



UNIVERSIDAD DE CÓRDOBA

FACULTAD DE CIENCIAS  
DEPARTAMENTO DE BIOQUÍMICA Y BIOLOGÍA MOLECULAR

**TESIS DOCTORAL**

**"FUNCTIONAL CHARACTERIZATION OF  
STRAWBERRY (*FRAGARIA* x *ANANASSA*) FRUIT-  
SPECIFIC AND RIPENING-RELATED GENES  
INVOLVED IN AROMA AND ANTHOCHYANINS  
BIOSYNTHESIS"**

Memoria de Tesis Doctoral presentada por Guadalupe Cumplido Laso, Licenciada en Biología, para optar al grado de Doctor por la Universidad de Córdoba con la mención de *Doctorado Internacional*.  
Córdoba, Diciembre de 2012

TITULO: *FUNCTIONAL CHARACTERIZATION OF STRAWBERRY (FRAGARIA  
x ANANASSA) FRUIT-SPECIFIC AND RIPENING-RELATED GENES  
INVOLVED IN AROMA AND ANTHOCHYANINS BIOSYNTHESIS*

AUTOR: *GUADALUPE CUMPLIDO LASO*

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**Certificamos**

Que GUADALUPE CUMPLIDO LASO, Licenciada en Biología por la Universidad de Extremadura, ha realizado bajo nuestra dirección el trabajo de investigación correspondiente a su Tesis Doctoral titulada "Functional characterization of strawberry (*Fragaria x ananassa*) fruit-specific and ripening-related genes involved in aroma and anthocyanins biosynthesis".

Revisado el presente trabajo estimamos que reúne todos los requisitos exigidos por la Normativa vigente para optar al grado de Doctor y que puede ser presentado al Tribunal que ha de evaluarlo, por ello autorizamos la defensa de esta Tesis en la Universidad de Córdoba.

Córdoba, Diciembre de 2012.



Dr. D. Juan  
Muñoz Blanco



Dra. Dña. Rosario  
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**TÍTULO DE LA TESIS: “Functional characterization of strawberry (*Fragaria x ananassa*) fruit-specific and ripening-related genes involved in aroma and anthocyanins biosynthesis”**

**DOCTORANDO/A: Guadalupe Cumplido Laso**

**INFORME RAZONADO DEL/DE LOS DIRECTOR/ES DE LA TESIS**

(se hará mención a la evolución y desarrollo de la tesis, así como a trabajos y publicaciones derivados de la misma).

La Lda. Guadalupe Cumplido Laso ha desarrollado en el seno del grupo BIO-278 liderado por el Dr. Juan Muñoz Blanco el trabajo de investigación llamado “**Functional characterization of strawberry (*Fragaria x ananassa*) fruit-specific and ripening-related genes involved in aroma and anthocyanins biosynthesis**” que constituye el tema de su tesis doctoral. Este trabajo de investigación ha sido dirigido y supervisado por el Dr. Juan Muñoz Blanco y la Dra. Rosario Blanco Portales, ambos miembros del Departamento de Bioquímica y Biología Molecular de la Universidad de Córdoba. Durante el periodo de investigación en el que se ha desarrollado esta tesis, la Lda. Cumplido Laso, además de haber desarrollado un correcto aprendizaje en el laboratorio que la ha permitido adquirir una amplia experiencia en diferentes técnicas de Biología Molecular (Microarrays, extracción de RNA, amplificación de RNA, generación de construcciones mediante tecnología Gateway, obtención e inducción de proteínas recombinantes, transformación de plantas de fresa de forma estable y transitoria, cultivo “in vitro” de plantas de fresa y las demás mostradas en el apartado de materiales y métodos de la tesis presentada) ha realizado tres estancias cortas (13 meses en total) en el grupo de investigación dirigido por el Dr. Willfried Schwab en el Departamento “Biomolecular food technology” de la Universidad Técnica de Munich (TUM), donde se realizaron parte de los análisis presentados en la tesis. Así, durante el desarrollo de esta tesis doctoral se han aislado varios genes, *FaAAT2* y *FaMyb10*, directamente relacionados con la producción del aroma y la síntesis de antocianinas respectivamente, en el fruto de fresa. El hecho de que ambos genes estén involucrados en el desarrollo de dos características tan determinantes de las propiedades organolépticas finales del fruto de fresa hace este trabajo de investigación especialmente interesante desde el punto de vista biotecnológico y abre las puertas a la obtención en el futuro de frutos de fresa mejorados. Por otra parte, los resultados mostrados en la tesis y las colaboraciones realizadas por la Lda. Cumplido-Laso dentro del grupo BIO-278 y con otros grupos de investigación de la Universidad de Málaga y de Munich han dado lugar a 11 comunicaciones a congresos, nacionales e internacionales, además de a tres publicaciones (dos de ellas bajo revisión) en revistas de alto índice de impacto en el

campo de la investigación en plantas superiores que avalan su interés para la comunidad científica.

