inibição do ABA endógeno (Figura 4 U e X).

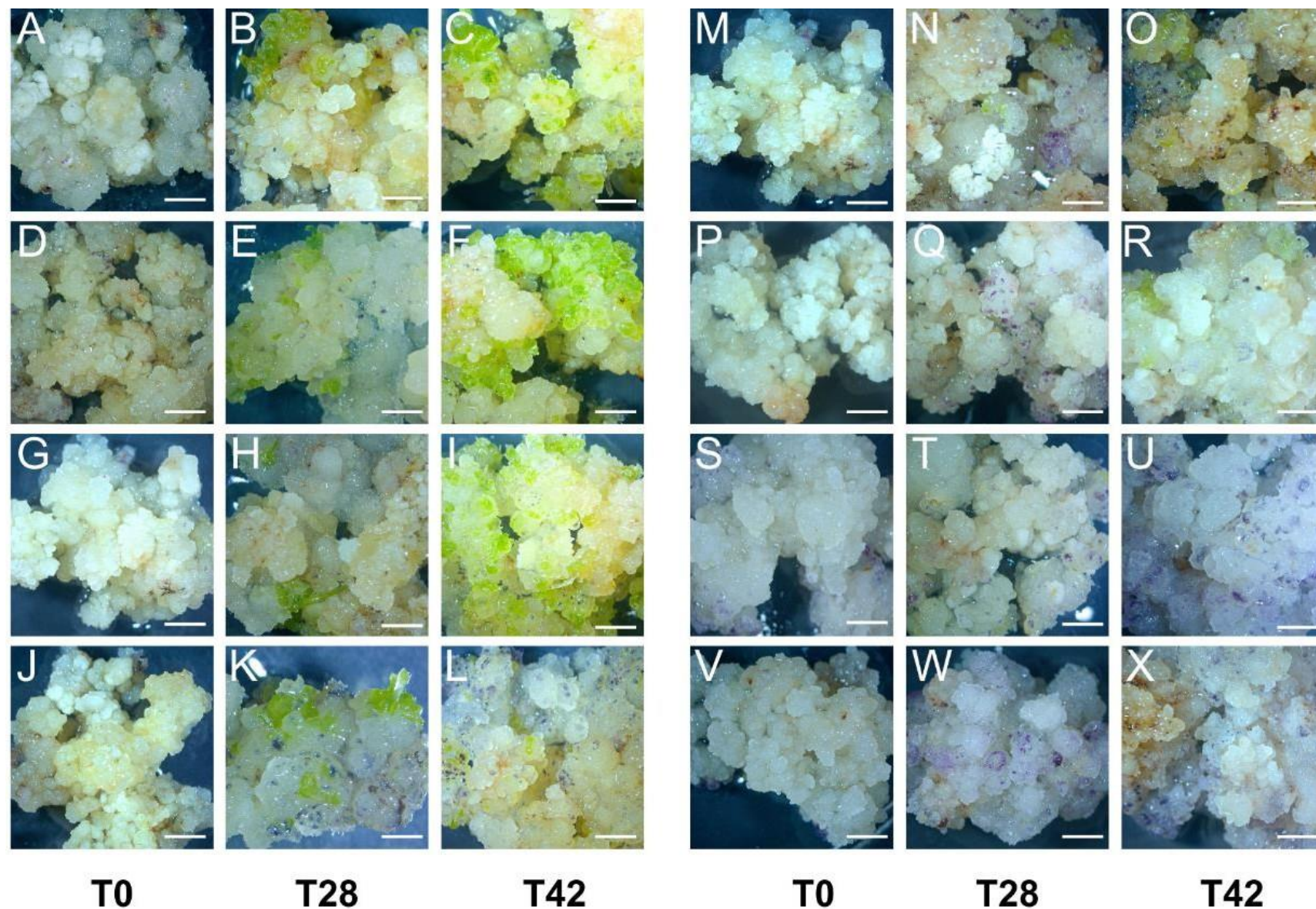


Figura 4. Aspectos morfológicos de calos embriogênicos submetidos ao tratamento controle e a diferentes doses de ABA e FDN (controle = A-C; 1 μ M ABA = D-F; 10 μ M ABA = G-I; 50 μ M ABA = J-L; 100 μ M ABA = M-O; 0,1 μ M fluridona = P-R; 1 μ M fluridona = S-U; 10 μ M fluridona = V-X). Tempo 0 (T0) de maturação A, D,G,J,M,P,S,V | Tempo 28 (T28) de maturação B,E,H,K,N,Q,T,W | Tempo 42 (T42) C,F,I,L,O,R,U,X. As barras indicam 0.5 mm.

O desenvolvimento dos embriões somáticos foi analisado através da contagem do número de embriões após 42 dias de incubação. Inicialmente, os resultados mostraram que as culturas sem qualquer tratamento produziram mais embriões somáticos em comparação com os calos tratados com FDN, com uma média de embriões somáticos de 32,6 no tratamento controle e 13,1 em 0,1 μ M de FDN (Tabela 1). Além disso, em comparação com o controle, a adição de ABA ao meio de cultura não apresentou efeito significativo quanto ao número de embriões somáticos. Vale ressaltar que houve diferença estatística ao comparar os calos do tratamento controle com os tratados com FDN. Em razão do tratamento de 0,1 μ M FDN apresentar ainda formação de um número reduzido de embriões em relação ao controle, deu-se prosseguimento às análises hormonais, proteômicas e fosfoproteômicas destes dois contrastes.

Tabela 1. Avaliação dos efeitos de diferentes concentrações de ABA e fluridona (FDN) no desenvolvimento de embriões somáticos em calos embriogênicos de cana-de-açúcar.

Tratamentos	Número de embriões somáticos
Controle	32,53 a
ABA 1	25,31 ab
ABA 10	32,69 a
ABA 50	24,97 ab
ABA 100	19,84 b
FDN 0,1	13,13 b
FDN 1	0,00 c
FDN 10	0,00 c

Médias seguidas pelas mesmas letras não diferem entre si pelo teste Tukey a 5% de probabilidade. Coeficiente de variação (CV)= 24,50%. n=8

4.2 Perfil hormonal

A análise de hormônios livres revelou os diferentes níveis de ABA, ACC, IAA e JA no tratamento controle e 0,1 μ M de FDN após 0, 14 e 28 dias de cultivo (Tabela 2). Foram detectados aumentos significativos nos níveis de ABA

endógeno nos tempos 0 e 14 dos calos no tratamento controle, cerca de 10 vezes mais, sugerindo um papel relevante do ABA neste evento. Nos calos em que o FDN estava presente no meio de cultura, esse comportamento nos tempos 0 e 14 manteve-se, embora com uma magnitude menor quando comparado com o controle (Tabela 2).

Tabela 2. Concentração dos níveis endógenos de ABA, ACC, IAA e JA (pg/g MF) em calos de cana-de-açúcar com a suplementação exógena de fluridona (FDN) e sem fluridona (Controle) durante a maturação na embriogênese somática.

Tratamento	Tempo de cultivo	IAA	ABA	ACC	JA
Controle	0	23,6 b	212,0 a	4359,1 c	14,9 a
	14	16,5 b	222,9 a	10468,1 bc	3,0 bc
	28	100,9 a	25,4 b	49823,9 a	0,0 c
FDN	0	13,5 b	23,5 b	2784,6 c	14,8 a
	14	16,1 b	34,3 b	18907,4 b	1,1 c
	28	21,9 b	17,7 b	11367,7 bc	0,1 c

Médias seguidas pelas mesmas letras não diferem entre si pelo teste T a 5% de probabilidade. ABA = ácido abscísico; ACC = ácido 1-aminociclopropanocarboxílico; IAA = ácido 3-indoleacético; JA = ácido jasmônico. N=5.

A concentração de ACC e IAA também foi menor nos calos que amadureceram no meio de cultura contendo FDN quando comparados aos calos que não estavam na presença de FDN, semelhante ao observado com ABA (Tabela 2). Parece que a presença do inibidor exógeno não inibe completamente a presença de alguns hormônios, indicando que as células podem encontrar alguma via alternativa, pois os comportamentos ao longo do tempo se mantiveram, apenas a magnitude foi bem menor quando o inibidor estava presente. A presença de FDN no meio de maturação dos calos de cana-de-açúcar parece não afetar as concentrações de JA, que manteve um comportamento semelhante independentemente da presença de FDN.

4.3 Análise proteômica e fosfoproteômica

Por meio de análises proteômicas e fosfoproteômicas *shotgun* (Apêndice 2), foram identificadas um total de 3.479 proteínas. A análise proteômica comparativa revelou 19 proteínas down acumuladas e 47 proteínas up-acumuladas no calo do tratamento controle em comparação com o tratamento com FDN. Além disso, 101 proteínas eram exclusivas na condição controle e 17 no tratamento com FDN.

Na análise fosfoproteômica, foram identificados 2.461 fosfopeptídeos com uma probabilidade de fosforilação de pelo menos 75% nas amostras de calos embriogênicos do tratamento controle e 0,1 uM FDN, correspondendo a 1147 fosfoproteínas (Apêndice 3). Foi descoberto um total de 2724 sítios de fosforilação entre os fosfopeptídeos identificados (Figura 5A). Foi também possível observar que 90% dos locais de fosforilação se situavam em resíduos de serina (S), 10% em resíduos de treonina (T) e menos de 1% em resíduos de tirosina (Y) (Figura 5B). Além disso, a análise comparativa revelou 138 fosfopeptídeos diferencialmente regulados na comparação FDN/controle.

4.4 Análise funcional das proteínas diferencialmente acumuladas

Com a análise proteômica e fosfoproteômica, foi possível identificar várias proteínas quinases, fatores de transcrição e reguladores de transcrição em calos embriogênicos de cana-de-açúcar (Tabela 3 e 4). Desta forma, foi possível identificar 48 classes de proteínas quinases e 55 famílias de fatores/reguladores de transcrição. As classes com maior número de quinases foram CAMK_CDPK (11 membros), RLK-Pelle_LRR-III (10 membros), TKL-PI-4 (6 membros), RLK-Pelle_LRR-V (5 membros) e CMGC_MAPK (5 membros). Entre os fatores/reguladores de transcrição, as classes C3H (20 membros), bZIP (11 membros), SWI/SNF-BAF60b (10 membros), SNF2 (10 membros) e C2H2 (8 membros) foram as mais representativas. Assim, verificou-se que 21 proteínas quinases e reguladores transcricionais estavam diferencialmente acumulados ou fosforilados na comparação FDN/controle (Tabela 3 e 4).

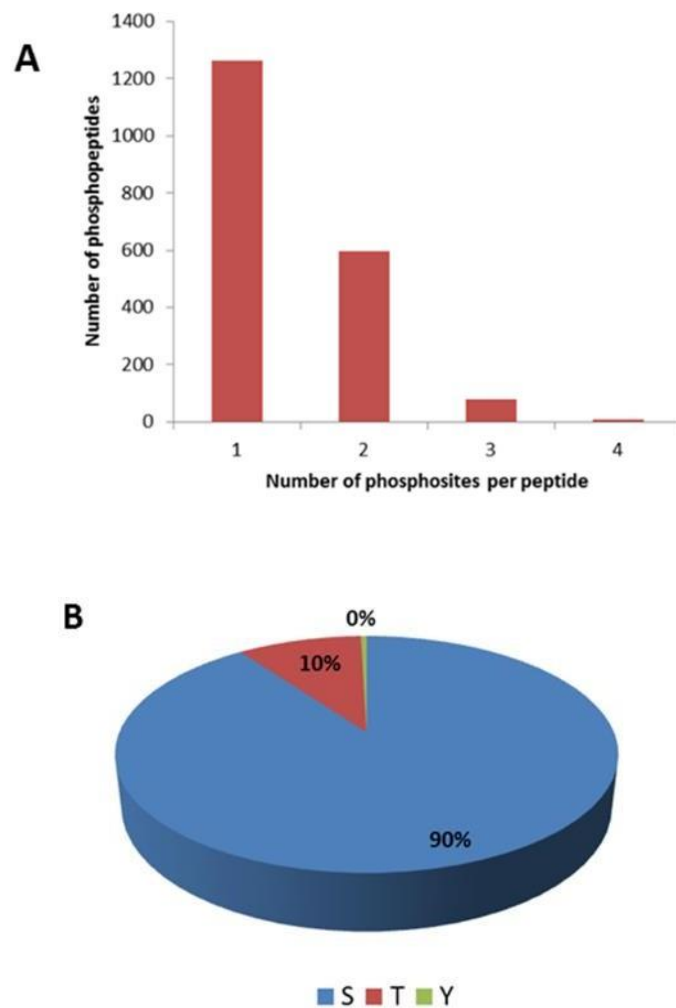


Figura 5. Número de sítios de fosforilação por peptídeo e número de resíduos S T Y fosforilados.(A) Número de fosfopeptídeos com 1, 2, 3 ou 4 sítios de fosforilação. (B). Proporção de resíduos de serina, treonina e tirosina fosforilados.

Tabela 3. Proteínas quinases moduladas por níveis endógenos de ABA em calos embriogênicos de cana-de-açúcar.

Protein ID	Annotation OmicsBox	Protein regulation	Phosphosite regulation	Kinase class
Sspon.05G0018860-4D	ATP binding protein	Unchanged	Down	TKL-PI-4
Sspon.04G0016580-1P	PTI1-like tyrosine-protein kinase At3g15890	Unchanged	Unique C	RLK-Pelle_RLCK-XV
Sspon.03G0001020-2B	PTI1-like tyrosine-protein kinase 3	Unique C		RLK-Pelle_RLCK-VIII
Sspon.01G0029040-3C	Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM1	-	Unique C	RLK-Pelle_LRR-XI-1
Sspon.03G0003820-1P	Leucine-rich repeat protein kinase family protein	Unique C	Unique C	RLK-Pelle_LRR-VIII-1
Sspon.05G0021270-1A	brassinosteroid LRR receptor kinase precursor	Unique C		RLK-Pelle_LRR-III
Sspon.01G0020370-2B	ATP binding protein	-	Unique C	CMGC_SRPK
Sspon.08G0008450-2B	CAK1AT	Down	Up	CMGC_CDK-CCRK
Sspon.02G0003320-2B	CDPK-related kinase 5	-	Up	CAMK_CDPK

Unique_C: Proteínas encontradas apenas no controle

Tabela 4. Fatores de transcrição e reguladores transcricionais modulados por níveis endógenos de ABA em calos embriogênicos de cana-de-açúcar.

Protein ID	Annotation OmicsBox	Protein regulation	Phosphosite regulation	TF class
Sspon.04G0005920-2D	Protein PHOTOPERIOD-INDEPENDENT EARLY FLOWERING 1	Unique C	Unique C	SNF2
Sspon.01G0007930-2B	enhancer of zeste3	Down		SET
Sspon.06G0015190-1A	CCAAT-HAP5-transcription factor 59	Unique C		NF-YC
Sspon.01G0015090-2C	BAH domain	Unchanged	Up	IWS1
Sspon.03G0009470-1A	HMG1/2-like protein	-	Unique C	HMG
Sspon.05G0022730-2D	N-terminal acetyltransferase A complex catalytic subunit NAA10-like	Unique T		GNAT
Sspon.01G0010590-1A	putative transcription factor	Up		GeBP
Sspon.06G0011880-1A	zinc finger CCCH domain-containing protein 55-like	Unchanged	Up	C3H
Sspon.02G0011780-2P	zinc finger protein WIP2	-	Up	C2H2
Sspon.03G0013820-1A	transcription factor HY5-like	Unchanged	Unique C	bZIP
Sspon.06G0003650-3C	DNA binding protein	Unchanged	Down	bZIP
Sspon.01G0036380-2C	F-box protein SKIP22	Unique C	Unique C	bHLH

Unique_C: Proteínas encontradas apenas no controle e Unique_T: Proteínas encontradas apenas no tratamento com FDN

4.5 Identificação de motivos e sítios de fosforilação de proteínas associadas ao ABA

No total, foram identificados 26 motivos de fosforilação entre os fosfopeptídeos. Além disso, 21 motivos estão presentes em fosfopeptídeos que foram regulados em calos provenientes do controle e/ou do tratamento com FDN (Figura 6). Esta análise permitiu também identificar 10 motivos que foram exclusivamente fosforilados ou mais regulados no tratamento de controle, incluindo os motivos [S-x-x-pS/T], [S-x-pS/T], [pS/T-P-R], [pS/T-P-x-x-S-P], [pS/T-G], [pS/T-D-S], [pS/T-D-E], [pS/T-D-D], [pS/T-D] e [pS/T-x-S]. Por outro lado, 2 motivos foram regulados após o tratamento com FDN, incluindo [pS/T-P-S-P] e [pS/T-x-x-S]. Após a análise funcional dos dados de proteínas e fosfoproteínas, foi possível gerar uma lista de candidatos que podem desempenhar um papel nas respostas ao ácido abscísico durante a ES da cana-de-açúcar (Tabela 5).

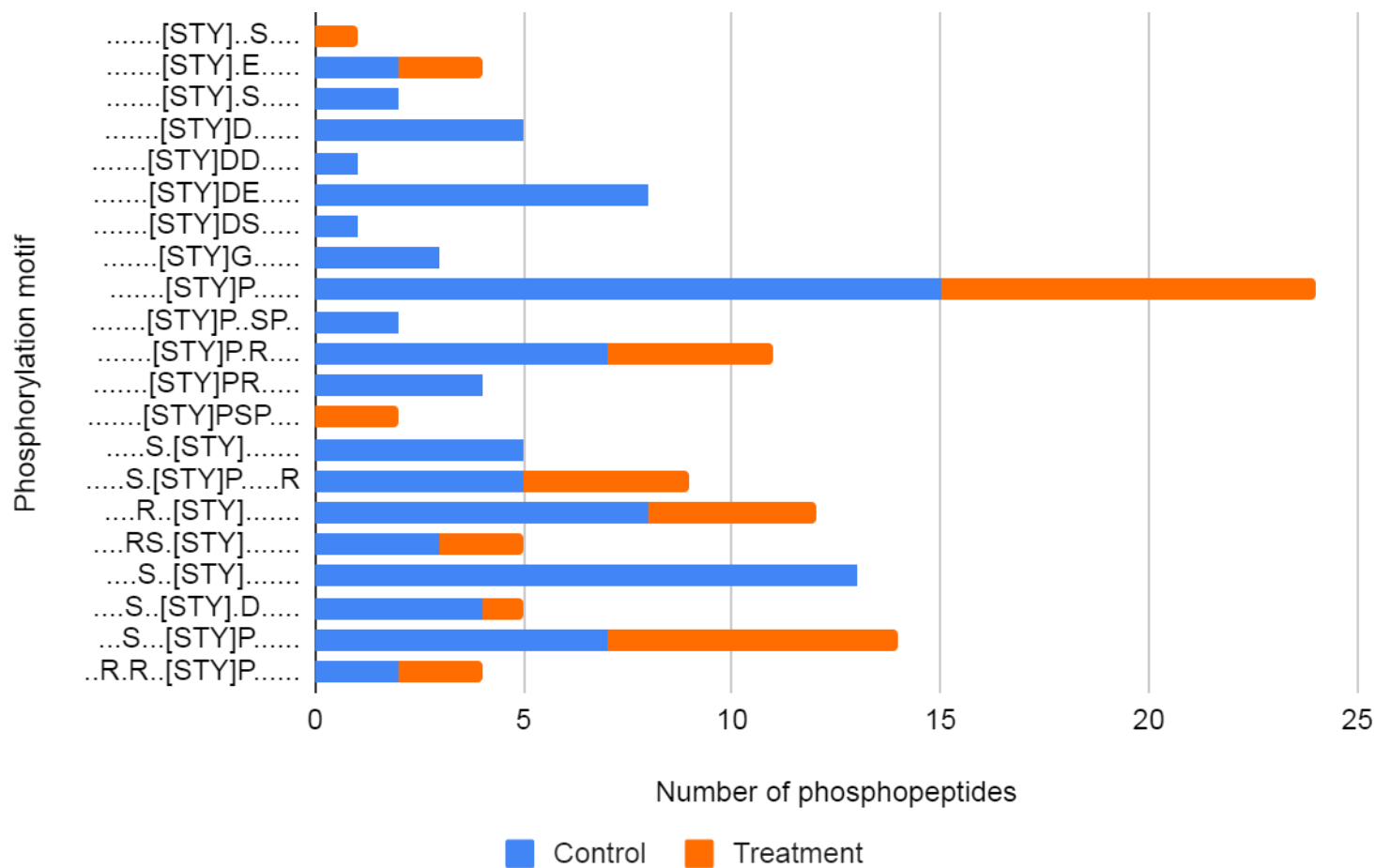


Figura 6. Gráfico de barras que mostra a distribuição dos motifs de fosforilação identificados nos tratamentos de controle e com fluridona. Todos os *motifs* de fosforilação identificados após análise de enriquecimento usando Motifer e a comparação entre DRPs

Tabela 5. Lista de proteínas e fosfoproteínas que podem desempenhar um papel nas respostas ao ABA durante a embriogênese somática em calos de cana-de-açúcar.

Protein ID	Annotation OmicsBox	Protein regulation	Phosphosite regulation	Phosphorylation motif	Site position
Sspon.05G0022390-2D	ABC transporter B family member 19	Unchanged	Up	R..[STY].....	657
Sspon.08G0022540-3D	Sucrose synthase 1	Down			
Sspon.08G0008450-2B	CAK1AT	Down	Up	[STY]DS.....	456
Sspon.01G0029040-3C	Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM1	-	Unique C	...S...[STY]P.....	1206
Sspon.06G0010720-3D	ramosa 1 enhancer locus 2	Down			
Sspon.02G0027830-4D	protein STABILIZED1	Unique_C			
Sspon.05G0021270-1A	brassinosteroid LRR receptor kinase precursor	Unique_C			
Sspon.03G0010360-3C	putative auxin efflux carrier component 3a	Unique_C			
Sspon.07G0016240-2C	AGO1a	Unchanged	Unique C	S.[STY].....	1053
Sspon.04G0011130-4D	Starch branching enzyme IIa	Unique_C			
Sspon.08G0016530-2B	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	Down			
Sspon.05G0023810-1B	Protein CTR9-like protein	Unchanged	Unique T	R..[STY].....	240
Sspon.02G0005420-1A	Lysine-specific demethylase JMJ25	Unique_C	Up	-	223
Sspon.06G0000390-3D	S-adenosyl-L-methionine-dependent methyltransferase superfamily protein	Unique_C	Unique C	[STY]D.....	857
Sspon.06G0007980-2B	auxin transport protein BIG	Unchanged	Up	S.[STY].....	1317

Unique_C: Proteínas encontradas apenas no controle e Unique_T: Proteínas encontradas apenas no tratamento com FDN

4.6 Redes de interação proteína-proteína

Foi possível determinar uma rede de interação proteína-proteína entre estes alvos e prever grupos que podem trabalhar em conjunto para integrar o desenvolvimento celular, transcriptômico, pós-embriogênico da planta (Figura 7), como por exemplo as proteínas *Sucrose Sintase 1*, *Starch Branching Enzyme IIa* e *Glycosyl Hydrolase Family 31 Protein* que estão intimamente interligadas e desempenham papéis cruciais no metabolismo energético das plantas, o que pode estar garantindo a disponibilidade adequada de energia para suportar o crescimento, o desenvolvimento e outras funções fisiológicas essenciais, além das proteínas fosforiladas envolvidas em respostas hormonais, como *Auxin transport protein BIG* e *ABC transporter B family member 19*.

Dessa forma, é possível observar que os níveis endógenos de ABA, além de regularem o acúmulo e a fosforilação de proteínas, também podem estar associados a interações importantes para a progressão da ES em cana-de-açúcar.

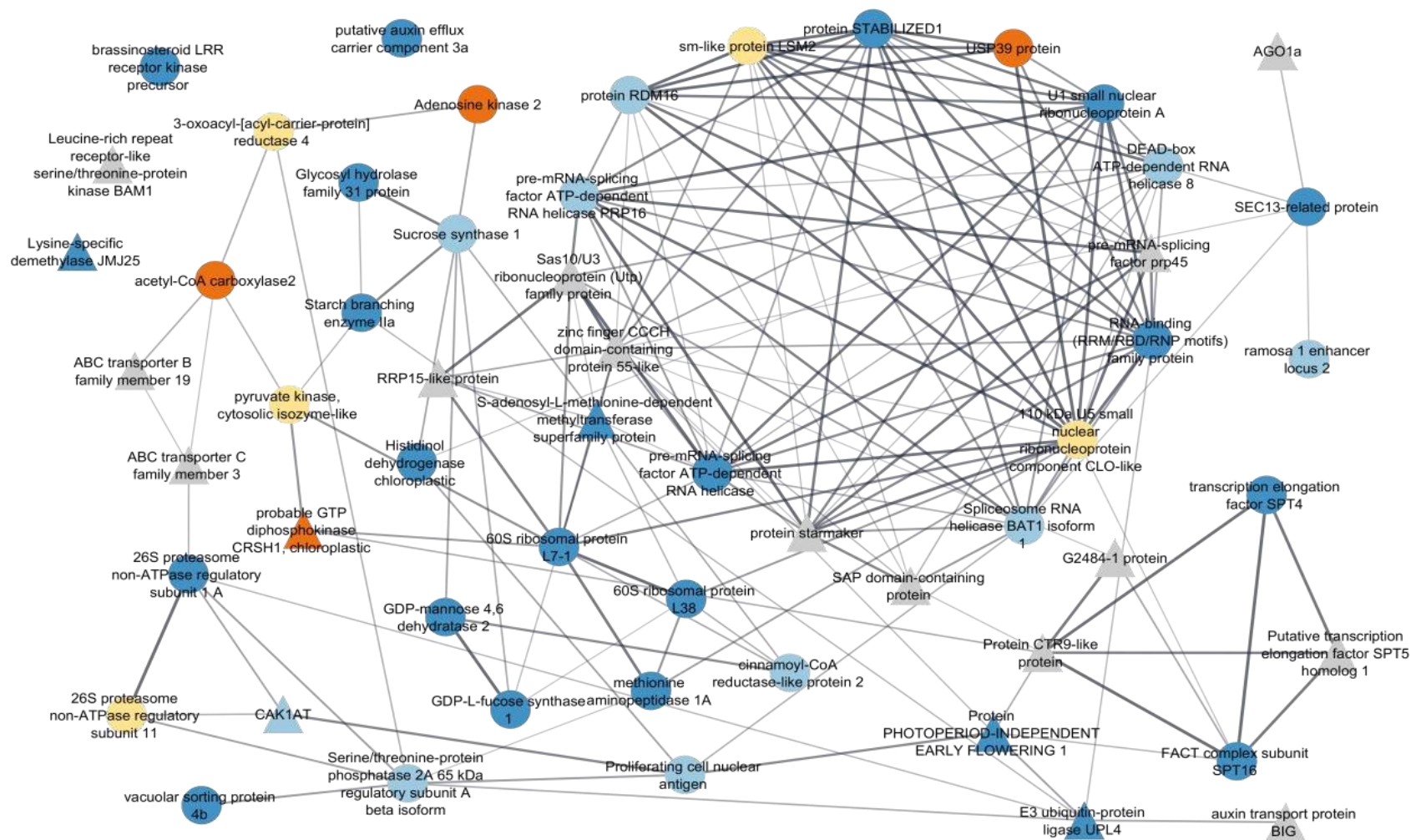


Figura 7. Rede de interação proteína-proteína prevista entre DAPs e DRPs associada às respostas ABA e à embriogênese somática da cana-de-açúcar. Análise realizada utilizando ortólogos de *Oryza sativa* identificados no STRING utilizando sequência de aminoácidos de proteínas de cana-de-açúcar. As elipses em azul escuro e azul claro representam Únicas no controle e Down-acumulada, respectivamente. As elipses em laranja escuro e laranja claro representam Única no tratamento e Up-acumulada, respectivamente. Em cinza, as Unchanged e as representadas por triângulo são as proteínas fosforiladas.

5. Discussão

O desenvolvimento do embrião somático é um processo que envolve a associação de inúmeras proteínas durante as fases de indução, desenvolvimento e a maturação do embrião somático. Neste estudo, observamos o papel crucial do ABA na regulação de proteínas-chave para o processo de diferenciação de embriões somáticos em cana-de-açúcar.

5.1 Impacto do acúmulo do ABA no desenvolvimento de embriões somáticos e metabolismo de reserva em cana-de-açúcar

Níveis elevados de ABA exercem influência sobre vários aspectos da ES, particularmente durante a fase de maturação, onde regula o acúmulo de reservas de armazenamento e o metabolismo para induzir a dormência. De acordo com os resultados, a inibição da biossíntese de ABA leva a uma redução na formação e desenvolvimento de embriões somáticos de cana-de-açúcar. Isto alinha-se com estudos semelhantes que demonstram que FDN afeta negativamente a formação de embriões somáticos durante a ES de *Medicago sativa* (Von Arnold et al., 2002). A análise proteômica revelou que a *Sucrose Sintase 1* (Sspon.08G0022540-3D) foi identificada como menos abundante no tratamento FDN em relação ao controle (Tabela 5). Na cana-de-açúcar, as proteínas da sacarose sintase são cruciais na síntese e decomposição da sacarose (Verma et al., 2011). Isso promove a geração de UDPG a partir da sacarose para o material da parede celular e a biossíntese de amido (Vasanth et al., 2022). Além disso, os produtos de degradação da sacarose estão disponíveis em várias vias metabólicas, como a produção de energia, metabólitos primários e a síntese de carboidratos complexos. Assim, a diminuição do número de embriões somáticos observada em calos embriogênicos de cana-de-açúcar tratados com FDN pode estar relacionada com alterações no acúmulo de reservas e no metabolismo energético causadas pela redução dos níveis endógenos de ABA.

O acúmulo de reservas de armazenamento nos embriões em desenvolvimento, incluindo o amido, é induzida pelo ABA (Finkelstein & Gibson, 2002). Neste contexto, *Starch branching enzyme IIa* (Sspon.04G0011130-4D), identificada como exclusiva no controle,

desempenha um papel crucial na biossíntese do amido, contribuindo para a síntese de amilopectina juntamente com outras enzimas (Pei et al., 2015). Além disso, esta proteína interage com outras proteínas envolvidas no metabolismo energético, incluindo a *Sucrose Sintase 1* e *Glycosyl hydrolase Family 31 protein* (Figura 7). Em *Ipomoea batatas* L. (batata-doce), o padrão de expressão da *Starch branching enzyme IIa* está ligado ao gene AGPase S, indicando uma interligação entre as *Starch branching enzyme* e a *ADP-glicose pirofosforilase*, a principal enzima reguladora da via biossintética do amido (Qin et al., 2013).

O ABA já foi identificado como um potente indutor da *Starch branching enzyme*, sugerindo uma resposta a sinais hormonais e acrescentando uma camada adicional de complexidade à regulação destas enzimas (Qin et al., 2013). Os genes da família da *Starch branching enzyme* demonstram uma atividade transcricional elevada em resposta à seca, ao sal e à aplicação externa de ABA nas folhas, sublinhando o seu potencial para influenciar a via biossintética do amido em diversas condições ambientais (Vasanth et al., 2022). A ausência da *Starch branching enzyme IIa* nos calos embriogênicos após o tratamento com FDN pode perturbar a biossíntese e o acúmulo de amido, reduzindo as reservas para o desenvolvimento de embriões somáticos.

Dessa forma, durante a ES, os embriões somáticos em desenvolvimento dependem das reservas de armazenamento para fornecer energia e nutrientes essenciais, como o amido e açúcar. Inicialmente, as células somáticas submetidas a estímulos reprogramam seu metabolismo para aumentar a produção de açúcares, a fim de fornecer energia e substratos necessários para a divisão celular e a formação de embriões somáticos, além disso podem ser alvos importantes para otimização de protocolos de cultura de tecidos e melhoria da regeneração de plantas em programas de melhoramento genético. Assim, em cana-de-açúcar já foi visto que o desenvolvimento eficiente dos embriões somáticos parece ser precedido pelo acúmulo eficiente de reservas de armazenamento nos calos (Reis et al., 2021).

5.2 As respostas hormonais envolvidas na embriogênese somática estão ligadas à acumulação e fosforilação de proteínas induzidas pelo ABA

A capacidade dos embriões maduros de *Arabidopsis* para manter o ambiente de maturação de sementes com ABA é identificada como um passo crucial para estabelecer a competência para a totipotência celular através da auxina (B. Chen et al., 2021), mostrando que o papel do ABA vai além da resposta ao stress abiótico.

Neste sentido, os nossos dados mostram que diferentes proteínas envolvidas nas respostas e transporte de auxinas, incluindo a proteína *Putative auxin efflux carrier component 3a* (Sspon.03G0010360-3C, ortóloga da *Arabidopsis* PIN4), identificada como exclusiva do controle, é um transportador de efluxo de auxinas, a proteína *Auxin transport protein BIG* (Sspon.06G0007980-2B, fosforilada a S1317) e *ABC transporter B family member 19* (Sspon.05G0022390-2D, fosforilado a S657). Assim, os calos embriogênicos de *Arabidopsis* submetidos ao tratamento com FDN diminuiram a biossíntese de auxinas e o transporte polar, demonstrando um papel importante do ABA na interação com outros hormônios para modular a ES e o desenvolvimento das plantas (Su et al., 2013). Em nosso trabalho é possível observar que também houve uma diminuição do IAA (auxina endógena) nos CE tratados com FDN (Tabela 2). Além disso, a caracterização molecular da proteína *BIG* mostra o seu envolvimento nas respostas hormonais e a luz, estando também relacionada com o crescimento dos órgãos através da expansão e divisão celular, impulsionando as respostas à auxina (Guo et al., 2013). A *ABC transporter B family member 19* é um componente primário do transporte de auxina, atuando como um regulador negativo da sinalização luminosa para promover o alongamento do hipocótilo da interação com o PIN1 (Noh et al., 2001). Já se sabe que a auxina controla muitos aspectos do desenvolvimento vegetal e que as proteínas transportadoras de auxina têm um papel crítico na regulação desses processos (Cecchetti et al., 2015). Dessa forma, níveis de auxina durante a ES pode afetar significativamente a expressão de genes e proteínas relacionados ao transporte e sinalização de auxina, bem como outros processos de desenvolvimento. A interação entre o ABA e a auxina revela uma complexa rede de sinalização hormonal que

influencia a competência das células para a totipotência e a formação de embriões somáticos. Possivelmente o ABA não está intermediando apenas a sinalização, mas também o transporte de outros hormônios. Além da relação a respostas relacionadas a outros hormônio, como a auxina, as proteínas *Auxin transport protein BIG* e *ABC transporter B family member 19* estão relacionadas as vias fotossintéticas, de respostas a luz e de antocianinas.

A indução da competência embriogênica e da diferenciação de embriões somáticos na cana-de-açúcar depende da regulação de diferentes repressores (Xavier et al., 2022). O corepressor transcricional *Ramosa 1 enhancer locus 2* (Sspon.06G0010720-3D, REL2) pertence à família *TOPLESS (TPL)* foi identificada como menos abundante no tratamento FDN em relação ao controle (Tabela 5). Os corepressores REL2/TPL interagem com diferentes fatores de transcrição de uma forma complexa, o que pode ter implicações em muitas vias hormonais e de desenvolvimento, como a via de sinalização da auxina (Liu et al., 2019). As mutações no rel2 conduziram a uma série de fenótipos vegetativos e reprodutivos, principalmente associados a problemas na iniciação e manutenção dos meristemas (Liu et al., 2019). Assim, as respostas de ABA dependem nas interações com diferentes hormônios vegetais, incluindo a giberelina e a auxina durante a ES e os nossos dados esclarecem a forma como os níveis endógenos de ABA, que apresentaram um aumento nos dias 0 e 14 de maturação (Tabela 2), nas células embriogênicas são integrados na sinalização da auxina por meio da acumulação e fosforilação de alvos específicos durante a ES.

Os brassinosteróides são hormônios vegetais envolvidos em diferentes processos fisiológicos e de desenvolvimento, incluindo o alongamento celular, a resposta à luz, a diferenciação vascular e a resistência ao estresse (H. Wang & Mao, 2014). O *Brassinosteroid LRR receptor kinase precursor* (Sspon.05G0021270-1A), identificado como exclusivo no controle, é rico em leucina (Kinoshita et al., 2005). Em *Arabidopsis*, para a ativação da rede de sinalização BR, a sua ligação requer a função de *Brassinosteroid insensitive 1* (BRI1), que é um receptor quinase rico em leucina (LRR) e está localizado na membrana plasmática, com a ligação desse hormônio, ocorre uma cascata de sinalização que resulta na regulação da expressão gênica e em várias

respostas fisiológicas (Zhi-Yong Wang et al., 2001). A ausência desta proteína nos calos de cana-de-açúcar tratados com FDN pode contribuir para o não desenvolvimento de embriões.

5.3 Os níveis endógenos de ABA modulam os mecanismos epigenéticos através da regulação das redes de interação de proteínas durante a embriogênese somática

Diferentes mecanismos epigenéticos são modulados em diferentes fases da ES, incluindo a acetilação/metilação de histonas e DNA, bem como microRNAs (Fehér, 2015; Wójcikowska et al., 2020). Os nossos dados mostram que a proteína *Argonaute (AGO1)* (Sspon.07G0016240-2C, AGO1, fosforilada em S1053), está relacionada com a regulação epigenética (Tabela 5). Em *Arabidopsis thaliana*, *AGO1* está envolvida no silenciamento de genes pós transcricionais dirigidos por miRNA e RNA interferentes (siRNAs) (P. Wang et al., 2013). Uma diminuição da *AGO1* confere hipersensibilidade ao ABA, enquanto um aumento do nível de *AGO1* conduz a uma hipossensibilidade ao ABA (Earley et al., 2010). Dessa forma, essa proteína possivelmente pode estar envolvida na mediação de respostas ao estresse causado por ABA na aquisição da competência embriogênica. A metilação/acetilação das histonas e do DNA desempenha um papel fundamental na regulação da expressão genética. Identificamos a ativação de várias proteínas que regulam este processo. A proteína *S-adenosyl-L-methionine-dependent (SAM)* (Sspon.06G0000390-3D fosforilada em S857) identificada exclusivamente no controle, é considerada uma doadora do grupo metil envolvida em diversas reações de metilação do DNA (R M et al., 2020) que são cruciais para a regulação da expressão gênica. Estes grupos metil podem então ser utilizados pela *CTR9-like* (Sspon.05G0023810-1B fosforilada em S240). Desta forma, alterações na expressão ou atividade dessa proteína podem impactar a metilação do DNA e a acetilação de histonas que são importantes modificações epigenéticas relacionadas à regulação da expressão gênica.

Além disso, os nossos dados mostram *Lysine-specific demethylase JMJ25* (Sspon.02G0005420-1A, fosforilada em S33) (Tabela 5), desempenha um importante papel na regulação epigenética das plantas, considerada uma histona demetilase, isso é, capaz de remover grupos metil da lisina em proteínas histonas, alterando assim o estado de metilação da cromatina e influenciando a expressão gênica. Sua capacidade de modular a metilação da cromatina permite que ela atue como regulador chave da expressão gênica, afetando a transcrição de genes envolvidos em vias metabólicas, diferenciação

celular, desenvolvimento de órgãos e resposta a estresses (Luo et al., 2014). Além disso, a proteína *STABILIZED1* (Sspon.02G0027830-4D) identificada exclusivamente no controle, envolvida na metilação do DNA, sugere que o ABA exerce influência sobre a metilação do DNA na cana-de-açúcar e, como se pode ver na rede de interação proteína-proteína (Figura 7), essa proteína realiza várias interações com outras proteínas. Os nossos resultados mostram a ativação de proteínas bem conhecidas documentadas na literatura, juntamente com novas proteínas que têm informação limitada disponível até à data.

Dessa forma, a análise da metilação do DNA emerge como uma abordagem promissora para ser explorada durante a ES de cana, visto que durante esse processo, os padrões de metilação do DNA podem ser suscetíveis a mudanças dinâmicas em resposta a estímulos hormonais, condições ambientais e estágios de desenvolvimento. Assim, é possível que esse estudo pode ajudar a entender melhor os mecanismos epigenéticos subjacentes ao desenvolvimento embrionário e identificar marcadores epigenéticos associados à regeneração de plantas a partir de CE. Além disso, melhorar os protocolos de cultura de tecidos e aumentar a eficiência da regeneração de plantas em programas de melhoramento genético e produção de cana-de-açúcar.

5.4 A embriogênese somática da cana-de-açúcar é regulada por proteínas quinases e fosfatases envolvidas nas respostas ao ABA

As respostas do ABA em diferentes processos biológicos dependem da atividade de proteínas quinases e fosfatases específicas (Yang et al., 2017). No caso da ES da cana-de-açúcar, a redução dos níveis endógenos de ABA resultou numa diminuição da acumulação e fosforilação de diferentes proteínas quinases que podem estar associadas ao desenvolvimento de embriões somáticos (Tabela 1).

Neste contexto, *Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform* (Sspon.08G0016530-2B) foi identificada como menos abundante no tratamento FDN em relação ao controle. Em *Arabidopsis*, esta proteína é conhecida pelo seu papel nas respostas à auxina, onde está envolvida na localização celular das proteínas *PIN* através da

desfosforilação destes transportadores de auxina (Dai et al., 2012). Assim, os nossos dados sugerem que uma alteração nos níveis endógenos de ABA durante a ES pode afetar a sinalização de diferentes hormônios envolvidos no desenvolvimento através da regulação pós-traducional de proteínas reguladoras, como as fosfatases.

A proteína *CAK1AT* (Sspon.08G0008450-2B, fosforilada em S456) foi identificada como menos abundante no tratamento FDN em relação ao controle (Tabela 5). Em *Arabidopsis* demonstrou que *CAK1AT* é importante para fosforilar e ativar as quinases dependentes da ciclina (CDK), a fim de promover a divisão celular e a progressão do ciclo celular ao longo do desenvolvimento (Takatsuka et al., 2015). Outros estudos sobre a *CAK1AT* demonstram o papel desta quinase na regulação do ciclo celular e da proliferação, sugerindo a sua participação principalmente no desenvolvimento pós-embriônico (Takatsuka et al., 2009). Além disso, os nossos dados mostram que *CAK1AT* tem interações com a *Proliferating Cell Nuclear Antigen* (Sspon.04G0001130-3D, PCNA), também identificada como menos abundante no tratamento FDN em relação ao controle (Tabela 5; Figura 7). A proteína PCNA tem localização nuclear e é conservada em procariotas e eucariotas, onde desempenha um papel na regulação do ciclo celular e da replicação do DNA, processos fundamentais para o crescimento e o desenvolvimento (Strzalka & Ziemienowicz, 2011). Ao modular a acumulação e a fosforilação de proteínas associadas à progressão da divisão celular, estes dados sugerem que os níveis endógenos de ABA nos CE da cana-de-açúcar são importantes para regular a proliferação e o ciclo celular durante a diferenciação do embrião. As proteínas quinases de receptores de membrana desempenham um papel importante nos processos biológicos, especialmente na percepção de sinais extracelulares. Neste contexto, a proteína *Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM1* (Sspon.01G0029040-3C, BAM1, fosforilada em S1206) em *Arabidopsis* interage com *CLAVATA (CLV)* para regular a identidade das células presentes nos meristemas das plantas, mutantes duplos para *bame clv* mostram defeitos na especificação das células estaminais (DeYoung & Clark, 2008). Assim, a perda de função da *BAM1* também prejudica a formação de meristemas e órgãos vegetais, além de provocar um aumento do número de

embriões de *Arabidopsis* abortados (DeYoung et al., 2006). Os estudos sobre o papel da *BAM1* sugerem também que a atividade de quinase é importante para as funções desta proteína nos meristemas das plantas (Shimizu et al., 2015). Consequentemente, a alteração no nível de fosforilação de *BAM1* em CE pode estar associada à diminuição do número de embriões somáticos de cana-de-açúcar observada após o tratamento com FDN. No entanto, ainda não está claro como os níveis endógenos de ABA em calos embriogênicos modulam a fosforilação de *BAM1* durante a ES.

No tratamento de CE de cana-de-açúcar, foi possível encontrar duas proteínas ricas em serina/arginina (SR), das quais são importantes fatores de *splicing*. A proteína *Serine/arginine-rich SC35-like splicing factor SCL30 (SCL)* (Sspon.02 G0029150-1P fosforilada em S36 e S219), sendo um fosfopeptídeo identificado exclusivamente no controle no local de fosforilação 36, enquanto no local de fosforilação 219 foi exclusivo no tratamento com FDN, esta fosforilação pode estar associada ao nível de ABA endógeno e a *Serine/arginine-rich splicing factor SC35 (SC35)* (Sspon.02G0003220-2B fosforilado em S116). Em estudos com *Arabidopsis* utilizando RNA-seq, descobriu-se que as proteínas *SCL* e *SC35* desempenham papéis no *splicing* do pré-mRNA (Yan et al., 2017). Nas plantas, as proteínas SR estão envolvidas no crescimento e desenvolvimento, na transdução de sinais, nas respostas aos estresses abiótico e biótico e no metabolismo, bem como na regulação dos genes durante o desenvolvimento (Jin, 2022). Estudos revelaram, através de análises genéticas, que a perda de função das proteínas *SC35/SCL* influencia o desenvolvimento das plantas e, em *Arabidopsis*, a *SC35-like (SCL)* e a *SC35* causam alterações pleiotrópicas na morfologia e no desenvolvimento das plantas, incluindo folhas serrilhadas, floração tardia e raízes mais curtas (Yan et al., 2017). Para além do efeito no crescimento e desenvolvimento, as proteínas SR também atuam em resposta a estresses e hormônios.

6. Conclusões

Com base nos resultados obtidos, podemos concluir que:

- Através técnica de cultura de tecido pode-se observar que ao longo do período de maturação, houve uma progressiva

diferenciação dos embriões somáticos, especialmente nos CE controle e tratados com ABA, em que foi possível observar o desenvolvimento de estruturas embrionárias mais avançadas, evidenciadas pela presença de pontuações clorofiladas na superfície dos calos, no entanto através de análises estáticas, evidenciamos que não houve diferença estatística com a suplementação do ABA comparado com o controle, sendo assim o ABA endógeno é suficiente para formação de embriões somáticos na cana-de-açúcar.

- Houve diferença significativa nos CE tratados com fluridona, e ainda resultaram em uma redução de estruturas embrionárias no CE tratados com 0,1 fluridona e inibição do desenvolvimento embrionário nas demais concentrações testadas, evidenciando a importância do ABA endógeno nos CE de cana-de-açúcar.
- Os nossos dados elucidam uma parte do processo pela forma como o ABA modula os mecanismos epigenéticos, transcricionais, hormonais e metabólicos, regulando o acúmulo e a fosforilação de proteínas envolvidas em diferentes processos biológicos.
- Proteínas encontradas nesse trabalho como *Putative auxin efflux carrier component 3a*, *Auxin transport protein BIG*, *ABC transporter B family member 19*, *REL2* e *brassinosteroid LRR receptor kinase* estão envolvidas em mecanismos hormonais, evidenciando a sua importância durante a ES. E ainda, observamos que proteínas de acúmulo de reservas nas plantas desempenham um papel crucial em seu metabolismo e desenvolvimento, podendo atuar como fonte de energia e nutrientes para a planta, é o caso da *Sucrose Sintase 1* e *Starch branching enzyme lia*. É possível compreender que a regulação da expressão da embriogênese somática acontece sob a influência da regulação epigenética, e dessa forma proteínas que foram fosforiladas como *AGO1*, *SAM*, *CTR9-like* e *Lysine-specific*

demethylase JMJ25 sugerem que a fosforilação é crucial para reprogramação da expressão gênica, influenciando as respostas ao estresse.

- A manutenção dos níveis endógenos de ABA em calos durante a ES é um fator importante que regula o acúmulo e a fosforilação de proteínas importantes para a diferenciação e o progresso do desenvolvimento de embriões somáticos de cana-de-açúcar. Essas descobertas podem ser aplicadas para explicar a baixa taxa de regeneração de embriões somáticos exibida pelas variedades de cana-de-açúcar, além de fornecer informações importantes para otimizar os protocolos modulando as respostas de ABA.

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Apêndices

Apêndice 1. Lista das funções configuradas em modo de monitorização de reações múltiplas (MRM), com modo de ionização, período em que se monitoriza a massa do precursor e dos fragmentos, tensão do cone e energia de colisão em função do metabólito, obtidas por infusão direta dos padrões (10 pg/μL) e injeção em modo Radar Scan.

Função	Nome	Fórmula	MW	Ion Mode	Start (min)	End (min)	Precursor	Fragmento	Dwell	Cone (V)	Colisão (eV)
ACC	1-Aminocyclopropanecarboxylic acid	C ₄ H ₇ NO ₂	101,1	ES+	0,0	1,0	102,03	55,95	0,33	25	8
IAA	3-Indoleacetic acid	C ₁₀ H ₉ NO ₂	175,18	ES+	3,8	4,8	176	130	0,025	25	15
JA	Jasmonic acid	C ₁₂ H ₁₈ O ₃	210,27	ES-	4,6	5,6	209,05	58,99	0,054	16	12
ABA	Absciscic acid	C ₁₅ H ₂₀ O ₄	264,32	ES-	4,3	5,3	263,02	152,94	0,025	20	10
				ES-	4,3	5,3	263,02	219,02	0,025	20	12

Apêndice 2. Lista completa de proteínas

Acesso	Descrição	Cobertura [%]	Regulação Proteômica	Regulação Fosfoproteômica
Sspon.03G0017600-1A	Zinc knuckle (CCHC-type) family protein	9,9	Unique T	Yes
Sspon.02G0025530-1A	putative disease resistance protein RGA4 isoform X1	1,7	Unique T	Yes
Sspon.07G0012350-3C	probable GTP diphosphokinase CRSH1, chloroplastic	2,8	Unique T	Yes
Sspon.01G0008150-1A	cAMP-regulated phosphoprotein 19-related protein	13,8	Unique T	Yes
Sspon.04G0005920-2D	Protein PHOTOPERIOD-INDEPENDENT EARLY FLOWERING 1	0,5	Unique C	Yes
Sspon.03G0030090-1P	putative ADP-ribosylation factor GTPase-activating protein AGD14	7,5	Unique C	Yes
Sspon.03G0003820-1P	Leucine-rich repeat protein kinase family protein	0,9	Unique C	Yes
Sspon.07G0005710-1P	ribosome export associated1	2,2	Unique C	Yes
Sspon.05G0032730-1C	myosin-2	8,7	Unique C	Yes
Sspon.07G0023250-1B	E3 ubiquitin-protein ligase UPL4	1,7	Unique C	Yes
Sspon.02G0005420-1A	Lysine-specific demethylase JMJ25	27,2	Unique C	Yes
Sspon.01G0036380-2C	F-box protein SKIP22	5,8	Unique C	Yes
Sspon.01G0000170-2D	sphingomyelin phosphodiesterase 4	1,8	Unique C	Yes
Sspon.04G0014710-1A	protein phosphatase 1 regulatory subunit pprA	11,6	Unique C	Yes
Sspon.03G0014830-1A	binding	5,7	Unique C	Yes
Sspon.06G0000390-3D	S-adenosyl-L-methionine-dependent methyltransferase superfamily protein	1,5	Unique C	Yes
Sspon.06G0011880-1A	zinc finger CCCH domain-containing protein 55-like	3,1	Unchanged	Yes
Sspon.01G0007790-2P	splicing factor PWI domain-containing protein	30,3	Unchanged	Yes
Sspon.02G0029150-4D	Serine/arginine-rich SC35-like splicing factor SCL30	30,3	Unchanged	Yes
Sspon.07G0014850-1A	Serine/arginine-rich splicing factor RS2Z32	23	Unchanged	Yes
Sspon.08G0024800-1C	transformer-2 protein	48	Unchanged	Yes
Sspon.01G0015090-2C	BAH domain	5,4	Unchanged	Yes
Sspon.04G0008510-2C	serine/arginine-rich splicing factor RSZ23-like	41,5	Unchanged	Yes
Sspon.03G0020230-4D	Octicosapeptide/Phox/Bem1p family protein	21,3	Unchanged	Yes
Sspon.04G0019310-3C	Patellin-6	4,4	Unchanged	Yes
Sspon.04G0015290-1A	NSP (nuclear shuttle protein)-interacting GTPase	8,5	Unchanged	Yes
Sspon.01G0041200-3D	G2484-1 protein	7,4	Unchanged	Yes
Sspon.07G0004490-2D	hypothetical protein	20,7	Unchanged	Yes
Sspon.02G0050370-2D	ENT domain containing protein	16	Unchanged	Yes
Sspon.05G0006100-1A	sphingoid long-chain bases kinase 1	2,4	Unchanged	Yes
Sspon.03G0013820-1A	transcription factor HY5-like	16,5	Unchanged	Yes
Sspon.04G0016580-1P	PTI1-like tyrosine-protein kinase At3g15890	6,3	Unchanged	Yes
Sspon.05G0018860-4D	ATP binding protein	17,1	Unchanged	Yes
Sspon.04G0004650-1A	enhancer of mRNA-decapping protein 4	16,4	Unchanged	Yes
Sspon.02G0019440-2B	aquaporin PIP2.1	20,7	Unchanged	Yes
Sspon.07G0016240-2C	AGO1a	4	Unchanged	Yes
Sspon.08G0020400-2C	ATP/GTP-binding protein family	18,1	Unchanged	Yes
Sspon.06G0007980-2B	auxin transport protein BIG	0,3	Unchanged	Yes
Sspon.07G0033930-1C	E3 ubiquitin-protein ligase UPL1	8,3	Unchanged	Yes
Sspon.06G0000140-1A	Mediator of RNA polymerase II transcription subunit 15a	3,2	Unchanged	Yes
Sspon.08G0005170-1P	Phox (PX) domain-containing protein	3,6	Unchanged	Yes
Sspon.05G0008970-1T	Plant intracellular Ras-group-related LRR protein 3	10,6	Unchanged	Yes
Sspon.05G0001710-1A	Protein IQ-DOMAIN 32	17	Unchanged	Yes
Sspon.07G0015770-1A	Pumilio homolog 3	4,3	Unchanged	Yes
Sspon.06G0009700-1A	Putative nucleolin-like family protein	37,6	Unchanged	Yes
Sspon.06G0003650-3C	DNA binding protein	12,5	Unchanged	Yes
Sspon.01G0041370-3D	RING/FYVE/PHD zinc finger superfamily protein	1,4	Unchanged	Yes
Sspon.05G0022390-2D	ABC transporter B family member 19	4,2	Unchanged	Yes
Sspon.08G0015120-1A	RNA-binding protein 1-like	18,2	Unchanged	Yes
Sspon.05G0023810-1B	Protein CTR9-like protein	17,4	Unchanged	Yes
Sspon.05G0024490-1B	senescence regulator	7	Unchanged	Yes
Sspon.04G0007340-2B	Autophagy-related protein 13a	5,5	Unchanged	Yes
Sspon.01G0042410-1P	RING/U-box superfamily protein	3,6	Unchanged	Yes
Sspon.02G0034150-1B	acidic leucine-rich nuclear phosphoprotein 32-related protein 1	11,1	Unchanged	Yes
Sspon.05G0038190-1D	Exocyst complex component SEC5A	4,4	Unchanged	Yes
Sspon.05G0031560-1C	Golgin candidate 2	2,9	Unchanged	Yes
Sspon.01G0052200-1P	branchpoint-bridging protein	15,6	Unchanged	Yes
Sspon.03G0043900-1C	ABC transporter C family member 3	2,6	Unchanged	Yes
Sspon.06G0015530-3D	BSD domain-containing protein	11,9	Unchanged	Yes
Sspon.06G0015400-1P	DUF724 domain-containing protein 2	12,2	Unchanged	Yes
Sspon.02G0004780-1A	Protein TIME FOR COFFEE	3,2	Unchanged	Yes
Sspon.02G0029090-3C	Heat shock protein 70	50,4	Unchanged	Yes
Sspon.06G0028040-1C	Sas10/U3 ribonucleoprotein (Utp) family protein	15,2	Unchanged	Yes
Sspon.02G0026090-3C	RRP15-like protein	3,5	Unchanged	Yes
Sspon.01G0023310-1A	Transducin/WD40 repeat-like superfamily protein	4,5	Unchanged	Yes
Sspon.02G0047000-1C	SAP domain-containing protein	4,2	Unchanged	Yes
Sspon.04G0033500-1C	protein starmaker	4,4	Unchanged	Yes
Sspon.04G0008860-1A	Glyceraldehyde-3-phosphate dehydrogenase 3, cytosolic	80,7	Unchanged	Yes
Sspon.02G0005420-4D	Lysine-specific demethylase JMJ25	13,9	Unchanged	Yes
Sspon.04G0005750-4D	60S ribosomal protein L12	52,4	Unchanged	Yes
Sspon.08G0016070-2B	BUD13 homolog	3,4	Down	Yes

Sspon.02G0049380-1C	65-kDa microtubule-associated protein 6	5,9	Down	Yes
Sspon.08G0008450-2B	CAK1AT	3,8	Down	Yes
Sspon.04G0008840-3C	Transcription factor GTE8	5,6	Down	Yes
Sspon.03G0008300-1T	Nuclear pore complex protein NUP50A	14,4	Down	Yes
Sspon.08G0013930-1A	Putative AP2/EREBP transcription factor superfamily protein	13,3	Down	Yes
Sspon.06G0024480-1B	60S acidic ribosomal protein P1	26,1	Down	Yes
Sspon.02G0013380-1A	heat shock protein	3,8	-	Yes
Sspon.01G0029040-3C	Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM1	1,6	-	Yes
Sspon.01G0041200-2C	G2484-1 protein	7,9	-	Yes
Sspon.06G0011170-3C	DNA topoisomerase 1 beta	17,1	-	Yes
Sspon.03G0009470-1A	HMG1/2-like protein	12,4	-	Yes
Sspon.03G0008790-3D	65-kDa microtubule-associated protein 3	2,4	-	Yes
Sspon.04G0008880-1A	glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform-like	22,4	-	Yes
Sspon.02G0028410-2B	Trafficking protein particle complex II-specific subunit 130-like protein	3,8	-	Yes
Sspon.02G0003220-2B	Serine/arginine-rich splicing factor SC35	8,6	-	Yes
Sspon.02G0003320-2B	CDPK-related kinase 5	1,8	-	Yes
Sspon.07G0021540-2D	Sugar transporter ERD6-like 6	15	-	Yes
Sspon.07G0001380-1T	Sugar transporter ERD6-like 6	4,5	-	Yes
Sspon.02G0011780-2P	zinc finger protein WIP2	2,8	-	Yes
Sspon.02G0029150-1P	Serine/arginine-rich SC35-like splicing factor SCL30	25,5	-	Yes
Sspon.04G0027470-2C	hypothetical protein BDA96_04G101600	7,7	-	Yes
Sspon.01G0020370-2B	ATP binding protein	2	-	Yes
Sspon.05G0005580-3D	SPT2 chromatin protein	3,1	-	Yes
Sspon.04G0022140-2C	pre-mRNA-splicing factor prp45	11,5	-	Yes
Sspon.04G0002680-2C	Remorin family protein	6,6	-	Yes
Sspon.02G0022230-1A	KH domain-containing protein SPIN1	12,5	-	Yes
Sspon.04G0002500-2P	Putative transcription elongation factor SPT5 homolog 1	4,6	-	Yes
Sspon.03G0035590-1B	nucleolin-like	5,3	-	Yes
Sspon.05G0031010-1P	uncharacterized protein LOC8063953	18,1	-	Yes
Sspon.03G0031100-3D	Phosphoenolpyruvate carboxylase 3	12,2	-	Yes
Sspon.03G0005570-1P	Topoisomerase II-associated protein PAT1	1,1	-	Yes
Sspon.01G0010590-1A	putative transcription factor	11,1	Up	-
Sspon.01G0037660-2P	tetratricopeptide repeat protein 38-like	4,1	Up	-
Sspon.01G0049640-2D	Glucan endo-1,3-beta-glucosidase 3	22,8	Up	-
Sspon.01G0053970-2D	nonsense-mediated mRNA decay NMD3 family protein	12	Up	-
Sspon.01G0024520-3C	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1	23	Up	-
Sspon.01G0008700-1A	pyruvate kinase, cytosolic isozyme-like	12,6	Up	-
Sspon.01G0020770-4D	Monothiol glutaredoxin-S11	21	Up	-
Sspon.01G0029350-1A	WW domain-binding protein 11	4,7	Up	-
Sspon.04G0011920-1A	3-oxoacyl-[acyl-carrier-protein] reductase 4	7,3	Up	-
Sspon.03G0005580-1A	eukaryotic translation initiation factor 3 subunit M-like	46,9	Up	-
Sspon.02G0030070-1A	Adenine phosphoribosyltransferase 1	25,3	Up	-
Sspon.08G0006100-2B	110 kDa U5 small nuclear ribonucleoprotein component CLO-like	21,1	Up	-
Sspon.04G0001490-1P	ATPase 6, plasma membrane-type-like	4,9	Up	-
Sspon.03G0010210-1P	malate dehydrogenase, mitochondrial-like	24,2	Up	-
Sspon.07G0003280-2B	Mitochondrial outer membrane protein porin 2	61,9	Up	-
Sspon.04G0033220-1C	Os05g0188100	24,1	Up	-
Sspon.05G0016070-3C	serine carboxypeptidase-like 42	15,6	Up	-
Sspon.06G0019170-3C	sm-like protein LSM2	33,7	Up	-
Sspon.02G0053710-2D	26S proteasome non-ATPase regulatory subunit 11	27	Up	-
Sspon.08G0003330-3D	USP39 protein	10,8	Unique T	-
Sspon.05G0022730-2D	N-terminal acetyltransferase A complex catalytic subunit NAA10-like	25,9	Unique T	-
Sspon.01G0006460-3C	erwinia induced protein 2	10,1	Unique T	-
Sspon.03G0017460-3C	Epoxide hydrolase 2	10,5	Unique T	-
Sspon.04G0012000-2B	fruit protein PKIW1502	10,6	Unique T	-
Sspon.01G0014850-3C	Metacaspase-1	14,8	Unique T	-
Sspon.05G0013780-2B	acetyl-CoA carboxylase2	0,7	Unique T	-
Sspon.04G0008080-3P	Adenosine kinase 2	20,1	Unique T	-
Sspon.06G0009270-2D	adenosylmethionine aminotransferase1	10,6	Unique T	-
Sspon.05G0011480-3D	COP9 signalosome complex subunit 8	15,8	Unique T	-
Sspon.07G0004180-1A	cyclic phosphodiesterase	20,7	Unique T	-
Sspon.08G0007750-1P	peroxidase P7	10,2	Unique T	-
Sspon.02G0027830-4D	protein STABILIZED1	10,3	Unique C	-
Sspon.04G0035160-1D	P-loop NTPase domain-containing protein LPA1 homolog 1	2,2	Unique C	-
Sspon.03G0004750-1A	probable glutamyl endopeptidase, chloroplastic	5,1	Unique C	-
Sspon.03G0010360-3C	putative auxin efflux carrier component 3a	6,4	Unique C	-
Sspon.05G0021270-1A	brassinosteroid LRR receptor kinase precursor	6,9	Unique C	-
Sspon.03G0001020-2B	PTI1-like tyrosine-protein kinase 3	7,4	Unique C	-
Sspon.04G0013740-3C	vacuolar protein sorting 29	12,2	Unique C	-
Sspon.02G0007120-2C	Regulator of nonsense transcripts 1-like protein	2,7	Unique C	-
Sspon.02G0039190-2C	Ubiquitin-conjugating enzyme E2 variant 1C	52,6	Unique C	-
Sspon.02G0027230-1A	ubiquitin C-terminal hydrolase 12-like isoform X2	11,2	Unique C	-
Sspon.01G0036750-1P	transmembrane 9 superfamily protein member 1 precursor	8,1	Unique C	-
Sspon.01G0020150-4D	aquaporin TIP3-1	8,1	Unique C	-
Sspon.01G0045910-2D	qLTG3-1	5,2	Unique C	-

Sspon.02G0010400-4D	arabinogalactan protein	24,9	Unique C	-
Sspon.01G0016610-2D	pre-mRNA-splicing factor ATP-dependent RNA helicase	5,4	Unique C	-
Sspon.01G0041040-3D	protein STRICTOSIDINE SYNTHASE-LIKE 5-like	10,6	Unique C	-
Sspon.02G0003270-3D	transcription elongation factor SPT4	13,5	Unique C	-
Sspon.01G0047830-2D	FACT complex subunit SPT16	2,9	Unique C	-
Sspon.03G0020260-1A	vacuolar sorting protein 4b	5,1	Unique C	-
Sspon.03G0024060-1A	SEC13-related protein	2,9	Unique C	-
Sspon.02G0005750-2B	60S ribosomal protein L38	40,6	Unique C	-
Sspon.03G0035150-3D	Pollen-specific protein like	9,9	Unique C	-
Sspon.03G0006300-3C	reticulon-4-interacting protein 1	5	Unique C	-
Sspon.03G0016620-1P	Glucosidase 2 subunit beta	4,6	Unique C	-
Sspon.03G0007410-2D	NADP-dependent malic enzyme6	8,3	Unique C	-
Sspon.02G0031860-1P	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1	40,8	Unique C	-
Sspon.04G0022860-1B	GPI-anchored protein	8,3	Unique C	-
Sspon.01G0046700-2D	E3 ubiquitin-protein ligase HOS1	2,8	Unique C	-
Sspon.01G0029580-2B	Histidinol dehydrogenase chloroplastic	7,4	Unique C	-
Sspon.01G0031750-3D	Galactokinase	6,8	Unique C	-
Sspon.04G0029560-1B	bifunctional protein FOLD 4, chloroplastic	13,2	Unique C	-
Sspon.01G0023710-3C	Nucleic acid binding protein	2,1	Unique C	-
Sspon.03G0028120-1B	stearoyl-acyl-carrier-protein desaturase1	4,2	Unique C	-
Sspon.01G0012480-2B	Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain	6,7	Unique C	-
Sspon.01G0053650-1C	dnaJ homolog subfamily C member 2-like	3,2	Unique C	-
Sspon.02G0001420-1A	RING finger and CHY zinc finger domain-containing protein 1 isoform 1	16,3	Unique C	-
Sspon.03G0008740-1P	alpha/beta-Hydrolases superfamily protein	11,2	Unique C	-
Sspon.04G0011690-1T	Isoleucine--tRNA ligase cytoplasmic	11,1	Unique C	-
Sspon.02G0038250-2D	probable endo-1,3(4)-beta-glucanase ARB_01444	12,7	Unique C	-
Sspon.04G0031440-2C	probable methionine--tRNA ligase	6,2	Unique C	-
Sspon.01G0023200-1T	Inosine triphosphate pyrophosphatase	11,2	Unique C	-
Sspon.03G0012990-2B	3'-5' exonuclease domain-containing protein / K homology domain-containing protein / KH domain-containing protein	14,4	Unique C	-
Sspon.01G0014700-4D	malonyl CoA-acyl carrier protein transacylase-like	16	Unique C	-
Sspon.01G0018970-4D	RNA-binding (RRM/RBD/RNP motifs) family protein	14,6	Unique C	-
Sspon.04G0020900-2C	L-lactate dehydrogenase	10,6	Unique C	-
Sspon.03G0039430-1C	Calreticulin-3	6,6	Unique C	-
Sspon.01G0022950-3C	peptidyl-prolyl cis-trans isomerase E	15,1	Unique C	-
Sspon.01G0016590-1A	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase 1	41,7	Unique C	-
Sspon.04G0000220-3C	AT-hook motif nuclear-localized protein 9	10,8	Unique C	-
Sspon.01G0046680-1P	Alba DNA/RNA-binding protein	14,7	Unique C	-
Sspon.06G0008960-1A	26S proteasome non-ATPase regulatory subunit 1 A	14,5	Unique C	-
Sspon.08G0011340-1A	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	6,8	Unique C	-
Sspon.06G0022830-1B	60S ribosomal protein L7-1	30,4	Unique C	-
Sspon.07G0014250-2B	acetylornithine aminotransferase, mitochondrial	5,2	Unique C	-
Sspon.07G0035840-1D	Cysteine--tRNA ligase 1 cytoplasmic	11,6	Unique C	-
Sspon.08G0006300-1A	D-aminoacyl-tRNA deacylase	10,2	Unique C	-
Sspon.07G0017350-2D	embryo defective 1379	4,9	Unique C	-
Sspon.05G0027020-1P	eukaryotic peptide chain release factor GTP-binding subunit ERF3A	20,7	Unique C	-
Sspon.07G0014210-2B	eyes absent homolog	13,4	Unique C	-
Sspon.08G0019340-1B	GDP-L-fucose synthase 1	9,8	Unique C	-
Sspon.08G0015940-1A	GDP-mannose 4,6 dehydratase 2	8,3	Unique C	-
Sspon.05G0013680-3C	Glucose-6-phosphate 1-dehydrogenase 2, chloroplastic	7,5	Unique C	-
Sspon.08G0018720-1B	Glycosyl hydrolase family 31 protein	17,8	Unique C	-
Sspon.05G0001250-2D	glyoxalase III	13,2	Unique C	-
Sspon.08G0013010-1A	Homogentisate 1,2-dioxygenase	14,6	Unique C	-
Sspon.08G0003660-4D	L-ascorbate oxidase homolog	7,7	Unique C	-
Sspon.01G0008640-2B	late embryogenesis abundant protein 1-like	14,9	Unique C	-
Sspon.04G0008620-3P	LETM1-like protein	6,7	Unique C	-
Sspon.04G0024770-2D	LETM1-like protein	9,5	Unique C	-
Sspon.07G0005330-1A	methionine aminopeptidase 1A	4,7	Unique C	-
Sspon.05G0021880-2D	Molybdopterin biosynthesis protein CNX1	9,2	Unique C	-
Sspon.06G0005670-1A	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	6,8	Unique C	-
Sspon.06G0023760-1B	Nicalin precursor	9,2	Unique C	-
Sspon.06G0007020-1A	NKAP family protein UM04995-like isoform X1	4	Unique C	-
Sspon.04G0010720-2P	pectinesterase inhibitor domain containing protein	16,5	Unique C	-
Sspon.08G0007750-3D	peroxidase P7-like	14,7	Unique C	-
Sspon.05G0021990-2C	plastidic glutamine synthetase	11,4	Unique C	-
Sspon.04G0005690-3D	P-loop containing nucleoside triphosphate hydrolase superfamily protein	4,8	Unique C	-
Sspon.08G0022350-2C	Putative DUF1296 domain containing family protein	4,1	Unique C	-
Sspon.07G0011050-2D	Serine/threonine-protein phosphatase 5	13	Unique C	-
Sspon.07G0005910-3C	sorting and assembly machinery component 50 homolog A-like	8,6	Unique C	-
Sspon.04G0011130-4D	Starch branching enzyme IIa	9,6	Unique C	-
Sspon.01G0026140-2B	succinate dehydrogenase subunit 5, mitochondrial	26,5	Unique C	-
Sspon.07G0012600-2B	U1 small nuclear ribonucleoprotein A	16,7	Unique C	-
Sspon.02G0004240-1A	WPP domain-containing protein 2	9,1	Unique C	-

Sspon.06G0015190-1A	CCAAT-HAP5-transcription factor 59	14,5	Unique C	-
Sspon.04G0001930-2D	splicing factor, arginine/serine-rich 7	20,7	Unique C	-
Sspon.02G0001270-1P	Stress-related protein-like	30,5	Unique C	-
Sspon.04G0014930-3P	elongation factor 1-gamma 3	45,3	Unique C	-
Sspon.05G0011000-3D	Zinc finger CCCH domain-containing protein 28	10,4	Unchanged	-
Sspon.08G0025320-2D	Zinc finger CCCH domain-containing protein 40	21,9	Unchanged	-
Sspon.03G0044930-1D	cell division cycle 5-like protein	9	Unchanged	-
Sspon.01G0010690-3D	serine/arginine-rich SC35-like splicing factor SCL33 isoform X1	19,1	Unchanged	-
Sspon.02G0029150-3C	Serine/arginine-rich SC35-like splicing factor SCL30	32	Unchanged	-
Sspon.01G0043020-2D	endonuclease/Exonuclease/phosphatase family protein	9,2	Unchanged	-
Sspon.01G0042420-2D	KH domain-containing protein SPIN1	17,2	Unchanged	-
Sspon.01G0050080-1B	Putative clathrin assembly protein	4,4	Unchanged	-
Sspon.04G0019890-4D	putative arginine/serine-rich splicing factor	19,2	Unchanged	-
Sspon.06G0006970-4D	serine/arginine-rich splicing factor SR45a	7,3	Unchanged	-
Sspon.03G0023530-4D	Protein BRASSINAZOLE-RESISTANT 1	5,8	Unchanged	-
Sspon.01G0007550-2D	zinc finger CCCH domain-containing protein 24	5,2	Unchanged	-
Sspon.06G0013930-2C	Zinc finger CCCH domain-containing protein 33	2,6	Unchanged	-
Sspon.07G0014300-1A	zinc finger CCCH domain-containing protein 33-like	3,8	Unchanged	-
Sspon.01G0015090-3D	unnamed protein product	2,4	Unchanged	-
Sspon.08G0021620-1B	Chromatin structure-remodeling complex protein SYD	2	Unchanged	-
Sspon.03G0006600-1A	Zinc finger CCCH domain-containing protein 19	3,1	Unchanged	-
Sspon.02G0014690-2P	ZF-HD homeobox protein	4	Unchanged	-
Sspon.01G0026770-3D	putative serine/threonine protein kinase IREH1	3,2	Unchanged	-
Sspon.05G0025670-1B	Putative MAPKKK family protein kinase	7,2	Unchanged	-
Sspon.03G0009180-3C	ATP binding protein	4	Unchanged	-
Sspon.05G0010190-1P	ubiquitin carboxyl-terminal hydrolase 4	5	Unchanged	-
Sspon.02G0048040-1P	Microtubule-associated protein TORTIFOLIA1	3,8	Unchanged	-
Sspon.03G0012430-3C	protein ALTERED PHOSPHATE STARVATION RESPONSE 1	2,6	Unchanged	-
Sspon.04G0031850-1P	Pseudouridine synthase family protein	19,6	Unchanged	-
Sspon.03G0026060-1B	Serine/arginine-rich splicing factor SR45	29,4	Unchanged	-
Sspon.01G0010390-4D	serine/arginine-rich SC35-like splicing factor SCL28 isoform X4	21,8	Unchanged	-
Sspon.02G0036650-3D	Serine/arginine-rich splicing factor SR45a	12,1	Unchanged	-
Sspon.03G0013340-1A	DEAD-box ATP-dependent RNA helicase 40	7,1	Unchanged	-
Sspon.03G0013340-2B	DEAD-box ATP-dependent RNA helicase 40	10	Unchanged	-
Sspon.04G0017040-3C	Protein CYPRO4	11,1	Unchanged	-
Sspon.04G0003600-4D	auxin efflux carrier component 1a	6,2	Unchanged	-
Sspon.04G0005920-1A	Protein PHOTOPERIOD-INDEPENDENT EARLY FLOWERING 1	4,9	Unchanged	-
Sspon.01G0016840-1A	phosphoenolpyruvate carboxykinase1	18,9	Unchanged	-
Sspon.04G0033150-1C	putative pre-mRNA-splicing factor ATP-dependent RNA helicase DEAH5	0,8	Unchanged	-
Sspon.01G0022790-2B	DEK domain-containing chromatin associated protein	27,8	Unchanged	-
Sspon.04G0004670-4D	KH domain-containing protein	10,5	Unchanged	-
Sspon.01G0052740-1C	SNF1-related protein kinase regulatory subunit beta-1-like	9	Unchanged	-
Sspon.03G0023940-4D	Transcription factor GTE4	8,8	Unchanged	-
Sspon.03G0026480-3D	Putative regulator of chromosome condensation (RCC1) family protein	7,6	Unchanged	-
Sspon.02G0010610-2B	hydroxyproline-rich glycoprotein family protein	10,2	Unchanged	-
Sspon.02G0022880-2D	heterogeneous nuclear ribonucleoprotein 1	8,2	Unchanged	-
Sspon.01G0021790-3C	probable serine incorporator isoform X1	3,6	Unchanged	-
Sspon.04G0030940-1P	Octicosapeptide/Phox/Bem1p family protein	7,4	Unchanged	-
Sspon.04G0030940-2P	Octicosapeptide/Phox/Bem1p family protein	7,7	Unchanged	-
Sspon.01G0048480-2D	FHA domain containing protein	3,2	Unchanged	-
Sspon.01G0015540-2C	protein ENHANCED DISEASE RESISTANCE 2-like	2,6	Unchanged	-
Sspon.02G0023480-4D	Peptidyl-prolyl cis-trans isomerase CYP63	5,9	Unchanged	-
Sspon.01G0051400-1C	guanine-nucleotide-exchange protein	3,5	Unchanged	-
Sspon.04G0001800-1A	Autophagy-related protein 18b	5,6	Unchanged	-
Sspon.04G0030610-1C	Pumilio homolog 4	5,6	Unchanged	-
Sspon.01G0058010-1D	ABC transporter B family member 6	3	Unchanged	-
Sspon.06G0014050-2B	DNA replication licensing factor MCM2	20,4	Unchanged	-
Sspon.06G0022260-1B	KH domain-containing protein	6,1	Unchanged	-
Sspon.08G0011540-2B	Kinesin-like protein KCA2	2,7	Unchanged	-
Sspon.06G0010570-1A	Nuclear factor 1 A-type isoform 2	3,2	Unchanged	-
Sspon.05G0030930-1P	OSJNBa0008M17.14-like protein	3	Unchanged	-
Sspon.07G0010230-4D	patellin-5	3,9	Unchanged	-
Sspon.04G0015360-4D	peptidyl-prolyl cis-trans isomerase CYP95 isoform X3	29	Unchanged	-
Sspon.04G0014380-3D	Phosphoenolpyruvate carboxylase 1	39,4	Unchanged	-
Sspon.05G0020310-4D	probable auxin efflux carrier component 1b	13,8	Unchanged	-
Sspon.08G0001290-3C	protein PSK SIMULATOR 2 isoform X1	2,2	Unchanged	-
Sspon.07G0002100-3C	Putative sucrose-phosphate synthase family protein isoform 1	8	Unchanged	-
Sspon.06G0017850-1P	Sodium/hydrogen exchanger	2,8	Unchanged	-
Sspon.06G0004690-1A	Structural maintenance of chromosomes (SMC) family protein	13,8	Unchanged	-
Sspon.05G0025860-2C	ubiquitin interaction motif-containing protein	5	Unchanged	-
Sspon.05G0037470-1D	Ubiquitin-specific protease family C19-related protein	17,6	Unchanged	-
Sspon.01G0015550-3D	unnamed protein product	1	Unchanged	-
Sspon.05G0010420-1A	unnamed protein product	3,3	Unchanged	-
Sspon.04G0017770-2P	zinc finger CCCH domain-containing protein 13-like isoform X1	19,4	Unchanged	-
Sspon.01G0036970-1B	bZIP transcription factor 1-A-like isoform X1	6,7	Unchanged	-
Sspon.01G0027330-2B	Protein kinase superfamily protein	4,5	Unchanged	-

Sspon.01G0011010-4D	Putative SAP DNA-binding domain family protein isoform 1	16,8	Unchanged	-
Sspon.01G0011010-1A	Putative SAP DNA-binding domain family protein isoform 1	18	Unchanged	-
Sspon.03G0006980-1A	seed maturation protein isoform X1	32,2	Unchanged	-
Sspon.01G0008330-4D	phytochrome B	12,3	Unchanged	-
Sspon.04G0033660-1C	RNA-binding (RRM/RBD/RNP motifs) family protein	26,9	Unchanged	-
Sspon.06G0006090-3C	14-3-3-like protein	66,9	Unchanged	-
Sspon.05G0009790-3C	14-3-3-like protein GF14-6	70,5	Unchanged	-
Sspon.07G0000490-1A	26S proteasome regulatory subunit RPN13	11,5	Unchanged	-
Sspon.01G0052600-2D	dehydrin HIRD11-like	42,6	Unchanged	-
Sspon.06G0002450-3D	FK506-binding protein 2-1	6,4	Unchanged	-
Sspon.07G0005070-4D	global transcription factor group B1	5	Unchanged	-
Sspon.02G0005470-1A	Transcription factor bHLH130	6,6	Unchanged	-
Sspon.02G0041140-1B	EM binding protein 1-like protein	4,4	Unchanged	-
Sspon.04G0006470-4D	naked endosperm1	4,8	Unchanged	-
Sspon.06G0029080-2D	GLABROUS1 enhancer-binding protein-like	16,9	Unchanged	-
Sspon.06G0031000-2D	RING/FYVE/PHD-type zinc finger family protein	5,8	Unchanged	-
Sspon.07G0000130-2B	Putative casein kinase family protein	7,8	Unchanged	-
Sspon.03G0017500-1A	topless-related1	15,1	Unchanged	-
Sspon.04G0005660-3C	TOM1-like protein 2	8,4	Unchanged	-
Sspon.04G0016930-3C	Protein RRC1	6,9	Unchanged	-
Sspon.04G0018430-3C	Eukaryotic translation initiation factor 5	11	Unchanged	-
Sspon.02G0026180-1A	Outer arm dynein light chain 1 protein	5,5	Unchanged	-
Sspon.03G0001110-1A	Sister chromatid cohesion 1 protein 4	8,6	Unchanged	-
Sspon.02G0023330-1A	glycine-rich RNA-binding protein RZ1C-like	30,5	Unchanged	-
Sspon.01G0047220-1T	oxysterol-binding protein-related protein 1C	3,6	Unchanged	-
Sspon.01G0019170-2B	nucleolin 2-like	26,8	Unchanged	-
Sspon.01G0005820-1P	BTB/POZ domain-containing protein NPY4-like	2,2	Unchanged	-
Sspon.02G0024210-3C	IAP-like protein 1	29,5	Unchanged	-
Sspon.01G0010820-3D	RNA-binding KH domain-containing protein	29,2	Unchanged	-
Sspon.02G0011160-2B	MTD1	12,8	Unchanged	-
Sspon.01G0025220-1A	transcription initiation factor TFIID subunit 4-like isoform X2	3,6	Unchanged	-
Sspon.03G0038330-2P	eukaryotic translation initiation factor 4E	14,5	Unchanged	-
Sspon.03G0005640-2B	Branched-chain-amino-acid aminotransferase 5 chloroplastic	11,8	Unchanged	-
Sspon.02G0007100-2C	Casein kinase II subunit beta-1	8,4	Unchanged	-
Sspon.04G0010440-3C	Alkaline/neutral invertase CINV2	19,3	Unchanged	-
Sspon.04G0000170-1P	callose synthase 3-like	1,7	Unchanged	-
Sspon.06G0002930-4D	ADP-ribosylation factor GTPase-activating protein AGD3	2,1	Unchanged	-
Sspon.06G0026890-1B	AAA-type ATPase family protein	3,2	Unchanged	-
Sspon.08G0016550-1A	aldo-keto reductase-like protein	20,2	Unchanged	-
Sspon.04G0007950-4D	aquaporin PIP2-5	3,1	Unchanged	-
Sspon.05G0005190-1A	argonaute1c	6,2	Unchanged	-
Sspon.03G0006890-2P	ATP-dependent 6-phosphofructokinase 3	23,6	Unchanged	-
Sspon.06G0008730-4D	cysteine-type endopeptidase/ ubiquitin thiolesterase	17,6	Unchanged	-
Sspon.04G0029020-3D	DNA-binding protein BIN4	14,1	Unchanged	-
Sspon.03G0008190-2B	fibrous sheath CABYR-binding protein-like	15,3	Unchanged	-
Sspon.03G0027940-2D	GYF domain-containing protein	6,3	Unchanged	-
Sspon.05G0002010-1P	putative glucose-6-phosphate 1-epimerase	15,7	Unchanged	-
Sspon.04G0008430-4D	Sister chromatid cohesion protein PDS5 B-B	16	Unchanged	-
Sspon.08G0000310-1A	Transcription elongation factor (TFIIS) family protein	2,8	Unchanged	-
Sspon.08G0026910-1C	tRNA(adenine(34)) deaminase chloroplastic	3,9	Unchanged	-
Sspon.02G0040370-1B	unnamed protein product	11,8	Unchanged	-
Sspon.08G0009580-1A	WW domain-containing protein	2,3	Unchanged	-
Sspon.05G0018880-1P	transcription factor VIP1-like	13,5	Unchanged	-
Sspon.01G0021690-1A	Zinc finger CCCH domain-containing protein 19	2,4	Unchanged	-
Sspon.08G0006590-1A	probable protein phosphatase 2C 57	2,3	Unchanged	-
Sspon.01G0024010-1A	Protein kinase superfamily protein	4,5	Unchanged	-
Sspon.02G0036550-1B	SH3 domain-containing protein 3	10,4	Unchanged	-
Sspon.03G0024450-3C	Aspartate--tRNA ligase 2 cytoplasmic	32,1	Unchanged	-
Sspon.04G0007580-3C	Vacuolar protein-sorting protein bro1	3,2	Unchanged	-
Sspon.05G0007450-3C	CLIP-associated protein	5,6	Unchanged	-
Sspon.08G0019980-1P	E3 ubiquitin-protein ligase RGLG1	3,2	Unchanged	-
Sspon.07G0003020-4D	plant/F18B13-26 protein	20,2	Unchanged	-
Sspon.05G0029760-2C	protein ROH1-like	1,6	Unchanged	-
Sspon.07G0007130-1A	Protein S-acyltransferase 8	5,4	Unchanged	-
Sspon.04G0037990-1D	Protein transport protein SEC16B-like protein	0,9	Unchanged	-
Sspon.06G0002200-1A	Pumilio homolog 5	2,5	Unchanged	-
Sspon.08G0012650-2B	splicing factor, arginine/serine-rich 7	47,8	Unchanged	-
Sspon.02G0012380-3C	Transcription factor BIM3	5,8	Unchanged	-
Sspon.01G0060800-1D	protein FAR1-RELATED SEQUENCE 6-like	0,9	Unchanged	-
Sspon.08G0006350-3D	Putative MYB DNA-binding domain superfamily protein	4,2	Unchanged	-
Sspon.02G0009460-2P	SHI	23,5	Unchanged	-
Sspon.01G0039160-2C	serine/threonine protein kinase OSK3	6,5	Unchanged	-
Sspon.01G0004620-1A	leucine-rich transmembrane protein kinase1	2,9	Unchanged	-
Sspon.01G0017190-1A	Protein STRUBBELIG-RECEPTOR FAMILY 7 precursor	2,4	Unchanged	-
Sspon.05G0002130-2D	MAP3K epsilon protein kinase 1	1	Unchanged	-
Sspon.02G0006260-2D	Villin-4	11,3	Unchanged	-

Sspon.02G0025830-1A	Protein LEO1-like protein	13,5	Unchanged	-
Sspon.01G0007120-2C	SH3 domain-containing protein	2,3	Unchanged	-
Sspon.03G0028140-1P	Sucrose-phosphate synthase	1,4	Unchanged	-
Sspon.01G0048910-2D	Heat stress transcription factor A-6b	12,1	Unchanged	-
Sspon.01G0028270-2D	stem-specific protein TSJT1	39,9	Unchanged	-
Sspon.01G0042450-1P	zinc finger protein-like 1	5,7	Unchanged	-
Sspon.03G0006890-2B	ATP-dependent 6-phosphofructokinase 3	4,9	Unchanged	-
Sspon.01G0004770-1A	dentin sialophosphoprotein-related	8,1	Unchanged	-
Sspon.01G0013660-1P	hexose transporter	27	Unchanged	-
Sspon.04G0026610-2C	Guanylate-binding family protein	21,1	Unchanged	-
Sspon.02G0018410-3C	P-loop NTPase domain-containing protein LPA1 homolog isoform X1	1,7	Unchanged	-
Sspon.01G0016070-1A	Ras-related small GTP-binding family protein	4	Unchanged	-
Sspon.02G0010160-1A	flowering time control protein FPA	10,5	Unchanged	-
Sspon.01G0005950-2B	Mannose-1-phosphate guanylyltransferase 1	9,2	Unchanged	-
Sspon.01G0018330-2B	perakine reductase-like isoform X2	12,1	Unchanged	-
Sspon.04G0005180-4D	protein CROWDED NUCLEI 1	7,9	Unchanged	-
Sspon.02G0008850-1A	unnamed protein product	6,6	Unchanged	-
Sspon.02G0005500-1A	Eukaryotic translation initiation factor 4G	8,7	Unchanged	-
Sspon.01G0027500-1A	adenylyl cyclase-associated protein	6,1	Unchanged	-
Sspon.01G0045610-2C	Serine/threonine-protein phosphatase BSL3	3,7	Unchanged	-
Sspon.03G0002830-2C	pumilio homolog 1-like isoform X1	5	Unchanged	-
Sspon.08G0010530-3D	alpha/beta-Hydrolases superfamily protein	5,1	Unchanged	-
Sspon.06G0012710-2B	AT-hook motif nuclear-localized protein 1-like	8,4	Unchanged	-
Sspon.07G0002960-2C	DNAJ heat shock N-terminal domain-containing protein	20,1	Unchanged	-
Sspon.05G0000380-1A	FT-interacting protein 3-like	1,5	Unchanged	-
Sspon.07G0014610-3C	interactor of constitutive active ROPs 2, chloroplastic isoform X3	7,8	Unchanged	-
Sspon.05G0019540-2B	IQ domain-containing protein IQM3	2,2	Unchanged	-
Sspon.07G0011920-2B	NADH-ubiquinone oxidoreductase 10.5 kDa subunit	22,6	Unchanged	-
Sspon.07G0018360-1A	protein FLX-like 3	19,3	Unchanged	-
Sspon.06G0019270-1B	Protein gar2	6,3	Unchanged	-
Sspon.07G0013370-3C	Serine/threonine-protein phosphatase BSL1	2,5	Unchanged	-
Sspon.05G0013010-4D	SNF1-related protein kinase regulatory subunit gamma-1	12,5	Unchanged	-
Sspon.05G0000690-1A	stem-specific protein TSJT1	70,5	Unchanged	-
Sspon.01G0002370-1A	Tetratricopeptide repeat (TPR)-like superfamily protein	5,3	Unchanged	-
Sspon.07G0019810-3C	thioredoxin M1	2,2	Unchanged	-
Sspon.08G0022780-2C	unnamed protein product	7,3	Unchanged	-
Sspon.08G0004460-2B	villin-3 isoform X1	3	Unchanged	-
Sspon.05G0015270-1A	Zn-finger, RanBP-type, containing protein	3,2	Unchanged	-
Sspon.06G0016630-2B	transcription factor BHLH062-like isoform X2	5	Unchanged	-
Sspon.03G0009500-2C	Transducin/WD40 repeat-like superfamily protein	9,8	Unchanged	-
Sspon.02G0011530-4D	DNA binding protein	8	Unchanged	-
Sspon.04G0029120-2C	CASP-like protein 4A1	7,8	Unchanged	-
Sspon.06G0027750-1B	Serine/arginine-rich SC35-like splicing factor SCL30	21,6	Unchanged	-
Sspon.07G0014860-2D	serine/arginine-rich splicing factor RS2Z33-like	26,9	Unchanged	-
Sspon.02G0010890-3P	Uridine kinase-like protein 2 chloroplastic	12,5	Unchanged	-
Sspon.03G0028220-1P	Zinc finger CCCH domain-containing protein 33	3,9	Unchanged	-
Sspon.02G0013560-1A	GLABROUS1 enhancer-binding protein-like	9,8	Unchanged	-
Sspon.04G0026550-2D	Tyrosine specific protein phosphatase-like	9,4	Unchanged	-
Sspon.03G0031920-2D	Trihelix transcription factor ASIL2	9,6	Unchanged	-
Sspon.06G0007930-1A	WRKY transcription factor 4	4,9	Unchanged	-
Sspon.04G0016130-1A	protein kinase	2,9	Unchanged	-
Sspon.01G0056690-1C	Mitogen-activated protein kinase kinase kinase 1	5	Unchanged	-
Sspon.01G0021560-2B	Protein kinase superfamily protein	3,4	Unchanged	-
Sspon.03G0034410-1B	FAM91A1-like protein	0,9	Unchanged	-
Sspon.01G0011620-2C	Chaperone DnaJ-domain superfamily protein	17,2	Unchanged	-
Sspon.01G0000780-4D	RNA binding protein	9,5	Unchanged	-
Sspon.01G0000800-1A	Protein kinase superfamily protein	5,3	Unchanged	-
Sspon.03G0005680-3C	BSD domain containing protein	7,7	Unchanged	-
Sspon.03G0022770-3C	hexokinase1	4	Unchanged	-
Sspon.02G0027980-2D	putative histone H2AXb	20,6	Unchanged	-
Sspon.03G0034930-1B	multidomain cystatin	55,6	Unchanged	-
Sspon.03G0040870-1C	putative serine/threonine-protein kinase	3,5	Unchanged	-
Sspon.03G0034420-1B	ATP-citrate synthase beta chain protein 1	32,7	Unchanged	-
Sspon.06G0025370-3D	14-3-3-like protein	72,9	Unchanged	-
Sspon.08G0009140-1A	65-kDa microtubule-associated protein 1	8,4	Unchanged	-
Sspon.04G0014630-4D	aquaporin NIP1-1	3,6	Unchanged	-
Sspon.08G0029600-1D	D-tagatose-1,6-bisphosphate aldolase subunit GatY	16,4	Unchanged	-
Sspon.04G0003840-3P	dynammin-2A	10,1	Unchanged	-
Sspon.07G0024870-3D	Phosphoribosylformylglycinamide cyclo-ligase	13,2	Unchanged	-
Sspon.08G0012940-1A	polymerase II transcription-mediator3	1,5	Unchanged	-
Sspon.07G0006010-3D	probable apyrase 7	3,1	Unchanged	-
Sspon.07G0017190-2B	probable protein NAP1	1,3	Unchanged	-
Sspon.02G0017920-1A	Protein SAWADEE HOMEODOMAIN HOMOLOG 1	15,2	Unchanged	-
Sspon.07G0009200-3C	protein unc-13 homolog	1,1	Unchanged	-
Sspon.07G0031480-2D	putative magnesium transporter NIPA4	5,6	Unchanged	-
Sspon.05G0019670-2B	Pyruvate kinase 1, cytosolic	40,6	Unchanged	-

Sspon.06G0000500-2B	unnamed protein product	8,3	Unchanged	-
Sspon.04G0016570-2B	unnamed protein product	11,3	Unchanged	-
Sspon.01G0031590-1A	unnamed protein product	18,6	Unchanged	-
Sspon.03G0004240-1A	WAS/WASL-interacting protein family member 3-like	3,4	Unchanged	-
Sspon.04G0020720-3C	nephrocystin-3	7	Unchanged	-
Sspon.04G0015310-1A	SPOC domain / Transcription elongation factor S-II protein	5,1	Unchanged	-
Sspon.08G0017960-2D	Serrate RNA effector molecule	6,6	Unchanged	-
Sspon.03G0022840-3C	Zinc finger CCCH domain-containing protein 2	6,4	Unchanged	-
Sspon.07G0006160-1P	nuclear factor YB2	21,8	Unchanged	-
Sspon.02G0034560-1B	putative WRKY transcription factor 20	8,6	Unchanged	-
Sspon.02G0018300-3C	LRR receptor-like serine/threonine-protein kinase GHR1	4,4	Unchanged	-
Sspon.04G0028050-2C	RING/U-box superfamily protein	11,2	Unchanged	-
Sspon.02G0012610-1A	glucose-6-phosphate isomerase	19,5	Unchanged	-
Sspon.01G0014220-3D	peptide methionine sulfoxide reductase A4, chloroplastic-like	9,1	Unchanged	-
Sspon.02G0017770-1A	RNA binding	10,6	Unchanged	-
Sspon.04G0002280-1A	ARM repeat superfamily protein	1	Unchanged	-
Sspon.02G0013960-2C	putative polygalacturonase	2,3	Unchanged	-
Sspon.04G0000310-1A	ATG8-interacting protein 1-like isoform X1	4,7	Unchanged	-
Sspon.06G0026490-1B	Nuclear pore complex protein NUP107	3,7	Unchanged	-
Sspon.05G0010970-1P	OSJNBa0006B20.20-like protein	3,8	Unchanged	-
Sspon.03G0005280-3C	USP family protein	35,6	Unchanged	-
Sspon.05G0018740-3C	putative mediator of RNA polymerase II transcription subunit 26c	3,2	Unchanged	-
Sspon.08G0004020-1A	unnamed protein product	4,6	Unchanged	-
Sspon.02G0033540-2C	chromatin remodeling factor18	2,6	Unchanged	-
Sspon.02G0033710-2C	putative inactive receptor kinase	1,4	Unchanged	-
Sspon.02G0028610-4D	DNA ligase 1-like	2,2	Unchanged	-
Sspon.02G0017130-3D	RNA recognition motif (RRM)-containing protein	3	Unchanged	-
Sspon.03G0026060-2P	Serine/arginine-rich splicing factor SR45	30,1	Unchanged	-
Sspon.01G0032640-1A	Nucleic acid-binding proteins superfamily	4,6	Unchanged	-
Sspon.01G0019920-2B	Probable prefoldin subunit 5	33,1	Unchanged	-
Sspon.04G0022560-1B	Nuclear-pore anchor	7,6	Unchanged	-
Sspon.04G0018480-2C	splicing factor 3B subunit 1-like	13,7	Unchanged	-
Sspon.02G0009000-1A	nucleosome/chromatin assembly factor 104	19,8	Unchanged	-
Sspon.01G0055900-1C	methyl binding domain115	24,6	Unchanged	-
Sspon.01G0020010-2B	DNA ligase	12,6	Unchanged	-
Sspon.02G0001390-1A	CW-type Zinc Finger	1,4	Unchanged	-
Sspon.03G0006070-3C	Putative HCNGP-related transcriptional regulator family protein	5,7	Unchanged	-
Sspon.03G0011800-1A	C3HC zinc finger-like	2,6	Unchanged	-
Sspon.01G0037490-1B	Protease Do-like 9	3,9	Unchanged	-
Sspon.01G0011730-2B	Splicing factor arginine/serine-rich	5,7	Unchanged	-
Sspon.06G0035100-1D	BSD domain-containing protein	12,4	Unchanged	-
Sspon.03G0020210-2B	cytochrome P450 family 77 protein	2,9	Unchanged	-
Sspon.06G0009940-2C	Polyadenylation and cleavage factor homolog 5	1,4	Unchanged	-
Sspon.07G0021680-1B	splicing factor U2af 38 kDa subunit	20,2	Unchanged	-
Sspon.07G0005010-3C	structural maintenance of chromosomes protein 4	1,3	Unchanged	-
Sspon.05G0027780-2C	SWI/SNF complex subunit SWI3D-like	1,5	Unchanged	-
Sspon.03G0034870-3D	titan9	5,1	Unchanged	-
Sspon.05G0008480-4D	Topoisomerase-like protein	7,9	Unchanged	-
Sspon.08G0008330-3D	Transducin/WD40 repeat-like superfamily protein	2	Unchanged	-
Sspon.06G0003980-3D	ubiquitin carboxyl-terminal hydrolase 36	8,9	Unchanged	-
Sspon.06G0010140-3D	vesicle-associated protein 1-2-like	17,5	Unchanged	-
Sspon.03G0040670-1C	Nuclear pore complex protein NUP50A	10,6	Unchanged	-
Sspon.08G0021490-1B	asparagine synthetase	13,2	Unchanged	-
Sspon.07G0012910-3C	Nuclear pore complex protein NUP50A	16,3	Unchanged	-
Sspon.01G0005330-2B	zinc finger protein ENHYDROUS-like	3,4	Unchanged	-
Sspon.02G0057380-1D	ENTH/VHS family protein	3,4	Unchanged	-
Sspon.02G0030680-1A	Protein tesmin/TSO1-like CXC 4	6,7	Unchanged	-
Sspon.04G0008640-1A	protein FAR1-RELATED SEQUENCE 6-like	6,1	Unchanged	-
Sspon.01G0017970-2B	histone acetyl transferase GNAT/MYST 101	13,3	Unchanged	-
Sspon.03G0011690-2B	Transcriptional corepressor LEUNIG	2,8	Unchanged	-
Sspon.02G0022290-3C	histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH1-like	8,8	Unchanged	-
Sspon.02G0009460-1A	Protein SHI RELATED SEQUENCE 1	13,4	Unchanged	-
Sspon.04G0030220-3D	Trihelix transcription factor GTL2	5,5	Unchanged	-
Sspon.05G0016920-3C	zinc-finger homeodomain protein 4 isoform X2	2,8	Unchanged	-
Sspon.03G0011050-1A	calcium-dependent protein kinase, isoform 2	24,3	Unchanged	-
Sspon.07G0001090-2B	calcium-dependent protein kinase 15	9,8	Unchanged	-
Sspon.02G0032660-1A	Protein kinase superfamily protein	4,4	Unchanged	-
Sspon.03G0013960-2B	receptor protein kinase-like protein ZAR1	3,7	Unchanged	-
Sspon.03G0032650-2D	putative inactive receptor kinase	8	Unchanged	-
Sspon.05G0004920-1A	putative LRR receptor-like serine/threonine-protein kinase	1,7	Unchanged	-
Sspon.03G0006960-1A	diphosphonucleotide phosphatase2	19,2	Unchanged	-
Sspon.03G0011340-2B	UBP1-associated protein 2C	24	Unchanged	-
Sspon.01G0006700-1A	Protein TOPLESS	12,6	Unchanged	-
Sspon.04G0019930-3D	eukaryotic translation initiation factor 3 subunit 1 alpha, 35kDa	29,3	Unchanged	-
Sspon.03G0002200-2B	hemerythrin HHE cation-binding domain protein	4,5	Unchanged	-
Sspon.01G0030520-2D	PP2Ac-2 - Phosphatase 2A isoform 2 belonging to family 2	45,6	Unchanged	-

Sspon.02G0028680-3C	prefoldin subunit 3	12,7	Unchanged	-
Sspon.02G0009300-2C	pantothenate kinase 2	6,8	Unchanged	-
Sspon.02G0034520-2C	cell wall protein IFF6-like	33	Unchanged	-
Sspon.03G0007870-2B	WD-repeat protein RBAP2	43,7	Unchanged	-
Sspon.01G0031120-2D	Mitochondrial Rho GTPase 1	17,4	Unchanged	-
Sspon.03G0018340-1A	Mediator of RNA polymerase II transcription subunit 17	1,7	Unchanged	-
Sspon.01G0000290-3D	polymerase II transcription-mediator2	0,9	Unchanged	-
Sspon.02G0011320-2B	methyl binding domain protein 111 isoform X2	42,4	Unchanged	-
Sspon.02G0053370-2D	skin secretory protein xP2 isoform X2	35,5	Unchanged	-
Sspon.01G0044430-1B	Methionine aminopeptidase	27,9	Unchanged	-
Sspon.03G0010970-3C	ATP binding microtubule motor family protein	6,8	Unchanged	-
Sspon.03G0003330-3D	protein IQ-DOMAIN 1-like	5,7	Unchanged	-
Sspon.01G0023780-3C	F-box/LRR-repeat protein 17	3,9	Unchanged	-
Sspon.01G0020450-1A	Nucleic acid binding protein	14,9	Unchanged	-
Sspon.02G0002140-1A	probable protein phosphatase 2C 65 isoform X1	8,1	Unchanged	-
Sspon.02G0020250-4D	CASP-like protein 1D1	17,6	Unchanged	-
Sspon.03G0012670-1P	esterase	7,3	Unchanged	-
Sspon.04G0027390-2C	KH domain-containing protein	12,2	Unchanged	-
Sspon.01G0016880-2D	uncharacterized protein LOC8082297	2,3	Unchanged	-
Sspon.02G0004890-2B	exocyst complex component EXO84C	2	Unchanged	-
Sspon.01G0030480-1A	Exocyst complex component EXO84B	3,7	Unchanged	-
Sspon.03G0046550-1D	NEDD8-activating enzyme E1 catalytic subunit	10,5	Unchanged	-
Sspon.03G0036070-2C	protein DOG1-like 2	15,8	Unchanged	-
Sspon.04G0001820-3D	T-complex protein 1 subunit alpha	22,5	Unchanged	-
Sspon.03G0017410-2B	H/ACA ribonucleoprotein complex subunit 4	18,3	Unchanged	-
Sspon.01G0018450-3C	flavoprotein wrbA	7,8	Unchanged	-
Sspon.04G0000280-1P	Protein BTR1	32	Unchanged	-
Sspon.04G0000870-1A	alcohol dehydrogenase class 3	37,5	Unchanged	-
Sspon.06G0003350-1D	alpha,alpha-trehalose-phosphate synthase 5	2,2	Unchanged	-
Sspon.06G0021820-1B	Aminopeptidase M1	23,2	Unchanged	-
Sspon.07G0020880-2C	argonaute6	3,2	Unchanged	-
Sspon.02G0011530-1P	AT-hook motif nuclear-localized protein 10	5	Unchanged	-
Sspon.05G0029980-2C	AT-hook motif nuclear-localized protein 7-like isoform X1	3,7	Unchanged	-
Sspon.06G0002310-3C	Calcium-transporting ATPase 9 plasma membrane-type	3,4	Unchanged	-
Sspon.05G0002250-1A	CDT1-like protein a chloroplastic	3,8	Unchanged	-
Sspon.01G0027620-1A	COMPASS-like H3K4 histone methylase component WDR5A	22,8	Unchanged	-
Sspon.05G0002370-3D	dehydration responsive element binding protein	15,7	Unchanged	-
Sspon.06G0031110-1C	ENHANCER OF AG-4 protein 2	4,9	Unchanged	-
Sspon.05G0007660-1T	enolase-phosphatase E1	19,3	Unchanged	-
Sspon.05G0013190-2B	Eukaryotic translation initiation factor 3 subunit H	23,4	Unchanged	-
Sspon.06G0002580-2B	FHA domain-containing protein FHA2	5	Unchanged	-
Sspon.07G0019360-2D	filaggrin-2	2,4	Unchanged	-
Sspon.07G0013140-1A	glutathione S-transferase 4	27,7	Unchanged	-
Sspon.07G0013110-3C	glutathione S-transferase 4	22,5	Unchanged	-
Sspon.06G0007620-2T	Histone deacetylase	19	Unchanged	-
Sspon.07G0003330-2B	Histone deacetylase HDT3	33,9	Unchanged	-
Sspon.05G0011310-2B	hypothetical protein SHCRBa_185_O22_F_80	1,8	Unchanged	-
Sspon.06G0013080-3C	KH domain-containing protein	10,3	Unchanged	-
Sspon.06G0007490-1A	lipid phosphate phosphatase 2-like	4,8	Unchanged	-
Sspon.07G0016210-1A	MACPF domain-containing protein	2,1	Unchanged	-
Sspon.06G0025340-1B	Maf-like protein CV_0124	7,4	Unchanged	-
Sspon.08G0001400-4D	P-loop containing nucleoside triphosphate hydrolase superfamily protein	6,9	Unchanged	-
Sspon.07G0029050-3D	Protein FAR1-RELATED SEQUENCE 5	5,7	Unchanged	-
Sspon.05G0020320-1A	Protein kinase superfamily protein	2,4	Unchanged	-
Sspon.06G0012460-2B	protein STICHEL-like 2	1,5	Unchanged	-
Sspon.08G0030790-1D	Protein transport protein SEC16B-like protein	2,4	Unchanged	-
Sspon.08G0024470-2D	Protein transport protein SEC16B-like protein	2,2	Unchanged	-
Sspon.06G0013100-1A	Putative ARM repeat-containing protein containing family protein isoform 1	2,8	Unchanged	-
Sspon.07G0006150-1P	Putative SAC3/GANP family protein	1,9	Unchanged	-
Sspon.05G0006790-1A	putative sphingolipid transporter spinster 2	6,2	Unchanged	-
Sspon.07G0003640-2D	RING-H2 finger protein ATL67	14,3	Unchanged	-
Sspon.06G0014600-1A	RNA polymerase II C-terminal domain phosphatase-like 3	2,2	Unchanged	-
Sspon.06G0012370-3C	Serine/threonine protein phosphatase 2A 59 kDa regulatory subunit B' eta isoform	3,4	Unchanged	-
Sspon.06G0007400-3C	UAP56-interacting factor-like	8,1	Unchanged	-
Sspon.07G0004740-2B	universal stress protein PHOS32-like	42,8	Unchanged	-
Sspon.01G0015190-2B	Homeodomain leucine zipper family IV protein	2,5	Unchanged	-
Sspon.03G0036600-2C	FACT complex subunit SSRP1	9,7	Unchanged	-
Sspon.03G0004720-4D	ubiquitin-like protein SMT3	40,8	Unchanged	-
Sspon.02G0017270-2B	Peptidyl-prolyl cis-trans isomerase FKBP53	7,4	Unchanged	-
Sspon.02G0010610-4D	hydroxyproline-rich glycoprotein family protein	9,6	Unchanged	-
Sspon.03G0021940-4D	Retrovirus-related Pol polyprotein LINE-1	43,5	Unchanged	-
Sspon.08G0005280-3C	RNA-binding (RRM/RBD/RNP motifs) family protein	20,8	Unchanged	-
Sspon.04G0012730-4D	bidirectional sugar transporter SWEET4	6,3	Unchanged	-
Sspon.06G0024720-3D	protein mago nashi	59,1	Unchanged	-

Sspon.08G0005280-1A	RNA-binding (RRM/RBD/RNP motifs) family protein	49,3	Unchanged	-
Sspon.04G0016580-3C	PTI1-like tyrosine-protein kinase At3g15890	4,9	Unchanged	-
Sspon.02G0006890-3C	GCK-like kinase MIK	4,1	Unchanged	-
Sspon.01G0061090-1D	putative gag-pol polyprotein	2,3	Unchanged	-
Sspon.04G0030340-1P	heat shock 70 kDa protein 1	3,1	Unchanged	-
Sspon.02G0004110-3C	eukaryotic translation initiation factor 5A	46,9	Unchanged	-
Sspon.02G0029980-2D	protein misato homolog 1	3,1	Unchanged	-
Sspon.05G0008060-2B	uncharacterized protein LOC8060177 isoform X2	8,2	Unchanged	-
Sspon.02G0011690-3C	Eukaryotic translation initiation factor 3 subunit C	16,6	Unchanged	-
Sspon.01G0014960-3C	eukaryotic translation initiation factor 3 subunit B-like	31,4	Unchanged	-
Sspon.03G0035610-1B	transmembrane protein 214-A	7,7	Unchanged	-
Sspon.02G0022390-1P	DDRK domain-containing protein 1	6,1	Unchanged	-
Sspon.02G0034270-1B	40S ribosomal protein S3a	18,7	Unchanged	-
Sspon.01G0008280-1A	DEAD-box ATP-dependent RNA helicase 24	7,5	Unchanged	-
Sspon.02G0026030-1A	eukaryotic translation initiation factor 5A-1/2	34,4	Unchanged	-
Sspon.06G0000330-1A	14-3-3-like protein A	54,9	Unchanged	-
Sspon.06G0024260-2C	60S acidic ribosomal protein P0	49,2	Unchanged	-
Sspon.07G0021770-1B	60S acidic ribosomal protein P0	40,8	Unchanged	-
Sspon.07G0006870-1A	60S acidic ribosomal protein P2B	91,2	Unchanged	-
Sspon.08G0024840-1P	protein kri1	3,4	Unchanged	-
Sspon.08G0000160-1A	tetraspanin-18-like	5,6	Unchanged	-
Sspon.04G0011310-4D	TUDOR-SN protein 1	25,3	Unchanged	-
Sspon.01G0019010-3D	chromatin complex subunit A	1,7	Unchanged	-
Sspon.08G0012870-3C	Putative homeodomain-like transcription factor superfamily protein	3,3	Unchanged	-
Sspon.08G0004960-1A	Protein kinase superfamily protein with octicosapeptide/Phox/Bem1p domain	7,8	Unchanged	-
Sspon.01G0015020-3D	Tobamovirus multiplication protein 2A	14,7	Unchanged	-
Sspon.03G0037250-2C	RNA polymerase-associated protein LEO1	8,1	Unchanged	-
Sspon.01G0027420-1A	translational activator GCN1	3	Unchanged	-
Sspon.01G0002230-1A	coiled-coil domain-containing protein 94	6	Unchanged	-
Sspon.08G0026900-2D	G patch domain-containing protein TGH	0,9	Unchanged	-
Sspon.08G0013100-1P	IQ calmodulin-binding motif family protein	18	Unchanged	-
Sspon.06G0013850-4D	SKP1-like protein 1A	51,7	Unchanged	-
Sspon.08G0000620-4D	DNA-binding protein MNB1B	43,8	Unchanged	-
Sspon.06G0010940-2B	NAC domain-containing protein 14	10,2	Unchanged	-
Sspon.02G0003360-2C	poly polymerase 2 isoform X2	5,1	Unchanged	-
Sspon.02G0017790-2C	CCR4-NOT transcription complex subunit 10	1,8	Unchanged	-
Sspon.02G0000790-2T	zinc finger BED domain-containing protein RICESLEEPER 2-like	22,6	Unchanged	-
Sspon.03G0024190-1A	protein CWC15 homolog	9,4	Unchanged	-
Sspon.02G0025080-2B	TPR domain containing protein	20,8	Unchanged	-
Sspon.07G0002920-1A	anaphase-promoting complex subunit 10	14,1	Unchanged	-
Sspon.07G0008650-3D	Decapping nuclease DXO homolog chloroplastic	2,3	Unchanged	-
Sspon.08G0010730-3C	histone-lysine N-methyltransferase	1,9	Unchanged	-
Sspon.05G0007860-1A	La protein 1	23,4	Unchanged	-
Sspon.06G0002420-4D	ras-related protein RABA5c-like	12	Unchanged	-
Sspon.06G0009850-2C	homeobox-leucine zipper protein ROC1-like	1,5	Unchanged	-
Sspon.01G0032460-2B	Late embryogenesis abundant protein group 2	51,4	Unchanged	-
Sspon.04G0003870-3C	pyruvate dehydrogenase E1 component alpha subunit	35,9	Unchanged	-
Sspon.04G0011260-1A	acetyl-coenzyme A synthetase	13,6	Unchanged	-
Sspon.05G0025270-1P	18S pre-ribosomal assembly protein gar2-related	2,2	Unchanged	-
Sspon.05G0025290-2C	L10-interacting MYB domain-containing protein	4,6	Unchanged	-
Sspon.07G0036230-1D	Protein UPSTREAM OF FLC	3,7	Unchanged	-
Sspon.02G0041640-2D	SHL1	45,4	Unchanged	-
Sspon.04G0018820-1P	protein NLP3	3,6	Unchanged	-
Sspon.02G0017290-1A	Brassinosteroid LRR receptor kinase BRL1	1	Unchanged	-
Sspon.02G0023270-4D	Thioredoxin H-type	75,4	Unchanged	-
Sspon.02G0015320-1A	ubiquitin-protein ligase	2,2	Unchanged	-
Sspon.01G0018210-2B	Protein NETWORKED 1A	1,9	Unchanged	-
Sspon.01G0027860-1A	FIP1[V]-like protein	0,8	Unchanged	-
Sspon.03G0007150-3D	Protein STICHEL-like 3	5	Unchanged	-
Sspon.04G0025740-3D	copper transport protein ATX1-like isoform X2	74,8	Unchanged	-
Sspon.05G0009480-1A	Protection of telomeres protein 1b	3,8	Unchanged	-
Sspon.06G0010180-1P	Protein PAF1-like protein	9,1	Unchanged	-
Sspon.02G0019430-1P	SUPPRESSOR OF ABI3-5	1,4	Unchanged	-
Sspon.04G0019500-1A	unnamed protein product	1,7	Unchanged	-
Sspon.03G0022260-2B	FRIGIDA-like protein 4a	18,3	Unchanged	-
Sspon.03G0007800-1A	RNA-binding KH domain-containing protein	6	Unchanged	-
Sspon.07G0011260-1A	O-acyltransferase	3,8	Unchanged	-
Sspon.01G0042520-3D	Calmodulin-binding transcription activator 2	6,9	Unchanged	-
Sspon.01G0031910-2D	Acyl-CoA binding protein	10,7	Unchanged	-
Sspon.07G0004570-1A	TRAF-like superfamily protein	4	Unchanged	-
Sspon.02G0025830-1P	transposon protein, putative, CACTA, En/Spm sub-class	1,9	Unchanged	-
Sspon.07G0020500-4D	PHD finger protein ALFIN-LIKE 6	8,1	Unchanged	-
Sspon.03G0000710-2C	histone deacetylase HDT3	25,7	Unchanged	-
Sspon.05G0003520-2C	glycine-rich protein 2b	58	Unchanged	-
Sspon.04G0002550-2C	nucleolin	21,4	Unchanged	-

Sspon.06G0007360-4D	endothelial differentiation-related factor 1	21,8	Unchanged	-
Sspon.01G0026700-1P	SWIB/MDM2 domain containing protein	17,8	Unchanged	-
Sspon.06G0001440-4D	skin secretory protein xP2	20,6	Unchanged	-
Sspon.05G0018290-3C	calcium-dependent protein kinase 24	32,6	Unchanged	-
Sspon.05G0011250-1P	stress-induced protein kinase1	12,3	Unchanged	-
Sspon.01G0028760-1A	casein kinase II subunit alpha-2-like	6,8	Unchanged	-
Sspon.02G0025720-1A	casein kinase II subunit alpha	23,7	Unchanged	-
Sspon.01G0008980-1A	receptor-like protein kinase FERONIA	5,4	Unchanged	-
Sspon.04G0029160-2C	Cleavage and polyadenylation specificity factor (CPSF) A subunit protein	3,8	Unchanged	-
Sspon.04G0011810-2C	ubiquitin-activating enzyme E1 domain-containing protein 1	16,7	Unchanged	-
Sspon.03G0029220-2C	VAMP-like protein YKT61	15,1	Unchanged	-
Sspon.02G0046580-2D	xylose isomerase	51,5	Unchanged	-
Sspon.03G0019530-2B	Alpha-xylosidase 1	14,7	Unchanged	-
Sspon.01G0033570-1P	Protein EXPORTIN 1A	13,6	Unchanged	-
Sspon.01G0033570-1A	Protein EXPORTIN 1A	14,2	Unchanged	-
Sspon.02G0002670-1A	xylulose kinase	18,2	Unchanged	-
Sspon.04G0018380-2C	phosphatase 2C 59	24,6	Unchanged	-
Sspon.03G0027920-2D	Villin-2	12,4	Unchanged	-
Sspon.03G0009900-2B	V-type proton ATPase subunit E-like	27	Unchanged	-
Sspon.04G0033600-1C	V-type proton ATPase subunit B 2-like	26,5	Unchanged	-
Sspon.04G0017180-2B	V-type proton ATPase catalytic subunit A	39	Unchanged	-
Sspon.03G0007740-1P	outer mitochondrial membrane protein porin	45,7	Unchanged	-
Sspon.03G0012370-2B	outer plastidial membrane protein porin	40	Unchanged	-
Sspon.02G0016020-4D	voltage-dependent anion channel protein1b	46,4	Unchanged	-
Sspon.02G0008310-2B	UDP-glucose pyrophosphorylase2	63,4	Unchanged	-
Sspon.02G0009750-1A	bifunctional UDP-glucose 4-epimerase and UDP-xylose 4-epimerase 1-like	14,8	Unchanged	-
Sspon.01G0049620-1B	UDP-glucose 6-dehydrogenase	36	Unchanged	-
Sspon.01G0006050-2B	UDP-glucose 6-dehydrogenase 4-like	29	Unchanged	-
Sspon.04G0028350-1B	ubiquitin fusion degradation protein 1 homolog isoform X1	16,4	Unchanged	-
Sspon.03G0013410-1A	ubiquitin carboxyl-terminal hydrolase 6	8,8	Unchanged	-
Sspon.03G0022020-2P	Ubiquitin carboxyl-terminal hydrolase	11,2	Unchanged	-
Sspon.03G0022020-1P	Ubiquitin carboxyl-terminal hydrolase	21,2	Unchanged	-
Sspon.02G0027190-2C	Ubiquitin carboxyl-terminal hydrolase 13	5,7	Unchanged	-
Sspon.02G0039310-1P	ubiquitin-conjugating enzyme E2 5A-like	9,9	Unchanged	-
Sspon.01G0032950-2P	elongation factor Tu, mitochondrial	44,8	Unchanged	-
Sspon.04G0009080-1A	elongation factor Tu	31,1	Unchanged	-
Sspon.04G0017520-1A	tubulin beta chain	64,8	Unchanged	-
Sspon.03G0016270-1A	tubulin beta-5 chain	57,5	Unchanged	-
Sspon.01G0027630-2D	alpha tubulin1	51,7	Unchanged	-
Sspon.01G0029070-2D	tubulin alpha-3 chain	51,6	Unchanged	-
Sspon.03G0008460-1A	threonine synthase	21,4	Unchanged	-
Sspon.01G0030300-3C	thioredoxin H-type 5	22,6	Unchanged	-
Sspon.02G0015060-2B	Alpha,alpha-trehalose-phosphate synthase 6	10,5	Unchanged	-
Sspon.04G0001910-1P	trehalose-6-phosphate synthase	16,5	Unchanged	-
Sspon.04G0030560-1P	serine/threonine-protein phosphatase PP1	24,4	Unchanged	-
Sspon.01G0007220-2C	Serine/threonine-protein phosphatase PP1 isozyme 2	25,5	Unchanged	-
Sspon.03G0016680-2B	Mitochondrial import receptor subunit TOM40-1	23	Unchanged	-
Sspon.01G0002730-4D	aquaporin TIP1-1	7,5	Unchanged	-
Sspon.01G0034030-1P	probable mitochondrial import inner membrane translocase subunit TIM21	5,7	Unchanged	-
Sspon.02G0037250-1B	Triosephosphate isomerase, chloroplastic	30,6	Unchanged	-
Sspon.01G0004590-3C	Eukaryotic translation initiation factor 3 subunit K	25,7	Unchanged	-
Sspon.03G0009580-3C	Eukaryotic translation initiation factor 3 subunit D	17,1	Unchanged	-
Sspon.03G0022710-2B	Eukaryotic translation initiation factor 3 subunit A	11,3	Unchanged	-
Sspon.01G0024710-2B	Threonine--tRNA ligase mitochondrial 1	22,6	Unchanged	-
Sspon.02G0037480-2C	formate--tetrahydrofolate ligase	20,2	Unchanged	-
Sspon.04G0033310-1C	FAM10 family protein	9,9	Unchanged	-
Sspon.04G0030010-2C	translationally-controlled tumor protein	31,5	Unchanged	-
Sspon.03G0017060-3D	UBP1-associated protein 2A	7,3	Unchanged	-
Sspon.01G0025370-2B	nuclear transport factor 2	12,8	Unchanged	-
Sspon.02G0008920-3C	Thioredoxin superfamily protein	43,5	Unchanged	-
Sspon.02G0022690-2P	coatomeer subunit gamma	21,8	Unchanged	-
Sspon.02G0026680-3C	eukaryotic translation initiation factor 3 subunit I	37,4	Unchanged	-
Sspon.01G0025080-2C	Acidic leucine-rich nuclear phosphoprotein 32-related protein 2	26	Unchanged	-
Sspon.04G0004530-1P	aspartyl protease family protein At5g10770-like	9,6	Unchanged	-
Sspon.03G0008800-2B	65-kDa microtubule-associated protein 3	12,6	Unchanged	-
Sspon.01G0009760-4D	Nascent polypeptide-associated complex alpha subunit-like protein	42,4	Unchanged	-
Sspon.03G0001350-2B	fructokinase-1	31,2	Unchanged	-
Sspon.03G0001350-3C	fructokinase-1	65,3	Unchanged	-
Sspon.01G0010410-3P	chaperonin	59,2	Unchanged	-
Sspon.03G0013850-3C	protein usf-like	50,6	Unchanged	-
Sspon.02G0001640-2C	elongation factor 1-beta	30,6	Unchanged	-
Sspon.02G0001640-1A	elongation factor 1-beta	41,1	Unchanged	-
Sspon.02G0004020-3C	Pentatricopeptide repeat-containing protein mitochondrial	17,1	Unchanged	-
Sspon.04G0002700-2C	importin subunit beta-1	13,6	Unchanged	-

Sspon.04G0004570-2B	Retrotransposon protein Ty1-copia subclass	28,3	Unchanged	-
Sspon.04G0033170-1C	Apoptosis inhibitor 5-like protein API5	10,3	Unchanged	-
Sspon.01G0012000-1P	probable nucleoredoxin 1-1	44,5	Unchanged	-
Sspon.03G0033880-1B	Asparaginyl-tRNA synthetase, cytoplasmic 3	33,7	Unchanged	-
Sspon.01G0011850-2B	sucrose synthase 2 isoform X1	49,5	Unchanged	-
Sspon.03G0016920-4D	sad1/unc-84-like protein 2	3,8	Unchanged	-
Sspon.01G0009460-1A	Serine/arginine-rich-splicing factor SR34	30,9	Unchanged	-
Sspon.01G0024940-3D	UDP-sulfoquinovose synthase, chloroplastic-like	16,5	Unchanged	-
Sspon.02G0020240-4D	Spermidine synthase 1	22,2	Unchanged	-
Sspon.02G0029860-4D	serine hydroxymethyltransferase 4-like	12,8	Unchanged	-
Sspon.03G0010960-3D	Protein SGT1 homolog	21,6	Unchanged	-
Sspon.03G0026970-3D	S-formylglutathione hydrolase	21,1	Unchanged	-
Sspon.01G0023340-1A	protein Z	25,6	Unchanged	-
Sspon.02G0001870-3C	Protein transport protein SEC31 homolog B	19,1	Unchanged	-
Sspon.02G0021520-2B	SEC13-related protein isoform X3	31,9	Unchanged	-
Sspon.02G0058670-1D	Succinate dehydrogenase flavoprotein subunit, mitochondrial	14	Unchanged	-
Sspon.02G0007660-3D	Serine carboxypeptidase-like precursor	22,1	Unchanged	-
Sspon.04G0022010-3D	Serine carboxypeptidase 24	23,1	Unchanged	-
Sspon.03G0028270-1P	selenium-binding protein 2-like	8,8	Unchanged	-
Sspon.02G0032750-2C	GTP-binding protein SAR1A	34,2	Unchanged	-
Sspon.03G0017510-3C	GTP-binding protein SAR1A	42	Unchanged	-
Sspon.04G0019980-2B	histone deacetylase complex subunit SAP18	27,6	Unchanged	-
Sspon.02G0008020-1P	SUMO-activating enzyme subunit 2	16,1	Unchanged	-
Sspon.04G0012330-1A	Importin beta-like SAD2	8,9	Unchanged	-
Sspon.01G0031950-2D	Glycine-rich RNA-binding protein RZ1A	28,6	Unchanged	-
Sspon.04G0017110-1A	small nuclear ribonucleoprotein F	40,5	Unchanged	-
Sspon.02G0049650-1C	ubiquitin-NEDD8-like protein RUB1	39,9	Unchanged	-
Sspon.04G0015330-1A	26S protease regulatory subunit 8 homolog B	14	Unchanged	-
Sspon.04G0001300-2B	26S protease regulatory subunit 6A homolog A	41,6	Unchanged	-
Sspon.04G0015600-1A	26S protease regulatory subunit S10B homolog B	32,4	Unchanged	-
Sspon.01G0006140-2B	26S protease regulatory subunit 6B	36,9	Unchanged	-
Sspon.02G0036140-1B	26S proteasome regulatory subunit 4 homolog A	18,1	Unchanged	-
Sspon.04G0026340-2D	26S proteasome regulatory subunit 7A	63,4	Unchanged	-
Sspon.01G0004560-3C	40S ribosomal protein SA	45,9	Unchanged	-
Sspon.01G0001930-1A	40S ribosomal protein SA	43,2	Unchanged	-
Sspon.02G0027260-4D	40S ribosomal protein S9	36,4	Unchanged	-
Sspon.04G0003910-4D	40S ribosomal protein S8	51,5	Unchanged	-
Sspon.01G0016990-3D	40S ribosomal protein S7	16,5	Unchanged	-
Sspon.01G0052460-2D	40S ribosomal protein S7	31,8	Unchanged	-
Sspon.02G0033850-1B	40S ribosomal protein S6	27,5	Unchanged	-
Sspon.03G0017970-4D	40S ribosomal protein S5	48,2	Unchanged	-
Sspon.03G0017970-1A	40S ribosomal protein S5	48,2	Unchanged	-
Sspon.01G0032260-2B	40S ribosomal protein S4	48,7	Unchanged	-
Sspon.01G0005520-2D	40S ribosomal protein S3a	49,6	Unchanged	-
Sspon.02G0022460-2B	40S ribosomal protein S2-3	50,2	Unchanged	-
Sspon.02G0022460-2P	40S ribosomal protein S2-3	35,4	Unchanged	-
Sspon.01G0052750-2D	40S ribosomal protein S28	25,7	Unchanged	-
Sspon.01G0009630-2D	40S ribosomal protein S21	37	Unchanged	-
Sspon.01G0037240-3D	40S ribosomal protein S20	48,4	Unchanged	-
Sspon.01G0047190-3D	40S ribosomal protein S19	48,3	Unchanged	-
Sspon.02G0042000-1B	40S ribosomal protein S18	65,8	Unchanged	-
Sspon.01G0048570-2P	40S ribosomal protein S15	27,3	Unchanged	-
Sspon.01G0053990-1C	26S proteasome non-ATPase regulatory subunit 13 homolog A	23,4	Unchanged	-
Sspon.04G0008920-3C	26S proteasome non-ATPase regulatory subunit 6	13,1	Unchanged	-
Sspon.01G0032970-2P	26S proteasome non-ATPase regulatory subunit 12 homolog A-like	14,4	Unchanged	-
Sspon.03G0000580-2C	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	20,2	Unchanged	-
Sspon.04G0018460-2C	26S proteasome non-ATPase regulatory subunit 2 homolog A	21,5	Unchanged	-
Sspon.01G0037150-1B	26S proteasome non-ATPase regulatory subunit 4	16,8	Unchanged	-
Sspon.02G0028970-3C	60S ribosomal protein L2	23,4	Unchanged	-
Sspon.02G0010680-4D	60S ribosomal protein L7a	13,2	Unchanged	-
Sspon.01G0034580-2D	60S ribosomal protein L5-1	38,6	Unchanged	-
Sspon.03G0001320-1A	60S ribosomal protein L5-1	38,9	Unchanged	-
Sspon.02G0023390-1P	60S ribosomal protein L4-1	17,5	Unchanged	-
Sspon.02G0023390-1A	60S ribosomal protein L4-1	41,6	Unchanged	-
Sspon.03G0003040-2D	60S ribosomal protein L36-3-like	17,8	Unchanged	-
Sspon.02G0049990-2D	60S ribosomal protein L35a-2	39,4	Unchanged	-
Sspon.02G0011010-4D	60S ribosomal protein L32-1	54,1	Unchanged	-
Sspon.02G0003430-1A	60S ribosomal protein L27a-3	35,2	Unchanged	-
Sspon.03G0035820-1B	60S ribosomal protein L26-1	13,8	Unchanged	-
Sspon.01G0022850-3C	60S ribosomal protein L24	17,7	Unchanged	-
Sspon.04G0000890-2C	60S ribosomal protein L23	48,8	Unchanged	-
Sspon.01G0009440-4D	60S ribosomal protein L22-2	40,2	Unchanged	-
Sspon.02G0001150-2B	60S ribosomal protein L18-3	18,6	Unchanged	-
Sspon.03G0009390-4D	60S ribosomal protein L18a-like isoform X3	18,9	Unchanged	-
Sspon.02G0048360-1P	60S ribosomal protein L15	26	Unchanged	-
Sspon.04G0014530-2B	60S ribosomal protein L10-1	28,2	Unchanged	-

Sspon.03G0002250-2C	Hevamine-A	5,4	Unchanged	-
Sspon.04G0021530-2C	replication protein A 32 kDa subunit A-like	11,9	Unchanged	-
Sspon.01G0019110-3C	heterogeneous nuclear ribonucleoprotein 1-like	14,5	Unchanged	-
Sspon.03G0003410-1A	RuvB-like protein 1	14,6	Unchanged	-
Sspon.01G0003180-1A	DEAD-box ATP-dependent RNA helicase 38	26,2	Unchanged	-
Sspon.01G0030530-2D	DEAD-box ATP-dependent RNA helicase 37-like	15,7	Unchanged	-
Sspon.02G0022630-2B	DEAD-box ATP-dependent RNA helicase 52	18,8	Unchanged	-
Sspon.01G0022960-4D	Alpha-1,4-glucan-protein synthase	52,1	Unchanged	-
Sspon.03G0007520-3D	plasminogen activator inhibitor 1 RNA-binding protein	13,9	Unchanged	-
Sspon.03G0040220-1C	Protein RETICULATA-RELATED 3, chloroplastic	20,7	Unchanged	-
Sspon.03G0002470-1A	retrotransposon protein, putative, unclassified	2,5	Unchanged	-
Sspon.04G0005330-3D	pathogen induced protein 2-4	23	Unchanged	-
Sspon.02G0045790-1B	glycine-rich RNA binding protein	16,1	Unchanged	-
Sspon.01G0025010-1P	glycine-rich RNA-binding protein 2	23,8	Unchanged	-
Sspon.02G0027500-4D	Glycine-rich RNA-binding protein 3 mitochondrial	22,3	Unchanged	-
Sspon.03G0028260-1P	glycine-rich RNA-binding protein 2	27,3	Unchanged	-
Sspon.04G0008350-2C	RAN GTPase-activating protein 2	18,5	Unchanged	-
Sspon.01G0037900-3D	ran-binding protein 1	40,2	Unchanged	-
Sspon.02G0010410-2D	snRK1-interacting protein 1	39,8	Unchanged	-
Sspon.03G0005080-1A	snRK1-interacting protein 1	24,5	Unchanged	-
Sspon.02G0007140-2C	ras-related protein RABH1b	12	Unchanged	-
Sspon.04G0007070-1A	ypt homolog4	37,2	Unchanged	-
Sspon.01G0030710-4D	Cytochrome b-c1 complex subunit 7	39,7	Unchanged	-
Sspon.04G0008820-1A	pre-mRNA-splicing factor ISY1	7,2	Unchanged	-
Sspon.03G0023680-1T	peptide-N4-(N-acetyl-beta-glucosaminy)asparagine amidase A	8	Unchanged	-
Sspon.03G0005220-1A	RNA recognition motif	4,8	Unchanged	-
Sspon.01G0049240-1B	strictosidine synthase precursor	15,1	Unchanged	-
Sspon.03G0026410-3D	Os01g0953500	2,6	Unchanged	-
Sspon.01G0021230-2B	Prolyl carboxypeptidase like protein	30,8	Unchanged	-
Sspon.03G0015550-1A	universal stress protein	27,9	Unchanged	-
Sspon.03G0032540-2C	adaptin ear-binding	5,9	Unchanged	-
Sspon.03G0027870-1B	putative ADP-ribosylation factor GTPase-activating protein AGD11	5,3	Unchanged	-
Sspon.02G0007510-1A	beta-ureidopropionase	11,2	Unchanged	-
Sspon.04G0003970-3C	dihydropyrimidine dehydrogenase (NADP(+)), chloroplastic-like	39,4	Unchanged	-
Sspon.03G0035010-3D	Transcription factor Pur-alpha 1	18,6	Unchanged	-
Sspon.02G0012840-1P	phosphoribosylaminoimidazole-succinocarboxamide synthase, chloroplastic isoform X1	34,8	Unchanged	-
Sspon.01G0037380-1B	putative glucan 13-alpha-glucosidase	10,9	Unchanged	-
Sspon.01G0003170-3C	phosphoserine aminotransferase 1, chloroplastic-like	49,2	Unchanged	-
Sspon.03G0016970-2B	Peroxisome 2F, mitochondrial	35,8	Unchanged	-
Sspon.03G0011410-1A	Peroxisome 2C	12,3	Unchanged	-
Sspon.01G0055060-1C	Pre-mRNA-processing factor 19 homolog 2	25,2	Unchanged	-
Sspon.03G0026720-3D	pyrroline-5-carboxylate reductase	29,9	Unchanged	-
Sspon.03G0016300-3D	DNA-binding protein	13,1	Unchanged	-
Sspon.02G0016310-1A	Proton pump-interactor 1	12,7	Unchanged	-
Sspon.03G0021910-2B	phospholipase D alpha 1	41,3	Unchanged	-
Sspon.01G0049290-3D	phytochrome C	4,6	Unchanged	-
Sspon.02G0040450-1B	mitochondrial prohibitin complex protein 2	31,5	Unchanged	-
Sspon.01G0032350-1A	prohibitin4	34,1	Unchanged	-
Sspon.01G0008890-2B	2,3-bisphosphoglycerate-independent phosphoglycerate mutase-like	4,3	Unchanged	-
Sspon.03G0019670-3D	Plastidic glucose transporter 4	3,1	Unchanged	-
Sspon.02G0009630-1A	6-phosphogluconolactonase	28,3	Unchanged	-
Sspon.04G0017410-2B	Phosphoglycerate kinase	64,2	Unchanged	-
Sspon.01G0028910-1A	glucose-6-phosphate isomerase, cytosolic	45	Unchanged	-
Sspon.03G0027260-1P	6-phosphogluconate dehydrogenase, decarboxylating 1-like	25	Unchanged	-
Sspon.03G0013610-2B	peroxidase 72	29,4	Unchanged	-
Sspon.01G0022000-4D	peroxidase 27 precursor	32,8	Unchanged	-
Sspon.03G0015020-3C	peroxidase 2 precursor	29,9	Unchanged	-
Sspon.01G0009220-3C	peroxidase3	36	Unchanged	-
Sspon.02G0002610-1A	Peroxidase 2	20,5	Unchanged	-
Sspon.03G0034150-2C	peroxidase 1 precursor	24,5	Unchanged	-
Sspon.02G0012680-1A	peroxidase 17	40,9	Unchanged	-
Sspon.03G0038090-1C	cationic peroxidase SPC4-like	13,1	Unchanged	-
Sspon.01G0014190-3D	nucleic acid binding protein	22,3	Unchanged	-
Sspon.04G0030660-1P	3-ketoacyl-CoA thiolase 2, peroxisomal-like	33,3	Unchanged	-
Sspon.02G0026110-4D	Pyridoxal 5'-phosphate synthase-like subunit PDX1.2	24,3	Unchanged	-
Sspon.03G0014720-2B	protein disulfide isomerase-like 2-2	23,5	Unchanged	-
Sspon.01G0052330-1P	pyruvate decarboxylase	49,7	Unchanged	-
Sspon.02G0048980-2D	proteasome subunit beta type	39,5	Unchanged	-
Sspon.02G0010910-3D	proteasome subunit beta type 1	70,1	Unchanged	-
Sspon.01G0025420-3C	Proteasome subunit beta type-2	57,6	Unchanged	-
Sspon.07G0007390-4P	patellin-1	35,2	Unchanged	-
Sspon.02G0008840-2C	probable inactive purple acid phosphatase 29	7,1	Unchanged	-
Sspon.02G0044310-3D	purple acid phosphatase precursor	19,9	Unchanged	-
Sspon.04G0008070-3C	Phenylalanine/tyrosine ammonia-lyase	21,2	Unchanged	-
Sspon.02G0002320-3C	proteasome subunit alpha type 3	61,4	Unchanged	-

Sspon.01G0002910-3C	proteasome subunit alpha type 5	55,3	Unchanged	-
Sspon.02G0039620-1B	Polyadenylate-binding protein 2	34,9	Unchanged	-
Sspon.04G0007750-2C	proteasome subunit alpha type-2	36,2	Unchanged	-
Sspon.01G0004450-1A	Proteasome subunit alpha type	60,2	Unchanged	-
Sspon.07G0006600-2B	Delta-1-pyrroline-5-carboxylate synthase B	13,7	Unchanged	-
Sspon.04G0012460-1A	co-chaperone protein SBA1	29,9	Unchanged	-
Sspon.03G0022530-1P	glutaminyI-tRNA synthetase	12,3	Unchanged	-
Sspon.02G0034650-2D	zeamatin-like protein	26,8	Unchanged	-
Sspon.01G0051840-2P	Oxysterol-binding protein-related protein 3C	21,7	Unchanged	-
Sspon.04G0021470-1T	probable cytosolic oligopeptidase A	30,8	Unchanged	-
Sspon.04G0015800-2B	outer envelope protein 80, chloroplastic	14,4	Unchanged	-
Sspon.01G0033440-3P	Outer envelope pore protein 24A chloroplastic	20,8	Unchanged	-
Sspon.04G0004890-3C	protein translocase/ protein transporter	6,1	Unchanged	-
Sspon.03G0017910-3C	Cysteine synthase mitochondrial	29,8	Unchanged	-
Sspon.02G0031930-2B	cysteine synthase	46,2	Unchanged	-
Sspon.04G0000020-2B	Thioredoxin reductase NTRB	45,6	Unchanged	-
Sspon.01G0062290-1D	DNA-directed RNA polymerases I, II, and III 17.1 kDa polypeptide	28,3	Unchanged	-
Sspon.02G0018120-2B	DNA-directed RNA polymerases II, IV and V subunit 3	27,9	Unchanged	-
Sspon.02G0013140-1A	ARP protein (REF)	6,5	Unchanged	-
Sspon.01G0009840-1A	nucleolar protein NOP56-like protein	21,9	Unchanged	-
Sspon.03G0031530-2D	glycylpeptide N-tetradecanoyltransferase 1	14	Unchanged	-
Sspon.01G0051030-1C	Omega-amidase chloroplastic	29,3	Unchanged	-
Sspon.02G0038730-1B	cysteine desulfurase, mitochondrial-like	24,6	Unchanged	-
Sspon.01G0014210-3C	Identification and characterization of the first plant G-quadruplex binding protein encoded by the Zea mays L. nucleoside diphosphate1 gene, ZmNDPK1	59,1	Unchanged	-
Sspon.02G0007310-4D	Nucleoside diphosphate kinase family protein	53	Unchanged	-
Sspon.03G0023870-1A	Sodium/calcium exchanger NCL1 precursor	8,1	Unchanged	-
Sspon.01G0042010-3D	Betaine aldehyde dehydrogenase 2 mitochondrial	43,6	Unchanged	-
Sspon.01G0042010-2P	Betaine aldehyde dehydrogenase 2 mitochondrial	48	Unchanged	-
Sspon.03G0010070-4D	Transducin/WD40 repeat-like superfamily protein	2,1	Unchanged	-
Sspon.02G0028960-3C	translocon-associated protein beta (TRAPB) family protein	17	Unchanged	-
Sspon.02G0037880-1B	26S proteasome non-ATPase regulatory subunit 9	18,5	Unchanged	-
Sspon.01G0042430-1P	brown midrib2	30,4	Unchanged	-
Sspon.01G0045680-3D	histone-binding protein MSI1 homolog	33,2	Unchanged	-
Sspon.01G0020890-1A	membrane steroid-binding protein 2-like	15,4	Unchanged	-
Sspon.02G0031860-4D	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1	42	Unchanged	-
Sspon.03G0003520-1P	cinnamoyl-CoA reductase 1	12	Unchanged	-
Sspon.04G0002660-3P	Mitochondrial phosphate carrier protein 3, mitochondrial	21,2	Unchanged	-
Sspon.01G0006110-3D	Peptidase beta subunit	47,2	Unchanged	-
Sspon.03G0022790-2B	mitochondrial-processing peptidase alpha subunit	20,6	Unchanged	-
Sspon.04G0001730-3D	membrane steroid-binding protein 1	35	Unchanged	-
Sspon.01G0004230-3D	DAG protein	17,3	Unchanged	-
Sspon.02G0004530-4D	Succinate--CoA ligase subunit alpha-1 mitochondrial	32,6	Unchanged	-
Sspon.04G0018980-1A	putative ATP synthase 24 kDa subunit mitochondrial	33,3	Unchanged	-
Sspon.04G0018960-1A	putative ATP synthase 24 kDa subunit mitochondrial	15,1	Unchanged	-
Sspon.03G0014490-1A	glyoxysomal fatty acid beta-oxidation multifunctional protein MFP-a	26,5	Unchanged	-
Sspon.02G0042140-3D	small nuclear ribonucleoprotein-associated protein B	19,1	Unchanged	-
Sspon.04G0022970-1P	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	16,3	Unchanged	-
Sspon.01G0019480-4D	malate dehydrogenase, cytoplasmic	50,9	Unchanged	-
Sspon.02G0028590-3D	DNA replication licensing factor MCM7	20	Unchanged	-
Sspon.03G0013580-1A	DNA replication licensing factor mcm4	9,7	Unchanged	-
Sspon.03G0016650-1A	pyruvate kinase, cytosolic isozyme	22,4	Unchanged	-
Sspon.02G0008540-4D	chitin elicitor-binding protein	6,2	Unchanged	-
Sspon.03G0014960-3C	Dihydrolipoyl dehydrogenase 1, mitochondrial	47,9	Unchanged	-
Sspon.03G0001400-4D	lipoygenase	9	Unchanged	-
Sspon.01G0047700-2D	Elongation factor 2	48,2	Unchanged	-
Sspon.01G0031190-1A	leukotriene A-4 hydrolase homolog	32,1	Unchanged	-
Sspon.04G0001610-1T	Leucine aminopeptidase 2 chloroplastic	55,8	Unchanged	-
Sspon.02G0029040-2B	Importin subunit beta-1	16,5	Unchanged	-
Sspon.03G0005480-2C	3-methyl-2-oxobutanoate hydroxymethyltransferase	10,2	Unchanged	-
Sspon.02G0047490-2D	ruvB-like 2	22,7	Unchanged	-
Sspon.03G0016110-1A	mitochondrial glycoprotein	13,9	Unchanged	-
Sspon.01G0000160-1A	quinone oxidoreductase-like	31,4	Unchanged	-
Sspon.02G0019370-1A	phosphomannomutase/phosphoglucomutase-like isoform X1	22,5	Unchanged	-
Sspon.01G0005150-1A	inositol-3-phosphate synthase	22,8	Unchanged	-
Sspon.03G0029970-1B	vegetative incompatibility protein HET-E-1-like	46,4	Unchanged	-
Sspon.03G0035170-2C	Importin alpha-1b subunit, mRNA	31,9	Unchanged	-
Sspon.07G0012540-4D	Importin subunit alpha	22,1	Unchanged	-
Sspon.03G0013200-2B	IAA-amino acid hydrolase ILR1-like 1	11,2	Unchanged	-
Sspon.04G0019550-2C	3-isopropylmalate dehydratase large subunit, chloroplastic-like isoform X2	21,7	Unchanged	-
Sspon.01G0020440-3C	Eukaryotic translation initiation factor 2 subunit alpha	15,6	Unchanged	-
Sspon.02G0001740-1P	Histone H2B	48,3	Unchanged	-

Sspon.03G0020730-2C	Histone H2B.1	51	Unchanged	-
Sspon.02G0006030-4D	histone H2A	24,1	Unchanged	-
Sspon.01G0033080-2D	probable histone H2A.5	32,3	Unchanged	-
Sspon.02G0027750-1A	Heat shock protein 90-6 mitochondrial	16,9	Unchanged	-
Sspon.02G0011960-3C	Heat shock protein 90-2	45,2	Unchanged	-
Sspon.02G0037180-2D	Heat shock protein 90-2	47,8	Unchanged	-
Sspon.03G0001660-1A	Heat shock 70 kDa protein 6 chloroplastic	15,2	Unchanged	-
Sspon.01G0025470-1A	Heat shock 70 kDa protein 6 chloroplastic	16,7	Unchanged	-
Sspon.07G0006270-4D	putative mediator of RNA polymerase II transcription subunit 37c	42,4	Unchanged	-
Sspon.01G0021320-1T	heat shock 70 kDa protein	37,8	Unchanged	-
Sspon.03G0011920-1A	pop3 peptide	43	Unchanged	-
Sspon.04G0007360-2B	Hsp70-Hsp90 organizing protein 3	44,2	Unchanged	-
Sspon.01G0038840-2D	Rho GTPase activation protein (RhoGAP) with PH domain	14	Unchanged	-
Sspon.01G0007650-1A	Beta-hexosaminidase 2	11,4	Unchanged	-
Sspon.03G0022050-3C	2-hydroxyphytanoyl-CoA lyase	26,6	Unchanged	-
Sspon.02G0012850-1P	glutathione transferase GST 23	26,3	Unchanged	-
Sspon.01G0029750-1A	probable glutathione S-transferase GSTU1	36,8	Unchanged	-
Sspon.01G0029750-4D	putative glutathione S-transferase parA	9,4	Unchanged	-
Sspon.01G0013420-2B	glutathione S-transferase L2, chloroplastic-like	7,9	Unchanged	-
Sspon.01G0013330-1P	Glutathione S-transferase U17	12,7	Unchanged	-
Sspon.01G0013400-2B	probable glutathione S-transferase GSTU6	15,8	Unchanged	-
Sspon.03G0044920-1D	glutathione S-transferase 3	52,1	Unchanged	-
Sspon.03G0005720-3D	glutathione S-transferase GSTF2	39,7	Unchanged	-
Sspon.03G0014110-2B	glutathione transferase 8 isoform X1	35,6	Unchanged	-
Sspon.04G0021790-1P	Glutathione reductase cytosolic	32,7	Unchanged	-
Sspon.01G0018000-3D	GDP-mannose 35-epimerase	41,3	Unchanged	-
Sspon.04G0010990-3C	2-hydroxy-3-oxopropionate reductase	28,8	Unchanged	-
Sspon.03G0009080-3C	Glutamate synthase 1 chloroplastic	11,7	Unchanged	-
Sspon.03G0016170-3C	germin-like protein 1-1	17,4	Unchanged	-
Sspon.04G0004050-3C	Crystal Structure of the Maize Glutamine Synthetase complexed with ADP and Methionine sulfoximine Phosphate	36,2	Unchanged	-
Sspon.01G0026870-2D	glutamine synthetase root isoform 2	13,6	Unchanged	-
Sspon.01G0012730-1A	probable indole-3-acetic acid-amido synthetase GH3.8	23,7	Unchanged	-
Sspon.04G0009330-3C	glycerophosphodiester phosphodiesterase GDPDL3	13,9	Unchanged	-
Sspon.01G0048650-2D	glutamate dehydrogenase	18,3	Unchanged	-
Sspon.04G0011780-2C	mitochondrial NADH ubiquinone oxidoreductase 29 kDa subunit	25	Unchanged	-
Sspon.02G0033350-1B	Gamma carbonic anhydrase 2, mitochondrial	25,6	Unchanged	-
Sspon.03G0016220-2B	Gamma carbonic anhydrase 1 mitochondrial	22,8	Unchanged	-
Sspon.01G0009280-1A	fumarate hydratase 1, mitochondrial-like	22,2	Unchanged	-
Sspon.03G0039290-1C	Peptidyl-prolyl cis-trans isomerase FKBP15-1 precursor	26,5	Unchanged	-
Sspon.04G0000320-2B	probable mediator of RNA polymerase II transcription subunit 36b	29,8	Unchanged	-
Sspon.03G0000790-3D	fructose-bisphosphate aldolase, cytoplasmic isoform	65,9	Unchanged	-
Sspon.03G0018970-1A	putative fructose-bisphosphate aldolase 3, chloroplastic	21,7	Unchanged	-
Sspon.04G0015770-1A	Fumarylacetoacetase	24,2	Unchanged	-
Sspon.01G0020450-2B	Nucleic acid binding protein	13,4	Unchanged	-
Sspon.01G0032240-1A	tol-Pal system protein TolB-like	13,9	Unchanged	-
Sspon.03G0023220-2B	Coatomer subunit alpha-1	10,6	Unchanged	-
Sspon.03G0032440-3D	putative aldo-keto reductase 1	48,4	Unchanged	-
Sspon.03G0032470-3D	putative aldo-keto reductase 1	38,6	Unchanged	-
Sspon.02G0028120-1P	Tryptophan--tRNA ligase, cytoplasmic	29,4	Unchanged	-
Sspon.01G0033600-2D	Transducin/WD40 repeat-like superfamily protein	3,1	Unchanged	-
Sspon.01G0023480-3D	N-acetyl-gamma-glutamyl-phosphate reductase	33	Unchanged	-
Sspon.03G0024710-2B	RNA polymerase I-associated factor PAF67	13	Unchanged	-
Sspon.01G0012260-3D	EF hand family protein	32,7	Unchanged	-
Sspon.01G0029440-4D	inosine-5'-monophosphate dehydrogenase	23,6	Unchanged	-
Sspon.03G0016320-1A	Coatomer subunit beta-2	17,2	Unchanged	-
Sspon.04G0029530-2C	NADP-dependent D-sorbitol-6-phosphate dehydrogenase	23,5	Unchanged	-
Sspon.03G0017900-1P	NADP-dependent oxidoreductase P1	41,3	Unchanged	-
Sspon.03G0020240-2C	Protein ASPARTIC PROTEASE IN GUARD CELL 1	3,1	Unchanged	-
Sspon.03G0042140-1C	SIT4 phosphatase-associated family protein	12,9	Unchanged	-
Sspon.04G0011690-1A	Isoleucine--tRNA ligase cytoplasmic	8,8	Unchanged	-
Sspon.01G0034330-2D	putative transcription factor Hap3/NF-YB family	11,5	Unchanged	-
Sspon.01G0024610-2B	lactoylglutathione lyase	27,4	Unchanged	-
Sspon.01G0007600-4D	beta-glucosidase BoGH3B-like	22,7	Unchanged	-
Sspon.02G0010980-1A	glucan endo-1,3-beta-glucosidase A6 precursor	17,3	Unchanged	-
Sspon.01G0002360-2B	Glutamate--tRNA ligase cytoplasmic	17,5	Unchanged	-
Sspon.01G0005410-1A	Serine--tRNA ligase cytoplasmic	22,8	Unchanged	-
Sspon.02G0006910-4D	probable protein phosphatase 2C 62	33,4	Unchanged	-
Sspon.03G0025190-2C	OB-fold nucleic acid binding domain containing protein	45,2	Unchanged	-
Sspon.04G0008600-3C	acetolactate synthase/ amino acid binding protein	14	Unchanged	-
Sspon.01G0028050-3D	Nucleic acid-binding OB-fold-like protein	31,4	Unchanged	-
Sspon.01G0051180-2D	Alcohol dehydrogenase-like 2	5,4	Unchanged	-
Sspon.01G0026180-1A	microsomal glutathione S-transferase 3-like	20	Unchanged	-
Sspon.04G0015280-1A	Coatomer subunit beta'-3	8,8	Unchanged	-
Sspon.01G0042980-3D	uncharacterized oxidoreductase At4g09670	8,1	Unchanged	-
Sspon.02G0028370-4D	fiber protein Fb19	20,9	Unchanged	-

Sspon.02G0022190-2B	nitrile-specifier protein 5	30,4	Unchanged	-
Sspon.01G0048350-2D	predicted protein	42	Unchanged	-
Sspon.02G0023950-2B	Phosphatidylglycerol/phosphatidylinositol transfer protein	20,8	Unchanged	-
Sspon.03G0022180-1A	eukaryotic translation initiation factor 3 subunit M-like	50,3	Unchanged	-
Sspon.04G0011890-2B	ubiquitin-associated (UBA)/TS-N domain-containing protein	7,1	Unchanged	-
Sspon.03G0023320-1A	phosphoribosylaminoimidazole carboxylase family protein / AIR carboxylase family protein	14,2	Unchanged	-
Sspon.03G0001620-2B	signal recognition particle subunit SRP72-like	16,1	Unchanged	-
Sspon.04G0035140-1P	NADH dehydrogenase 1 alpha subcomplex subunit 9, mitochondrial-like	20,7	Unchanged	-
Sspon.01G0028570-1A	aspartate-semialdehyde dehydrogenase	24	Unchanged	-
Sspon.01G0048030-1B	alpha-expansin 6 precursor	15,8	Unchanged	-
Sspon.01G0008860-3P	hydroxyproline-rich glycoprotein family protein	32,5	Unchanged	-
Sspon.01G0008860-4D	ricin B-like lectin R40C1	64,6	Unchanged	-
Sspon.03G0018250-1A	ricin B-like lectin R40G3	18,6	Unchanged	-
Sspon.02G0034390-2P	eukaryotic peptide chain release factor subunit 1-3-like	12,1	Unchanged	-
Sspon.02G0028010-3C	bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase, chloroplastic isoform X3	20	Unchanged	-
Sspon.03G0033870-1B	shikimate biosynthesis protein aroDE	17,4	Unchanged	-
Sspon.01G0011150-2B	P-loop containing nucleoside triphosphate hydrolase superfamily protein	5,4	Unchanged	-
Sspon.02G0034720-2C	importin-5	7,7	Unchanged	-
Sspon.01G0026900-1A	NADH dehydrogenase iron-sulfur protein 1, mitochondrial	19,2	Unchanged	-
Sspon.02G0026030-4D	eukaryotic translation initiation factor 5A-1/2	34,8	Unchanged	-
Sspon.04G0021450-2T	RNA helicase 2	17,1	Unchanged	-
Sspon.02G0033080-2D	Eukaryotic translation initiation factor 2 subunit beta	18,3	Unchanged	-
Sspon.02G0005080-2P	eukaryotic translation initiation factor 2 subunit gamma	31,1	Unchanged	-
Sspon.03G0012740-1A	elongation factor Ts, mitochondrial	16,1	Unchanged	-
Sspon.02G0034040-1B	elongation factor 1-delta 1	50,2	Unchanged	-
Sspon.01G0008350-3C	3-hydroxybutyryl-CoA dehydratase	30,2	Unchanged	-
Sspon.01G0025100-1A	deoxyuridine 5'-triphosphate nucleotidohydrolase	13,2	Unchanged	-
Sspon.03G0033550-2C	DNA-damage-repair/toleration protein DRT102	8	Unchanged	-
Sspon.03G0000450-2C	Dynamin-related protein 3A	9,3	Unchanged	-
Sspon.01G0056850-1C	Dynamin-related protein 1C	11,3	Unchanged	-
Sspon.03G0035230-3D	sphingosine-1-phosphate lyase	9,7	Unchanged	-
Sspon.04G0015680-1A	protein DNA-DAMAGE INDUCIBLE 1-like isoform X2	22,8	Unchanged	-
Sspon.01G0052770-1P	putative LL-diaminopimelate aminotransferase, chloroplastic	34,8	Unchanged	-
Sspon.01G0044460-3D	cytochrome b5	25,4	Unchanged	-
Sspon.01G0036320-2D	allene oxide synthase	31,8	Unchanged	-
Sspon.04G0011250-1A	peptidyl-prolyl cis-trans isomerase	18,7	Unchanged	-
Sspon.04G0016470-2B	peptidyl-prolyl cis-trans isomerase	42,7	Unchanged	-
Sspon.01G0043790-3D	cyanate hydratase	16,3	Unchanged	-
Sspon.04G0028200-2C	Kynurenine formamidase	17	Unchanged	-
Sspon.01G0017090-3D	Protein CutA 1, chloroplastic	9,8	Unchanged	-
Sspon.03G0020430-3C	triosephosphate isomerase, cytosolic	56,9	Unchanged	-
Sspon.03G0002980-1A	triosephosphate isomerase, cytosolic-like isoform X1	19,8	Unchanged	-
Sspon.04G0015990-1A	citrate synthase 4, mitochondrial-like	42,4	Unchanged	-
Sspon.04G0014600-3C	citrate synthase, glyoxysomal-like	27	Unchanged	-
Sspon.02G0007340-3D	COP9 signalosome complex subunit 7	38,6	Unchanged	-
Sspon.01G0000970-3D	COP9 signalosome complex subunit 1	17,5	Unchanged	-
Sspon.01G0009830-2B	superoxide dismutase 2	8,6	Unchanged	-
Sspon.01G0033710-2P	RuBisCO large subunit-binding protein subunit alpha, chloroplastic	33,6	Unchanged	-
Sspon.01G0019080-1A	chaperonin 60	49	Unchanged	-
Sspon.04G0002180-2D	chaperonin10	23,6	Unchanged	-
Sspon.01G0010410-3C	chaperonin	42,4	Unchanged	-
Sspon.01G0028990-2D	Cytochrome c oxidase subunit 6a, mitochondrial	6,3	Unchanged	-
Sspon.03G0011500-2B	putative cytochrome c oxidase subunit 5b-like	50,6	Unchanged	-
Sspon.03G0005560-1P	Copper transporter 1	8,5	Unchanged	-
Sspon.04G0016830-2C	Chaperone protein ClpB3, mitochondrial	6,3	Unchanged	-
Sspon.03G0010040-4D	Cytosolic isocitrate dehydrogenase	44,2	Unchanged	-
Sspon.02G0021430-1A	protein CIA1	7,6	Unchanged	-
Sspon.01G0053870-1C	CHY1	13	Unchanged	-
Sspon.03G0028600-1B	cysteine proteinase EP-B 2	15,7	Unchanged	-
Sspon.01G0018700-2B	Cell division control protein 48 homolog D	50,4	Unchanged	-
Sspon.01G0002980-1A	Cell division control protein 48 homolog D	42,3	Unchanged	-
Sspon.04G0017920-1A	T-complex protein 1 subunit eta	30,3	Unchanged	-
Sspon.02G0025520-4D	T-complex protein 1 subunit epsilon	24,4	Unchanged	-
Sspon.01G0001060-2B	T-complex protein 1 subunit delta	36	Unchanged	-
Sspon.03G0017690-3C	T-complex protein 1 subunit beta	42,9	Unchanged	-
Sspon.01G0057070-2D	CBS domain-containing protein CBSX3, mitochondrial-like	52,7	Unchanged	-
Sspon.03G0013810-1A	NADH-cytochrome b5 reductase-like protein	29,8	Unchanged	-
Sspon.04G0011010-1A	calmodulin binding protein1	11,4	Unchanged	-
Sspon.04G0017070-1A	calmodulin-binding protein 60 B-like	4,7	Unchanged	-
Sspon.02G0036590-1B	Cathepsin B-like cysteine proteinase 3	26,1	Unchanged	-
Sspon.01G0026910-1A	Exportin-2	14,9	Unchanged	-
Sspon.03G0012910-2B	carbamoyl-phosphate synthase large chain, chloroplastic	8,8	Unchanged	-
Sspon.02G0007270-1A	protein C2-DOMAIN ABA-RELATED 8-like	40,6	Unchanged	-
Sspon.04G0017510-3C	Cullin-associated NEDD8-dissociated protein 1	18,1	Unchanged	-

Sspon.04G0016410-1A	cinnamyl alcohol dehydrogenase 2	6,6	Unchanged	-
Sspon.02G0002630-1P	DExH-box ATP-dependent RNA helicase DEXH12	12,6	Unchanged	-
Sspon.04G0021340-2B	luminal-binding protein	36,3	Unchanged	-
Sspon.03G0015310-3C	dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex	19,7	Unchanged	-
Sspon.01G0031220-1A	NEDD8-activating enzyme E1 regulatory subunit AXR1	30,8	Unchanged	-
Sspon.04G0001370-3D	pyrophosphate-energized vacuolar membrane proton pump-like	14,1	Unchanged	-
Sspon.01G0006220-1P	ATP synthase subunit gamma mitochondrial	23,3	Unchanged	-
Sspon.04G0005220-4D	ATP synthase subunit O, mitochondrial-like	34,3	Unchanged	-
Sspon.03G0009090-3C	splicing factor SF3a60 homolog	6	Unchanged	-
Sspon.01G0022650-2B	Lysine--tRNA ligase cytoplasmic	40,8	Unchanged	-
Sspon.02G0023060-1A	Os07g0189700	12,8	Unchanged	-
Sspon.04G0001470-3C	plastidic aspartate aminotransferase	17,3	Unchanged	-
Sspon.03G0006020-1A	aspartate aminotransferase, cytoplasmic	42,9	Unchanged	-
Sspon.04G0014500-1A	aspartate aminotransferase	41,4	Unchanged	-
Sspon.01G0037840-1B	asparagine synthetase	37,1	Unchanged	-
Sspon.01G0000620-2B	Actin-related protein 4	13,9	Unchanged	-
Sspon.01G0062670-1D	ADP-ribosylation factor	47	Unchanged	-
Sspon.01G0003310-1A	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase 2	47,1	Unchanged	-
Sspon.01G0052180-1P	Chain A, L-ascorbate peroxidase	67,6	Unchanged	-
Sspon.02G0000380-1A	L-ascorbate peroxidase 2, cytosolic	50	Unchanged	-
Sspon.04G0015030-3C	aminopeptidase M1-A	23	Unchanged	-
Sspon.04G0003110-2C	annexin p35	52,5	Unchanged	-
Sspon.02G0015130-1A	Annexin D5	23,1	Unchanged	-
Sspon.02G0013220-3C	alpha-amylase isozyme 3C	19,3	Unchanged	-
Sspon.04G0031260-2D	alpha-amylase precursor	41,2	Unchanged	-
Sspon.02G0015350-3C	alpha-amylase type A isozyme-like	31	Unchanged	-
Sspon.01G0052060-1C	THO complex subunit 4	19,5	Unchanged	-
Sspon.02G0013850-3C	cysteine proteinase 2	17,5	Unchanged	-
Sspon.02G0013900-2C	aldehyde dehydrogenase family 7 member A1	20	Unchanged	-
Sspon.02G0023160-3D	Methylmalonate-semialdehyde dehydrogenase, mitochondrial	32,5	Unchanged	-
Sspon.04G0004330-2B	aldehyde dehydrogenase2	31,1	Unchanged	-
Sspon.02G0037150-2C	Alanine--tRNA ligase	19,2	Unchanged	-
Sspon.02G0003400-3C	alanine aminotransferase 2-like	19	Unchanged	-
Sspon.01G0017210-1T	Alanine aminotransferase 2	64	Unchanged	-
Sspon.03G0045300-1D	putative NADPH-dependent aldo-keto reductase, chloroplastic	3,2	Unchanged	-
Sspon.04G0015700-1A	ADP-ribosylation factor GTPase-activating protein AGD12	4,9	Unchanged	-
Sspon.01G0027980-2D	alcohol dehydrogenase 1	64,2	Unchanged	-
Sspon.01G0029430-3D	actin-depolymerizing factor 6	11,3	Unchanged	-
Sspon.01G0031280-1A	actin-depolymerizing factor 3	64	Unchanged	-
Sspon.03G0029260-2C	actin-7	45,2	Unchanged	-
Sspon.01G0027140-2C	actin-1	53,9	Unchanged	-
Sspon.02G0009020-2B	acyl carrier protein 3	18,3	Unchanged	-
Sspon.01G0002150-4D	Aconitate hydratase 3, mitochondrial-like	25,4	Unchanged	-
Sspon.03G0042170-1C	1-aminocyclopropane-1-carboxylate oxidase 1	26,8	Unchanged	-
Sspon.02G0028800-3C	ATP-citrate synthase alpha chain protein 3	9	Unchanged	-
Sspon.01G0009690-3D	Nuclear cap-binding protein subunit 1	13,4	Unchanged	-
Sspon.01G0062350-1D	zerumbone synthase	12,3	Unchanged	-
Sspon.02G0032500-2B	acetyl-CoA acetyltransferase, cytosolic 1	17,6	Unchanged	-
Sspon.02G0015440-3C	putative acyl-activating enzyme 17 peroxisomal	13,2	Unchanged	-
Sspon.01G0001680-4D	ADP,ATP carrier protein 1, mitochondrial-like	24,5	Unchanged	-
Sspon.04G0022930-3D	adenine nucleotide translocator	21	Unchanged	-
Sspon.04G0002890-2B	2-cys peroxiredoxin BAS1	28,8	Unchanged	-
Sspon.06G0008960-2C	26S proteasome non-ATPase regulatory subunit 1 homolog B	20,3	Unchanged	-
Sspon.05G0010680-3C	26S proteasome non-ATPase regulatory subunit 11 homolog	27,3	Unchanged	-
Sspon.06G0004000-4D	26S proteasome non-ATPase regulatory subunit 3 homolog A	37,1	Unchanged	-
Sspon.06G0009170-2B	26S proteasome non-ATPase regulatory subunit 8	34,5	Unchanged	-
Sspon.07G0028350-2D	2-isopropylmalate synthase 1 chloroplastic	38	Unchanged	-
Sspon.08G0000180-1A	2-oxoglutarate dehydrogenase, mitochondrial-like	25	Unchanged	-
Sspon.05G0009080-1A	2-oxoglutarate-dependent dioxygenase DAO-like	18	Unchanged	-
Sspon.08G0022510-2C	3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplastic	23,5	Unchanged	-
Sspon.05G0002580-1A	40S ribosomal protein S11	37,7	Unchanged	-
Sspon.07G0001500-1A	40S ribosomal protein S12	52,9	Unchanged	-
Sspon.07G0006500-1A	40S ribosomal protein S15a-1	8,8	Unchanged	-
Sspon.05G0030370-1B	40S ribosomal protein S16	20,7	Unchanged	-
Sspon.08G0016200-3D	40S ribosomal protein S20	44,2	Unchanged	-
Sspon.08G0020480-1P	40S ribosomal protein S24	26,3	Unchanged	-
Sspon.06G0004380-4D	40S ribosomal protein S25-1	42,6	Unchanged	-
Sspon.07G0005730-2B	40S ribosomal protein S26	29,5	Unchanged	-
Sspon.06G0010630-4D	40S ribosomal protein S3-3	61,8	Unchanged	-
Sspon.06G0032650-2D	40S ribosomal protein S5	36,4	Unchanged	-
Sspon.06G0004210-1P	60S ribosomal protein L10a-1	40,3	Unchanged	-
Sspon.08G0007670-1A	60S ribosomal protein L11	33,7	Unchanged	-
Sspon.07G0001820-3C	60S ribosomal protein L13-2	42,3	Unchanged	-
Sspon.07G0014870-4D	60S ribosomal protein L13a-4-like	32,5	Unchanged	-
Sspon.05G0007070-4D	60S ribosomal protein L14-1-like	19,3	Unchanged	-