Así, las comunicaciones presentadas a congresos han sido:

***“Searching for the Strawberry genes by functional genomic as valuable biotechnological tools”.***

Muñoz-Blanco, José Luis Caballero, Rosario Blanco-Portales, Mari Luz Bellido Cabello de Alba, **Guadalupe Cumplido Laso**, Bridget Moreno Suárez, Carmen García Limones, Francisco Amil-Ruíz, Sonia Encinas Villarejo, Aureliano Bombarely, José Sánchez Sevilla and Victoriano Valpuesta. VI Internacional Strawberry Symposium ISHS (2008) (Huelva). Comunicación oral.

***“Caracterización molecular de genes relacionados en procesos de resistencia a patógenos y en la maduración del fruto de fresa”.***

Bridget Moreno-Suárez, **Guadalupe Cumplido-Laso**, Laura Medina Puche, M Luz Bellido Cabello de Alba, José Luis Caballero, Juan Muñoz-Blanco y Rosario Blanco Portales. IX Reunión de Biología Molecular de Plantas (2008) (Santiago de Compostela).

***“Estudios de expresión y función fisiológica de una alcohol acil transferasa (FaAAT2) del fruto de fresa (Fragaria x ananassa)”.***

**Guadalupe Cumplido-Laso**, Laura Medina Puche, Bridget Moreno-Suárez, MLuz Bellido Cabello de Alba, Carmen García-Limones, Nicolás García Caparrós, Jose Luis Caballero, Juan Muñoz-Blanco y Rosario Blanco Portales. IX Reunión de Biología Molecular de Plantas (2008) (Santiago de Compostela).

***“Estudios funcionales de genes potencialmente reguladores del proceso de maduración de la fresa (Fragaria x ananassa)”.***

Rosario Blanco Portales, **Guadalupe Cumplido-Laso**, Bridget Moreno-Suárez, Laura Medina Puche, Carmen García-Limones, M Luz Bellido Cabello de Alba, Enriqueta Moyano Cañete, José Luis Caballero, Juan Muñoz-Blanco. IX Reunión de Biología Molecular de Plantas (2008) (Santiago de Compostela).

***“MADS-BOX genes involved in strawberry fruit ripening: identification of putative target genes regulated by FAMADS1 using microarrays”.***

M Luz Bellido Cabello de Alba, Rosario Blanco Portales, Enriqueta Moyano Cañete, Carmen García-Limones, **Guadalupe Cumplido-Laso**, Bridget Moreno-Suárez, Laura Medina Puche, José Luis Caballero y Juan Muñoz-Blanco. IX Reunión de Biología Molecular de Plantas (2008) (Santiago de Compostela).

***“Determinación del papel que desempeña el ácido abscísico en la maduración de la fresa mediante estudios funcionales de los genes NCEDs”.***

Laura Medina Puche, Rosario Blanco Portales, **Guadalupe Cumplido-Laso**, Bridget Moreno-Suárez, M Luz Bellido Cabello de Alba, Carmen García-Limones, Nicolás García Caparrós, José Luis Caballero y Juan Muñoz-Blanco. IX Reunión de Biología Molecular de Plantas (2008) (Santiago de Compostela).

***“Using of an fruit derived ESTs microarray platform to discover new candidate genes with potential biotechnological roles in strawberry fruit development, ripening and senescence”.***

Blanco-Portales R, Bellido-Cabello de Alba M Luz, **Cumplido-Laso G**, Medina-Puche, L, González A, Trelles O, Schwab W, Caballero JL, Muñoz-Blanco J. Plant GEMs (2009) (Lisboa)

***“Caracterización funcional de un gen que codifica a una alcohol acil trasferasa (Faaat2) de fruto de fresa (Fragaria x ananassa).***

**Guadalupe Cumplido-Laso**, Laura Medina-Puche, Bridget Moreno-Suárez, Enriqueta Moyano-Cañete, Wilfried Schwab, Juan Muñoz-Blanco, Rosario Blanco-Portales. XXXIII Congreso de la Sociedad Española de Bioquímica y Biología Molecular (SEBBM) (2010) (Córdoba). Comunicación oral.

***“Estudios funcionales de una aldo-ceto reductasa (FaAKR3) en el proceso de maduración del fruto de fresa (Fragaria x ananassa)”.***

José Antonio Mérida, Henrik Keränen, Laura Medina, **Guadalupe Cumplido-Laso**, Rosario Blanco-Portales, Juan Muñoz, Enriqueta Moyano. XXXIII Congreso de la Sociedad Española de Bioquímica y Biología Molecular (SEBBM) (2010) (Córdoba).

***“Using of an strawberry oligo microarray platform to discover new candidate genes with potential biotechnological roles in strawberry fruit development, ripening and senescence”.***

Blanco-Portales, Rosario; Moyano, Enriqueta; **Cumplido-Laso, Guadalupe**; Medina-Puche, Laura; Trelles, Oswaldo; Caballero, José Luis; Muñoz-Blanco, Juan. 28th International Horticultural Congress. IHC (2010) (Lisboa).

***“Using of an derived ESTs microarray platform to discover new candidate genes with potential biotechnological roles in strawberry fruit development, ripening and senescence”.***

Blanco-Portales, Rosario; Moyano, Enriqueta; **Cumplido-Laso, Guadalupe**; Medina-Puche, Laura; Muñoz-Mérida, Antonio; Trelles, Oswaldo; Schwab, Wilfried; Caballero, José Luis; Muñoz-Blanco, Juan. 28th International Horticultural Congress. IHC (2010) (Lisboa). Charla invitada.

Los artículos de investigación publicados o bajo revisión han sido:

***“The fruit ripening-related gene FaAAT2 encodes an acyl transferase involved in strawberry aroma biogenesis”.*** **Cumplido-Laso G**, Medina-Puche L, Moyano E, Hoffmann T, Sinz Q, Ring L, Studart-Wittkowski C, Caballero JL, Schwab W, Muñoz-Blanco J, Blanco-Portales R. (2012). Journal of Experimental Botany, 63(11): 4275-90.

Índice de impacto: 5,3

***“FaMYB10 plays a major role in the regulation of the flavonoid/phenylpropanoid metabolism during the ripening of Fragaria x ananassa fruits”.*** **Guadalupe Cumplido Laso**; Laura Medina Puche; Francisco Amil Ruiz; Bridget Moreno Suarez;

Ludwig Ring; Antonio Rodriguez Franco; José Luis Caballero; Wilfried Schwab; Juan Muñoz Blanco; Rosario Blanco Portales. Plant Physiology (bajo revisión).

Índice de impacto: 7,05.

***“Using of a fruit derived ESTs microarray platform to discover new candidate genes with potential biotechnological roles in strawberry fruit development and ripening”.***

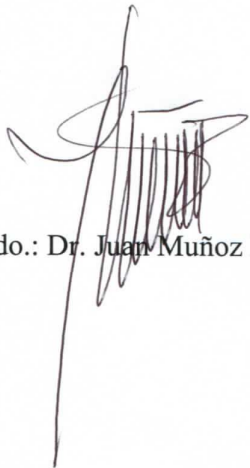
Blanco-Portales R, Bellido M Luz, **Cumplido-Laso G**, Medina-Puche L, López-Raéz JA, Moyano-Cañete E, Rodríguez-Franco A, Schwab W, Caballero JL, Muñoz-Blanco J  
BMC Genomics (bajo revisión).

Índice de impacto: 3,92.

Por todo ello, se autoriza la presentación de la tesis doctoral.