Sspon.06G0002660-1A	60S ribosomal protein L17	37,9	Unchanged	-
Sspon.07G0032650-1C	60S ribosomal protein L18	23,4	Unchanged	-
Sspon.07G0002090-1A	60S ribosomal protein L18a	44,9	Unchanged	-
Sspon.08G0022630-2D	60S ribosomal protein L19-1-like	16,8	Unchanged	-
Sspon.05G0003730-2C	60S ribosomal protein L23a	34,9	Unchanged	-
Sspon.05G0018670-4D	60S ribosomal protein L3	37,8	Unchanged	-
Sspon.05G0003860-1A	60S ribosomal protein L3	40,1	Unchanged	-
Sspon.07G0005360-2B	60S ribosomal protein L30	58	Unchanged	-
Sspon.08G0027020-1C	60S ribosomal protein L31	34,1	Unchanged	-
Sspon.02G0014780-6P	60S ribosomal protein L34	31,1	Unchanged	-
Sspon.06G0003440-2C	60S ribosomal protein L38	36,2	Unchanged	-
Sspon.04G0024940-3D	60S ribosomal protein L6	27,9	Unchanged	-
Sspon.05G0009180-2D	60S ribosomal protein L6	38,8	Unchanged	-
Sspon.05G0003770-4D	60S ribosomal protein L7-2	36,9	Unchanged	-
Sspon.08G0013240-3P	60S ribosomal protein L9	49,5	Unchanged	-
Sspon.08G0024210-1B	6-phosphogluconate dehydrogenase, decarboxylating 1	19,6	Unchanged	-
Sspon.04G0005910-3D	Acetylornithine deacetylase	17,2	Unchanged	-
Sspon.06G0023260-2C	aconitase1	35,3	Unchanged	-
Sspon.07G0007050-2B	actin-1	49,2	Unchanged	-
Sspon.05G0018830-2B	Actin-7	57,8	Unchanged	-
Sspon.07G0016040-2B	actin-97	61,5	Unchanged	-
Sspon.08G0014240-1A	Acyl-coenzyme A oxidase	23,4	Unchanged	-
Sspon.07G0006650-3C	Adenine nucleotide alpha hydrolase-like superfamily protein	23,7	Unchanged	-
Sspon.04G0008080-4D	Adenosine kinase 2	44,4	Unchanged	-
Sspon.06G0013840-2B	adenosylhomocysteinase	53,4	Unchanged	-
Sspon.06G0010370-4P	Adenylate kinase 4	42,7	Unchanged	-
Sspon.07G0037810-1D	Alanine--tRNA ligase	17,8	Unchanged	-
Sspon.05G0016040-3C	alcohol dehydrogenase 1	59,4	Unchanged	-
Sspon.05G0034560-2T	Alcohol dehydrogenase 2	53,6	Unchanged	-
Sspon.05G0010010-2B	aldose 1-epimerase	10,3	Unchanged	-
Sspon.02G0013220-3P	alpha-amylase isozyme 3D-like protein	25,5	Unchanged	-
Sspon.07G0000040-1A	amidophosphoribosyltransferase, chloroplastic-like	18	Unchanged	-
Sspon.08G0011920-1A	aminoacylase-1	7,9	Unchanged	-
Sspon.08G0001950-2B	aminolevulinic acid dehydratase	23	Unchanged	-
Sspon.06G0015030-3C	Aminopeptidase P1	22,7	Unchanged	-
Sspon.06G0003280-1P	Ankyrin repeat domain-containing protein 2A	32,1	Unchanged	-
Sspon.08G0011360-4D	annexin p33	50,2	Unchanged	-
Sspon.05G0015190-3C	Arginase 1 mitochondrial	30,7	Unchanged	-
Sspon.07G0012250-1P	Arginine--tRNA ligase chloroplastic/mitochondrial	17	Unchanged	-
Sspon.07G0037760-1P	Argininosuccinate synthase chloroplastic	20,2	Unchanged	-
Sspon.07G0009550-1T	ASF/SF2-like pre-mRNA splicing factor SRP31	25,1	Unchanged	-
Sspon.08G0010330-1A	asparagine synthetase	13,6	Unchanged	-
Sspon.03G0009670-1P	Aspartic proteinase A1	16	Unchanged	-
Sspon.07G0013790-2B	aspartic proteinase-like	6,4	Unchanged	-
Sspon.08G0016000-2B	AT-hook motif nuclear-localized protein 18-like	6,1	Unchanged	-
Sspon.03G0008800-2P	ATP synthase beta chain	40,7	Unchanged	-
Sspon.06G0004770-3D	ATP synthase subunit d, mitochondrial-like	48,5	Unchanged	-
Sspon.05G0008110-1A	ATP/GTP binding protein	13,3	Unchanged	-
Sspon.07G0029210-1B	Beta-galactosidase 9	5,9	Unchanged	-
Sspon.07G0017510-3D	bifunctional aspartokinase/homoserine dehydrogenase	9,6	Unchanged	-
Sspon.05G0002620-1A	bifunctional purine biosynthesis protein PurH	14,7	Unchanged	-
Sspon.06G0024440-1B	calmodulin	61,5	Unchanged	-
Sspon.05G0012190-3D	calnexin precursor	24,1	Unchanged	-
Sspon.04G0021320-4D	catalase	39,6	Unchanged	-
Sspon.08G0000830-3C	catalase	53,7	Unchanged	-
Sspon.06G0006520-3C	cell division control protein 48 homolog D	4,1	Unchanged	-
Sspon.04G0010760-4D	cell wall invertase	26	Unchanged	-
Sspon.07G0020790-3C	chaperone protein ClpC2, chloroplastic	10,7	Unchanged	-
Sspon.08G0022480-1B	chaperonin	33,3	Unchanged	-
Sspon.07G0003140-3D	Chaperonin CPN60-like 2, mitochondrial	11,1	Unchanged	-
Sspon.08G0024680-2P	chitinase	40,5	Unchanged	-
Sspon.08G0024680-1P	chitinase	40,2	Unchanged	-
Sspon.05G0017040-1A	Chitinase 2	12,2	Unchanged	-
Sspon.04G0008670-1P	chitinase B	48	Unchanged	-
Sspon.06G0027590-1P	chitinase CLP-like	30,2	Unchanged	-
Sspon.06G0027590-1B	chitinase CLP-like	43,7	Unchanged	-
Sspon.07G0027940-1B	Clathrin heavy chain 2 -like protein	34,2	Unchanged	-
Sspon.01G0026820-3D	Coatomer subunit alpha-3	17,7	Unchanged	-
Sspon.06G0001040-4D	COP9 signalosome complex subunit 6a	14,4	Unchanged	-
Sspon.08G0001890-2B	CUE domain containing protein	8,5	Unchanged	-
Sspon.07G0013010-3C	Cullin-1	13,3	Unchanged	-
Sspon.07G0004180-2B	cyclic phosphodiesterase	19	Unchanged	-
Sspon.01G0033960-1A	cystatin	37,3	Unchanged	-
Sspon.01G0040770-2C	cystatin 6 precursor	37,5	Unchanged	-
Sspon.07G0005080-1P	cystatin3	51,4	Unchanged	-
Sspon.05G0001300-1P	cysteine protease 1 precursor	12,1	Unchanged	-

Sspon.07G0012310-2B	cysteine-rich repeat secretory protein 55	26,4	Unchanged	-
Sspon.07G0000980-1A	Cysteine--tRNA ligase 1 cytoplasmic	12,4	Unchanged	-
Sspon.07G0027630-2D	Cytochrome b5	42,9	Unchanged	-
Sspon.05G0026170-1B	Cytochrome b-c1 complex subunit Rieske, mitochondrial	9,5	Unchanged	-
Sspon.06G0004340-1A	Cytochrome c1 1 heme protein mitochondrial	32,5	Unchanged	-
Sspon.05G0002180-1A	D-3-phosphoglycerate dehydrogenase 1, chloroplastic	31,2	Unchanged	-
Sspon.08G0011200-1A	DCD (Development and Cell Death) domain protein	20,3	Unchanged	-
Sspon.06G0016290-2B	defence-related protein precursor	19,1	Unchanged	-
Sspon.07G0015180-1A	dehydroascorbate reductase like3	21,4	Unchanged	-
Sspon.08G0000430-2P	delta(24)-sterol reductase-like	29,3	Unchanged	-
Sspon.07G0018540-4D	Diaminopimelate decarboxylase 2 chloroplastic	23,5	Unchanged	-
Sspon.04G0014970-4D	Dihydrolipoyllysine-residue acetyltransferase component 2 of pyruvate dehydrogenase complex mitochondrial	36,5	Unchanged	-
Sspon.06G0006040-3C	Dihydrolipoyllysine-residue acetyltransferase component 4 of pyruvate dehydrogenase complex chloroplastic	11,3	Unchanged	-
Sspon.07G0019700-2B	Dihydrolipoyllysine-residue acetyltransferase component 5 of pyruvate dehydrogenase complex chloroplastic	12,2	Unchanged	-
Sspon.05G0012560-3C	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	11,7	Unchanged	-
Sspon.05G0004840-2B	dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	12,2	Unchanged	-
Sspon.06G0004460-3C	Dihydroxy-acid dehydratase chloroplastic	22,7	Unchanged	-
Sspon.04G0013430-3D	dipeptidyl aminopeptidase 4-like	5,7	Unchanged	-
Sspon.07G0020390-1A	disease resistance protein RGA2-like isoform X1	4,4	Unchanged	-
Sspon.06G0016210-3D	DJ-1 protein homolog E-like	24,8	Unchanged	-
Sspon.05G0030110-1B	DNA-directed RNA polymerase V subunit 5A-like	13,4	Unchanged	-
Sspon.07G0009630-3T	DUF538 family protein	8,7	Unchanged	-
Sspon.03G0009040-3P	dynammin-related protein 1A	25,1	Unchanged	-
Sspon.07G0009240-1P	Elongation factor 1-alpha	45,3	Unchanged	-
Sspon.02G0008140-1T	elongation factor 1-alpha-like	43,4	Unchanged	-
Sspon.04G0014930-4D	elongation factor 1-gamma 2	35,2	Unchanged	-
Sspon.04G0014930-6P	elongation factor 1-gamma 3	45,3	Unchanged	-
Sspon.05G0031550-2D	endonuclease 2-like	11	Unchanged	-
Sspon.07G0005350-2B	Endoplasmic reticulum vesicle transporter protein	14,1	Unchanged	-
Sspon.08G0001270-3C	Endoplasmin homolog precursor	30,2	Unchanged	-
Sspon.08G0016040-3D	enolase 1	72	Unchanged	-
Sspon.07G0033790-2D	enolase 2	62,6	Unchanged	-
Sspon.08G0003190-2B	ervatamin-B-like	15,8	Unchanged	-
Sspon.05G0027020-1B	eukaryotic peptide chain release factor GTP-binding subunit ERF3A	18,5	Unchanged	-
Sspon.08G0015320-1A	eukaryotic translation initiation factor 1A	33,3	Unchanged	-
Sspon.07G0003290-2D	Eukaryotic translation initiation factor 3 subunit F	22	Unchanged	-
Sspon.06G0012570-3C	eukaryotic translation initiation factor 3 subunit G-like	20,7	Unchanged	-
Sspon.06G0000240-3C	eukaryotic translation initiation factor 6	15,8	Unchanged	-
Sspon.05G0007780-1P	Eukaryotic translation initiation factor isoform 4G-2	23,9	Unchanged	-
Sspon.04G0013020-3D	Fatty acid oxidation complex subunit alpha	15,5	Unchanged	-
Sspon.07G0016700-2B	ferritin	29,4	Unchanged	-
Sspon.08G0026860-1C	formate dehydrogenase 1, mitochondrial	44,3	Unchanged	-
Sspon.06G0012930-3C	fructokinase-2	56	Unchanged	-
Sspon.06G0008490-2B	Galactose mutarotase-like superfamily protein	30	Unchanged	-
Sspon.05G0002790-2C	Gamma-soluble NSF attachment protein	34,6	Unchanged	-
Sspon.06G0016170-1P	GDP-mannose 3,5-epimerase 2	40,7	Unchanged	-
Sspon.08G0014550-2B	GDSL esterase/lipase	22,9	Unchanged	-
Sspon.04G0010070-4D	gibberellin receptor GID1L2	29,4	Unchanged	-
Sspon.01G0024930-1P	globulin-1 S allele-like	34,4	Unchanged	-
Sspon.01G0024930-3D	globulin-1 S allele-like	35,8	Unchanged	-
Sspon.06G0019020-3C	glucan endo-1,3-beta-glucosidase-like	14,1	Unchanged	-
Sspon.05G0006050-1A	glutamic dehydrogenase2	29,9	Unchanged	-
Sspon.05G0007380-3D	glutaredoxin-C6-like	43,8	Unchanged	-
Sspon.07G0013110-1T	glutathione S-transferase 4	26,1	Unchanged	-
Sspon.06G0012300-2B	Glyceraldehyde-3-phosphate dehydrogenase 1, cytosolic	81,3	Unchanged	-
Sspon.08G0001560-1A	Glyceraldehyde-3-phosphate dehydrogenase 1, cytosolic	79,5	Unchanged	-
Sspon.05G0009290-3D	glycerophosphodiester phosphodiesterase GDPDL3	5,2	Unchanged	-
Sspon.04G0024950-1B	glycine-rich cell wall structural protein precursor	27,9	Unchanged	-
Sspon.06G0011710-3C	glycine-rich RNA-binding protein 4, mitochondrial	20,7	Unchanged	-
Sspon.06G0002990-2B	Glycine--tRNA ligase mitochondrial 1	16,8	Unchanged	-
Sspon.05G0012390-4D	Glycine--tRNA ligase, mitochondrial 1	24,6	Unchanged	-
Sspon.08G0018720-2D	Glycosyl hydrolase family 31 protein	18	Unchanged	-
Sspon.06G0013250-3C	GroES-like zinc-binding alcohol dehydrogenase family protein	29,3	Unchanged	-
Sspon.08G0026340-1P	GTP-binding nuclear protein	24	Unchanged	-
Sspon.07G0030170-1C	GTP-binding nuclear protein Ran-2	46,9	Unchanged	-
Sspon.07G0002670-2B	guanine nucleotide-binding protein beta subunit-like protein	65,5	Unchanged	-
Sspon.07G0007790-1A	Guanosine nucleotide diphosphate dissociation inhibitor 2	35,1	Unchanged	-
Sspon.07G0011510-1P	Heat shock 70 kDa protein 14	35,4	Unchanged	-
Sspon.07G0011520-1A	Heat shock protein 4	37,3	Unchanged	-
Sspon.07G0011510-1A	Heat shock protein 4	46	Unchanged	-
Sspon.03G0006720-3P	hexokinase-5	18,7	Unchanged	-

Sspon.07G0011410-3D	hexokinase-7	13,3	Unchanged	-
Sspon.08G0016410-2B	histone H1	46	Unchanged	-
Sspon.06G0022030-3D	hypersensitive-induced response protein 1	22,3	Unchanged	-
Sspon.07G0000350-1A	hypersensitive-induced response protein-like protein 1	21,3	Unchanged	-
Sspon.07G0004450-1A	import inner membrane translocase subunit TIM50	5,1	Unchanged	-
Sspon.03G0010040-3P	isocitrate dehydrogenase	40,2	Unchanged	-
Sspon.05G0007390-1A	isocitrate dehydrogenase-like	25,7	Unchanged	-
Sspon.05G0008810-1A	isocitrate dehydrogenase	17,1	Unchanged	-
Sspon.07G0007940-4D	Isopentenyl-diphosphate Delta-isomerase I	19,7	Unchanged	-
Sspon.03G0010130-1P	ketol-acid reductoisomerase, chloroplastic	30,5	Unchanged	-
Sspon.05G0013800-2B	lactoylglutathione lyase	23,6	Unchanged	-
Sspon.06G0009730-1T	Lactoylglutathione lyase	43,6	Unchanged	-
Sspon.07G0019530-1A	L-ascorbate peroxidase S chloroplastic/mitochondrial	26,6	Unchanged	-
Sspon.04G0010390-3P	L-ascorbate peroxidase S chloroplastic/mitochondrial	31,2	Unchanged	-
Sspon.07G0015170-4D	legumin-like protein	44,7	Unchanged	-
Sspon.05G0001560-1A	Leucine--tRNA ligase, cytoplasmic	14	Unchanged	-
Sspon.06G0002800-1A	lipid transfer protein	14,4	Unchanged	-
Sspon.06G0004330-2D	low molecular weight protein-tyrosine-phosphatase slr0328	7,3	Unchanged	-
Sspon.06G0012450-2B	MA3 DOMAIN-CONTAINING TRANSLATION REGULATORY FACTOR 1-like	29,7	Unchanged	-
Sspon.05G0002290-4D	maize insect resistance3	15,3	Unchanged	-
Sspon.06G0021590-3D	malate dehydrogenase, chloroplastic-like	26,5	Unchanged	-
Sspon.05G0008290-1A	Malate synthase, glyoxysomal	46,3	Unchanged	-
Sspon.07G0008690-1A	Mannosylglycoprotein endo-beta-mannosidase	10,2	Unchanged	-
Sspon.04G0006050-3D	Metal-dependent protein hydrolase	29,7	Unchanged	-
Sspon.06G0030720-2D	methionine aminopeptidase 2B-like	15,3	Unchanged	-
Sspon.06G0029340-1C	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	4,2	Unchanged	-
Sspon.07G0011030-2B	Mitochondrial dicarboxylate/tricarboxylate transporter DTC	18,8	Unchanged	-
Sspon.07G0003890-1A	mitochondrial-processing peptidase subunit alpha-like	18	Unchanged	-
Sspon.05G0009630-4D	MLP-like protein 423	41,8	Unchanged	-
Sspon.06G0004300-2D	monodehydroascorbate reductase-like	29,8	Unchanged	-
Sspon.06G0027390-1P	mRNA splicing factor1	17,1	Unchanged	-
Sspon.05G0002650-2D	myosin-14-like	4,3	Unchanged	-
Sspon.06G0001460-2B	---NA---	37,3	Unchanged	-
Sspon.07G0004670-2B	NAD(P)H dehydrogenase (quinone) FQR1-like	17,2	Unchanged	-
Sspon.05G0010450-1P	NAD(P)-linked oxidoreductase superfamily protein	25,9	Unchanged	-
Sspon.06G0006030-1A	NADH-ubiquinone oxidoreductase 20.9 kDa subunit-like	46,1	Unchanged	-
Sspon.06G0020090-1B	Nascent polypeptide-associated complex alpha subunit-like protein	35,3	Unchanged	-
Sspon.05G0019030-4P	NDR1/HIN1-like protein 1	9,4	Unchanged	-
Sspon.07G0026090-3D	NifU-like protein 4, mitochondrial	10,1	Unchanged	-
Sspon.07G0003490-2B	non-classical arabinogalactan protein 31-like	27,6	Unchanged	-
Sspon.01G0011020-3C	Non-specific lipid transfer protein-like 1	25,3	Unchanged	-
Sspon.06G0020440-3D	Nuclear speckle RNA-binding protein A	26,6	Unchanged	-
Sspon.07G0003200-2B	Nucleosome assembly protein 1	20	Unchanged	-
Sspon.06G0009570-3D	Obg-like ATPase 1	39,6	Unchanged	-
Sspon.06G0009570-2B	Obg-like ATPase 1	39,3	Unchanged	-
Sspon.07G0001540-3C	Oleosin family protein	5,5	Unchanged	-
Sspon.06G0032610-2D	Os11g0484500	24,2	Unchanged	-
Sspon.06G0002940-1A	OVARIAN TUMOR DOMAIN-containing deubiquitinating enzyme 1-like	22	Unchanged	-
Sspon.05G0000400-2D	Oxalate--CoA ligase	11,5	Unchanged	-
Sspon.06G0017440-1A	patatin-like protein 1	18,9	Unchanged	-
Sspon.05G0022560-1P	Pathogenesis-related protein 1	90	Unchanged	-
Sspon.01G0058110-1D	Pathogenesis-related protein 1	55,1	Unchanged	-
Sspon.02G0026770-3C	pentatricopeptide repeat-containing protein At5g64320, mitochondrial	2,8	Unchanged	-
Sspon.07G0006410-1A	Peptidyl-prolyl cis-trans isomerase FKBP20-1	17,2	Unchanged	-
Sspon.08G0017570-1B	Peptidyl-prolyl cis-trans isomerase, microsomal	9,4	Unchanged	-
Sspon.06G0002460-1T	peptidyl-prolyl isomerase	37,8	Unchanged	-
Sspon.08G0009190-4D	peroxidase 1	41,4	Unchanged	-
Sspon.08G0002660-3C	Peroxidase 16	32,2	Unchanged	-
Sspon.04G0011700-2D	peroxidase 2-like	39,2	Unchanged	-
Sspon.07G0014010-1A	peroxidase 2-like	14,8	Unchanged	-
Sspon.08G0018620-2C	Peroxidase 3	10,6	Unchanged	-
Sspon.04G0014420-2P	peroxidase P7	41,2	Unchanged	-
Sspon.04G0016140-2P	Peroxiredoxin-2E-1, chloroplastic	18,4	Unchanged	-
Sspon.05G0030840-1C	peroxisomal (S)-2-hydroxy-acid oxidase GLO3 isoform X2	6,9	Unchanged	-
Sspon.08G0011680-3C	peroxisomal multifunctional enzyme type 2	55,7	Unchanged	-
Sspon.06G0007580-2B	phosphofructose kinase2	37,9	Unchanged	-
Sspon.03G0004290-3C	Phosphoglycerate kinase	19,4	Unchanged	-
Sspon.08G0023270-1B	pleckstrin homology domain containing, family A	48	Unchanged	-
Sspon.05G0007530-2P	polyadenylate-binding protein 2	21,3	Unchanged	-
Sspon.02G0004830-2B	polygalacturonase inhibitor 1 precursor	34,1	Unchanged	-
Sspon.07G0007120-1A	Polypyrimidine tract-binding protein homolog 3	24,2	Unchanged	-
Sspon.05G0001800-3D	predicted protein	42,9	Unchanged	-
Sspon.08G0013830-3D	Pre-mRNA-processing-splicing factor 8A	12,5	Unchanged	-
Sspon.08G0026670-1P	probable aquaporin TIP2-2	10,9	Unchanged	-
Sspon.05G0020050-2B	probable calcium-transporting ATPase 9, plasma membrane-type	8,7	Unchanged	-

Sspon.05G0020050-2P	probable calcium-transporting ATPase 9, plasma membrane-type	9,9	Unchanged	-
Sspon.08G0022550-1B	probable cinnamyl alcohol dehydrogenase 1 isoform X1	9,3	Unchanged	-
Sspon.06G0016180-1P	probable histone H2A variant 3	30,1	Unchanged	-
Sspon.06G0003940-1A	probable L-ascorbate peroxidase 4, peroxisomal	44,7	Unchanged	-
Sspon.07G0019530-2B	probable L-ascorbate peroxidase 6, chloroplastic/mitochondrial	33,6	Unchanged	-
Sspon.05G0005600-3D	probable phospholipid hydroperoxide glutathione peroxidase 6, mitochondrial	16,1	Unchanged	-
Sspon.08G0013210-1A	probable polygalacturonase	16,9	Unchanged	-
Sspon.08G0014800-2B	profilin-2	58	Unchanged	-
Sspon.04G0025040-1P	prohibitin	32,8	Unchanged	-
Sspon.07G0004440-2B	proline iminopeptidase-like	6,9	Unchanged	-
Sspon.08G0000290-1A	Protease 2	14,9	Unchanged	-
Sspon.08G0013780-1A	proteasome subunit alpha type	32,8	Unchanged	-
Sspon.04G0029110-3D	proteasome subunit alpha type 1	49,6	Unchanged	-
Sspon.06G0003910-2B	proteasome subunit alpha type-7-A	28,1	Unchanged	-
Sspon.08G0015870-1A	Proteasome subunit beta type-6	61,2	Unchanged	-
Sspon.06G0016810-2B	protein ALTERED PHOSPHATE STARVATION RESPONSE 1	1,9	Unchanged	-
Sspon.05G0017460-2B	protein disulfide isomerase	42,8	Unchanged	-
Sspon.03G0014720-3P	protein disulfide isomerase7	34,7	Unchanged	-
Sspon.07G0003260-2B	putative aldehyde dehydrogenase MIS1	26,3	Unchanged	-
Sspon.06G0032680-1C	putative alpha-mannosidase	15,3	Unchanged	-
Sspon.07G0005850-3D	Putative aminotransferase class III superfamily protein	24	Unchanged	-
Sspon.06G0009260-4D	Putative aminotransferase class III superfamily protein	18,2	Unchanged	-
Sspon.06G0014070-1T	putative bifunctional methylthioribulose-1-phosphate dehydratase/enolase-phosphatase E1 Methylthioribulose-1-phosphate dehydratase Enolase-phosphatase E1	34,8	Unchanged	-
Sspon.05G0013340-2D	putative inactive purple acid phosphatase 27	13,3	Unchanged	-
Sspon.07G0005770-1A	putative mini-chromosome maintenance (MCM) complex protein family	16,7	Unchanged	-
Sspon.06G0019180-2C	putative proteasome inhibitor	19,9	Unchanged	-
Sspon.08G0013440-2C	Pyrophosphate-energized vacuolar membrane proton pump	14	Unchanged	-
Sspon.08G0010790-2D	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta	29,6	Unchanged	-
Sspon.08G0021760-2C	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta	35,9	Unchanged	-
Sspon.07G0005790-1A	pyruvate decarboxylase 1	16,7	Unchanged	-
Sspon.02G0010620-1P	pyruvate dehydrogenase E1 component subunit beta-1, mitochondrial	25,8	Unchanged	-
Sspon.05G0036690-1C	pyruvate kinase 1, cytosolic	51,4	Unchanged	-
Sspon.05G0000820-3D	pyruvate kinase, cytosolic isozyme	47,6	Unchanged	-
Sspon.07G0008260-1P	pyruvate orthophosphate dikinase1	20,4	Unchanged	-
Sspon.07G0010060-2B	ran-binding protein 1	37,1	Unchanged	-
Sspon.08G0007650-4D	ras-related protein RIC2	32,5	Unchanged	-
Sspon.05G0005050-1A	Replication factor C subunit 4	14,1	Unchanged	-
Sspon.08G0010120-3D	Restorer of fertility2	37,8	Unchanged	-
Sspon.05G0013570-1A	Rhodanese-like domain-containing protein 19 mitochondrial	25,7	Unchanged	-
Sspon.05G0024940-2C	ribosome recycling factor	16,2	Unchanged	-
Sspon.06G0012780-3D	RNA-binding (RRM/RBD/RNP motifs) family protein	34,3	Unchanged	-
Sspon.06G0023150-2C	RNA-binding KH domain-containing protein	18,7	Unchanged	-
Sspon.04G0021090-2D	ruBisCO large subunit-binding protein subunit beta	33,7	Unchanged	-
Sspon.03G0015850-4D	S-adenosylmethionine synthase 1-like isoform X2	33,6	Unchanged	-
Sspon.04G0022010-4P	Serine carboxypeptidase K10B2.2 precursor	11,9	Unchanged	-
Sspon.06G0013830-2B	serine hydroxymethyltransferase	33,3	Unchanged	-
Sspon.06G0032400-1C	sex determination protein tasselseed-2-like	9	Unchanged	-
Sspon.04G0021150-3D	SKP1-like protein 1	28,4	Unchanged	-
Sspon.07G0007080-3P	soluble inorganic pyrophosphatase	28,2	Unchanged	-
Sspon.06G0003710-1T	sorbitol dehydrogenase	44,8	Unchanged	-
Sspon.07G0010190-1P	sorting nexin 2B	2,9	Unchanged	-
Sspon.07G0000580-1A	Spliceosome RNA helicase BAT1 isoform 1	28,1	Unchanged	-
Sspon.07G0016560-1A	stem-specific protein TSJT1-like	24,3	Unchanged	-
Sspon.02G0001270-2D	Stress-related protein-like	21,8	Unchanged	-
Sspon.07G0000690-3C	structural maintenance of chromosomes protein 3-like	10,3	Unchanged	-
Sspon.06G0012970-3D	Succinate dehydrogenase subunit 6, mitochondrial	20,4	Unchanged	-
Sspon.06G0012470-1A	succinate dehydrogenase2	17,3	Unchanged	-
Sspon.04G0008180-1P	Succinate--CoA ligase subunit beta mitochondrial	42,9	Unchanged	-
Sspon.06G0014320-2B	SUMO-activating enzyme subunit 1A	24,3	Unchanged	-
Sspon.04G0016510-4D	SUN domain protein1	13,6	Unchanged	-
Sspon.07G0024880-3D	superoxide dismutase	54,9	Unchanged	-
Sspon.07G0001660-1A	T-complex protein 1 subunit theta	32,3	Unchanged	-
Sspon.06G0016820-1A	Thioredoxin domain-containing protein PLP3B	16,9	Unchanged	-
Sspon.07G0000910-1A	Thioredoxin H-type	54,6	Unchanged	-
Sspon.08G0004210-1A	Thioredoxin O1 mitochondrial	28,8	Unchanged	-
Sspon.08G0009320-2C	thioredoxin-like protein 5	47,1	Unchanged	-
Sspon.06G0011180-1A	transaldolase-like	12,4	Unchanged	-
Sspon.06G0002790-2B	Transmembrane emp24 domain-containing protein p24beta2	35,8	Unchanged	-
Sspon.06G0023950-1P	tyrosyl-tRNA synthetase	23	Unchanged	-
Sspon.05G0020120-3D	ubiquinol-cytochrome c reductase complex 8.0 kDa protein	30,2	Unchanged	-
Sspon.07G0027970-2D	Ubiquitin-activating enzyme E1 2	29	Unchanged	-

Sspon.04G0013370-2D	ubiquitin-conjugating enzyme spm2	57,4	Unchanged	-
Sspon.05G0022650-3D	UBP1-associated protein 2A	17,7	Unchanged	-
Sspon.05G0011080-3C	ultraviolet-B receptor UVR8-like	28,7	Unchanged	-
Sspon.06G0018510-1T	uncharacterized protein LOC101759868	3,6	Unchanged	-
Sspon.06G0005130-4D	uncharacterized protein LOC8083498	35,6	Unchanged	-
Sspon.07G0032490-2D	USP family protein	38,9	Unchanged	-
Sspon.05G0006430-3C	vacuolar-processing enzyme beta-isozyme 1-like	8,1	Unchanged	-
Sspon.06G0010530-4D	Valine--tRNA ligase mitochondrial 1	14,4	Unchanged	-
Sspon.07G0003280-1A	voltage-dependent anion channel protein 2	55,6	Unchanged	-
Sspon.04G0017180-1P	V-type proton ATPase catalytic subunit A	34,2	Unchanged	-
Sspon.07G0017570-4D	V-type proton ATPase subunit C	22,8	Unchanged	-
Sspon.02G0028660-4D	WD repeat-containing protein VIP3-like	25,5	Unchanged	-
Sspon.05G0016310-1A	xylanase inhibitor protein 1	21,1	Unchanged	-
Sspon.02G0041800-3D	xylanase inhibitor protein 1 precursor	36	Unchanged	-
Sspon.02G0026790-4D	xylanase inhibitor protein 1-like	31	Unchanged	-
Sspon.05G0016310-1P	xylanase inhibitor protein 1-like	26	Unchanged	-
Sspon.05G0016310-2C	xylanase inhibitor protein 1-like	30,4	Unchanged	-
Sspon.06G0016650-1T	xylanase inhibitor protein 2-like	31,7	Unchanged	-
Sspon.02G0034570-2C	Protein indeterminate-domain 11	2	Unchanged	-
Sspon.04G0016490-1A	glycine-rich protein 2-like	33,6	Unchanged	-
Sspon.05G0005240-4D	nucleosome/chromatin assembly factor D	16,1	Unchanged	-
Sspon.04G0030800-2D	transcriptional corepressor LEUNIG_HOMOLOG-like isoform X2	4,6	Unchanged	-
Sspon.08G0026570-1C	unnamed protein product	3,8	Unchanged	-
Sspon.04G0013510-1A	DNA binding protein	27	Unchanged	-
Sspon.05G0004600-1A	calcium dependent protein kinase 13	6,6	Unchanged	-
Sspon.05G0008090-2B	cyclin-dependent kinase G-2	4,7	Unchanged	-
Sspon.08G0014700-3D	MAP kinase7	16,1	Unchanged	-
Sspon.08G0008800-1P	G-type lectin S-receptor-like serine/threonine-protein kinase SD2-5	1,5	Unchanged	-
Sspon.02G0042210-1B	Ubiquitin carboxyl-terminal hydrolase 13	14,6	Unchanged	-
Sspon.03G0017470-4D	Syntaxin-22	7,4	Unchanged	-
Sspon.02G0035070-2C	vesicle-associated protein 4-2-like	4,8	Unchanged	-
Sspon.01G0004170-1A	adenylosuccinate synthetase	25,2	Unchanged	-
Sspon.01G0012640-2D	putative ubiquitin conjugation factor E4	5,8	Unchanged	-
Sspon.01G0012990-1A	pyruvate, phosphate dikinase 2 isoform X1	19,4	Unchanged	-
Sspon.01G0026990-1A	Protein POLLEN DEFECTIVE IN GUIDANCE 1	9,1	Unchanged	-
Sspon.01G0026860-2D	phosphoglucomutase1	33,9	Unchanged	-
Sspon.03G0025530-2B	protein MLN51 homolog	1,5	Unchanged	-
Sspon.04G0012290-2B	fructose-bisphosphate aldolase 1, cytoplasmic	58,7	Unchanged	-
Sspon.03G0036420-2C	acyl-protein thioesterase 2	22	Unchanged	-
Sspon.04G0003680-2C	melanoma-associated antigen 1 isoform X2	19,9	Unchanged	-
Sspon.02G0030260-1A	negatively light-regulated protein	23,6	Unchanged	-
Sspon.01G0030480-3C	exocyst complex component EXO84B	2,3	Unchanged	-
Sspon.01G0051950-1P	SART-1 family protein DOT2	1,9	Unchanged	-
Sspon.01G0035900-2P	T-complex protein 1 subunit gamma	22	Unchanged	-
Sspon.04G0026410-1B	autophagy-related protein 101-like isoform X1	4,7	Unchanged	-
Sspon.04G0012270-3D	40S ribosomal protein S27	14,4	Unchanged	-
Sspon.05G0033160-2D	60S acidic ribosomal protein P2A-like	76,8	Unchanged	-
Sspon.08G0002100-2B	60S acidic ribosomal protein P3	44,5	Unchanged	-
Sspon.06G0023260-3D	aconitase1	31,7	Unchanged	-
Sspon.07G0005270-4D	Calmodulin	57	Unchanged	-
Sspon.07G0008660-4D	E3 ubiquitin-protein ligase KEG	1	Unchanged	-
Sspon.06G0012920-2B	EMBRYO DEFECTIVE 140	11,7	Unchanged	-
Sspon.07G0033790-1C	enolase 2	66,2	Unchanged	-
Sspon.07G0010050-3C	ERBB-3 BINDING PROTEIN 1	42,6	Unchanged	-
Sspon.04G0018470-2B	eukaryotic initiation factor 4A-3	50,1	Unchanged	-
Sspon.06G0000720-2C	Heterogeneous nuclear ribonucleoprotein 1	10,5	Unchanged	-
Sspon.06G0006110-4D	HMG-Y-related protein A	46,3	Unchanged	-
Sspon.05G0000450-2D	K(+) efflux antiporter 2 chloroplastic	2,8	Unchanged	-
Sspon.05G0021500-3D	mRNA turnover protein 4	11,7	Unchanged	-
Sspon.05G0000210-2C	nudix hydrolase 26, chloroplastic-like	5,1	Unchanged	-
Sspon.07G0007390-2B	patellin-3-like	19,8	Unchanged	-
Sspon.05G0001970-2B	Plasma membrane ATPase	24,8	Unchanged	-
Sspon.08G0014730-1P	Proteasome subunit beta type	35	Unchanged	-
Sspon.07G0009230-2D	Protein BONZAI 3	7	Unchanged	-
Sspon.08G0013000-1P	Protein MEI2-like 5	1,4	Unchanged	-
Sspon.07G0000790-2C	Pseudouridine synthase family protein	6,6	Unchanged	-
Sspon.07G0006270-2B	putative mediator of RNA polymerase II transcription subunit 37c	40,8	Unchanged	-
Sspon.08G0003760-4D	RING/U-box superfamily protein	1,8	Unchanged	-
Sspon.01G0038980-2C	RNA-binding (RRM/RBD/RNP motifs) family protein	26	Unchanged	-
Sspon.01G0027920-1A	Serine/threonine-protein kinase TOR	9,1	Unchanged	-
Sspon.06G0017840-3C	sister-chromatid cohesion protein 3	7,3	Unchanged	-
Sspon.08G0022540-2C	Sucrose synthase 1	27,1	Unchanged	-
Sspon.05G0006700-2B	uncharacterized protein LOC8082862	4,5	Unchanged	-
Sspon.02G0028160-2B	Uveal autoantigen with coiled-coil domains and ankyrin repeats isoform 4	16,3	Unchanged	-
Sspon.03G0008250-1A	VIP1 protein	15,8	Unchanged	-
Sspon.02G0015770-2B	VQ motif-containing protein	2,7	Unchanged	-

Sspon.03G0029130-1B	protein PSK SIMULATOR 1-like	2,3	Down	-
Sspon.03G0024550-1T	P-loop containing nucleoside triphosphate hydrolase superfamily protein	5,1	Down	-
Sspon.07G0019280-2D	CBS domain containing protein	5,3	Down	-
Sspon.01G0032930-1P	ankyrin repeat and SAM domain-containing protein 6-like	7,5	Down	-
Sspon.04G0016190-3C	protein FLX-like 2	4,4	Down	-
Sspon.01G0049940-1B	DEAD-box ATP-dependent RNA helicase 8	12,1	Down	-
Sspon.02G0032530-3D	ATPase 11 plasma membrane-type-related	16,8	Down	-
Sspon.02G0036520-2C	pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16	8,8	Down	-
Sspon.08G0005310-2C	Zinc finger C-x8-C-x5-C-x3-H type family protein	2,7	Down	-
Sspon.04G0014010-4D	protein RDM16	1,5	Down	-
Sspon.01G0007930-2B	enhancer of zeste3	3,6	Down	-
Sspon.02G0018830-3C	Structure and catalytic mechanism of monodehydroascorbate reductase, MDHAR, from <i>Oryza sativa</i> L. japonica	30,3	Down	-
Sspon.06G0010720-3D	ramosa 1 enhancer locus 2	22,2	Down	-
Sspon.05G0013520-1A	SNARE-interacting protein KEULE	2,4	Down	-
Sspon.04G0007530-1A	unnamed protein product	9,4	Down	-
Sspon.02G0015630-1A	RNA ligase/cyclic nucleotide phosphodiesterase family protein	9,8	Down	-
Sspon.02G0021920-2C	Peroxidase 1	17,2	Down	-
Sspon.04G0001130-3D	Proliferating cell nuclear antigen	51,3	Down	-
Sspon.02G0018440-3C	Calcium-dependent lipid-binding (CaLB domain) family protein	30,2	Down	-
Sspon.03G0003060-2C	osmotin-like protein precursor	45,8	Down	-
Sspon.04G0013460-1T	cinnamoyl-CoA reductase-like protein 2	39,8	Down	-
Sspon.02G0021530-2B	calreticulin	36,1	Down	-
Sspon.08G0003560-3C	40S ribosomal protein S14	49,3	Down	-
Sspon.08G0012290-1A	40S ribosomal protein S17-4	39,5	Down	-
Sspon.07G0003170-1A	60S ribosomal protein L28-1	43,8	Down	-
Sspon.04G0006710-4D	Aquaporin PIP1-2	6,6	Down	-
Sspon.04G0009800-4D	NAP1-related protein 2	42,6	Down	-
Sspon.08G0014990-1A	Nucleosome assembly protein 1	20,5	Down	-
Sspon.06G0020430-1B	Proline--tRNA ligase cytoplasmic	41,4	Down	-
Sspon.08G0011050-3C	pro-resilin precursor	22,6	Down	-
Sspon.06G0000200-2D	puromycin-sensitive aminopeptidase	25,8	Down	-
Sspon.08G0016530-2B	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	17,4	Down	-
Sspon.08G0022540-3D	Sucrose synthase 1	37,1	Down	-
Sspon.05G0012970-3C	uncharacterized LOC100277287	33,8	Down	-
Sspon.03G0005570-3C	Topoisomerase II-associated protein PAT1	1,1	Down	-
Sspon.03G0004220-4D	cysteine proteinase inhibitor	31	Down	-
Sspon.05G0011390-2D	40S ribosomal protein S10-1	29,7	Down	-
Sspon.05G0000700-2T	clathrin light chain 1-like	12,4	Down	-
Sspon.04G0025590-2D	NF-180	10,8	Down	-
Sspon.07G0000580-3C	Spliceosome RNA helicase BAT1 isoform 1	41,6	Down	-
Sspon.03G0020370-1A	Transcription elongation factor (TFIIS) family protein	4,4	-	-
Sspon.01G0011270-1A	Splicing factor, arginine/serine-rich 2	5,6	-	-
Sspon.01G0035370-2C	nuclear pore complex protein NUP96	2,5	-	-
Sspon.01G0017490-2C	endonuclease/Exonuclease/phosphatase family protein	3,8	-	-
Sspon.03G0040490-2D	myosin heavy chain-related	1,6	-	-
Sspon.04G0007600-1A	pre-mRNA-processing ATP-dependent RNA helicase prp5	2,8	-	-
Sspon.08G0001590-3C	midasin	2,1	-	-
Sspon.02G0004860-3D	Zinc finger CCCH domain-containing protein 50	1,6	-	-
Sspon.07G0003620-2D	CCCH transcription factor	4,9	-	-
Sspon.07G0005250-4D	myb family transcription factor PHL7-like	7,5	-	-
Sspon.03G0030130-2C	transcription factor GAMYB	3,5	-	-
Sspon.03G0000150-1A	cell division cycle 5-like protein	10,2	-	-
Sspon.06G0004620-1A	putative kinase-like protein TMKL1	1,5	-	-
Sspon.01G0007870-3D	LRR receptor-like serine/threonine-protein kinase FEI 1	5,6	-	-
Sspon.05G0016020-2B	mitogen-activated protein kinase kinase kinase 3	4,3	-	-
Sspon.02G0030220-3D	extra-large guanine nucleotide-binding protein 1	2,7	-	-
Sspon.03G0006540-1A	VQ motif-containing protein 4-like	6,2	-	-
Sspon.03G0026510-2D	Villin-2	12,7	-	-
Sspon.01G0003730-1A	DNA topoisomerase 3-alpha	2,9	-	-
Sspon.04G0001790-2B	probable serine incorporator	3,6	-	-
Sspon.04G0001790-4D	Serinc-domain containing serine and sphingolipid biosynthesis protein	6,2	-	-
Sspon.04G0030650-1C	TBC1 domain family member 22A	2,8	-	-
Sspon.02G0003570-2B	DUF1677 family protein	13,2	-	-
Sspon.02G0036650-2C	Serine/arginine-rich splicing factor SR45a	10,9	-	-
Sspon.03G0027240-2C	Protein kinase superfamily protein	11,7	-	-
Sspon.01G0052130-1P	Ankyrin repeat-containing protein ITN1	2,1	-	-
Sspon.01G0020130-4D	RING/U-box superfamily protein	2,3	-	-
Sspon.03G0028780-3D	Formin-like protein 1	3,2	-	-
Sspon.01G0024650-2C	unnamed protein product	9,2	-	-
Sspon.01G0056510-2D	protein SOSEKI 2-like	5,5	-	-
Sspon.03G0030920-2C	putative calcium-binding protein CML41	8,4	-	-
Sspon.02G0044580-3D	boron transporter 1	2	-	-
Sspon.01G0055130-1C	Serine/threonine protein phosphatase 2A regulatory subunit B"alpha	8	-	-
Sspon.03G0026850-3D	Serine/arginine repetitive matrix protein 2 isoform 4	1	-	-

Sspon.02G0028420-3C	Chaperone protein dnaJ 15	8,1	-	-
Sspon.08G0000560-2C	Calcium-binding EF hand family protein	4,2	-	-
Sspon.08G0007050-2B	Histone deacetylase 11	7,8	-	-
Sspon.08G0012140-2B	Mechanosensitive ion channel protein 10	3,1	-	-
Sspon.07G0012590-1A	mediator of RNA polymerase II transcription subunit 28-like	16,9	-	-
Sspon.07G0003030-1T	mov34/MPN/PAD-1 family protein	7,5	-	-
Sspon.06G0004510-2B	Protein UPSTREAM OF FLC	2,8	-	-
Sspon.08G0010430-1A	putative 1-phosphatidylinositol-3-phosphate 5-kinase FAB1C	3,6	-	-
Sspon.06G0011120-1T	RNA polymerase II large subunit family protein	2,4	-	-
Sspon.05G0001820-1P	serine/arginine repetitive matrix protein 2 isoform X2	1	-	-
Sspon.07G0012280-4D	serine/arginine-rich splicing factor RS2Z33	4,1	-	-
Sspon.06G0000480-3C	Serine/arginine-rich splicing factor SC35	6,6	-	-
Sspon.05G0037510-1D	uncharacterized abhydrolase domain-containing protein DDB_G0269086-like	1,9	-	-
Sspon.05G0012530-1A	zinc finger CCCH domain-containing protein 27-like	8,4	-	-
Sspon.01G0027830-1A	putative LRR receptor-like serine/threonine-protein kinase	1,8	-	-
Sspon.02G0019470-2B	putative serine/threonine-protein kinase WNK3	4	-	-
Sspon.03G0009320-1A	P-loop containing nucleoside triphosphate hydrolase superfamily protein	2,5	-	-
Sspon.01G0035430-3D	origin recognition complex subunit 2	4,8	-	-
Sspon.03G0005390-1T	Vps51/Vps67 family (components of vesicular transport) protein	1,1	-	-
Sspon.07G0022560-1P	homeobox2	8,8	-	-
Sspon.05G0025570-1T	peptidyl-prolyl cis-trans isomerase FKBP53	14,9	-	-
Sspon.03G0037330-3D	uncharacterized protein LOC8081378 isoform X1	7,1	-	-
Sspon.03G0037330-2C	uncharacterized protein LOC8081378 isoform X1	8,2	-	-
Sspon.02G0009710-2B	Homeodomain leucine zipper family IV protein	3,4	-	-
Sspon.07G0011500-1P	chromatin complex subunit A	3	-	-
Sspon.02G0042090-1B	BTB/POZ and MATH domain-containing protein 4	2,8	-	-
Sspon.02G0036030-3D	trihelix transcription factor ASIL2-like	5,1	-	-
Sspon.02G0014690-1A	ZF-HD homeobox protein	9,4	-	-
Sspon.01G0030900-1P	Protein kinase domain	2,1	-	-
Sspon.06G0003120-1A	Chitin elicitor receptor kinase 1	3,3	-	-
Sspon.01G0030390-3D	Actin cross-linking protein	4,1	-	-
Sspon.01G0042830-3D	Putative WEB family protein chloroplastic	1,4	-	-
Sspon.01G0021810-2B	Putative E3 ubiquitin-protein ligase RING1a	6,3	-	-
Sspon.01G0030850-2B	remorin 4.1-like	4,7	-	-
Sspon.02G0019410-3P	aquaporin PIP2-6	3,1	-	-
Sspon.07G0025720-1P	Calcium-dependent lipid-binding (CaLB domain) family protein	6,1	-	-
Sspon.02G0047570-1C	protein IQ-DOMAIN 1-like	4,3	-	-
Sspon.03G0022310-1P	type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2	1,8	-	-
Sspon.04G0015140-2P	RPD3 histone deacetylase-like protein	10	-	-
Sspon.03G0026000-1B	putative leucine-rich repeat-containing protein DDB_G0290503	0,9	-	-
Sspon.02G0006280-2B	cysteine-rich receptor-like protein kinase 10	3,6	-	-
Sspon.04G0004560-3C	neutral/alkaline invertase	6,5	-	-
Sspon.02G0039360-1P	histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20specific	7,4	-	-
Sspon.03G0019170-2B	SLL2	7,4	-	-
Sspon.06G0003220-4D	14-3-3-like protein GF14-C	69,9	-	-
Sspon.05G0005980-4D	ELMO domain-containing protein A	5,6	-	-
Sspon.07G0013420-3D	Inosine triphosphate pyrophosphatase	12,4	-	-
Sspon.08G0005950-3C	Microtubule-associated protein MAP65-1a	8,6	-	-
Sspon.08G0024630-1C	monosaccharide-sensing protein 2-like isoform X1	7,4	-	-
Sspon.01G0000470-2B	Myosin heavy chain-related protein	1,6	-	-
Sspon.05G0010950-4D	nuclear speckle splicing regulatory protein 1-like	13,5	-	-
Sspon.01G0044620-1B	Pentatricopeptide repeat-containing protein	2,2	-	-
Sspon.04G0003600-3C	putative auxin efflux carrier	8,6	-	-
Sspon.05G0001670-2C	RNA recognition water-stress protein1	10,3	-	-
Sspon.05G0008440-3D	Steroid nuclear receptor ligand-binding	2	-	-
Sspon.07G0011120-1A	Translocase of chloroplast 159 chloroplastic	4,7	-	-
Sspon.07G0029110-1B	trihelix transcription factor	2,7	-	-
Sspon.05G0025680-1P	U-box domain-containing protein 33	1,3	-	-
Sspon.02G0036840-1B	unnamed protein product	4,1	-	-
Sspon.05G0001290-1A	unnamed protein product	2,3	-	-
Sspon.08G0022970-1P	probable protein phosphatase 2C 54	2,6	-	-
Sspon.02G0038070-1B	Protein TIFY 6b	3,3	-	-
Sspon.01G0060750-1D	putative WRKY transcription factor 74	2,4	-	-
Sspon.01G0023740-1P	protein WRKY1-like	2,2	-	-
Sspon.02G0009270-2B	serine/threonine-protein kinase NAK	2,6	-	-
Sspon.08G0012270-2B	Serine/threonine-protein kinase RIPK	2,1	-	-
Sspon.02G0018760-2B	Single-stranded nucleic acid binding R3H protein	4,9	-	-
Sspon.01G0040480-1B	Ca2+/calmodulin-dependent protein kinase phosphatase	3,1	-	-
Sspon.03G0011960-3C	Serine/threonine protein phosphatase 2A 55 kDa regulatory subunit B beta isoform	4,6	-	-
Sspon.01G0036140-2C	Protein OBERON 4	0,6	-	-
Sspon.02G0014480-4D	probable monogalactosyldiacylglycerol synthase 1, chloroplastic	1,3	-	-
Sspon.03G0036100-1B	Golgi to ER traffic protein 4 homolog isoform X1	3,3	-	-
Sspon.03G0029290-1P	unnamed protein product	3,9	-	-

Sspon.01G0019680-3C	RING/U-box superfamily protein	7,2	-	-
Sspon.04G0012250-2B	Polyadenylate-binding protein-interacting protein 3	2,3	-	-
Sspon.08G0020140-3D	MAPK kinase substrate protein At1g80180-like	10,3	-	-
Sspon.06G0004940-1T	nitrate reductase	2,3	-	-
Sspon.06G0004940-2B	nitrate reductase	1,4	-	-
Sspon.06G0002350-3C	oligopeptide transporter-like protein	4,9	-	-
Sspon.05G0033360-2D	Protein AUXIN SIGNALING F-BOX 3	1,6	-	-
Sspon.08G0001160-3D	Protein FREE1	3,6	-	-
Sspon.07G0005840-1A	protein transporter	4,1	-	-
Sspon.07G0027030-2C	protein-tyrosine-phosphatase MKP1	1,1	-	-
Sspon.05G0016000-2B	Putative phosphatidylinositol kinase	1	-	-
Sspon.06G0010190-1A	sec34-like family protein	7,6	-	-
Sspon.07G0014850-2B	Serine/arginine-rich splicing factor RS2Z32	20,5	-	-
Sspon.08G0019100-1B	Ypt/Rab-GAP domain of gyp1p superfamily protein	3,1	-	-
Sspon.03G0014450-1A	Basic leucine zipper 25	4,4	-	-
Sspon.02G0033160-1B	Transcription factor RF2b	4,8	-	-
Sspon.04G0004590-2B	Zinc finger protein CONSTANS-LIKE 9	2	-	-
Sspon.07G0009010-3C	CCT motif family protein	4,8	-	-
Sspon.05G0008360-2B	glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform-like	5,9	-	-
Sspon.08G0001620-1T	protein SHI RELATED SEQUENCE 1	18,8	-	-
Sspon.04G0016270-3D	protein STRUBBELIG-RECEPTOR FAMILY 8	1,3	-	-
Sspon.08G0022930-2C	serine/threonine-protein kinase ste20 isoform X1	7,6	-	-
Sspon.03G0035570-2C	putative ubiquitin-conjugating enzyme E2 23	2,5	-	-
Sspon.03G0023370-1A	Nuclear pore complex protein NUP35	3,4	-	-
Sspon.01G0036290-1B	Nuclear pore complex protein NUP133	2,8	-	-
Sspon.02G0028810-2B	modifier of snc1	0,9	-	-
Sspon.03G0005070-1A	Mitotic spindle checkpoint protein MAD1	2,1	-	-
Sspon.01G0035870-1P	nucleotidyltransferase	1,2	-	-
Sspon.01G0054390-1C	Outer arm dynein light chain 1 protein	1,2	-	-
Sspon.02G0028510-3D	transmembrane protein 205-like	5,7	-	-
Sspon.04G0021430-1P	ARM repeat superfamily protein	3,1	-	-
Sspon.01G0035970-2D	homerin isoform X1	3,4	-	-
Sspon.04G0011870-2B	exocyst complex component EXO70A1-like	1,5	-	-
Sspon.01G0012130-1A	Protein ELF4-LIKE 4	9,5	-	-
Sspon.01G0038040-2D	Calcium-binding protein CML42	24,4	-	-
Sspon.02G0035690-2C	Calmodulin-binding transcription activator 5	1,3	-	-
Sspon.02G0003150-1A	Calmodulin-binding transcription activator 2	6,1	-	-
Sspon.02G0014140-1A	protein binding protein	5,7	-	-
Sspon.01G0052070-1P	probable ADP-ribosylation factor GTPase-activating protein AGD6	3,5	-	-
Sspon.02G0003810-3C	ninja-family protein 5	3,6	-	-
Sspon.06G0015720-1A	E3 ubiquitin-protein ligase RHF2A	3,5	-	-
Sspon.05G0008790-3D	eukaryotic translation initiation factor 4B	16,4	-	-
Sspon.08G0017950-2C	exocyst complex component EXO70A1-like	3,2	-	-
Sspon.08G0001630-2D	NF-E2 inducible protein-like	2	-	-
Sspon.06G0003780-1A	Plant UBX domain-containing protein 8	9,5	-	-
Sspon.05G0013160-3C	Sterile alpha motif (SAM) domain-containing protein	14,7	-	-
Sspon.07G0019040-1A	Transducin/WD40 repeat-like superfamily protein	6,8	-	-
Sspon.04G0036150-1D	unnamed protein product	7,9	-	-
Sspon.08G0001790-3C	WAT1-related protein At5g45370-like	4,1	-	-
Sspon.03G0008770-2D	arginine/serine-rich coiled coil protein 1	2,9	-	-
Sspon.02G0033590-1B	Serine/arginine-rich SC35-like splicing factor SCL33	8,2	-	-
Sspon.05G0014330-3C	phosphoglycerate mutase family protein	7,2	-	-
Sspon.06G0015210-2C	unnamed protein product	6,7	-	-
Sspon.02G0031260-3C	nuclear transcription factor Y subunit A-7	4,3	-	-
Sspon.07G0009290-2B	Protein kinase superfamily protein	4,5	-	-
Sspon.03G0010650-3C	Protein kinase superfamily protein	5	-	-
Sspon.03G0007480-1P	mitogen-activated protein kinase kinase 1-like	6,2	-	-
Sspon.07G0032640-1C	salt-inducible protein kinase	6	-	-
Sspon.04G0002670-3C	THO complex subunit 5B	2,8	-	-
Sspon.01G0048200-2D	SCAR-like protein 1 isoform X1	8,2	-	-
Sspon.01G0027580-2B	Os03g0724500	16,7	-	-
Sspon.01G0047350-1B	COP1-interacting protein-related	2,3	-	-
Sspon.01G0003420-1A	XS domain containing protein expressed	8,5	-	-
Sspon.02G0004820-1A	uncharacterized protein LOC8083896	1,5	-	-
Sspon.01G0041320-2C	DnaJ homolog subfamily C GRV2	0,9	-	-
Sspon.01G0005570-1A	peptidyl-prolyl cis-trans isomerase CYP65	2	-	-
Sspon.01G0043200-1B	calcium-dependent protein kinase 3	2,2	-	-
Sspon.04G0009220-1A	chloride channel	1,1	-	-
Sspon.02G0005150-1P	HOPM interactor 7	4,5	-	-
Sspon.02G0042010-1B	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein	5,4	-	-
Sspon.07G0030090-2D	auxin-like 1 protein	1,4	-	-
Sspon.01G0042110-2D	Coilin	5,2	-	-
Sspon.07G0033930-2D	E3 ubiquitin-protein ligase UPL1	10,4	-	-
Sspon.08G0005120-1A	formamidopyrimidine-DNA glycosylase	3,5	-	-
Sspon.07G0012190-4D	fructose-6-phosphate-2-kinase/fructose-2,6-bisphosphatase	1,4	-	-

Sspon.05G0003670-3C	Gamma-tubulin complex component 2	1,3	-	-
Sspon.05G0029560-1B	---NA---	6,1	-	-
Sspon.07G0022500-3D	oxidative stress 3	6,5	-	-
Sspon.06G0017190-2C	Phosphatidate phosphatase PAH2	2,4	-	-
Sspon.07G0023140-3D	PLAC8 family protein	1,4	-	-
Sspon.08G0013000-3C	Protein MEI2-like 5	6	-	-
Sspon.05G0001580-3D	putative plastid-lipid-associated protein 13 chloroplastic	11	-	-
Sspon.07G0016080-2C	unnamed protein product	1,8	-	-
Sspon.05G0025730-1B	zinc-finger homeodomain protein 8-like	4,3	-	-
Sspon.03G0027700-2C	coiled-coil domain-containing protein SCD2-like	3,8	-	-
Sspon.03G0006070-2B	Putative HCNGP-related transcriptional regulator family protein	5,7	-	-
Sspon.07G0002130-1A	Guanylate-binding family protein	7,9	-	-
Sspon.08G0008210-1T	intracellular protein transport protein USO1-related	6,4	-	-
Sspon.03G0044130-2D	protein indeterminate-domain 7	3,7	-	-
Sspon.02G0017090-2C	myb family transcription factor-related protein	6,4	-	-
Sspon.06G0003160-1A	Retinoblastoma-related protein 1	3,3	-	-
Sspon.03G0021000-2B	kinesin-like protein KIF27	3	-	-
Sspon.04G0002790-2C	Methionine aminopeptidase 1D chloroplastic/mitochondrial	3,3	-	-
Sspon.02G0029350-1A	unnamed protein product	4,6	-	-
Sspon.03G0012600-2B	selT/selW/selH selenoprotein domain containing protein	8,3	-	-
Sspon.01G0002270-4D	splicing factor U2af large subunit B-like	0,7	-	-
Sspon.02G0013960-1A	putative polygalacturonase	3	-	-
Sspon.04G0005180-1A	protein CROWDED NUCLEI 1	13,7	-	-
Sspon.08G0003280-1A	Auxin-independent growth promoter-like protein, mRNA	8,3	-	-
Sspon.06G0015690-2B	lymphoid organ expressed yellow head virus receptor protein	4,7	-	-
Sspon.06G0012450-1A	MA3 DOMAIN-CONTAINING TRANSLATION REGULATORY FACTOR 1-like	31,4	-	-
Sspon.05G0015400-2B	Phosphoglycerate mutase-like protein	4	-	-
Sspon.05G0008970-1A	Plant intracellular Ras-group-related LRR protein 3	12,9	-	-
Sspon.03G0008190-1A	retinitis pigmentosa 1-like 1 protein	16,8	-	-
Sspon.06G0019900-3D	uncharacterized protein LOC8062431	5,2	-	-
Sspon.04G0019230-2C	beta-amylase 8 isoform X2	2,4	-	-
Sspon.07G0011300-1A	Zinc finger CCCH domain-containing protein 35	3,8	-	-
Sspon.05G0001240-2D	Zinc finger C-x8-C-x5-C-x3-H type family protein	3,2	-	-
Sspon.02G0037080-2C	DNA-binding bromodomain-containing protein	1,1	-	-
Sspon.01G0008840-4P	NAC transcription factor	4,1	-	-
Sspon.07G0008640-3D	Putative cyclin-dependent kinase family protein	2,6	-	-
Sspon.01G0017620-4D	Protein kinase 2B chloroplastic	4,4	-	-
Sspon.03G0004340-1A	putative E3 ubiquitin-protein ligase RING1a isoform X1	1,9	-	-
Sspon.03G0029190-1B	DNA polymerase alpha catalytic subunit	0,4	-	-
Sspon.04G0023700-1B	N6-adenosine-methyltransferase MT-A70-like protein	6,4	-	-
Sspon.02G0021640-3C	protein phosphatase inhibitor 2-like isoform X1	22,3	-	-
Sspon.01G0025570-3C	histone H3.v1	3,3	-	-
Sspon.04G0027410-1B	putative pre-mRNA-splicing factor cwc-22	2,9	-	-
Sspon.07G0030600-2D	KH domain-containing protein	5	-	-
Sspon.02G0034070-1P	DGCR14 protein	2	-	-
Sspon.03G0011150-1A	Extra-large G-protein-like	1,8	-	-
Sspon.01G0030140-1A	putative zinc metalloprotease EGY1 chloroplastic	1,1	-	-
Sspon.01G0053850-2D	Transcriptional adapter ADA2b	1,8	-	-
Sspon.08G0008970-2B	AT-hook motif nuclear-localized protein 10	2,5	-	-
Sspon.05G0002390-1A	Crossover junction endonuclease EME1B	2,1	-	-
Sspon.06G0013200-3D	DNA-binding bromodomain-containing protein	2,3	-	-
Sspon.05G0005950-3D	DNAJ heat shock N-terminal domain-containing protein	5,6	-	-
Sspon.06G0029200-1C	exocyst complex component EXO70B1-like	2	-	-
Sspon.04G0013830-3D	intracellular protein transport protein USO1-related	6	-	-
Sspon.05G0005310-1A	lysine histidine transporter-like 8	3	-	-
Sspon.04G0008810-4D	protein phosphatase inhibitor 2	12,6	-	-
Sspon.03G0004340-2B	Putative E3 ubiquitin-protein ligase RING1a	2,7	-	-
Sspon.08G0010450-2B	unnamed protein product	7,2	-	-
Sspon.05G0006340-1A	Vesicle-associated protein 1-1	9,7	-	-
Sspon.01G0021790-2B	Serinc-domain containing serine and sphingolipid biosynthesis protein	6,5	-	-
Sspon.01G0008570-1A	protein ROLLING AND ERECT LEAF 2-like	3,1	-	-
Sspon.02G0007350-1A	RanBP2-type zinc finger protein	5,9	-	-
Sspon.02G0011270-1P	chaperone protein dnaJ 10	5,7	-	-
Sspon.05G0012470-1A	histone H2A.Z-specific chaperone CHZ1-like	17	-	-
Sspon.06G0014860-3C	Retinoblastoma-related protein 1	12,3	-	-
Sspon.02G0012440-2P	Methyl-CpG-binding domain-containing protein 8	1,2	-	-
Sspon.03G0017350-1T	zinc finger CCCH type domain-containing protein ZFN-like 1	3,6	-	-
Sspon.03G0000320-3D	Calmodulin-binding transcription activator 4	1,1	-	-
Sspon.07G0007610-3C	scarecrow-like protein 1	5	-	-
Sspon.03G0031530-1B	Putative casein kinase family protein	4,7	-	-
Sspon.07G0014400-1A	Putative MYB DNA-binding domain superfamily protein	2,3	-	-
Sspon.03G0001860-4D	NAC domain-containing protein 48	7,1	-	-
Sspon.06G0007040-2C	Protein Dr1-like protein	5,4	-	-
Sspon.01G0008130-2D	BRCT domain-containing protein	1,7	-	-
Sspon.01G0027480-2D	chromatin complex subunit A 106	2,5	-	-

Sspon.02G0007200-1A	Protein CHROMATIN REMODELING 4	0,3	-	-
Sspon.01G0028710-1P	BTB/POZ domain-containing protein At3g50780	2,8	-	-
Sspon.03G0031400-3D	trihelix transcription factor ASIL1	4,5	-	-
Sspon.04G0024860-1P	cyclin-dependent kinase G-2	4	-	-
Sspon.02G0058460-1D	probable LRR receptor-like serine/threonine-protein kinase At1g56130 isoform X4	2,8	-	-
Sspon.07G0021120-3D	probable inactive receptor kinase At2g26730	4,3	-	-
Sspon.04G0017150-2B	protein STRUBBELIG-RECEPTOR FAMILY 3 isoform X1	3	-	-
Sspon.02G0007590-1A	G-type lectin S-receptor-like serine/threonine-protein kinase At2g19130	2,8	-	-
Sspon.01G0012490-2B	nucleolar complex protein 3 homolog	1,4	-	-
Sspon.01G0034930-1P	Ubiquitin-conjugating enzyme E2 4	34,4	-	-
Sspon.01G0032980-2P	U2 small nuclear ribonucleoprotein A'	28,3	-	-
Sspon.03G0042840-2D	uridine-cytidine kinase C	2,2	-	-
Sspon.03G0017500-4D	topless-related1	14,1	-	-
Sspon.02G0036390-2D	Transcription initiation factor IIB-2	3,2	-	-
Sspon.03G0029320-2C	Transcription initiation factor TFIID subunit 12	3	-	-
Sspon.01G0047470-2D	HIT zinc finger	2,3	-	-
Sspon.01G0051410-1C	Translation initiation factor IF-2	5,1	-	-
Sspon.02G0017130-2B	RNA recognition motif (RRM)-containing protein	2,2	-	-
Sspon.04G0015530-2B	SWR1-complex protein 4	8,8	-	-
Sspon.01G0038290-1T	guanine nucleotide exchange factor SPIKE 1	3	-	-
Sspon.03G0010960-1A	Protein SGT1 homolog	23,4	-	-
Sspon.03G0024540-3C	Reticulon-like protein B4	10,2	-	-
Sspon.04G0001930-1A	Serine/arginine-rich splicing factor RSZ22	42,2	-	-
Sspon.02G0022070-3C	Cytochrome b5 domain-containing protein RLF	5,9	-	-
Sspon.01G0032740-3D	RPM1-interacting protein 4-like	4	-	-
Sspon.02G0026820-2B	Cleavage and polyadenylation specificity factor (CPSF) A subunit protein	1,9	-	-
Sspon.01G0019810-1T	Pre-mRNA-processing protein 40C	2	-	-
Sspon.01G0017250-1P	protein PHYTOCHROME-DEPENDENT LATE-FLOWERING-like isoform X2	1,3	-	-
Sspon.04G0015440-2B	Nuclear pore complex protein NUP205	2,7	-	-
Sspon.02G0000180-1A	sodium/proton antiporter	8,5	-	-
Sspon.01G0018420-1P	DWNN domain a CCHC-type zinc finger	4,3	-	-
Sspon.04G0025320-2C	nucleic acid binding protein	6,1	-	-
Sspon.01G0040340-2C	Protein HUA2-LIKE 3	2,4	-	-
Sspon.01G0008600-2P	zinc-binding protein	44,2	-	-
Sspon.01G0039070-3D	IN2-1 protein	13,3	-	-
Sspon.01G0024510-2B	protein FAR1-RELATED SEQUENCE 5-like	3,7	-	-
Sspon.02G0034300-1B	FRIGIDA-like protein 3	7,6	-	-
Sspon.02G0034540-2D	RNA-binding (RRM/RBD/RNP motifs) family protein	1,9	-	-
Sspon.04G0005740-1A	titin isoform X1	3,6	-	-
Sspon.02G0026670-3C	unnamed protein product	1,2	-	-
Sspon.01G0027970-1P	Oryza sativa unknown protein AAP03423	8,9	-	-
Sspon.01G0009900-2C	Protein EARLY RESPONSIVE TO DEHYDRATION 15	5,8	-	-
Sspon.04G0001070-2C	Clathrin interactor EPSIN 2	2,2	-	-
Sspon.02G0015690-1A	enolase	21,7	-	-
Sspon.01G0038080-2D	ycf54-like protein	9	-	-
Sspon.02G0022310-1A	DUF724 domain-containing protein 3-like	2,7	-	-
Sspon.04G0003840-1A	dynammin-2A	7	-	-
Sspon.02G0034530-2D	U-box domain-containing protein 4	3,8	-	-
Sspon.02G0023480-3C	Peptidyl-prolyl cis-trans isomerase CYP63	5,5	-	-
Sspon.04G0000280-4D	Protein BTR1	27,4	-	-
Sspon.01G0027110-1P	anthranilate synthase beta subunit 2, chloroplastic-like	5,6	-	-
Sspon.02G0009710-3C	Homeodomain leucine zipper family IV protein	1,8	-	-
Sspon.02G0016200-2D	argonaute4a	10,9	-	-
Sspon.06G0008440-4D	afadin- and alpha-actinin-binding protein-like isoform X1	3,7	-	-
Sspon.06G0019100-1A	alkylated DNA repair protein alkB homolog 8 isoform X1	8,8	-	-
Sspon.08G0008910-3C	AT-hook motif nuclear-localized protein 25-like	8,7	-	-
Sspon.03G0014830-2C	binding	3,4	-	-
Sspon.03G0032240-1B	chromatin modification-related protein eaf-1	1,9	-	-
Sspon.07G0013440-2T	Embryonic flower 1-like protein	5,2	-	-
Sspon.07G0009920-2B	FHA domain-containing protein DDL	5,8	-	-
Sspon.06G0001680-1A	G patch domain-containing protein 11	5,1	-	-
Sspon.05G0019420-2P	heat shock 70 kDa protein 14-like	4,2	-	-
Sspon.03G0031960-1P	homeobox-DDT domain protein RLT2 isoform X3	7,4	-	-
Sspon.08G0006850-1A	hypothetical protein SHCRBa_152_D05_R_340	5,2	-	-
Sspon.04G0026370-1P	hypothetical protein ZEAMMB73_Zm00001d053372	1,4	-	-
Sspon.04G0032340-2D	iron-stress related protein	10,3	-	-
Sspon.06G0016670-1A	MEIOTIC F-BOX protein MOF-like	1,6	-	-
Sspon.05G0003020-3D	myosin heavy chain-related	1,8	-	-
Sspon.07G0004910-1A	myosin heavy chain-related	1,7	-	-
Sspon.06G0007350-1A	NOL1/NOP2/sun family protein	4,1	-	-
Sspon.08G0020440-1B	Nuclear poly(A) polymerase 2	2,9	-	-
Sspon.08G0012680-2D	Nuclear pore complex protein NUP98A	6,9	-	-
Sspon.07G0002580-3C	O-acyltransferase WSD1	3,3	-	-
Sspon.05G0013650-3C	OSJNBa0065B15.1-like protein	6,4	-	-

Sspon.05G0004410-1A	OSJNBa0086O06.9-like protein	21,2	-	-
Sspon.07G0000740-1A	phosphatase 2C 76	7,2	-	-
Sspon.06G0011840-3D	polycomb group protein FIE2	7,3	-	-
Sspon.06G0001080-3C	probable protein S-acyltransferase 7 isoform X2	3,5	-	-
Sspon.05G0003050-2C	putative cinnamyl alcohol dehydrogenase 1	0,7	-	-
Sspon.07G0016630-2B	putative inactive poly polymerase SRO1	2,4	-	-
Sspon.04G0024300-3D	putative metal-nicotianamine transporter YSL7	4,4	-	-
Sspon.04G0020380-4D	Remorin family protein	5,1	-	-
Sspon.08G0025170-2D	RNA polymerase I specific transcription initiation factor RRN3 protein	1,8	-	-
Sspon.08G0000340-2P	ROOT HAIRLESS 1	2,2	-	-
Sspon.04G0025680-3D	serine/arginine-rich splicing factor 4-like isoform X2	5,1	-	-
Sspon.05G0003930-2B	Serine/threonine-protein kinase ppk15	2,8	-	-
Sspon.02G0003120-1A	splicing factor, arginine/serine-rich 7	6,6	-	-
Sspon.05G0027560-1T	Sterol 3-beta-glucosyltransferase UGT80A2	7,1	-	-
Sspon.07G0016990-3C	suppressor of mec-8 and unc-52 protein homolog 2-like isoform X1	8,6	-	-
Sspon.04G0017550-4D	thiosulfate/3-mercaptopyruvate sulfurtransferase 1, mitochondrial	28,7	-	-
Sspon.01G0040960-2C	unnamed protein product	2,5	-	-
Sspon.07G0037580-1D	WEB family protein	4,1	-	-
Sspon.07G0007990-2B	Transcription factor MYBC1	3,4	-	-
Sspon.01G0061070-1D	leunig-related3	1,7	-	-
Sspon.03G0030600-2C	histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH1-like	2	-	-
Sspon.03G0014310-2B	Respiratory burst oxidase homolog protein B	3	-	-
Sspon.01G0010660-3C	Protein phosphatase 2C 32	2,5	-	-
Sspon.01G0051260-1C	Nuclear pore complex protein NUP155	5,3	-	-
Sspon.01G0058960-1D	ubiquitin-fusion protein	8,5	-	-
Sspon.01G0061280-1D	GRF1-interacting factor 1	8,2	-	-
Sspon.01G0017260-1A	Transcription factor TFIIIE alpha subunit	7	-	-
Sspon.03G0009250-2B	Callose synthase 11	0,9	-	-
Sspon.07G0014260-3D	Glutamate--cysteine ligase chloroplastic	11,2	-	-
Sspon.07G0022400-1B	Pentatricopeptide repeat-containing protein	4,7	-	-
Sspon.08G0005640-1A	RNA-binding (RRM/RBD/RNP motifs) family protein	16,4	-	-
Sspon.05G0026360-3D	U6 snRNA-associated Sm-like protein LSM6	26	-	-
Sspon.02G0019770-1A	Protein PHOSPHATE STARVATION RESPONSE 1	5,9	-	-
Sspon.02G0027860-4D	DNA binding	6,7	-	-
Sspon.03G0034940-1B	Rab escort protein 1	3,1	-	-
Sspon.02G0017530-1P	Ras-related protein RGP1	12,8	-	-
Sspon.01G0019170-4D	nucleolin 2-like	24,4	-	-
Sspon.04G0002330-3D	DENN (AEX-3) domain-containing protein	8,2	-	-
Sspon.02G0033600-1B	DNAJ heat shock N-terminal domain-containing protein	1,8	-	-
Sspon.02G0020350-4D	Retrovirus-related Pol polyprotein LINE-1	4,3	-	-
Sspon.07G0026940-1B	E3 SUMO-protein ligase Siz1	3,8	-	-
Sspon.07G0001040-4D	protein LAZ1-like	5,5	-	-
Sspon.02G0032880-1B	PWWP domain containing protein	14,4	-	-
Sspon.04G0020470-3D	brahma1	2,4	-	-
Sspon.03G0013310-1A	Protein MICRORCHIDIA 6	6,3	-	-
Sspon.01G0005610-1A	Elongator complex protein 5	5,5	-	-
Sspon.02G0046530-1C	F-actin-capping protein subunit alpha	4,5	-	-
Sspon.01G0036410-1P	Branched-chain-amino-acid aminotransferase	13,7	-	-
Sspon.06G0009700-3D	Putative nucleolin-like family protein	28,7	-	-
Sspon.05G0004340-3D	unnamed protein product	26,3	-	-
Sspon.05G0014350-2P	AT-rich interactive domain-containing protein 2	2,5	-	-
Sspon.02G0034000-1B	protein FAR1-RELATED SEQUENCE 5-like isoform X1	7,2	-	-
Sspon.04G0021750-1B	Galactose oxidase/kelch repeat superfamily protein	2,3	-	-
Sspon.02G0001320-2D	nucleolar protein 58 isoform X1	12,4	-	-
Sspon.04G0024970-2C	phosphoinositide binding	3,9	-	-
Sspon.04G0012950-2P	Protein CONTINUOUS VASCULAR RING 1	12,9	-	-
Sspon.03G0022100-2B	aromatic aminotransferase ISS1-like	3,8	-	-
Sspon.02G0028230-2D	condensin-2 complex subunit D3	0,9	-	-
Sspon.08G0003680-3C	Decaprenyl-diphosphate synthase subunit 1	4,3	-	-
Sspon.06G0015200-3D	DNA ligase 1 isoform X2	9	-	-
Sspon.07G0014110-4D	RNA binding protein	14,2	-	-
Sspon.08G0021330-1B	SMAD/FHA domain-containing protein	3,8	-	-
Sspon.04G0003800-2B	unnamed protein product	12,3	-	-
Sspon.03G0034640-1B	unnamed protein product	5,3	-	-
Sspon.02G0012130-1A	WPP domain-interacting protein 2	3,5	-	-
Sspon.04G0008020-3C	Auxin response factor 8	2,1	-	-
Sspon.05G0016410-1A	serine/threonine-protein kinase-like protein CCR4	1,8	-	-
Sspon.02G0008880-1A	ATP binding protein	7,3	-	-
Sspon.01G0009420-3D	ATP-dependent RNA helicase DDX41	8,1	-	-
Sspon.03G0030820-2D	zinc knuckle (CCHC-type) family protein	1,1	-	-
Sspon.01G0041800-1B	Callose synthase 10	10,6	-	-
Sspon.08G0017310-3D	hypothetical protein SORBI_3010G267900, partial	29,1	-	-
Sspon.05G0002650-1P	myosin-14-like	2	-	-
Sspon.06G0001750-4D	Protein EMSY-LIKE 4	6,7	-	-
Sspon.07G0002640-1A	syntaxin-71-like	7,5	-	-
Sspon.04G0011540-2B	unnamed protein product	2	-	-

Sspon.04G0011540-1P	unnamed protein product	2,8	-	-
Sspon.02G0047390-1C	Putative MO25-like protein	7,4	-	-
Sspon.01G0014350-2B	putative histone H2AXb	20,6	-	-
Sspon.01G0000390-2C	SKP1-like protein 21	4,2	-	-
Sspon.06G0013130-2B	putative methylesterase 14, chloroplastic	2,6	-	-
Sspon.01G0015180-4D	ADP-ribosylation factor GTPase-activating protein AGD10	13,2	-	-
Sspon.03G0018720-1A	Paired amphipathic helix protein Sin3-like 3	4	-	-
Sspon.04G0005130-1A	Histone-lysine N-methyltransferase SUVVR5	1,3	-	-
Sspon.06G0020970-1B	Histone-lysine N-methyltransferase SUVVR4	7,4	-	-
Sspon.01G0007740-1A	probable inactive receptor kinase At1g48480	3,1	-	-
Sspon.03G0015070-3C	probable receptor-like protein kinase At5g18500 isoform X1	3,1	-	-
Sspon.01G0037620-2D	receptor-like serine/threonine-protein kinase At2g45590	1,5	-	-
Sspon.06G0013570-4D	putative ACT-domain containing protein kinase family protein	4,1	-	-
Sspon.07G0018980-1T	Serine/threonine-protein kinase STY46	4,8	-	-
Sspon.03G0014980-3C	protein FAM192A isoform X1	10,2	-	-
Sspon.03G0016300-1P	DNA-binding protein	15,5	-	-
Sspon.04G0029830-1B	DNA-directed RNA polymerase II 16 kDa polypeptide	24,5	-	-
Sspon.01G0024340-4D	Myosin-binding protein 7	3,4	-	-
Sspon.03G0016670-3C	YEATS domain-containing protein 2-like	3,1	-	-
Sspon.03G0025260-1A	uncharacterized protein LOC8078069	4,9	-	-
Sspon.05G0006880-2B	ABC transporter G family member 11	1,8	-	-
Sspon.07G0022130-1B	DNA-directed RNA polymerase I subunit 1	4,5	-	-
Sspon.02G0010970-2D	FK506-binding protein 2-1	3,4	-	-
Sspon.04G0006600-4P	mechanosensitive ion channel protein 6	0,4	-	-
Sspon.06G0011440-3D	nucleolin	9,2	-	-
Sspon.08G0024140-1P	Os06g0113900	8,2	-	-
Sspon.05G0021080-1A	protein ENHANCED DISEASE RESISTANCE 4	3,1	-	-
Sspon.06G0001600-1A	RNA binding (RRM/RBD/RNP motifs) family protein	3,4	-	-
Sspon.01G0018990-1P	shugoshin-1	7,6	-	-
Sspon.08G0008940-2B	uncharacterized LOC100283220	24,9	-	-
Sspon.04G0008760-1A	unnamed protein product	20,4	-	-
Sspon.08G0001740-2C	unnamed protein product	8,4	-	-
Sspon.07G0016330-1A	Vacuolar sorting protein 39	1,9	-	-
Sspon.03G0030280-2C	WAS/WASL-interacting protein family member 3-like	3,4	-	-
Sspon.02G0036620-2D	DNA-binding bromodomain-containing protein	1,3	-	-
Sspon.08G0020810-2C	DEAD-box ATP-dependent RNA helicase 31	3,4	-	-
Sspon.01G0005000-3D	calmodulin-binding transcription activator 1 isoform X2	3	-	-
Sspon.02G0007330-2B	Protein VASCULAR ASSOCIATED DEATH 1 chloroplastic	3,1	-	-
Sspon.03G0017090-2C	pre-mRNA-splicing factor SPF27 homolog	20,9	-	-
Sspon.01G0003500-3D	glutathione reductase, chloroplastic-like	5,6	-	-
Sspon.06G0014630-3C	coiled-coil domain-containing protein SCD2-like isoform X2	2,5	-	-
Sspon.05G0006230-1A	required to maintain repression 2	6,4	-	-
Sspon.07G0002130-2B	Guanylate-binding family protein	6,8	-	-
Sspon.05G0015390-4D	phosphoglycerate mutase-like protein 1 isoform X4	12,7	-	-
Sspon.07G0016180-3D	PHD finger protein ALFIN-LIKE 7	9,4	-	-
Sspon.02G0041840-3D	transcription factor UNE12-like	5,7	-	-
Sspon.04G0021980-1P	bHLH transcription factor RHL1	4,4	-	-
Sspon.02G0048970-1C	transcription factor RF2a	6	-	-
Sspon.08G0002360-3C	GATA transcription factor 24	8,6	-	-
Sspon.02G0038490-1B	Zinc finger CCCH domain-containing protein 59	4,3	-	-
Sspon.03G0011250-1A	Zinc finger CCCH domain-containing protein 37	3,7	-	-
Sspon.05G0001570-2B	Zinc finger CCCH domain-containing protein 31	6,2	-	-
Sspon.08G0019740-3D	Zinc finger CCCH domain-containing protein 52	3,9	-	-
Sspon.04G0032670-2D	RNA polymerase II transcriptional coactivator KIWI	9,9	-	-
Sspon.02G0030680-3C	Protein tesmin/TSO1-like CXC 4	8,6	-	-
Sspon.06G0007600-2B	Protein PHR1-LIKE 3	4,6	-	-
Sspon.08G0011950-2D	STOREKEEPER protein	17,5	-	-
Sspon.01G0034990-2C	probable acetyltransferase NATA1-like	16,1	-	-
Sspon.03G0011560-3C	N-alpha-acetyltransferase 50-like	5,5	-	-
Sspon.02G0029230-3D	scarecrow-like protein 34	3,9	-	-
Sspon.02G0004400-1P	chitin-inducible gibberellin-responsive protein 2-like	2,4	-	-
Sspon.01G0046970-1P	DWARF8	2,9	-	-
Sspon.01G0062660-1D	transcription elongation factor A protein 2	12	-	-
Sspon.05G0021870-2D	Mediator of RNA polymerase II transcription subunit 7a	9,3	-	-
Sspon.04G0004480-3C	nuclear transcription factor Y subunit B-6	4,9	-	-
Sspon.02G0011880-3D	Nuclear transcription factor Y subunit C-6	25	-	-
Sspon.02G0015230-3C	Chromatin remodeling protein EBS	14,9	-	-
Sspon.02G0015230-1P	DNA binding protein	9,8	-	-
Sspon.05G0002570-2C	Cell differentiation Rcd1-like protein	6,9	-	-
Sspon.07G0005310-1A	Histone-lysine N-methyltransferase H3 lysine-9 specific SUVH3	7,7	-	-
Sspon.04G0019330-1A	SWIB domain-containing protein	13,1	-	-
Sspon.02G0027630-2D	upstream activation factor subunit spp27-like	12,6	-	-
Sspon.01G0028580-3D	upstream activation factor subunit UAF30-like	17,7	-	-
Sspon.02G0033360-1B	SWI/SNF complex component SNF12 homolog	6,3	-	-
Sspon.05G0001540-1A	SWIB complex BAF60b domain-containing protein	8,6	-	-
Sspon.05G0001540-2D	SWIB complex BAF60b domain-containing protein	15,3	-	-

Sspon.06G0011620-4D	lysine-specific histone demethylase 1 homolog 2-like	6,7	-	-
Sspon.03G0015130-2B	sequence-specific DNA binding transcription factor	2,3	-	-
Sspon.01G0021620-1P	Trihelix transcription factor GT-2	1,4	-	-
Sspon.03G0003760-4D	probable LRR receptor-like serine/threonine-protein kinase IRK	3,6	-	-
Sspon.02G0006720-4D	calcium dependent protein kinase3	8	-	-
Sspon.05G0018290-2P	calcium-dependent protein kinase 28	12,5	-	-
Sspon.01G0061760-1D	SnRK2 serine threonine protein kinase8	20	-	-
Sspon.01G0014770-3D	Serine/threonine-protein kinase SRK2C	10,3	-	-
Sspon.03G0010350-2B	Putative MAP kinase family protein	2,5	-	-
Sspon.01G0052190-2D	MAP kinase1	8,5	-	-
Sspon.01G0039020-2C	Receptor-like protein kinase HERK 1	3,2	-	-
Sspon.06G0010230-1P	Putative leucine-rich repeat receptor-like protein kinase family protein	6,6	-	-
Sspon.01G0026830-2C	atypical receptor-like kinase MARK	11,5	-	-
Sspon.07G0016760-3C	probable leucine-rich repeat receptor-like protein kinase IMK3	5,9	-	-
Sspon.01G0027230-3D	Receptor-like kinase TMK2	3,3	-	-
Sspon.07G0010860-4D	proline-rich receptor-like protein kinase PERK1	3,3	-	-
Sspon.02G0019910-2B	PTI1-like tyrosine-protein kinase 3	3,8	-	-
Sspon.03G0015870-4P	PTI1-like tyrosine-protein kinase 3	14	-	-
Sspon.04G0011640-1A	MKK4 - putative MAPKK	6,7	-	-
Sspon.01G0045270-1B	zinc finger protein 4	2,8	-	-
Sspon.03G0006960-2D	diphosphonucleotide phosphatase2	19,2	-	-
Sspon.01G0028350-1A	NADH-ubiquinone oxidoreductase 23 kDa subunit	22	-	-
Sspon.02G0019450-2D	ylmG homolog protein 1-2, chloroplastic-like	6,3	-	-
Sspon.03G0006870-1T	haloacid dehalogenase-like hydrolase family protein	3,6	-	-
Sspon.01G0028070-3D	DNA repair protein XRCC4	6,4	-	-
Sspon.02G0020070-3D	exportin 1A	8,8	-	-
Sspon.02G0036370-1B	protein XAP5 CIRCADIAN TIMEKEEPER	6,8	-	-
Sspon.01G0022670-3C	inositol monophosphatase 3	28,3	-	-
Sspon.01G0009050-3D	Vacuolar-sorting receptor 1	4,8	-	-
Sspon.01G0016740-2B	Vacuolar protein sorting-associated protein 9A	4,6	-	-
Sspon.01G0030320-1A	Vacuolar protein sorting-associated protein 35B	8,1	-	-
Sspon.03G0011240-3P	Vacuolar protein sorting-associated protein 32 homolog 1	15,4	-	-
Sspon.02G0005840-3C	V-type proton ATPase subunit H	12,3	-	-
Sspon.02G0041180-3D	vacuolar ATP synthase subunit G	8,2	-	-
Sspon.02G0001340-3D	vacuolar ATP synthase subunit F	6,9	-	-
Sspon.03G0012320-1A	probable V-type proton ATPase subunit d	18,8	-	-
Sspon.01G0037280-2C	V-type proton ATPase subunit a3	7,1	-	-
Sspon.01G0005630-2B	Mitochondrial outer membrane protein porin 5	45,5	-	-
Sspon.07G0003280-1P	outer mitochondrial membrane protein porin	38,1	-	-
Sspon.01G0048460-3D	vesicle-associated membrane protein 725	18,2	-	-
Sspon.01G0009450-1P	UDP-glucuronic acid decarboxylase 4	13	-	-
Sspon.03G0015230-2B	UDP-glucuronic acid decarboxylase 4	17,7	-	-
Sspon.02G0025860-3C	Urease	6,7	-	-
Sspon.01G0032480-2D	LUC7 related protein	4,7	-	-
Sspon.04G0002160-3C	UMP-CMP kinase family protein	22,3	-	-
Sspon.03G0008260-2T	anthocyanidin 5,3-O-glucosyltransferase	2,2	-	-
Sspon.03G0006820-1P	UDP-glycosyltransferase 88F3	1,9	-	-
Sspon.03G0010440-2P	scopoletin glucosyltransferase	4,8	-	-
Sspon.02G0055460-1D	Chain A, UDP-glucose 4-epimerase	5,3	-	-
Sspon.01G0028180-1A	cytochrome b-c1 complex subunit 8-1, mitochondrial-like	9,4	-	-
Sspon.04G0000290-3C	ubiquitin carboxyl-terminal hydrolase 2-like isoform X1	9,6	-	-
Sspon.03G0013410-3C	Ubiquitin carboxyl-terminal hydrolase	29,8	-	-
Sspon.03G0003080-2C	ubiquitin-conjugating enzyme E2 7	19,1	-	-
Sspon.03G0009210-2P	ubiquitin-conjugating enzyme E2 36	33,3	-	-
Sspon.01G0049010-2D	ubiquitin-conjugating enzyme E2 2	11,2	-	-
Sspon.02G0000460-2B	ubiquitin-activating enzyme E1 3 isoform X2	7,6	-	-
Sspon.01G0000280-3D	tubulin beta-2 chain	62,3	-	-
Sspon.01G0029450-2C	tubulin beta-4 chain	55,8	-	-
Sspon.01G0027630-1A	tubulin alpha chain	40,2	-	-
Sspon.02G0004590-1A	alpha-tubulin	41,8	-	-
Sspon.01G0007630-2C	tubulin alpha-2 chain	21	-	-
Sspon.01G0011480-2C	5-hydroxyisourate hydrolase	11,7	-	-
Sspon.02G0047010-1C	Multifunctional methyltransferase subunit TRM112-like protein	7,7	-	-
Sspon.04G0004490-1A	tRNA (guanine(9)-N1)-methyltransferase	9,4	-	-
Sspon.03G0000100-1P	transaldolase 2	28,4	-	-
Sspon.03G0031200-3D	trehalose-6-phosphate synthase15	11,5	-	-
Sspon.02G0030660-2B	stress-induced-phosphoprotein 1-like isoform X1	4,9	-	-
Sspon.04G0006800-2B	Tripeptidyl-peptidase 2	9,4	-	-
Sspon.01G0045120-2C	Mitochondrial import receptor subunit TOM5-like protein	24,5	-	-
Sspon.01G0008650-2B	Mitochondrial import receptor subunit TOM40-1	31,3	-	-
Sspon.03G0000390-2D	mitochondrial import receptor subunit TOM20	24,1	-	-
Sspon.01G0015360-3C	TOM1-like protein 2	3,8	-	-
Sspon.02G0034760-1B	protein TOC75, chloroplastic-like	3,6	-	-
Sspon.01G0036990-1B	translocon of outer membrane of chloroplast35	8	-	-
Sspon.04G0001460-1A	transmembrane 9 superfamily member 11-like	13,9	-	-
Sspon.03G0021080-2C	mitochondrial import inner membrane translocase subunit TIM14	8,3	-	-

Sspon.02G0040910-1B	Eukaryotic translation initiation factor 3 subunit E	28,4	-	-
Sspon.01G0020110-2B	Protein TIC110 chloroplastic	3,4	-	-
Sspon.02G0017150-2B	THO complex subunit 3	4,8	-	-
Sspon.01G0000570-1A	THO complex subunit 1	3	-	-
Sspon.03G0017680-1A	protein TRIGALACTOSYLDIACYLGLYCEROL 4, chloroplastic	3,5	-	-
Sspon.04G0030730-2D	tubulin-folding cofactor A-like isoform X1	15,2	-	-
Sspon.03G0021360-3D	transcription initiation factor TFIID subunit 15b	3,4	-	-
Sspon.01G0032670-1A	Tetratricopeptide repeat protein KIAA0103	5,9	-	-
Sspon.02G0029050-1A	Osmotin-like protein precursor	10,4	-	-
Sspon.01G0006300-2B	glucan endo-1,3-beta-glucosidase 3 precursor	12,6	-	-
Sspon.02G0013470-1A	probable N-succinylidiaminopimelate aminotransferase DapC	4,8	-	-
Sspon.01G0004360-1A	tubulin--tyrosine ligase-like protein 12	4,6	-	-
Sspon.03G0017000-2C	phenazine biosynthesis protein	4,7	-	-
Sspon.02G0038400-1P	CD2 antigen cytoplasmic tail-binding protein 2 homolog isoform X2	7,2	-	-
Sspon.03G0017020-1A	putative splicing factor 3A subunit 1	15,7	-	-
Sspon.01G0012500-2B	SPFH/Band 7/PHB domain-containing membrane-associated protein family	11,3	-	-
Sspon.01G0007780-2D	Putative Nonclathrin coat protein gamma - like protein	13	-	-
Sspon.03G0025440-1A	2-oxoglutarate-Fe(II) type oxidoreductase isoform X1	7	-	-
Sspon.02G0002210-1A	Tetratricopeptide repeat (TPR)-like superfamily protein	6,8	-	-
Sspon.02G0012030-3C	protein ASPARTIC PROTEASE IN GUARD CELL 2-like	7,3	-	-
Sspon.01G0008190-3D	argininosuccinate lyase	19,6	-	-
Sspon.01G0012400-3D	protein LRP16	13,7	-	-
Sspon.03G0008800-1A	ATP synthase subunit beta, mitochondrial-like	40,7	-	-
Sspon.06G0002720-1P	exosome complex exonuclease RRP43	11,8	-	-
Sspon.02G0014440-1A	HAD-superfamily hydrolase subfamily IG 5'-nucleotidase	7,1	-	-
Sspon.02G0004010-2B	RNA-binding (RRM/RBD/RNP motifs) family protein	9,3	-	-
Sspon.03G0013850-1P	protein usf-like	40,1	-	-
Sspon.01G0006940-2B	splicing factor 3A subunit 2	3,1	-	-
Sspon.02G0002930-2D	Transmembrane emp24 domain-containing protein p24delta9	17	-	-
Sspon.02G0005730-1A	USP family protein	18	-	-
Sspon.03G0008880-3C	Rho-related protein from plants 1	10,1	-	-
Sspon.03G0007570-4D	NADH-ubiquinone oxidoreductase 20 kDa subunit	9,5	-	-
Sspon.03G0026470-2C	protein MEMO1-like	13,7	-	-
Sspon.03G0009270-3D	Adenine nucleotide alpha hydrolase-like superfamily protein	40,4	-	-
Sspon.04G0004380-1A	h/ACA ribonucleoprotein complex subunit 2	16	-	-
Sspon.02G0036850-2C	bromodomain protein 103	2,9	-	-
Sspon.02G0022120-4D	protein LURP-one-related 15-like	12,9	-	-
Sspon.04G0027330-1B	early nodulin 93	17,3	-	-
Sspon.01G0056930-1C	Dihydroxyacetone kinase	12	-	-
Sspon.02G0014820-3C	Peptidyl-prolyl cis-trans isomerase	11,4	-	-
Sspon.01G0018660-2B	translin	7,9	-	-
Sspon.01G0019670-4D	uncharacterized protein LOC8070473	22,9	-	-
Sspon.03G0021580-1A	proactivator polypeptide-like 1 isoform X1	20,7	-	-
Sspon.02G0013530-2B	Aspartic proteinase nepenthesin-1	2,2	-	-
Sspon.07G0005410-2B	ADP-ribosylation factor 1	47	-	-
Sspon.03G0011320-3C	10-deacetylbaecatin III-10-O-acetyl transferase	14	-	-
Sspon.03G0022570-1P	Acyl transferase 9	16,1	-	-
Sspon.01G0038140-1P	Vicilin-like seed storage protein	11	-	-
Sspon.01G0041560-3D	putative NADH dehydrogenase 1 alpha subcomplex subunit 12	11,5	-	-
Sspon.01G0043730-1B	RNase H family protein	4,4	-	-
Sspon.01G0039460-1B	branched-chain-amino-acid aminotransferase-like protein 1	9,7	-	-
Sspon.06G0005380-2C	Carbohydrate-binding-like fold	7,5	-	-
Sspon.03G0015630-2B	Carbohydrate-binding-like fold	6,3	-	-
Sspon.01G0019380-2C	NADPH-dependent aldehyde reductase-like protein, chloroplastic	12,9	-	-
Sspon.01G0011410-2B	unnamed protein product	5,7	-	-
Sspon.02G0003250-1A	unnamed protein product	11,9	-	-
Sspon.02G0028480-1A	CTP synthase family protein	9,1	-	-
Sspon.01G0048510-1B	Histone H1	6,6	-	-
Sspon.03G0025970-1B	syntxin-61	8,7	-	-
Sspon.02G0026640-1A	syntxin 132	11,9	-	-
Sspon.03G0001970-3C	Bidirectional sugar transporter SWEET1a	5,6	-	-
Sspon.02G0030830-4D	Sulfurtransferase	14	-	-
Sspon.04G0016910-3C	Nucleoid-associated protein chloroplastic	17,4	-	-
Sspon.04G0023960-1B	3-isopropylmalate dehydratase small subunit 2	13,8	-	-
Sspon.03G0004630-3D	Signal recognition particle 54 kDa protein 3	10,1	-	-
Sspon.01G0026250-1A	Signal peptide peptidase	3,1	-	-
Sspon.01G0040510-3D	protein SPIRAL1-like 1	17	-	-
Sspon.04G0022440-1B	DIS3-like exonuclease 2	1,4	-	-
Sspon.03G0039770-2D	Sorting nexin 1	4,7	-	-
Sspon.02G0017820-2B	probable small nuclear ribonucleoprotein G	27,5	-	-
Sspon.01G0033510-2D	Sucrose nonfermenting 4-like protein	8,9	-	-
Sspon.03G0033260-2C	Suppressor of mec-8 and unc-52 protein homolog 1	7,3	-	-
Sspon.03G0033260-1B	Suppressor of mec-8 and unc-52 protein homolog 1	12,2	-	-
Sspon.01G0006450-1A	small nuclear ribonucleoprotein Sm D3	19,1	-	-
Sspon.04G0032460-1C	small nuclear ribonucleoprotein SmD1a	13	-	-

Sspon.01G0027940-1A	serine hydroxymethyltransferase, mitochondrial	2,8	-	-
Sspon.01G0023340-1T	protein Z	9,2	-	-
Sspon.02G0001440-2C	Exocyst complex component SEC8	6,6	-	-
Sspon.02G0040230-2D	tropinone reductase-like 3	14,9	-	-
Sspon.02G0052170-1C	Fumarate reductase/succinate dehydrogenase, FAD-binding site	27,4	-	-
Sspon.02G0001930-2B	serine carboxypeptidase 1 precursor	2,5	-	-
Sspon.02G0042810-1B	serine carboxypeptidase 2-like	9,5	-	-
Sspon.03G0029730-2C	Serine carboxypeptidase 27	4,4	-	-
Sspon.03G0021100-2C	Serine carboxypeptidase-like 27	2,4	-	-
Sspon.04G0002120-1A	subtilisin-like protease SBT1.4	6	-	-
Sspon.03G0014760-3C	GTP-binding protein SAR1A	29,2	-	-
Sspon.03G0015040-1A	S-adenosylmethionine synthase	29,6	-	-
Sspon.02G0019070-2C	thiol protease SEN102 precursor	4	-	-
Sspon.03G0001990-2D	Stearoyl-[acyl-carrier-protein] 9-desaturase 1, chloroplastic	3,9	-	-
Sspon.02G0023330-4D	glycine-rich RNA-binding protein RZ1C-like	26,4	-	-
Sspon.02G0002950-1A	Exosome complex component RRP41-like	11,7	-	-
Sspon.02G0003020-2P	40S ribosomal protein S9-2	25,8	-	-
Sspon.01G0048160-3P	40S ribosomal protein S23	14,7	-	-
Sspon.01G0025590-1A	40S ribosomal protein S21	23,5	-	-
Sspon.02G0022200-1A	40S ribosomal protein S12	61,7	-	-
Sspon.07G0029580-3D	40S ribosomal protein S10	11,7	-	-
Sspon.04G0021660-1B	26S proteasome non-ATPase regulatory subunit 12 homolog A-like	12,7	-	-
Sspon.03G0016950-4D	26S proteasome non-ATPase regulatory subunit 14 homolog	18,9	-	-
Sspon.04G0024940-2C	60S ribosomal protein L6	29,8	-	-
Sspon.01G0040060-2C	60S ribosomal protein L37	11,7	-	-
Sspon.04G0002040-1A	60S ribosomal protein L35a-2	27,7	-	-
Sspon.04G0017420-1A	60S ribosomal protein L27a-3	25	-	-
Sspon.01G0034700-3D	60S ribosomal protein L21-2	16,5	-	-
Sspon.04G0014520-2B	60S ribosomal protein L11	33,7	-	-
Sspon.03G0002250-1A	60S ribosomal protein L10a	27,6	-	-
Sspon.02G0023550-1A	ribose-5-phosphate isomerase	8	-	-
Sspon.02G0007560-3C	Rop guanine nucleotide exchange factor 3	2,6	-	-
Sspon.01G0015860-1T	U1 snRNP	3,7	-	-
Sspon.04G0005710-3C	protein RMD5 homolog A	3,7	-	-
Sspon.02G0006700-2C	reactive Intermediate Deaminase A, chloroplastic-like	52	-	-
Sspon.01G0052050-1P	Trifunctional UDP-glucose 46-dehydratase/UDP-4-keto-6-deoxy-D-glucose 35-epimerase/UDP-4-keto-L-rhamnose-reductase RHM2	10,7	-	-
Sspon.01G0058300-1P	RGS1-HXK1-interacting protein 1-like	11,7	-	-
Sspon.02G0031000-1A	DEAD-box ATP-dependent RNA helicase 53	9,6	-	-
Sspon.02G0031000-2B	DEAD-box ATP-dependent RNA helicase 53	6,3	-	-
Sspon.03G0011200-3C	P-loop containing nucleoside triphosphate hydrolase superfamily protein	2,9	-	-
Sspon.01G0046920-1B	DEAD-box ATP-dependent RNA helicase 21	3,4	-	-
Sspon.03G0023090-1A	DEAD-box ATP-dependent RNA helicase 20	10,7	-	-
Sspon.03G0023090-2B	DEAD-box ATP-dependent RNA helicase 20	5,5	-	-
Sspon.03G0011900-3D	RGG repeats nuclear RNA binding protein A	14,7	-	-
Sspon.01G0029600-1T	Chain A, ferredoxin-NADP reductase	25	-	-
Sspon.01G0029600-2P	ferredoxin--NADP reductase, embryo isozyme, chloroplastic	17,5	-	-
Sspon.01G0030130-1A	Replication factor C subunit 5	8,5	-	-
Sspon.03G0018300-3D	Protein RER1A	10,1	-	-
Sspon.02G0021520-3C	Putative pol polyprotein	5,1	-	-
Sspon.03G0009530-1P	ribokinase	14,6	-	-
Sspon.01G0050990-2D	Polyadenylate-binding protein RBP47B'	9,1	-	-
Sspon.02G0006630-1A	Polyadenylate-binding protein RBP45C	9,4	-	-
Sspon.02G0027500-3C	Glycine-rich RNA-binding protein 3 mitochondrial	25,3	-	-
Sspon.03G0010240-1A	GTP-binding nuclear protein Ran-2	48,4	-	-
Sspon.03G0010510-2C	rae1-like protein	9	-	-
Sspon.02G0014930-3D	Ubiquitin receptor RAD23c	10,2	-	-
Sspon.07G0002670-3P	guanine nucleotide-binding protein subunit beta-like protein A	32,8	-	-
Sspon.01G0024860-1A	ras-related protein RHN1	10,1	-	-
Sspon.02G0022790-2C	ras-related protein RABE1d-like	17,1	-	-
Sspon.03G0033290-2C	ras-related protein RIC1	34	-	-
Sspon.04G0007050-2B	Ubiquitin carboxyl-terminal hydrolase 3	26,2	-	-
Sspon.02G0008290-2B	nicotinate-nucleotide pyrophosphorylase, chloroplastic	9,9	-	-
Sspon.01G0030710-3P	ubiquinol-cytochrome c reductase complex 14 kDa protein	16,3	-	-
Sspon.01G0016300-3C	aldose 1-epimerase	17,6	-	-
Sspon.04G0003660-1A	DCN1-like protein 2	7,2	-	-
Sspon.03G0000640-1A	Ribosomal protein S24/S35 mitochondrial	3,5	-	-
Sspon.02G0042940-2C	transducin family protein / WD-40 repeat family protein	4,3	-	-
Sspon.04G0030420-1C	predicted protein	5,8	-	-
Sspon.02G0034110-2P	unnamed protein product	16,7	-	-
Sspon.02G0021540-2B	probable polygalacturonase isoform X2	3	-	-
Sspon.01G0021240-3D	putative serine protease EDA2	3,6	-	-
Sspon.02G0033310-2C	COX VIIa-like protein	16,2	-	-
Sspon.01G0025600-1A	unnamed protein product	8,9	-	-
Sspon.01G0002060-1A	NHP2-like protein 1	17,7	-	-
Sspon.06G0001580-1P	complex I subunit	22,8	-	-

Sspon.04G0022220-2C	ER6 protein	20,4	-	-
Sspon.03G0020320-2B	EKC/KEOPS complex subunit TPRKB-like	12,2	-	-
Sspon.01G0023300-3C	translation initiation factor eIF-2B subunit gamma-like	2,6	-	-
Sspon.01G0001020-4D	riboflavin biosynthesis protein PYRD, chloroplastic	6,9	-	-
Sspon.02G0007510-3D	beta-ureidopropionase	9,4	-	-
Sspon.02G0004760-1A	Insulin-degrading enzyme-like 1 peroxisomal	7	-	-
Sspon.02G0004760-2B	Insulin-degrading enzyme-like 1 peroxisomal	11,6	-	-
Sspon.01G0026970-2D	probable phosphoribosylformylglycinamide synthase, chloroplastic/mitochondrial	12,8	-	-
Sspon.04G0004930-2B	Ribose-phosphate pyrophosphokinase 4	28	-	-
Sspon.03G0033600-1B	Pre-mRNA-processing protein 40A	8,9	-	-
Sspon.04G0002780-1A	presequence protease 1, chloroplastic/mitochondrial	5	-	-
Sspon.03G0023060-1A	PRA1 family protein F3-like	5,7	-	-
Sspon.02G0017410-1A	serine/threonine-protein phosphatase PP-X isozyme 2	12,3	-	-
Sspon.02G0017190-2B	phosphate/phosphoenolpyruvate translocator	9	-	-
Sspon.04G0022360-1P	inorganic pyrophosphatase	16,1	-	-
Sspon.01G0035250-1B	PP2Ac-5 - Phosphatase 2A isoform 5 belonging to family 2	25,9	-	-
Sspon.01G0006680-3D	phosphomevalonate kinase	4,3	-	-
Sspon.03G0028970-1B	probable pectinesterase/pectinesterase inhibitor 51	7,2	-	-
Sspon.03G0015350-2B	pectinesterase-like	2,5	-	-
Sspon.01G0029050-2B	Malate dehydrogenase, glyoxysomal	6,7	-	-
Sspon.01G0047180-1P	phospholipase A2	12,8	-	-
Sspon.03G0009790-2B	Plastidial pyruvate kinase 2	11,3	-	-
Sspon.01G0048960-2C	Pyruvate kinase	9,2	-	-
Sspon.01G0048960-1B	pyruvate kinase isozyme A, chloroplastic	5,2	-	-
Sspon.01G0015080-4D	Plant intracellular Ras-group-related LRR protein 5	1,5	-	-
Sspon.02G0019440-4D	aquaporin PIP2.1	20,7	-	-
Sspon.03G0004650-1A	Alpha-glucan phosphorylase, H isozyme	2,7	-	-
Sspon.04G0025040-1B	prohibitin-3, mitochondrial-like	20,3	-	-
Sspon.01G0028910-2B	phosphohexose isomerase1	50	-	-
Sspon.04G0033060-1C	prefoldin subunit 1	10,9	-	-
Sspon.03G0013610-1A	peroxidase 72	6,6	-	-
Sspon.03G0043010-1C	Peroxidase 72	31,4	-	-
Sspon.01G0010500-3C	peroxidase 2-like	10,6	-	-
Sspon.01G0039610-1B	Peroxidase 2	11,3	-	-
Sspon.03G0015020-1A	Peroxidase 1 precursor	12,9	-	-
Sspon.04G0033440-1C	peroxidase 52-like isoform X2	16,5	-	-
Sspon.03G0015030-2P	Peroxidase 64	19,9	-	-
Sspon.04G0011700-1A	peroxidase 2-like	35	-	-
Sspon.03G0015740-2B	Peroxidase 2	2,8	-	-
Sspon.02G0002490-1A	Peroxidase 2	7,2	-	-
Sspon.02G0033400-1B	peroxidase 2	7,8	-	-
Sspon.02G0002650-1A	peroxidase 2-like	14,1	-	-
Sspon.01G0060870-1D	Peroxidase 2	24,3	-	-
Sspon.02G0002640-1A	peroxidase 2-like	11,7	-	-
Sspon.03G0025980-2P	Cationic peroxidase SPC4	15,2	-	-
Sspon.03G0025980-5P	Cationic peroxidase SPC4	11,9	-	-
Sspon.02G0053200-1C	Cationic peroxidase SPC4	21,1	-	-
Sspon.02G0033420-1B	1-Cys peroxiredoxin PER1	10,8	-	-
Sspon.02G0013570-1A	Protein disulfide isomerase-like 2-3	24,5	-	-
Sspon.03G0014720-1A	protein disulfide isomerase-like 2-2	23,8	-	-
Sspon.04G0021200-1A	protein disulfide isomerase3	14,6	-	-
Sspon.02G0031490-1A	pyruvate dehydrogenase E1 component subunit beta	2,6	-	-
Sspon.03G0042680-1C	Pyruvate decarboxylase 4	44,3	-	-
Sspon.01G0052330-1C	pyruvate decarboxylase	44,3	-	-
Sspon.03G0024960-1A	Plasma membrane-associated cation-binding protein 1	13,4	-	-
Sspon.01G0001540-4D	Anthranilate phosphoribosyltransferase, chloroplastic	3,6	-	-
Sspon.02G0040120-2C	poly polymerase 1	2,8	-	-
Sspon.01G0048710-1B	Globulin-2	25,9	-	-
Sspon.01G0036870-1T	purple acid phosphatase 1	19,5	-	-
Sspon.01G0036860-1B	Purple acid phosphatase 3	12,7	-	-
Sspon.02G0029300-3D	Nucleotide pyrophosphatase/phosphodiesterase	12,2	-	-
Sspon.01G0047170-2C	Phytanoyl-CoA dioxygenase	29	-	-
Sspon.03G0030170-2P	proteasome subunit alpha type	41,6	-	-
Sspon.06G0003910-1P	Proteasome subunit alpha type	25,1	-	-
Sspon.01G0044780-3D	putative prolyl 4-hydroxylase 12	5,4	-	-
Sspon.01G0010960-3C	prostaglandin E synthase 3	14	-	-
Sspon.01G0013070-2B	5-oxoprolinase-like	2,2	-	-
Sspon.04G0005370-4D	Ornithine carbamoyltransferase chloroplastic	16,4	-	-
Sspon.02G0018050-3D	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	10,7	-	-
Sspon.01G0022020-2B	probable dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 3	3,1	-	-
Sspon.01G0001750-1A	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit	9,8	-	-
Sspon.04G0024750-1B	Outer envelope pore protein 37, chloroplastic	5	-	-

Sspon.01G0038520-2C	outer envelope pore protein 16-2, chloroplastic-like	7,6	-	-
Sspon.02G0031930-3C	cysteine synthase	47,1	-	-
Sspon.01G0009750-1A	nuclear pore complex protein NUP93A	10,7	-	-
Sspon.03G0002330-1A	Nuclear pore complex protein NUP62	8,4	-	-
Sspon.03G0039780-1C	nuclear pore complex protein NUP62-like isoform X1	14,4	-	-
Sspon.02G0013490-2B	nucleoporin p58/p45	5,4	-	-
Sspon.02G0020060-3D	Nuclear pore complex protein NUP54	2,8	-	-
Sspon.02G0010740-1A	nuclear transport factor 2-like	11,4	-	-
Sspon.04G0025950-2C	Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain	6,6	-	-
Sspon.03G0004100-2B	DNA-directed RNA polymerases II and IV subunit 5A	5,4	-	-
Sspon.02G0018120-1A	DNA-directed RNA polymerases II, IV and V subunit 3	34	-	-
Sspon.01G0055960-2D	DNA-directed RNA polymerase II subunit 2	5,9	-	-
Sspon.03G0026400-2C	putative NADPH:quinone oxidoreductase 1	6,2	-	-
Sspon.03G0020290-3D	protein NRT1/ PTR FAMILY 8.1-like	5	-	-
Sspon.03G0000280-2B	probable nucleolar protein 5-2	14	-	-
Sspon.01G0009770-3D	putative nucleolar protein 5-1	11,8	-	-
Sspon.04G0008300-2B	H/ACA ribonucleoprotein complex subunit 3-like protein	11,5	-	-
Sspon.04G0013140-2B	putative inactive nicotinamidase	5,3	-	-
Sspon.04G0008700-2B	nicotinamidase 1	5,6	-	-
Sspon.01G0006900-3C	Eukaryotic translation initiation factor NCBP	10,9	-	-
Sspon.04G0008870-3C	cytosolic Fe-S cluster assembly factor NBP35-like	8,2	-	-
Sspon.02G0029930-1A	nucleobase-ascorbate transporter 3	2,1	-	-
Sspon.01G0024440-1P	Nicotianamine synthase 3	5,5	-	-
Sspon.01G0020930-2B	Malic enzyme	6,3	-	-
Sspon.02G0007160-1A	Malic enzyme	4,4	-	-
Sspon.03G0041730-1C	acetyltransferase 1-like protein	11,1	-	-
Sspon.03G0032500-1B	acetyltransferase 1-like protein	8,9	-	-
Sspon.01G0003140-3C	Splicing factor CC1-like	2,2	-	-
Sspon.01G0041470-1B	NADH dehydrogenase 1 beta subcomplex subunit 10-B-like	13,5	-	-
Sspon.01G0057570-1D	uncharacterized protein LOC100276776	4,5	-	-
Sspon.01G0047520-2D	Splicing factor 3B subunit 6-like protein	30	-	-
Sspon.02G0007240-1A	ubiquinol-cytochrome C chaperone family protein	7,2	-	-
Sspon.02G0004130-2B	Saccharopine dehydrogenase	6,6	-	-
Sspon.03G0038270-1C	Nuclear transport factor 2 (NTF2) family protein	10,5	-	-
Sspon.01G0022870-2B	acyl carrier protein 3, mitochondrial	8,7	-	-
Sspon.01G0009870-1A	acyl carrier protein	17,6	-	-
Sspon.01G0010270-3D	Peptide methionine sulfoxide reductase B5	6,7	-	-
Sspon.04G0018840-2B	DNA polymerase V family	2,6	-	-
Sspon.01G0047320-1B	unnamed protein product	1,4	-	-
Sspon.02G0004250-2B	nuclear transport factor 2-like isoform X2	19,8	-	-
Sspon.02G0007110-2C	ATP synthase subunit delta', mitochondrial	9,9	-	-
Sspon.02G0005590-4D	mitochondrial pyruvate carrier 4-like	9,2	-	-
Sspon.01G0030580-1A	brain protein 44-like protein	15,2	-	-
Sspon.03G0005630-4D	Putative serine peptidase S28 family protein	8,8	-	-
Sspon.03G0010210-3C	malate dehydrogenase, mitochondrial	16,1	-	-
Sspon.02G0028050-2B	Cofactor-independent phosphoglycerate mutase	11,7	-	-
Sspon.01G0031120-1A	Mitochondrial Rho GTPase	12,6	-	-
Sspon.04G0004060-1P	mitochondrial metalloendopeptidase OMA1-like	4,1	-	-
Sspon.04G0026530-1B	unnamed protein product	14,1	-	-
Sspon.04G0014440-2C	uncharacterized protein LOC103654780	3,9	-	-
Sspon.02G0017390-1P	Co-chaperone GrpE family protein	9,5	-	-
Sspon.02G0035980-3D	mediator of RNA polymerase II transcription subunit 8	2,1	-	-
Sspon.04G0001500-3D	DNA replication licensing factor MCM5	17,2	-	-
Sspon.04G0026620-1B	Guanylate-binding family protein	4,7	-	-
Sspon.02G0030710-3D	methylcrotonoyl-CoA carboxylase subunit alpha	7,4	-	-
Sspon.03G0033790-1B	NAD dependent epimerase/dehydratase family protein	9,5	-	-
Sspon.01G0038720-1B	catalytic/ oxidoreductase, acting on NADH or NADPH	26,4	-	-
Sspon.01G0028400-2D	putative helicase MAGATAMA 3	5,7	-	-
Sspon.01G0001950-3D	Chitin elicitor-binding protein	12,1	-	-
Sspon.04G0011290-2B	WD40 repeat protein	19,2	-	-
Sspon.03G0003670-4D	nonspecific lipid-transfer protein precursor	19,5	-	-
Sspon.01G0030730-1A	Dihydrolipoyllysine-residue acetyltransferase component 1 of pyruvate dehydrogenase complex mitochondrial	6,5	-	-
Sspon.03G0029230-1P	Sm-like protein lsm3b	22,9	-	-
Sspon.02G0023570-2D	leucine-rich repeat extensin-like protein 4	12,7	-	-
Sspon.03G0014960-1P	Dihydrolipoyl dehydrogenase 1, mitochondrial	47,9	-	-
Sspon.03G0014790-3C	dihydrolipoyl dehydrogenase	8,6	-	-
Sspon.03G0028860-2D	lipoxigenase2	11,8	-	-
Sspon.01G0025830-2B	lipoxigenase4	23,2	-	-
Sspon.01G0062210-1D	leukotriene A-4 hydrolase homolog	31,9	-	-
Sspon.01G0009980-3D	COMPASS-like H3K4 histone methylase component WDR5B	8,1	-	-
Sspon.01G0038980-1B	RNA-binding (RRM/RBD/RNP motifs) family protein	20	-	-
Sspon.04G0009390-2B	armadillo repeat-containing protein LFR	3,5	-	-
Sspon.04G0007470-1A	L-type lectin-domain containing receptor kinase SIT1-like	3,3	-	-
Sspon.01G0021450-1A	Lecithin-cholesterol acyltransferase-like 1	5,6	-	-

Sspon.04G0001610-1A	Leucine aminopeptidase 2 chloroplastic	51,9	-	-
Sspon.01G0033470-1A	ATP-dependent DNA helicase 2 subunit KU80	2,9	-	-
Sspon.03G0023950-2B	KIN17-like protein	4	-	-
Sspon.01G0011870-3D	3-oxoacyl-[acyl-carrier-protein] synthase II, chloroplastic-like	13,4	-	-
Sspon.02G0023970-4D	FAD-dependent oxidoreductase family protein	7,1	-	-
Sspon.02G0027060-3C	putative mediator of RNA polymerase II transcription subunit 26	6,5	-	-
Sspon.04G0018590-1A	glucan endo-1,3-beta-glucosidase 6	5,6	-	-
Sspon.01G0027750-3C	prostamide/prostaglandin F synthase-like	8	-	-
Sspon.02G0019390-2B	phosphomannomutase/phosphoglucomutase isoform X1	31,2	-	-
Sspon.01G0015220-3D	Chain A, Inositol-tetrakisphosphate 1-kinase 1	11	-	-
Sspon.03G0022100-1A	aromatic aminotransferase ISS1-like	11,6	-	-
Sspon.02G0012620-3D	isoamylase-type starch debranching enzyme3	4	-	-
Sspon.02G0006000-3D	putative isopentenyl pyrophosphate:dimethylallyl pyrophosphate isomerase	24,1	-	-
Sspon.03G0020960-1P	Importin subunit alpha	3,8	-	-
Sspon.03G0010610-2B	protein INVOLVED IN DE NOVO 2-like	5,2	-	-
Sspon.03G0016690-2B	Isocitrate dehydrogenase catalytic subunit 5 mitochondrial	38,9	-	-
Sspon.02G0028730-1A	Metallopeptidase M24 family protein	10,8	-	-
Sspon.02G0006430-2B	isocitrate lyase	15,7	-	-
Sspon.04G0004800-1A	Protein-tyrosine-phosphatase IBR5	15,1	-	-
Sspon.02G0011520-2B	heat shock 70 kDa protein	10,2	-	-
Sspon.01G0051970-1C	heat shock cognate 70 kDa protein 2	35,5	-	-
Sspon.01G0051580-1C	17.9 kDa class I heat shock protein	8,2	-	-
Sspon.03G0004950-2C	ERAD-associated E3 ubiquitin-protein ligase component HRD3A	3,1	-	-
Sspon.03G0026940-1B	hexokinase-3	5	-	-
Sspon.01G0001590-1A	Heavy metal-associated isoprenylated plant protein 39	7,6	-	-
Sspon.03G0022200-2B	DExH-box ATP-dependent RNA helicase DExH10	5	-	-
Sspon.02G0026630-3C	histone deacetylase	10,6	-	-
Sspon.04G0017850-2B	protein SCO1 homolog 1, mitochondrial	11,9	-	-
Sspon.02G0016190-2B	Histone acetyltransferase type B catalytic subunit	5,9	-	-
Sspon.03G0016850-1A	DNA gyrase subunit B, chloroplastic/mitochondrial	6,7	-	-
Sspon.01G0048420-1B	DNA gyrase subunit A chloroplastic/mitochondrial	7,7	-	-
Sspon.04G0025250-1P	glutathione S-transferase	12,8	-	-
Sspon.03G0026600-2C	putative glutathione S-transferase	6	-	-
Sspon.03G0037900-1C	glutathione S-transferase GST 21 isoform X1	4,7	-	-
Sspon.01G0013410-3P	probable glutathione S-transferase GSTU6	15,9	-	-
Sspon.01G0013350-1A	putative glutathione S-transferase GSTU6	1,3	-	-
Sspon.01G0013410-2P	probable glutathione S-transferase GSTU6	14,4	-	-
Sspon.01G0002010-2D	glutathione transferase10	7,9	-	-
Sspon.03G0036410-2C	monothiol glutaredoxin-S4, mitochondrial	26,7	-	-
Sspon.04G0024540-1B	Grx_C2.1 - glutaredoxin subgroup I	13,2	-	-
Sspon.01G0038060-2D	Hydroxyacylglutathione hydrolase cytoplasmic	20,9	-	-
Sspon.01G0007760-2B	glutamine synthetase	22	-	-
Sspon.02G0027310-1A	SSXT protein	17	-	-
Sspon.01G0036810-3D	LisH and RanBPM domains containing protein	15,9	-	-
Sspon.01G0040550-2C	indole-3-acetic acid amido synthetase	10,4	-	-
Sspon.03G0005770-3D	putative indole-3-acetic acid-amido synthetase GH3.2	14,9	-	-
Sspon.02G0026050-2B	Pentatricopeptide repeat-containing protein ELI1 chloroplastic	28,7	-	-
Sspon.04G0016440-2B	Glycerophosphodiester phosphodiesterase GDPDL3	4,9	-	-
Sspon.04G0009330-2B	glycerophosphodiester phosphodiesterase GDPDL3	13,9	-	-
Sspon.03G0005820-1A	Glycerophosphodiester phosphodiesterase GDPD5	5,3	-	-
Sspon.01G0045110-2D	Glycerophosphoryl diester phosphodiesterase	6,8	-	-
Sspon.03G0030310-1B	protein GAMETE CELL DEFECTIVE 1, mitochondrial	5	-	-
Sspon.02G0028110-1A	Golgin candidate 6	4	-	-
Sspon.02G0018910-2D	Nuclear pore complex protein GP210	3,9	-	-
Sspon.04G0017360-1A	glyceraldehyde-3-phosphate dehydrogenase, cytosolic	15	-	-
Sspon.04G0017360-2B	glyceraldehyde-3-phosphate dehydrogenase, cytosolic	16,2	-	-
Sspon.01G0031750-1A	Galactokinase	6,7	-	-
Sspon.01G0008460-2D	Glucose-6-phosphate 1-dehydrogenase 4 chloroplastic	3,4	-	-
Sspon.03G0008570-1A	Serine/threonine-protein phosphatase	17,6	-	-
Sspon.03G0028800-1B	Peroxin domain-containing protein	3,1	-	-
Sspon.01G0000640-2B	folylpolyglutamate synthase	3,5	-	-
Sspon.04G0004870-3C	Clustered mitochondria protein	4,5	-	-
Sspon.02G0036540-2C	Protein FLX-like 1	4,6	-	-
Sspon.01G0029890-1A	Fasciclin-like arabinogalactan protein 16	4,5	-	-
Sspon.02G0011030-2B	FK506-binding protein 2-1 precursor	19,5	-	-
Sspon.01G0003150-1A	FH protein interacting protein FIP2-like isoform X1	7	-	-
Sspon.01G0016730-3C	bifunctional riboflavin kinase/FMN phosphatase-like isoform X1	5,4	-	-
Sspon.01G0047970-2D	Fes1A	8,1	-	-
Sspon.03G0020410-4D	Factor of DNA methylation 4	9	-	-
Sspon.01G0031930-3D	ferredoxin-3, chloroplastic	9,3	-	-
Sspon.04G0012290-3C	fructose-bisphosphate aldolase 1, cytoplasmic	58,7	-	-
Sspon.03G0003730-1A	non-green plastid inner envelope membrane protein	8	-	-
Sspon.01G0047810-2D	Fumarylacetoacetate (FAA) hydrolase family	21,6	-	-
Sspon.02G0010900-2B	Ribulose-phosphate 3-epimerase	15,8	-	-
Sspon.01G0025980-1A	pinin/SDK/memA/ protein conserved region containing protein	4,7	-	-

Sspon.02G0011390-1T	Proton pump-interactor 1	2,1	-	-
Sspon.03G0007010-1A	Phenylalanine--tRNA ligase, chloroplastic/mitochondrial	7,9	-	-
Sspon.03G0032440-1B	putative aldo-keto reductase 1	33,3	-	-
Sspon.03G0032470-2C	putative aldo-keto reductase 4	31,7	-	-
Sspon.03G0015140-1A	caffeoylshikimate esterase-like	11,6	-	-
Sspon.04G0013460-1P	cinnamoyl-CoA reductase-like protein 2	35,3	-	-
Sspon.02G0000720-3D	rhodanese-like/PpiC domain-containing protein 12, chloroplastic isoform X2	14,6	-	-
Sspon.02G0003050-1A	Ribonuclease 1	22,5	-	-
Sspon.04G0012080-1A	2-oxoglutarate-dependent dioxygenase DAO-like	17,9	-	-
Sspon.02G0033600-2C	DNAJ heat shock N-terminal domain-containing protein	4,9	-	-
Sspon.02G0048760-1C	trafficking protein particle complex subunit 2-like protein	9,7	-	-
Sspon.01G0031790-1A	huntingtin-interacting protein K-like	15,4	-	-
Sspon.04G0018360-1A	pyridoxamine 5-phosphate oxidase family protein	5,7	-	-
Sspon.01G0056570-2D	oleosin 18 kDa	5,1	-	-
Sspon.04G0017730-3C	FAD/NAD(P)-binding oxidoreductase family protein	4	-	-
Sspon.03G0034250-1B	serine/threonine-protein phosphatase 4 regulatory subunit 3-like	3,9	-	-
Sspon.03G0001310-4D	Rhodanese/Cell cycle control phosphatase superfamily protein	2	-	-
Sspon.03G0013190-1A	cysteine sulfinate desulfinase/cysteine desulfurase and related enzymes	13,7	-	-
Sspon.02G0020090-3C	uncharacterized protein LOC8057932	8,7	-	-
Sspon.04G0003620-2C	VW domain-binding protein 11	9,5	-	-
Sspon.04G0025350-2C	Ligatin	1,9	-	-
Sspon.04G0015420-3C	Alba DNA/RNA-binding protein	18,4	-	-
Sspon.02G0015930-1A	unnamed protein product	23,3	-	-
Sspon.04G0007270-1A	receptor-like protein kinase precursor	9,5	-	-
Sspon.04G0007270-2B	receptor-like protein kinase precursor	3	-	-
Sspon.03G0000530-3C	AP-4 complex subunit epsilon	4,1	-	-
Sspon.03G0013170-1A	UPF0587 protein F46B6.12-like	38,6	-	-
Sspon.02G0008950-2D	DUF1279 family protein	9,1	-	-
Sspon.02G0011220-4D	probable sarcosine oxidase	3,4	-	-
Sspon.03G0038680-1C	putative sarcosine oxidase	3,6	-	-
Sspon.01G0035440-2D	NADH-ubiquinone oxidoreductase B16.6 subunit	11,9	-	-
Sspon.02G0018530-1P	Short-chain dehydrogenase TIC 32 chloroplastic	18	-	-
Sspon.02G0032430-1P	alpha/beta-Hydrolases superfamily protein	6,2	-	-
Sspon.04G0007020-1A	ribosomal RNA small subunit methyltransferase nep-1	10,4	-	-
Sspon.01G0035630-2D	Vicilin-like seed storage protein	14,3	-	-
Sspon.01G0035630-2P	Vicilin-like seed storage protein	17,4	-	-
Sspon.04G0000130-1P	unnamed protein product	17	-	-
Sspon.02G0048990-1C	ferredoxin	6,5	-	-
Sspon.01G0062710-1D	multiple inositol polyphosphate phosphatase 1-like isoform X1	4,9	-	-
Sspon.03G0011540-4D	yip1 domain family member 1	9,3	-	-
Sspon.02G0012540-2B	glutamyl-tRNA reductase-binding protein, chloroplastic	6,1	-	-
Sspon.02G0047360-2D	alpha-L-fucosidase 2 precursor	14,6	-	-
Sspon.04G0000940-2C	Trimeric LpxA-like enzyme	11,1	-	-
Sspon.03G0045570-1D	Pentatricopeptide (PPR) repeat protein-like	8,4	-	-
Sspon.03G0032640-1B	ATP synthase epsilon chain, mitochondrial	17,7	-	-
Sspon.03G0025090-1A	RNA-binding KH domain-containing protein RCF3-like isoform X1	3,7	-	-
Sspon.03G0040840-1C	probable 3-hydroxyisobutyrate dehydrogenase-like 1, mitochondrial	5,1	-	-
Sspon.03G0017030-1A	Translin family protein	5,3	-	-
Sspon.04G0031020-2D	quinone oxidoreductase	9,7	-	-
Sspon.04G0001210-3D	quinone oxidoreductase PIG3-like	9,5	-	-
Sspon.01G0036080-2D	Methionine--tRNA ligase cytoplasmic	7,6	-	-
Sspon.01G0020810-1A	pentatricopeptide repeat-containing protein At4g21705, mitochondrial	3,9	-	-
Sspon.01G0038790-2C	NADH dehydrogenase 1 alpha subcomplex subunit 8-B	11,8	-	-
Sspon.01G0025300-3D	p8MTCP1	33,1	-	-
Sspon.02G0045520-1B	protein YIF1A	6	-	-
Sspon.01G0017560-2B	oxidoreductase	5	-	-
Sspon.03G0020720-4D	universal stress protein PHOS34-like	8,2	-	-
Sspon.04G0027380-1B	Xaa-Pro dipeptidase	14,3	-	-
Sspon.03G0001080-2C	pentatricopeptide repeat-containing protein	2,1	-	-
Sspon.03G0011480-2C	GTP-binding nuclear protein Ran-3	6,3	-	-
Sspon.02G0002080-1A	BSD domain-containing protein 1-like	4,4	-	-
Sspon.03G0027150-2C	basic 7S globulin-like	7,8	-	-
Sspon.03G0027150-1B	basic 7S globulin-like	5,5	-	-
Sspon.03G0004430-2B	F1F0-ATPase inhibitor protein	16,1	-	-
Sspon.08G0005130-1P	mucin-2	3	-	-
Sspon.01G0016620-1A	Adenylosuccinate lyase	16,7	-	-
Sspon.03G0022180-1P	eukaryotic translation initiation factor 3 subunit M-like	51,2	-	-
Sspon.03G0010130-4D	ketol-acid reductoisomerase, chloroplastic-like	26,3	-	-
Sspon.03G0025610-2C	transducin family protein / WD-40 repeat family protein	8,5	-	-
Sspon.01G0001800-4D	NADH-ubiquinone oxidoreductase B18 subunit	20,4	-	-
Sspon.01G0011960-1A	Ubiquinone biosynthesis protein COQ9, mitochondrial	8	-	-
Sspon.01G0045710-1B	Protein transport protein Sec61 subunit alpha	7,6	-	-
Sspon.04G0021120-1A	ribosomal S subunit	3,8	-	-
Sspon.03G0031160-1B	3-hydroxyisobutyryl-CoA hydrolase/ catalytic	3,8	-	-
Sspon.02G0043580-2D	Membrane magnesium transporter	10,6	-	-

Sspon.02G0012750-2B	Coatomer subunit zeta-2	13,7	-	-
Sspon.03G0003340-2B	ureidoglycolate hydrolase	10,9	-	-
Sspon.01G0014040-3C	3-hydroxyisobutryl-CoA hydrolase-like protein 2, mitochondrial-like	5,8	-	-
Sspon.01G0054990-2D	unnamed protein product	10,8	-	-
Sspon.01G0045920-1P	cortical cell-delineating protein-like	18,1	-	-
Sspon.01G0014180-4D	beta-expansin 1a precursor	10,9	-	-
Sspon.01G0014180-3C	expansin-B2	5,6	-	-
Sspon.01G0014160-4D	expansin-B3	14,4	-	-
Sspon.01G0014170-2D	Expansin-B4 precursor	14,8	-	-
Sspon.04G0003560-2D	expansin-A5	6,5	-	-
Sspon.04G0002980-3C	phi-1-like phosphate-induced protein	18,5	-	-
Sspon.01G0008860-1T	ricin B-like lectin R40C1	13,4	-	-
Sspon.03G0018250-2B	ricin B-like lectin R40G3	15,9	-	-
Sspon.01G0047560-1B	electron transfer flavoprotein subunit alpha, mitochondrial	20,1	-	-
Sspon.02G0024200-4D	CSC1-like protein ERD4	4,5	-	-
Sspon.01G0000850-1A	early nodulin-like protein 1 precursor	6,2	-	-
Sspon.01G0007890-3C	enolase	10,4	-	-
Sspon.02G0015690-4D	enolase 1, chloroplastic-like	4,5	-	-
Sspon.01G0004760-1P	Protein EMBRYO DEFECTIVE 514-like	19,7	-	-
Sspon.03G0011990-3C	pentatricopeptide repeat-containing protein At3g49240, mitochondrial-like	9,9	-	-
Sspon.04G0018470-3C	eukaryotic initiation factor 4A	48,5	-	-
Sspon.01G0026470-1P	Eukaryotic translation initiation factor isoform 4E-2	10,5	-	-
Sspon.02G0023760-1P	evolutionarily conserved C-terminal region 2	2,8	-	-
Sspon.01G0050300-1C	evolutionarily conserved C-terminal region 2	2,7	-	-
Sspon.01G0039030-1B	Calcium-transporting ATPase 4, endoplasmic reticulum-type	15,3	-	-
Sspon.01G0013740-3C	Ubiquitin domain-containing protein DSK2b	5,7	-	-
Sspon.03G0033550-1B	DNA-damage-repair/toleration protein DRT102	11,3	-	-
Sspon.03G0037170-2C	phosphoacetylglucosamine mutase	5,9	-	-
Sspon.01G0014940-3C	dynamamin-related protein 1E-like	8,3	-	-
Sspon.01G0021830-2B	dormancy-associated protein 1	26,6	-	-
Sspon.02G0002980-2B	developmentally-regulated GTP-binding protein 1	9,2	-	-
Sspon.01G0030960-3D	phosphatase 2C 55	3,9	-	-
Sspon.03G0017420-4D	Dynein light chain type 1 family protein	12,9	-	-
Sspon.01G0002860-3C	Os03g0149200	15,8	-	-
Sspon.01G0032870-1A	unnamed protein product	10,7	-	-
Sspon.03G0037130-2D	Protein DJ-1 homolog B	2,5	-	-
Sspon.02G0050950-2D	PVR3-like protein	12,6	-	-
Sspon.02G0009080-4D	3-dehydroquinate synthase chloroplastic	9	-	-
Sspon.01G0026110-2B	ornithine-oxo-acid transaminase	14,8	-	-
Sspon.04G0005030-2P	protease Do-like 7 isoform X1	10,1	-	-
Sspon.02G0002130-2C	39S ribosomal protein L46, mitochondrial-like	4,2	-	-
Sspon.03G0018600-2B	Protein decapping 5	5,2	-	-
Sspon.02G0043590-1B	diaminopimelate epimerase chloroplastic isoform X2	8	-	-
Sspon.02G0023300-3C	probable D-2-hydroxyglutarate dehydrogenase, mitochondrial	5,3	-	-
Sspon.03G0038400-1P	cytochrome b5	22,2	-	-
Sspon.03G0028290-2C	cysteine proteinase inhibitor 4-like	9,2	-	-
Sspon.02G0019300-4D	Trans-cinnamate 4-monooxygenase	10,4	-	-
Sspon.01G0047450-1P	peptidyl-prolyl cis-trans isomerase H	33,3	-	-
Sspon.02G0039790-1B	Peptidyl-prolyl cis-trans isomerase CYP19-3	11,3	-	-
Sspon.07G0007070-4P	Fructose-1,6-bisphosphatase, cytosolic	18,8	-	-
Sspon.01G0029980-2C	putative carboxylesterase 15	10	-	-
Sspon.03G0020950-1P	putative carboxylesterase 15	10,1	-	-
Sspon.01G0029760-1A	Cullin-4	5,6	-	-
Sspon.03G0014150-1A	cullin-1-like protein	0,9	-	-
Sspon.03G0020430-4D	triosephosphate isomerase, cytosolic	49,6	-	-
Sspon.03G0003800-2B	Protein kinase family protein with ARM repeat domain	2,1	-	-
Sspon.01G0005320-1A	COP9 signalosome complex subunit 4	33,2	-	-
Sspon.03G0016550-1A	COP9 signalosome complex subunit 2	9,6	-	-
Sspon.02G0021530-1A	Calreticulin-2	34,8	-	-
Sspon.01G0047800-1B	calreticulin-like	32,6	-	-
Sspon.01G0052030-1P	Cysteine-rich repeat secretory protein 55	13,7	-	-
Sspon.02G0011500-2B	NAD(P)-binding Rossmann-fold superfamily protein	13,3	-	-
Sspon.01G0020780-1A	predicted protein	13,6	-	-
Sspon.02G0006160-1A	Receptor-like protein kinase RK20-1	4,2	-	-
Sspon.01G0032140-1A	Cleavage and polyadenylation specificity factor subunit 2	2,2	-	-
Sspon.03G0034520-1T	putative L-cysteine desulfhydrase 1	17	-	-
Sspon.02G0013970-1T	20 kDa chaperonin, chloroplastic-like	10,7	-	-
Sspon.01G0014920-4D	CHL-CPN10	15,7	-	-
Sspon.04G0010820-1A	N-carbamoylputrescine amidase	17,8	-	-
Sspon.02G0018980-1A	RNA-binding protein CP31B chloroplastic	14,5	-	-
Sspon.01G0011390-1P	cytochrome c oxidase subunit 6b-1-like	11,3	-	-
Sspon.01G0007130-2C	Coronatine-insensitive protein 1	2,5	-	-
Sspon.01G0004030-2B	Conserved oligomeric Golgi complex subunit 4	2,1	-	-
Sspon.02G0003340-2B	caltractin	6,6	-	-
Sspon.04G0016890-2B	chorismate mutase2	14,8	-	-

Sspon.01G0006590-4D	ATP-dependent Clp protease ATP-binding subunit CLPT1 chloroplastic	17,2	-	-
Sspon.03G0034850-2D	ATP-dependent Clp protease proteolytic subunit-related protein 4, chloroplastic-like	10,9	-	-
Sspon.01G0008260-3D	ATP-dependent Clp protease proteolytic subunit 5, chloroplastic-like	4,9	-	-
Sspon.01G0015500-1A	ATP-dependent Clp protease proteolytic subunit	20,6	-	-
Sspon.03G0022700-2B	Chain A, Cytokinin dehydrogenase 1	6,7	-	-
Sspon.02G0002180-3C	NADH dehydrogenase flavoprotein 1, mitochondrial	23,6	-	-
Sspon.01G0013780-4D	chitinase 8-like	7,7	-	-
Sspon.01G0010750-3C	Cystathionine gamma-synthase 1 chloroplastic	3,1	-	-
Sspon.02G0032960-1B	T-complex protein 1 subunit zeta	22,2	-	-
Sspon.02G0032960-2C	T-complex protein 1 subunit zeta	22,2	-	-
Sspon.04G0017280-1A	choline-phosphate cytidylyltransferase 1	10,9	-	-
Sspon.07G0029590-2C	ubiquitin-fold modifier 1	28,3	-	-
Sspon.03G0012400-2B	SNF1-related protein kinase regulatory subunit gamma-1-like	3,3	-	-
Sspon.03G0030050-2C	cytochrome b5 reductase	12,1	-	-
Sspon.04G0032300-1T	nuclear cap-binding protein subunit 2	5	-	-
Sspon.01G0050630-1P	catalase-1	10,4	-	-
Sspon.01G0026910-2C	Exportin-2	13	-	-
Sspon.04G0018570-2B	Cycloartenol synthase	9,4	-	-
Sspon.03G0016830-3D	calmodulin-3	57	-	-
Sspon.01G0028540-2B	isoflavone 3'-hydroxylase-like	8,6	-	-
Sspon.01G0019710-1A	Basic transcription factor 3	11,7	-	-
Sspon.01G0032880-3P	Basic transcription factor 3	14,6	-	-
Sspon.01G0020510-1P	Endosomal targeting BRO1-like domain-containing protein	2,5	-	-
Sspon.01G0015140-2P	mitochondrial carnitine/acylcarnitine carrier-like protein	7,7	-	-
Sspon.01G0025920-4D	beta-glucosidase 7	7,4	-	-
Sspon.03G0018780-1A	Os01g0508000	6,7	-	-
Sspon.02G0010510-2B	beta-glucosidase 31-like	5,3	-	-
Sspon.01G0051490-1C	Beta-galactosidase	11,1	-	-
Sspon.03G0045220-1D	Beta-galactosidase 3	3,5	-	-
Sspon.03G0032130-1B	carbonic anhydrase3	31,8	-	-
Sspon.01G0043450-1B	universal stress protein YxiE-like	16,8	-	-
Sspon.01G0042820-1B	NagB/RpiA/CoA transferase-like superfamily protein	3,9	-	-
Sspon.03G0038490-1P	UDP-D-apiose/UDP-D-xylose synthase 2	12,5	-	-
Sspon.02G0031900-3C	copper chaperone	29,1	-	-
Sspon.01G0029830-1A	DnaJ protein	11,6	-	-
Sspon.03G0023790-1A	heme-binding protein 2	5,8	-	-
Sspon.01G0019390-2B	calcium ion binding	2,9	-	-
Sspon.01G0022530-1A	alpha-soluble NSF attachment protein	20,9	-	-
Sspon.01G0047030-3D	Chemocyanin	29,7	-	-
Sspon.01G0043400-2D	Actin-related protein 7	11,1	-	-
Sspon.01G0003310-3C	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase 2	34,8	-	-
Sspon.02G0000860-1A	Apyrase 1	4,1	-	-
Sspon.01G0031820-1A	Pumilio homolog 24	2,7	-	-
Sspon.04G0024680-2C	adenine phosphoribosyltransferase 2	23	-	-
Sspon.03G0038160-1C	adenine phosphoribosyltransferase1	8,7	-	-
Sspon.02G0017170-3D	glucose-1-phosphate adenyllyltransferase small subunit, chloroplastic/amyloplastic-like	10,1	-	-
Sspon.03G0026810-1B	RNA-binding (RRM/RBD/RNP motifs) family protein	9,4	-	-
Sspon.03G0008150-3C	AP-1 complex subunit mu-2	4,9	-	-
Sspon.01G0012880-3C	Allene oxide cyclase, chloroplastic	15,5	-	-
Sspon.03G0004310-3D	metacaspase-5-like	8,3	-	-
Sspon.02G0022030-4D	THO complex subunit 4B	14,1	-	-
Sspon.04G0011740-1A	acetolactate synthase ALS1	12,6	-	-
Sspon.02G0010390-1A	Ankyrin repeat domain-containing protein 2A	10,2	-	-
Sspon.02G0017280-1A	Bifunctional aspartokinase/homoserine dehydrogenase 2, chloroplastic	4,8	-	-
Sspon.01G0023750-4D	prefoldin subunit 4	55,6	-	-
Sspon.03G0035580-2C	Actin-interacting protein 1-2	17,9	-	-
Sspon.04G0013020-1A	Peroxisomal fatty acid beta-oxidation multifunctional protein	10	-	-
Sspon.01G0025350-1A	ATPase 4 plasma membrane-type	11,6	-	-
Sspon.01G0035360-2D	alanine--glyoxylate aminotransferase 2 homolog 1, mitochondrial	4	-	-
Sspon.02G0000970-4D	Alpha-galactosidase 3	13,3	-	-
Sspon.01G0020210-2B	alpha-galactosidase-like	20,2	-	-
Sspon.02G0039490-1B	alpha-galactosidase	4,3	-	-
Sspon.01G0046650-2D	Endoplasmic reticulum oxidoreductin-1	2,7	-	-
Sspon.01G0029170-1P	protein AE7-like 1	19,4	-	-
Sspon.01G0004730-1A	aspartyl protease 25-like	4,9	-	-
Sspon.01G0052390-2D	Arogenate dehydratase/prephenate dehydratase 2 chloroplastic	21,5	-	-
Sspon.04G0000870-2B	alcohol dehydrogenase class 3	21	-	-
Sspon.01G0027970-2D	alcohol dehydrogenase 1	34,3	-	-
Sspon.03G0021150-2B	glutaryl-CoA dehydrogenase	4,3	-	-
Sspon.03G0002780-3C	acyl-coenzyme A oxidase 3, peroxisomal-like	5	-	-
Sspon.01G0031940-2B	actin-3	48,5	-	-
Sspon.04G0002530-2B	1-aminocyclopropane-1-carboxylate oxidase 1	6,5	-	-
Sspon.01G0042470-2C	Acetyl-CoA carboxylase 1	1,8	-	-
Sspon.02G0051760-1C	ABC transporter F family member 4	6	-	-

Sspon.02G0027040-1A	ABC transporter F family member 1	5	-	-
Sspon.01G0036530-2C	ABC transporter E family member 2	6	-	-
Sspon.04G0015320-2B	Plastidic ATP/ADP-transporter	12,9	-	-
Sspon.03G0018740-1A	acetyl-CoA acetyltransferase, cytosolic 1-like isoform X1	11	-	-
Sspon.01G0059620-1D	Acylamino-acid-releasing enzyme	4,1	-	-
Sspon.01G0029940-2P	aldehyde oxidase4	5	-	-
Sspon.02G0015440-1A	putative acyl-activating enzyme 17 peroxisomal	15,3	-	-
Sspon.03G0031010-1B	Long-chain-fatty-acid-CoA ligase-like protein	2,1	-	-
Sspon.03G0018740-2C	putative acetyl-CoA acetyltransferase cytosolic 2	12,6	-	-
Sspon.02G0005260-1A	elongation factor 1-alpha	34,3	-	-
Sspon.01G0035220-2C	TATA-binding protein-associated factor 2N-like isoform X1	10,6	-	-
Sspon.04G0015820-2B	Chaperone protein dnaJ 6	4,9	-	-
Sspon.02G0034610-2C	5-formyltetrahydrofolate cyclo-ligase, mitochondrial-like isoform X1	6	-	-
Sspon.02G0050510-2D	coumaroyl-CoA:anthocyanidin 3-O-glucoside-6'	3,7	-	-
Sspon.08G0029260-1D	12-oxophytodienoate reductase 1-like	5,8	-	-
Sspon.08G0004110-1P	14 kDa zinc-binding protein-like	10,8	-	-
Sspon.08G0023150-2D	26S proteasome regulatory subunit 6A homolog	27,6	-	-
Sspon.07G0034100-1C	2-alkenal reductase (NADP(+)-dependent)-like	18,7	-	-
Sspon.07G0017060-2C	2-isopropylmalate synthase B	27,4	-	-
Sspon.05G0012790-1A	2-oxoglutarate dehydrogenase E1 component	12,1	-	-
Sspon.06G0008900-2B	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ-like	10,7	-	-
Sspon.08G0006670-3C	3-hydroxyisobutyryl-CoA hydrolase-like protein 3 mitochondrial	13,5	-	-
Sspon.04G0011920-4D	3-oxoacyl-[acyl-carrier-protein] reductase 4-like	21,8	-	-
Sspon.05G0013240-2B	3-oxoacyl-[acyl-carrier-protein] reductase 4-like	17,3	-	-
Sspon.07G0007540-3C	40S ribosomal protein S12	23	-	-
Sspon.06G0013710-1T	40S ribosomal protein S13	41	-	-
Sspon.04G0010770-4D	40S ribosomal protein S14	47,1	-	-
Sspon.06G0021050-1B	40S ribosomal protein S15a-1-like	16,5	-	-
Sspon.08G0020480-2C	40S ribosomal protein S24-1	13,4	-	-
Sspon.06G0017470-3C	40S ribosomal protein S29	37,5	-	-
Sspon.08G0023090-2D	40S ribosomal protein S30-like	16,1	-	-
Sspon.07G0027860-2C	4F5 protein family protein	3,8	-	-
Sspon.04G0028680-3D	4-hydroxyphenylpyruvate dioxygenase-like	5,1	-	-
Sspon.05G0031760-2D	4-hydroxy-tetrahydrodipicolinate synthase 2 chloroplastic	15,4	-	-
Sspon.08G0016210-1A	5-enolpyruvylshikimate-3-phosphate synthase	7	-	-
Sspon.06G0002830-2P	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 2	8,3	-	-
Sspon.05G0036910-1P	6,7-dimethyl-8-ribityllumazine synthase	9,5	-	-
Sspon.07G0001510-3C	60S acidic ribosomal protein P2A	63,4	-	-
Sspon.08G0003610-4D	60S ribosomal protein L27	21,8	-	-
Sspon.08G0003610-2B	60S ribosomal protein L27	36,7	-	-
Sspon.04G0025860-3D	60S ribosomal protein L35	19,5	-	-
Sspon.05G0026500-2C	60S ribosomal protein L37a-1 isoform X2	26,1	-	-
Sspon.04G0026120-2D	7-dehydrocholesterol reductase	6,3	-	-
Sspon.05G0018980-4D	AB hydrolase superfamily protein YfhM-like	8,9	-	-
Sspon.05G0000040-1A	ABC transporter G family member 5	14,8	-	-
Sspon.05G0018690-4D	Abscisic stress ripening protein	35,3	-	-
Sspon.04G0010580-2B	Abscisic stress-ripening protein 1	22,6	-	-
Sspon.05G0017090-1A	Acetolactate synthase small subunit 1 chloroplastic	10,2	-	-
Sspon.05G0015490-1A	aconitase2	11,7	-	-
Sspon.06G0004970-2B	Activator of 90 kDa heat shock protein ATPase	13,3	-	-
Sspon.06G0003960-4D	acyl carrier protein 3	11,5	-	-
Sspon.05G0005690-4D	Acyl-acyl carrier protein thioesterase ATL3 chloroplastic	6,3	-	-
Sspon.08G0011600-2B	acylaminoacyl-peptidase1	8,7	-	-
Sspon.06G0010700-3C	acyl-CoA-binding protein	38	-	-
Sspon.08G0017120-1A	acyl-CoA-binding protein	15,4	-	-
Sspon.08G0010360-1A	acylphosphatase	16,3	-	-
Sspon.06G0010370-1A	Adenylate kinase 4	32,6	-	-
Sspon.06G0008240-2B	ADP-ribosylation factor 3	6,2	-	-
Sspon.06G0016130-3D	ADP-ribosylation factor-like protein 5	7,1	-	-
Sspon.07G0019960-2C	aladin-like	10,3	-	-
Sspon.07G0037860-1D	Alanine--tRNA ligase	27,5	-	-
Sspon.07G0037800-1D	alanine--tRNA ligase	11	-	-
Sspon.05G0029720-1B	Alba DNA/RNA-binding protein	4,3	-	-
Sspon.05G0017870-1A	Aldehyde dehydrogenase	8	-	-
Sspon.08G0014030-2B	alpha/beta-Hydrolases superfamily protein	13,4	-	-
Sspon.02G0013220-2T	alpha-amylase isozyme	15,8	-	-
Sspon.02G0013220-2B	alpha-amylase isozyme 3D	18,4	-	-
Sspon.02G0013220-1P	alpha-amylase isozyme 3D	43,5	-	-
Sspon.05G0020400-1P	Alpha-L-arabinofuranosidase 1	12,7	-	-
Sspon.05G0023980-1B	alpha-L-fucosidase 1 precursor	6,3	-	-
Sspon.06G0022450-1B	Alpha-soluble NSF attachment protein 2	32,6	-	-
Sspon.05G0004030-1A	alternative oxidase 1	9,1	-	-
Sspon.06G0019680-2D	aminoacylase-1	12,4	-	-
Sspon.05G0002990-3D	aminomethyltransferase, mitochondrial-like	3	-	-
Sspon.05G0019710-1P	AMP-binding protein	9,2	-	-
Sspon.07G0016340-1A	Ankyrin-1	5,1	-	-

Sspon.08G0013820-3D	AP-1 complex subunit gamma-1	5,7	-	-
Sspon.07G0012250-3C	Arginine--tRNA ligase chloroplastic/mitochondrial	15,9	-	-
Sspon.07G0002480-2B	ARM repeat superfamily protein	4,8	-	-
Sspon.08G0012420-2B	ARM repeat superfamily protein	3,5	-	-
Sspon.06G0026450-2C	Armadillo/beta-catenin-like repeat family protein	2,1	-	-
Sspon.06G0008230-2B	aspartate carbamoyltransferase 1	14,7	-	-
Sspon.05G0029210-1B	aspartic proteinase Asp1 precursor	15,2	-	-
Sspon.05G0000280-1A	aspartic proteinase nepenthesin-2 precursor	4,2	-	-
Sspon.01G0011620-1P	AT hook-containing MAR binding 1-like protein	2	-	-
Sspon.07G0022770-2P	atherin-like	5	-	-
Sspon.05G0004350-3D	AT-hook motif nuclear-localized protein 23	6,8	-	-
Sspon.04G0014220-4D	AT-hook motif nuclear-localized protein 24-like	5,8	-	-
Sspon.08G0017040-2B	ATOZ11	16,7	-	-
Sspon.02G0011850-2B	ATP phosphoribosyltransferase, chloroplastic-like	15,3	-	-
Sspon.05G0032260-1C	ATP synthase E chain	23,7	-	-
Sspon.05G0015870-2B	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	11,1	-	-
Sspon.05G0015870-4D	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	9,7	-	-
Sspon.03G0006890-3P	ATP-dependent 6-phosphofructokinase 3	21,5	-	-
Sspon.07G0000320-1A	ATP-dependent Clp protease proteolytic subunit	1,9	-	-
Sspon.08G0016010-1A	ATP-dependent Clp protease proteolytic subunit	5,9	-	-
Sspon.04G0007720-2P	ATP-dependent Clp protease proteolytic subunit	11,5	-	-
Sspon.07G0023300-1B	ATP-dependent zinc metalloprotease FTSH 10 mitochondrial	2,6	-	-
Sspon.06G0002400-3D	auxin-induced in root cultures protein 12-like	17	-	-
Sspon.08G0010760-4D	B12D protein	17,8	-	-
Sspon.08G0010290-2D	basic blue protein-like	10,6	-	-
Sspon.05G0022470-2D	Beta-D-xylosidase 4	5,4	-	-
Sspon.07G0015160-2B	Beta-hexosaminidase 1 precursor	4,4	-	-
Sspon.05G0009730-4D	betaine aldehyde dehydrogenase	2,7	-	-
Sspon.06G0007610-4D	Bifunctional aspartokinase/homoserine dehydrogenase 2 chloroplastic	7,9	-	-
Sspon.07G0017370-1A	Bifunctional bis(5'-adenosyl)-triphosphatase/adenylylsulfatase FHIT	16,3	-	-
Sspon.07G0017370-2C	Bifunctional bis(5'-adenosyl)-triphosphatase/adenylylsulfatase FHIT	12,1	-	-
Sspon.06G0014140-1A	Bifunctional dihydrofolate reductase-thymidylate synthase	7,8	-	-
Sspon.04G0006320-4D	Bifunctional dTDP-4-dehydrorhamnose 3,5-epimerase/dTDP-4-dehydrorhamnose reductase	5	-	-
Sspon.05G0014650-2P	bifunctional L-3-cyanoalanine synthase/cysteine synthase 2, mitochondrial	22,1	-	-
Sspon.08G0009820-3C	binding	9,3	-	-
Sspon.05G0004240-2B	Binding partner of ACD11 1	7,3	-	-
Sspon.08G0024250-2D	Binding partner of ACD11 1	14,8	-	-
Sspon.06G0003330-2B	biotin synthase, mitochondrial-like	8,3	-	-
Sspon.05G0025080-2D	Bowman-Birk type bran trypsin inhibitor	7,7	-	-
Sspon.08G0013970-2B	caffeoyl-CoA 3-O-methyltransferase 1	19,9	-	-
Sspon.06G0000920-2B	caffeoyl-CoA O-methyltransferase 1	15,1	-	-
Sspon.08G0018540-1P	calcium homeostasis endoplasmic reticulum protein-like	4,6	-	-
Sspon.07G0022470-1B	carnitine racemase/ catalytic	14,1	-	-
Sspon.05G0000370-2C	CASP-like protein 1	9,3	-	-
Sspon.08G0000830-1A	catalase	53,7	-	-
Sspon.07G0006910-2B	Cell division protein FtsZ homolog 2-2 chloroplastic	4	-	-
Sspon.06G0008280-3D	cell wall integrity protein scw1	10	-	-
Sspon.07G0005380-1A	centromeric histone H3	10,3	-	-
Sspon.08G0024130-2D	Chaperonin 60 subunit beta 2 chloroplastic	35	-	-
Sspon.05G0017050-2C	chitinase	17,1	-	-
Sspon.04G0008670-3P	chitinase	59,6	-	-
Sspon.07G0008410-2B	chitinase 2-like	23,5	-	-
Sspon.06G0012240-1P	Chloroplast J-like domain 1	7,5	-	-
Sspon.01G0041910-2D	Chromo domain-containing protein LHP1	12	-	-
Sspon.05G0036590-1C	Clathrin heavy chain 2 -like protein	30,4	-	-
Sspon.05G0002510-3P	coatomer subunit epsilon	11,2	-	-
Sspon.07G0006260-2B	Coatomer subunit zeta-1	13,6	-	-
Sspon.08G0025700-1C	Conserved oligomeric Golgi complex subunit 7	2,6	-	-
Sspon.06G0030810-1C	COP9 signalosome complex subunit 3	26	-	-
Sspon.05G0009020-1A	Copper amine oxidase family protein	3,2	-	-
Sspon.08G0006690-4D	crocin glucosyltransferase, chloroplastic	5,1	-	-
Sspon.06G0006290-3D	Crystal structure of aminoaldehyde dehydrogenase 1a from Zea mays (ZmAMADH1a)	21,8	-	-
Sspon.06G0010440-1A	Cullin-3B	4	-	-
Sspon.07G0003080-3C	Cyclin/Brf1-like TBP-binding protein	6,7	-	-
Sspon.07G0001360-3D	cycloartenol-C-24-methyltransferase 1	6,3	-	-
Sspon.08G0013630-1A	Cystathionine beta-lyase, chloroplastic	2,5	-	-
Sspon.04G0026080-2D	cysteine protease1	6	-	-
Sspon.04G0010610-1A	Cytochrome b-c1 complex subunit 6	11,6	-	-
Sspon.04G0011390-4D	Cytochrome b-c1 complex subunit Rieske, mitochondrial	7,8	-	-
Sspon.05G0002180-2C	D-3-phosphoglycerate dehydrogenase 3 chloroplastic	32,9	-	-
Sspon.07G0012130-3C	DCD (Development and Cell Death) domain protein	1,5	-	-
Sspon.06G0018770-3C	DEAD-box ATP-dependent RNA helicase 40	3,1	-	-
Sspon.06G0010830-2B	DEAD-box ATP-dependent RNA helicase 42-like	2,2	-	-

Sspon.06G0016530-1A	DEAD-box ATP-dependent RNA helicase 52C	13,2	-	-
Sspon.07G0015180-1T	dehydroascorbate reductase like3	41,9	-	-
Sspon.07G0019700-1A	Dihydrolipoyllysine-residue acetyltransferase component 5 of pyruvate dehydrogenase complex chloroplastic	12,3	-	-
Sspon.05G0000910-2C	dihydroorotate dehydrogenase	4,6	-	-
Sspon.05G0018140-2C	disease resistance response protein 206	19,7	-	-
Sspon.07G0000280-1A	DNA damage-binding protein 1a	5	-	-
Sspon.05G0017770-1A	DNA polymerase delta catalytic subunit	1,3	-	-
Sspon.06G0000180-1A	DNA-binding protein	14,2	-	-
Sspon.07G0019570-2B	DNA-directed RNA polymerase II 8.2 kDa polypeptide	12,5	-	-
Sspon.04G0029780-3D	DNA-directed RNA polymerases I and III subunit rpac1-like	11,7	-	-
Sspon.07G0020240-1A	DNA-directed RNA polymerases I and III subunit RPAC2-like	17,3	-	-
Sspon.05G0008270-4D	DNA-directed RNA polymerases II and IV subunit 5A-like	10,6	-	-
Sspon.05G0014760-4D	DNA-directed RNA polymerases II, IV and V subunit 11-like	35,8	-	-
Sspon.07G0002150-1A	DnaJ subfamily B member 13	8	-	-
Sspon.05G0012370-1P	Double Clip-N motif-containing P-loop nucleoside triphosphate hydrolase superfamily protein	12,1	-	-
Sspon.08G0005240-2T	E3 ubiquitin-protein ligase KEG-like	17,7	-	-
Sspon.05G0013610-3C	E3 ubiquitin-protein ligase UPL3	2,1	-	-
Sspon.07G0014920-3D	E3 UFM1-protein ligase 1-like protein	5	-	-
Sspon.04G0017720-2P	early nodulin-like protein 1	7	-	-
Sspon.06G0029810-1C	early nodulin-like protein 1	7,5	-	-
Sspon.08G0018190-2C	EH domain-containing protein 1	16	-	-
Sspon.05G0013920-1P	Electron transfer flavoprotein subunit beta mitochondrial	29,4	-	-
Sspon.05G0006570-4D	Elicitor-responsive protein 3	6,5	-	-
Sspon.08G0000910-1A	endochitinase A-like	17,7	-	-
Sspon.08G0016040-1A	enolase 1	72	-	-
Sspon.07G0025210-1B	ER membrane protein complex subunit 1	7,7	-	-
Sspon.08G0005150-3P	ESCRT-related protein CHMP1	10,3	-	-
Sspon.05G0020790-4D	Ethanolamine-phosphate cytidyltransferase	4,7	-	-
Sspon.07G0000260-3C	eukaryotic translation initiation factor 2 (eIF-2) family protein	3	-	-
Sspon.04G0032390-2D	eukaryotic translation initiation factor 2A isoform X1	12,1	-	-
Sspon.03G0009580-1P	Eukaryotic translation initiation factor 3 subunit D	9,2	-	-
Sspon.06G0008990-3D	evolutionarily conserved C-terminal region 10	7,7	-	-
Sspon.07G0033840-1C	exonuclease 1 isoform X1	0,8	-	-
Sspon.07G0006310-1T	exosome complex component RRP41 homolog	9,7	-	-
Sspon.03G0003660-2P	expansin-A4	5,6	-	-
Sspon.06G0024090-2C	External alternative NAD(P)H-ubiquinone oxidoreductase B4 mitochondrial	4,5	-	-
Sspon.03G0041150-2P	farnesyl pyrophosphate synthase1	6,5	-	-
Sspon.05G0004990-1P	fasciclin-like arabinogalactan protein 10 precursor	5,1	-	-
Sspon.07G0012270-2B	fasciclin-like arabinogalactan protein 2	7,8	-	-
Sspon.05G0015370-1A	fatty acid amide hydrolase	8,1	-	-
Sspon.05G0037030-1D	FBD-associated F-box protein At2g26860-like	5,6	-	-
Sspon.06G0035620-1D	F-box/LRR-repeat protein At4g14096	2,2	-	-
Sspon.04G0006020-3D	FCS-Like Zinc finger 2	12,6	-	-
Sspon.03G0002230-1P	ferredoxin-6	9,1	-	-
Sspon.06G0011410-1A	ferric-chelate reductase (NADH)2	10,8	-	-
Sspon.07G0022340-1B	Flap endonuclease 1	9,3	-	-
Sspon.06G0001520-1A	frataxin isoform X1	7,1	-	-
Sspon.07G0007070-1A	Fructose-16-bisphosphatase cytosolic	15	-	-
Sspon.04G0009830-3P	galactose mutarotase-like	11,9	-	-
Sspon.05G0025460-1B	Gamma-glutamyltranspeptidase 1	8,5	-	-
Sspon.08G0014550-3D	GDSL esterase/lipase	9,9	-	-
Sspon.08G0014550-1A	GDSL esterase/lipase	23,3	-	-
Sspon.01G0048710-2D	Globulin-2	30	-	-
Sspon.07G0002550-3C	glutamate synthase 2, chloroplastic-like	1,9	-	-
Sspon.07G0005200-1A	glutamate-1-semialdehyde 2,1-aminomutase	13,5	-	-
Sspon.07G0028390-1B	glutamate-rich WD repeat-containing protein 1	4,6	-	-
Sspon.08G0004480-3C	glutaredoxin-C8-like	9,6	-	-
Sspon.07G0012160-1A	glutaryl-CoA dehydrogenase	4,3	-	-
Sspon.07G0013110-1A	glutathione S-transferase 4	17,6	-	-
Sspon.08G0011000-3C	Glutathione S-transferase DHAR3 chloroplastic	12,9	-	-
Sspon.06G0016540-2B	Glutathione S-transferase T1	3,5	-	-
Sspon.05G0002870-2C	glutathione transferase19	14,7	-	-
Sspon.06G0012300-4D	Glyceraldehyde-3-phosphate dehydrogenase 1, cytosolic	76,2	-	-
Sspon.07G0015240-2B	glyceraldehyde-3-phosphate dehydrogenase 3, cytosolic	44,8	-	-
Sspon.05G0002420-3D	Glycerol kinase	5	-	-
Sspon.07G0027890-1B	glycine dehydrogenase (decarboxylating), mitochondrial-like	2,5	-	-
Sspon.08G0003790-4D	Glycosyl hydrolase family 31 protein	17	-	-
Sspon.07G0023710-2C	Guanosine nucleotide diphosphate dissociation inhibitor 2	34,1	-	-
Sspon.08G0004240-1A	haloacid dehalogenase-like hydrolase domain-containing protein 3	20,1	-	-
Sspon.08G0024290-1P	Haloacid dehalogenase-like hydrolase domain-containing protein Sgpp	6,3	-	-
Sspon.07G0011510-2B	Heat shock 70 kDa protein 14	35,1	-	-
Sspon.08G0010010-1A	heat shock factor-binding protein 1	14,8	-	-
Sspon.05G0027810-1B	heat shock protein 81-1	5,5	-	-