Córdoba, 7 de Diciembre de 2012

Firma del/de los director/es



Fdo.: Dr. Juan Muñoz Blanco



Fdo.: Dra. Rosario Blanco Portales





*A mi familia*



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## ABREVIATURAS

<b>Aa</b>	Aminoácido
<b>AAT</b>	Alcohol acil transferasa
<b>ABA</b>	Ácido abscísico
<b>ACP</b>	“Acyl carrier protein” (Proteína transportadora de acilos)
<b>ADH</b>	Alcohol deshidrogenasa
<b>ADN</b>	Ácido desoxirribonucleico
<b>ADNasa</b>	Desoxirribonucleasa
<b>ADNc</b>	Ácido desoxirribonucleico copia
<b>AGPs</b>	Arabinogalatan proteínas
<b>AKR</b>	Aldo ceto reductasa
<b>ANS/LDOX</b>	Antocianidin sintasa/Leucoantocianidin dioxigenasa
<b>ANR</b>	Antocianidin reductasa
<b>ARN</b>	Ácido ribonucleico
<b>ARNa</b>	Ácido ribonucleico amplificado
<b>ARNasa</b>	Ribonucleasa
<b>ARNi</b>	Ácido ribonucleico interferente
<b>ARNm</b>	Ácido ribonucleico mensajero
<b>ARNr</b>	Ácido ribonucleico ribosómico
<b>BA</b>	N <sup>6</sup> -benciladenina
<b>bHLH</b>	Basic helix-loop-helix
<b>2-BE</b>	Etilenglicol monobutil éter, 2-butoxietanol
<b>BrEt</b>	Bromuro de etidio
<b>BSA</b>	Seroalbúmina bovina
<b>CAD</b>	Cinamil alcohol deshidrogenasa
<b>CCR</b>	Cinamoil CoA reductasa
<b>C4H</b>	Cinamato-4-hydroxylasa
<b>CIAP</b>	Fosfatasa alcalina
<b>CHI</b>	Chalcona isomerasa
<b>CHS</b>	Chalcona sintasa
<b>4CL</b>	4-coumarato-CoA ligasa
<b>CoA</b>	Coenzima A
<b>CRKs</b>	“Cysteine rich kinases” (Kinasas ricas en cisteína)
<b>Ct</b>	Ciclo umbral
<b>cv.</b>	Cultivar
<b>CYP</b>	Citocromo P450
<b>2,4-D</b>	Ácido 2,4-diclorofenoxiacético
<b>Da</b>	Dalton
<b>DFR</b>	Dihidroflavonol 4-reductasa
<b>DEPC</b>	Dietil pirocarbonato
<b>dNTPs</b>	Desoxirribonucleótidos
<b>DMSO</b>	Dimetil sulfóxido
<b>DTT</b>	Ditiotreitol
<b>DO</b>	Densidad optica
<b>DsADN</b>	“Double strand ADN” (ADN de doble cadena)
<b>EDTA-Na<sub>2</sub></b>	Ácido etilendiamino tetraacético (sal disódica)
<b>EBGs</b>	“Early regulated Biosynthesis Genes” (Genes tempranos reguladores de la biosíntesis del metabolismo de flavonoides/fenilpropanoides)