Sspon.07G0004160-3D	hemoglobin 2	14,9	-	-
Sspon.07G0012950-4D	Histidine--tRNA ligase cytoplasmic	7,1	-	-
Sspon.08G0016380-1A	Histone domain-containing protein	10,8	-	-
Sspon.08G0016410-1T	histone H1	23	-	-
Sspon.01G0015100-1A	histone H1-like protein	8,2	-	-
Sspon.05G0012470-2B	histone H2A.Z-specific chaperone CHZ1-like	7,6	-	-
Sspon.06G0000650-1P	histone H2B.3	49	-	-
Sspon.03G0039930-1P	histone H2B-like	71,2	-	-
Sspon.06G0006110-2B	HMG-Y-related protein A	31,8	-	-
Sspon.06G0006110-3C	HMG-Y-related protein A	46,8	-	-
Sspon.06G0006940-2B	Hydroxyproline O-galactosyltransferase HPGT1	7,4	-	-
Sspon.08G0008870-1T	hypothetical protein ZEAMMB73_Zm00001d045938	7,2	-	-
Sspon.01G0045890-2D	immediate-early protein RSP40	18,1	-	-
Sspon.06G0008530-2B	indole-3-glycerol phosphate synthase, chloroplastic	3,1	-	-
Sspon.07G0019770-2B	Inositol monophosphatase family protein	11,7	-	-
Sspon.04G0009130-3D	isocitrate dehydrogenase regulatory subunit 1, mitochondrial isoform X2	5,9	-	-
Sspon.05G0007390-2B	isocitrate dehydrogenase-like	21,8	-	-
Sspon.07G0014420-1A	Isovaleryl-CoA dehydrogenase mitochondrial	5,6	-	-
Sspon.07G0000930-1A	jacalin-related lectin 3	15,5	-	-
Sspon.07G0000930-3C	jacalin-related lectin 3	13,1	-	-
Sspon.05G0007860-2C	La protein 1	23,1	-	-
Sspon.05G0033150-1C	late embryogenesis abundant protein-related / LEA protein-related	10,1	-	-
Sspon.05G0019790-2B	L-galactono-1,4-lactone dehydrogenase 2, mitochondrial	5,1	-	-
Sspon.05G0020530-1T	Long chain acyl-CoA synthetase 8	15,5	-	-
Sspon.01G0021020-1A	low-temperature-induced 65 kDa protein	5,1	-	-
Sspon.05G0030670-1P	macrophage migration inhibitory factor	11,5	-	-
Sspon.07G0011420-4D	Malic enzyme	16,7	-	-
Sspon.05G0012870-2B	mediator of RNA polymerase II transcription subunit 30-like	15,3	-	-
Sspon.07G0023960-1B	methyl-binding domain protein MBD101	12,2	-	-
Sspon.05G0001320-2D	methylthioribose kinase	7,1	-	-
Sspon.07G0010760-1A	minichromosome maintenance protein	12,5	-	-
Sspon.01G0055830-1C	mitochondrial import receptor subunit TOM6 homolog	39,3	-	-
Sspon.06G0027850-3D	Mitochondrial uncoupling protein 1	13	-	-
Sspon.08G0013070-1A	Monocopper oxidase-like protein SKU5	9,4	-	-
Sspon.06G0011470-3C	Monodehydroascorbate reductase 5 mitochondrial	15,9	-	-
Sspon.05G0019160-3C	mRNA-decapping enzyme-like protein	2,5	-	-
Sspon.08G0016880-2B	multiple organellar RNA editing factor 2, chloroplastic-like	9,4	-	-
Sspon.06G0002220-1A	myosin heavy chain-related	8,1	-	-
Sspon.08G0017430-2D	NADH ubiquinone oxidoreductase B22-like subunit	28,1	-	-
Sspon.06G0019200-2D	NADH:quinone reductase-like	6,7	-	-
Sspon.06G0000430-1A	NADH:quinone reductase-like	10,3	-	-
Sspon.07G0034100-2D	NADP-dependent oxidoreductase P2	22,4	-	-
Sspon.04G0025370-3D	NADPH-dependent pterin aldehyde reductase	4	-	-
Sspon.05G0025410-1B	NAP1-related protein 1	11,3	-	-
Sspon.08G0002160-1A	NEDD8-conjugating enzyme Ubc12-like	9	-	-
Sspon.08G0009810-1T	nitrate-induced NOI protein	28,8	-	-
Sspon.07G0014080-2C	nitrogen regulatory protein P-II homolog	7	-	-
Sspon.07G0003500-1A	non-classical arabinogalactan protein 31-like	21,3	-	-
Sspon.07G0018120-3C	Non-specific lipid-transfer protein	24,2	-	-
Sspon.07G0010220-1A	N-terminal acetyltransferase B complex auxiliary subunit NAA25	2	-	-
Sspon.04G0032300-2D	Nuclear cap-binding protein subunit 2	7,6	-	-
Sspon.08G0016720-2B	Nuclear speckle RNA-binding protein A	17	-	-
Sspon.06G0020080-3D	Nuclear transport factor 2	35,8	-	-
Sspon.06G0009700-2B	Nucleolin 1	34,5	-	-
Sspon.08G0024530-1B	OB-fold nucleic acid binding domain containing protein	35,8	-	-
Sspon.05G0005940-2C	oleosin Zm-I	7,7	-	-
Sspon.05G0000960-3D	oligosaccharyl transferase STT3 subunit	3,4	-	-
Sspon.06G0028320-2D	Oligouridylate-binding protein 1C	11,2	-	-
Sspon.06G0010980-4D	O-methyltransferase	18	-	-
Sspon.04G0033430-2D	Os02g0246300	19,4	-	-
Sspon.05G0005050-2B	Os04g0569000	7,1	-	-
Sspon.07G0010540-4D	Os05g0368300	37,3	-	-
Sspon.08G0014940-3D	Os06g0150100	6,6	-	-
Sspon.08G0022470-3D	Os06g0198500	11,2	-	-
Sspon.05G0020020-3D	Os12g0137100	11,3	-	-
Sspon.04G0007550-2B	OSJNBa0074L08.7-like protein	2,3	-	-
Sspon.02G0029080-1A	osmotin-like protein	7,2	-	-
Sspon.07G0015580-2B	outer envelope pore protein 16, chloroplastic	22,6	-	-
Sspon.04G0017650-4D	OVARIAN TUMOR DOMAIN-containing deubiquitinating enzyme 2-like	13	-	-
Sspon.06G0006340-1P	oxidoreductase	8,6	-	-
Sspon.05G0031020-1C	oxygen-dependent coproporphyrinogen-III oxidase, chloroplastic	13,1	-	-
Sspon.04G0008560-2D	ozone-responsive stress-like protein (DUF1138)	15,1	-	-
Sspon.08G0008980-4D	pantothenate kinase 4	11,6	-	-
Sspon.02G0022820-1A	Pathogenesis-related protein 1	45,7	-	-
Sspon.02G0022820-2B	Pathogenesis-related protein 1	75,6	-	-
Sspon.04G0010730-3C	Pectinesterase inhibitor 8	23,8	-	-

Sspon.07G0000420-4D	Pentatricopeptide repeat-containing protein	11,1	-	-
Sspon.07G0003220-3D	pentatricopeptide repeat-containing protein At1g10270	3,5	-	-
Sspon.04G0027930-1B	pentatricopeptide repeat-containing protein At3g02490, mitochondrial-like	6,2	-	-
Sspon.07G0026450-1B	pentatricopeptide repeat-containing protein At4g35850, mitochondrial	25,8	-	-
Sspon.06G0000200-2P	Peptidase M1 family protein	22	-	-
Sspon.06G0004360-2B	peptidyl-prolyl cis-trans isomerase CYP18-2-like	17,9	-	-
Sspon.08G0011560-1A	peptidyl-prolyl cis-trans isomerase CYP40-like isoform X1	6	-	-
Sspon.06G0004310-3D	peptidyl-prolyl cis-trans isomerase CYP71-like	5,5	-	-
Sspon.08G0009200-1A	peroxidase 1	19,1	-	-
Sspon.07G0016910-2B	peroxidase 4-like isoform X1	4,9	-	-
Sspon.03G0015020-1T	peroxidase 5	7,3	-	-
Sspon.07G0013950-1A	Peroxidase 5	30,8	-	-
Sspon.05G0011490-1A	Peroxidase 72	7,5	-	-
Sspon.07G0016490-1A	Peroxisomal membrane protein PEX14	2,6	-	-
Sspon.05G0032150-1C	peroxygenase-like	18,6	-	-
Sspon.07G0012880-1A	phenylalanine--tRNA ligase beta subunit, cytoplasmic	15,7	-	-
Sspon.06G0000420-2B	PHI-1	19,9	-	-
Sspon.05G0007550-1P	Phosphoenolpyruvate carboxylase family protein	10,3	-	-
Sspon.06G0007580-4D	phosphofructose kinase2	36,4	-	-
Sspon.03G0004290-4D	Phosphoglycerate kinase	19,5	-	-
Sspon.04G0017410-3P	phosphoglycerate kinase, cytosolic	52,4	-	-
Sspon.05G0015390-3C	Phosphoglycerate mutase-like protein	31,8	-	-
Sspon.08G0006320-3C	phospholipase D alpha 2	8,5	-	-
Sspon.05G0000480-1A	Phosphomannomutase	14,5	-	-
Sspon.06G0023470-1B	phosphopantothenate--cysteine ligase	6	-	-
Sspon.08G0022420-2C	phosphopantothenoylcysteine decarboxylase isoform X1	4,2	-	-
Sspon.07G0003130-3D	Phosphoribosylamine--glycine ligase chloroplastic	9,2	-	-
Sspon.05G0011260-2B	phosphoribosylglycinamide formyltransferase, chloroplastic	7,3	-	-
Sspon.07G0016410-3C	Photosynthetic NDH subunit of lumenal location 5, chloroplastic	36,1	-	-
Sspon.05G0009710-2C	Plant UBX domain-containing protein 4	5,6	-	-
Sspon.07G0000500-1A	Plasminogen activator inhibitor 1 RNA-binding protein	5,5	-	-
Sspon.07G0031390-2D	PLASMODESMATA CALLOSE-BINDING PROTEIN 2	35,5	-	-
Sspon.03G0004230-3P	plastidic phosphate translocator-like protein1	4,3	-	-
Sspon.08G0011450-2B	polyadenylate-binding protein 2	21,4	-	-
Sspon.05G0003180-1A	Polyadenylate-binding protein RBP45C	9,3	-	-
Sspon.05G0019980-3C	PP2A regulatory subunit TAP46	8,9	-	-
Sspon.02G0048770-2D	predicted protein	5,4	-	-
Sspon.05G0016210-1A	predicted protein	3	-	-
Sspon.05G0025490-3D	predicted protein	7,4	-	-
Sspon.08G0014420-3D	predicted protein	40,6	-	-
Sspon.06G0020440-1B	predicted protein	30,1	-	-
Sspon.06G0025630-2C	prefoldin subunit 2	25	-	-
Sspon.05G0000420-1A	pre-mRNA cleavage factor Im 25 kDa subunit 2	31,5	-	-
Sspon.07G0005810-4D	prenylated Rab receptor 2	6,9	-	-
Sspon.05G0013460-4D	primary amine oxidase	5,2	-	-
Sspon.07G0002050-2C	Probable 3-hydroxyisobutyrate dehydrogenase-like 3, mitochondrial	8,2	-	-
Sspon.06G0002960-1A	probable aldo-keto reductase 2	9,6	-	-
Sspon.07G0004220-2B	probable alpha,alpha-trehalose-phosphate synthase 7	8,8	-	-
Sspon.07G0017620-2C	probable apyrase 3	7,1	-	-
Sspon.05G0013550-1A	probable cleavage and polyadenylation specificity factor subunit 1 isoform X3	4,5	-	-
Sspon.08G0023050-2D	probable galactinol--sucrose galactosyltransferase 6	7,1	-	-
Sspon.05G0020510-4D	probable inactive serine/threonine-protein kinase bub1 isoform X1	2,5	-	-
Sspon.08G0016320-1A	probable lysophospholipase BODYGUARD 3	2,2	-	-
Sspon.05G0028340-1B	probable non-inhibitory serpin-z9	3,7	-	-
Sspon.03G0007550-2P	probable serine acetyltransferase 5	7,1	-	-
Sspon.05G0010590-1A	probable signal peptidase complex subunit 2	22,2	-	-
Sspon.05G0002120-1A	probable UDP-arabinopyranose mutase 2 isoform X1	13,5	-	-
Sspon.07G0003950-1A	proline-rich receptor-like protein kinase PERK12 isoform X1	25,3	-	-
Sspon.06G0015880-1T	proline-rich receptor-like protein kinase PERK2	5,1	-	-
Sspon.08G0000260-2C	proline-rich spliceosome-associated (PSP) family protein	9,4	-	-
Sspon.07G0018250-1A	prosaposin-like	4,9	-	-
Sspon.05G0013630-3C	prostaglandin E synthase 2-like	13,8	-	-
Sspon.06G0003910-3C	Proteasome subunit alpha type-7-A	31,3	-	-
Sspon.08G0005160-1A	Proteasome subunit beta type	18,6	-	-
Sspon.08G0024390-1B	proteasome subunit beta type-7-A-like	13,8	-	-
Sspon.08G0009020-1A	protein adenyltransferase SeLO-like	8,4	-	-
Sspon.06G0007330-3D	protein aq_1857	7,6	-	-
Sspon.07G0011680-2B	protein binding protein	9	-	-
Sspon.08G0011080-2B	Protein BOBBER 1	3,9	-	-
Sspon.08G0017370-2C	protein BRE	5,9	-	-
Sspon.05G0017460-4D	protein disulfide isomerase	45,8	-	-
Sspon.05G0017460-1A	protein disulfide isomerase	45,2	-	-
Sspon.05G0011220-3D	protein disulfide isomerase10	4,5	-	-
Sspon.03G0014720-1P	protein disulfide isomerase-like 2-1	33,1	-	-

Sspon.08G0007950-4D	Protein DJ-1 homolog B	14,4	-	-
Sspon.07G0010260-2B	protein EARLY RESPONSIVE TO DEHYDRATION 15-like	29,6	-	-
Sspon.08G0011400-4D	Protein EXORDIUM	8	-	-
Sspon.05G0028720-1B	protein FAM136A	10,6	-	-
Sspon.05G0009360-1P	Protein FATTY ACID EXPORT 1 chloroplastic	21,7	-	-
Sspon.05G0019890-1P	Protein FLX-like 3	17,3	-	-
Sspon.04G0024720-3D	protein grpE	4,8	-	-
Sspon.06G0011260-1P	Protein MICRORCHIDIA 1	2,2	-	-
Sspon.08G0000350-2P	Protein pelota	5,6	-	-
Sspon.05G0010760-4D	Protein phosphatase methylesterase 1	6,9	-	-
Sspon.05G0014400-4P	Protein pleiotropic regulatory locus 1	3,5	-	-
Sspon.02G0003600-1A	protein PYRICULARIA ORYZAE RESISTANCE 21-like	5,3	-	-
Sspon.05G0001700-1T	protein RCC2	16	-	-
Sspon.07G0024170-2C	Protein RETICULATA-RELATED 4, chloroplastic	17,1	-	-
Sspon.05G0018240-2B	Protein TPLATE	1,6	-	-
Sspon.08G0009570-2C	protein translocase subunit SecA	15,7	-	-
Sspon.02G0013040-1P	protein transport protein SEC23	5,2	-	-
Sspon.05G0014860-3C	Protein transport protein Sec24-like	5,2	-	-
Sspon.06G0014000-2B	Protein transport protein Sec24-like CEF	2,1	-	-
Sspon.02G0012960-1A	protein transport protein SEC31	3,7	-	-
Sspon.06G0004810-3C	protein transport protein sec31	5,3	-	-
Sspon.07G0027060-1B	protein transport protein Sec61 beta subunit	28	-	-
Sspon.05G0019750-2B	protein TRAUCO-like	4,1	-	-
Sspon.05G0008130-2B	protoporphyrinogen oxidase 2, chloroplastic/mitochondrial	6,5	-	-
Sspon.07G0000800-2B	Pseudouridine synthase family protein	4,7	-	-
Sspon.08G0005110-4D	purple acid phosphatase precursor	21,3	-	-
Sspon.08G0000450-3C	putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase 2	10,1	-	-
Sspon.06G0009110-2B	putative alcohol dehydrogenase superfamily protein	8,4	-	-
Sspon.06G0014650-1A	putative alpha-mannosidase	14,7	-	-
Sspon.05G0006550-1A	putative beta-D-xylosidase 6	3,4	-	-
Sspon.06G0014070-4D	putative bifunctional methylthioribulose-1-phosphate dehydratase/enolase-phosphatase E1 Methylthioribulose-1-phosphate dehydratase Enolase-phosphatase E1	32,2	-	-
Sspon.04G0030670-1P	putative brown planthopper-induced resistance protein 1	13,4	-	-
Sspon.06G0020470-1T	putative carboxylesterase 8	13,2	-	-
Sspon.05G0023090-3D	putative disease resistance protein RGA3	0,3	-	-
Sspon.04G0015420-1P	putative DNA/RNA-binding protein Alba	28,1	-	-
Sspon.05G0024890-2D	putative E3 ubiquitin-protein ligase ARI8	4,7	-	-
Sspon.08G0023060-1B	putative galactinol-sucrose galactosyltransferase 6	4	-	-
Sspon.06G0017190-3D	putative GRF-interacting factor 2	5,6	-	-
Sspon.06G0015890-1A	Putative H/ACA ribonucleoprotein complex subunit 1-like protein 1	5,7	-	-
Sspon.06G0008450-2B	putative HAD-superfamily hydrolase	11,6	-	-
Sspon.07G0004680-2C	putative indole-3-acetic acid-amido synthetase GH3.1	3,7	-	-
Sspon.07G0010820-2P	putative lactoylglutathione lyase chloroplastic	12,5	-	-
Sspon.05G0013130-2B	putative low-specificity L-threonine aldolase 1	5,9	-	-
Sspon.07G0005770-2C	putative mini-chromosome maintenance (MCM) complex protein family	19,6	-	-
Sspon.07G0007260-1A	putative NOT transcription complex subunit VIP2	2,7	-	-
Sspon.08G0015620-2B	Putative pentatricopeptide repeat-containing protein mitochondrial	7,4	-	-
Sspon.07G0006170-1A	Putative PWWP domain family protein	5,4	-	-
Sspon.07G0006170-1P	Putative PWWP domain family protein	3,1	-	-
Sspon.07G0026980-1B	putative RNA-directed DNA polymerase	1,1	-	-
Sspon.06G0028980-1C	putative rnase H family protein isoform X3	8,9	-	-
Sspon.06G0005490-1A	putative splicing factor 3B subunit 5/RDS3 complex subunit 10	12,6	-	-
Sspon.04G0013130-3D	putative tocopherol cyclase, chloroplastic	10,7	-	-
Sspon.03G0002360-1A	putative ubiquitin-like-specific protease 2B	9	-	-
Sspon.08G0002580-2T	putative xyloglucan endotransglycosylase	6,5	-	-
Sspon.06G0021350-1B	Pyridoxal phosphate (PLP)-dependent transferase superfamily protein	3,7	-	-
Sspon.08G0013440-1A	Pyrophosphate-energized vacuolar membrane proton pump	14	-	-
Sspon.05G0014950-4D	pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic	17,7	-	-
Sspon.05G0016160-2B	Pyruvate kinase	4,9	-	-
Sspon.07G0007790-3C	Rab GDP dissociation inhibitor alpha	26,1	-	-
Sspon.06G0001990-1A	RanBP2-type zinc finger protein	9	-	-
Sspon.05G0025240-3D	ras-related protein Rab-2-A	30	-	-
Sspon.07G0004190-3D	Ras-related protein RABG3f	45,6	-	-
Sspon.06G0008870-1A	receptor-like protein EIX2	6,3	-	-
Sspon.06G0006070-2B	regulator of chromosome condensation3	6,6	-	-
Sspon.07G0016860-1A	Regulatory-associated protein of TOR 1	2,1	-	-
Sspon.05G0025900-1B	repetitive proline-rich cell wall protein-like	2,7	-	-
Sspon.04G0024310-2P	replication protein A 32 kDa subunit B-like	19,4	-	-
Sspon.08G0008320-2B	reticulon	3,9	-	-
Sspon.07G0028690-2C	retrotransposon protein, putative, LINE subclass	1,1	-	-
Sspon.02G0044210-1B	retrotransposon protein, putative, Ty1-copia subclass	3,2	-	-
Sspon.07G0035480-1D	RGG repeats nuclear RNA binding protein A-like isoform X1	17,7	-	-
Sspon.04G0020990-2D	RGS1-HXK1-interacting protein 1-like	8,9	-	-
Sspon.02G0018980-2P	ribonucleoprotein	14,5	-	-
Sspon.08G0013730-1A	Ribonucleoside-diphosphate reductase large subunit	5,6	-	-

Sspon.05G0039820-1D	ribose-5-phosphate isomerase	11,7	-	-
Sspon.06G0013000-3C	Ribosome-recycling factor chloroplastic	11,9	-	-
Sspon.08G0017540-1T	ripening-related protein	6,6	-	-
Sspon.01G0041860-2D	RNA-binding (RRM/RBD/RNP motifs) family protein	5,3	-	-
Sspon.07G0017130-2P	RNA-binding (RRM/RBD/RNP motifs) family protein	7,5	-	-
Sspon.07G0026710-2D	RNA-binding protein 8A	18	-	-
Sspon.06G0019260-1T	RNA-binding protein cabeza-like	6,6	-	-
Sspon.06G0023270-3D	RNA-binding protein L-like	6,8	-	-
Sspon.05G0013270-2C	RNA-binding protein-like	8,3	-	-
Sspon.05G0012000-2C	salutaridine reductase-like	4,9	-	-
Sspon.05G0006640-1A	salutaridine reductase-like	4,5	-	-
Sspon.03G0030590-2D	secretory carrier-associated membrane protein 2	19,2	-	-
Sspon.05G0004070-1A	seed specific protein Bn15D1B	24	-	-
Sspon.05G0004070-3D	seed specific protein Bn15D1B	20	-	-
Sspon.04G0020460-4D	serine carboxypeptidase 3	34,5	-	-
Sspon.05G0027600-1B	Serine/arginine-rich splicing factor RS31A	16	-	-
Sspon.08G0006290-2B	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	18,7	-	-
Sspon.08G0006310-1A	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	14,5	-	-
Sspon.08G0011420-1A	serine/threonine-protein phosphatase 2A activator 2	8,5	-	-
Sspon.07G0012610-2C	serine/threonine-protein phosphatase PP1-like	6,6	-	-
Sspon.08G0006940-3D	Serine/threonine-protein phosphatase PP2A-5 catalytic subunit	23,4	-	-
Sspon.06G0015920-1P	serpin-ZXA-like	3,5	-	-
Sspon.06G0002300-2C	Serrate RNA effector molecule	3,1	-	-
Sspon.08G0017960-1B	Serrate RNA effector molecule	9,1	-	-
Sspon.08G0010500-1A	Signal recognition particle 9 kDa protein	23,3	-	-
Sspon.07G0028040-2C	signal recognition particle receptor subunit beta	10,5	-	-
Sspon.06G0007100-2D	signal recognition particle receptor subunit beta-like	10,5	-	-
Sspon.05G0010620-1P	small nuclear ribonucleoprotein LSM1	17,1	-	-
Sspon.07G0015650-3C	small nuclear ribonucleoprotein Sm D2-like	26	-	-
Sspon.07G0008820-2B	sm-like protein LSM5	18,8	-	-
Sspon.07G0000470-2B	Sm-like protein LSM8	16,2	-	-
Sspon.07G0005230-2B	SNF1-related protein kinase regulatory subunit beta-1	6,6	-	-
Sspon.04G0020180-4D	Spermine synthase	16,5	-	-
Sspon.06G0006390-1A	splicing factor PWI domain-containing protein / RNA recognition motif (RRM)-containing protein	4,5	-	-
Sspon.06G0017490-1T	Splicing factor U2af large subunit A	9,6	-	-
Sspon.05G0008660-1A	Stachyose synthase	1,7	-	-
Sspon.05G0013050-1A	Stearoyl-[acyl-carrier-protein] 9-desaturase 5, chloroplastic	7	-	-
Sspon.07G0017770-4D	Sterol 14-demethylase	3,9	-	-
Sspon.06G0010910-3C	Stomatin-like protein 2, mitochondrial	17,9	-	-
Sspon.07G0014690-1A	Structural constituent of ribosome	7,3	-	-
Sspon.06G0004690-2C	Structural maintenance of chromosomes (SMC) family protein	7	-	-
Sspon.06G0004700-1A	Structural maintenance of chromosomes (SMC) family protein	10,4	-	-
Sspon.06G0005200-2C	subtilisin-like protease SBT1.5	1,4	-	-
Sspon.04G0017250-4D	succinate semialdehyde dehydrogenase	12,5	-	-
Sspon.06G0002680-1A	sulfite oxidase	16,4	-	-
Sspon.07G0013160-3D	sulfite oxidase-like isoform X1	16,9	-	-
Sspon.07G0004610-2B	Sulfite reductase, chloroplastic	20,2	-	-
Sspon.06G0014320-1A	SUMO-activating enzyme subunit 1A	20,2	-	-
Sspon.06G0020870-2C	superoxide dismutase	10,9	-	-
Sspon.04G0031690-2D	survival motor neuron protein	5	-	-
Sspon.07G0019490-3D	Switch/sucrose nonfermenting 3C	4,5	-	-
Sspon.01G0002680-2B	Tankyrase 1	17,4	-	-
Sspon.07G0001660-2C	T-complex protein 1 subunit theta	30,8	-	-
Sspon.06G0005730-1A	Temperature-induced lipocalin-1	7,7	-	-
Sspon.06G0008290-2B	thioredoxin domain-containing protein 9 homolog	17,1	-	-
Sspon.08G0008900-4D	thioredoxin reductase 2	35,7	-	-
Sspon.05G0000940-1A	thioredoxin X	8,4	-	-
Sspon.05G0024210-2D	Thioredoxin-like protein CXXS1	13,1	-	-
Sspon.06G0006140-2B	THO complex subunit 4C	4,7	-	-
Sspon.07G0002850-3C	Threonine synthase, chloroplastic	17,2	-	-
Sspon.05G0007620-2D	trafficking protein particle complex II-specific subunit 120 homolog	1,2	-	-
Sspon.07G0000880-2B	Transcription initiation factor IIF beta subunit	11	-	-
Sspon.08G0004850-2B	Transcription initiation factor TFIID subunit 5	4,8	-	-
Sspon.05G0003900-1A	Transducin family protein / WD-40 repeat family protein	2	-	-
Sspon.07G0019350-3C	Transducin/WD40 repeat-like superfamily protein	4,7	-	-
Sspon.08G0025430-2D	Transducin/WD40 repeat-like superfamily protein	30,5	-	-
Sspon.05G0008820-1P	transglutaminase15	5,4	-	-
Sspon.08G0016220-1A	transketolase, chloroplastic	23	-	-
Sspon.08G0003300-1A	translation machinery associated protein TMA7	19,4	-	-
Sspon.05G0010920-2B	translocon Tic40	5,6	-	-
Sspon.05G0018080-1A	transmembrane 9 superfamily member 1-like	5,5	-	-
Sspon.08G0007110-2B	transmembrane 9 superfamily member 7-like	6,5	-	-
Sspon.06G0007940-3C	transmembrane 9 superfamily member 9	2,8	-	-

Sspon.06G0013770-2D	transmembrane 9 superfamily protein member 1 precursor	4,4	-	-
Sspon.06G0013470-3C	transmembrane protein 18	17,5	-	-
Sspon.05G0000110-1A	Transportin-1	3,4	-	-
Sspon.01G0040430-1B	Transposable element protein, putative, Retrotrans_gag	2,4	-	-
Sspon.02G0015500-3P	trehalose-6-phosphate synthase4	3,7	-	-
Sspon.05G0001280-2D	trypsin family protein isoform X1	2,1	-	-
Sspon.06G0011870-1A	Tryptophan synthase beta chain 2, chloroplastic	10,2	-	-
Sspon.07G0007950-2B	tubulin beta-5 chain	41,4	-	-
Sspon.08G0018850-2C	tubulin beta-7 chain	59,2	-	-
Sspon.04G0015920-4D	Tubulin binding cofactor C domain-containing protein	10	-	-
Sspon.08G0025650-1C	twinkle homolog protein, chloroplastic/mitochondrial	1,7	-	-
Sspon.06G0011250-2B	tyrosyl-tRNA synthetase	23,3	-	-
Sspon.05G0005630-2B	U4/U6 small nuclear ribonucleoprotein Prp31 homolog	6,9	-	-
Sspon.08G0025880-1C	U5 small nuclear ribonucleoprotein 40 kDa protein-like	10	-	-
Sspon.08G0014790-3D	ubiquinone biosynthesis O-methyltransferase, mitochondrial	6,5	-	-
Sspon.08G0010390-1A	Ubiquitin receptor RAD23c	8,3	-	-
Sspon.08G0014390-3D	Ubiquitin-associated/translation elongation factor EF1B protein	7,1	-	-
Sspon.08G0008230-1T	ubiquitin-conjugating enzyme E2 28	12,9	-	-
Sspon.03G0003080-1P	Ubiquitin-conjugating enzyme E2 7	17,8	-	-
Sspon.05G0030090-1P	ubiquitin-like protein 5	30,1	-	-
Sspon.07G0009570-3C	UDP-glucuronic acid decarboxylase 4	13,6	-	-
Sspon.08G0002150-3C	UDP-sugar pyrophosphorylase	4,7	-	-
Sspon.05G0027890-1B	UMP-CMP kinase 2-like	10,7	-	-
Sspon.03G0005490-1A	uncharacterized LOC100283563	12,6	-	-
Sspon.08G0011590-2B	uncharacterized LOC100286291	11,4	-	-
Sspon.06G0008090-2D	uncharacterized protein LOC8073282	12,1	-	-
Sspon.07G0037340-1D	uncharacterized protein LOC8079369	11,1	-	-
Sspon.04G0021850-1B	uncharacterized protein LOC8155353 isoform X2	17,2	-	-
Sspon.07G0004740-1A	universal stress protein PHOS32-like	15,4	-	-
Sspon.05G0029650-3D	unnamed protein product	2,6	-	-
Sspon.05G0012400-3C	unnamed protein product	5,9	-	-
Sspon.06G0003610-2B	unnamed protein product	4,2	-	-
Sspon.06G0006230-4D	unnamed protein product	7,3	-	-
Sspon.07G0006110-1A	unnamed protein product	10,9	-	-
Sspon.04G0029840-1B	unnamed protein product	8	-	-
Sspon.07G0000550-2B	unnamed protein product	7,2	-	-
Sspon.05G0029640-2C	unnamed protein product	3,3	-	-
Sspon.02G0054580-2D	unnamed protein product	39,3	-	-
Sspon.02G0054570-2D	unnamed protein product	16	-	-
Sspon.07G0006570-2C	Uracil phosphoribosyltransferase	19,2	-	-
Sspon.07G0002070-2C	Urease accessory protein G	11,6	-	-
Sspon.04G0021210-2D	uridine kinase-like protein 3 isoform X1	12	-	-
Sspon.06G0027950-1C	UvrB/uvrC motif family protein	1,4	-	-
Sspon.05G0030500-1B	Vacuolar-sorting receptor 1	4,2	-	-
Sspon.06G0007710-1A	Vacuolar-sorting receptor 4	3	-	-
Sspon.05G0000260-2C	VAMP protein SEC22	6,8	-	-
Sspon.06G0023740-1B	vesicle-associated membrane protein 714	18,4	-	-
Sspon.06G0004120-3D	vignain precursor	2,7	-	-
Sspon.03G0008250-3D	VIP1 protein	24,2	-	-
Sspon.07G0035400-1D	VIP1 protein	4,7	-	-
Sspon.07G0029200-1B	V-type proton ATPase 16 kDa proteolipid subunit	10,9	-	-
Sspon.07G0000200-2B	V-type proton ATPase subunit C	24,4	-	-
Sspon.05G0036980-1T	V-type proton ATPase subunit D	13,4	-	-
Sspon.05G0009330-3C	WPP domain-interacting protein 2	5,3	-	-
Sspon.05G0016350-1A	xylanase inhibitor protein 1-like	11,1	-	-
Sspon.08G0002570-1T	xyloglucan endotransglucosylase/hydrolase protein 23	19	-	-
Sspon.01G0031300-2D	zinc knuckle (CCHC-type) family protein	11,2	-	-
Sspon.01G0013880-1A	zinc knuckle (CCHC-type) family protein	5,1	-	-
Sspon.02G0013320-4D	bZIP transcription factor TRAB1	5,9	-	-
Sspon.07G0001780-1P	G-box binding factor	4,9	-	-
Sspon.07G0007110-3C	G-box-binding factor 4	5,8	-	-
Sspon.01G0031320-3C	Dof zinc finger protein DOF3.6	4,6	-	-
Sspon.04G0035020-1P	zinc finger C-x8-C-x5-C-x3-H type family protein	5,3	-	-
Sspon.03G0017360-2D	Zinc finger CCCH domain-containing protein 58	8	-	-
Sspon.07G0000810-1T	Protein tesmin/TSO1-like CXC 4	7,6	-	-
Sspon.04G0004810-2C	probable glucosamine 6-phosphate N-acetyltransferase 2	8,9	-	-
Sspon.01G0026220-2B	Growth-regulating factor 2	3	-	-
Sspon.01G0046230-2D	BEL1-like homeodomain protein 3	1,7	-	-
Sspon.06G0011860-1A	homeobox-leucine zipper protein ROC7-like	3,6	-	-
Sspon.02G0016800-3D	Protein SAWADEE HOMEODOMAIN HOMOLOG 2	12,6	-	-
Sspon.02G0008370-4D	High mobility group B protein 2	17,5	-	-
Sspon.02G0013390-3C	heat stress transcription factor B-4c-like	3,7	-	-
Sspon.01G0018350-2D	heat shock factor protein HSF30 isoform X1	5,4	-	-
Sspon.01G0038610-2C	pollen-specific protein SF3	8,4	-	-
Sspon.04G0010480-1A	Homeodomain-like superfamily protein	1,8	-	-
Sspon.07G0034910-1C	atherin	1,8	-	-

Sspon.06G0010940-1A	NAC domain-containing protein 14	9,1	-	-
Sspon.06G0001440-2B	skin secretory protein xP2	30,5	-	-
Sspon.08G0009070-2B	BTB/POZ domain-containing protein	1,7	-	-
Sspon.03G0022650-2C	Putative AGC protein kinase family protein	2	-	-
Sspon.02G0004840-4D	Calcium-dependent protein kinase 7	1,8	-	-
Sspon.01G0062050-1D	Nuclear pore complex protein NUP1	0,3	-	-
Sspon.02G0012830-1P	Serine/threonine-protein kinase PEPKR2	1,8	-	-
Sspon.03G0012930-1A	casein kinase 1-like protein 2 isoform X1	5	-	-
Sspon.07G0024900-1B	casein kinase 1-like protein HD16 isoform X2	2,2	-	-
Sspon.02G0001430-4D	putative serine/threonine-protein kinase	1,4	-	-
Sspon.01G0027600-1A	cyclin-dependent kinase C-2	2,6	-	-
Sspon.07G0008780-1T	cyclin-dependent kinase C-2	3,5	-	-
Sspon.05G0028120-2C	mitogen-activated protein kinase 15-like isoform X1	2,5	-	-
Sspon.08G0002270-2B	mitogen-activated protein kinase 4	3	-	-
Sspon.04G0014610-1A	probable LRR receptor-like serine/threonine-protein kinase At1g53440 isoform X1	1,4	-	-
Sspon.05G0002810-3D	serine/threonine-protein kinase receptor isoform X3	4,9	-	-
Sspon.06G0003120-2B	Chitin elicitor receptor kinase 1	4,4	-	-
Sspon.01G0017620-1P	Protein kinase 2B chloroplastic	2,6	-	-
Sspon.04G0011160-1A	Serine/threonine-protein kinase CTR1	2,3	-	-
Sspon.04G0020150-2B	Serine/threonine-protein kinase STY46	4,7	-	-
Sspon.02G0004650-1A	Serine/threonine-protein kinase WNK2	1,4	-	-
Sspon.02G0019240-3D	glycosyl hydrolase family 10 protein / carbohydrate-binding domain-containing protein	1,8	-	-
Sspon.04G0021070-1A	Extra-large guanine nucleotide-binding protein 3	1,7	-	-
Sspon.02G0027450-3D	Vacuolar protein sorting-associated protein 26A	5,9	-	-
Sspon.03G0026510-1P	Villin-2	10,9	-	-
Sspon.03G0003300-3C	V-type proton ATPase subunit a1	3,5	-	-
Sspon.02G0015600-4D	transcription initiation factor TFIID subunit 10	10,4	-	-
Sspon.03G0004730-2D	mucin-5AC	2,2	-	-
Sspon.03G0001120-3D	ARM repeat superfamily protein	6,3	-	-
Sspon.03G0039740-2D	uricase	18,6	-	-
Sspon.01G0044030-2C	senescence regulator	7,4	-	-
Sspon.02G0002120-2C	leaf blight resistance	1,1	-	-
Sspon.02G0018020-3D	protein ROLLING AND ERECT LEAF 2	1,5	-	-
Sspon.04G0005450-1T	syntaxin-22-like	4,6	-	-
Sspon.01G0046290-1B	Glycine-rich RNA-binding protein RZ1C	18,7	-	-
Sspon.01G0060070-1D	Rho GTPase activator	13,3	-	-
Sspon.02G0036860-2D	DEAD-box ATP-dependent RNA helicase 28	5,9	-	-
Sspon.03G0007760-3C	ras-related protein Rab7-like	28,5	-	-
Sspon.02G0017530-3C	Ras-related protein RGP1	13,1	-	-
Sspon.04G0011450-3C	RING finger protein 10	1,7	-	-
Sspon.02G0022300-2C	uncharacterized protein LOC8078442	5	-	-
Sspon.02G0015490-3C	Potassium transporter 23	1,3	-	-
Sspon.03G0031460-1B	protein PLASTID MOVEMENT IMPAIRED 1-RELATED 1	0,8	-	-
Sspon.01G0002890-2P	putative inorganic phosphate transporter 1-8	3,7	-	-
Sspon.07G0006750-2P	protein OCTOPUS-like	1,5	-	-
Sspon.02G0046390-1C	Nuclear pore complex protein NUP214	0,8	-	-
Sspon.02G0018440-1A	Calcium-dependent lipid-binding (CaLB domain) family protein	48	-	-
Sspon.01G0013680-1A	barley mlo defense gene homolog2	6,4	-	-
Sspon.02G0019150-4D	Fiber protein Fb34	10,3	-	-
Sspon.04G0033450-1C	uncharacterized protein LOC103627005	6	-	-
Sspon.02G0045390-2C	GTPase LSG1-2-like	3,5	-	-
Sspon.04G0000040-1A	DCD (Development and Cell Death) domain protein	3,5	-	-
Sspon.01G0028600-2B	arginine N-methyltransferase 2	5,7	-	-
Sspon.01G0063150-1D	transcriptional repressor ILP1	2,4	-	-
Sspon.01G0053000-1C	Protein HUA2-LIKE 3	4,8	-	-
Sspon.02G0026630-2B	histone deacetylase	9,1	-	-
Sspon.03G0045900-1D	zinc finger BED domain-containing protein RICESLEEPER 1 isoform X2	0,9	-	-
Sspon.02G0004620-3C	Protein FREE1	2,4	-	-
Sspon.01G0029440-1A	inosine-5'-monophosphate dehydrogenase	23,6	-	-
Sspon.03G0041810-2D	ARM repeat superfamily protein	2	-	-
Sspon.01G0000270-2B	signal recognition particle protein subunit 9	1,4	-	-
Sspon.03G0009650-2B	GBF-interacting protein 1	4,7	-	-
Sspon.02G0024060-2B	melanoma-associated antigen 1 isoform X2	22,9	-	-
Sspon.03G0024310-1A	ethylene insensitive 2	0,9	-	-
Sspon.02G0022840-2B	DDT domain-containing protein DDR4	2,2	-	-
Sspon.01G0010070-4D	Beta-adaptin-like protein C	12,3	-	-
Sspon.01G0044610-1B	Sec20 family protein	10,4	-	-
Sspon.01G0022650-1A	Lysine--tRNA ligase cytoplasmic	36,6	-	-
Sspon.02G0036750-2C	ATG8-interacting protein 1	3,4	-	-
Sspon.02G0000320-2D	AMP deaminase	4,7	-	-
Sspon.02G0024140-1A	187-kDa microtubule-associated protein AIR9	3,4	-	-
Sspon.02G0039040-1B	ABC transporter G family member 40	1,2	-	-
Sspon.02G0027390-2C	ABC transporter D family member 1-like	1,3	-	-
Sspon.01G0011760-2C	uncharacterized protein LOC8080442 isoform X2	1	-	-

Sspon.04G0014670-3C	abscisic acid receptor PYL9-like	8	-	-
Sspon.07G0008450-4D	alpha/beta-Hydrolases superfamily protein	40,6	-	-
Sspon.07G0025510-2C	aquaporin NIP1-3-like	4,4	-	-
Sspon.05G0024290-1P	Autophagy-related protein 13a	2,7	-	-
Sspon.06G0004630-3C	brachytic2	1	-	-
Sspon.03G0022140-1A	brain acid soluble protein 1 homolog	14,2	-	-
Sspon.07G0025390-3D	CAPIP1	10,2	-	-
Sspon.07G0011140-1A	Casein kinase I-RAG8-like protein	3,2	-	-
Sspon.08G0000280-3P	coiled-coil domain-containing protein 12-like	12,9	-	-
Sspon.07G0009080-4D	Conserved oligomeric Golgi complex subunit 5	1	-	-
Sspon.05G0008450-2C	dentin sialophosphoprotein	4,5	-	-
Sspon.06G0002970-2D	disease resistance protein RGA2	1,2	-	-
Sspon.05G0018800-1A	disease resistance protein RPM1-like	1,5	-	-
Sspon.05G0016710-4D	disease resistance protein RPP13	1,6	-	-
Sspon.08G0011940-3C	DNA-binding protein	4,8	-	-
Sspon.07G0032070-2D	DnaJ protein ERDJ2A	7,4	-	-
Sspon.04G0021710-2P	DUF2146 family protein	1,9	-	-
Sspon.05G0002790-1A	gamma-soluble NSF attachment protein-like	19,9	-	-
Sspon.07G0021260-1P	GBF-interacting protein 1	3,5	-	-
Sspon.04G0003420-2P	Glutaredoxin family protein	2,4	-	-
Sspon.07G0002270-2D	hydroxyproline-rich glycoprotein family protein	3,2	-	-
Sspon.06G0002040-1A	isoamylase 1, chloroplastic	2,1	-	-
Sspon.04G0033010-2D	MACPF domain-containing protein	2	-	-
Sspon.04G0004000-3D	Microtubule-associated protein 70-1	2,1	-	-
Sspon.05G0008320-1P	mitotic spindle checkpoint protein MAD2	3	-	-
Sspon.07G0009460-3C	nucleolar protein 16	13,9	-	-
Sspon.04G0012260-2D	Os02g0478550-like protein	3,7	-	-
Sspon.08G0020090-2C	peroxidase P7-like	7,3	-	-
Sspon.08G0008410-1A	PHD finger protein-related	4,6	-	-
Sspon.08G0017480-1B	Polyadenylate-binding protein-interacting protein 3	2,2	-	-
Sspon.05G0016820-1A	predicted protein	1,5	-	-
Sspon.05G0021610-2B	protein DWARF 53	1,1	-	-
Sspon.07G0000600-1A	protein EARLY FLOWERING 3-like isoform X1	2	-	-
Sspon.06G0021550-2C	protein ENHANCED DISEASE RESISTANCE 2-like	3,5	-	-
Sspon.05G0022030-2D	Protein KAKU4	7,6	-	-
Sspon.07G0004580-3C	Protein RNA-directed DNA methylation 3	3	-	-
Sspon.02G0030680-2B	Protein tesmin/TSO1-like CXC 4	6,1	-	-
Sspon.08G0006240-1A	Protein WVD2-like 5	3,1	-	-
Sspon.05G0014050-1A	Pumilio homolog 3	2,1	-	-
Sspon.06G0031100-1C	putative B3 DNA binding domain family protein	8,4	-	-
Sspon.07G0010840-1A	putative serine/threonine-protein kinase WNK3	6,2	-	-
Sspon.07G0002100-1A	Putative sucrose-phosphate synthase family protein isoform 1	7,6	-	-
Sspon.05G0019380-1P	Rac GTPase activating protein 1	3,9	-	-
Sspon.03G0031670-1B	RE1-silencing transcription factor-like isoform X1	1,8	-	-
Sspon.06G0024530-1B	Retrovirus-related Pol polyprotein from transposon TNT 1-94	5,2	-	-
Sspon.07G0027200-2C	Retrovirus-related Pol polyprotein LINE-1	3,9	-	-
Sspon.08G0024150-2D	RING/FYVE/PHD zinc finger superfamily protein	0,9	-	-
Sspon.05G0009700-2B	RING/U-box superfamily protein	3,1	-	-
Sspon.06G0012780-1A	RNA-binding (RRM/RBD/RNP motifs) family protein	26,6	-	-
Sspon.05G0002470-1P	Syntaxin-51	4	-	-
Sspon.06G0022720-2C	tobamovirus multiplication protein 2A-like	4,2	-	-
Sspon.04G0034470-2D	transducin family protein / WD-40 repeat family protein	1,7	-	-
Sspon.05G0001490-1A	Ubiquitin carboxyl-terminal hydrolase 3	11,8	-	-
Sspon.02G0028160-3C	Uveal autoantigen with coiled-coil domains and ankyrin repeats isoform 4	16,1	-	-
Sspon.06G0004410-2B	vesicle-associated membrane protein 727	11,9	-	-
Sspon.06G0001310-1A	wall-associated receptor kinase 3-like	11,7	-	-

Apêndice 3. Lista completa de fosfopetídeos

Acesso	Fosfopeptídeo	Motif fosfopeptídeo	Posição fosforilação	Amino-ácido	Regulation FDN/Controle
Sspon.01G0007790-2P	IGAGDSS(0.993)PREKS(0.995)PFSLR	...[STY]PR...	628	S	Down
Sspon.01G0007790-2P	EKS(1)PFS(1)LR	...[STY]P...	633	S	Down
Sspon.01G0007790-2P	EKS(1)PFS(1)LR	...[STY]P...	636	S	Down
Sspon.01G0015090-2C	SAS(0.969)AGSFDDPSVTGGR	...RS.[STY]...	567	S	Down
Sspon.01G0023310-1A	TLYGVVDDGS(1)S(1)DEDESTSK	...[STY]DE...	839	S	Down
Sspon.01G0023310-1A	TLYGVVDDGS(1)S(1)DEDESTSK	...[STY]DE...	838	S	Down
Sspon.01G0041200-3D	VTESSGGS(0.992)PPDNSNIGGNIK	...S...[STY]P...	787	S	Down
Sspon.01G0052200-1P	SRWEQSNDDSAANNS(1)GGEGGTGGR	...[STY]G...	62	S	Down
Sspon.02G0003220-2B	SRS(0.959)YSPDDYKR	...RS.[STY]...	116	S	Down
Sspon.02G0003320-2B	TES(1)GIFR	...R...[STY]...	133	S	Down
Sspon.02G0005420-1A	GDS(1)PPPLPDHLR	-	223	S	Down
Sspon.02G0011780-2P	EALPLLSQS(0.92)PTR	...S.[STY]P...R	83	S	Down
Sspon.02G0022230-1A	TLS(1)PQIR	...[STY]P...	16	S	Down
Sspon.02G0026090-3C	KVPLSDS(0.989)S(0.994)DEE	...[STY]DE...	311	S	Down
Sspon.02G0026090-3C	KVPLSDS(0.989)S(0.994)DEE	...[STY]DE...	312	S	Down
Sspon.02G0029090-3C	MYQGAGADMGGAGGMDEDAPAGS(1)GGPGPK	...[STY]G...	638	S	Down
Sspon.02G0049380-1C	SSLGSAT(1)PELLT(1)PR	...S.[STY]P...R	188	T	Down
Sspon.02G0049380-1C	SSLGSAT(1)PELLT(1)PR	...S.[STY]P...R	193	T	Down
Sspon.03G0005570-1P	SS(0.965)EPILLHR	-	187	S	Down
Sspon.03G0008300-1T	APDVQLKT(1)PENS(1)PKAEV	...[STY]P...SP..	459	S	Down
Sspon.03G0008300-1T	APDVQLKT(1)PENS(1)PKAEV	...[STY]P...SP..	455	T	Down
Sspon.03G0031100-3D	ATS(0.987)IDAQLR	-	11	S	Down
Sspon.03G0035590-1B	ENSNLIDADD(1)DELR	...[STY]DE...	100	S	Down
Sspon.03G0043900-1C	DALAEIDTIDAANESNEGS(0.928)PSR	...[STY]P.R...	238	S	Down
Sspon.04G0002500-2P	DNWEDGNPATWGSS(0.814)PAYQPGT(0.991)PQAR	...[STY]P...	754	T	Down
Sspon.04G0002680-2C	DVGTQMS(0.997)PEDSISSSPK	...[STY]P...	313	S	Down
Sspon.04G0004650-1A	MLS(0.999)STSS(0.855)KVPR	...S...[STY]...	157	S	Down
Sspon.04G0005750-4D	DLQQEIDDGEVEIPS(1)A	-	165	S	Down
Sspon.04G0008840-3C	GYTETVGESEVAAGS(0.999)PVRVDESDSSAPK	...[STY]P.R...	64	S	Down
Sspon.04G0008860-1A	LTGMS(1)FR	-	234	S	Down
Sspon.04G0008880-1A	NS(1)FSS(0.989)PLSSFK	...[STY]P...	19	S	Down
Sspon.04G0008880-1A	NS(1)FSS(0.989)PLSSFK	...[STY]P...	16	S	Down
Sspon.04G0015290-1A	YFEVDDRS(0.986)GKTT(0.959)PVQR	...S...[STY]P...	204	T	Down
Sspon.04G0022140-2C	ASGS(0.949)PPVPMVMS(1)PPR	...[STY]P.R...	236	S	Down
Sspon.04G0022140-2C	ASGS(0.833)PPVPMVMS(1)PPR	...[STY]P.R...	244	S	Down
Sspon.04G0033500-1C	DALEEQGYT(0.997)DGEIEER	...[STY]D...	91	T	Down
Sspon.05G0001710-1A	ILVCAGSGSDPAAGS(0.999)DADADDHPDENK	...[STY]D...	25	S	Down
Sspon.05G0008970-1T	T(1)APSS(1)PSAGEFELVER	...[STY]P...	51	S	Down
Sspon.05G0022390-2D	NLS(0.994)YQYS(0.828)TGADGR	...R...[STY]...	657	S	Down
Sspon.05G0031010-1P	GASSASAMDVEMS(1)DEGNR	...[STY]DE...	73	S	Down
Sspon.05G0031560-1C	S(1)ADDLLDVPPR	...S.[STY]...	57	S	Down
Sspon.05G0038190-1D	SLEVDS(1)AIGDS(1)PR	...[STY]PR...	493	S	Down
Sspon.05G0038190-1D	SLEVDS(1)AIGDS(1)PR	...[STY]PR...	498	S	Down
Sspon.06G0000140-1A	DTSAMPLNVSS(0.981)AGS(0.974)VNDLTK	...S...[STY]...	825	S	Down
Sspon.06G0000140-1A	DTSAMPLNVSS(0.804)AGS(0.996)VNDLTK	...S...[STY]...	828	S	Down
Sspon.06G0007980-2B	TSGSSFGSGS(0.903)LILK	...S.[STY]...	1317	S	Down
Sspon.06G0011880-1A	S(1)RS(0.999)PYFADR	..R.R...[STY]P...	186	S	Down
Sspon.06G0011880-1A	S(1)RS(0.999)PYFADR	..R.R...[STY]P...	184	S	Down
Sspon.06G0015530-3D	SIANSLATEDEPEASDPGPSAS(0.919)PGSTSPPR	...[STY]P...	29	S	Down
Sspon.06G0024480-1B	EEVKEES(1)DDDMGFSFLD	...[STY]DD...	59	S	Down
Sspon.06G0028040-1C	DFGLDDGES(1)DEENNATK	...[STY]DE...	180	S	Down
Sspon.07G0001380-1T	LGS(1)S(1)AFSLR	...R...[STY]...	56	S	Down
Sspon.07G0001380-1T	LGS(1)S(1)AFSLR	...R...[STY]...	55	S	Down
Sspon.07G0015770-1A	GPGTIGGLHS(0.852)SNS(0.936)LR	...S...[STY]...	183	S	Down
Sspon.07G0033930-1C	LRPGQPDVQEAATS(0.837)DMEDASTSSGGQR	-	3172	S	Down
Sspon.08G0005170-1P	KDS(1)AES(1)IGSDLSSLR	...S...[STY]...	306	S	Down
Sspon.08G0005170-1P	KDS(1)AES(1)IGSDLSSLR	...S...[STY]...	303	S	Down
Sspon.08G0008450-2B	DGVS(1)DSDFDEFGSMDVTK	...[STY]DS...	456	S	Down
Sspon.08G0013930-1A	NPDLNREPT(1)PDT(0.983)SDDE	...[STY]P...	116	T	Down
Sspon.08G0013930-1A	NPDLNREPT(1)PDT(0.979)SDDE	...[STY]P...	113	T	Down
Sspon.08G0016070-2B	HIS(1)EEPQDTS(0.99)PPR	...[STY]P.R...	231	S	Down
Sspon.08G0016070-2B	HIS(1)EEPQDTS(0.975)PPR	...[STY]P.R...	224	S	Down
Sspon.01G0008150-1A	AYFDS(1)ADWVLGK	-	44	S	Unique T
Sspon.02G0025530-1A	LT(1)KEGLDQSSPPEK	...[STY].E...	497	T	Unique T
Sspon.02G0029150-1P	HRS(0.982)YS(0.842)PASR	...[STY]P...	219	S	Unique T
Sspon.02G0029150-4D	HRS(0.953)YS(0.972)PASR	...[STY]P...	209	S	Unique T
Sspon.02G0029150-4D	HRS(0.982)YS(0.842)PASR	...[STY]P...	207	S	Unique T
Sspon.03G0017600-1A	AYSGPVASAANS(0.999)VT(0.999)PK	...[STY]P...	40	S	Unique T
Sspon.03G0017600-1A	AYSGPVASAANS(0.999)VT(0.999)PK	...[STY]P...	42	T	Unique T
Sspon.04G0007340-2B	FSGVFSS(0.784)SGS(0.854)PR	...S.[STY]P...R	89	S	Unique T
Sspon.05G0001710-1A	SNS(0.772)SSHLDGVS	...RS.[STY]...	560	S	Unique T
Sspon.05G0005580-3D	DYSFLLSDDADLS(1)PS(1)PK	...[STY]PSP...	179	S	Unique T

Sspon.05G0005580-3D	DYSFLLSDDADLS(1)PS(1)PK	...[STY]PSP...	181	S	Unique T
Sspon.05G0006100-1A	ASSLSSIDS(1)IMT(0.977)PSR	...[STY]P.R...	438	T	Unique T
Sspon.05G0006100-1A	ASSLSSIDS(1)IMT(0.977)PSR	...[STY]P.R...	435	S	Unique T
Sspon.05G0023810-1B	AWS(1)ES(1)EDDEPVK	...R...[STY]...	240	S	Unique T
Sspon.05G0023810-1B	AWS(1)ES(1)EDDEPVK	...R...[STY]...	242	S	Unique T
Sspon.06G0011170-3C	SDDS(0.99)DDEVPGLR	...S...[STY].D...	139	S	Unique T
Sspon.06G0015400-1P	ELCS(0.984)PNS(0.792)SLDVTR	...[STY]P...	325	S	Unique T
Sspon.06G0015400-1P	ELCS(0.999)PNSSLDVTR	...[STY]P...	322	S	Unique T
Sspon.07G0012350-3C	LHT(1)IDSAGLIHVYRK	...[STY]..S...	519	T	Unique T
Sspon.07G0014850-1A	ERS(0.951)YS(0.993)RS(1)PT(1)PR	...S.[STY]P...R	153	S	Unique T
Sspon.07G0014850-1A	ERS(0.951)YS(0.993)RS(1)PT(1)PR	...S.[STY]P...R	155	S	Unique T
Sspon.07G0014850-1A	ERS(0.951)YS(0.993)RS(1)PT(1)PR	...S.[STY]P...R	157	T	Unique T
Sspon.08G0024800-1C	DYS(0.997)PHRDPR	...[STY]P.R...	223	S	Unique T
Sspon.01G0000170-2D	LVASS(0.983)PASDEVK	...[STY]P...	481	S	Unique C
Sspon.01G0020370-2B	AEAEAAGS(0.831)LSR	...[STY].S...	9	S	Unique C
Sspon.01G0029040-3C	EQQQQPSSQSS(0.93)PTTDLISM	...S...[STY]P...	1206	S	Unique C
Sspon.01G0036380-2C	NPS(0.996)PGSGTAASIAEAVDR	...[STY]P...	104	S	Unique C
Sspon.01G0041200-2C	AHS(1)PVWS(1)PFPR	...S...[STY]P...	636	S	Unique C
Sspon.01G0041200-2C	AHS(1)PVWS(1)PFPR	...S...[STY]P...	640	S	Unique C
Sspon.01G0041370-3D	TQS(0.987)SISALSR	...R...[STY]...	269	S	Unique C
Sspon.01G0042410-1P	DGDNAAASSS(0.931)DTESTNR	...S.[STY]...	538	S	Unique C
Sspon.02G0004780-1A	LSDDIDGSS(0.962)DLADKK	...[STY]D...	30	S	Unique C
Sspon.02G0005420-1A	ATEPEPELEEAVES(1)EIEAGDAK	-	33	S	Unique C
Sspon.02G0013380-1A	VSAS(0.996)PS(1)PR	...S...[STY]P...	25	S	Unique C
Sspon.02G0028410-2B	TMS(0.989)GPATSETSLPVDR	...R...[STY]...	111	S	Unique C
Sspon.02G0029150-1P	GRS(1)PPPPPR	-	36	S	Unique C
Sspon.02G0034150-1B	DDDAS(0.844)GSGDDSEDDGIEDLRPFK	...[STY].S...	467	S	Unique C
Sspon.02G0047000-1C	TLMSGYTS(0.921)DIDLDR	...[STY]D...	324	S	Unique C
Sspon.03G0003820-1P	S(1)LLSRFS(0.995)VK	...S...[STY]...	595	S	Unique C
Sspon.03G0003820-1P	S(1)LLSRFS(0.949)VK	...S...[STY]...	589	S	Unique C
Sspon.03G0008790-3D	SIAADSWSVRS(0.893)EYGST(0.899)LDDDQR	...S...[STY]...	1207	T	Unique C
Sspon.03G0009470-1A	ESGEMS(0.871)EESDYDELIS	...[STY].E...	119	S	Unique C
Sspon.03G0013820-1A	RVPEMGGASAS(0.985)ASS(0.934)GAGADER	...S...[STY]...	62	S	Unique C
Sspon.03G0013820-1A	RVPEMGGASAS(0.995)ASSGAGADER	...S...[STY]...	59	S	Unique C
Sspon.03G0014830-1A	GLEKEEEDYFNEDS(0.999)DEEDSGSGR	...[STY]DE...	224	S	Unique C
Sspon.03G0030090-1P	TASSGSFGS(0.999)FDGSSVSNK	...S...[STY].D...	241	S	Unique C
Sspon.03G0030090-1P	TASSGS(0.868)FGSFDGSSVSNK	...S...[STY]...	238	S	Unique C
Sspon.04G0005920-2D	SSFISEALS(1)PR	...S...[STY]P...	1663	S	Unique C
Sspon.04G0014710-1A	ASGEGVVDQLS(1)GAAGGEAEAK	...[STY]G...	12	S	Unique C
Sspon.04G0014710-1A	AS(1)GEGVVDQLSGAAGGEAEAK	...[STY].E...	3	S	Unique C
Sspon.04G0016580-1P	ADAIEEAVDSSETVPS(0.991)AR	-	280	S	Unique C
Sspon.04G0027470-2C	EIS(1)RS(1)PPPPR	...S.[STY]P...R	6	S	Unique C
Sspon.04G0027470-2C	EIS(1)RS(1)PPPPR	...S.[STY]P...R	8	S	Unique C
Sspon.05G0032730-1C	SES(1)DDLELQIK	...RS.[STY]...	87	S	Unique C
Sspon.06G0000390-3D	ASDIEIS(1)DAKDAE	...[STY]D...	857	S	Unique C
Sspon.07G0005710-1P	SVSS(0.882)DIDDESQLGDSK	...S...[STY]...	277	S	Unique C
Sspon.07G0016240-2C	FYMEPDTTDSGS(0.943)MASGATPSR	...S.[STY]...	1053	S	Unique C
Sspon.07G0021540-2D	QSS(0.883)LNAAGTSS(0.785)MAVLR	...R...[STY]...	51	S	Unique C
Sspon.07G0023250-1B	TAVNPEANDS(1)PR	...[STY]PR...	201	S	Unique C
Sspon.08G0016070-2B	HDS(0.999)MES(0.811)EDISPPR	...S...[STY].D...	260	S	Unique C
Sspon.08G0016070-2B	HDS(0.999)MES(0.811)EDISPPR	...S...[STY].D...	257	S	Unique C
Sspon.01G0007790-2P	RGS(1)PS(0.994)LSRYPS(0.863)PSSR	...S...[STY]P...	284	S	Up
Sspon.01G0007790-2P	YPS(0.999)PSSR	...S...[STY]P...	290	S	Up
Sspon.01G0007790-2P	RGS(1)PS(0.964)LSRYPPSSR	...S...[STY]P...	282	S	Up
Sspon.02G0029150-4D	S(0.999)RS(0.978)YS(0.835)PASR	...R.R...[STY]P...	166	S	Up
Sspon.02G0029150-4D	S(0.999)RS(0.978)YS(0.835)PASR	...R.R...[STY]P...	164	S	Up
Sspon.03G0020230-4D	HPHDVQS(1)VPDS(1)PMLDK	...S...[STY]P...	271	S	Up
Sspon.03G0020230-4D	HPHDVQS(1)VPDS(1)PMLDK	...S...[STY]P...	275	S	Up
Sspon.04G0008510-2C	NNS(1)RS(1)PPGAR	...[STY]P...	206	S	Up
Sspon.04G0008510-2C	NNS(1)RS(1)PPGAR	...[STY]P...	208	S	Up
Sspon.05G0018860-4D	FQDGGGAMT(0.991)AETGTYR	...[STY].E...	239	T	Up
Sspon.05G0024490-1B	AAS(1)MS(1)VHEGIGR	...R...[STY]...	153	S	Up
Sspon.05G0024490-1B	AAS(1)MS(1)VHEGIGR	...R...[STY]...	155	S	Up
Sspon.06G0003650-3C	SLS(0.877)MDS(1)FMGK	...RS.[STY]...	252	S	Up
Sspon.07G0004490-2D	MDNVES(1)APDS(1)PAQAPPSSASSLPK	...S...[STY]P...	6	S	Up
Sspon.07G0004490-2D	MDNVES(1)APDS(1)PAQAPPSSASSLPK	...S...[STY]P...	10	S	Up
Sspon.01G0000270-2B	LQPALS(1)QK	-	141	S	-
Sspon.01G0000290-3D	EQSS(0.999)PGLTAGTNQIK	...[STY]P...	301	S	-
Sspon.01G0000390-2C	S(0.794)ESELAVIKPEALK	...[STY].S...	2	S	-
Sspon.01G0000470-2B	DDSFS(0.917)ESS(0.853)MSNADELQR	...S...[STY]...	257	S	-
Sspon.01G0000470-2B	DDSFS(0.917)ESS(0.853)MSNADELQR	...S...[STY]...	254	S	-
Sspon.01G0000780-4D	NRPYELYSDDSDS(0.999)GSDA	...S.[STY]...	164	S	-
Sspon.01G0000780-4D	NRPYELYSDDSDS(0.899)DSGSDA	...[STY]DS...	162	S	-
Sspon.01G0000780-4D	NRPYELYS(0.999)DSDSGSDA	...[STY]DS...	160	S	-
Sspon.01G0000800-1A	ASANLS(1)APIR	-	267	S	-
Sspon.01G0000800-1A	SAS(0.994)VGDWSVNDK	...S.[STY]...	330	S	-

Sspon.01G0002230-1A	QTNVLQSLCQNYDS(0.99)DDSE	[STY]DD...	295	S	-
Sspon.01G0002270-4D	LGGYS(0.991)PR	[STY]PR...	404	S	-
Sspon.01G0002370-1A	TCS(1)EDNLASLAVR	...R..[STY]....	69	S	-
Sspon.01G0002890-2P	SLEEMSGEADDAEEEA VGS(1)R	-	530	S	-
Sspon.01G0003420-1A	AAPSTSART(0.997)PT(0.995)PTR	[STY]P.R...	55	T	-
Sspon.01G0003420-1A	AAPSTSART(0.997)PT(0.995)PTR	[STY]P.R...	53	T	-
Sspon.01G0003420-1A	NPAS(1)PAAAR	[STY]P...	81	S	-
Sspon.01G0003420-1A	S(0.967)VSDQNPLLVETDIR	...S.[STY]....	405	S	-
Sspon.01G0003500-3D	LLVY(1)AS(0.969)KYSR	[STY]..S...	77	S	-
Sspon.01G0003500-3D	LLVY(1)AS(0.969)KYSR	[STY]..S...	75	Y	-
Sspon.01G0003730-1A	SQS(0.999)ATPVYK	...RS.[STY]....	253	S	-
Sspon.01G0003730-1A	SQS(0.998)AT(0.855)PVYK	...S...[STY]P...	255	T	-
Sspon.01G0004620-1A	NKS(1)FDDDDDFSNKPIAK	...R..[STY]....	249	S	-
Sspon.01G0004770-1A	VVDDLNLNLS(0.966)SS(0.7)PR	[STY]PR...	299	S	-
Sspon.01G0004770-1A	VVDDLNLNLS(0.952)SS(0.989)PR	[STY]PR...	301	S	-
Sspon.01G0004770-1A	VVDDLNLNLS(0.899)S(0.762)SPR	[STY].S...	300	S	-
Sspon.01G0004770-1A	IDIVGS(1)PLAATDGK	[STY]P...	202	S	-
Sspon.01G0004770-1A	ADITS(0.793)PTGSLSEHKR	[STY]P...	460	S	-
Sspon.01G0004770-1A	IDNS(0.933)DSENVVYPDR	[STY]DS...	769	S	-
Sspon.01G0004770-1A	DSSS(0.841)DDDNLF FSK	...S.[STY]....	856	S	-
Sspon.01G0004770-1A	DSS(0.977)SDDDNLF FSK	...R..[STY]....	855	S	-
Sspon.01G0004770-1A	ELS(1)DLELGELR	...R..[STY]....	659	S	-
Sspon.01G0005000-3D	TQSS(0.87)SLSEMLK	[STY]..S...	292	S	-
Sspon.01G0005000-3D	VQS(1)FQR	-	720	S	-
Sspon.01G0005000-3D	VKS(0.999)MAQYPEAR	-	878	S	-
Sspon.01G0005330-2B	GAQATPWERNPS(0.991)SS(0.807)PIL	[STY]P...	499	S	-
Sspon.01G0005330-2B	GAQATPWERNPS(0.775)SS(0.995)PIL	[STY]P...	501	S	-
Sspon.01G0005570-1A	S(0.88)FTSTSYDPVTK	...S.[STY]....	318	S	-
Sspon.01G0005610-1A	DSDDEQPDS(0.999)DEDPDDDLDI	[STY]DE...	334	S	-
Sspon.01G0005820-1P	ADS(1)IGIGS(0.913)YESSR	...R..[STY]....	477	S	-
Sspon.01G0005820-1P	ADS(1)IGIGS(0.913)YESSR	...R..[STY]....	472	S	-
Sspon.01G0005820-1P	ADS(0.993)IGIGSYES(0.896)SR	...S...[STY]....	480	S	-
Sspon.01G0005950-2B	VSS(0.988)FEALHSATK	...R..[STY]....	251	S	-
Sspon.01G0006700-1A	T(0.78)PTTANPGMDYPGSDHISK	[STY]P...	286	T	-
Sspon.01G0007120-2C	KES(1)FENPLAGR	...R..[STY]....	982	S	-
Sspon.01G0007550-2D	STNSISS(0.985)PVSSPTAEDAR	[STY]P..SP..	208	S	-
Sspon.01G0007550-2D	STNSISS(0.979)PVSS(0.95)PTAEDAR	...S...[STY]P...	212	S	-
Sspon.01G0007550-2D	ASALGS(0.999)PLSSWSK	...S...[STY]P...	627	S	-
Sspon.01G0007550-2D	SSS(0.99)FELR	...RS.[STY]....	660	S	-
Sspon.01G0007740-1A	QAPDS(1)AEGDEPSL	[STY].E...	659	S	-
Sspon.01G0007740-1A	AS(1)AEVLGK	-	377	S	-
Sspon.01G0007790-2P	NSGKPIPSQGSTDT(0.908)SGDEEGSR	...S...[STY]....	587	T	-
Sspon.01G0007790-2P	RHSPRST(0.965)PS(0.967)ISR	...S...[STY]P...	267	T	-
Sspon.01G0007790-2P	HSDQLS(0.983)ESSEDLVGR	[STY]..S...	653	S	-
Sspon.01G0007790-2P	IGGHHS(1)PDS(1)EHR	[STY]P...	545	S	-
Sspon.01G0007790-2P	IGGHHS(1)PDS(1)EHR	[STY]P...	548	S	-
Sspon.01G0007790-2P	HSDQLS(0.971)ES(0.96)SEDELVGR	...S.[STY]....	655	S	-
Sspon.01G0007790-2P	VNEDS(0.95)HSEDGS(1)PLKK	...S...[STY]P...	724	S	-
Sspon.01G0007790-2P	VNEDS(0.95)HSEDGS(1)PLKK	...S...[STY]P...	730	S	-
Sspon.01G0007790-2P	KPWS(1)RS(1)PIR	[STY]P.R...	448	S	-
Sspon.01G0007790-2P	KPWS(1)RS(1)PIR	[STY]P.R...	450	S	-
Sspon.01G0007790-2P	RPRS(1)PS(1)PGR	...S.[STY]P...R	358	S	-
Sspon.01G0007790-2P	RPRS(1)PS(1)PGR	...S.[STY]P...R	360	S	-
Sspon.01G0007790-2P	SLRS(1)PNYEER	[STY]P...	558	S	-
Sspon.01G0007790-2P	RPRS(0.999)PS(0.997)PGSR	..R.R..[STY]P...	440	S	-
Sspon.01G0007790-2P	RPRS(0.999)PS(0.997)PGSR	..R.R..[STY]P...	438	S	-
Sspon.01G0007790-2P	RHS(0.965)PRSTPS(0.985)ISR	[STY]PR...	269	S	-
Sspon.01G0007790-2P	RHS(1)PRSTPS(0.883)ISR	[STY]PR...	263	S	-
Sspon.01G0007790-2P	RHS(0.998)PRS(0.938)TPSISR	[STY]PR...	266	S	-
Sspon.01G0007790-2P	RPS(1)PS(1)PVRR	...S.[STY]P...R	348	S	-
Sspon.01G0007790-2P	RPS(1)PS(1)PVRR	...S.[STY]P...R	350	S	-
Sspon.01G0007790-2P	QRS(1)IS(1)PR	..R.R..[STY]P...	223	S	-
Sspon.01G0007790-2P	QRS(1)IS(1)PR	..R.R..[STY]P...	225	S	-
Sspon.01G0007790-2P	S(1)PS(1)PGWR	...S.[STY]P...R	378	S	-
Sspon.01G0007790-2P	S(1)PS(1)PGWR	...S.[STY]P...R	380	S	-
Sspon.01G0007790-2P	S(1)RS(1)IS(1)LS(1)PR	...S...[STY]P...	210	S	-
Sspon.01G0007790-2P	S(1)RS(1)IS(1)LS(1)PR	...S...[STY]P...	212	S	-
Sspon.01G0007790-2P	S(1)RS(1)IS(1)LS(1)PR	...S...[STY]P...	214	S	-
Sspon.01G0007790-2P	S(1)RS(1)IS(1)LS(1)PR	...S...[STY]P...	216	S	-
Sspon.01G0007790-2P	S(0.905)TSPRRS(0.99)VS(0.997)PR	...S.[STY]P...R	250	S	-
Sspon.01G0007790-2P	S(0.905)TSPRRS(0.99)VS(0.997)PR	...S.[STY]P...R	256	S	-
Sspon.01G0007790-2P	S(0.905)TSPRRS(0.99)VS(0.997)PR	...S.[STY]P...R	258	S	-
Sspon.01G0007790-2P	S(1)LS(1)RDIQK	...RS.[STY]....	500	S	-
Sspon.01G0007790-2P	S(1)LS(1)RDIQK	...RS.[STY]....	502	S	-
Sspon.01G0007870-3D	VVQMLESDVIT(0.997)PCPS(0.89)DFYDSE	...S...[STY]P...	370	S	-
Sspon.01G0007870-3D	VVQMLESDVIT(0.997)PCPS(0.89)DFYDSE	...S...[STY]P...	366	T	-

Sspon.01G0007930-2B	VDVNIMS(0.995)ESED5NR	[STY].S...	401	S	-
Sspon.01G0007930-2B	DICGES(0.885)PTTTTNDVGR	[STY]P...	535	S	-
Sspon.01G0008130-2D	TNDITGQDS(0.995)PDS(0.921)GLLASSAK	[STY]P...	140	S	-
Sspon.01G0008130-2D	TNDITGQDS(0.995)PDS(0.921)GLLASSAK	[STY]P...	137	S	-
Sspon.01G0008280-1A	AVDAGMMEYDS(0.997)DDNPIVVDKK	[STY]DD...	151	S	-
Sspon.01G0008280-1A	AGYDS(1)DEEYVAAAK	[STY]DE...	131	S	-
Sspon.01G0008330-4D	QNS(0.997)DGTDTLFI	[STY]D...	1085	S	-
Sspon.01G0008330-4D	S(1)FDYSQSLR	...S..[STY].D...	84	S	-
Sspon.01G0008570-1A	VLDISMYE5DET(0.985)PVT5PLK	[STY]P..SP..	361	T	-
Sspon.01G0008600-2P	EAALAAVPNDS(0.877)PTIFDK	[STY]P...	16	S	-
Sspon.01G0008840-4P	AEAPATLLMS(0.923)PSR	[STY]P.R...	286	S	-
Sspon.01G0009420-3D	EVIENTLS(1)DNK	[STY]D...	114	S	-
Sspon.01G0009900-2C	ALNLT5(0.941)PK	[STY]P...	100	S	-
Sspon.01G0010390-4D	SHSYSPS(0.897)PS(1)PVRR	...S..[STY]P...R	153	S	-
Sspon.01G0010390-4D	SHSYSPS(0.993)PSPVR	...S...[STY]P...	151	S	-
Sspon.01G0010390-4D	SHSYS(0.962)PSPS(0.948)PVRR	...S..[STY]P...R	149	S	-
Sspon.01G0010390-4D	DDYS(0.992)PEYSHS(0.988)PRPR	...S..[STY]P...R	169	S	-
Sspon.01G0010390-4D	DDYS(0.945)PEYSHS(0.999)PRPR	...S..[STY]P...R	175	S	-
Sspon.01G0010390-4D	RYS(0.989)RS(0.999)PPR	[STY]P.R...	20	S	-
Sspon.01G0010390-4D	RYS(0.989)RS(0.999)PPR	[STY]P.R...	22	S	-
Sspon.01G0010390-4D	EIS(1)IVYAEENR	...R..[STY]....	103	S	-
Sspon.01G0010390-4D	SHS(0.958)YSPS(0.924)PSPVR	...S...[STY]P...	147	S	-
Sspon.01G0010660-3C	GSGFMS(1)GPLDK	[STY]G...	182	S	-
Sspon.01G0010660-3C	S(1)FGETTFR	-	95	S	-
Sspon.01G0010690-3D	SYDYS(0.998)PS(1)PPR	...S..[STY]P...R	14	S	-
Sspon.01G0010690-3D	SYDYS(0.998)PS(1)PPR	...S..[STY]P...R	16	S	-
Sspon.01G0010690-3D	QRS(1)LS(1)VSE	...RS..[STY]....	217	S	-
Sspon.01G0010690-3D	QRS(1)LS(1)VSE	...RS..[STY]....	215	S	-
Sspon.01G0010690-3D	LRS(1)RS(0.999)PGYSDS(0.786)PR	..R.R..[STY]P...	156	S	-
Sspon.01G0010690-3D	LRS(1)RS(0.999)PGYSDS(0.786)PR	..R.R..[STY]P...	150	S	-
Sspon.01G0010690-3D	LRS(1)RS(0.999)PGYSDS(0.786)PR	..R.R..[STY]P...	148	S	-
Sspon.01G0010690-3D	S(0.995)HS(0.968)PSYS(0.836)PAPK	..R.R..[STY]P...	169	S	-
Sspon.01G0010690-3D	S(0.995)HS(0.968)PSYS(0.836)PAPK	..R.R..[STY]P...	165	S	-
Sspon.01G0010690-3D	S(0.995)HS(0.968)PSYS(0.836)PAPK	..R.R..[STY]P...	163	S	-
Sspon.01G0010820-3D	VASSNS(0.957)DPDDDCIITVSAK	...S...[STY]....	321	S	-
Sspon.01G0011010-1A	SDSTASVDS(1)PKER	[STY]P...	494	S	-
Sspon.01G0011010-1A	SDSTAS(0.994)VDSPKER	...S...[STY].D...	491	S	-
Sspon.01G0011010-1A	KDS(1)PEAGS(1)PEKLNDR	[STY]P...	352	S	-
Sspon.01G0011010-1A	KDS(1)PEAGS(1)PEKLNDR	[STY]P...	357	S	-
Sspon.01G0011010-1A	ALS(0.998)QTGPETPK	-	464	S	-
Sspon.01G0011010-1A	SDS(0.96)TASVDSPK	...RS..[STY]....	488	S	-
Sspon.01G0011010-1A	SS(0.991)GDES(1)MEEDVAEIK	[STY].E...	367	S	-
Sspon.01G0011010-1A	SS(0.991)GDES(1)MEEDVAEIK	[STY].E...	371	S	-
Sspon.01G0011010-1A	S(0.96)FGRSDSTASVSPK	-	482	S	-
Sspon.01G0011010-4D	SDSTASVDS(1)PEER	[STY]P...	521	S	-
Sspon.01G0011010-4D	SDSTAS(0.999)VDSPEER	...S...[STY].D...	518	S	-
Sspon.01G0011010-4D	SDS(0.948)TASVDS(0.998)PEER	[STY]P...	515	S	-
Sspon.01G0011270-1A	HRT(1)RS(1)IS(0.99)PDYDR	..R.R..[STY]P...	166	S	-
Sspon.01G0011270-1A	HRT(1)RS(1)IS(0.99)PDYDR	..R.R..[STY]P...	164	S	-
Sspon.01G0011270-1A	HRT(1)RS(1)IS(0.99)PDYDR	..R.R..[STY]P...	162	T	-
Sspon.01G0011620-2C	MDFSAGGSGSGS(0.981)GGGGGGGGGGDGGPGDGR	...S..[STY]....	12	S	-
Sspon.01G0011730-2B	IEYITEFGGS(0.881)DDTSEPK	[STY]DD...	353	S	-
Sspon.01G0011730-2B	VSGIS(1)PPSSPIR	[STY]P..SP..	365	S	-
Sspon.01G0011730-2B	VSGIS(0.997)PPSS(0.994)PIR	[STY]P.R...	369	S	-
Sspon.01G0012130-1A	AAS(1)EGGS(0.996)VGTVR	...R...[STY]....	106	S	-
Sspon.01G0012130-1A	AAS(1)EGGS(0.996)VGTVR	...R...[STY]....	102	S	-
Sspon.01G0012490-2B	EFVALS(1)PDVLQK	[STY]P...	773	S	-
Sspon.01G0012640-2D	SAAVS(0.957)EIGEADGADMAE	-	1038	S	-
Sspon.01G0012990-1A	GGMT(0.915)SHAAVVAR	-	472	T	-
Sspon.01G0013660-1P	EGDDYASDHGGDDIEDNLQS(1)PLIS(1)R	[STY]P...	281	S	-
Sspon.01G0013660-1P	EGDDYASDHGGDDIEDNLQS(1)PLIS(1)R	[STY]P...	285	S	-
Sspon.01G0013660-1P	MPEIMGS(1)MR	[STY]..S...	230	S	-
Sspon.01G0013660-1P	EGDDYAS(0.996)DHGGDDIEDNLQS(0.999)PLISR	[STY]P...	268	S	-
Sspon.01G0013660-1P	GQS(1)ALGS(1)ALGLIS(1)R	...R...[STY]....	187	S	-
Sspon.01G0013660-1P	GQS(1)ALGS(1)ALGLIS(1)R	...R...[STY]....	191	S	-
Sspon.01G0013660-1P	GQS(1)ALGS(1)ALGLIS(1)R	...R...[STY]....	197	S	-
Sspon.01G0014220-3D	LGLSGLGGS(1)PR	[STY]PR...	64	S	-
Sspon.01G0014350-2B	GKAEIGS(0.955)ASQEF	[STY].S...	131	S	-
Sspon.01G0014960-3C	DGEAS(1)DEEEYEAK	[STY]DE...	689	S	-
Sspon.01G0015020-3D	AMNKPAEYDS(1)DDEIIAIGR	[STY]DD...	194	S	-
Sspon.01G0015090-2C	AALQSGGRS(0.979)PK	[STY]P.R...	150	S	-
Sspon.01G0015090-2C	SELVS(0.999)PASS(0.99)PR	...S...[STY]P...	726	S	-
Sspon.01G0015090-2C	SELVS(1)PASS(0.955)PR	...S...[STY]P...	722	S	-
Sspon.01G0015090-2C	GATGS(0.908)EEGDKS(1)PCAILDDDNSR	[STY]P...	628	S	-
Sspon.01G0015090-2C	GATGS(0.908)EEGDKS(1)PCAILDDDNSR	[STY]P...	634	S	-
Sspon.01G0015090-2C	SAS(0.911)AGS(1)FDDPSVTGGR	...RS..[STY]....	570	S	-