<b>ENODLs</b>	“Early nodulin like proteins” (Nodulinas tempranas)
<b>ERF</b>	“Ethylene Response Elements” (Elementos de respuesta al etileno)
<b>EST</b>	“Expressed sequence tag” (Secuencia de ADNc expresada)
<b>EtOH</b>	Etanol
<b>ET</b>	Etileno
<b>Fds</b>	Ferredoxina
<b>Fig.</b>	Figura
<b>F3H</b>	Flavonona-3-hidroxilasa
<b>F3'H</b>	Flavonona-3'-hidroxilasa
<b>F3'5'H</b>	Flavonona-3'-5'-hidroxilasa
<b>FKF</b>	“Flavin binding kelch repeat F-box”
<b>FLS</b>	Flavonol sintasa
<b>FT</b>	Factor de transcripción
<b>GAs</b>	Giberelinas
<b>GC-MS</b>	Cromatografía de gases-espectrometría de masas
<b>Grx</b>	Glutarredoxina
<b>GST</b>	Glutation-S-transferasa
<b>HDMF</b>	2,5-dimethyl-4-hydroxy-3(2H)-furanone (Furaneol)
<b>HMDF</b>	4-hidroxi-2,5-dimetil-3(2H)-furanona
<b>HPLC</b>	Cromatografía líquida de alta presión
<b>IAA</b>	Ácido indolacético
<b>IPTG</b>	Isopropil- $\beta$ -D-galactósido
<b>IVT</b>	Transcripción <i>in vitro</i>
<b>Kb</b>	Kilobase
<b>MMA</b>	Murashige y Skoog Sal morfina ácido etanosulfónico acetosiringona
<b>LB</b>	Medio de cultivo Luria-Bertani
<b>LAR</b>	Antocianidin reductasa
<b>LAGs</b>	“Late-regulated Biosynthesis Genes” (Genes tardíos reguladores de la biosíntesis del metabolismo de flavonoides/fenilpropanoides)
<b>LRR-RLKs</b>	“Leucine Rich repeat like kinases” (Kinasas ricas en leucina)
<b>MAPKs</b>	“Mitogen activated protein kinases” (Proteínas kinasas activadas por mitógenos)
<b>MATE</b>	“Multidrug and toxic efflux” (Proteínas implicadas en el flujo de múltiples fármacos y tóxicos)
<b>MeJA</b>	Metil Jasmonato
<b>MOPS</b>	Ácido 3(N-morfolino)propanosulfónico
<b>MS</b>	Medio de cultivo Murashige y Skoog
<b>NAA</b>	Ácido naftalenacético
<b>NaAC</b>	Acetato sódico
<b>NBT</b>	Nitroblue tetrazolium
<b>NCBI</b>	“National Center for Biotechnology Information” (Centro Nacional de Información sobre Biotecnología)
<b>NCED</b>	9-cis-epoxicarotenoide dioxigenasa
<b>NDGA</b>	Ácido nordihidroguaiarético
<b>NIP</b>	“Nodulin intrinsic protein”
<b>NPR</b>	“Non expressor of pathogenesis related”
<b>nptII</b>	Neomicina fosfotransferasa II
<b>NZ-amina</b>	Hidrolizado de caseína
<b>NZY</b>	Medio de cultivo de microorganismos

<b>OMT</b>	O-metiltransferasa
<b>OPT</b>	“Oligopeptides transporters” (Oligopéptidos transportadores)
<b>ORF</b>	“Open Reading frame” (Marco abierto de lectura)
<b>PAGE</b>	Electroforesis en gel de poliacrilamida
<b>PAE</b>	Pectin acetil esterasa
<b>PAL</b>	Fenilalanina amonio liasa
<b>Pb</b>	Pares de bases
<b>PCR</b>	Reacción en cadena de la polimerasas
<b>PEG</b>	Polietilenglicol
<b>pI</b>	Punto isoeléctrico
<b>PL</b>	Pectato liasa
<b>ppm</b>	Partes por millón
<b>PRE</b>	Paclbutrazol resistente
<b>PTR</b>	“Peptides transporters” (Péptidos transportadores)
<b>QR</b>	Quinona reductasa
<b>QRTPCR</b>	“Quantitative real time PCR” (PCR cuantitativa en tiempo real)
<b>rpm</b>	Revoluciones por minuto
<b>RACE</b>	“Rapid Amplification of cDNA Ends” (Amplificación rápida de extremos de un ADNc”
<b>RG</b>	Ramnogalacturonano
<b>RLKs</b>	“Receptor like kinase” (Receptor de kinasa)
<b>RT</b>	Reacción de retrotranscripción
<b>RT-PCR</b>	Retrotranscripción y reacción en cadena de la polimerasa
<b>RZS</b>	Rapsberry cetona/ziringona sintasa
<b>SCAI</b>	Servicio Central de Apoyo a la Investigación
<b>SD</b>	Desviación estándar
<b>SDS</b>	Dodecil sulfato sódico
<b>SGR</b>	“Stay green proteins”
<b>SKDH</b>	Sikimato deshidrogenasa
<b>Sp.</b>	Especie
<b>Spp.</b>	Subespecie
<b>ssADN</b>	“Single strand ADN” (ADN de cadena simple)
<b>SM</b>	Solución tampón para los fagos
<b>SPME</b>	Solid phase microextraction (Microextracción en fase sólida)
<b>Supl.</b>	Suplemento
<b>TAE</b>	Tampón tris-acetato-EDTA-Na <sub>2</sub>
<b>TBE</b>	Tampón Tris-bórico-EDTA-Na <sub>2</sub>
<b>TBS</b>	Tampón tris-HCl-NaCl
<b>TE</b>	Tampón TRIS-HCl 10 mM, EDTA-Na <sub>2</sub> 1 mM
<b>TIPs</b>	“Tonoplast intrinsic proteins” (Proteínas intrínsecas del tonoplasto)
<b>Tm</b>	Temperatura de <i>melting</i> (Temperatura de fusión)
<b>TMV</b>	“Tobacco mosaic virus” (Virus del mosaico del tabaco)
<b>TF</b>	Factor de transcripción
<b>TPR</b>	“Tetracopeptide repeat motifs”
<b>Tris</b>	Tris (hidroximetil) aminometano
<b>Trx</b>	Tiorredoxina
<b>TTBS</b>	Tampón TBS con tritrón X-100
<b>UFGT</b>	UDP glucosa:flavonoide-3-O-glucosiltransferasas
<b>UV</b>	Radiación Ultravioleta
<b>Wt</b>	“Wild type” (Planta silvestre)