Sspon.01G0015090-2C	QT(0.974)TPS(0.974)PELADSK	[STY]P...	788	S	-
Sspon.01G0015090-2C	QT(0.974)TPS(0.974)PELADSK	[STY]P...	785	T	-
Sspon.01G0015090-3D	STSGGS(0.976)LEDPSVTGGR	...S...[STY]...	544	S	-
Sspon.01G0015090-3D	SELVS(1)PSSSPR	...S...[STY]P...	700	S	-
Sspon.01G0015090-3D	SELVS(0.87)PSSS(0.803)PR	...S...[STY]P...	704	S	-
Sspon.01G0015090-3D	SELVS(0.997)PS(0.899)SSPR	...S...[STY]P...	702	S	-
Sspon.01G0015090-3D	S(1)AGIELDLNR	-	1198	S	-
Sspon.01G0015180-4D	SSTEDGNTS(0.92)WPSPPVAASQAPNQDAAPDLK	[STY]P.SP..	160	S	-
Sspon.01G0015180-4D	S(0.991)ISSSQFFGDQASFEK	[STY]..S...	226	S	-
Sspon.01G0015190-2B	GQGAGVSGVEPVAAAGS(1)D	[STY]D...	730	S	-
Sspon.01G0015190-2B	GQGAGVS(1)GVEPVAAAGSD	[STY]G...	720	S	-
Sspon.01G0015540-2C	ENDLGISNQGS(1)PDQVFSR	...S...[STY]P...	205	S	-
Sspon.01G0015550-3D	EVLSGCTS(0.972)QPVVS(0.999)PDFK	...S...[STY]P...	1417	S	-
Sspon.01G0015550-3D	EVLSGCTS(0.924)QPVVS(1)PDFK	...S...[STY]P...	1421	S	-
Sspon.01G0016070-1A	RVS(1)S(1)GNLVDVAR	...R...[STY]....	141	S	-
Sspon.01G0016070-1A	RVS(1)S(1)GNLVDVAR	...R...[STY]....	142	S	-
Sspon.01G0016840-1A	S(0.986)APTTPIK	...R...[STY]....	47	S	-
Sspon.01G0016840-1A	S(0.913)APTT(0.885)PIKDGAAAS(1)PFAAALSEEER	...S...[STY]P...	51	T	-
Sspon.01G0016840-1A	S(0.913)APTT(0.885)PIKDGAAAS(1)PFAAALSEEER	...S...[STY]P...	59	S	-
Sspon.01G0016880-2D	LNQDS(1)PLDGYQELPK	[STY]P...	283	S	-
Sspon.01G0017190-1A	NQS(1)FDDDDFANKPVAK	...R...[STY]....	335	S	-
Sspon.01G0017250-1P	APSGPMVQS(0.999)PVS(0.908)SK	[STY]P...	565	S	-
Sspon.01G0017250-1P	APSGPMVQS(1)PVSSK	[STY]P...	562	S	-
Sspon.01G0017260-1A	LADLNAEAQES(1)GDDEDDNVWEEG	[STY]G...	315	S	-
Sspon.01G0017490-2C	DAS(1)PDVVELCDSAGK	..R.R...[STY]P...	89	S	-
Sspon.01G0017620-4D	RLS(0.77)GSAS(0.954)PLPAAAAGS(1)PLR	[STY]P.R...	408	S	-
Sspon.01G0017620-4D	RLS(0.77)GSAS(0.954)PLPAAAAGS(1)PLR	[STY]P.R...	412	S	-
Sspon.01G0017620-4D	RLS(0.77)GSAS(0.954)PLPAAAAGS(1)PLR	[STY]P.R...	421	S	-
Sspon.01G0017970-2B	MDGLAAPS(0.924)PSHS(0.962)GATSGGGASHR	[STY]P...	12	S	-
Sspon.01G0017970-2B	MDGLAAPS(0.971)PSHS(0.883)GATSGGGASHR	[STY]P...	8	S	-
Sspon.01G0017970-2B	MDGLAAPS(0.921)PSHSGAT(0.751)SGGGASHR	[STY]P...	15	T	-
Sspon.01G0018210-2B	LAATS(0.959)TEIQELK	[STY].E...	330	S	-
Sspon.01G0018330-2B	VPS(0.83)ESLLSK	...R...[STY]....	227	S	-
Sspon.01G0018420-1P	ASTPVEES(0.998)PDAESLNGAK	[STY]P...	253	S	-
Sspon.01G0018420-1P	LRS(1)PAVS(1)AAS(1)KEEAK	[STY]P...	233	S	-
Sspon.01G0018420-1P	LRS(1)PAVS(1)AAS(1)KEEAK	[STY]P...	237	S	-
Sspon.01G0018420-1P	LRS(1)PAVS(1)AAS(1)KEEAK	[STY]P...	240	S	-
Sspon.01G0018450-3C	EAPEEEAANAAS(1)PAAAAAGR	[STY]P...	43	S	-
Sspon.01G0018990-1P	VTTY(0.988)KEMPLHVK	[STY].E...	146	Y	-
Sspon.01G0019010-3D	TVIIES(1)DDDMQIDNK	[STY]DD...	432	S	-
Sspon.01G0019170-2B	KVESSSSDSEEDSSDS(0.892)EVEVPVK	-	137	S	-
Sspon.01G0019170-2B	KVESSSSDSEEDSS(0.762)DSEVEVPVK	-	135	S	-
Sspon.01G0019170-2B	KVESSSSDSEEDS(0.851)SDSEVEVPVK	-	134	S	-
Sspon.01G0019170-2B	HDSSSSDSSS(0.96)DEDEKSAANLK	-	270	S	-
Sspon.01G0019170-2B	KVESSSSDS(0.952)EEDSSDSEVEVPVKK	-	130	S	-
Sspon.01G0019170-2B	HDSS(0.828)SSDSSSDEDEKSAANLK	-	264	S	-
Sspon.01G0019170-2B	HDS(0.982)SSSDS(0.866)SSDEDEKSAANLK	...S...[STY]....	268	S	-
Sspon.01G0019170-2B	HDS(0.982)SSSDS(0.866)SSDEDEKSAANLK	...S...[STY]....	263	S	-
Sspon.01G0019170-4D	KVESSSSDSEEDSS(0.839)DSEVEVK	[STY]DS...	105	S	-
Sspon.01G0019680-3C	SDS(0.918)FDDYEQCR	...RS.[STY]....	108	S	-
Sspon.01G0019810-1T	ATPAS(0.975)PVS(0.996)DVGDQPVEEPSQAK	[STY]P...	6	S	-
Sspon.01G0019810-1T	ATPAS(0.965)PVS(0.996)DVGDQPVEEPSQAK	[STY]P...	9	S	-
Sspon.01G0019920-2B	AS(1)PGRIELDK	[STY]P.R...	3	S	-
Sspon.01G0020010-2B	GPAAAAQLDAAKENS(1)PS(1)PKR	[STY]P.R...	104	S	-
Sspon.01G0020010-2B	GPAAAAQLDAAKENS(1)PS(1)PKR	[STY]P.R...	106	S	-
Sspon.01G0020130-4D	QES(1)PGAATPLR	...S...[STY]P...	284	S	-
Sspon.01G0020370-2B	AEAEAAGSLS(0.98)R	...S.[STY]....	11	S	-
Sspon.01G0020450-1A	EYPSGS(0.964)PMFTSNAPSAAAYER	-	410	S	-
Sspon.01G0020450-1A	EYPS(0.937)GS(0.949)PMFTSNAPSAAAYER	[STY]P...	408	S	-
Sspon.01G0020450-1A	FSS(0.787)TIELR	-	507	S	-
Sspon.01G0021560-2B	SAS(0.875)JGDCLVNPK	...S.[STY]....	593	S	-
Sspon.01G0021690-1A	SSGWQQSSS(0.958)PDGSR	[STY]P...	757	S	-
Sspon.01G0021690-1A	SGS(0.985)FTQGVTK	...RS.[STY]....	788	S	-
Sspon.01G0021790-2B	AGSSTTFLS(0.978)PPTSPR	[STY]P..SP..	174	S	-
Sspon.01G0021790-3C	AGSSTTFLS(0.989)PPSS(0.974)PR	...S...[STY]P...	314	S	-
Sspon.01G0021790-3C	AGSSTTFLS(1)PPSS(0.854)PR	...S...[STY]P...	310	S	-
Sspon.01G0021810-2B	AAAAAAESSDS(0.827)ESEDADAAK	...S...[STY]....	74	S	-
Sspon.01G0021810-2B	ENFSTS(0.907)PLR	[STY]P.R...	309	S	-
Sspon.01G0022650-1A	ADGAGS(0.983)ASGLEEK	-	7	S	-
Sspon.01G0022790-2B	MTEADAGS(0.843)TEVK	[STY].E...	114	S	-
Sspon.01G0022790-2B	GGESASKT(0.981)PDST(0.965)PSR	...S.[STY]P...R	407	T	-
Sspon.01G0022790-2B	GGESASKT(0.996)PDSTPSR	...S.[STY]P...R	403	T	-
Sspon.01G0022790-2B	LLNT(0.996)PS(0.881)PYGTDRPQR	...S...[STY]P...	233	S	-
Sspon.01G0022790-2B	LLNT(0.996)PS(0.881)PYGTDRPQR	...S...[STY]P...	231	T	-
Sspon.01G0022790-2B	QVDS(1)GDVET(1)DADTKEDATAK	[STY]..D...D	87	T	-
Sspon.01G0022790-2B	QVDS(1)GDVETDADTK	[STY]G...	82	S	-

Sspon.01G0023740-1P	SNS(0.997)GISLK	...RS.[STY]....	188	S	-
Sspon.01G0023780-3C	ALS(1)FDEAGTTPPS(0.992)PEK	[STY]P...	83	S	-
Sspon.01G0023780-3C	ALS(1)FDEAGTTPPS(0.991)PEK	[STY]P...	73	S	-
Sspon.01G0024010-1A	SGS(0.982)LGSNDTYVR	...RS.[STY]....	20	S	-
Sspon.01G0024340-4D	GGLYADEVLS(1)EEDVEAR	[STY].E...	294	S	-
Sspon.01G0024510-2B	IAS(0.921)PSDAATIK	[STY]P...	629	S	-
Sspon.01G0024650-2C	LMS(1)GATS(0.991)PTKPR	...S...[STY]P...	24	S	-
Sspon.01G0024650-2C	LMS(1)GATS(0.991)PTKPR	...S...[STY]P...	20	S	-
Sspon.01G0025220-1A	LGGSGPSQYSSSL(0.888)SGLGR	...S...[STY]....	920	S	-
Sspon.01G0025220-1A	LGGSGPSQYSSS(0.994)LSSGLGR	...S.[STY]....	918	S	-
Sspon.01G0025220-1A	LGGSGPSQYSSS(0.922)LSS(0.884)GLGR	...S...[STY]....	921	S	-
Sspon.01G0025570-3C	SPATFSTAS(0.813)PSR	[STY]P.R...	307	S	-
Sspon.01G0026770-3D	VSSSINEESDGPS(0.996)PK	...S...[STY]P...	650	S	-
Sspon.01G0026770-3D	DLPNAAVS(1)PDVAK	[STY]P...	631	S	-
Sspon.01G0026770-3D	S(1)LRAS(1)PVHPVKDR	...S...[STY]P...	829	S	-
Sspon.01G0026770-3D	S(1)LRAS(1)PVHPVKDR	...S...[STY]P...	833	S	-
Sspon.01G0026860-2D	ATGAFILTAS(0.967)HNPGGPTEDFGIK	-	177	S	-
Sspon.01G0026990-1A	SPPIDEAAS(1)EGEQQPR	-	63	S	-
Sspon.01G0027110-1P	IIEGYEALNCS(1)P	[STY]P...	212	S	-
Sspon.01G0027330-2B	NSSAS(0.778)YDETEDTTNVR	...S...[STY].D...	688	S	-
Sspon.01G0027330-2B	S(1)IGVGISSDAADIGS(1)EVR	...S...[STY]....	530	S	-
Sspon.01G0027330-2B	S(1)IGVGISSDAADIGS(1)EVR	...S...[STY]....	544	S	-
Sspon.01G0027330-2B	S(1)IGVGISS(0.974)DAADIGSEVR	...S...[STY]....	537	S	-
Sspon.01G0027420-1A	AILEGGS(1)DDEGASTEAGGR	[STY]DD...	1720	S	-
Sspon.01G0027480-2D	IADEVEPQGEES(1)PVEEK	[STY]P...	185	S	-
Sspon.01G0027500-1A	AGS(0.987)FSFK	...R...[STY]....	321	S	-
Sspon.01G0027580-2B	EAEVESALPLQTSVS(0.918)Q	...S.[STY]....	95	S	-
Sspon.01G0027600-1A	SFSSDHNGNLT(1)NR	-	198	T	-
Sspon.01G0027620-1A	AAPAADASAS(0.985)PGYVLR	[STY]P...	12	S	-
Sspon.01G0027830-1A	EIFPEPSGS(0.975)RDT(0.994)ED	...S...[STY].D...	782	S	-
Sspon.01G0027830-1A	EIFPEPSGS(0.975)RDT(0.994)ED	...S...[STY].D...	785	T	-
Sspon.01G0027860-1A	EIES(1)S(1)NEVIPR	[STY].E...	607	S	-
Sspon.01G0027860-1A	EIES(1)S(1)NEVIPR	[STY].E...	608	S	-
Sspon.01G0027920-1A	DSS(0.896)NNQEVETDLVEGR	-	21	S	-
Sspon.01G0027970-1P	SDES(0.999)PPPAQAAEK	[STY]P...	5	S	-
Sspon.01G0028270-2D	VDS(1)QGQMCGSTFK	...R...[STY]....	217	S	-
Sspon.01G0028270-2D	VGS(1)AADWSNQF	...R...[STY]....	245	S	-
Sspon.01G0028710-1P	NLQSENYGVS(0.999)PVLK	[STY]P...	257	S	-
Sspon.01G0029440-1A	AASS(1)ADLADDGFAAPR	-	5	S	-
Sspon.01G0029440-1A	AAS(0.879)SADLADDGFAAPR	-	4	S	-
Sspon.01G0030140-1A	DLAAS(0.936)PTR	[STY]P.R...	605	S	-
Sspon.01G0030390-3D	LESSLS(0.994)FHAPLHK	...S...[STY]....	224	S	-
Sspon.01G0030390-3D	LES(0.985)SLS(0.985)FHAPLHK	...S...[STY]....	221	S	-
Sspon.01G0030480-1A	EVNS(0.992)PTAS(0.98)VSAQSVSSAR	[STY]P...	755	S	-
Sspon.01G0030480-1A	EVNS(0.809)PTASVSAQSVSS(0.779)AR	[STY]P...	767	S	-
Sspon.01G0030480-1A	EVNS(0.894)PTASVSAQS(0.924)VSSAR	[STY]P...	764	S	-
Sspon.01G0030480-1A	EVNS(0.936)PTAS(0.99)VSAQS(0.849)VSSAR	[STY]P...	759	S	-
Sspon.01G0030480-3C	LSSINQS(1)MDDLRL	-	421	S	-
Sspon.01G0030520-2D	SS(0.771)PHGGLDDQIER	[STY]P...	3	S	-
Sspon.01G0030850-2B	S(0.973)FSSEEQFMTMSR	...S...[STY]....	66	S	-
Sspon.01G0030900-1P	QRFS(1)NLS(1)LK	...S...[STY]....	409	S	-
Sspon.01G0030900-1P	QRFS(1)NLS(1)LK	...S...[STY]....	412	S	-
Sspon.01G0031120-2D	AGATS(0.999)PAAAAANLAGK	[STY]P...	6	S	-
Sspon.01G0031590-1A	VDGFLPGGGSGDDDAADSPS(0.863)R	...S.[STY]....	109	S	-
Sspon.01G0031590-1A	VDGFLPGGGSGDDDAADS(0.911)PSR	[STY]P.R...	107	S	-
Sspon.01G0031910-2D	VIEPEAEIS(1)QDGK	-	378	S	-
Sspon.01G0031910-2D	EIAMDS(0.825)ADSDLNNR	[STY].S...	390	S	-
Sspon.01G0032460-2B	S(0.862)SSAENDPTTVTER	[STY].S...	2	S	-
Sspon.01G0032640-1A	VIPLEADQS(1)PDR	[STY]P.R...	164	S	-
Sspon.01G0032740-3D	GGVSS(0.952)PSWER	[STY]P...	139	S	-
Sspon.01G0032930-1P	DAS(1)GDES(1)DGVAWGLPNGR	...R...[STY]....	300	S	-
Sspon.01G0032930-1P	DAS(1)GDES(1)DGVAWGLPNGR	...R...[STY]....	304	S	-
Sspon.01G0032980-2P	MDTDGQNQGEADGQKQDDEST(0.953)PIQED	[STY]P...	278	T	-
Sspon.01G0034930-1P	YAKPEDAGIT(1)PEDK	[STY]P...	155	T	-
Sspon.01G0034930-1P	SSDEELS(0.958)EEEDDSGDEAILGNPDP	[STY].E...	166	S	-
Sspon.01G0035370-2C	LRS(1)LS(1)PLHVSSQK	..R.R...[STY]P...	251	S	-
Sspon.01G0035370-2C	LRS(1)LS(1)PLHVSSQK	..R.R...[STY]P...	249	S	-
Sspon.01G0035430-3D	AAAS(0.887)SGS(0.972)EDEEEEVGFSR	...S...[STY].D...	11	S	-
Sspon.01G0035430-3D	AAAS(0.887)SGS(0.972)EDEEEEVGFSR	...S...[STY].D...	14	S	-
Sspon.01G0035870-1P	S(0.787)SPELTDSSAEGFR	...R...[STY]....	512	S	-
Sspon.01G0035900-2P	QPQIET(1)EGDADNEQMIPE	-	511	T	-
Sspon.01G0035970-2D	SAMQVGQAS(0.998)RGAS(0.954)LDPTEEK	...R...[STY]....	279	S	-
Sspon.01G0035970-2D	SAMQVGQAS(0.998)RGAS(0.954)LDPTEEK	...R...[STY]....	275	S	-
Sspon.01G0036140-2C	SES(0.998)FSGFR	...RS.[STY]....	81	S	-
Sspon.01G0036290-1B	KGS(0.987)CNETIAEEK	...R...[STY]....	176	S	-
Sspon.01G0036410-1P	VDRS(0.99)DEESGGGEIDWDK	[STY]DE...	57	S	-

Sspon.01G0036970-1B	DIVLS(1)DPAIQDER	[STY]D...	315	S	-
Sspon.01G0036970-1B	GS(1)LGS(1)LDVVAVK	...S..[STY].D...	173	S	-
Sspon.01G0036970-1B	GS(1)LGS(1)LDVVAVK	...S..[STY].D...	176	S	-
Sspon.01G0036970-1B	S(0.999)KGS(0.946)LGSLDVVAVK	...S..[STY]....	170	S	-
Sspon.01G0037490-1B	ASPPS(0.989)PDRSS(0.78)PSPAAAPAPAGR	[STY]P.R...	30	S	-
Sspon.01G0037490-1B	ASPPS(0.989)PDRSS(0.78)PSPAAAPAPAGR	[STY]P.R...	25	S	-
Sspon.01G0037490-1B	AS(0.999)PPS(0.953)PDRSSPSPAAAPAPAGR	[STY]P.R...	22	S	-
Sspon.01G0037620-2D	DWAS(1)GEFVVK	[STY].E...	530	S	-
Sspon.01G0038040-2D	KPSPS(0.999)FR	...S..[STY]....	20	S	-
Sspon.01G0038040-2D	NGS(1)LNALR	...R..[STY]....	27	S	-
Sspon.01G0038080-2D	AVAVDADQQGS(1)PEPPEQEK	[STY]P...	64	S	-
Sspon.01G0038290-1T	VS(0.999)PQLSS(0.981)PNQPYSLR	[STY]P...	125	S	-
Sspon.01G0038290-1T	VS(0.999)PQLSS(0.981)PNQPYSLR	[STY]P...	120	S	-
Sspon.01G0038290-1T	S(1)PDVEHPAS(1)PK	[STY]P...	73	S	-
Sspon.01G0038290-1T	S(1)PDVEHPAS(1)PK	[STY]P...	81	S	-
Sspon.01G0038980-2C	GADAAEGS(1)GPEDEEER	-	79	S	-
Sspon.01G0039070-3D	ASALPVS(1)PK	[STY]P...	8	S	-
Sspon.01G0039160-2C	ATS(0.795)GYLGADYQESMDR	...R..[STY]....	337	S	-
Sspon.01G0040340-2C	SQLDS(0.99)PVDEIDASNK	[STY]P...	397	S	-
Sspon.01G0040340-2C	S(1)PFDNIQPK	-	821	S	-
Sspon.01G0040480-1B	SIS(0.93)MEGLHTLK	...RS.[STY]....	339	S	-
Sspon.01G0040960-2C	ECSSEFPEVNNTSVDS(0.983)PCWK	[STY]P...	213	S	-
Sspon.01G0041200-2C	SLYTSLET(0.989)PTSAR	-	801	T	-
Sspon.01G0041200-2C	SLYTSLET(0.885)PTS(0.796)AR	[STY]P...	804	S	-
Sspon.01G0041200-2C	ASAS(0.995)PEQQPVFASPQLK	-	989	S	-
Sspon.01G0041200-2C	NIES(1)APGS(0.982)EDASAAGGDR	-	608	S	-
Sspon.01G0041200-2C	SGNS(0.997)PTDSTVVPTK	-	17	S	-
Sspon.01G0041200-2C	NIES(1)APGS(0.982)EDASAAGGDR	-	604	S	-
Sspon.01G0041200-2C	ASAS(0.815)PEQQPVFAS(1)PQLK	[STY]P...	998	S	-
Sspon.01G0041200-3D	S(1)FGFVGR	...S..[STY]....	1785	S	-
Sspon.01G0041320-2C	SDEDSQS(0.883)QYDEAPLSR	...S..[STY]....	762	S	-
Sspon.01G0041370-3D	SYS(1)LGNMVMNAK	...RS.[STY]....	688	S	-
Sspon.01G0041800-1B	ELDGILDSS(0.845)DAETAK	[STY]D...	12	S	-
Sspon.01G0041800-1B	ELDGILDS(0.824)SDAETAK	-	11	S	-
Sspon.01G0042110-2D	ADEEES(0.888)DT(0.85)SEEIVPVVVR	...S..[STY]....	70	T	-
Sspon.01G0042110-2D	ADEEES(0.975)DT(0.785)SEEIVPVVVRPGHIR	...S..[STY]....	68	S	-
Sspon.01G0042410-1P	GSDDT(0.983)DS(0.812)DTERDLELER	[STY]DS...	329	S	-
Sspon.01G0042410-1P	GSDDT(0.983)DS(0.812)DTERDLELER	[STY]DS...	327	T	-
Sspon.01G0042420-2D	SGLYSQGFS(1)PAR	-	10	S	-
Sspon.01G0042420-2D	SGLYS(0.968)QGFS(1)PAR	[STY]P.R...	6	S	-
Sspon.01G0042420-2D	NLS(1)PQIR	[STY]P...	16	S	-
Sspon.01G0042420-2D	FRS(0.999)PS(0.968)PMSS(0.995)PNPR	..R.R..[STY]P...	86	S	-
Sspon.01G0042420-2D	FRS(1)PS(0.997)PMSS(0.98)PNPR	..R.R..[STY]P...	82	S	-
Sspon.01G0042420-2D	FRS(1)PS(0.997)PMSS(0.98)PNPR	..R.R..[STY]P...	80	S	-
Sspon.01G0042420-2D	S(0.995)GLYSQGFS(1)PAR	[STY]P.R...	2	S	-
Sspon.01G0042450-1P	QNS(1)EISYYADDEDGNR	...R..[STY]....	252	S	-
Sspon.01G0042520-3D	TQSS(0.995)NLSILK	[STY]..S...	406	S	-
Sspon.01G0042520-3D	TQSS(0.892)NLSILKDS(1)FK	[STY]..S...	415	S	-
Sspon.01G0042830-3D	GLDSSAASEES(0.998)K	...S..[STY]....	301	S	-
Sspon.01G0043020-2D	DAS(1)PDVVELCDSAEK	..R.R..[STY]P...	88	S	-
Sspon.01G0043020-2D	ERS(1)AS(1)PPPQR	[STY]P...	71	S	-
Sspon.01G0043020-2D	ERS(1)AS(1)PPPQR	[STY]P...	73	S	-
Sspon.01G0043200-1B	FNSLS(0.986)MK	...S..[STY]....	267	S	-
Sspon.01G0044030-2C	ILGAEYAGS(0.967)CAAAR	-	110	S	-
Sspon.01G0044430-1B	PGALASQQS(0.999)PEGWK	[STY]P...	60	S	-
Sspon.01G0044620-1B	LSASAASPKT(0.86)AKPT(0.86)R	...S..[STY]....	41	T	-
Sspon.01G0044620-1B	LSASAASPKT(0.86)AKPT(0.86)R	...S..[STY]....	37	T	-
Sspon.01G0045610-2C	QLS(1)IDQFENEGR	...R..[STY]....	349	S	-
Sspon.01G0045610-2C	QMS(1)INSVPK	...R..[STY]....	380	S	-
Sspon.01G0046290-1B	ERS(0.987)YER	-	231	S	-
Sspon.01G0047220-1T	DFLSSSS(0.876)FK	...S..[STY]....	367	S	-
Sspon.01G0047350-1B	S(1)VDDSILLAER	...S..[STY]....	493	S	-
Sspon.01G0047470-2D	NNGS(1)PDNPQLVPR	[STY]P...	128	S	-
Sspon.01G0048200-2D	QAVGSDDDEDADSW(0.843)DT	...S..[STY]....	194	S	-
Sspon.01G0048480-2D	SENTIYSAS(0.958)PATS(0.899)PPSNAEQPK	...S...[STY]P...	481	S	-
Sspon.01G0048480-2D	SENTIYSAS(0.958)PATS(0.899)PPSNAEQPK	...S...[STY]P...	477	S	-
Sspon.01G0048910-2D	VGS(1)AADWSSQY	...R..[STY]....	239	S	-
Sspon.01G0048910-2D	VDS(0.999)KGEVCGTTYTVDSAK	...R..[STY]....	213	S	-
Sspon.01G0049940-1B	TAPQLDAVDSSS(0.816)QDWK	...S..[STY]....	103	S	-
Sspon.01G0050080-1B	WGS(1)PDYPGR	..R.R..[STY]P...	182	S	-
Sspon.01G0050080-1B	S(0.993)PSYSSPPGYGGYDDYR	[STY]P...	190	S	-
Sspon.01G0050080-1B	S(0.977)PSYSS(0.998)PPGYGGYDDYR	[STY]P...	195	S	-
Sspon.01G0051260-1C	SADKS(0.955)S(0.965)GLATAVDPASR	[STY]G...	933	S	-
Sspon.01G0051260-1C	SADKS(0.955)S(0.965)GLATAVDPASR	[STY]G...	934	S	-
Sspon.01G0051400-1C	LKDNPSNS(0.916)NPPS(0.993)PHLTNDGK	...S...[STY]P...	1244	S	-
Sspon.01G0051400-1C	LKDNPSNS(0.872)NPPS(0.999)PHLTNDGK	...S...[STY]P...	1248	S	-

Sspon.01G0051410-1C	AGEEDAAAAS(1)PAAVR	[STY]P...	11	S	-
Sspon.01G0052070-1P	NQS(0.998)VGSFAAAGASGR	...R...[STY]....	171	S	-
Sspon.01G0052130-1P	LDQSSPASS(0.787)PAPVR	...S...[STY]P...	102	S	-
Sspon.01G0052130-1P	LDQSS(0.958)PASSPAPVR	[STY]P..SP..	98	S	-
Sspon.01G0052200-1P	ASAETLARS(0.993)PS(0.997)REPS(0.94)SDPPR	[STY]P.R...	16	S	-
Sspon.01G0052200-1P	ASAETLARS(1)PS(1)REPS(0.877)SDPPR	[STY]P.R...	10	S	-
Sspon.01G0052200-1P	ASAETLARS(1)PS(1)REPS(0.877)SDPPR	[STY]P.R...	12	S	-
Sspon.01G0052200-1P	S(1)PS(1)PEPVYDNLGIR	[STY]PSP...	132	S	-
Sspon.01G0052200-1P	S(1)PS(1)PEPVYDNLGIR	[STY]PSP...	134	S	-
Sspon.01G0052600-2D	HGEGHDHDGHSSSS(0.98)S(0.99)DSD	...S...[STY].D...	98	S	-
Sspon.01G0052600-2D	KHGEHDHDGHSS(0.922)S(0.952)SSSDSD	...S...[STY]....	96	S	-
Sspon.01G0052600-2D	KHGEHDHDGHSS(0.967)S(0.946)SSSDSD	[STY]..S...	95	S	-
Sspon.01G0052600-2D	HGEGHDHDGHSS(0.996)SSS(0.991)SDSD	...S...[STY].D...	97	S	-
Sspon.01G0052600-2D	HGEGHDHDGHSS(0.996)SSS(0.991)SDSD	...S...[STY].D...	94	S	-
Sspon.01G0052740-1C	ACSVGVVGGGGGAGS(0.881)PPGS(0.881)PGHSLS(0.853)PR	...S...[STY]P...	75	S	-
Sspon.01G0052740-1C	ACSVGVVGGGGGAGS(1)PPGS(0.962)PGHSLSPR	...S...[STY]P...	69	S	-
Sspon.01G0052740-1C	ACSVGVVGGGGGAGS(1)PPGS(0.962)PGHSLSPR	...S...[STY]P...	65	S	-
Sspon.01G0053850-2D	AES(1)PFS(0.978)PSR	[STY]P.R...	164	S	-
Sspon.01G0053850-2D	AES(1)PFS(0.977)PSR	[STY]P.R...	161	S	-
Sspon.01G0054390-1C	LVS(1)IVEEER	...R...[STY]....	289	S	-
Sspon.01G0055130-1C	GSGAGPSSLSGS(0.967)PLK	...S...[STY]P...	113	S	-
Sspon.01G0055900-1C	ATES(1)PEGEKT(1)PK	[STY]P.R...	104	S	-
Sspon.01G0055900-1C	ATES(1)PEGEKT(1)PK	[STY]P.R...	110	T	-
Sspon.01G0056510-2D	TQLPAS(0.984)GSAS(0.999)PVEFR	...S...[STY]P...	203	S	-
Sspon.01G0056510-2D	TQLPAS(0.984)GSAS(0.999)PVEFR	...S...[STY]P...	207	S	-
Sspon.01G0056690-1C	ISGS(0.99)VEGEVDELCL	...S...[STY]....	84	S	-
Sspon.01G0056690-1C	IS(0.882)GSVEGEVDELCL	[STY].S...	82	S	-
Sspon.01G0056690-1C	S(1)LDLAPGADLR	...S...[STY]....	70	S	-
Sspon.01G0058010-1D	NSEPDS(1)PIS(1)PLLTSDPK	...S...[STY]P...	759	S	-
Sspon.01G0058010-1D	NSEPDS(1)PIS(1)PLLTSDPK	...S...[STY]P...	762	S	-
Sspon.01G0058010-1D	QSSKNS(0.966)EPDSPISPLLTSDPK	[STY].P.SP..	755	S	-
Sspon.01G0058010-1D	QSS(0.839)KNSEPDS(1)PISPLLTSDPK	...S...[STY]P...	752	S	-
Sspon.01G0058960-1D	S(1)GVQEQFEIK	[STY]G...	2	S	-
Sspon.01G0060070-1D	SS(0.905)APVAGAAFER	-	3	S	-
Sspon.01G0060750-1D	SNS(0.998)GINLK	...RS.[STY]....	174	S	-
Sspon.01G0060800-1D	LES(1)FVQR	...R...[STY]....	269	S	-
Sspon.01G0061070-1D	NTLVS(1)GGVR	[STY]G...	457	S	-
Sspon.01G0061090-1D	ASSEGQPDSS(0.865)DS(0.944)EGDSLHFVITPR	[STY]DS...	2137	S	-
Sspon.01G0061090-1D	ASSEGQPDSS(0.865)DS(0.944)EGDSLHFVITPR	[STY]DS...	2139	S	-
Sspon.01G0061090-1D	ASSEGQPDSS(0.854)S(0.779)DSEGDSLHFVITPR	[STY]DS...	2136	S	-
Sspon.01G0061090-1D	ASS(0.991)EGQPDSSDSEGDSLHFVITPR	-	2130	S	-
Sspon.01G0061280-1D	GGTSSGAQS(1)GDGEYLK	[STY]G...	179	S	-
Sspon.01G0062050-1D	SNMMS(0.968)FR	-	746	S	-
Sspon.02G0000180-1A	LLLPAASNTVPS(0.938)EPSSPK	[STY].P.SP..	353	S	-
Sspon.02G0000180-1A	GFVPFSPGS(0.854)PTEQS(0.979)VHDGR	[STY]P...	426	S	-
Sspon.02G0000180-1A	GFVPFSPGS(0.854)PTEQS(0.979)VHDGR	[STY]P...	431	S	-
Sspon.02G0000790-2T	LSPSTGGT(0.998)DNDGEGTIERPTK	[STY]D...	153	T	-
Sspon.02G0001270-1P	VFSSPEAEPLAES(1)Q	-	265	S	-
Sspon.02G0001320-2D	AAAGDLS(1)DDEKR	[STY]DD...	8	S	-
Sspon.02G0001390-1A	TSPIELSSS(0.954)PQR	[STY]P.R...	423	S	-
Sspon.02G0001390-1A	TS(0.909)PIELSSSPQR	[STY]P...	415	S	-
Sspon.02G0001430-4D	LGGS(1)FANK	-	86	S	-
Sspon.02G0002120-2C	SLIQPIT(1)LVPR	-	636	T	-
Sspon.02G0002140-1A	SAATGMQS(0.935)PSSGS(0.871)PTER	[STY]P...	136	S	-
Sspon.02G0002140-1A	SAATGMQS(0.994)PSSGS(0.834)PTER	[STY]P...	131	S	-
Sspon.02G0003120-1A	GRSSPS(0.972)PDAGR	[STY]P...	82	S	-
Sspon.02G0003150-1A	KFDS(0.999)FSR	[STY].S...	36	S	-
Sspon.02G0003150-1A	S(1)MNQYPEAR	...R...[STY]....	567	S	-
Sspon.02G0003220-2B	SRSYS(0.869)PDDYKR	...S...[STY]P...R	118	S	-
Sspon.02G0003360-2C	LLEDDSS(0.994)DQDDPLYAR	[STY]D...	379	S	-
Sspon.02G0003570-2B	GAS(1)APPS(1)PAGS(1)PDDLIALR	...S...[STY]P...	74	S	-
Sspon.02G0003570-2B	GAS(1)APPS(1)PAGS(1)PDDLIALR	...S...[STY]P...	78	S	-
Sspon.02G0003570-2B	GAS(1)APPS(1)PAGS(1)PDDLIALR	...S...[STY]P...	82	S	-
Sspon.02G0003810-3C	TSS(0.798)LPAEYMEDR	...R...[STY]....	98	S	-
Sspon.02G0004110-3C	S(1)DS(1)EEHHFESK	[STY]DS...	2	S	-
Sspon.02G0004110-3C	S(1)DS(1)EEHHFESK	[STY]DS...	4	S	-
Sspon.02G0004620-3C	SGS(0.967)ALFDDYGR	-	140	S	-
Sspon.02G0004650-1A	LQS(1)FHIGK	-	482	S	-
Sspon.02G0004780-1A	SSNAPVAGS(0.939)PSNSVSK	[STY]P...	831	S	-
Sspon.02G0004820-1A	SVS(0.902)SGSDEDSWVDVK	...S...[STY]....	150	S	-
Sspon.02G0004840-4D	DGS(1)LQMTSTR	-	535	S	-
Sspon.02G0004860-3D	SSLS(0.991)PITVDR	...S...[STY]P...	211	S	-
Sspon.02G0004890-2B	NDDLESPVYFT(1)DPES	[STY]D...	757	T	-
Sspon.02G0004890-2B	NDDLES(1)PVYFT(0.999)DPES	[STY]P...	752	S	-
Sspon.02G0005150-1P	DGLSSS(0.82)GDDWLR	...S...[STY]....	1120	S	-

Sspon.02G0005420-1A	AEEAAATEAEAKPDASDAEDEEGGET(0.988)GS(0.993)DRE ADAK	...[STY]..D...D	118	T	-
Sspon.02G0005420-1A	AEEAAATEAEAKPDASDAEDEEGGET(0.988)GS(0.993)DRE ADAK	...[STY]..D...D	120	S	-
Sspon.02G0005420-1A	SINPPMS(1)PQAATTDR	-	296	S	-
Sspon.02G0005420-1A	AAT(1)PDDEPEETPTPSR	-	197	T	-
Sspon.02G0005420-1A	AAT(0.999)PDDEPEETPT(0.797)PSR	...[STY]P.R...	207	T	-
Sspon.02G0005420-4D	LSAAQQTETMS(0.996)T	-	637	S	-
Sspon.02G0005470-1A	GQLS(0.999)FSSR	...[STY]..S...	199	S	-
Sspon.02G0005470-1A	GQLS(0.989)FSS(0.83)R	...S..[STY]....	202	S	-
Sspon.02G0005470-1A	AAS(1)PDAAAADNVFSR	...[STY]P...	51	S	-
Sspon.02G0005500-1A	ADDQQAAPTQSVRVPVS(0.954)R	...R..[STY]....	273	S	-
Sspon.02G0005500-1A	TPASSQSAGPSQRPAS(0.974)QEGR	...R..[STY]....	963	S	-
Sspon.02G0006260-2D	SRS(1)MSFS(0.99)PER	...S.[STY]P...R	614	S	-
Sspon.02G0006260-2D	SMS(1)FS(1)PERVR	...S.[STY]P...R	616	S	-
Sspon.02G0006260-2D	SMS(1)FS(1)PERVR	...S.[STY]P...R	618	S	-
Sspon.02G0006260-2D	NLS(0.997)TPPPVVK	...R..[STY]....	647	S	-
Sspon.02G0006260-2D	S(0.764)RSMSFS(0.996)PER	...S.[STY]P...R	612	S	-
Sspon.02G0006280-2B	ITSLAVSSDS(0.99)FGESSCR	...S..[STY]....	454	S	-
Sspon.02G0006890-3C	S(0.945)DSASMAAAIEAR	...[STY]DS...	2	S	-
Sspon.02G0007100-2C	LVPSS(0.977)VSSIPK	...[STY]..S...	55	S	-
Sspon.02G0007100-2C	LVPSS(0.948)VSS(0.865)IPK	...S..[STY]....	58	S	-
Sspon.02G0007100-2C	LVPSS(0.84)SVSSIPK	...[STY]..S...	54	S	-
Sspon.02G0007200-1A	MDLS(1)PNK	...[STY]P...	377	S	-
Sspon.02G0007330-2B	S(0.811)ASSSEENGVLLEGAK	...[STY]..S...	191	S	-
Sspon.02G0007350-1A	GACGAPRPS(0.981)PS(0.942)PSPR	...[STY]P..SP..	44	S	-
Sspon.02G0007350-1A	GACGAPRPS(0.981)PS(0.942)PSPR	...[STY]P..SP..	42	S	-
Sspon.02G0007590-1A	LLNAVTTGGS(0.992)PT	...[STY]P...	391	S	-
Sspon.02G0008850-1A	RLS(1)AAAKEDQMK	...R..[STY]....	453	S	-
Sspon.02G0008880-1A	AVQVSPILDGNQT(0.992)DADSNAGEEVASR	...[STY]D...	138	T	-
Sspon.02G0008880-1A	AQSGVMT(1)AETGTyr	...[STY]E...	469	T	-
Sspon.02G0009000-1A	MDGGSST(0.989)PAS(1)PPR	...[STY]P.R...	7	T	-
Sspon.02G0009000-1A	MDGGSST(0.989)PAS(1)PPR	...[STY]P.R...	10	S	-
Sspon.02G0009000-1A	MDGGSST(0.977)TPASPPR	...[STY]P..SP..	6	S	-
Sspon.02G0009270-2B	SIS(0.984)SLYEER	...RS.[STY]....	83	S	-
Sspon.02G0009300-2C	GGIDS(0.997)PSWR	...[STY]P...	263	S	-
Sspon.02G0009460-1A	LSVAT(0.998)PTTS(0.976)SGDQQMVTVAER	...[STY]P...	391	S	-
Sspon.02G0009460-1A	LSVAT(1)PTTSSGDQQMVTVAER	...[STY]P...	387	T	-
Sspon.02G0009460-1A	LSVAT(0.967)PTT(0.818)SSGDQQMVTVAER	...[STY]P...	390	T	-
Sspon.02G0009460-1A	LSVAT(0.826)PTTS(0.943)S(0.973)GDQQMVTVAER	...[STY]P...	392	S	-
Sspon.02G0009460-1A	ARLS(0.999)VAT(0.905)PTTSSGDQQMVTVAER	...[STY]P...	384	S	-
Sspon.02G0009460-2P	DAGAQPSSTTATTS(0.876)S(0.841)GEQQQQMAVVAER	...[STY]E...	182	S	-
Sspon.02G0009460-2P	DAGAQPSSTTATTS(0.823)S(0.92)GEQQQQMAVVAER	...[STY]E...	183	S	-
Sspon.02G0009460-2P	EVS(0.995)SEALFR	...R..[STY]....	202	S	-
Sspon.02G0009710-2B	MGLIGSGGSGSGGDGDS(0.998)LGR	-	86	S	-
Sspon.02G0009710-2B	MGLIGSGGS(0.989)GS(0.996)GGDGDLSGR	...S..[STY]....	78	S	-
Sspon.02G0009710-2B	MGLIGSGGS(0.989)GS(0.996)GGDGDLSGR	...S..[STY]....	80	S	-
Sspon.02G0009710-3C	SALQASIVT(1)P	...[STY]P...	556	T	-
Sspon.02G0010160-1A	AEWSEASS(0.988)FNCR	-	201	S	-
Sspon.02G0010160-1A	AGS(0.949)TGLYSAGYR	...R..[STY]....	399	S	-
Sspon.02G0010610-2B	IVSQS(0.996)APLFPEK	-	251	S	-
Sspon.02G0010610-2B	GSFS(0.994)GPIASR	-	377	S	-
Sspon.02G0010610-2B	SFS(1)IPSR	-	494	S	-
Sspon.02G0010610-2B	VS(1)PGNS(1)PPPISS(0.988)PK	...S...[STY]P...	421	S	-
Sspon.02G0010610-2B	VS(1)PGNS(1)PPPISS(0.988)PK	...S...[STY]P...	411	S	-
Sspon.02G0010610-2B	VS(1)PGNS(1)PPPISS(0.988)PK	...S...[STY]P...	415	S	-
Sspon.02G0010610-2B	S(0.938)TENIDVISAAPR	-	386	S	-
Sspon.02G0010610-4D	ATSQIASGNPTS(0.975)GPLESK	...[STY]G...	371	S	-
Sspon.02G0010890-3P	LSSSSLS(0.989)PSSSPSR	...S.[STY]P...R	30	S	-
Sspon.02G0010970-2D	ELNTVQS(0.99)IGNFEANK	-	664	S	-
Sspon.02G0010970-2D	VLLAEAS(1)MENQVK	...[STY]E...	757	S	-
Sspon.02G0011160-2B	SFSLSDLHNSSTDGGS(0.975)D	...[STY]D...	256	S	-
Sspon.02G0011160-2B	GLSSFY(0.91)GK	...S..[STY]....	117	S	-
Sspon.02G0011160-2B	NGLGS(1)FR	...[STY]..S...	235	S	-
Sspon.02G0011160-2B	SFS(1)LSDLHNSSTDGSD	...RS.[STY]....	243	S	-
Sspon.02G0011160-2B	S(0.952)FSLSDLHNSSTDGSD	...S..[STY]....	241	S	-
Sspon.02G0011270-1P	NIDNMDDNDGSS(0.908)PDSSPKR	...[STY]P..SP..	284	S	-
Sspon.02G0011320-2B	MESSKS(1)PQSSK	...[STY]P...	6	S	-
Sspon.02G0011530-1P	VAPTTGMGPNS(0.99)PPS(0.999)R	...[STY]P...	263	S	-
Sspon.02G0011530-1P	VAPTTGMGPNS(0.999)PPSR	...[STY]P...	260	S	-
Sspon.02G0011530-4D	APNTALSAS(0.992)PDGAK	...S.[STY]P...R	150	S	-
Sspon.02G0011530-4D	MMEVS(1)PS(1)PEQGVMAGR	...[STY]PSP...	5	S	-
Sspon.02G0011530-4D	MMEVS(1)PS(1)PEQGVMAGR	...[STY]PSP...	7	S	-
Sspon.02G0011690-3C	FWGQGDSESEEEEEVES(0.972)EQGSDSDDDGGR	-	123	S	-
Sspon.02G0011690-3C	NQEDDS(0.996)DESDTGH	...[STY]DE...	155	S	-
Sspon.02G0012130-1A	VLFPDGHQS(1)DDEPPSGDLR	...[STY]DD...	258	S	-

Sspon.02G0012380-3C	EVSS(0.974)S(0.998)LQDLTVR	...S.[STY]....	200	S	-
Sspon.02G0012380-3C	EVS(1)S(0.985)SLQDLTVR	...R..[STY]....	199	S	-
Sspon.02G0012380-3C	EVS(1)S(0.985)SLQDLTVR	...R..[STY]....	198	S	-
Sspon.02G0012440-2P	MATAGS(0.998)PPPGSISK	[STY]P...	858	S	-
Sspon.02G0012610-1A	ALIAEGSCGS(1)PR	[STY]PR...	612	S	-
Sspon.02G0012830-1P	S(1)LQDLASR	-	20	S	-
Sspon.02G0013320-4D	DFGS(1)MNMDLLR	-	58	S	-
Sspon.02G0013380-1A	VSAS(0.995)PS(1)PR	...S...[STY]P...	27	S	-
Sspon.02G0013380-1A	DRS(1)PIPYR	..R.R..[STY]P...	47	S	-
Sspon.02G0013380-1A	VS(0.795)ASPS(0.995)PR	...S...[STY]P...	23	S	-
Sspon.02G0013560-1A	SAAAGPTSAEDSTAAGSDSEAYDS(0.803)DADHRPPPR	[STY]D...	71	S	-
Sspon.02G0013560-1A	SAAAGPTSAEDSTAAGSDS(0.986)EAYDSADHRPPPR	...S.[STY]....	65	S	-
Sspon.02G0013560-1A	SAAAGPTSAEDST(0.918)AAGSDSEAYDSADHRPPPR	-	59	T	-
Sspon.02G0013560-1A	SAAAGPTSAEDS(0.952)TAAGSDS(0.77)EAYDSADHRPPPR	...S.[STY]....	58	S	-
Sspon.02G0013560-1A	KAAAAAS(0.957)PSR	[STY]P.R...	87	S	-
Sspon.02G0013960-1A	MLETAAAAAS(1)PR	[STY]PR...	10	S	-
Sspon.02G0013960-2C	MLETAAAASS(0.96)PR	[STY]PR...	10	S	-
Sspon.02G0014140-1A	ELS(1)ILTESSGDQDGNR	...R..[STY]....	156	S	-
Sspon.02G0014480-4D	SYS(0.99)FLVK	...RS.[STY]....	203	S	-
Sspon.02G0014690-1A	HHPGVVDADDSDSDSEGS(0.917)EYDEER	...S..[STY]....	136	S	-
Sspon.02G0014690-2P	VQPSTASGGGS(1)PQSS	...S...[STY]P...	372	S	-
Sspon.02G0014690-2P	VQPSTASGGGS(0.996)PQS(0.809)S	...S...[STY]P...	375	S	-
Sspon.02G0015320-1A	ELGVSS(0.989)CGNT(1)AEF	[STY].E...	571	S	-
Sspon.02G0015320-1A	ELGVSS(0.886)CGNT(1)AEF	[STY].E...	575	T	-
Sspon.02G0015490-3C	VDEDIS(0.879)SFR	-	205	S	-
Sspon.02G0015630-1A	ELVSYPLGGS(1)GSAGAD	[STY].S...	248	S	-
Sspon.02G0015690-1A	YAGEAFRS(1)P	[STY]P...	445	S	-
Sspon.02G0015770-2B	GEGLDPWICTS(0.998)E	-	444	S	-
Sspon.02G0016200-2D	TPANGS(0.996)PGNDSPPGSDR	[STY]P...	148	S	-
Sspon.02G0016800-3D	DVEASS(0.879)VVEDDDEVQVVDK	-	364	S	-
Sspon.02G0017090-2C	DASYLLDAQSGMS(0.944)VS(0.968)PR	[STY]PR...	128	S	-
Sspon.02G0017090-2C	DASYLLDAQSGMS(0.944)VS(0.968)PR	[STY]PR...	130	S	-
Sspon.02G0017130-2B	SFVAPYS(0.97)PQPSAR	[STY]P...	287	S	-
Sspon.02G0017130-3D	FQQSNPDYSS(0.789)PNRKS(0.993)LER	[STY]P.R...	551	S	-
Sspon.02G0017130-3D	FQQSNPDYSS(0.789)PNRKS(0.993)LER	[STY]P.R...	556	S	-
Sspon.02G0017130-3D	HLS(0.999)PENTIDK	-	156	S	-
Sspon.02G0017270-2B	IFDS(1)GDDDTPTVTKPVDKR	[STY]G...	203	S	-
Sspon.02G0017290-1A	S(1)GEAELYQYLK	[STY].E...	985	S	-
Sspon.02G0017530-1P	NLVANEES(0.957)DSSGNSSLLK	[STY]DS...	193	S	-
Sspon.02G0017770-1A	GGPAFGGPGFS(1)PR	[STY]PR...	309	S	-
Sspon.02G0017790-2C	ALVERDS(1)DGEDSVAPSVTK	[STY]D...	958	S	-
Sspon.02G0017920-1A	STS(0.854)ASEVNVSVSK	...S.[STY]....	114	S	-
Sspon.02G0018300-3C	GGLVS(1)ADELVT(1)PR	[STY]PR...	702	S	-
Sspon.02G0018300-3C	GGLVS(1)ADELVT(1)PR	[STY]PR...	708	T	-
Sspon.02G0018300-3C	FSWS(0.984)PDS(0.996)GEAYGQEGLAR	[STY]P...	740	S	-
Sspon.02G0018300-3C	FSWS(0.956)PDS(1)GEAYGQEGLAR	[STY]P...	743	S	-
Sspon.02G0018300-3C	FS(0.992)WS(0.976)PDSGEAYGQEGLAR	[STY]P...	738	S	-
Sspon.02G0018410-3C	S(1)APELVSVCK	...R..[STY]....	558	S	-
Sspon.02G0018440-1A	EDS(0.836)YGGGGYGGGYDDYGGDDDY	-	302	S	-
Sspon.02G0018760-2B	STS(0.95)LELNSSNR	...RS.[STY]....	259	S	-
Sspon.02G0018830-3C	VLGAFLEGG(1)PDENK	[STY]P...	401	S	-
Sspon.02G0019150-4D	DAAGGAPYGG(0.84)SIGMGPNY	-	177	S	-
Sspon.02G0019240-3D	LEEKGSS(0.85)TNYLSIAR	-	139	S	-
Sspon.02G0019410-3P	GYGS(0.997)FRS(1)NA	...S..[STY]....	281	S	-
Sspon.02G0019410-3P	GYGS(0.997)FRS(1)NA	...S..[STY]....	284	S	-
Sspon.02G0019430-1P	S(1)VDEGFPR	[STY].DE...	135	S	-
Sspon.02G0019440-2B	ALGS(1)FRS(1)NA	...S..[STY]....	285	S	-
Sspon.02G0019440-2B	ALGS(1)FRS(1)NA	...S..[STY]....	288	S	-
Sspon.02G0019470-2B	SSASSAGS(0.995)LDDYMSAAAAAR	...S...[STY].D...	435	S	-
Sspon.02G0019770-1A	TTS(0.865)DSEIPESSTVK	[STY]DS...	190	S	-
Sspon.02G0020250-4D	ATVDVAT(1)PTAESGK	[STY]P...	8	T	-
Sspon.02G0020250-4D	QAPS(1)PPPPAAR	[STY]P...	19	S	-
Sspon.02G0020350-4D	MSYSDLES(0.94)AS(0.845)DSEGFSEIDNSR	[STY]DS...	277	S	-
Sspon.02G0020350-4D	MSYSDLES(0.94)AS(0.845)DSEGFSEIDNSR	[STY]DS...	275	S	-
Sspon.02G0021640-3C	TPYHPMIDDGGS(0.994)LS(0.903)PTRPFDK	[STY]P.R...	44	S	-
Sspon.02G0021640-3C	TPYHPMIDDGGS(0.996)LS(0.871)PTRPFDK	[STY]P.R...	42	S	-
Sspon.02G0022070-3C	VSSAENDGQPES(1)PK	[STY]P...	131	S	-
Sspon.02G0022290-3C	DSESS(0.914)PQPPSAAAPAESGK	[STY]P...	252	S	-
Sspon.02G0022300-2C	S(1)LLANDVESGLR	-	223	S	-
Sspon.02G0022310-1A	TIS(0.82)PADATSSDDEGLQR	[STY]P...	191	S	-
Sspon.02G0022390-1P	NVVEDDAES(1)DEEEVPEGR	[STY]DE...	74	S	-
Sspon.02G0022880-2D	SNASSIGS(0.994)PGPGR	...S...[STY]P...	102	S	-
Sspon.02G0022880-2D	SNASS(0.824)IGSPGPGR	...[STY]..S...	99	S	-
Sspon.02G0022880-2D	EQS(1)PGPVVRS(1)PVGVGQNYAMNR	[STY]P...	197	S	-
Sspon.02G0022880-2D	EQS(1)PGPVVR	[STY]P...	190	S	-

Sspon.02G0023270-4D	AS(1)EEGVVIACHTK	[STY].E...	3	S	-
Sspon.02G0023330-1A	YAPAADRYSGDRYS(0.894)GADR	-	216	S	-
Sspon.02G0023330-1A	YASSSFASERS(0.846)YER	...S..[STY]....	231	S	-
Sspon.02G0023330-1A	YAPAADRYYS(0.918)GDRYSGADR	-	211	S	-
Sspon.02G0023330-1A	S(1)GGDVVPAASDDCFK	-	110	S	-
Sspon.02G0023480-3C	QTVTTVNRS(0.954)QS(0.979)PDGSKPSNK	[STY]P...	228	S	-
Sspon.02G0023480-3C	QTVTTVNRS(0.888)QS(0.982)PDGSKPSNK	[STY]P...	230	S	-
Sspon.02G0023480-3C	RS(1)RS(1)PAEPR	[STY]P...	429	S	-
Sspon.02G0023480-3C	RS(1)RS(1)PAEPR	[STY]P...	431	S	-
Sspon.02G0023480-4D	SSS(0.995)PDGNKGLVSY	...S...[STY]P...	209	S	-
Sspon.02G0024060-2B	ATS(0.922)DELAQIDISK	-	4	S	-
Sspon.02G0024140-1A	FALGTASS(0.948)IK	-	34	S	-
Sspon.02G0024210-3C	DCDEVDDAAQDS(1)GAR	[STY]G...	529	S	-
Sspon.02G0024210-3C	WLPNVQDWEENS(1)T(1)R	[STY]..S...	292	S	-
Sspon.02G0024210-3C	WLPNVQDWEENS(1)T(1)R	[STY]..S...	293	T	-
Sspon.02G0024210-3C	WLPNVQDWEENS(0.809)TRS(0.841)AR	...S..[STY]....	295	S	-
Sspon.02G0024210-3C	DLIIGQPTGS(0.87)ELGGHAAS(0.997)FES(0.998)R	...S..[STY]....	469	S	-
Sspon.02G0024210-3C	DLIIGQPTGS(0.87)ELGGHAAS(0.997)FES(0.998)R	...S..[STY]....	477	S	-
Sspon.02G0024210-3C	DLIIGQPTGS(0.87)ELGGHAAS(0.997)FES(0.998)R	...S..[STY]....	480	S	-
Sspon.02G0024210-3C	NLEEGGS(0.915)TADKPINR	-	495	S	-
Sspon.02G0024210-3C	LQPADS(1)IEGT(1)VIDR	[STY].E...	509	S	-
Sspon.02G0024210-3C	LQPADS(1)IEGT(1)VIDR	[STY].E...	513	T	-
Sspon.02G0024210-3C	FDTS(0.967)NAEGPSALR	-	572	S	-
Sspon.02G0024210-3C	GIS(0.99)ATS(0.998)GINGLVAEGAER	...S..[STY]....	394	S	-
Sspon.02G0024210-3C	GIS(1)ATS(0.967)GINGLVAEGAER	...S..[STY]....	391	S	-
Sspon.02G0025080-2B	AQEEES(1)DFLGNVPK	[STY]D...	105	S	-
Sspon.02G0025830-1A	ADLDQGESDGDVKVQS(0.999)S(1)PERELDDQR	[STY]P.R...	138	S	-
Sspon.02G0025830-1A	ADLDQGESDGDVKVQS(0.999)S(1)PERELDDQR	[STY]P.R...	139	S	-
Sspon.02G0025830-1A	ADLDQGES(1)DGDVKVQSSPER	[STY]D...	131	S	-
Sspon.02G0025830-1A	KAVVFDD(1)DED	[STY]DE...	672	S	-
Sspon.02G0025830-1A	DVFGES(1)DEDEPAPYR	[STY]DE...	224	S	-
Sspon.02G0025830-1A	EELVS(1)EDDYDDDDSPPR	[STY]..D...D	644	S	-
Sspon.02G0025830-1A	GMDS(1)EDEGYQQR	[STY].DE...	158	S	-
Sspon.02G0025830-1A	YES(0.978)DDNRELKPK	...R..[STY]....	272	S	-
Sspon.02G0025830-1P	REELVS(1)EDDDDDDDSPPR	[STY]..D...D	860	S	-
Sspon.02G0026030-1A	S(1)DEEHHFESK	[STY]DE...	2	S	-
Sspon.02G0026090-3C	KVPLS(0.962)DSSDEE	[STY]DS...	309	S	-
Sspon.02G0026180-1A	STGST(0.997)EENFVR	[STY].E...	236	T	-
Sspon.02G0026180-1A	STGS(0.977)T(0.996)EENFVR	...S..[STY]....	235	S	-
Sspon.02G0026180-1A	SQS(1)LGNMLQK	...S..[STY]....	50	S	-
Sspon.02G0026180-1A	ST(0.864)GST(0.864)EENFVR	[STY].E...	233	T	-
Sspon.02G0026630-2B	ASFVGS(0.92)PSR	-	481	S	-
Sspon.02G0026670-3C	METSIS(0.831)PPGTSK	[STY]P...	6	S	-
Sspon.02G0026820-2B	HDNVAFCGEGDDICNNS(1)PPK	[STY]P...	477	S	-
Sspon.02G0027390-2C	YLTGS(0.994)LGLR	-	96	S	-
Sspon.02G0027830-4D	LSDSVSGLT(0.999)VVDPK	...S..[STY]....	160	T	-
Sspon.02G0027830-4D	LSDS(0.945)VSGLT(0.996)VVDPK	...S..[STY]....	155	S	-
Sspon.02G0027860-4D	LFAQVS(0.998)DS(0.996)DEDIALNSQADAQDGTASSATDR	[STY]DS...	257	S	-
Sspon.02G0027860-4D	LFAQVS(0.998)DS(0.996)DEDIALNSQADAQDGTASSATDR	[STY]DS...	255	S	-
Sspon.02G0027980-2D	GKADIGSAS(0.97)QEF	...S..[STY]....	133	S	-
Sspon.02G0028230-2D	RLQPFES(0.993)DDES	[STY]DD...	1280	S	-
Sspon.02G0028410-2B	SAS(0.996)NLMTR	...RS.[STY]....	103	S	-
Sspon.02G0028420-3C	YTVEQSIPES(0.974)PENGSDVGR	...S...[STY]P...	379	S	-
Sspon.02G0028510-3D	DLS(1)IGEEVGWSK	...R..[STY]....	152	S	-
Sspon.02G0028610-4D	EFLLNAPS(1)PER	[STY]P.R...	84	S	-
Sspon.02G0028680-3C	AAAASAST(0.914)PQGVAER	[STY]P...	9	T	-
Sspon.02G0028810-2B	S(0.986)AETRPGSS(0.774)QLSR	...R..[STY]....	151	S	-
Sspon.02G0028810-2B	S(0.925)AETRPGS(0.886)QLSR	...R..[STY]....	150	S	-
Sspon.02G0028810-2B	S(0.986)AETRPGSS(0.774)QLSR	...R..[STY]....	143	S	-
Sspon.02G0029150-1P	SADES(1)PVRSD	-	269	S	-
Sspon.02G0029150-1P	EYSGS(0.988)PPGS(1)R	...S..[STY]P...R	257	S	-
Sspon.02G0029150-1P	EYSGS(0.988)PPGS(1)R	...S..[STY]P...R	261	S	-
Sspon.02G0029150-1P	RYS(0.994)PPYRSPPR	-	19	S	-
Sspon.02G0029150-1P	SYS(1)PASR	[STY]P...	221	S	-
Sspon.02G0029150-1P	RYS(0.955)PPYRS(0.993)PPR	[STY]P.R...	24	S	-
Sspon.02G0029150-1P	KRS(1)PLPDSGDS(0.984)PPHR	[STY]P...	236	S	-
Sspon.02G0029150-1P	RS(0.998)PLPDSGDS(0.998)PPHR	[STY]P...	244	S	-
Sspon.02G0029150-1P	S(1)ADESPVR	-	265	S	-
Sspon.02G0029150-1P	S(1)PKEYS(0.836)GS(0.776)PPGSR	[STY]P...	255	S	-
Sspon.02G0029150-1P	S(1)PKEYS(0.836)GS(0.776)PPGSR	[STY]P...	250	S	-
Sspon.02G0029150-3C	RRDDYS(0.982)AS(1)PR	[STY]P.R...	191	S	-
Sspon.02G0029150-3C	RRDDYS(0.867)AS(1)PR	[STY]P.R...	193	S	-
Sspon.02G0029150-3C	SYS(1)PAPR	..R.R..[STY]P...	181	S	-
Sspon.02G0029150-3C	RS(0.998)PLPDSGDS(0.998)PPHR	[STY]P...	245	S	-
Sspon.02G0029150-3C	RS(0.998)PLPDSGDS(0.998)PPHR	[STY]P...	237	S	-
Sspon.02G0029150-3C	S(0.999)RS(0.984)YS(0.959)PAPR	..R.R..[STY]P...	179	S	-

Sspon.02G0029150-3C	S(1)RS(0.969)YS(0.959)PAPR	..R.R..[STY]P...	177	S	-
Sspon.02G0029150-4D	SYS(1)PASR	[STY]P...	168	S	-
Sspon.02G0029350-1A	ESSPDYTCGANYPVS(0.996)PR	[STY]PR...	158	S	-
Sspon.02G0029980-2D	MLRPFYPEDMLTS(0.993)DSDD	[STY]DS...	544	S	-
Sspon.02G0029980-2D	MLRPFYPEDMLT(0.998)S(0.941)DSDD	[STY]DS...	543	T	-
Sspon.02G0030220-3D	AAAGQSSGS(0.938)LS(0.995)PAHWR	...S...[STY]P...	189	S	-
Sspon.02G0030220-3D	AAAGQSSGS(0.938)LS(0.995)PAHWR	...S...[STY]P...	191	S	-
Sspon.02G0030260-1A	AYFDS(1)ADWALG	-	86	S	-
Sspon.02G0030680-1A	QLS(1)PIPPS(1)PVS(1)R	[STY]P...	250	S	-
Sspon.02G0030680-1A	QLS(1)PIPPS(1)PVS(1)R	[STY]P...	255	S	-
Sspon.02G0030680-1A	QLS(1)PIPPS(1)PVS(1)R	[STY]P...	258	S	-
Sspon.02G0031260-3C	TSVVQSVS(0.917)GDHR	...S.[STY]....	9	S	-
Sspon.02G0032530-3D	GLDIETIQQSYT(1)V	...S.[STY]....	773	T	-
Sspon.02G0032660-1A	TIGVSGLGEYS(1)PKS(1)ER	[STY]P...	494	S	-
Sspon.02G0032660-1A	TIGVSGLGEYS(1)PKS(1)ER	[STY]P...	497	S	-
Sspon.02G0032660-1A	TIGVS(1)GLGEYS(1)PK	[STY]P...	488	S	-
Sspon.02G0032660-1A	S(1)ADMFCDDIFGES(1)PAGIR	[STY]P...	500	S	-
Sspon.02G0032660-1A	S(1)ADMFCDDIFGES(1)PAGIR	[STY]P...	512	S	-
Sspon.02G0032880-1B	GAT(1)DSDSDVDFDR	[STY]DS...	257	T	-
Sspon.02G0033160-1B	AAETSS(0.971)PPRPAK	[STY]P.R...	109	S	-
Sspon.02G0033160-1B	S(1)EVAFR	...R..[STY]....	59	S	-
Sspon.02G0033540-2C	FGTVEALS(0.921)PSR	[STY]P.R...	99	S	-
Sspon.02G0033590-1B	GYS(0.945)YS(0.977)PS(0.999)PPR	...S.[STY]P...R	21	S	-
Sspon.02G0033590-1B	GYS(0.98)YSPS(0.995)PPR	...S.[STY]P...R	19	S	-
Sspon.02G0033590-1B	GYS(0.945)YS(0.977)PS(0.999)PPR	...S.[STY]P...R	23	S	-
Sspon.02G0033600-1B	QWEMS(0.991)DSDSD	[STY]DS...	548	S	-
Sspon.02G0033710-2C	FLEEPVAFEVYS(0.986)PDR	[STY]P.R...	754	S	-
Sspon.02G0034000-1B	ILTELQSGEALS(0.935)DDSVVPTTK	[STY]DD...	236	S	-
Sspon.02G0034070-1P	MLRS(1)PGNS(1)PR	[STY]P.R...	4	S	-
Sspon.02G0034070-1P	MLRS(1)PGNS(1)PR	[STY]P.R...	8	S	-
Sspon.02G0034150-1B	AVEAALHAGGEGSSS(0.888)PAR	[STY]P.R...	23	S	-
Sspon.02G0034150-1B	DDDASGS(0.984)GDDSEDDGIEDLRPFK	...S.[STY]....	469	S	-
Sspon.02G0034270-1B	VFEVSLADLQS(0.996)DEDQAYR	[STY]DE...	83	S	-
Sspon.02G0034300-1B	ASEENTPASGSGEAS(0.963)PVETKPR	[STY]P...	168	S	-
Sspon.02G0034300-1B	ASEENTPASGSGEAS(0.841)EAS(0.868)PVETKPR	[STY]P...	165	S	-
Sspon.02G0034300-1B	ECS(1)LGPLQK	-	441	S	-
Sspon.02G0034520-2C	KPAAAGQQEKPS(1)PK	[STY]P...	359	S	-
Sspon.02G0034520-2C	LVETFST(0.817)DNSTADSVGAFR	[STY]..S...	268	T	-
Sspon.02G0034530-2D	SALLQPDSSPGSTS(0.854)PAPR	[STY]P...	50	S	-
Sspon.02G0034540-2D	EQS(1)PGPIAR	[STY]P...	187	S	-
Sspon.02G0034560-1B	ADSPNPSSGDLPAAGGS(1)PEK	[STY]P...	19	S	-
Sspon.02G0034560-1B	DILPS(1)PR	[STY]PR...	105	S	-
Sspon.02G0035070-2C	YLAQQQVEVDS(1)V	-	269	S	-
Sspon.02G0035690-2C	QNS(1)LGLWK	...R..[STY]....	53	S	-
Sspon.02G0036030-3D	EVRPADSDANVS(0.903)SPRS(0.868)K	...S..[STY]....	217	S	-
Sspon.02G0036030-3D	EVRPADSDANVS(0.903)SPRS(0.868)K	...S..[STY]....	213	S	-
Sspon.02G0036030-3D	EVRPADS(0.996)DANVSS(0.963)PR	[STY]PR...	214	S	-
Sspon.02G0036030-3D	EVRPADS(0.996)DANVSS(0.963)PR	[STY]PR...	208	S	-
Sspon.02G0036390-2D	EEDLKNLCT(1)P	[STY]P...	311	T	-
Sspon.02G0036520-2C	SPMLAAS(1)PDAR	[STY]P...	259	S	-
Sspon.02G0036520-2C	SAAS(0.902)PWDNVS(1)PS(1)PAPIR	[STY]PSP...	279	S	-
Sspon.02G0036520-2C	SAAS(0.902)PWDNVS(1)PS(1)PAPIR	[STY]PSP...	285	S	-
Sspon.02G0036520-2C	SAAS(0.902)PWDNVS(1)PS(1)PAPIR	[STY]PSP...	287	S	-
Sspon.02G0036520-2C	LVS(1)PWLGGNT(1)PR	[STY]PR...	266	S	-
Sspon.02G0036520-2C	LVS(1)PWLGGNT(1)PR	[STY]PR...	273	T	-
Sspon.02G0036550-1B	SDS(0.977)VVIDEVELQR	...RS.[STY]....	36	S	-
Sspon.02G0036550-1B	S(0.818)DSVVIDEVELQR	[STY]DS...	34	S	-
Sspon.02G0036620-2D	VEQDDQGYIS(0.777)CDEEAVK	[STY].DE...	537	S	-
Sspon.02G0036650-2C	NGSSTPDNQFDS(1)PPDR	-	279	S	-
Sspon.02G0036650-2C	DVGDLVHS(1)ES(1)PPVR	[STY]P...	347	S	-
Sspon.02G0036650-2C	DVGDLVHS(1)ES(1)PPVR	[STY]P...	349	S	-
Sspon.02G0036650-2C	LERDT(1)PT(1)PDGRVS(1)PER	[STY]P.R...	299	S	-
Sspon.02G0036650-2C	LERDT(1)PT(1)PDGRVS(1)PER	[STY]P.R...	291	T	-
Sspon.02G0036650-2C	LERDT(1)PT(1)PDGRVS(1)PER	[STY]P.R...	293	T	-
Sspon.02G0036650-2C	NGS(0.839)S(0.872)TPDNQFDSPPDR	...R..[STY]....	270	S	-
Sspon.02G0036650-2C	NGS(0.839)S(0.872)TPDNQFDSPPDR	...R..[STY]....	271	S	-
Sspon.02G0036650-2C	SAS(0.965)AS(0.987)PESSMK	...S...[STY]P...	92	S	-
Sspon.02G0036650-2C	SAS(0.965)AS(0.987)PESSMK	...S...[STY]P...	94	S	-
Sspon.02G0036650-2C	AS(0.919)SRELS(0.999)PHAR	...S...[STY]P...	370	S	-
Sspon.02G0036650-2C	AS(0.919)SRELS(0.999)PHAR	...S...[STY]P...	375	S	-
Sspon.02G0036650-3D	ELS(1)PHAQHSSPVER	...S...[STY]P...	375	S	-
Sspon.02G0036650-3D	ELS(1)PHAQHSS(0.887)PVER	...S...[STY]P...	382	S	-
Sspon.02G0036840-1B	IVPSTDSSLAS(0.948)DVGENSR	...S..[STY]....	219	S	-
Sspon.02G0036860-2D	FDPDS(0.812)SDDEASGPPAR	-	11	S	-
Sspon.02G0037080-2C	LNQS(1)PPR	[STY]P.R...	525	S	-
Sspon.02G0038070-1B	SAS(0.758)SSNLDSPVPK	...RS.[STY]....	276	S	-

Sspon.02G0039360-1P	VGS(0.885)SSSVPGVK	...R..[STY]....	6	S	-
Sspon.02G0039360-1P	VGS(0.791)SSS(0.836)VPGVK	...S..[STY]....	9	S	-
Sspon.02G0040370-1B	NQYRPVEPVTQEEQES(1)IPNQK	-	297	S	-
Sspon.02G0040370-1B	VRSTDVETSVNNNSQS(0.919)AANDSQK	...S.[STY]....	318	S	-
Sspon.02G0040370-1B	VRSTDVETSVNNNS(1)QSAANDSQK	[STY].S...	316	S	-
Sspon.02G0040370-1B	NQYRPVEPVT(1)QEEQES(1)IPNQK	[STY].E...	290	T	-
Sspon.02G0040370-1B	EVPQDGFDTDS(0.783)SGT(0.914)KWIR	...S..[STY]....	589	S	-
Sspon.02G0040370-1B	EVPQDGFDTDS(0.783)SGT(0.914)KWIR	...S..[STY]....	592	T	-
Sspon.02G0040370-1B	DQPKDDFPS(1)PK	[STY]P...	608	S	-
Sspon.02G0040370-1B	VRSTDVETS(0.889)VNNNS(0.847)QSAANDSQK	[STY].S...	311	S	-
Sspon.02G0041140-1B	SGNTS(0.992)AEGEPSQTAVVR	[STY].E...	174	S	-
Sspon.02G0041140-1B	SGNT(0.79)S(0.882)AEGEPSQTAVVR	...S..[STY]....	173	T	-
Sspon.02G0041140-1B	S(0.814)GNTSAEGEPSQTAVVR	[STY]G...	170	S	-
Sspon.02G0041640-2D	MVENS(0.989)HEATAQS(0.964)EEKPVESK	[STY].E...	206	S	-
Sspon.02G0041640-2D	MVENS(0.989)HEATAQS(0.964)EEKPVESK	[STY].E...	199	S	-
Sspon.02G0042010-1B	HSSS(0.801)CEDMLATL TESK	...S.[STY]....	240	S	-
Sspon.02G0042090-1B	DNCPS(1)LQS(1)EILK	...S..[STY]....	382	S	-
Sspon.02G0042090-1B	DNCPS(1)LQS(1)EILK	...S..[STY]....	385	S	-
Sspon.02G0044580-3D	ITS(0.821)SGGT(0.893)PVaelK	...S...[STY]P...	580	S	-
Sspon.02G0046530-1C	S(1)DEGGAGEPLSDR	[STY]DE...	2	S	-
Sspon.02G0047000-1C	SSGDES(0.999)MDEDVMESK	[STY].DE...	353	S	-
Sspon.02G0047390-1C	EGLVQLDLHS(0.963)GSR	[STY].S...	30	S	-
Sspon.02G0047570-1C	SVLS(0.921)VQS(1)ERPR	...S..[STY]....	170	S	-
Sspon.02G0047570-1C	SVLS(0.903)VQS(1)ERPR	...S..[STY]....	173	S	-
Sspon.02G0048040-1P	GGGPALGFDSS(0.91)PGR	[STY]P.R...	616	S	-
Sspon.02G0048040-1P	SESFDDSSPDS(0.937)PSNNVK	...S...[STY]P...	392	S	-
Sspon.02G0050370-2D	MEYRPSDSSGT(0.865)DDDL PQFPNSR	...S..[STY].D...	11	T	-
Sspon.02G0050370-2D	LAEAS(1)DGES(1)DGHNr	[STY]D...	428	S	-
Sspon.02G0050370-2D	LAEAS(1)DGES(1)DGHNr	[STY]D...	432	S	-
Sspon.02G0053370-2D	VFDS(1)PEGEKIPK	[STY]P...	96	S	-
Sspon.02G0057380-1D	QGS(1)PNPAESDFYPSR	[STY]P...	631	S	-
Sspon.02G0058460-1D	EIDPLTQS(0.812)PTITGAS(0.953)QELEGR	[STY]P...	742	S	-
Sspon.02G0058460-1D	EIDPLTQS(0.812)PTITGAS(0.953)QELEGR	[STY]P...	749	S	-
Sspon.03G0000150-1A	TLLASYS(0.999)QT(1)PR	...S...[STY]P...	326	S	-
Sspon.03G0000150-1A	TLLASYS(0.978)QT(1)PR	...S...[STY]P...	328	T	-
Sspon.03G0000150-1A	EIQT(1)PNPMAT(1)PLAS(1)PGPGIT(1)PR	[STY]P..SP..	402	S	-
Sspon.03G0000150-1A	EIQT(1)PNPMAT(1)PLAS(1)PGPGIT(1)PR	[STY]P..SP..	392	T	-
Sspon.03G0000150-1A	EIQT(1)PNPMAT(1)PLAS(1)PGPGIT(1)PR	[STY]P..SP..	398	T	-
Sspon.03G0000150-1A	EIQT(1)PNPMAT(1)PLAS(1)PGPGIT(1)PR	[STY]P..SP..	408	T	-
Sspon.03G0000320-3D	VSCIIGS(1)PK	[STY]P...	813	S	-
Sspon.03G0001110-1A	LNELS(0.898)TS(0.991)EFAEPEK	...S.[STY]....	439	S	-
Sspon.03G0001110-1A	LNELS(0.898)TS(0.991)EFAEPEK	...S.[STY]....	441	S	-
Sspon.03G0001110-1A	GTAES(0.941)DGS(0.997)NIIGSLTSR	...S..[STY]....	475	S	-
Sspon.03G0001110-1A	GTAES(0.941)DGS(0.997)NIIGSLTSR	...S..[STY]....	478	S	-
Sspon.03G0001110-1A	VHES(1)PVLS(1)PQRK	[STY]P.R...	264	S	-
Sspon.03G0001110-1A	VHES(1)PVLS(1)PQRK	[STY]P.R...	268	S	-
Sspon.03G0001860-4D	LHADSSCSEQVLS(1)PEQLACDR	[STY]P...	235	S	-
Sspon.03G0001860-4D	LHADSSCS(0.926)EQVLS(1)PEQLACDR	[STY]P...	230	S	-
Sspon.03G0002200-2B	S(0.994)PS(0.994)VSAAAVDAEDAGVVR	[STY]P...	45	S	-
Sspon.03G0002200-2B	S(0.992)PS(0.994)VSAAAVDAEDAGVVR	[STY]P...	47	S	-
Sspon.03G0002830-2C	S(1)FADILQDNIGR	...R..[STY]....	214	S	-
Sspon.03G0003300-3C	FLGTSEMDPDS(1)EPDS(1)AR	-	353	S	-
Sspon.03G0003300-3C	FLGTSEMDPDS(1)EPDS(1)AR	-	357	S	-
Sspon.03G0003330-3D	NPS(1)IGTVR	-	222	S	-
Sspon.03G0003330-3D	AIS(1)IQRPAT(1)PNK	[STY]P...	235	S	-
Sspon.03G0003330-3D	AIS(1)IQRPAT(1)PNK	[STY]P...	241	T	-
Sspon.03G0004220-4D	ELQEFKPVEEGAS(1)A	-	128	S	-
Sspon.03G0004240-1A	GLPIPGNDGGS(0.909)SSEEEQR	[STY].S...	285	S	-
Sspon.03G0004240-1A	GLPIPGNDGGS(0.868)S(0.824)SSEEEQR	[STY].E...	286	S	-
Sspon.03G0004240-1A	GLPIPGNDGGS(0.8)SS(0.8)EEEQR	...S.[STY]....	287	S	-
Sspon.03G0004340-1A	EFLATS(0.99)PLR	[STY]P.R...	347	S	-
Sspon.03G0004340-2B	DFVTAS(1)PLR	[STY]P.R...	176	S	-
Sspon.03G0004720-4D	S(1)GAGEEDKKPAEGGAHINLK	[STY]G...	2	S	-
Sspon.03G0004750-1A	LDLRY(0.999)AT(0.999)WVLS PDK	...R..[STY]....	414	T	-
Sspon.03G0004750-1A	LDLRY(0.999)AT(0.999)WVLS PDK	...R..[STY]....	412	Y	-
Sspon.03G0005070-1A	AGS(0.828)SAGDDADLALLK	...R..[STY]....	15	S	-
Sspon.03G0005280-3C	LSAAAQAAAIQPSS(0.907)PR	[STY]PR...	35	S	-
Sspon.03G0005280-3C	LSAAAQAAAIQPS(0.829)SPR	-	34	S	-
Sspon.03G0005390-1T	AS(0.999)FDSLVS(0.993)FTPR	...S..[STY].D...	648	S	-
Sspon.03G0005390-1T	AS(1)FDSLVS(0.92)FTPR	...S...[STY].D...	642	S	-
Sspon.03G0005570-3C	SS(0.94)EPIVLPK	-	178	S	-
Sspon.03G0005640-2B	GPHNTQAGELAS(1)S(1)DDVLLVNGK	[STY]DD...	917	S	-
Sspon.03G0005640-2B	GPHNTQAGELAS(1)S(1)DDVLLVNGK	[STY]DD...	918	S	-
Sspon.03G0005640-2B	VIGGEIDSNCs(0.928)PSVLEEK	[STY]P...	882	S	-
Sspon.03G0005640-2B	VIGGEIDS(0.962)NCSPSVLEEK	[STY].S...	879	S	-
Sspon.03G0005640-2B	S(1)AGGGVAGDEAIWR	...S..[STY]....	6	S	-

Sspon.03G0005680-3C	TGNPTAVGEEEDVSFS(1)DLEDD	...S.[STY]...	399	S	-
Sspon.03G0006070-2B	TLAS(0.989)PYPS(0.986)PAR	[STY]P.R...	80	S	-
Sspon.03G0006070-2B	TLAS(0.989)PYPS(0.986)PAR	[STY]P.R...	76	S	-
Sspon.03G0006070-2B	SSS(0.873)PFAASS(0.79)PSPLR	[STY]PSP...	102	S	-
Sspon.03G0006070-2B	SSS(0.873)PFAASS(0.79)PSPLR	[STY]PSP...	96	S	-
Sspon.03G0006070-3C	TLAS(1)PHPS(1)PAR	[STY]P.R...	76	S	-
Sspon.03G0006070-3C	TLAS(1)PHPS(1)PAR	[STY]P.R...	80	S	-
Sspon.03G0006070-3C	T(0.961)LASPHPS(1)PAR	[STY]P.R...	73	T	-
Sspon.03G0006540-1A	LSSPVT(0.999)PLTGDPFNR	...S...[STY]P...	177	T	-
Sspon.03G0006540-1A	LSS(0.935)PVT(0.994)PLTGDPFNR	...S...[STY]P...	174	S	-
Sspon.03G0006600-1A	SGELPDTNEEEVNS(0.861)ESSSSGR	[STY]..S...	533	S	-
Sspon.03G0006600-1A	DSESVGT(0.998)STSSAEASWASK	...S...[STY]...	613	T	-
Sspon.03G0006600-1A	DSESVGT(0.802)STS(0.791)SAEEASWASK	...S...[STY]...	616	S	-
Sspon.03G0006600-1A	DSESVGT(0.836)ST(0.883)SSAEASWASK	...S...[STY]...	615	T	-
Sspon.03G0006600-1A	SES(0.863)PNIGAQTvk	...S...[STY]P...	1037	S	-
Sspon.03G0006890-2B	ISRDS(0.996)YPNLR	-	63	S	-
Sspon.03G0006890-2B	NAS(0.923)TMALHDDDAAFVK	...R...[STY]...	74	S	-
Sspon.03G0006890-2P	NAS(1)SVS(1)LADAAVVK	...S...[STY]...	79	S	-
Sspon.03G0006890-2P	NAS(1)SVS(1)LADAAVVK	...S...[STY]...	82	S	-
Sspon.03G0006890-2P	NAS(1)S(0.998)VSLADAAVVK	...R...[STY]...	80	S	-
Sspon.03G0006960-1A	DNTAVS(1)PLEEPS(1)PK	[STY]P...	133	S	-
Sspon.03G0006960-1A	DNTAVS(1)PLEEPS(1)PK	[STY]P...	139	S	-
Sspon.03G0006960-1A	IQMSS(0.854)PAEGVPDK	-	149	S	-
Sspon.03G0006980-1A	FHGGDSSSSS(0.888)SDSDDDKKK	...S...[STY].D...	30	S	-
Sspon.03G0007150-3D	VAS(1)S(1)EEDSGEVALAER	[STY].E...	316	S	-
Sspon.03G0007150-3D	VAS(1)S(1)EEDSGEVALAER	[STY].E...	315	S	-
Sspon.03G0007480-1P	FLTASGT(0.915)FK	...S.[STY]...	30	T	-
Sspon.03G0007480-1P	FLTAS(0.94)GTFK	[STY]G...	28	S	-
Sspon.03G0007760-3C	DQDIYFQS(0.999)VAEPVPETEQR	-	163	S	-
Sspon.03G0007800-1A	AS(1)EDEANAAAAVAEDAAEQGR	[STY].DE...	3	S	-
Sspon.03G0007870-2B	SVVLWSIQDHISALGDSSSS(0.786)PGASGSK	[STY]P...	223	S	-
Sspon.03G0008190-1A	AAAS(1)EPDEEER	-	15	S	-
Sspon.03G0008190-1A	MES(0.964)SEEMVTPR	-	3	S	-
Sspon.03G0008190-1A	MES(0.771)SEEMVT(1)PR	[STY]PR...	9	T	-
Sspon.03G0008190-2B	VDASEDSMES(1)S(1)EEMVT(1)PR	[STY]PR...	71	S	-
Sspon.03G0008190-2B	VDASEDSMES(1)S(1)EEMVT(1)PR	[STY]PR...	72	S	-
Sspon.03G0008190-2B	VDASEDSMES(1)S(1)EEMVT(1)PR	[STY]PR...	77	T	-
Sspon.03G0008190-2B	VDASEDS(1)MES(0.952)SEEMVT(1)PR	[STY]PR...	68	S	-
Sspon.03G0008190-2B	VDAS(1)EDS(0.998)MESEEMVTPR	...S...[STY]...	65	S	-
Sspon.03G0008250-1A	MENGDETLAS(0.981)PTAAAEK	-	10	S	-
Sspon.03G0008300-1T	DGSS(0.902)SGPLFGLK	-	277	S	-
Sspon.03G0008770-2D	SSS(0.964)PPLS(1)PPR	...S.[STY]P...R	88	S	-
Sspon.03G0008770-2D	SSS(0.964)PPLS(1)PPR	...S.[STY]P...R	92	S	-
Sspon.03G0008790-3D	SIAADSWSVRS(0.965)EYGS(0.767)TLDDDQR	...S...[STY]...	1206	S	-
Sspon.03G0008790-3D	SIAADSW(0.953)VRS(0.992)EY(0.805)GSTLDDDQR	...RS.[STY]...	1202	S	-
Sspon.03G0008790-3D	SIAADSW(0.75)VRS(0.956)EY(0.865)GSTLDDDQR	...RS.[STY]...	1204	Y	-
Sspon.03G0008790-3D	SIAADS(1)WS(1)VR	...S.[STY]...	1197	S	-
Sspon.03G0008790-3D	SIAADS(1)WS(1)VR	...S.[STY]...	1199	S	-
Sspon.03G0009180-3C	AVS(1)LPSS(0.967)PHEYR	...S...[STY]P...	403	S	-
Sspon.03G0009180-3C	AVS(1)LPSS(0.967)PHEYR	...S...[STY]P...	399	S	-
Sspon.03G0009180-3C	SIS(0.855)ITPEIGDDIVR	...RS.[STY]...	323	S	-
Sspon.03G0009180-3C	S(0.971)ISITPEIGDDIVR	...R...[STY]...	321	S	-
Sspon.03G0009250-2B	DGVAGGS(0.854)GYYSR	[STY]G...	1035	S	-
Sspon.03G0009320-1A	IAPVYIGGGS(1)ENЕК	-	580	S	-
Sspon.03G0009320-1A	AGDSVGSAS(0.987)IDNTGLPR	...S...[STY].D...	1617	S	-
Sspon.03G0009320-1A	APVVLDT(0.904)PLPS(0.986)PR	[STY]P.R...	77	S	-
Sspon.03G0009320-1A	APVVLDT(0.888)PLPS(0.999)PR	[STY]P.R...	81	S	-
Sspon.03G0009320-1A	AGDSVGS(0.828)SAS(0.969)IDNTGLPR	...S...[STY].D...	1614	S	-
Sspon.03G0009320-1A	AGDS(0.959)VGSAS(0.845)IDNTGLPR	...S...[STY].D...	1611	S	-
Sspon.03G0009470-1A	ESGEMSEES(0.909)DYDELIS	...S...[STY]...	122	S	-
Sspon.03G0009500-2C	MDGYGEADNAAMEVEAEAS(1)PCR	[STY]P.R...	19	S	-
Sspon.03G0009500-2C	SSPVLGS(0.971)PSQNSDR	...S.[STY]P...R	32	S	-
Sspon.03G0010360-3C	PSNLTGAEIYS(0.849)MSSSR	[STY]..S...	241	S	-
Sspon.03G0010360-3C	ASSFGAAELYS(0.857)MHSSR	[STY]..S...	291	S	-
Sspon.03G0010360-3C	LGS(0.981)SS(0.906)TMAELR	...S.[STY]...	464	S	-
Sspon.03G0010360-3C	LGS(0.981)SS(0.906)TMAELR	...S.[STY]...	462	S	-
Sspon.03G0010650-3C	TGSMDIESIAEGSNS(0.9)AEFGK	...S.[STY]...	382	S	-
Sspon.03G0010960-1A	VVEGS(1)PPDGMELK	[STY]P...	313	S	-
Sspon.03G0010970-3C	LLNENNVLLYDQS(1)P	[STY]P...	1134	S	-
Sspon.03G0011050-1A	VVAENLS(1)DEEIMGLK	[STY]DE...	377	S	-
Sspon.03G0011050-1A	NNS(1)PEIVPNR	[STY]P...	519	S	-
Sspon.03G0011150-1A	AEGLSFS(0.892)PSR	[STY]P.R...	220	S	-
Sspon.03G0011340-2B	GQDPQGGMS(1)PPGPGAR	[STY]P...	634	S	-
Sspon.03G0011690-2B	S(1)PQLPGPAQGIK	[STY]P...	274	S	-
Sspon.03G0011800-1A	LDEASNVEQPETGS(0.906)PSR	[STY]P.R...	543	S	-
Sspon.03G0011960-3C	SLS(0.908)TLTR	...RS.[STY]...	406	S	-

Sspon.03G0012430-3C	CSEVAVIHS(1)GAAS(0.999)PAICS	...S...[STY]P...	698	S	-
Sspon.03G0012430-3C	CSEVAVIHS(1)GAAS(0.999)PAICS	...S...[STY]P...	694	S	-
Sspon.03G0012600-2B	RKS(0.786)PATAAAPAGS(1)PR	[STY]PR...	7	S	-
Sspon.03G0012600-2B	RKS(0.786)PATAAAPAGS(1)PR	[STY]PR...	17	S	-
Sspon.03G0012670-1P	ELSDAVVEAITSSSEAGETT(0.999)P	[STY]P...	272	T	-
Sspon.03G0013310-1A	SLGAEVIELS(1)S(1)DEDEEVPSTTALAR	[STY]DE...	12	S	-
Sspon.03G0013310-1A	SLGAEVIELS(1)S(1)DEDEEVPSTTALAR	[STY]DE...	11	S	-
Sspon.03G0013340-1A	YVKPSGKPEPAS(1)PGR	[STY]P.R...	1126	S	-
Sspon.03G0013340-1A	ASAS(0.871)MS(0.994)PNVQPEADAK	...S...[STY]P...	1102	S	-
Sspon.03G0013340-1A	ASAS(0.871)MS(0.994)PNVQPEADAK	...S...[STY]P...	1104	S	-
Sspon.03G0013340-2B	VDLDRS(1)PS(1)PQDDK	[STY]PSP...	676	S	-
Sspon.03G0013340-2B	VDLDRS(1)PS(1)PQDDK	[STY]PSP...	678	S	-
Sspon.03G0013340-2B	VDLDRS(1)PS(1)PQDDKSAPYS(0.921)PVYNGK	...S...[STY]P...	688	S	-
Sspon.03G0013820-1A	RVPEMGGASAS(0.881)AS(0.861)SGAGADER	...S.[STY]....	61	S	-
Sspon.03G0013820-1A	EGGVES(1)DEEIR	[STY]DE...	43	S	-
Sspon.03G0013960-2B	LANIAGAS(1)PFVQS(1)DR	[STY]P...	266	S	-
Sspon.03G0013960-2B	LANIAGAS(1)PFVQS(1)DR	[STY]P...	271	S	-
Sspon.03G0014310-2B	AVDDGGS(1)GHGGGFDGLSLVSPSSSR	[STY]G...	157	S	-
Sspon.03G0014450-1A	CPS(0.999)EWYFQK	...R..[STY]....	49	S	-
Sspon.03G0014450-1A	VAS(1)LEHLQK	...R..[STY]....	389	S	-
Sspon.03G0014830-2C	DVGSM(0.995)PEK	[STY]P...	229	S	-
Sspon.03G0014980-3C	ATLGSLVAYDDDDDES(1)GEDDD	[STY].E...	211	S	-
Sspon.03G0015070-3C	DAGFQS(1)AEEGSGTFR	[STY].E...	141	S	-
Sspon.03G0016300-1P	NDAGLT(0.905)SEDSSDEDADELGLPDVDADAKPEK	[STY].E...	111	T	-
Sspon.03G0016670-3C	TGGDES(1)EEEDVMLR	[STY].E...	89	S	-
Sspon.03G0017090-2C	ELGMPMDNTGTNS(0.996)QAS	[STY]..S...	251	S	-
Sspon.03G0017350-1T	TQTSTSVGSSS(0.896)PGGGR	[STY]P...	436	S	-
Sspon.03G0017410-2B	SSATPAVAS(0.955)PASEHSK	[STY]P...	10	S	-
Sspon.03G0017470-4D	S(1)FQDLEAGHVR	-	2	S	-
Sspon.03G0017500-1A	TPASSATS(0.991)NPAADQIQR	-	1038	S	-
Sspon.03G0017500-1A	TPASSAT(0.803)SNPAADQIQR	-	1037	T	-
Sspon.03G0017500-1A	TPASS(0.96)ATS(0.888)NPAADQIQR	...S..[STY]....	1035	S	-
Sspon.03G0017500-1A	IS(1)EEKPDK	-	700	S	-
Sspon.03G0017500-4D	AS(1)PVS(1)VPLAAVPK	[STY]P...	213	S	-
Sspon.03G0017500-4D	AS(1)PVS(1)VPLAAVPK	[STY]P...	216	S	-
Sspon.03G0017600-1A	AYSGPVAS(0.985)AANS(0.82)VTPK	-	36	S	-
Sspon.03G0017600-1A	GKHS(0.916)PSS(0.932)PK	[STY]P...	195	S	-
Sspon.03G0017600-1A	GKHS(0.916)PSS(0.932)PK	[STY]P...	198	S	-
Sspon.03G0017600-1A	DKS(1)DDEDEAPDPAVPTDFTSR	...R..[STY]....	57	S	-
Sspon.03G0018340-1A	MSADS(1)PELEK	[STY]P...	585	S	-
Sspon.03G0018720-1A	TGNETLLS(0.987)AEGGETGR	[STY].E...	737	S	-
Sspon.03G0019170-2B	SVAADSW(0.914)IKS(0.859)DYGSTLDDDQR	...S..[STY]....	18	S	-
Sspon.03G0019170-2B	SVAADSW(0.914)IKS(0.859)DYGSTLDDDQR	...S..[STY]....	15	S	-
Sspon.03G0020210-2B	MDPSLSSSSS(0.868)PLR	[STY]P.R...	10	S	-
Sspon.03G0020230-4D	MEPLPSATAAGVGPGPGPGYPESTESSPRS(0.797)R	...S..[STY]....	31	S	-
Sspon.03G0020230-4D	GISTDSAS(0.977)VNCLLGLEDDSS(0.759)VHSR	...S.[STY]....	226	S	-
Sspon.03G0020230-4D	GISTDSAS(0.977)VNCLLGLEDDSS(0.759)VHSR	...S.[STY]....	214	S	-
Sspon.03G0020370-1A	GRS(1)PT(1)PVHGDDGGAGSSSKPR	..R.R..[STY]P...	35	T	-
Sspon.03G0020370-1A	GRS(1)PT(1)PVHGDDGGAGSSSKPR	..R.R..[STY]P...	33	S	-
Sspon.03G0021000-2B	ALQEVEAEVGGSGGS(1)PR	[STY]PR...	102	S	-
Sspon.03G0021940-4D	NLAVAGDAAVS(1)GGEGQR	[STY]G...	23	S	-
Sspon.03G0022100-2B	YGS(0.963)DGLPELR	[STY]DD...	66	S	-
Sspon.03G0022140-1A	ETQEAADGSEETAS(0.816)AGPDEDTTAVDVK	-	208	S	-
Sspon.03G0022260-2B	TALVS(0.977)GDEEDPEEVEPEALEK	[STY].DE...	293	S	-
Sspon.03G0022310-1P	S(1)FKS(1)FRGS(1)FR	...S..[STY]....	251	S	-
Sspon.03G0022310-1P	S(1)FKS(1)FRGS(1)FR	...S..[STY]....	254	S	-
Sspon.03G0022310-1P	S(1)FKS(1)FRGS(1)FR	...S..[STY]....	258	S	-
Sspon.03G0022650-2C	DLS(1)FVGTYK	-	484	S	-
Sspon.03G0022770-3C	HADDGSEIGAALIAAS(1)QS(1)Q	...S.[STY]....	478	S	-
Sspon.03G0022770-3C	HADDGSEIGAALIAAS(1)QS(1)Q	...S.[STY]....	480	S	-
Sspon.03G0022840-3C	VLPTTQHQQSS(0.907)PR	[STY]PR...	511	S	-
Sspon.03G0023370-1A	DLSSPISS(0.758)FR	...S.[STY]....	26	S	-
Sspon.03G0023370-1A	DLS(0.827)SPISSFR	...R..[STY]....	20	S	-
Sspon.03G0023530-4D	MCT(0.997)PGQS(0.901)GTCS(0.98)PAIPGMMPR	...S...[STY]P...	266	S	-
Sspon.03G0023530-4D	MCT(1)PGQS(0.99)GTCS(0.908)PAIPGMMPR	...S...[STY]P...	262	S	-
Sspon.03G0023530-4D	MCT(1)PGQS(0.99)GTCS(0.908)PAIPGMMPR	...S...[STY]P...	258	T	-
Sspon.03G0023940-4D	FVGESS(0.972)PGHLEDQK	[STY]P...	442	S	-
Sspon.03G0023940-4D	ASGPPS(0.999)PSGKPYSR	...S...[STY]P...	7	S	-
Sspon.03G0023940-4D	AS(0.999)GPPS(0.955)PSGKPYSR	...S...[STY]P...	3	S	-
Sspon.03G0023940-4D	S(0.801)DSTVHAAGMEATPK	[STY]DS...	264	S	-
Sspon.03G0024190-1A	EIDADD(1)DVEPK	[STY]D...	99	S	-
Sspon.03G0024310-1A	NPYSS(0.899)MPLDPQR	-	836	S	-
Sspon.03G0024450-3C	SW(0.995)EIGDLDDSAAGR	...RS.[STY]....	84	S	-
Sspon.03G0024540-3C	AEQPQPHEEGGAS(1)PK	[STY]P...	14	S	-
Sspon.03G0024550-1T	IVDMDS(1)DEELDDR	[STY]DE...	297	S	-
Sspon.03G0024550-1T	SSES(1)MTNLPK	...S..[STY]....	191	S	-

Sspon.03G0024550-1T	TSS(0.989)WTFDEK	...R..[STY]....	228	S	-
Sspon.03G0024550-1T	SIS(0.999)ETTLER	...RS.[STY]....	148	S	-
Sspon.03G0025260-1A	GGYDS(0.983)GEEDDKATQQEIAVCK	[STY].E...	64	S	-
Sspon.03G0025530-2B	RYSEMNF(1)Q	-	592	S	-
Sspon.03G0026000-1B	SLSSNLS(0.974)QGAEDVVK	...S..[STY]....	1542	S	-
Sspon.03G0026060-1B	SDSSYSRS(0.986)PT(0.994)PPPR	...S...[STY]P...	348	S	-
Sspon.03G0026060-1B	SDSSYSRS(0.927)PT(1)PPPRK	...S...[STY]P...	350	T	-
Sspon.03G0026060-1B	RRPDPS(1)PVR	-	256	S	-
Sspon.03G0026060-1B	RKPAS(1)PPR	-	218	S	-
Sspon.03G0026060-1B	KGRS(1)PS(1)PPPK	[STY]PSP...	69	S	-
Sspon.03G0026060-1B	KGRS(1)PS(1)PPPK	[STY]PSP...	71	S	-
Sspon.03G0026060-1B	KAS(1)PPAESAVLCIDHLSR	-	85	S	-
Sspon.03G0026060-1B	AAS(1)PMKAPPPPK	-	176	S	-
Sspon.03G0026060-1B	GVS(1)S(1)AEKDAQQRPR	[STY].E...	197	S	-
Sspon.03G0026060-1B	GVS(1)S(1)AEKDAQQRPR	[STY].E...	198	S	-
Sspon.03G0026060-1B	AES(1)PRRPPDPS(1)PR	[STY]P.R...	231	S	-
Sspon.03G0026060-1B	AES(1)PRRPPDPS(1)PR	[STY]P.R...	239	S	-
Sspon.03G0026060-2P	S(1)PMRPS(1)PR	[STY]P.R...	265	S	-
Sspon.03G0026060-2P	S(1)PMRPS(1)PR	[STY]P.R...	270	S	-
Sspon.03G0026480-3D	RSSPLSS(0.916)PFSSNDSIHK	...S...[STY]P...	104	S	-
Sspon.03G0026480-3D	LSSMES(0.996)FKHLDSR	...S..[STY]....	699	S	-
Sspon.03G0026480-3D	SDILS(0.911)SGATSPR	-	86	S	-
Sspon.03G0026480-3D	FFSAS(0.961)VPGS(0.995)R	...S..[STY]....	754	S	-
Sspon.03G0026480-3D	FFSAS(0.826)VPGS(1)R	...S..[STY]....	758	S	-
Sspon.03G0026480-3D	SDILS(0.837)SGATS(0.953)PR	...S...[STY]P...	91	S	-
Sspon.03G0026480-3D	STT(0.994)PTPTLGGLTS(0.915)PR	[STY]PR...	789	S	-
Sspon.03G0026480-3D	STT(0.994)PTPTLGGLTS(0.915)PR	[STY]PR...	779	T	-
Sspon.03G0026480-3D	S(0.953)DVSSDLGGIR	[STY]..S...	2	S	-
Sspon.03G0026510-1P	FESWPVGNAAGS(1)PGAEEGR	-	163	S	-
Sspon.03G0026510-2D	VVITPAGPS(0.986)GPSSPQSEAGESNVFHQEK	-	719	S	-
Sspon.03G0026510-2D	VVITPAGPS(0.953)GPSS(0.888)PQS(0.998)EAGESNVFHQEK	...S...[STY]P...	723	S	-
Sspon.03G0026510-2D	VVITPAGPS(0.953)GPSS(0.888)PQS(0.998)EAGESNVFHQEK	...S...[STY]P...	726	S	-
Sspon.03G0026850-3D	GGLEYIS(0.961)QPST(0.945)PAASNK	...S...[STY]P...	2569	T	-
Sspon.03G0026850-3D	GGLEYIS(0.961)QPST(0.945)PAASNK	...S...[STY]P...	2565	S	-
Sspon.03G0027240-2C	SGLDDMDLTGSQVGS(0.84)PAQTGR	...S...[STY]P...	135	S	-
Sspon.03G0027700-2C	ADIDQAS(1)LAMENQ	-	545	S	-
Sspon.03G0027700-2C	S(0.961)PSPALGR	[STY]PSP...	123	S	-
Sspon.03G0027940-2D	QGSSAS(0.995)LAGDDTDFAEAAVSK	...S...[STY]....	179	S	-
Sspon.03G0027940-2D	KQGSS(0.78)ASLAGDDTDFAEAAVSK	[STY].S...	177	S	-
Sspon.03G0027940-2D	QGS(0.871)SASLAGDDTDFAEAAVSK	[STY]..S...	176	S	-
Sspon.03G0028140-1P	NFS(1)DLTVWSDDNK	...R..[STY]....	157	S	-
Sspon.03G0028220-1P	RLLGSPS(0.964)GSGYAS	...S..[STY]....	330	S	-
Sspon.03G0028220-1P	RLLGS(0.948)PSGSGYAS	[STY]P...	328	S	-
Sspon.03G0028220-1P	RLLGS(0.947)PSGS(0.994)GYAS	[STY]P...	332	S	-
Sspon.03G0028780-3D	AGFSDESSAASVSS(0.988)P	[STY]P...	933	S	-
Sspon.03G0028780-3D	AGFSDESSAASVS(0.815)SP	...S..[STY]....	932	S	-
Sspon.03G0028780-3D	AGFS(0.965)DDESSAASVSSP	[STY]DD...	922	S	-
Sspon.03G0028780-3D	S(1)PALS(1)PPPQAANFR	...S...[STY]P...	442	S	-
Sspon.03G0028780-3D	S(1)PALS(1)PPPQAANFR	...S...[STY]P...	446	S	-
Sspon.03G0029130-1B	GASITLS(1)PNK	...S...[STY]P...	350	S	-
Sspon.03G0029190-1B	IDS(1)PMR	[STY]P.R...	581	S	-
Sspon.03G0029290-1P	SLS(0.982)CDPIPDSPLR	...RS.[STY]....	31	S	-
Sspon.03G0029320-2C	NQTPKPPAPAS(1)P	[STY]P...	403	S	-
Sspon.03G0030090-1P	RPSSYHSYSQS(0.893)PPYDFQYEDR	...S...[STY]P...	108	S	-
Sspon.03G0030090-1P	FSDFS(0.996)ASSTGDFR	...S...[STY]....	173	S	-
Sspon.03G0030130-2C	IS(0.999)PAQS(0.991)PSMGSGEQALEPK	...S...[STY]P...	474	S	-
Sspon.03G0030130-2C	IS(0.999)PAQS(0.991)PSMGSGEQALEPK	...S...[STY]P...	470	S	-
Sspon.03G0030280-2C	GLPIPGNDGGS(1)S(1)EEEEQR	[STY].E...	319	S	-
Sspon.03G0030280-2C	GLPIPGNDGGS(1)S(1)EEEEQR	[STY].E...	320	S	-
Sspon.03G0030600-2C	SFFAFGGEDAS(1)GGK	[STY]G...	108	S	-
Sspon.03G0030820-2D	GGVS(1)DFIVGPS(1)DNK	[STY]D...	730	S	-
Sspon.03G0030820-2D	GGVS(1)DFIVGPS(1)DNK	[STY]D...	737	S	-
Sspon.03G0030920-2C	ATAVSS(0.935)PPDS(0.931)PTAATGAR	...S...[STY]P...	46	S	-
Sspon.03G0030920-2C	ATAVSS(0.88)PPDS(0.982)PTAATGAR	...S...[STY]P...	50	S	-
Sspon.03G0031400-3D	RLEEDGDEQNNSAMDAS(0.997)P	[STY]P...	399	S	-
Sspon.03G0031400-3D	LEEDGDEQNNS(0.999)AMDASP	-	394	S	-
Sspon.03G0031460-1B	ALS(1)LDPSAR	-	34	S	-
Sspon.03G0031530-1B	TTDAS(1)PGAFR	[STY]P...	876	S	-
Sspon.03G0031920-2D	AAAAAAAAAAESDSEDGYNNNDYDDDEGSQQSPS(0.945)R	...S..[STY]....	202	S	-
Sspon.03G0031920-2D	AAAAAAAAAAESDSEDGYNNNDYDDDEGSQQS(0.986)PSR	[STY]P.R...	200	S	-
Sspon.03G0031920-2D	AAAAAAAAAAESDSEDGYNNNDYDDDEGS(0.827)QQSPSR	[STY]..S...	197	S	-

Sspon.03G0031960-1P	PAPVEES(0.983)PQS(0.788)SGADEWGLETR	[STY]P...	150	S	-
Sspon.03G0031960-1P	PAPVEES(0.999)PQSSGADEWGLETR	[STY]P...	147	S	-
Sspon.03G0032240-1B	TES(0.999)PAAGHPIGQGSLDLEK	[STY]P...	470	S	-
Sspon.03G0032650-2D	TTTEESEGVRTSEEERS(0.991)R	[STY].S...	679	S	-
Sspon.03G0032650-2D	SGGT(1)PPAAPT(1)P	[STY]P...	684	T	-
Sspon.03G0032650-2D	SGGT(0.985)PPAAPT(1)P	[STY]P...	690	T	-
Sspon.03G0034410-1B	ALINSIS(0.992)GR	...S.[STY]....	853	S	-
Sspon.03G0034420-1B	S(0.992)GGMSNEMYNTIAR	...S.[STY]....	176	S	-
Sspon.03G0034640-1B	SLFEGFS(1)DDEDVK	[STY]DD...	152	S	-
Sspon.03G0034870-3D	TPESILENSTPMS(0.968)PK	[STY]P.R...	151	S	-
Sspon.03G0034930-1B	SLEGAFVLNQHQPAEHDESSS(0.947)Q	...S.[STY]....	242	S	-
Sspon.03G0034930-1B	SLEGAFVLNQHQPAEHDESS(0.774)SQ	-	241	S	-
Sspon.03G0034940-1B	KSAPVYGDDDS(1)DSAE	[STY]DS...	477	S	-
Sspon.03G003570-2C	LAS(1)DLFAR	...R..[STY]....	743	S	-
Sspon.03G0035610-1B	IAAATGAAYS(0.981)DDEDS(1)DEAAAPR	[STY]DE...	98	S	-
Sspon.03G0035610-1B	IAAATGAAYS(0.981)DDEDS(1)DEAAAPR	[STY]DE...	103	S	-
Sspon.03G0036070-2C	DGHAGNAAAAAAS(0.981)PSE	[STY]P...	314	S	-
Sspon.03G0036100-1B	SLS(0.993)MRGS(1)MR	...RS.[STY]....	6	S	-
Sspon.03G0036100-1B	SLS(0.993)MRGS(1)MR	...RS.[STY]....	10	S	-
Sspon.03G0036420-2C	S(0.99)FGGSSSLASGAK	-	2	S	-
Sspon.03G0036600-2C	GEATADVDS(1)GNESD	[STY]G...	530	S	-
Sspon.03G0037250-2C	EDGDESDEAKGHSAPAT(0.956)R	[STY]..S...	259	T	-
Sspon.03G0037250-2C	SSPGLEVS(1)DGEVDYK	[STY]D...	507	S	-
Sspon.03G0037250-2C	DAIEVS(1)DDEEGADAVGANK	[STY]DD...	84	S	-
Sspon.03G0037330-2C	SADT(0.928)SDEEPEIDIMR	...S..[STY].D...	64	T	-
Sspon.03G0037330-3D	SADT(0.833)SDEEPEIDIMK	...S..[STY].D...	64	T	-
Sspon.03G0038330-2P	ADEIDTRPAS(1)AGS(1)R	...S..[STY]....	11	S	-
Sspon.03G0038330-2P	ADEIDTRPAS(1)AGS(1)R	...S..[STY]....	14	S	-
Sspon.03G0039740-2D	AENFQLQS(1)R	-	9	S	-
Sspon.03G0040490-2D	VQS(0.998)PSLA AVR	..R.R..[STY]P...	45	S	-
Sspon.03G0040670-1C	APEAPLKT(1)PENS(1)PK	[STY]P..SP..	504	S	-
Sspon.03G0040670-1C	APEAPLKT(1)PENS(1)PK	[STY]P..SP..	500	T	-
Sspon.03G0040870-1C	SYS(0.785)TNLAYTPPEYLR	...S.[STY]....	188	S	-
Sspon.03G0042840-2D	LSIDDELVS(0.818)PK	[STY]P...	396	S	-
Sspon.03G0042840-2D	LSIDDELVS(0.76)SPK	-	395	S	-
Sspon.03G0044130-2D	SLPGNPDPDAEVIAS(1)PR	[STY]PR...	64	S	-
Sspon.03G0044930-1D	SAS(0.943)PDL SR	..R.R..[STY]P...	2233	S	-
Sspon.03G0046550-1D	AS(1)PD AEQPAPTEPER	[STY]P...	3	S	-
Sspon.04G0000170-1P	IHIGSENS(0.995)S(0.995)EDDVER	...S..[STY]....	1569	S	-
Sspon.04G0000170-1P	IHIGSENS(0.995)S(0.995)EDDVER	...S..[STY]....	1570	S	-
Sspon.04G0000170-1P	IHIGS(0.998)ENS(0.866)SEDDVER	...S..[STY]....	1566	S	-
Sspon.04G0000170-1P	NTTS(0.978)FIIR	-	1374	S	-
Sspon.04G0000280-1P	MEAPGSPY(0.764)ASSPESAPK	-	8	Y	-
Sspon.04G0000280-1P	MEAPGS(1)PYAS(0.999)S(0.998)PESAPK	[STY]P...	11	S	-
Sspon.04G0000280-1P	MEAPGS(1)PYAS(0.999)S(0.998)PESAPK	[STY]P...	10	S	-
Sspon.04G0000280-1P	MEAPGS(1)PYASS(0.994)PESAPK	[STY]P...	6	S	-
Sspon.04G0000280-1P	MEAPGS(0.97)PYASSPES(0.995)APKR	[STY]P...	14	S	-
Sspon.04G0000280-1P	S(1)PPQQQQPPS(1)EEGDDKEKPTH LR	[STY]P...	31	S	-
Sspon.04G0000280-1P	S(1)PPQQQQPPSEEGDDKEKPTH LR	[STY]P...	22	S	-
Sspon.04G0000280-4D	S(1)PPQQQQPPS(1)EEGDDKEKPTH LR	[STY]P...	22	S	-
Sspon.04G0000280-4D	S(1)PPQQQQPPS(1)EEGDDKEKPTH LR	[STY]P...	30	S	-
Sspon.04G0000310-1A	MEPGQSGTEQTS(0.926)PR	[STY]PR...	12	S	-
Sspon.04G0000870-1A	AS(1)PTQGGVITCK	[STY]P...	3	S	-
Sspon.04G0001070-2C	KLS(1)NQQIAS(1)PPPNYEDVTR	[STY]P...	194	S	-
Sspon.04G0001070-2C	KLS(1)NQQIAS(1)PPPNYEDVTR	[STY]P...	188	S	-
Sspon.04G0001790-2B	AGSSATVLS(0.999)APDS(1)PR	...S...[STY]P...	310	S	-
Sspon.04G0001790-2B	AGSSATVLS(0.999)APDS(1)PR	...S...[STY]P...	314	S	-
Sspon.04G0001790-4D	AGSSATVLS(0.995)PPDS(0.999)PR	...S...[STY]P...	137	S	-
Sspon.04G0001790-4D	AGSSATVLS(0.995)PPDS(0.999)PR	...S...[STY]P...	141	S	-
Sspon.04G0001800-1A	EFNLLDSCSGS(0.982)PK	...S...[STY]P...	222	S	-
Sspon.04G0001820-3D	AITATT(0.974)PDILGER	[STY]P...	7	T	-
Sspon.04G0001930-1A	IGSGGLGS(1)GR	-	91	S	-
Sspon.04G0001930-1A	YRRS(0.999)PS(0.968)YSR	[STY]P...	112	S	-
Sspon.04G0001930-1A	YRRS(0.999)PS(0.968)YSR	[STY]P...	110	S	-
Sspon.04G0001930-1A	IGS(1)GGLGSGR	-	86	S	-
Sspon.04G0002280-1A	ADVDM AELPQT(1)PR	[STY]PR...	12	T	-
Sspon.04G0002330-3D	NFDTQES(0.918)DSEEPSSIGDGLVR	[STY]DS...	243	S	-
Sspon.04G0002500-2P	DNWEDGNPATWGSS(0.829)PAYQPGT(0.99)PQAR	[STY]P...	747	S	-
Sspon.04G0002670-3C	LSISQS(0.998)FGR	...S.[STY]....	608	S	-
Sspon.04G0002680-2C	WILS(1)PVS(1)CDGMGR	[STY]P...	156	S	-
Sspon.04G0002680-2C	WILS(1)PVS(1)CDGMGR	[STY]P...	159	S	-
Sspon.04G0002790-2C	MASLSS(0.887)PR	[STY]PR...	6	S	-
Sspon.04G0003420-2P	SSTLGTL S(0.885)LD R	-	53	S	-
Sspon.04G0003600-3C	MAVAS(1)PR	[STY]PR...	366	S	-
Sspon.04G0003600-3C	S(0.855)SNFGAGDAFGLR	-	255	S	-
Sspon.04G0003600-3C	S(1)MGFSGTTPR	...S..[STY]....	209	S	-

Sspon.04G0003600-4D	PSNLTNAEIYS(0.846)LQSSRNPT(0.964)PR	...S...[STY]P...	242	S	-
Sspon.04G0003600-4D	PSNLTNAEIYS(0.846)LQSSRNPT(0.964)PR	...S...[STY]P...	250	T	-
Sspon.04G0003600-4D	SS(0.851)NFGAADAFGVR	-	269	S	-
Sspon.04G0003680-2C	ATS(0.922)DELAQIDISK	-	4	S	-
Sspon.04G0003800-2B	EAVVGES(1)DDEKEK	[STY]DD...	92	S	-
Sspon.04G0003840-1A	ASS(0.826)PQTGSDEAGGNLK	[STY]P...	534	S	-
Sspon.04G0003840-3P	QSNS(0.991)DGALDTMAR	...S.[STY]....	719	S	-
Sspon.04G0003840-3P	ASS(0.99)PQTDAEQGGSLK	[STY]P...	537	S	-
Sspon.04G0003870-3C	YHGHS(0.999)MSDPGSTYR	[STY].S...	293	S	-
Sspon.04G0004560-3C	ASSQAS(0.986)LADPDDFDLTR	...S...[STY]....	14	S	-
Sspon.04G0004560-3C	ASS(0.84)QASLADPDDFDLTR	[STY]..S...	11	S	-
Sspon.04G0004590-2B	ADS(0.928)SLCIPVR	...R...[STY]....	382	S	-
Sspon.04G0004650-1A	MLS(0.99)STSS(0.989)KVPR	...S...[STY]....	161	S	-
Sspon.04G0004650-1A	MLS(0.987)STS(0.817)SKVPR	...S...[STY]....	160	S	-
Sspon.04G0004670-4D	YMAYSPS(0.857)PSTTPHSPR	[STY]P...	12	S	-
Sspon.04G0004670-4D	SGS(0.986)AS(0.999)PFHNSLGMK	...S...[STY]P...	269	S	-
Sspon.04G0004670-4D	SGS(0.928)AS(1)PFHNSLGMK	...S...[STY]P...	271	S	-
Sspon.04G0005130-1A	LMTTVAIENS(1)GEK	[STY].E...	267	S	-
Sspon.04G0005180-1A	DIESLHLS(0.967)K	-	688	S	-
Sspon.04G0005180-1A	KCS(1)T(1)LFKFS(1)PR	[STY]PR...	776	S	-
Sspon.04G0005180-1A	KCS(1)T(1)LFKFS(1)PR	[STY]PR...	782	S	-
Sspon.04G0005180-1A	KCS(1)T(1)LFKFS(1)PR	[STY]PR...	777	T	-
Sspon.04G0005180-4D	GGDVAAAEAGS(1)PR	[STY]PR...	1534	S	-
Sspon.04G0005180-4D	QNS(1)LSFTGSNDESR	...R...[STY]....	1742	S	-
Sspon.04G0005450-1T	S(1)FADLEAGALR	-	2	S	-
Sspon.04G0005660-3C	DNESLAPIFT(1)PPR	[STY]P.R...	195	T	-
Sspon.04G0005660-3C	MTAGMSSMS(0.998)FK	...S...[STY]....	35	S	-
Sspon.04G0005660-3C	MTAGMS(0.816)SMS(0.798)FK	...S...[STY]....	32	S	-
Sspon.04G0005740-1A	VMAVEEQQGS(1)PLPR	[STY]P...	77	S	-
Sspon.04G0005920-1A	ESS(0.839)PDSNDMLSDLGSK	...S...[STY]P...	277	S	-
Sspon.04G0005920-1A	ESS(0.815)PDS(0.999)NDMLSDLGSK	...S...[STY]P...	280	S	-
Sspon.04G0006470-4D	TMPDPDAEVALS(1)PK	[STY]P...	68	S	-
Sspon.04G0006470-4D	AS(0.904)NSS(0.956)AAAFFGVR	...S...[STY]....	3	S	-
Sspon.04G0006470-4D	AS(0.904)NSS(0.956)AAAFFGVR	...S...[STY]....	6	S	-
Sspon.04G0006600-4P	S(1)VEEAIAR	[STY].E...	1812	S	-
Sspon.04G0007340-2B	FSGVFSSSGS(0.987)PR	...S.[STY]P...R	92	S	-
Sspon.04G0007340-2B	FSGVFS(0.998)SSGS(0.785)PR	...S.[STY]P...R	88	S	-
Sspon.04G0007530-1A	QQNTAGSLLGLAYES(1)S(1)DEE	[STY]DE...	199	S	-
Sspon.04G0007530-1A	QQNTAGSLLGLAYES(1)S(1)DEE	[STY]DE...	200	S	-
Sspon.04G0007580-3C	SAS(0.978)LSEILDPK	...RS.[STY]....	332	S	-
Sspon.04G0007600-1A	S(1)HS(1)PVEYK	..R.R..[STY]P...	10	S	-
Sspon.04G0007600-1A	S(1)HS(1)PVEYK	..R.R..[STY]P...	8	S	-
Sspon.04G0007950-4D	LGSS(0.925)ASFSR	[STY].S...	286	S	-
Sspon.04G0007950-4D	LGS(0.998)SAS(1)FSR	...S...[STY]....	285	S	-
Sspon.04G0007950-4D	LGS(0.998)SAS(1)FSR	...S...[STY]....	288	S	-
Sspon.04G0008020-3C	RLTILTDAGS(0.999)DNLGS	[STY]D...	702	S	-
Sspon.04G0008430-4D	DTVDDGKLS(0.998)ERT(0.997)IS(0.995)DELPQESSK	[STY]DE...	285	T	-
Sspon.04G0008430-4D	DTVDDGKLS(0.998)ERT(0.997)IS(0.995)DELPQESSK	[STY]DE...	282	S	-
Sspon.04G0008430-4D	AAEIEQEAS(0.999)GNASTGK	[STY]G...	808	S	-
Sspon.04G0008430-4D	DETLS(0.994)EDDPAKDLSLK	[STY]..D...D	506	S	-
Sspon.04G0008430-4D	AALDS(0.997)DKS(0.853)TELKPSDK	...S...[STY]....	381	S	-
Sspon.04G0008430-4D	AALDS(0.997)DKS(0.853)TELKPSDK	...S...[STY]....	378	S	-
Sspon.04G0008430-4D	TIS(1)DELPQESSK	[STY]DE...	287	S	-
Sspon.04G0008510-2C	RSYS(0.99)PR	-	146	S	-
Sspon.04G0008510-2C	YRRS(0.984)PS(0.977)YGR	[STY]P...	139	S	-
Sspon.04G0008510-2C	YRRS(0.997)PS(0.876)YGR	[STY]P...	137	S	-
Sspon.04G0008510-2C	DAS(1)RS(1)PPPPPDAR	[STY]P...	216	S	-
Sspon.04G0008510-2C	DAS(1)RS(1)PPPPPDAR	[STY]P...	218	S	-
Sspon.04G0008510-2C	DMS(1)RS(1)PPPPPPR	...S.[STY]P...R	194	S	-
Sspon.04G0008510-2C	DMS(1)RS(1)PPPPPPR	...S.[STY]P...R	196	S	-
Sspon.04G0008510-2C	RS(0.983)YSRSPGQQPQR	[STY].S.SP..	228	S	-
Sspon.04G0008510-2C	RS(0.906)YS(0.926)RS(0.976)PGQQPQR	...S.[STY]P...R	230	S	-
Sspon.04G0008510-2C	RS(0.906)YS(0.926)RS(0.976)PGQQPQR	...S.[STY]P...R	232	S	-
Sspon.04G0008510-2C	S(1)LS(1)RS(1)PPLPPPPPR	...S...[STY]P...	168	S	-
Sspon.04G0008510-2C	S(1)LS(1)RS(1)PPLPPPPPR	...S...[STY]P...	170	S	-
Sspon.04G0008510-2C	S(1)LS(1)RS(1)PPLPPPPPR	...S...[STY]P...	172	S	-
Sspon.04G0008640-1A	GVEVPQDLGGIS(1)PK	[STY]P...	52	S	-
Sspon.04G0008640-1A	EVILVDDNDS(1)GQEDGGEGK	[STY]G...	72	S	-
Sspon.04G0008760-1A	ALENMGMGDVDMVS(0.932)AEESSEAAK	[STY].E...	76	S	-
Sspon.04G0008810-4D	TPYHPMIDEDEGPVS(1)PLR	[STY]P.R...	52	S	-
Sspon.04G0008880-1A	SGGS(0.946)SESSPLSGR	...S...[STY]....	5	S	-
Sspon.04G0009220-1A	TSGS(0.949)FVLR	...S.[STY]....	633	S	-
Sspon.04G0010440-3C	GGFDGMY(0.999)PGGGRLR	[STY]P...	67	S	-
Sspon.04G0010440-3C	SASHTSL(0.86)ESDDFELTR	...S.[STY]....	19	S	-
Sspon.04G0010440-3C	SASHTS(1)LSSESDDFELTR	...S...[STY]....	17	S	-
Sspon.04G0010440-3C	SASHTS(0.908)LSSES(0.872)DDFELTR	...S...[STY]....	21	S	-

Sspon.04G0010440-3C	SAS(0.976)HTS(0.927)LSESDDFELTR	...RS.[STY]....	14	S	-
Sspon.04G0011160-1A	DGTQRGS(0.771)QDGNFMQQR	-	401	S	-
Sspon.04G0011260-1A	HVES(0.999)MSELPSEGAGK	[STY].S...	24	S	-
Sspon.04G0011310-4D	IWQYGDVES(1)DEEEQAPAAAR	[STY]DE...	909	S	-
Sspon.04G0011540-1P	ASSAGNS(0.97)DVAPMNASVLQNK	[STY]D...	669	S	-
Sspon.04G0011540-2B	ASSVGNS(0.998)DVAPMNASVLQNK	[STY]D...	782	S	-
Sspon.04G0011870-2B	ILS(1)GFDNR	...R..[STY]....	105	S	-
Sspon.04G0012250-2B	SSS(0.878)DGFINSSENGIK	...RS.[STY]....	43	S	-
Sspon.04G0012260-2D	NLNFQTEPS(0.997)FR	-	278	S	-
Sspon.04G0012270-3D	LTEGCS(0.998)FR	-	140	S	-
Sspon.04G0012290-2B	GILAADES(0.927)TGITIGKR	-	32	S	-
Sspon.04G0012730-4D	TDQVAMTEVVVDGS(1)GR	[STY]G...	241	S	-
Sspon.04G0012950-2P	TVADS(0.991)DDDESKPSSASAAAAAQTGR	[STY]DD...	46	S	-
Sspon.04G0013510-1A	VERPHPDS(1)JEWER	-	148	S	-
Sspon.04G0013830-3D	TSLFCEGTTS(0.964)GDLGNVGSPTTR	[STY]G...	609	S	-
Sspon.04G0013830-3D	AGPAT(0.989)PTPS(0.892)WK	[STY]P...	74	S	-
Sspon.04G0013830-3D	S(0.986)PTRS(0.835)LGIMGR	[STY]P.R...	200	S	-
Sspon.04G0013830-3D	S(0.986)PTRS(0.835)LGIMGR	[STY]P.R...	196	S	-
Sspon.04G0014010-4D	S(0.999)VS(0.939)PSESPPPSAK	[STY]P..SP..	99	S	-
Sspon.04G0014010-4D	S(0.999)VS(0.752)PSESPPPSAK	[STY]P..SP..	97	S	-
Sspon.04G0014380-3D	DPSFQVS(1)PQPPLSK	...S...[STY]P...	910	S	-
Sspon.04G0014380-3D	HQS(1)IDAQLR	...R..[STY]....	7	S	-
Sspon.04G0014630-4D	STS(0.932)FLKS(1)MNR	...S.[STY]....	268	S	-
Sspon.04G0014630-4D	STS(0.922)FLKS(1)MNR	...S.[STY]....	272	S	-
Sspon.04G0014930-3P	LKDDNPLLS(0.946)SR	-	86	S	-
Sspon.04G0015140-2P	MDPSSAGS(0.803)GGNSLPSVGPDGQK	...S...[STY]....	8	S	-
Sspon.04G0015290-1A	TISSASSIGS(0.938)SEGTSQTK	...S...[STY]....	312	S	-
Sspon.04G0015290-1A	YFEVDDRS(0.999)GKTT(0.806)PVQR	...S...[STY]P...	200	S	-
Sspon.04G0015290-1A	TISSASS(0.946)IGSSEGTSEQTK	...S...[STY]....	309	S	-
Sspon.04G0015290-1A	KPDSGS(0.899)PDFQK	[STY]P...	224	S	-
Sspon.04G0015290-1A	EADGSS(0.976)PVVVRPVR	[STY]P...	235	S	-
Sspon.04G0015310-1A	DGELNKSS(0.886)PS(1)PGKGAEAK	[STY]PSP...	245	S	-
Sspon.04G0015310-1A	DGELNKSS(0.917)PS(0.994)PGKGAEAK	[STY]PSP...	243	S	-
Sspon.04G0015310-1A	DGELNKSS(0.766)SPS(0.996)PGKGAEAK	[STY]P...	242	S	-
Sspon.04G0015310-1A	LES(0.917)PGHTAVPNSDLTEPR	[STY]P...	220	S	-
Sspon.04G0015360-4D	IIKGDSEAEAST(0.96)SDSSSEDAR	[STY]..S...	289	T	-
Sspon.04G0015360-4D	SRSPPVHRPS(0.987)PPDS(0.954)PSLK	...S...[STY]P...	753	S	-
Sspon.04G0015360-4D	SRSPPVHRPS(0.987)PPDS(0.954)PSLK	...S...[STY]P...	749	S	-
Sspon.04G0015360-4D	GLVSYGDGS(1)PDS(1)AGK	[STY]P...	792	S	-
Sspon.04G0015360-4D	GLVSYGDGS(1)PDS(1)AGK	[STY]P...	795	S	-
Sspon.04G0015360-4D	NAAVMPVLT(1)GNRS(1)K	[STY].S...	378	S	-
Sspon.04G0015360-4D	NAAVMPVLT(1)GNRS(1)K	[STY].S...	374	T	-
Sspon.04G0015360-4D	TSVIS(1)PLR	[STY]P.R...	524	S	-
Sspon.04G0015360-4D	TSVIS(0.998)PLRS(1)VS(1)RS(1)PAR	[STY]P.R...	528	S	-
Sspon.04G0015360-4D	TSVIS(0.998)PLRS(1)VS(1)RS(1)PAR	[STY]P.R...	530	S	-
Sspon.04G0015360-4D	TSVIS(0.998)PLRS(1)VS(1)RS(1)PAR	[STY]P.R...	532	S	-
Sspon.04G0015360-4D	GGGYS(0.961)KS(0.999)PVRS(1)LS(1)PPPR	...S.[STY]P...R	706	S	-
Sspon.04G0015360-4D	GGGYS(0.961)KS(0.999)PVRS(1)LS(1)PPPR	...S.[STY]P...R	708	S	-
Sspon.04G0015360-4D	GGGYS(0.961)KS(0.999)PVRS(1)LS(1)PPPR	...S.[STY]P...R	712	S	-
Sspon.04G0015360-4D	GGGYS(0.961)KS(0.999)PVRS(1)LS(1)PPPR	...S.[STY]P...R	714	S	-
Sspon.04G0015360-4D	NISRS(0.768)PS(0.925)PHRR	[STY]P.R...	589	S	-
Sspon.04G0015360-4D	NISRS(0.768)PS(0.925)PHRR	[STY]P.R...	591	S	-
Sspon.04G0015360-4D	GLVS(0.986)YGDGS(0.994)PDSAGK	[STY]P...	787	S	-
Sspon.04G0015360-4D	SKAS(0.869)SQVS(0.996)EENLAAVAALK	...S...[STY]....	311	S	-
Sspon.04G0015360-4D	DVGS(1)IEIDK	[STY].E...	153	S	-
Sspon.04G0015360-4D	GAS(1)RS(1)PHIRS(1)PVK	[STY]P...	463	S	-
Sspon.04G0015360-4D	GAS(1)RS(1)PHIRS(1)PVK	[STY]P...	465	S	-
Sspon.04G0015360-4D	GAS(1)RS(1)PHIRS(1)PVK	[STY]P...	470	S	-
Sspon.04G0015360-4D	SMS(0.999)IS(1)PR	[STY]P.R...	396	S	-
Sspon.04G0015360-4D	SMS(0.999)IS(1)PR	[STY]P.R...	398	S	-
Sspon.04G0015360-4D	ASS(0.998)QVS(1)EENLAAVAALK	...S...[STY]....	312	S	-
Sspon.04G0015360-4D	ASS(0.977)QVS(1)EENLAAVAALK	...S...[STY]....	315	S	-
Sspon.04G0015360-4D	QQS(0.999)ISRS(0.858)PAR	[STY]P.R...	445	S	-
Sspon.04G0015360-4D	QQS(0.999)ISRS(1)PAR	[STY]P.R...	449	S	-
Sspon.04G0015360-4D	RS(1)VS(1)RS(1)PVR	[STY]P.R...	571	S	-
Sspon.04G0015360-4D	RS(1)VS(1)RS(1)PVR	[STY]P.R...	573	S	-
Sspon.04G0015360-4D	RS(1)VS(1)RS(1)PVR	[STY]P.R...	575	S	-
Sspon.04G0015360-4D	S(1)VS(1)PS(1)PPLEK	...S.[STY]P...R	504	S	-
Sspon.04G0015360-4D	S(1)VS(1)PS(1)PPLEK	...S.[STY]P...R	506	S	-
Sspon.04G0015360-4D	S(1)VS(1)PS(1)PPLEK	...S.[STY]P...R	508	S	-
Sspon.04G0015360-4D	S(1)PS(0.989)RSLER	[STY]P.R...	493	S	-
Sspon.04G0015360-4D	S(0.997)MSIS(0.894)PR	[STY]P.R...	394	S	-
Sspon.04G0015360-4D	S(1)PS(0.989)RSLER	[STY]P.R...	491	S	-
Sspon.04G0015360-4D	S(0.992)LSRS(0.987)PVR	...S.[STY]P...R	563	S	-
Sspon.04G0015360-4D	S(0.992)LSRS(0.987)PVR	...S.[STY]P...R	559	S	-
Sspon.04G0015360-4D	S(1)RS(1)PVRT(1)PR	...S.[STY]P...R	425	S	-

Sspon.04G0015360-4D	S(1)RS(1)PVRT(1)PR	...S.[STY]P...R	427	S	-
Sspon.04G0015360-4D	S(1)RS(1)PVRT(1)PR	...S.[STY]P...R	431	T	-
Sspon.04G0015440-2B	AMTALS(0.99)PYGPPR	[STY]P...	328	S	-
Sspon.04G0015530-2B	FIDAPPS(0.989)PPQSK	[STY]P...	122	S	-
Sspon.04G0016130-1A	VVIDVSS(0.963)S(0.97)AEYGALASGK	...S.[STY]....	295	S	-
Sspon.04G0016130-1A	VVIDVSS(0.963)S(0.97)AEYGALASGK	...S.[STY]....	296	S	-
Sspon.04G0016190-3C	TTPTGLADPLSGS(1)PGGTGLR	...S.[STY]P...R	310	S	-
Sspon.04G0016190-3C	TT(0.85)PTGLADPLSGS(0.999)PGGTGLR	...S.[STY]P...R	299	T	-
Sspon.04G0016270-3D	EGDLRDL(1)F	...R..[STY]....	712	S	-
Sspon.04G0016490-1A	SYGGS(1)WGGGR	-	108	S	-
Sspon.04G0016570-2B	MDSGSDS(0.919)DGAPEELTAVQGVK	...S.[STY]....	7	S	-
Sspon.04G0016570-2B	MDSGSDS(0.925)DSDGAPEELTAVQGVK	[STY]DS...	5	S	-
Sspon.04G0016570-2B	MDS(0.995)GSDSDGAPEELTAVQGVK	[STY]..S...	3	S	-
Sspon.04G0016580-1P	ADAIEEAVDSSET(0.979)VPSAR	...S..[STY]....	277	T	-
Sspon.04G0016580-1P	ADAIEEAVDS(0.991)SETVPSAR	[STY]..E...	274	S	-
Sspon.04G0016580-3C	ADAIEEATDS(0.912)SETVPSAR	[STY]..E...	363	S	-
Sspon.04G0016580-3C	ADAIEEAT(0.988)DS(0.839)SETVPSAR	[STY]DS...	361	T	-
Sspon.04G0016930-3C	GLGLSYSS(0.983)GS(0.99)DIADDLGK	...S..[STY]....	360	S	-
Sspon.04G0016930-3C	GLGLSYSS(0.953)GS(0.999)DIADDLGK	...S..[STY]....	362	S	-
Sspon.04G0016930-3C	GLGLSYS(0.965)SGS(0.963)DIADDLGK	...S..[STY]....	359	S	-
Sspon.04G0016930-3C	GLGLS(0.822)YSSGS(0.912)DIADDLGK	...S..[STY]....	357	S	-
Sspon.04G0016930-3C	FGES(1)PNGDELDVSR	[STY]P...	289	S	-
Sspon.04G0017040-3C	EDLDLSDSDS(1)EDAESR	...S.[STY]....	17	S	-
Sspon.04G0017040-3C	EDLDLSDS(0.983)DSEDAESR	[STY]DS...	15	S	-
Sspon.04G0017040-3C	EDLDLS(0.933)DSDSEDAESR	[STY]DS...	13	S	-
Sspon.04G0017040-3C	YSVSDS(0.968)PEAPLVVATPMK	...S...[STY]P...	626	S	-
Sspon.04G0017040-3C	YSVSDS(0.947)PEAPLVVAT(1)PMK	...S...[STY]P...	635	T	-
Sspon.04G0017150-2B	IVGASGEVS(1)E	-	632	S	-
Sspon.04G0017150-2B	LPS(1)PPPVKE	[STY]P...	364	S	-
Sspon.04G0017550-4D	HDVPVYDGSWTEWAQS(0.802)DSDYPK	[STY]DS...	204	S	-
Sspon.04G0017550-4D	ASGFNVENAS(1)PDDAVLK	[STY]P...	116	S	-
Sspon.04G0017770-2P	GANEEVSS(0.82)INVDDDPNGSYERS(0.772)PNAATAK	...S...[STY]P...	257	S	-
Sspon.04G0017770-2P	GANEEVSS(0.755)INVDDDPNGSYERS(0.851)PNAATAK	...S...[STY]P...	271	S	-
Sspon.04G0017770-2P	SIPYST(0.969)S(0.985)EEAKAVK	...S.[STY]....	286	T	-
Sspon.04G0017770-2P	SIPYST(0.969)S(0.985)EEAKAVK	...S.[STY]....	287	S	-
Sspon.04G0017770-2P	ETLLS(1)GDDKEDHEIQLK	[STY]G...	161	S	-
Sspon.04G0017770-2P	SLS(0.99)VS(1)DNNDDRKK	...RS.[STY]....	146	S	-
Sspon.04G0017770-2P	SLS(0.989)VS(1)DNNDDR	...RS.[STY]....	148	S	-
Sspon.04G0017770-2P	S(0.995)LSVSDNNDDR	...S..[STY]....	144	S	-
Sspon.04G0018430-3C	ATAAGSDEHSTSPTRS(0.941)R	-	219	S	-
Sspon.04G0018430-3C	ATAAGSDEHST(0.876)PTRS(0.9)R	[STY]P.R...	215	S	-
Sspon.04G0018430-3C	PFVEWLQSAES(1)EEEDDE	...S..[STY]....	439	S	-
Sspon.04G0018430-3C	ATAAGSDEHDS(0.877)TS(0.752)PTRS(0.939)R	[STY]P.R...	213	S	-
Sspon.04G0018470-2B	VHACVGGT(1)S(1)VREDQR	-	148	S	-
Sspon.04G0018470-2B	VHACVGGT(1)S(1)VREDQR	-	147	T	-
Sspon.04G0018470-2B	AGMAPEGS(1)QFDAK	-	9	S	-
Sspon.04G0018480-2C	TSSDWDAPDAT(1)PGIGR	[STY]P...	226	T	-
Sspon.04G0018480-2C	MVDADAT(1)PAAGGAT(0.999)PGAT(0.933)PSGAWDAT(0.888)PK	[STY]P...	277	T	-
Sspon.04G0018480-2C	MVDADAT(1)PAAGGAT(0.999)PGAT(0.852)PSGAWDAT(0.966)PK	[STY]P...	285	T	-
Sspon.04G0018480-2C	MVDADAT(1)PAAGGAT(0.999)PGAT(0.852)PSGAWDAT(0.966)PK	[STY]P...	273	T	-
Sspon.04G0018480-2C	MVDADAT(1)PAAGGAT(0.999)PGAT(0.852)PSGAWDAT(0.966)PK	[STY]P...	266	T	-
Sspon.04G0018480-2C	LPGGV(1)PT(1)PGKK	[STY]P...	293	T	-
Sspon.04G0018480-2C	LPGGV(1)PT(1)PGKK	[STY]P...	295	T	-
Sspon.04G0018480-2C	LLAT(1)PT(1)PLGT(0.999)PLYAIPENR	[STY]P...	415	T	-
Sspon.04G0018480-2C	LLAT(1)PT(1)PLGT(0.985)PLYAIPENR	[STY]P...	411	T	-
Sspon.04G0018480-2C	LLAT(1)PT(1)PLGT(0.985)PLYAIPENR	[STY]P...	409	T	-
Sspon.04G0018480-2C	WDET(1)PT(1)PGR	[STY]P.R...	254	T	-
Sspon.04G0018480-2C	WDET(1)PT(1)PGR	[STY]P.R...	256	T	-
Sspon.04G0018480-2C	WDAT(1)PGRVGDAT(1)PS(1)VRR	[STY]P.R...	245	S	-
Sspon.04G0018480-2C	WDAT(1)PGRVGDAT(1)PS(1)VRR	[STY]P.R...	235	T	-
Sspon.04G0018480-2C	WDAT(1)PGRVGDAT(1)PS(1)VRR	[STY]P.R...	243	T	-
Sspon.04G0018820-1P	LMVQEVAEIHGS(1)S(1)CGSSE	[STY]..S...	750	S	-
Sspon.04G0018820-1P	LMVQEVAEIHGS(1)S(1)CGSSE	[STY]..S...	749	S	-
Sspon.04G0018820-1P	TVS(0.955)LEELQR	[STY]..E...	516	S	-
Sspon.04G0019230-2C	GFASAPASAAGGS(0.997)PR	[STY]P.R...	35	S	-
Sspon.04G0019310-3C	S(0.99)PTTTPS(0.995)PAPVAAPASK	[STY]P...	2	S	-
Sspon.04G0019310-3C	S(0.987)PTTT(0.997)PS(1)PAPVAAPASK	...S...[STY]P...	6	T	-
Sspon.04G0019310-3C	S(0.987)PTTT(0.997)PS(1)PAPVAAPASK	...S...[STY]P...	8	S	-
Sspon.04G0019500-1A	GSTDAIS(1)GDEDAWR	[STY]..DE...	78	S	-
Sspon.04G0019890-4D	SKERGS(0.995)PDYGR	[STY]P...	217	S	-
Sspon.04G0019890-4D	ERGS(1)PDYGRS(0.988)K	[STY]P...	212	S	-
Sspon.04G0019890-4D	ERGS(1)PDYGR	[STY]P...	206	S	-

Sspon.04G0019890-4D	GVS(1)PINGGR	[STY]P...	234	S	-
Sspon.04G0019890-4D	RRS(1)PS(0.999)PYGR	..R.R..[STY]P...	196	S	-
Sspon.04G0019890-4D	RRS(1)PS(0.986)PYGR	..R.R..[STY]P...	194	S	-
Sspon.04G0019890-4D	RS(0.957)PSPY(0.865)GR	[STY]PSP...	198	Y	-
Sspon.04G0019890-4D	S(0.982)PTNARPTK	...S...[STY]P...	87	S	-
Sspon.04G0019930-3D	QCASTSAEEPDEPPLS(0.874)PTSEK	[STY]P...	86	S	-
Sspon.04G0019930-3D	MEDWDS(1)EDFQPVAPVVK	-	6	S	-
Sspon.04G0020380-4D	DMGTEMT(1)PIAS(0.991)QEPSR	[STY]P...	66	S	-
Sspon.04G0020380-4D	DMGTEMT(1)PIAS(0.991)QEPSR	[STY]P...	62	T	-
Sspon.04G0020470-3D	LTYLSGSGEGS(0.777)AER	[STY].E...	1624	S	-
Sspon.04G0020470-3D	EIDDEDLEES(0.947)DEDSEER	[STY]DE...	1370	S	-
Sspon.04G0020470-3D	LTYLS(0.854)GSGEGSAER	[STY].S...	1618	S	-
Sspon.04G0020720-3C	PGLAASDNS(0.994)PPSAAPPPR	[STY]P...	10	S	-
Sspon.04G0020720-3C	RAPPS(0.956)PSPSASSR	[STY]PSP...	32	S	-
Sspon.04G0020720-3C	LSS(0.982)PLPR	[STY]P...	23	S	-
Sspon.04G0021070-1A	EFEEMS(1)EQYVAVTK	-	176	S	-
Sspon.04G0021430-1P	EVPSLGAS(1)PLQEQNQK	[STY]P...	1155	S	-
Sspon.04G0021430-1P	EVPSLGAS(0.991)AS(1)PLQEQNQK	[STY]P...	1153	S	-
Sspon.04G0021430-1P	APFGHS(0.999)PVDPR(0.937)PSYSK	[STY]P...	318	T	-
Sspon.04G0021430-1P	APFGHS(1)PVDPR(0.913)PSYSK	[STY]P...	312	S	-
Sspon.04G0021430-1P	NVS(1)GNLSWR	..R..[STY]....	674	S	-
Sspon.04G0021710-2P	NS(1)QQQLQLR	-	184	S	-
Sspon.04G0021750-1B	WVAGSAEVS(1)DDE	[STY]DD...	518	S	-
Sspon.04G0022560-1B	AAVEPDQS(0.99)PITQSGAADAS(0.96)PSR	[STY]P.R...	1841	S	-
Sspon.04G0022560-1B	AAVEPDQS(1)PITQSGAADAS(0.855)PSR	[STY]P.R...	1830	S	-
Sspon.04G0022560-1B	DMEESSS(0.948)PFR	[STY]P.R...	1523	S	-
Sspon.04G0022560-1B	SDVDM(1)EIEGETTAER	-	1812	S	-
Sspon.04G0022560-1B	TADAS(0.999)PAREPS(1)PNPVQAGATSR	[STY]P.R...	1849	S	-
Sspon.04G0022560-1B	TADAS(0.993)PAREPS(1)PNPVQAGATSR	[STY]P.R...	1855	S	-
Sspon.04G0023700-1B	AAYPDVEVSPPS(0.993)PPR	[STY]P.R...	626	S	-
Sspon.04G0024300-3D	APHTTAAGGGGSGGGGEDEVSEAAAAS(1)PALR	[STY]P...	28	S	-
Sspon.04G0024860-1P	YLKS(1)PDPLEEQR	[STY]P...	669	S	-
Sspon.04G0024860-1P	S(1)VS(1)PADPSVAGQWK	[STY]P...	241	S	-
Sspon.04G0024860-1P	S(1)VS(1)PADPSVAGQWK	[STY]P...	243	S	-
Sspon.04G0024970-2C	QLEEQEILGEAEDS(1)DDDLAAIIR	[STY]DD...	363	S	-
Sspon.04G0025320-2C	LEYEEGELSEQAEAS(0.999)PPK	[STY]P...	400	S	-
Sspon.04G0025590-2D	ADVLPVAAAEVDQADVS(1)R	-	53	S	-
Sspon.04G0025680-3D	FKAHSPTYS(0.911)AHSSSK	[STY]..S...	386	S	-
Sspon.04G0025680-3D	FKAHS(0.961)PTYSAHSSSK	[STY]P...	382	S	-
Sspon.04G0025740-3D	VAMS(1)CEGCAGAVR	[STY].E...	13	S	-
Sspon.04G0026370-1P	DSNIILS(1)PK	[STY]P...	237	S	-
Sspon.04G0026410-1B	VLNSGHPYS(0.983)L	-	212	S	-
Sspon.04G0026550-2D	RPPQAAANNADSSEADS(0.992)ESD TDVQAFQMR	[STY].S...	64	S	-
Sspon.04G0026550-2D	RPPQAAANNADSSEADS(0.986)ES(0.875)DTDVQAFQMR	...S.[STY]....	66	S	-
Sspon.04G0026550-2D	RPPQAAANNADSS(0.851)EADS(0.956)ESD TDVQAFQMR	[STY]..D...D	60	S	-
Sspon.04G0026550-2D	RPPQAAANNADS(0.798)SEADS(0.962)ESD TDVQAFQMR	[STY].E...	59	S	-
Sspon.04G0026550-2D	LSEEAATTAS(0.885)PSK	[STY]P...	387	S	-
Sspon.04G0026550-2D	LSEEAATT(0.803)ASPSK	[STY].S...	385	T	-
Sspon.04G0026610-2C	EDSVTVS(0.865)TDVKDGNPDGYKK	-	572	S	-
Sspon.04G0026610-2C	EDSVT(0.869)VSTDVKDGNPDGYKK	...S.[STY]....	570	T	-
Sspon.04G0026610-2C	LVET(1)ALDS(1)KLR	-	508	S	-
Sspon.04G0026610-2C	LVET(1)ALDS(1)KLR	-	504	T	-
Sspon.04G0026610-2C	LDS(1)IQDMDIDPPERS(1)R	...R..[STY]....	528	S	-
Sspon.04G0026610-2C	LDS(1)IQDMDIDPPERS(1)R	...R..[STY]....	540	S	-
Sspon.04G0026610-2C	EDS(0.872)VTVST(0.874)DVKDGNPDGYKK	...R..[STY]....	568	S	-
Sspon.04G0026610-2C	EDS(0.872)VTVST(0.874)DVKDGNPDGYKK	...R..[STY]....	573	T	-
Sspon.04G0027390-2C	KYDDPS(1)PPRR	[STY]P...	16	S	-
Sspon.04G0027410-1B	AASASAS(0.991)PPR	[STY]P.R...	8	S	-
Sspon.04G0027470-2C	TRS(0.976)PS(0.999)PLWDR	[STY]PSP...	44	S	-
Sspon.04G0027470-2C	TRS(0.976)PS(0.999)PLWDR	[STY]PSP...	46	S	-
Sspon.04G0028050-2C	DSIELGLDAES(1)PR	[STY]PR...	701	S	-
Sspon.04G0029020-3D	DMVTLS(0.999)SDSDASLGNSPSR	...S..[STY]....	89	S	-
Sspon.04G0029020-3D	DMVTLS(0.797)SDSDASLGNSPSR	[STY]..S...	83	S	-
Sspon.04G0029120-2C	ALQAQAQQATSS(0.893)PS(0.833)PSPS(0.796)PTR	...S.[STY]P...R	20	S	-
Sspon.04G0029120-2C	ALQAQAQQATSS(0.893)PS(0.833)PSPS(0.796)PTR	...S.[STY]P...R	16	S	-
Sspon.04G0029120-2C	ALQAQAQQATSS(0.893)PS(0.833)PSPS(0.796)PTR	...S.[STY]P...R	14	S	-
Sspon.04G0029830-1B	S(1)GEEENAAELK	[STY].E...	2	S	-
Sspon.04G0030220-3D	QAS(1)S(1)ELLDVVK	[STY].E...	664	S	-
Sspon.04G0030220-3D	QAS(1)S(1)ELLDVVK	[STY].E...	665	S	-
Sspon.04G0030220-3D	VAT(1)PES(1)PAPAAAANYFK	[STY]P...	287	S	-
Sspon.04G0030220-3D	VAT(1)PES(1)PAPAAAANYFK	[STY]P...	284	T	-
Sspon.04G0030340-1P	AEQFYTVAS(0.996)DSETTGEDK	[STY]DS...	10	S	-
Sspon.04G0030610-1C	SDSMNGLRS(0.946)GSTSPSLVR	[STY].S.SP..	264	S	-
Sspon.04G0030610-1C	STT(0.759)PDPQLIR	...S.[STY]P...R	298	T	-
Sspon.04G0030610-1C	QQS(0.958)SEWLGR	...R..[STY]....	182	S	-
Sspon.04G0030610-1C	SGS(0.978)TS(0.97)PSLVR	...S...[STY]P...	268	S	-

Sspon.04G0030610-1C	SGS(0.978)TS(0.97)PSLVR	...S...[STY]P...	266	S	-
Sspon.04G0030610-1C	T(1)PS(1)PCLPPVGV	[STY]PSP...	309	S	-
Sspon.04G0030610-1C	T(1)PS(1)PCLPPVGV	[STY]PSP...	307	T	-
Sspon.04G0030650-1C	SEPLS(0.997)PPDYS(0.795)PR	...S...[STY]P...	51	S	-
Sspon.04G0030650-1C	SEPLS(0.997)PPDYS(0.795)PR	...S...[STY]P...	46	S	-
Sspon.04G0030940-1P	NDERHPNPANAGDHVAVS(1)PVVS(1)PAK	...S...[STY]P...	314	S	-
Sspon.04G0030940-1P	NDERHPNPANAGDHVAVS(1)PVVS(1)PAK	...S...[STY]P...	318	S	-
Sspon.04G0030940-1P	QESVFAQQSSS(0.994)PPQAK	-	218	S	-
Sspon.04G0030940-2P	NDERHPNPANAGDHVAVS(1)PVVS(1)PAK	...S...[STY]P...	317	S	-
Sspon.04G0030940-2P	NDERHPNPANAGDHVAVS(1)PVVS(1)PAK	...S...[STY]P...	321	S	-
Sspon.04G0031850-1P	VGAIVENIEEAQMPSGNLS(1)E	-	576	S	-
Sspon.04G0031850-1P	MSSSS(0.934)DPEADAEPSTASAAVEGADPAQR	...S...[STY]...	22	S	-
Sspon.04G0031850-1P	AAAS(1)PPPS(1)PPHAK	...S...[STY]P...	5	S	-
Sspon.04G0031850-1P	AAAS(1)PPPS(1)PPHAK	...S...[STY]P...	9	S	-
Sspon.04G0032340-2D	ALDAHTEVAS(1)PVDWTN	[STY]P...	150	S	-
Sspon.04G0033010-2D	TEWTNAPAAS(1)QK	-	504	S	-
Sspon.04G0033150-1C	FSIDMS(1)PVK	...S...[STY]P...	457	S	-
Sspon.04G0033450-1C	FATPATEESTLATEES(0.996)IPATEE	-	866	S	-
Sspon.04G0033500-1C	KKGDVES(1)DVES(1)GELVPGK	[STY].E...	174	S	-
Sspon.04G0033500-1C	KKGDVES(1)DVES(1)GELVPGK	[STY].E...	178	S	-
Sspon.04G0033660-1C	AAEMHNMDS(1)DNDKDR	[STY]D...	179	S	-
Sspon.04G0033660-1C	GRDS(1)RDLSSSSDDLQNDGK	-	199	S	-
Sspon.04G0033660-1C	DLS(0.85)SS(0.946)SDDLQNDGK	...R...[STY]...	205	S	-
Sspon.04G0033660-1C	DLS(1)S(0.996)SSDDLQNDGK	...R...[STY]...	204	S	-
Sspon.04G0033660-1C	DLS(1)S(0.994)SSDDLQNDGK	...R...[STY]...	203	S	-
Sspon.04G0033660-1C	DLS(0.85)SSS(0.993)DDLQNDGK	...S...[STY].D...	206	S	-
Sspon.04G0035160-1D	SNS(0.863)SIPFELYK	...RS.[STY]...	59	S	-
Sspon.04G0036150-1D	AASLS(0.76)LS(0.98)GVVGR	...S.[STY]...	140	S	-
Sspon.04G0036150-1D	AAS(0.999)LS(0.967)LSGVVGR	...R...[STY]...	138	S	-
Sspon.04G0036150-1D	AAS(1)LS(0.932)LSGVVGR	...R...[STY]...	136	S	-
Sspon.04G0037990-1D	SVS(1)EPDFGR	...RS.[STY]...	849	S	-
Sspon.05G0000210-2C	HFAPYQSDPTAS(0.937)S	-	275	S	-
Sspon.05G0000380-1A	MYS(0.992)AASQQPMDYALK	...R...[STY]...	230	S	-
Sspon.05G0000690-1A	QVAHAPQELNS(1)PR	[STY]PR...	18	S	-
Sspon.05G0000690-1A	VDT(0.998)FTKINS(0.999)MPR	-	240	T	-
Sspon.05G0000690-1A	INS(1)MPR	-	246	S	-
Sspon.05G0000690-1A	VGS(1)ATNWAAAWDDAI	...R...[STY]...	252	S	-
Sspon.05G0000690-1A	VDS(1)EGAMCGATFK	...R...[STY]...	227	S	-
Sspon.05G0000700-2T	AS(1)FFGDDGADDLPR	-	3	S	-
Sspon.05G0001240-2D	INGPSTAIS(0.998)PER	[STY]P.R...	353	S	-
Sspon.05G0001240-2D	S(0.854)SEIVSTVR	[STY].E...	453	S	-
Sspon.05G0001290-1A	SSLS(0.999)MQS(0.998)LSSR	...S...[STY]...	255	S	-
Sspon.05G0001290-1A	SSLS(0.999)MQS(0.998)LSSR	...S...[STY]...	252	S	-
Sspon.05G0001580-3D	LEGPQPNPGDGTADAVISEY(0.782)ES	...S.[STY]...	297	Y	-
Sspon.05G0001580-3D	LEGPQPNPGDGTADAVIS(0.889)EYES	-	295	S	-
Sspon.05G0001670-2C	GSDVGGSSSYSLYS(0.922)GR	...S...[STY]...	763	S	-
Sspon.05G0001670-2C	RQPS(1)PLLQQPVVEEK	[STY]P...	65	S	-
Sspon.05G0001710-1A	AVEELIEEPDETIS(0.985)VSSTGPK	[STY]..S...	218	S	-
Sspon.05G0001710-1A	FEELSTNSIVS(1)R	...S...[STY]...	556	S	-
Sspon.05G0001710-1A	SVASYATPEGT(0.942)PMSR	[STY]P...	722	T	-
Sspon.05G0001710-1A	SLASPGSES(0.784)VGR	...S.[STY]...	768	S	-
Sspon.05G0001710-1A	FEELSTNS(0.984)IVS(1)R	...S...[STY]...	553	S	-
Sspon.05G0001710-1A	ITES(0.951)PTDEPAEK	[STY]P...	160	S	-
Sspon.05G0001820-1P	TSMS(0.872)PS(0.995)PPK	...S.[STY]P...R	833	S	-
Sspon.05G0001820-1P	TSMS(0.872)PS(0.995)PPK	...S.[STY]P...R	835	S	-
Sspon.05G0001820-1P	TS(0.975)MSPS(0.959)PPK	...S...[STY]P...	831	S	-
Sspon.05G0001970-2B	GLDIDTIQQNYT(1)V	-	647	T	-
Sspon.05G0001970-2B	GLDIDT(1)IQQNYT(0.98)V	-	641	T	-
Sspon.05G0002010-1P	LELSAVPSSYYS(0.836)GQLDPDR	...S...[STY]...	336	S	-
Sspon.05G0002130-2D	S(1)GQLDPSVLESCK	...R...[STY]...	744	S	-
Sspon.05G0002250-1A	SFEEDS(1)PVFFTDK	[STY]P...	449	S	-
Sspon.05G0002250-1A	S(0.996)EANTTQLELEK	-	2	S	-
Sspon.05G0002370-3D	VKNPDLNRAPS(0.966)PES(0.872)SDAE	[STY]P...	111	S	-
Sspon.05G0002370-3D	VKNPDLNRAPS(0.999)PESSDAE	[STY]P...	108	S	-
Sspon.05G0002390-1A	DFLDAFS(1)PS(1)PPR	[STY]P.R...	49	S	-
Sspon.05G0002390-1A	DFLDAFS(1)PS(1)PPR	[STY]P.R...	51	S	-
Sspon.05G0002470-1P	EDLLGQS(1)K	-	113	S	-
Sspon.05G0002650-1P	EAHNDEDDGT(1)GS(1)DGFELIDVK	[STY]D...	55	S	-
Sspon.05G0002650-1P	EAHNDEDDGT(1)GS(1)DGFELIDVK	[STY]D...	53	T	-
Sspon.05G0002790-1A	KADDGEES(1)LDEDDL	-	275	S	-
Sspon.05G0003020-3D	NEVSS(0.877)PIS(0.999)VLER	[STY]P...	150	S	-
Sspon.05G0003020-3D	NEVSS(0.877)PIS(0.999)VLER	[STY]P...	153	S	-
Sspon.05G0003050-2C	SDDGMAS(0.999)PVVEPPKR	[STY]P...	8	S	-
Sspon.05G0003670-3C	S(0.988)FSLDSFSR	...S.[STY]...	38	S	-
Sspon.05G0003930-2B	HGS(0.875)GSPASGGIHGS(1)PLGK	[STY]P...	445	S	-
Sspon.05G0003930-2B	HGS(0.875)GSPASGGIHGS(1)PLGK	[STY]P...	456	S	-

Sspon.05G0004340-3D	TLDSLDDENGQDS(0.987)ES(0.942)DETGLQR	[STY]DE...	44	S	-
Sspon.05G0004340-3D	TLDSLDDENGQDS(0.987)ES(0.942)DETGLQR	[STY]DE...	42	S	-
Sspon.05G0004410-1A	AS(0.999)PGASAPAEFTQMEAR	[STY]P...	3	S	-
Sspon.05G0004600-1A	T(1)MRNS(1)LNIS(1)MR	-	442	S	-
Sspon.05G0004600-1A	T(1)MRNS(1)LNIS(1)MR	-	446	S	-
Sspon.05G0004600-1A	T(1)MRNS(1)LNIS(1)MR	-	438	T	-
Sspon.05G0004920-1A	VGPDISSADPT(0.962)SQPS(0.815)PA	[STY]P...	1038	T	-
Sspon.05G0004920-1A	VGPDI(0.978)SADPTS(0.998)QPS(1)PA	[STY]P...	1039	S	-
Sspon.05G0004920-1A	VGPDI(1)S(1)ADPTSQPS(0.998)PA	[STY]P...	1034	S	-
Sspon.05G0004920-1A	VGPDI(1)S(1)ADPTSQPS(0.998)PA	[STY]P...	1033	S	-
Sspon.05G0004920-1A	VGPDI(0.978)SADPTS(0.998)QPS(1)PA	[STY]P...	1042	S	-
Sspon.05G0005190-1A	FYMEPDTS(0.878)GAS	...S..[STY]...	1044	S	-
Sspon.05G0005190-1A	FYMEPD(0.981)S(0.866)DSGSMASGAR	[STY]DS...	1036	T	-
Sspon.05G0005190-1A	FYMEPD(0.968)S(0.985)DSGSMASGAR	[STY]DS...	1037	S	-
Sspon.05G0005190-1A	FYMEPD(0.831)SDS(0.865)GSMASGAR	...S..[STY]....	1039	S	-
Sspon.05G0005190-1A	FYMEPD(0.851)SDSGS(0.943)MASGAR	...S..[STY]....	1041	S	-
Sspon.05G0005240-4D	AAKS(1)EVEDDDEQDGNEDDE	-	103	S	-
Sspon.05G0005310-1A	AMAT(1)PLAS(1)PVRK	[STY]P.R...	71	S	-
Sspon.05G0005310-1A	AMAT(1)PLAS(1)PVRK	[STY]P.R...	67	T	-
Sspon.05G0005950-3D	SGKS(0.911)VS(0.993)PNREEPPQANFDVQNK	[STY]P.R...	77	S	-
Sspon.05G0005950-3D	SGKS(0.911)VS(0.993)PNREEPPQANFDVQNK	[STY]P.R...	79	S	-
Sspon.05G0005980-4D	MDGSAGS(0.957)FVAVR	...S..[STY]...	7	S	-
Sspon.05G0006100-1A	ASSLSS(0.907)IDSIMT(0.857)PSR	[STY]P.R...	432	S	-
Sspon.05G0006100-1A	ASSLSS(0.89)IDSIMT(0.812)R	...S..[STY].D...	440	S	-
Sspon.05G0006230-1A	YEAPLVSSSDGECVS(0.841)DPSPGR	[STY]..S...	67	S	-
Sspon.05G0006340-1A	VVYVPPPKPPS(0.998)PVREGS(0.985)EEGSSPR	[STY]P.R...	141	S	-
Sspon.05G0006340-1A	VVYVPPPKPPS(0.998)PVREGS(0.985)EEGSSPR	[STY]P.R...	135	S	-
Sspon.05G0006790-1A	SNLRPLDENDEPRTS(0.8)D	[STY]D...	559	S	-
Sspon.05G0006790-1A	GG(1)PVAQVQDASDDADAR	[STY]P...	4	S	-
Sspon.05G0006880-2B	GYVVDPELGS(1)NEG	[STY].E...	713	S	-
Sspon.05G0007450-3C	SYDQVDFGTSS(0.795)EDGYALTSK	-	922	S	-
Sspon.05G0007450-3C	STS(0.914)LDLGVDPSSR	...RS.[STY]....	482	S	-
Sspon.05G0007450-3C	YAS(0.993)PSLR	[STY]P...	381	S	-
Sspon.05G0007660-1T	DNETLVASELS(0.999)PETNDGDKK	[STY]P...	444	S	-
Sspon.05G0007660-1T	DNETLVASELS(0.932)PET(0.958)NDGDKK	[STY]P...	447	T	-
Sspon.05G0007660-1T	WEFIAEEQDT(1)DPDAPSNIR	[STY]D...	672	T	-
Sspon.05G0007660-1T	EDAVSDKDT(0.999)DEDISLK	[STY]DE...	561	T	-
Sspon.05G0007660-1T	DNETLVAS(0.935)ELSPETNDGDKK	[STY]..S...	441	S	-
Sspon.05G0007660-1T	QKQELTS(0.932)GDEQTPDSSK	[STY].DE...	360	S	-
Sspon.05G0007660-1T	SVSDES(1)PQETSK	[STY]P...	287	S	-
Sspon.05G0007660-1T	LSEKS(0.926)VS(0.998)DESPQETSK	[STY]DE...	284	S	-
Sspon.05G0007660-1T	LSEKS(0.999)VS(0.988)DESPQETSK	[STY]DE...	282	S	-
Sspon.05G0007860-1A	GNVSEAQS(1)DAVEELK	[STY]D...	324	S	-
Sspon.05G0008060-2B	KIDFDAVS(1)DS(1)DKE	[STY]DS...	153	S	-
Sspon.05G0008060-2B	KIDFDAVS(1)DS(1)DKE	[STY]DS...	155	S	-
Sspon.05G0008320-1P	LHS(0.969)FDTK	-	225	S	-
Sspon.05G0008360-2B	RNS(1)FNLSLR	...R..[STY]....	97	S	-
Sspon.05G0008440-3D	MLS(1)QKS(1)MGK	...S..[STY]....	420	S	-
Sspon.05G0008440-3D	MLS(1)QKS(1)MGK	...S..[STY]....	423	S	-
Sspon.05G0008480-4D	AAEEGAMS(0.995)PTR	[STY]P.R...	9	S	-
Sspon.05G0008790-3D	YPS(1)LGSGGGFR	...R..[STY]....	210	S	-
Sspon.05G0008970-1A	APTSSEFDIEQPPVHT(1)PS(1)PR	[STY]PR...	42	T	-
Sspon.05G0008970-1A	APTSSEFDIEQPPVHT(1)PS(1)PR	[STY]PR...	44	S	-
Sspon.05G0008970-1A	TTPSS(0.833)PSAGEFELVER	[STY]P...	51	S	-
Sspon.05G0008970-1T	TAPSSPS(0.997)AGEFELVER	...S..[STY]....	53	S	-
Sspon.05G0008970-1T	T(1)APSS(0.919)PSAGEFELVER	[STY]P...	47	T	-
Sspon.05G0009480-1A	LLGNPEQEDS(1)EEGAPLTR	[STY].E...	435	S	-
Sspon.05G0009700-2B	QAS(1)FPASIGNR	-	243	S	-
Sspon.05G0009790-3C	QAFDEAISELD(0.84)EESYK	[STY].E...	216	S	-
Sspon.05G0009790-3C	DNLTLWTS(0.997)DIS(1)EDPAEEIR	...S..[STY].D...	239	S	-
Sspon.05G0009790-3C	DNLTLWTS(0.997)DIS(1)EDPAEEIR	...S..[STY].D...	242	S	-
Sspon.05G0009790-3C	EAPKRDS(0.988)SEGQ	[STY].E...	257	S	-
Sspon.05G0010190-1P	LARS(0.972)PTAS(0.972)PPAAAAER	...S..[STY]P...	7	S	-
Sspon.05G0010190-1P	LARS(0.829)PTAS(0.996)PPAAAAER	...S..[STY]P...	11	S	-
Sspon.05G0010420-1A	DSTS(0.933)NPVS(1)PVLGR	...S..[STY]P...	627	S	-
Sspon.05G0010420-1A	DSTS(0.823)NPVS(1)PVLGR	...S..[STY]P...	631	S	-
Sspon.05G0010950-4D	ESSVGS(0.998)EGAKS(0.999)MEEPLASR	...S..[STY]....	236	S	-
Sspon.05G0010950-4D	ESS(0.808)VGS(0.997)EGAKS(0.999)MEEPLASR	...S..[STY]....	233	S	-
Sspon.05G0010950-4D	ESS(0.808)VGS(0.997)EGAKS(0.999)MEEPLASR	...S..[STY]....	241	S	-
Sspon.05G0010970-1P	GGDFDLESGS(0.996)PR	[STY]PR...	29	S	-
Sspon.05G0011000-3D	RLS(1)PS(0.999)AS(0.988)PTR	...S..[STY]P...R	42	S	-
Sspon.05G0011000-3D	RLS(1)PS(1)AS(0.918)PTR	...S..[STY]P...R	40	S	-
Sspon.05G0011000-3D	RLS(1)PS(1)AS(0.918)PTR	...S..[STY]P...R	38	S	-
Sspon.05G0011000-3D	SRS(0.966)RS(0.993)PQYLPDGK	..R.R..[STY]P...	71	S	-
Sspon.05G0011000-3D	SRS(0.966)RS(0.993)PQYLPDGK	..R.R..[STY]P...	73	S	-
Sspon.05G0011310-2B	DLNLIGS(1)PEVADMR	[STY]P...	589	S	-

Sspon.05G0011390-2D	GGAPAEFQPS(1)FR	-	144	S	-
Sspon.05G0012470-1A	ATADGEPQPVATDPAQVPAPAPS(0.796)PSPSPAK	[STY]P..SP..	24	S	-
Sspon.05G0012530-1A	ASSISGHTQSISSSES(0.978)PS(0.997)PVGK	...S...[STY]P...	178	S	-
Sspon.05G0012530-1A	ASSISGHTQSISSSES(0.978)PS(0.997)PVGK	...S...[STY]P...	180	S	-
Sspon.05G0013010-4D	VEDLWEVAEPQLS(0.971)PSEK	[STY]P...	27	S	-
Sspon.05G0013010-4D	MES(1)PRS(1)PEAEIGHR	[STY]PR...	3	S	-
Sspon.05G0013010-4D	MES(1)PRS(1)PEAEIGHR	[STY]PR...	6	S	-
Sspon.05G0013010-4D	LGS(1)FTFR	...R..[STY]....	135	S	-
Sspon.05G0013160-3C	QSS(0.957)QQGFTSTR	...R..[STY]....	77	S	-
Sspon.05G0013190-2B	ELEPES(1)PVTQCDFDR	[STY]P...	204	S	-
Sspon.05G0013520-1A	NS(1)DDGYSSDSVLK	[STY]DD...	469	S	-
Sspon.05G0013520-1A	NS(1)DDGYSS(0.781)DSVLK	[STY]DS...	475	S	-
Sspon.05G0013650-3C	MDSATVALAS(1)PAS(1)DDRR	[STY]P...	10	S	-
Sspon.05G0013650-3C	MDSATVALAS(1)PAS(1)DDRR	[STY]P...	13	S	-
Sspon.05G0014330-3C	MDMEDASGSSSS(0.858)PAILR	...S.[STY]P...R	12	S	-
Sspon.05G0014350-2P	NIDS(1)DDDEETEFR	[STY]DD...	471	S	-
Sspon.05G0015270-1A	LAS(1)EELANDWDNKR	...R..[STY]....	230	S	-
Sspon.05G0015390-4D	IPS(1)GIDLPSDDVAADK	[STY]..D...D	431	S	-
Sspon.05G0015400-2B	SMLGSYS(0.945)PR	[STY]PR...	195	S	-
Sspon.05G0016000-2B	SLS(0.971)FGPEESPR	...RS.[STY]....	11	S	-
Sspon.05G0016020-2B	MNMS(1)LPVS(0.841)PCSS(0.918)PLR	[STY]P.R...	281	S	-
Sspon.05G0016020-2B	MNMS(1)LPVS(0.933)PCSSPLR	...S...[STY]P...	277	S	-
Sspon.05G0016020-2B	MNMS(1)LPVS(0.933)PCSSPLR	...S...[STY]P...	273	S	-
Sspon.05G0016410-1A	SGTDQFDLTDT(0.996)D	[STY]D...	676	T	-
Sspon.05G0016410-1A	SGTDQFDLT(0.995)DTD	[STY]D...	674	T	-
Sspon.05G0016710-4D	VPPLGPHGDEAGGS(0.781)AGGSR	-	423	S	-
Sspon.05G0016920-3C	GGPGS(1)PLPLKLE	[STY]P...	426	S	-
Sspon.05G0018740-3C	VSGFQYS(0.998)PS(1)PQR	[STY]P.R...	252	S	-
Sspon.05G0018740-3C	VSGFQYS(0.998)PS(1)PQR	[STY]P.R...	254	S	-
Sspon.05G0018800-1A	LTTLKWEMY(0.999)ELK	-	740	Y	-
Sspon.05G0018860-4D	NEGSWS(0.79)GSESSASER	...S.[STY]....	59	S	-
Sspon.05G0018860-4D	NEGS(0.959)WSGSESSASER	[STY].S...	57	S	-
Sspon.05G0018860-4D	S(1)VPFLAQDCETDIDTR	...S...[STY]....	69	S	-
Sspon.05G0018880-1P	SGS(0.937)MDGATS(0.994)EGESALSGGLPDYAK	...RS.[STY]....	138	S	-
Sspon.05G0018880-1P	SGS(0.937)MDGATS(0.994)EGESALSGGLPDYAK	...RS.[STY]....	144	S	-
Sspon.05G0019420-2P	AAVPEPGS(1)PK	[STY]P...	123	S	-
Sspon.05G0019540-2B	TLS(1)GGLQSPR	...R..[STY]....	348	S	-
Sspon.05G0019670-2B	S(0.986)VDTISSCLK	...S.[STY]....	42	S	-
Sspon.05G0020310-4D	DLHMLVWS(0.912)SSAS(0.998)PVS(1)ER	...S...[STY]P...	327	S	-
Sspon.05G0020310-4D	DLHMLVWS(0.842)SSAS(1)PVS(1)ER	...S...[STY]P...	331	S	-
Sspon.05G0020310-4D	DLHMLVWS(0.842)SSAS(1)PVS(1)ER	...S...[STY]P...	334	S	-
Sspon.05G0020310-4D	LGSNS(0.973)TAQLYPK	...S.[STY]....	394	S	-
Sspon.05G0020310-4D	LGS(1)NSTAQLYPK	[STY].S...	392	S	-
Sspon.05G0020310-4D	VDS(1)DVVS(1)LAR	...R..[STY]....	190	S	-
Sspon.05G0020310-4D	VDS(1)DVVS(1)LAR	...R..[STY]....	194	S	-
Sspon.05G0020310-4D	LGS(0.997)NST(0.998)AQLYPK	...S...[STY]....	395	T	-
Sspon.05G0020310-4D	VS(0.98)NLSGVEIYS(0.999)LQSSR	[STY]..S...	260	S	-
Sspon.05G0020310-4D	VS(1)NLS(1)GVEIYS(0.996)LQSSR	...S...[STY]....	251	S	-
Sspon.05G0020310-4D	VS(1)NLS(1)GVEIYS(0.996)LQSSR	...S...[STY]....	254	S	-
Sspon.05G0020310-4D	VS(1)NLS(1)GVEIYSLQS(0.851)SRNPT(0.922)PR	...S...[STY]P...	263	S	-
Sspon.05G0020310-4D	VS(1)NLS(1)GVEIYSLQS(0.851)SRNPT(0.922)PR	...S...[STY]P...	268	T	-
Sspon.05G0020320-1A	MEDQS(1)PDHIS(1)VGS(1)APKK	[STY]P...	5	S	-
Sspon.05G0020320-1A	MEDQS(1)PDHIS(1)VGS(1)APKK	[STY]P...	10	S	-
Sspon.05G0020320-1A	MEDQS(1)PDHIS(1)VGS(1)APKK	[STY]P...	13	S	-
Sspon.05G0021080-1A	IGDIGT(0.827)SELSTTLYEK	[STY].E...	190	T	-
Sspon.05G0021500-3D	EGLMHLGADD(0.992)S	-	230	S	-
Sspon.05G0022030-2D	VAEANDVSS(0.751)TGITK	-	329	S	-
Sspon.05G0022390-2D	NLSYQYS(0.853)TGADGR	-	661	S	-
Sspon.05G0022390-2D	IEMIS(1)NADNDR	-	672	S	-
Sspon.05G0022390-2D	S(1)IHLTSSLS(0.985)TK	...RS.[STY]....	642	S	-
Sspon.05G0022390-2D	S(1)IHLTSSLS(0.985)TK	...RS.[STY]....	634	S	-
Sspon.05G0023810-1B	KPAAPPS(1)PGADGLS(1)E	[STY]P...	256	S	-
Sspon.05G0023810-1B	KPAAPPS(1)PGADGLS(1)E	[STY]P...	263	S	-
Sspon.05G0025270-1P	TDS(1)FSDLVNR	[STY].S...	229	S	-
Sspon.05G0025290-2C	ADEQAQS(0.977)SSCVELQR	[STY].S...	168	S	-
Sspon.05G0025570-1T	NPPTESLES(0.978)EDEDGFPVSFSESK	...S...[STY].D...	217	S	-
Sspon.05G0025670-1B	LQSLNIS(1)PK	[STY]P.R...	330	S	-
Sspon.05G0025670-1B	ANMST(0.919)PVSPCSSPLR	[STY]P...	261	T	-
Sspon.05G0025670-1B	ANMS(0.871)TPVS(0.991)PCSS(0.968)PLR	[STY]P.R...	268	S	-
Sspon.05G0025670-1B	ANMS(0.808)TPVS(0.999)PCSS(0.937)PLR	[STY]P.R...	264	S	-
Sspon.05G0025670-1B	ANMS(0.991)TPVS(0.997)PCSSPLR	...S...[STY]P...	260	S	-
Sspon.05G0025680-1P	ESSAS(0.929)VIS(0.831)SNVSK	...S...[STY]....	875	S	-
Sspon.05G0025680-1P	ESSAS(0.929)VIS(0.831)SNVSK	...S...[STY]....	872	S	-
Sspon.05G0025730-1B	AAVSSPS(0.93)PSPISV	[STY]PSP...	298	S	-
Sspon.05G0025730-1B	AAVSS(0.89)PSPSPISV	[STY]P..SP..	296	S	-
Sspon.05G0025860-2C	MSLQGS(1)PPAQPEPK	...S...[STY]P...	21	S	-

Sspon.05G0026360-3D	STGGADKPGS(0.759)GGGGAVK	[STY]G...	11	S	-
Sspon.05G0026360-3D	ST(0.87)GGADKPGSGGGGAVK	[STY]G...	3	T	-
Sspon.05G0027560-1T	SGDS(0.77)PLAAPSSSSADDR	[STY]P...	33	S	-
Sspon.05G0027780-2C	AASAAPSGS(0.99)PS(0.997)PKR	[STY]P.R...	38	S	-
Sspon.05G0027780-2C	AASAAPSGS(0.99)PS(0.997)PKR	[STY]P.R...	40	S	-
Sspon.05G0029560-1B	MRAASTPSSS(0.996)RR	...S.[STY]....	10	S	-
Sspon.05G0029760-2C	SLS(0.999)WSVSR	...RS.[STY]....	302	S	-
Sspon.05G0029760-2C	SLS(0.99)WSVS(0.941)R	...RS.[STY]....	306	S	-
Sspon.05G0029980-2C	ASPDINVSLT(1)PQE	[STY]P...	351	T	-
Sspon.05G0029980-2C	AS(1)PDINVSLTPQE	[STY]P...	343	S	-
Sspon.05G0030930-1P	FLS(1)GPTS(0.997)PTK	...S...[STY]P...	230	S	-
Sspon.05G0030930-1P	FLS(1)GPTS(0.997)PTK	...S...[STY]P...	226	S	-
Sspon.05G0033160-2D	VEEKEES(1)DDDMGFSLFD	-	102	S	-
Sspon.05G003360-2D	SVS(0.982)VDTLK	...RS.[STY]....	184	S	-
Sspon.05G0037470-1D	SSGPQS(1)GGVT(1)PMAR	...S...[STY]P...	137	T	-
Sspon.05G0037470-1D	SNYS(0.965)GSLSSSVPGAGGSAR	...S...[STY]....	95	S	-
Sspon.05G0037470-1D	SNYS(0.828)GSLSSSVPGAGGS(1)AR	...S...[STY]....	108	S	-
Sspon.05G0037470-1D	NTS(0.999)FGGAASNS(0.993)GPVSNAGGR	...R...[STY]....	74	S	-
Sspon.05G0037470-1D	NTS(0.959)FGGAASNS(1)GPVSNAGGR	...R...[STY]....	82	S	-
Sspon.05G0037470-1D	KVS(1)GPLDSAAS(1)MK	...S...[STY]....	177	S	-
Sspon.05G0037470-1D	KVS(1)GPLDSAAS(1)MK	...S...[STY]....	185	S	-
Sspon.05G0037470-1D	SNS(1)GPLNK	-	115	S	-
Sspon.05G0037470-1D	SS(0.925)GPQSGGVTPMAR	[STY]G...	129	S	-
Sspon.05G0037470-1D	SS(0.924)GPQS(1)GGVTPMAR	[STY]G...	133	S	-
Sspon.05G0037470-1D	S(1)GPLGNAPSR	...S...[STY]....	62	S	-
Sspon.05G0037510-1D	YLS(0.963)PTLS(0.943)PVAELAK	...S...[STY]P...	259	S	-
Sspon.05G0037510-1D	YLS(0.963)PTLS(0.943)PVAELAK	...S...[STY]P...	255	S	-
Sspon.05G0038190-1D	LITDASVSS(0.856)PISR	[STY]P...	206	S	-
Sspon.05G0038190-1D	LITDASVS(0.803)SPISR	...S.[STY]....	205	S	-
Sspon.06G0000140-1A	DTSAMPLNVS(0.966)SAGS(0.971)VNDSLK	...S...[STY]....	824	S	-
Sspon.06G0000330-1A	DNLTWTSMDMQEDGS(1)DEMR	[STY]DE...	285	S	-
Sspon.06G0000480-3C	S(1)AS(1)PHKS(1)PPPR	...S...[STY]P...	251	S	-
Sspon.06G0000480-3C	S(1)AS(1)PHKS(1)PPPR	...S...[STY]P...	253	S	-
Sspon.06G0000480-3C	S(1)AS(1)PHKS(1)PPPR	...S...[STY]P...	257	S	-
Sspon.06G0000500-2B	DISPSLAGEAMS(1)ND	-	166	S	-
Sspon.06G0000500-2B	DISPS(0.918)LAGEAMSND	...S.[STY]....	159	S	-
Sspon.06G0000500-2B	DIS(0.998)PSLAGEAMSND	[STY]P...	157	S	-
Sspon.06G0001080-3C	VAHAS(1)PDLR	[STY]P...	257	S	-
Sspon.06G0001310-1A	QVAEIAAMCLRT(1)K	-	38	T	-
Sspon.06G0001440-2B	AAAAAAPTPAES(1)PR	-	114	S	-
Sspon.06G0001600-1A	YVNNEES(0.873)EEESGELTMADR	[STY].E...	311	S	-
Sspon.06G0001680-1A	FLPPS(0.966)PSSSSPPK	[STY]P...	20	S	-
Sspon.06G0001750-4D	LDEAS(1)DRENDMMMLVGNR	[STY]D...	250	S	-
Sspon.06G0002040-1A	GQYYDVS(0.999)NVVDPYAK	-	176	S	-
Sspon.06G0002200-1A	SLS(0.998)VDAVK	...RS.[STY]....	341	S	-
Sspon.06G0002310-3C	AQGSSPPEIRS(1)PDDR	[STY]P...	13	S	-
Sspon.06G0002310-3C	AQGSS(0.859)PPPEIRS(1)PDDR	[STY]P...	6	S	-
Sspon.06G0002350-3C	SGS(0.956)GKPDPEEADR	...RS.[STY]....	21	S	-
Sspon.06G0002420-4D	GDES(1)DGEAEYLFK	[STY]D...	5	S	-
Sspon.06G0002450-3D	DGSGQQDWNS(1)PARLPVEK	[STY]P.R...	894	S	-
Sspon.06G0002450-3D	FSLTSTD(1)PEER	[STY]P...	691	S	-
Sspon.06G0002450-3D	DNVS(1)PVKPGS(1)PK	[STY]P...	876	S	-
Sspon.06G0002450-3D	DNVS(1)PVKPGS(1)PK	[STY]P...	882	S	-
Sspon.06G0002450-3D	SVGT(1)DDDLLQLGK	...S...[STY].D...	365	T	-
Sspon.06G0002580-2B	YLTQDDWS(1)PTETK	[STY]P...	237	S	-
Sspon.06G0002930-4D	ALLLQEQSTSPSNGS(0.768)SR	...S...[STY]....	685	S	-
Sspon.06G0002930-4D	ALLLQEQSTS(0.841)PSNGSSR	...S.[STY]P...R	680	S	-
Sspon.06G0002970-2D	LPDS(1)LGEMVIR	-	812	S	-
Sspon.06G0003120-1A	AALLPSSSED(0.849)TQLATTSMKD	...S...[STY]....	262	S	-
Sspon.06G0003120-1A	AALLPS(0.941)S(0.906)EDSTQLATTSMKD	[STY].E...	259	S	-
Sspon.06G0003120-1A	AALLPS(0.941)S(0.906)EDSTQLATTSMKD	[STY].E...	258	S	-
Sspon.06G0003160-1A	GSDVGPYPES(0.981)PR	[STY]PR...	928	S	-
Sspon.06G0003160-1A	MDTLLS(0.979)PSSK	[STY]P...	966	S	-
Sspon.06G0003160-1A	SISS(0.757)PNPMS(0.999)PPR	[STY]P.R...	429	S	-
Sspon.06G0003160-1A	SISS(0.752)PNPMS(1)PPR	[STY]P.R...	434	S	-
Sspon.06G0003220-4D	DNLTWTS(1)EEGIEEGK	...S...[STY]....	237	T	-
Sspon.06G0003650-3C	SLS(1)MDSFMGK	...RS.[STY]....	249	S	-
Sspon.06G0003650-3C	AGS(1)AAES(0.805)SENAESQSTSVDRK	...R...[STY]....	222	S	-
Sspon.06G0003650-3C	AGS(1)AAES(0.805)SENAESQSTSVDRK	...R...[STY]....	218	S	-
Sspon.06G0003650-3C	S(1)LS(0.995)MDSFMGK	...RS.[STY]....	247	S	-
Sspon.06G0003780-1A	QEGLYVADHS(0.986)PDLS(0.89)DKEGDQGGSR	[STY]P...	280	S	-
Sspon.06G0003780-1A	QEGLYVADHS(0.986)PDLS(0.89)DKEGDQGGSR	[STY]P...	276	S	-
Sspon.06G0003780-1A	AVS(0.997)LSLETAER	...R...[STY]....	253	S	-
Sspon.06G0003980-3D	ADEAAQAPS(0.914)PSR	[STY]P.R...	10	S	-
Sspon.06G0004410-2B	TETLQSQADS(0.996)FHR	-	197	S	-
Sspon.06G0004510-2B	NAPLS(0.998)EASS(0.911)PGPSEYR	...S...[STY]P...	263	S	-

Sspon.06G0004510-2B	NAPLS(0.999)EASS(0.864)PGPSEYR	...S...[STY]P...	259	S	-
Sspon.06G0004620-1A	S(0.997)ALYS(0.814)PTESR	...S...[STY]P...	675	S	-
Sspon.06G0004620-1A	S(0.997)ALYS(0.814)PTESR	...S...[STY]P...	671	S	-
Sspon.06G0004690-1A	NELETQMSELGS(1)PR	...S...[STY]P...	636	S	-
Sspon.06G0004940-1T	STS(0.755)TPFMSTSDGK	...RS.[STY]....	177	S	-
Sspon.06G0004940-2B	STS(0.938)TPFMNTTGGK	...RS.[STY]....	534	S	-
Sspon.06G0006090-3C	DNLTLWTSDLTDEGADEGKEAS(1)KGDAGEGQ	-	267	S	-
Sspon.06G0006090-3C	DNLTLWTSDLT(1)EDGADEGK	...S...[STY].D...	256	T	-
Sspon.06G0006110-4D	VRPAVPSET(0.919)AAA	-	200	T	-
Sspon.06G0006110-4D	VRPAVPS(0.934)ETAAA	-	198	S	-
Sspon.06G0006970-4D	ERT(1)PT(0.981)PGKYCGR	..R.R..[STY]P...	215	T	-
Sspon.06G0006970-4D	ERT(1)PT(0.981)PGKYCGR	..R.R..[STY]P...	213	T	-
Sspon.06G0006970-4D	S(1)IT(1)PPADR	[STY]P...	34	S	-
Sspon.06G0006970-4D	S(1)IT(1)PPADR	[STY]P...	36	T	-
Sspon.06G0007040-2C	LDTLDS(0.993)PK	[STY]P...	105	S	-
Sspon.06G0007350-1A	MDSDSS(0.925)PSAAPPAAAEAGR	[STY]P...	6	S	-
Sspon.06G0007400-3C	MES(1)PPLTAEIAFTEK	[STY]P...	3	S	-
Sspon.06G0007490-1A	DTS(0.993)PILESMESGR	[STY]P...	298	S	-
Sspon.06G0007490-1A	DTS(0.972)PILESMES(0.996)GRRP	[STY]P...	306	S	-
Sspon.06G0007490-1A	DTS(0.785)PILES(0.766)MESGRRP	[STY]P...	303	S	-
Sspon.06G0007490-1A	DT(0.803)SPILESMESGR	-	297	T	-
Sspon.06G0007620-2T	AASGEGASLPS(0.999)PAGGEDAHR	[STY]P...	12	S	-
Sspon.06G0007620-2T	LWSGGAYDS(0.992)DTEDPDNLK	[STY]D...	429	S	-
Sspon.06G0007620-2T	AAS(1)GEGASLPS(0.998)PAGGEDAHR	[STY]P...	4	S	-
Sspon.06G0007930-1A	LVNTEIVESST(0.995)PTCK	[STY]P...	347	T	-
Sspon.06G0007930-1A	DANS(1)ES(1)DKETTLEFGGEK	...S.[STY]....	505	S	-
Sspon.06G0007930-1A	DANS(1)ES(1)DKETTLEFGGEK	...S.[STY]....	503	S	-
Sspon.06G0007980-2B	TSGS(0.87)SFGSGS(0.811)LILK	...S.[STY]....	1311	S	-
Sspon.06G0007980-2B	TS(0.845)GSSFSGS(0.943)GSLILK	...S..[STY]....	1309	S	-
Sspon.06G0007980-2B	TS(0.845)GSSFSGS(0.943)GSLILK	...S..[STY]....	1315	S	-
Sspon.06G0007980-2B	T(0.784)SGSSFSGSLILK	...S..[STY]....	1308	T	-
Sspon.06G0008440-4D	QESGSPQS(1)PLGGK	[STY]P...	240	S	-
Sspon.06G0008440-4D	QESGS(0.976)PQS(1)PLGGK	[STY]P...	237	S	-
Sspon.06G0008730-4D	SSGPQS(0.98)AGVTPMAR	-	129	S	-
Sspon.06G0008730-4D	SNYS(0.823)GSISSAVPGTGGSSR	...S...[STY]....	91	S	-
Sspon.06G0008730-4D	NTS(0.988)FGGAANNS(1)GPVSNVGR	...R..[STY]....	70	S	-
Sspon.06G0008730-4D	NTS(0.986)FGGAANNS(1)GPVSNVGR	...R..[STY]....	78	S	-
Sspon.06G0008730-4D	KVS(1)GPLDSSVS(1)MK	...S...[STY]....	181	S	-
Sspon.06G0008730-4D	KVS(1)GPLDSSVS(0.999)MK	...S...[STY]....	173	S	-
Sspon.06G0008730-4D	S(1)GPLGNQPSR	[STY]G...	58	S	-
Sspon.06G0009700-1A	KVESSSSGSEEDSES(0.999)EEEEVKVPK	-	77	S	-
Sspon.06G0009700-1A	KVESSSSGSEEDS(0.998)ESEEVEVKVPK	-	75	S	-
Sspon.06G0009700-1A	KEDSSGSESESDS(0.975)EVEDASK	...S.[STY]....	212	S	-
Sspon.06G0009700-1A	ASASSGSEDESS(0.766)EDDSDEDSEEPANTPK	-	303	S	-
Sspon.06G0009700-1A	ASASSGSEDES(0.888)SEDDSDDEDSEEPANTPK	-	302	S	-
Sspon.06G0009700-1A	MKDESSDDSDT(0.914)DEDGKPPQK	-	240	T	-
Sspon.06G0009700-1A	KEDSSGSESES(0.996)DSEVEDASK	[STY]DS...	210	S	-
Sspon.06G0009700-1A	KKEDPSESDS(0.826)DDDSDEEVPTK	-	179	S	-
Sspon.06G0009700-1A	KVESSSSGS(0.982)EEDSEEEEEVKVPK	-	71	S	-
Sspon.06G0009700-1A	EDSSGSES(0.998)ES(0.85)DSEVEDASK	[STY]DS...	208	S	-
Sspon.06G0009700-1A	KKEDPS(0.964)ESDSDSDSEEVPTK	-	175	S	-
Sspon.06G0009700-1A	KVES(0.925)SSSGS(0.906)EEDSEEEEEVKVPK	...S..[STY]....	66	S	-
Sspon.06G0009700-1A	ASAS(0.765)SGSEDESSDDSDDEDSEEPANTPK	-	295	S	-
Sspon.06G0009700-1A	KEDS(0.847)SGSESESDSEVEDASK	[STY]..S...	203	S	-
Sspon.06G0009700-1A	GS(0.944)SNSIFIR	-	448	S	-
Sspon.06G0009700-3D	QESSDDDDSSDATSES(0.903)DEEPAKKPAK	[STY]DE...	112	S	-
Sspon.06G0009850-2C	SDTLVDEFES(1)K	[STY].S...	74	S	-
Sspon.06G0009940-2C	S(1)PPLDVFPNMVS(1)PK	[STY]P.R...	294	S	-
Sspon.06G0009940-2C	S(1)PPLDVFPNMVS(1)PK	[STY]P.R...	305	S	-
Sspon.06G0010140-3D	VTYVAPPQPPSPVPEES(0.972)EEGS(0.798)PSR	[STY]P.R...	149	S	-
Sspon.06G0010140-3D	VTYVAPPQPPSPVPEES(0.972)EEGS(0.798)PSR	[STY]P.R...	145	S	-
Sspon.06G0010140-3D	VTYVAPPQPPS(0.997)PVPEESEEGSPSR	[STY]P...	139	S	-
Sspon.06G0010180-1P	SRVEDIDQYS(0.963)GEEYS(0.926)E	[STY].E...	329	S	-
Sspon.06G0010180-1P	VEDIDQYS(1)GEEYSE	[STY].E...	324	S	-
Sspon.06G0010190-1A	STS(0.834)LART(0.999)FSPR	...RS.[STY]....	19	S	-
Sspon.06G0010190-1A	STS(0.834)LART(0.999)FSPR	...RS.[STY]....	23	T	-
Sspon.06G0010570-1A	SGSPS(0.995)PDLLLELT	...S...[STY]P...	432	S	-
Sspon.06G0010570-1A	SGS(0.794)PSPDLELT	[STY]PSP...	430	S	-
Sspon.06G0010720-3D	T(0.949)PTSAPGIDYQSADSEHLMK	[STY]P...	289	T	-
Sspon.06G0010940-1A	DES(1)EDEVSCVVTDDR	-	431	S	-
Sspon.06G0010940-2B	DVAS(1)DGDEVESTGIVIR	[STY]D...	421	S	-
Sspon.06G0010940-2B	DVAS(1)DGDEVES(0.931)TGIVIR	[STY]D...	428	S	-
Sspon.06G0011120-1T	YSPSHAYS(0.889)PSSPR	...S...[STY]P...	1745	S	-
Sspon.06G0011170-3C	SGGDVS(0.98)EDS(0.999)EDEKPLAAR	...S..[STY].D...	233	S	-
Sspon.06G0011170-3C	SGGDVS(0.98)EDS(0.999)EDEKPLAAR	...S..[STY].D...	236	S	-
Sspon.06G0011170-3C	ADDS(1)DDDDKPLSLK	[STY]DD...	169	S	-

Sspon.06G0011440-3D	VRLEDLGGES(1)S(1)EDEADEVDK	[STY].E...	130	S	-
Sspon.06G0011440-3D	VRLEDLGGES(1)S(1)EDEADEVDK	[STY].E...	131	S	-
Sspon.06G0011840-3D	EQS(1)PGECSIDLQK	[STY]P...	255	S	-
Sspon.06G0011880-1A	EGS(1)HEVVEIS(0.99)EDESPDK	[STY].E...	25	S	-
Sspon.06G0011880-1A	EGS(1)HEVVEIS(0.986)EDESPDK	[STY].E...	18	S	-
Sspon.06G0012370-3C	ELAGAGPSLPS(0.827)PTSDAR	[STY]P...	32	S	-
Sspon.06G0012450-1A	IAVQNAETQS(1)LAS(1)PR	[STY]PR...	30	S	-
Sspon.06G0012450-1A	IAVQNAETQS(1)LAS(1)PR	[STY]PR...	33	S	-
Sspon.06G0012450-1A	NDPNYDS(0.947)GEEPVELVEAPVSTPLEDYKK	-	129	S	-
Sspon.06G0012460-2B	LADS(1)PINIHK	[STY]P...	96	S	-
Sspon.06G0012710-2B	TPS(0.96)SGDLK	...R..[STY]....	311	S	-
Sspon.06G0012780-1A	SDRQPS(0.874)EEPEEQVDLEGDDGMDDDGGYR	-	7	S	-
Sspon.06G0013080-3C	SVIAEAEAGGS(1)PALIAR	[STY]P...	222	S	-
Sspon.06G0013080-3C	GVS(0.988)PQSAAAGYGAGGQWTA	[STY]P...	682	S	-
Sspon.06G0013100-1A	ANIPGS(1)PEADVYLR	[STY]P...	307	S	-
Sspon.06G0013130-2B	IDAGAAS(0.776)LSR	[STY].S...	74	S	-
Sspon.06G0013200-3D	LAGPPSVENST(0.856)PDR	[STY]P.R...	200	T	-
Sspon.06G0013570-4D	LLEELS(1)LER	[STY].E...	146	S	-
Sspon.06G0013850-4D	AGS(1)DDVGAAANSTAAAGEDLK	[STY]DD...	81	S	-
Sspon.06G0013930-2C	SAS(0.999)FIASPR	...RS.[STY]....	122	S	-
Sspon.06G0013930-2C	SAS(0.862)FIAS(1)PR	...S...[STY]P...	126	S	-
Sspon.06G0013930-2C	S(0.904)ASFIAS(1)PR	...S...[STY]P...	120	S	-
Sspon.06G0014050-2B	SDDDGDGATPSS(0.995)PGR	[STY]P.R...	181	S	-
Sspon.06G0014050-2B	MDDSENNAPST(0.999)PGS(1)PGFSTDR	...S...[STY]P...	11	T	-
Sspon.06G0014050-2B	MDDSENNAPST(0.986)PGS(1)PGFSTDR	...S...[STY]P...	14	S	-
Sspon.06G0014050-2B	MDDSENNAPS(0.765)TPGS(0.873)PGFSTDR	...S...[STY]P...	10	S	-
Sspon.06G0014050-2B	MLHDQDT(1)DEDMNFR	[STY]DE...	143	T	-
Sspon.06G0014600-1A	SVFPSDDLPS(0.983)PTPS(0.918)GDEGK	[STY]P...	419	S	-
Sspon.06G0014600-1A	SVFPSDDLPS(0.909)PTPS(0.983)GDEGK	[STY]P...	423	S	-
Sspon.06G0014630-3C	AVYPDPTFAQS(0.843)TR	[STY]..S...	186	S	-
Sspon.06G0014860-3C	SS(0.765)PDPSPSTSTQOK	[STY]P..SP..	3	S	-
Sspon.06G0015190-1A	VPDLGGADS(1)CGDER	-	95	S	-
Sspon.06G0015200-3D	VFAES(0.997)DDENANDNSSDDPEAKDDHLSK	[STY]DD...	151	S	-
Sspon.06G0015210-2C	RRS(1)PS(1)PAR	...S.[STY]P...R	18	S	-
Sspon.06G0015210-2C	RRS(1)PS(1)PAR	...S.[STY]P...R	20	S	-
Sspon.06G0015530-3D	SIANSLLATEDEPEASDPGPSASPGSTS(0.846)PPR	[STY]P.R...	34	S	-
Sspon.06G0015530-3D	IPIADDEDVSFS(0.999)DLEEDDDAA	-	427	S	-
Sspon.06G0015530-3D	IPIADDEDVS(0.981)FSDLEEDDDAA	-	425	S	-
Sspon.06G0015690-2B	HKPANSATAASADGSVTCES(0.987)PR	[STY]PR...	358	S	-
Sspon.06G0015720-1A	NSS(0.92)VADLGSEVR	...R..[STY]....	250	S	-
Sspon.06G0016630-2B	ELQLFPGASSS(0.868)PER	...S.[STY]P...R	231	S	-
Sspon.06G0016670-1A	ASGGGGGGGS(1)PAGDLDDR	[STY]P...	851	S	-
Sspon.06G0017190-2C	S(0.993)LQSNAENNGIDPVK	...S.[STY]....	878	S	-
Sspon.06G0017840-3C	MEETLAS(0.999)LR	-	7	S	-
Sspon.06G0017850-1P	EASALS(0.998)EPSSPK	[STY].P.SP..	341	S	-
Sspon.06G0017850-1P	EAS(1)ALSEPSSPK	...R..[STY]....	338	S	-
Sspon.06G0017850-1P	EAS(1)ALSEPS(0.804)SPK	...S...[STY]....	344	S	-
Sspon.06G0017850-1P	EAS(1)ALSEPSS(0.845)PK	...S...[STY]P...	345	S	-
Sspon.06G0019100-1A	EAFGDSSGSDSTPAVVS(0.999)PGAGR	[STY]P...	35	S	-
Sspon.06G0019270-1B	EWS(1)GAPER	...R..[STY]....	371	S	-
Sspon.06G0019900-3D	SAGGGGEVVESDDEASAGDVT(0.954)PR	[STY]PR...	35	T	-
Sspon.06G0019900-3D	SAGGGGEVVES(0.856)DDEASAGDVTPR	[STY]DD...	25	S	-
Sspon.06G0020970-1B	DDLQYVYASHDDT(0.832)GEDDNETPLVK	[STY].E...	100	T	-
Sspon.06G0020970-1B	DDLQYVYAS(0.757)HDDTGEDDNETPLVK	[STY]..D..D	96	S	-
Sspon.06G0021550-2C	GESFEDESDDDDDAT(0.812)SPK	-	263	T	-
Sspon.06G0021820-1B	AAS(1)PDQFR	[STY]P...	4	S	-
Sspon.06G0022260-1B	SGS(0.932)VS(1)PFHNMGMK	...S...[STY]P...	198	S	-
Sspon.06G0022260-1B	SGS(0.932)VS(1)PFHNMGMK	...S...[STY]P...	200	S	-
Sspon.06G0022720-2C	YGVD(1)FDPNR	-	213	S	-
Sspon.06G0023260-3D	DMTMS(0.994)PPGPSAVK	-	744	S	-
Sspon.06G0024260-2C	APEPEEES(1)DEEMGFSLFDD	[STY]DE...	308	S	-
Sspon.06G0024720-3D	AAAGGENS(1)GAGEGEFYLR	[STY]G...	9	S	-
Sspon.06G0025340-1B	MDTGSS(0.986)PPASQQTFK	[STY]P...	6	S	-
Sspon.06G0025370-3D	DNLTLWTS(0.917)NEDGGDEIK	...S.[STY]....	245	T	-
Sspon.06G0025370-3D	DNLTLWTS(0.87)DTNEDGGDEIK	[STY]D...	243	S	-
Sspon.06G0025370-3D	SPS(0.895)EPTREESVYMAK	...S.[STY]....	4	S	-
Sspon.06G0025370-3D	MS(0.953)PSEPTREESVYMAK	[STY]P...	2	S	-
Sspon.06G0026490-1B	MEVDPS(1)PS(1)PR	[STY]PR...	6	S	-
Sspon.06G0026490-1B	MEVDPS(1)PS(1)PR	[STY]PR...	8	S	-
Sspon.06G0026890-1B	AEEDSVAGAAPARS(0.878)TGS(0.759)AEDAAAAAQK	...S...[STY]....	61	S	-
Sspon.06G0026890-1B	STGS(0.997)AEDAAAAAQK	...S...[STY]....	64	S	-
Sspon.06G0026890-1B	VES(1)PGS(0.993)PTASAPGR	[STY]P...	39	S	-
Sspon.06G0026890-1B	VES(1)PGS(0.993)PTASAPGR	[STY]P...	36	S	-
Sspon.06G0026890-1B	S(0.833)T(0.872)GSAEDAAAAAQK	[STY]..S...	62	T	-
Sspon.06G0027750-1B	RRDDYS(0.983)AS(0.997)PPR	[STY]P.R...	65	S	-
Sspon.06G0027750-1B	RRDDYS(0.976)AS(1)PPR	[STY]P.R...	67	S	-

Sspon.06G0027750-1B	S(1)PAGEEDEEPRR	[STY]P...	115	S	-
Sspon.06G0027750-1B	S(0.774)YT(0.994)PDDRNDNR	...S.[STY]P...R	93	S	-
Sspon.06G0027750-1B	S(0.774)YT(0.994)PDDRNDNR	...S.[STY]P...R	95	T	-
Sspon.06G0028040-1C	NAYYDAGEQS(0.999)GDDEVYEEAQR	[STY]G...	147	S	-
Sspon.06G0029080-2D	SDSDSDNSAAAAASDDDGAGAGDGDAS(0.821)PLPSAR	[STY]P...	163	S	-
Sspon.06G0029080-2D	RPAAAAIPGSVS(1)DAS(1)DGEAGAAR	...S..[STY]....	16	S	-
Sspon.06G0029080-2D	RPAAAAIPGSVS(1)DAS(1)DGEAGAAR	...S..[STY]....	19	S	-
Sspon.06G0029080-2D	DHLDS(1)DADADADAGTGR	[STY]..D...D	83	S	-
Sspon.06G0029080-2D	RPS(1)PHS(1)PEHQK	[STY]P...	207	S	-
Sspon.06G0029080-2D	RPS(1)PHS(1)PEHQK	[STY]P...	210	S	-
Sspon.06G0029200-1C	LAPPS(1)PAAVGS(1)PR	[STY]P.R...	59	S	-
Sspon.06G0029200-1C	LAPPS(1)PAAVGS(1)PR	[STY]P.R...	65	S	-
Sspon.06G0031000-2D	QAS(1)GVS(1)EIDVAEHR	...S..[STY]....	200	S	-
Sspon.06G0031000-2D	QAS(1)GVS(1)EIDVAEHR	...S..[STY]....	203	S	-
Sspon.06G0031000-2D	ELT(0.998)PPCDS(0.861)GHSTIPK	[STY]P...	234	S	-
Sspon.06G0031000-2D	ELT(0.998)PPCDS(0.861)GHSTIPK	[STY]P...	229	T	-
Sspon.06G0031100-1C	EPENS(1)EDLPAVVR	-	26	S	-
Sspon.06G0031110-1C	IAFPES(1)PGQR	[STY]P...	323	S	-
Sspon.06G0031110-1C	QAS(1)GS(1)PSGGTDAAIAR	[STY]P...	351	S	-
Sspon.06G0031110-1C	QAS(1)GS(1)PSGGTDAAIAR	[STY]P...	349	S	-
Sspon.06G0033530-1D	AS(0.998)PSAS(1)DSELSPPFVEAR	[STY]P...	3	S	-
Sspon.06G0033530-1D	AS(0.998)PSAS(1)DSELSPPFVEAR	[STY]P...	7	S	-
Sspon.06G0035100-1D	SIANSLLATEDEPEANDPGPSAS(0.984)PGSSS(0.842)PPR	[STY]P.R...	34	S	-
Sspon.06G0035100-1D	SIANSLLATEDEPEANDPGPSAS(0.984)PGSSS(0.842)PPR	[STY]P.R...	29	S	-
Sspon.07G0000130-2B	DAVFS(0.956)SSTFLGR	[STY].S...	378	S	-
Sspon.07G0000130-2B	TTDAS(1)PGAQFR	[STY]P...	416	S	-
Sspon.07G0000130-2B	DAVFS(0.947)SST(0.949)FLGR	...S..[STY]....	381	T	-
Sspon.07G0000490-1A	VPIEAEMSED(0.999)ADDDISSR	...S..[STY].D...	124	T	-
Sspon.07G0000490-1A	VPIEAEMS(0.999)EDT(0.994)ADDDISSR	...S..[STY].D...	121	S	-
Sspon.07G0000580-3C	ELPEQIDTSTYMPS(0.999)	-	344	S	-
Sspon.07G0000740-1A	FQHDKPGIGGGGGHS(0.949)PSS(0.852)PPGDKS	[STY]P...	519	S	-
Sspon.07G0000740-1A	FQHDKPGIGGGGGHS(0.949)PSS(0.852)PPGDKS	[STY]P...	516	S	-
Sspon.07G0000790-2C	LIGS(0.98)PDTLSK	-	1317	S	-
Sspon.07G0001040-4D	GIDDLPLISGSAS(0.815)DSGIVGK	[STY]DS...	265	S	-
Sspon.07G0001090-2B	NNS(1)PDIVPNR	[STY]P...	530	S	-
Sspon.07G0002100-1A	DIHDIS(1)LNLK	-	642	S	-
Sspon.07G0002100-1A	IGS(0.772)TDAIETWANQHK	-	169	S	-
Sspon.07G0002100-3C	NDVATEISEADS(1)PEDSLR	...S...[STY]P...	663	S	-
Sspon.07G0002100-3C	NDVATEIS(1)EADS(1)PEDSLR	...S...[STY]P...	659	S	-
Sspon.07G0002130-1A	GGS(0.922)PSPS(0.899)AGDAAPAMSEDGAAAGPARPLR	[STY]PSP...	15	S	-
Sspon.07G0002130-1A	GGS(0.922)PSPS(0.899)AGDAAPAMSEDGAAAGPARPLR	[STY]PSP...	11	S	-
Sspon.07G0002130-2B	GEAT(1)ES(1)VHDMIDEDSVR	[STY]..D...D	897	S	-
Sspon.07G0002130-2B	GEAT(1)ES(1)VHDMIDEDSVR	[STY]..D...D	895	T	-
Sspon.07G0002580-3C	EGDLEAAGEPMS(1)PAGR	[STY]P...	82	S	-
Sspon.07G0002640-1A	NMAS(1)DMNEELDR	[STY]D...	200	S	-
Sspon.07G0002920-1A	MES(1)DAEEEEAAATPAAAGAPGAGR	[STY]D...	3	S	-
Sspon.07G0002960-2C	ENS(1)LRVETGASQQATPSN	...R..[STY]....	323	S	-
Sspon.07G0003020-4D	VPPALDPPS(1)PR	[STY]PR...	72	S	-
Sspon.07G0003020-4D	SGS(0.9)SGLVWDDK	...RS.[STY]....	16	S	-
Sspon.07G0003030-1T	HPFSNQGS(0.994)PRS(1)PR	...S...[STY]P...	333	S	-
Sspon.07G0003030-1T	HPFSNQGS(0.994)PRS(1)PR	...S...[STY]P...	336	S	-
Sspon.07G0003330-2B	RPAENSLT(0.988)PLS(1)DKK	[STY]P...	132	T	-
Sspon.07G0003330-2B	RPAENSLT(0.988)PLS(1)DKK	[STY]P...	135	S	-
Sspon.07G0003620-2D	DECSPLSLSLS(0.78)PK	...S...[STY]P...	185	S	-
Sspon.07G0003640-2D	VVFVAEDYDS(0.999)PGSS(0.851)SR	[STY]P...	88	S	-
Sspon.07G0003640-2D	VVFVAEDYDS(0.999)PGSS(0.851)SR	[STY]P...	84	S	-
Sspon.07G0003640-2D	VVFVAEDYDS(0.998)PGSS(0.78)SSR	[STY]P...	87	S	-
Sspon.07G0004570-1A	VDALEEGS(0.99)SDGSDMPNR	-	347	S	-
Sspon.07G0004570-1A	VDALEEGS(0.982)S(0.965)DGSDMPNR	[STY]..S...	348	S	-
Sspon.07G0004740-2B	ATHPAS(0.986)PTAGAGGDR	-	7	S	-
Sspon.07G0004740-2B	ATHPAS(0.927)PTAGAGGDRS(0.985)PSGPPPVVR	[STY]P...	17	S	-
Sspon.07G0004910-1A	MPNAALS(1)PDLK	[STY]P...	592	S	-
Sspon.07G0005010-3C	AMEIS(1)PTQS(1)PPR	[STY]P.R...	6	S	-
Sspon.07G0005010-3C	AMEIS(0.977)PTQS(1)PPR	[STY]P.R...	10	S	-
Sspon.07G0005010-3C	AMEIS(0.802)PTQS(0.988)PPRT(1)PR	[STY]P.R...	14	T	-
Sspon.07G0005070-4D	SGFS(0.999)DDDGTGK	...S...[STY].D...	104	S	-
Sspon.07G0005250-4D	LSDSPPSLDDYPESMQPS(0.938)PK	...S...[STY]P...	207	S	-
Sspon.07G0005270-4D	ADQLT(1)DDQIAEFK	-	6	T	-
Sspon.07G0005840-1A	HDAIASGS(0.951)PLPVET(0.862)PSR	[STY]P.R...	260	T	-
Sspon.07G0005840-1A	HDAIASGS(0.952)PLPVET(0.82)PSR	[STY]P.R...	254	S	-
Sspon.07G0005840-1A	STS(0.988)MPSPK	...RS.[STY]....	587	S	-
Sspon.07G0006010-3D	LSSSLQDLPT(0.966)FTR	-	12	T	-
Sspon.07G0006010-3D	DGAVAS(0.97)FSK	[STY].S...	48	S	-
Sspon.07G0006010-3D	LSSS(0.758)LQDLPT(0.821)FTR	...S.[STY]....	6	S	-

Sspon.07G0006150-1P	YYASATALANS(1)PEEK	[STY]P...	631	S	-
Sspon.07G0006160-1P	ADAPAS(0.999)PGGGGGSHES(0.956)GS(0.995)PR	[STY]PR...	17	S	-
Sspon.07G0006160-1P	ADAPAS(1)PGGGGGSHESGS(0.997)PR	[STY]PR...	19	S	-
Sspon.07G0006160-1P	ADAPAS(1)PGGGGGSHESGS(0.99)PR	[STY]PR...	7	S	-
Sspon.07G0006160-1P	ADAPAS(0.998)PGGGGGGS(0.799)HESGS(0.935)PR	[STY]PR...	14	S	-
Sspon.07G0006870-1A	VEEKEES(1)DEDMGFLFD	[STY]DE...	103	S	-
Sspon.07G0007110-3C	SSSGIGS(0.999)MNMDDIIR	-	40	S	-
Sspon.07G0007130-1A	SAS(0.968)DVIER	...RS.[STY]....	369	S	-
Sspon.07G0007130-1A	S(1)GNWDMSSDVLTR	[STY]G...	354	S	-
Sspon.07G0007390-2B	TVEAIEETVAAAAAS(1)EPEAEAAPAPAAEPK	-	395	S	-
Sspon.07G0007610-3C	DIVSMDS(0.846)PKESS(0.833)PESSLCCLDSNIGEAR	[STY]P...	174	S	-
Sspon.07G0007610-3C	DIVSMDS(0.965)PKESSPESSLCCLDSNIGEAR	[STY]P...	169	S	-
Sspon.07G0007990-2B	ELTLFPTS(0.885)GDH	[STY]G...	322	S	-
Sspon.07G0008640-3D	MFGS(1)PGR	[STY]P.R...	223	S	-
Sspon.07G0008650-3D	DLFGS(1)DNEEYVR	[STY]D...	119	S	-
Sspon.07G0008660-4D	VGFPAS(1)JR	-	109	S	-
Sspon.07G0008780-1T	SFSNDHHANLT(0.995)NR	-	228	T	-
Sspon.07G0009010-3C	AYS(0.925)EGDIQNLGANTPR	...R..[STY]....	243	S	-
Sspon.07G0009200-3C	SQS(0.999)FDSPTK	...S.[STY]....	145	S	-
Sspon.07G0009230-2D	AAEIASQSLQYS(0.987)NNK	-	471	S	-
Sspon.07G0009290-2B	NSDT(0.887)GS(0.795)SDPSTLVEWGK	...S.[STY]....	46	S	-
Sspon.07G0009290-2B	NSDT(0.887)GS(0.795)SDPSTLVEWGK	...S.[STY]....	44	T	-
Sspon.07G0009920-2B	EYVLLHENST(0.763)E	-	565	T	-
Sspon.07G0009920-2B	VKS(1)PQS(1)PAK	[STY]P...	144	S	-
Sspon.07G0009920-2B	VKS(1)PQS(1)PAK	[STY]P...	147	S	-
Sspon.07G0010050-3C	S(0.916)SDDEVREEK	-	2	S	-
Sspon.07G0010230-4D	S(0.995)PTTT(0.969)PS(0.998)PAPVAASASK	...S...[STY]P...	2	S	-
Sspon.07G0010230-4D	S(0.899)PTTT(0.998)PS(1)PAPVAASASK	...S...[STY]P...	6	T	-
Sspon.07G0010230-4D	S(0.899)PTTT(0.998)PS(1)PAPVAASASK	...S...[STY]P...	8	S	-
Sspon.07G0011120-1A	ELAGSSGS(0.92)VSR	...S...[STY]....	507	S	-
Sspon.07G0011120-1A	ELAGGS(0.955)SGS(0.851)VSR	...S...[STY]....	504	S	-
Sspon.07G0011140-1A	MDDGDSVVR(0.989)VDK	-	10	S	-
Sspon.07G0011260-1A	ASFAADS(0.997)GDESGPGEPSRR	[STY].DE...	53	S	-
Sspon.07G0011300-1A	SPAGLYSLPST(0.829)PTR	[STY]P.R...	293	T	-
Sspon.07G0011300-1A	SPAGLYS(0.996)LPSTPTR	[STY]..S...	289	S	-
Sspon.07G0011500-1P	GSESEDCSQIS(1)GVK	...S...[STY]....	321	S	-
Sspon.07G0011500-1P	S(1)VENS(1)ADGASNPTWTPDK	...R..[STY]....	995	S	-
Sspon.07G0011500-1P	S(1)VENS(1)ADGASNPTWTPDK	...R..[STY]....	991	S	-
Sspon.07G0011920-2B	ECS(1)GVQPQLWAR	...R..[STY]....	54	S	-
Sspon.07G0012190-4D	S(1)VGTFPLQK	...S.[STY]....	277	S	-
Sspon.07G0012280-4D	GRSWS(0.86)YS(0.82)RSL(0.985)PR	...S...[STY]P...	268	S	-
Sspon.07G0012280-4D	GRSWS(0.86)YS(0.82)RSL(0.985)PR	...S...[STY]P...	266	S	-
Sspon.07G0012280-4D	GRSWS(0.86)YS(0.82)RSL(0.985)PR	...S...[STY]P...	272	S	-
Sspon.07G0012280-4D	GRS(0.945)WSYSRS(0.895)LS(0.958)PR	...S...[STY]P...	270	S	-
Sspon.07G0012280-4D	GRS(0.945)WSYSRS(0.895)LS(0.958)PR	...S...[STY]P...	264	S	-
Sspon.07G0012590-1A	ADPTPSQSPAQT(0.996)PPAQQAPAAGGR	...S...[STY]P...	13	T	-
Sspon.07G0012910-3C	APDAPLKT(1)PENS(1)PKAAEV	[STY]P..SP..	466	S	-
Sspon.07G0012910-3C	APDAPLKT(1)PENS(1)PKAAEV	[STY]P..SP..	462	T	-
Sspon.07G0013110-3C	VAEFMPVDAPGS(1)PK	[STY]P...	204	S	-
Sspon.07G0013140-1A	VAEFMPVDVPGS(1)PK	[STY]P...	219	S	-
Sspon.07G0013370-3C	QLS(1)LDQFENES(1)R	...R..[STY]....	87	S	-
Sspon.07G0013370-3C	QLS(1)LDQFENES(1)R	...R..[STY]....	95	S	-
Sspon.07G0013420-3D	EHFASASYTVQSNDS(0.907)A	...S...[STY]....	128	S	-
Sspon.07G0013440-2T	ISIEENGTDPPS(1)PK	[STY]P...	216	S	-
Sspon.07G0014110-4D	GGYTVEYDLSLES(0.868)EDSDR	[STY]..S...	72	S	-
Sspon.07G0014110-4D	VEVCS(1)DDEGFR	[STY]DD...	283	S	-
Sspon.07G0014260-3D	DDLVAYLVS(0.987)GCKPK	[STY]G...	73	S	-
Sspon.07G0014300-1A	VLLKS(1)PAAS(0.987)PSSS(0.981)PK	...S...[STY]P...	183	S	-
Sspon.07G0014300-1A	VLLKS(1)PAAS(0.987)PSSS(0.981)PK	...S...[STY]P...	179	S	-
Sspon.07G0014300-1A	VLLKS(1)PAAS(0.987)PSSS(0.981)PK	...S...[STY]P...	175	S	-
Sspon.07G0014300-1A	SQS(1)FIDR	...RS.[STY]....	506	S	-
Sspon.07G0014400-1A	SVNTEAATLEGS(0.773)PTGVTHNTENLSPSSGTSK	[STY]P...	475	S	-
Sspon.07G0014610-3C	LMSS(0.993)PFS(1)DEVDEESPK	[STY]P...	592	S	-
Sspon.07G0014610-3C	LMSS(0.989)PFS(1)DEVDEESPK	[STY]P...	595	S	-
Sspon.07G0014610-3C	LMSS(0.97)PFS(0.998)DEVDEES(1)PKRR	[STY]P.R...	602	S	-
Sspon.07G0014610-3C	TGS(0.937)LEPEYNNISIGGK	...R..[STY]....	576	S	-
Sspon.07G0014850-1A	ERS(0.987)YS(0.94)RS(0.999)PT(1)PR	...S.[STY]P...R	151	S	-
Sspon.07G0014850-1A	GRS(0.991)PSYSRS(0.917)R	...R.R..[STY]P...	171	S	-
Sspon.07G0014850-1A	GRS(0.991)PSYSRS(0.917)R	...R.R..[STY]P...	165	S	-
Sspon.07G0014850-1A	S(1)RS(1)PQDQVMS(1)PPPK	[STY]P...	234	S	-
Sspon.07G0014850-1A	S(1)RS(1)PQDQVMS(1)PPPK	[STY]P...	236	S	-
Sspon.07G0014850-1A	S(1)RS(1)PQDQVMS(1)PPPK	[STY]P...	243	S	-
Sspon.07G0014850-2B	DDRS(1)PS(1)PKGDNGDDER	[STY]PSP...	378	S	-
Sspon.07G0014850-2B	DDRS(1)PS(1)PKGDNGDDER	[STY]PSP...	380	S	-
Sspon.07G0014850-2B	DDVS(1)PPPKDNGAR	-	327	S	-
Sspon.07G0014850-2B	RGS(1)PRGS(1)QS(1)P	[STY]PR...	393	S	-

Sspon.07G0014850-2B	RGS(1)PRGS(1)QS(1)P	[STY]PR...	397	S	-
Sspon.07G0014850-2B	RGS(1)PRGS(1)QS(1)P	[STY]PR...	399	S	-
Sspon.07G0014850-2B	RS(1)VS(1)PAKEK	...S.[STY]P...R	298	S	-
Sspon.07G0014850-2B	RS(1)VS(1)PAKEK	...S.[STY]P...R	300	S	-
Sspon.07G0014850-2B	RS(0.999)RS(0.984)VS(0.848)YSR	...RS.[STY]....	288	S	-
Sspon.07G0014850-2B	RS(0.999)RS(0.984)VS(0.848)YSR	...RS.[STY]....	286	S	-
Sspon.07G0014850-2B	RS(0.999)RS(0.984)VS(0.848)YSR	...RS.[STY]....	284	S	-
Sspon.07G0014860-2D	ERS(0.965)YS(0.989)RS(0.998)PS(0.998)PR	...S.[STY]P...R	151	S	-
Sspon.07G0014860-2D	ERS(0.965)YS(0.989)RS(0.998)PS(0.998)PR	...S.[STY]P...R	153	S	-
Sspon.07G0014860-2D	ERS(0.965)YS(0.989)RS(0.998)PS(0.998)PR	...S.[STY]P...R	157	S	-
Sspon.07G0014860-2D	ERS(0.965)YS(0.989)RS(0.998)PS(0.998)PR	...S.[STY]P...R	155	S	-
Sspon.07G0015770-1A	GPGTIGGLHS(0.962)S(0.894)NSLR	[STY]..S...	181	S	-
Sspon.07G0015770-1A	GPGTIGGLHS(0.968)S(0.844)NSLR	[STY]..S...	180	S	-
Sspon.07G0015770-1A	SAS(1)PDPFLVR	...S.[STY]P...R	213	S	-
Sspon.07G0015770-1A	S(0.956)FSTVFQEDSYQR	...R..[STY]....	132	S	-
Sspon.07G0016080-2C	MDSISSPAGLSES(0.774)EGSAVAESK	...S.[STY]....	461	S	-
Sspon.07G0016080-2C	MDSISSPAGLS(0.868)ESEGSAVAESK	[STY].S...	459	S	-
Sspon.07G0016080-2C	MDSISS(0.924)PAGLSESEGSVAESK	[STY]P...	454	S	-
Sspon.07G0016210-1A	FVESS(0.989)PSSSYCTK	[STY]P...	250	S	-
Sspon.07G0016240-2C	FYMEPDTTDSGSMAS(0.86)GATPSR	...S..[STY]....	1056	S	-
Sspon.07G0016240-2C	FYMEPDT(0.864)TDS(0.99)GSMASGATPSR	[STY]..S...	1051	S	-
Sspon.07G0016240-2C	FYMEPDT(0.995)T(0.991)DSGSMASGATPSR	[STY]DS...	1049	T	-
Sspon.07G0016240-2C	FYMEPDT(0.997)T(0.966)DSGSMASGATPSR	[STY]DS...	1048	T	-
Sspon.07G0016330-1A	VGPPS(1)GEFAS(1)R	[STY].E...	55	S	-
Sspon.07G0016330-1A	VGPPS(1)GEFAS(1)R	[STY].E...	60	S	-
Sspon.07G0016630-2B	VANS(1)PPEVVK	[STY]P...	175	S	-
Sspon.07G0016630-2B	AS(1)PQESNSLCLK	[STY]P...	3	S	-
Sspon.07G0016990-3C	EMSQS(0.997)PVS(1)DMDESPHNHQK	[STY]P...	307	S	-
Sspon.07G0016990-3C	EMSQS(0.997)PVS(1)DMDESPHNHQK	[STY]P...	310	S	-
Sspon.07G0017190-2B	SGPLDFSVS(0.989)R	...S.[STY]....	756	S	-
Sspon.07G0017190-2B	S(1)GPLDFSISR	[STY]G...	748	S	-
Sspon.07G0018360-1A	EQS(1)VQQQLPVLK	...R..[STY]....	214	S	-
Sspon.07G0018980-1T	FQDQGGIMT(0.997)AETGTYR	[STY].E...	211	T	-
Sspon.07G0019040-1A	VGS(1)AGNTAGS(0.949)TRPR	...R..[STY]....	18	S	-
Sspon.07G0019040-1A	VGS(1)AGNTAGS(0.949)TRPR	...R..[STY]....	11	S	-
Sspon.07G0019040-1A	AS(0.995)LEGSAPVPVYK	[STY].E...	345	S	-
Sspon.07G0019280-2D	SEVS(1)LLLQS(1)EAGDGK	...S..[STY]....	185	S	-
Sspon.07G0019280-2D	SEVS(1)LLLQS(1)EAGDGK	...S..[STY]....	190	S	-
Sspon.07G0019360-2D	GGDDRY(0.968)HS(0.997)PGTEPIGIAR	[STY]P...	510	S	-
Sspon.07G0019360-2D	GGDDRY(0.968)HS(0.997)PGTEPIGIAR	[STY]P...	512	S	-
Sspon.07G0019810-3C	ANS(1)FNNLQYDWK	...R..[STY]....	530	S	-
Sspon.07G0020880-2C	AVGGS(1)PVHGS(0.995)PTQADK	[STY]P...	136	S	-
Sspon.07G0020880-2C	AVGGS(1)PVHGS(0.935)PTQADK	[STY]P...	131	S	-
Sspon.07G0021120-3D	GLT(0.938)PS(0.839)TPS(0.866)GDLTGADFTSSSK	[STY]P...	317	S	-
Sspon.07G0021120-3D	GLT(0.994)PS(0.976)TPSGDLTGADFTSSSK	[STY]P...	314	S	-
Sspon.07G0021120-3D	GLT(0.994)PS(0.976)TPSGDLTGADFTSSSK	[STY]P...	312	T	-
Sspon.07G0021540-2D	QSS(0.924)LNAAGTSSMAVLR	...R..[STY]....	43	S	-
Sspon.07G0021680-1B	ARS(1)PVRESS(0.818)EER	[STY]P.R...	290	S	-
Sspon.07G0021680-1B	ARS(1)PVRESS(0.818)EER	[STY]P.R...	284	S	-
Sspon.07G0021770-1B	APEPAEES(1)DEELGFSLFDD	[STY]DE...	303	S	-
Sspon.07G0022130-1B	NLEDVNEAYLS(0.986)EEDEDITK	[STY].E...	118	S	-
Sspon.07G0022400-1B	SAGEGALQGNPTES(0.867)GDDEEGEFQGNPTER	[STY]G...	593	S	-
Sspon.07G0022500-3D	SQS(0.754)FACMSEVR	...S.[STY]....	101	S	-
Sspon.07G0022500-3D	S(0.845)QSFACMSEVR	[STY].S...	99	S	-
Sspon.07G0022560-1P	SSSDESDFS(0.92)SDSDDFCK	...S..[STY].D...	155	S	-
Sspon.07G0023140-3D	FGASPS(0.996)FR	...S.[STY]....	69	S	-
Sspon.07G0024870-3D	SGLSLS(0.993)DQLPR	...S.[STY]....	251	S	-
Sspon.07G0024900-1B	MDDGDSAVRS(0.981)VDK	-	10	S	-
Sspon.07G0025510-2C	EITQTSS(0.869)FLR	-	225	S	-
Sspon.07G0025720-1P	SLTSTLS(0.972)R	...S..[STY]....	2679	S	-
Sspon.07G0026940-1B	LCLSLDT(0.997)DSE	[STY]DS...	577	T	-
Sspon.07G0027030-2C	SVS(0.931)WSEPR	...RS.[STY]....	23	S	-
Sspon.07G0027200-2C	YAGAS(0.987)NWTVK	-	246	S	-
Sspon.07G0029050-3D	TESLEIQCNQAS(0.99)PECTVK	[STY]P...	99	S	-
Sspon.07G0029110-1B	S(0.97)DPHSITVDINK	...S..[STY]....	341	S	-
Sspon.07G0030090-2D	DTTCDEVGSELS(0.97)GDEVVIK	...S.[STY]....	954	S	-
Sspon.07G0030600-2D	MDGLHGTACFS(0.995)PAR	[STY]P.R...	12	S	-
Sspon.07G0031480-2D	DMADGGLSTSSS(0.833)FR	...S.[STY]....	233	S	-
Sspon.07G0032640-1C	YTSQYAPFSGTAS(0.849)QR	[STY]..S...	518	S	-
Sspon.07G0032640-1C	S(0.998)EDSLNPELLIR	...S.[STY]....	677	S	-
Sspon.07G0033790-1C	DGGS(0.999)DYLK	-	65	S	-
Sspon.07G0033930-1C	DVEAVSQAS(0.987)S(0.954)GSGATLGESLR	...S..[STY]....	2448	S	-
Sspon.07G0033930-1C	DVEAVS(0.999)QASS(0.991)GSGATLGESLR	[STY]..S...	2449	S	-
Sspon.07G0033930-1C	DVEAVS(1)QASS(0.914)GSGATLGESLR	[STY]..S...	2445	S	-
Sspon.07G0033930-1C	DVEAVS(1)QASS(0.845)GSGAT(0.993)LGESLR	...S..[STY]....	2454	T	-
Sspon.07G0033930-2D	YHSSS(0.891)LFGMNS(1)R	...S.[STY]....	1328	S	-

Sspon.07G0033930-2D	YHSSS(0.768)LFGMNS(1)R	...S.[STY]...	1334	S	-
Sspon.07G0034910-1C	TLQIQRT(1)EAWR	-	576	T	-
Sspon.07G0036230-1D	DYFS(0.997)GSLIESSK	[STY].S...	301	S	-
Sspon.07G0037580-1D	TAEAQPSAGAEELGSAS(0.981)PPVPQTSAGK	[STY]P...	591	S	-
Sspon.08G0000160-1A	TVDYDS(1)DEDFVVIR	[STY]DE...	188	S	-
Sspon.08G0000280-3P	EKEALEES(1)QD	-	176	S	-
Sspon.08G0000310-1A	GPFCSSPDT(0.836)NSR	...S..[STY]...	410	T	-
Sspon.08G0000310-1A	GPFCSS(0.861)PDTNS(0.938)R	[STY]P...	412	S	-
Sspon.08G0000310-1A	GPFCSS(0.992)PDTNSR	[STY]P...	407	S	-
Sspon.08G0000310-1A	GPFCSS(0.95)S(0.855)PDTNSR	[STY]P...	406	S	-
Sspon.08G0000310-1A	NADS(1)PDLEAPR	[STY]P...	417	S	-
Sspon.08G0000340-2P	EIAEPHS(1)PK	[STY]P...	196	S	-
Sspon.08G0000560-2C	SVFDS(0.998)VPS(0.836)TPMQR	...S..[STY]...	415	S	-
Sspon.08G0000560-2C	SVFDS(0.998)VPS(0.836)TPMQR	...S..[STY]...	412	S	-
Sspon.08G0000560-2C	SIFDS(0.999)IPGT(1)PVQK	...S..[STY]P...	358	S	-
Sspon.08G0000560-2C	SIFDS(0.999)IPGT(1)PVQK	...S..[STY]P...	362	T	-
Sspon.08G0000620-4D	SEVNDEDDDEGS(1)EEDEDDDE	[STY].E...	152	S	-
Sspon.08G0000620-4D	SLTES(0.997)DKAPYVAK	[STY]D...	87	S	-
Sspon.08G0001160-3D	SGS(0.819)GSALFDDYGR	...RS.[STY]...	169	S	-
Sspon.08G0001290-3C	LTSFS(0.92)HPSS(0.964)PTFC	...S..[STY]P...	587	S	-
Sspon.08G0001290-3C	LTSFS(0.984)HPSS(0.775)PTFC	...S..[STY]P...	583	S	-
Sspon.08G0001290-3C	LTS(0.974)FSHPSS(0.776)PTFC	...S..[STY]P...	581	S	-
Sspon.08G0001400-4D	IVQNSQSEPQEPSS(0.98)P	[STY]P...	390	S	-
Sspon.08G0001590-3C	RRS(1)PAPPS(1)PR	..R.R..[STY]P...	6	S	-
Sspon.08G0001590-3C	RRS(1)PAPPS(1)PR	..R.R..[STY]P...	11	S	-
Sspon.08G0001620-1T	LPS(0.975)ANSAMVTTTSSGDDGGGR	...R..[STY]...	206	S	-
Sspon.08G0001630-2D	S(0.999)FDELTLNSTEPHK	...R..[STY]...	267	S	-
Sspon.08G0001740-2C	DQNFLGVFS(1)NEK	[STY].E...	140	S	-
Sspon.08G0001790-3C	WSS(0.764)S(0.913)VWAVSSSGR	...R..[STY]...	32	S	-
Sspon.08G0001790-3C	WSS(0.764)S(0.913)VWAVSSSGR	...R..[STY]...	33	S	-
Sspon.08G0002100-2B	EES(1)DDDMGFSLFD	-	109	S	-
Sspon.08G0002270-2B	GQFMT(0.999)EY(0.985)VVTR	-	194	Y	-
Sspon.08G0002270-2B	GQFMT(0.999)EY(0.985)VVTR	-	192	T	-
Sspon.08G0003280-1A	DAEASASSPLVAS(1)PR	[STY]PR...	37	S	-
Sspon.08G0003330-3D	DREEEGEDLS(1)DGGAEEK	[STY]D...	23	S	-
Sspon.08G0003680-3C	AIESLPDS(0.998)DDEDVLTSR	[STY]DD...	374	S	-
Sspon.08G0003760-4D	NIIPQNS(1)FR	-	89	S	-
Sspon.08G0004020-1A	EGNDMELGLVTGS(0.964)PSR	[STY]P.R...	301	S	-
Sspon.08G0004460-2B	SMS(0.999)FS(1)PDRVR	...S.[STY]P...R	757	S	-
Sspon.08G0004460-2B	SMS(0.999)FS(1)PDRVR	...S.[STY]P...R	759	S	-
Sspon.08G0004460-2B	NLS(0.992)TPPPAVR	...R..[STY]...	788	S	-
Sspon.08G0004960-1A	AATAGAS(1)DDGGS(1)VGGGGGGER	[STY]DD...	8	S	-
Sspon.08G0004960-1A	AATAGAS(1)DDGGS(1)VGGGGGGER	[STY]DD...	13	S	-
Sspon.08G0005120-1A	DSGT(0.762)EGEDADILPK	...S.[STY]...	302	T	-
Sspon.08G0005170-1P	DSAES(0.998)IGS(0.999)DLSSLR	...S..[STY]...	309	S	-
Sspon.08G0005280-1A	GLAEAEAAGNVDAAGGEDGRDADS(0.999)GGGDASGK	[STY]G...	35	S	-
Sspon.08G0005280-3C	DGAS(0.992)GYGDAGGEDGR	[STY]G...	37	S	-
Sspon.08G0005310-2C	IEENPSLYTPPS(0.993)PR	[STY]PR...	203	S	-
Sspon.08G0005640-1A	APFPQNNISEQAT(1)G	[STY]G...	237	T	-
Sspon.08G0005950-3C	DASRPVAPVNYVAIAKEDAAS(0.999)QAS(0.91)SN	...S..[STY]...	565	S	-
Sspon.08G0005950-3C	DASRPVAPVNYVAIAKEDAAS(0.999)QAS(0.91)SN	...S..[STY]...	562	S	-
Sspon.08G0005950-3C	LSALQS(1)GGR	[STY]G...	530	S	-
Sspon.08G0006240-1A	AQITPDEPGFS(1)A	-	383	S	-
Sspon.08G0006350-3D	YAS(0.98)TGSLQIPDETEK	...R..[STY]...	247	S	-
Sspon.08G0006590-1A	SIS(1)AEGLR	...RS.[STY]...	339	S	-
Sspon.08G0006850-1A	AAVVS(1)PAADAPPNIS(1)APR	[STY]P...	36	S	-
Sspon.08G0006850-1A	AAVVS(1)PAADAPPNIS(1)APR	[STY]P...	46	S	-
Sspon.08G0007050-2B	ASSSSS(0.971)PLPALAGEALR	...S..[STY]P...	7	S	-
Sspon.08G0008210-1T	AGHAT(0.999)PS(0.976)PSWK	[STY]PSP...	95	S	-
Sspon.08G0008210-1T	AGHAT(0.999)PS(0.976)PSWK	[STY]PSP...	93	T	-
Sspon.08G0008330-3D	VQVMPAAEGAAVEVDS(1)PR	[STY]P.R...	206	S	-
Sspon.08G0008450-2B	DGVSDS(0.895)DFDEFGSMDVTK	...S.[STY]...	458	S	-
Sspon.08G0008800-1P	NEDS(0.953)SLLDWDTR	-	594	S	-
Sspon.08G0008910-3C	SAPS(0.89)PENVDPGGDQPALEGS(0.933)GGSGGPTR	[STY]P...	49	S	-
Sspon.08G0008910-3C	SAPS(0.89)PENVDPGGDQPALEGS(0.933)GGSGGPTR	[STY]P...	65	S	-
Sspon.08G0008940-2B	VIIEIECVVQS(0.846)EESTADK	[STY].E...	91	S	-
Sspon.08G0008970-2B	FPTASS(0.923)PSR	[STY]P.R...	320	S	-
Sspon.08G0009070-2B	MDS(1)EPDVELR	-	3	S	-
Sspon.08G0009140-1A	EDAAS(1)QVSVTDPVPS(0.985)TP	...[STY]..S...	602	S	-
Sspon.08G0009140-1A	EDAAS(1)QVS(1)VTDPVPST(1)P	[STY]P...	603	T	-
Sspon.08G0009140-1A	EDAAS(1)QVS(1)VTDPVPST(1)P	[STY]P...	595	S	-
Sspon.08G0009140-1A	EDAAS(1)QVS(1)VTDPVPST(0.973)P	[STY]P...	592	S	-
Sspon.08G0009140-1A	EDAAS(0.99)QVSVT(0.986)DPVPSTP	...S.[STY]...	597	T	-
Sspon.08G0009580-1A	TSSASLVANS(0.976)NSDLSGLDK	...S..[STY]...	649	S	-
Sspon.08G0010430-1A	GSDDVDSFSFMNS(0.991)PR	...S..[STY]P...	228	S	-
Sspon.08G0010450-2B	IMQLCAANTAGS(0.998)GAAT(1)PER	[STY]P.R...	173	S	-

Sspon.08G0010450-2B	IMQLCAANTAGS(0.998)GAAT(1)PER	[STY]P.R...	177	T	-
Sspon.08G0010530-3D	LQS(1)FEVEHK	...R..[STY]....	365	S	-
Sspon.08G0010730-3C	DWNS(1)DIPGDVDNDQTLDK	[STY]D...	838	S	-
Sspon.08G0011540-2B	EEGGS(1)PIRNPPTAAEDAR	[STY]P.R...	910	S	-
Sspon.08G0011540-2B	S(1)PDVFASPVSDQK	...S...[STY]P...	540	S	-
Sspon.08G0011940-3C	VGPMDVGTKS(0.893)H	-	603	S	-
Sspon.08G0012140-2B	AAAGVSTPHT(0.944)PAEADDDDLFR	...S...[STY]P...	127	T	-
Sspon.08G0012270-2B	SLS(0.977)LQDLSR	...RS.[STY]....	48	S	-
Sspon.08G0012650-2B	GRSYS(0.995)RS(0.991)PQYK	...S.[STY]P...R	180	S	-
Sspon.08G0012650-2B	RRS(1)VS(1)PAR	[STY]P.R...	168	S	-
Sspon.08G0012650-2B	RRS(1)VS(1)PAR	[STY]P.R...	170	S	-
Sspon.08G0012650-2B	GRS(0.985)YS(0.996)RS(0.932)PQYK	...S.[STY]P...R	178	S	-
Sspon.08G0012650-2B	GRS(0.994)YS(0.826)RSPQYK	...RS.[STY]....	176	S	-
Sspon.08G0012650-2B	GRS(0.914)YSRSPQY(0.988)K	[STY].S.SP..	183	Y	-
Sspon.08G0012650-2B	S(0.994)YS(0.997)PAAR	...S.[STY]P...R	156	S	-
Sspon.08G0012650-2B	S(0.92)YS(1)PAAR	...S.[STY]P...R	158	S	-
Sspon.08G0012650-2B	S(0.778)YS(1)PAARS(1)PR	...S.[STY]P...R	163	S	-
Sspon.08G0012680-2D	VPFFADDEESPAT(0.992)PK	[STY]P...	686	T	-
Sspon.08G0012870-3C	YALDES(1)DDDLPLR	[STY]DD...	23	S	-
Sspon.08G0012940-1A	AVATEGDLVADADSMS(0.979)GR	...S.[STY]....	411	S	-
Sspon.08G0013000-1P	TGESSTDMAGS(1)L	-	841	S	-
Sspon.08G0013000-3C	LIFSDS(0.967)AHGTPSMDDTSAK	...S.[STY]....	45	S	-
Sspon.08G0013100-1P	IEEIS(1)DDNDAGCVAIK	[STY]DD...	239	S	-
Sspon.08G0014700-3D	TTSETDFMT(0.99)EY(0.999)VVTR	-	227	Y	-
Sspon.08G0014700-3D	TTSETDFMT(1)EY(0.999)VVTR	-	225	T	-
Sspon.08G0014730-1P	TPVEQEMTDAPTTS(0.969)A	-	279	S	-
Sspon.08G0014730-1P	TPVEQEMTDAPTT(0.796)SA	-	278	T	-
Sspon.08G0015120-1A	SSS(1)LGTGASIPDVER	...RS.[STY]....	109	S	-
Sspon.08G0015120-1A	SSS(0.955)LGT(1)GAS(1)IPDVER	...RS.[STY]....	115	S	-
Sspon.08G0015120-1A	SSS(0.955)LGT(1)GAS(1)IPDVER	...RS.[STY]....	112	T	-
Sspon.08G0015120-1A	SS(0.784)S(0.999)LGTGASIPDVER	...RS.[STY]....	108	S	-
Sspon.08G0016070-2B	GGAVREDLS(1)PVR	[STY]P.R...	152	S	-
Sspon.08G0016070-2B	HDS(0.998)MESEDIS(1)PPR	[STY]P.R...	264	S	-
Sspon.08G0016550-1A	DSETPPLSSWKS(0.983)E	...S..[STY]....	345	S	-
Sspon.08G0016550-1A	LVDSLS(0.989)EQDFR	...S.[STY]....	228	S	-
Sspon.08G0017310-3D	HNAPNDVPDEPVEGES(1)DGEALVNNPPKK	[STY]D...	84	S	-
Sspon.08G0017480-1B	IPSSTCHVDS(0.994)FNR	-	301	S	-
Sspon.08G0017950-2C	AGS(1)FQIK	...R..[STY]....	196	S	-
Sspon.08G0017960-2D	GGSS(0.941)PS(1)PPPYR	[STY]PSP...	82	S	-
Sspon.08G0017960-2D	GGSS(0.985)PS(1)PPPYR	[STY]PSP...	80	S	-
Sspon.08G0017960-2D	GGSS(0.95)SPS(1)PPPYR	[STY]P...	79	S	-
Sspon.08G0019100-1B	DPLGAASGYLS(0.981)R	[STY]..S...	570	S	-
Sspon.08G0019100-1B	SLS(0.909)NTELNVR	...RS.[STY]....	471	S	-
Sspon.08G0019980-1P	STS(0.991)FSQQSGVYS(0.989)R	...RS.[STY]....	353	S	-
Sspon.08G0019980-1P	STS(0.992)FSQQSGVYSR	...RS.[STY]....	344	S	-
Sspon.08G0020140-3D	SGS(0.916)SGLVWDER	...RS.[STY]....	16	S	-
Sspon.08G0020400-2C	QSVAEKGDS(1)VEGGEK	[STY].E...	1193	S	-
Sspon.08G0020400-2C	EKS(1)PGDS(1)KEQMKGELNK	[STY]P...	701	S	-
Sspon.08G0020400-2C	EKS(1)PGDS(1)KEQMKGELNK	[STY]P...	705	S	-
Sspon.08G0020400-2C	S(0.962)SSVRS(1)EKPVR	...S..[STY]....	427	S	-
Sspon.08G0020400-2C	S(0.962)SSVRS(1)EKPVR	...S..[STY]....	432	S	-
Sspon.08G0020440-1B	RSSVS(0.998)PVHPK	[STY]P...	543	S	-
Sspon.08G0020440-1B	S(0.997)PDTIVSAPR	[STY]P...	587	S	-
Sspon.08G0020810-2C	TDSFHLGLS(0.997)S(0.997)DEGDAPSTR	[STY].DE...	86	S	-
Sspon.08G0020810-2C	TDSFHLGLS(0.997)S(0.997)DEGDAPSTR	[STY].DE...	85	S	-
Sspon.08G0021330-1B	ASLEEEDDILS(1)DDDEFFDR	[STY]DD...	149	S	-
Sspon.08G0021490-1B	GLHPASLVT(1)PVAS(1)PTAV	[STY]P..SP..	450	S	-
Sspon.08G0021490-1B	GLHPASLVT(1)PVAS(0.999)PTAV	[STY]P..SP..	446	T	-
Sspon.08G0021490-1B	GLHPASLVT(1)PVASPT(0.785)AV	[STY]P..SP..	452	T	-
Sspon.08G0021620-1B	MVSAVEAAST(0.943)PDDLGR	[STY]P...	3111	T	-
Sspon.08G0021620-1B	MEASPTVGDS(1)PPAK	[STY]P...	1529	S	-
Sspon.08G0021620-1B	LCQVDS(1)PDS(1)PQPGGMSK	[STY]P...	1486	S	-
Sspon.08G0021620-1B	LCQVDS(1)PDS(1)PQPGGMSK	[STY]P...	1483	S	-
Sspon.08G0021620-1B	SSGIES(1)PAS(1)LQMEDTR	...S...[STY]P...	175	S	-
Sspon.08G0021620-1B	SSGIES(1)PAS(1)LQMEDTR	...S...[STY]P...	178	S	-
Sspon.08G0021620-1B	NS(0.966)PSEYSNER	[STY]P...	2420	S	-
Sspon.08G0022540-2C	LHS(1)LRER	-	449	S	-
Sspon.08G0022780-2C	VDS(1)LCCLIQK	...R..[STY]....	216	S	-
Sspon.08G0022930-2C	DSVASAGSSAHNSEASEYSGLVEGMS(1)PR	[STY]PR...	212	S	-
Sspon.08G0022930-2C	AAS(1)FGELLR	...R..[STY]....	70	S	-
Sspon.08G0022970-1P	SIS(0.969)AEGLNSLR	...RS.[STY]....	415	S	-
Sspon.08G0024140-1P	GEGMGGAVADS(0.961)GESR	[STY].E...	581	S	-
Sspon.08G0024140-1P	S(1)EQQLPQPR	-	2	S	-
Sspon.08G0024470-2D	EGGS(1)PGS(1)EKGIHTAIK	[STY]P...	454	S	-
Sspon.08G0024470-2D	EGGS(1)PGS(1)EKGIHTAIK	[STY]P...	451	S	-
Sspon.08G0024470-2D	SIS(1)EPDFGK	-	1460	S	-

Sspon.08G0024470-2D	AS(1)DFDETDEAFFDK	[STY]D...	3	S	-
Sspon.08G0024630-1C	IYHQQEGVAGS(1)R	-	237	S	-
Sspon.08G0024630-1C	GPS(0.987)MLGSLVLS(0.999)IGS(1)R	...S..[STY]....	60	S	-
Sspon.08G0024630-1C	FDS(1)MIS(0.99)ITDQHPK	...S..[STY]....	117	S	-
Sspon.08G0024630-1C	GPS(0.987)MLGSLVLS(0.999)IGS(1)R	...S..[STY]....	67	S	-
Sspon.08G0024630-1C	GPS(0.987)MLGSLVLS(0.999)IGS(1)R	...S..[STY]....	70	S	-
Sspon.08G0024630-1C	FDS(1)MIS(0.99)ITDQHPK	...S..[STY]....	114	S	-
Sspon.08G0024800-1C	GYS(0.999)PPPYGGGR	[STY]P...	241	S	-
Sspon.08G0024800-1C	ERS(1)IS(1)PYRMPEP	...S..[STY]P...R	257	S	-
Sspon.08G0024800-1C	ERS(1)IS(1)PYRMPEP	...S..[STY]P...R	255	S	-
Sspon.08G0024800-1C	RYS(0.983)RS(0.995)PS(0.95)YSR	[STY]P...	14	S	-
Sspon.08G0024800-1C	RYS(0.985)RS(0.916)PS(0.916)YSR	[STY]P...	10	S	-
Sspon.08G0024800-1C	RYS(0.983)RS(0.995)PS(0.95)YSR	[STY]P...	12	S	-
Sspon.08G0024800-1C	SQS(0.964)PARS(1)QS(1)RS(1)PVPDPR	...S..[STY]P...R	28	S	-
Sspon.08G0024800-1C	SQS(0.797)PARS(1)QS(1)RS(1)PVPDPR	...S..[STY]P...R	32	S	-
Sspon.08G0024800-1C	SQS(0.797)PARS(1)QS(1)RS(1)PVPDPR	...S..[STY]P...R	34	S	-
Sspon.08G0024800-1C	SQS(0.797)PARS(1)QS(1)RS(1)PVPDPR	...S..[STY]P...R	36	S	-
Sspon.08G0024800-1C	S(1)PPPVHASYSR	[STY]P...	188	S	-
Sspon.08G0024800-1C	T(1)PT(1)PGSYLGHR	..R.R..[STY]P...	148	T	-
Sspon.08G0024800-1C	T(1)PT(1)PGSYLGHR	..R.R..[STY]P...	146	T	-
Sspon.08G0024800-1C	S(1)HEREEDAVNR	...RS.[STY]....	51	S	-
Sspon.08G0024840-1P	KPVDILAGSDEDS(1)DGGEEDLSK	[STY]D...	27	S	-
Sspon.08G0024840-1P	KPVDILAGS(1)DESDGGEEDLSK	[STY]DE...	23	S	-
Sspon.08G0025170-2D	IRPS(1)VS(0.998)PPS	[STY]P...	503	S	-
Sspon.08G0025170-2D	IRPS(1)VS(0.998)PPS	[STY]P...	501	S	-
Sspon.08G0025320-2D	DRGGSPDAS(0.866)GPPPPFR	[STY]G...	13	S	-
Sspon.08G0025320-2D	SPDGGKT(0.751)DSSIS(0.941)FR	[STY]DS...	134	T	-
Sspon.08G0025320-2D	SPDGGKT(0.751)DSSIS(0.941)FR	[STY]DS...	139	S	-
Sspon.08G0025320-2D	EQGS(0.999)IGITANEDPYNANEMS(0.996)PSDQR	[STY]P...	260	S	-
Sspon.08G0025320-2D	EQGS(1)IGIT(1)ANEDPYNANEMS(0.963)PSDQR	[STY]P...	248	T	-
Sspon.08G0025320-2D	EQGS(1)IGIT(1)ANEDPYNANEMS(0.928)PSDQR	[STY]P...	244	S	-
Sspon.08G0025320-2D	RPIS(1)LPT(1)S(1)EEAK	...S..[STY]....	278	S	-
Sspon.08G0025320-2D	RPIS(1)LPT(1)S(1)EEAK	...S..[STY]....	282	S	-
Sspon.08G0025320-2D	RPIS(1)LPT(1)S(1)EEAK	...S..[STY]....	281	T	-
Sspon.08G0025320-2D	EQGS(0.982)IGITANEDPYNANEMS(0.99)PS(0.971)DQR	[STY]P...	262	S	-
Sspon.08G0025320-2D	RHS(1)PRYS(0.993)PER	[STY]P.R...	89	S	-
Sspon.08G0025320-2D	RHS(1)PRYS(0.993)PER	[STY]P.R...	85	S	-
Sspon.08G0025320-2D	GGG(1)PDASGPPPPFR	..R.R..[STY]P...	9	S	-
Sspon.08G0026900-2D	GVDS(1)DDEDLVVYGTPIER	[STY]DD...	5	S	-
Sspon.08G0026910-1C	TKGPADEMWDVQS(0.997)TTS(0.832)QETFK	...S..[STY]....	1069	S	-
Sspon.08G0026910-1C	TKGPADEMWDVQS(0.997)TTS(0.832)QETFK	...S..[STY]....	1066	S	-
Sspon.08G0026910-1C	SIVEGIASSS(0.957)PR	[STY]PR...	1049	S	-
Sspon.08G0026910-1C	SIVEGIAS(0.974)SSPR	[STY].S...	1047	S	-
Sspon.08G0026910-1C	ITTEGS(1)GEFFTCK	[STY].E...	1279	S	-
Sspon.08G0026910-1C	SED(0.998)DGEDVSLLR	...S..[STY]....	408	T	-
Sspon.08G0029600-1D	LSGS(0.867)EDGLTVEEYEAR	...S..[STY]....	568	S	-
Sspon.08G0030790-1D	S(1)PDGQIMQS(0.996)PSMPGK	[STY]P...	965	S	-
Sspon.08G0030790-1D	S(1)PDGQIMQS(0.996)PSMPGK	[STY]P...	957	S	-