**X-gal**  
**XTH**

5-Bromo-4-cloro-3-indolil  $\beta$ -galactósido  
Xiloglucan endotransglicosilasa/hidrolasa

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## FUNCTIONAL CHARACTERIZATION OF STRAWBERRY (*FRAGARIA* x *ANANASSA*) FRUIT-SPECIFIC AND RIPENING- RELATED GENES INVOLVED IN AROMA AND ANTHOCHYANINS BIOSYNTHESIS

Along the development of this thesis, we have studied the transcriptomic changes that occur in the receptacle of the strawberry fruit (*Fragaria x ananassa* cv Camarosa) during ripening using an oligo microarray platform of strawberry fruit. This analysis allowed us to select several target genes with biotechnological importance potentially involved in the process of fruit ripening, since they are determinants of some relevant organoleptic properties that directly influence the final quality of strawberry fruit.

One of the selected genes (*FaAAT2*) showed significant homology of sequence with genes of higher plants encoding alcohol acyltransferases (AATs), proteins involved in generating the characteristic aroma of ripe strawberry fruit. These enzymes are involved in the final step in the biosynthesis of volatile esters, catalyzing the esterification of acyl moiety of acyl-CoA with an alcohol. In this work, we have observed a clear correlation between the increase in *FaAAT2* gene expression and the increase of volatile esters biosynthesis along the strawberry maturation. Furthermore, it has been found that their expression is negatively regulated by auxin synthesized in the achenes.

On the other hand, we evaluated the enzymatic activity of FaAAT2 protein recombinant derived from the full-length *FaAAT2* cDNA using a wide variety of acyl-CoA and alcohols as substrates. The recombinant enzyme showed activity in the presence of straight chain alcohols and aromatic alcohols in combination with acetyl-CoA, although it had preference for the cinnamyl alcohol as acceptor of acyl groups. The analysis of potential substrates for this enzyme present in the strawberry fruit indicated that the FaAAT2 protein always has preference to C6-C10 alcohols, being more active with hexanol and heptanol followed by octanol. Therefore, our results suggest that the FaAAT2 protein can produce esters as hexyl acetate and octyl acetate present in the strawberry fruit.

After the transient silencing of *FaAAT2* gene expression, we observed a significant reduction of volatile esters in the transgenic strawberry fruit, suggesting that the FaAAT2 enzyme could be related with the synthesis of volatile compounds involved in the final aroma of the strawberry fruit.

The second gene selected for our study was a transcription factor belonging to the MYB family (*FaMYB10*), which is involved in regulating the metabolism of flavonoids/phenylpropanoids during the strawberry fruit ripening. The expression of this gene is fruit receptacle specific, inducible along its maturation and regulated by auxin and abscisic acid. Furthermore, transcriptome analysis of transgenic fruits with the *FaMYB10* expression transiently silenced indicated that many of the genes involved in the metabolism of flavonoids/phenylpropanoids [*Early-regulated Biosynthesis Genes* (EBGs): *CHS*, *CHI*, *F3H*, *FLS*; *Late-regulated Biosynthesis Genes* (LBGs): *DFR*, *UFGT*; and genes of the general pathway: *PAL*, *C4H*, *4CL*] may be regulated by this transcription factor which also seems to repress genes involved in the biosynthesis of proanthocyanidins (PAs) (Glycosyltransferases, *F3'5'H*, *LDOX/ANS*, *LAR*) in immature fruit receptacle. We have also found that the *FaMYB10* gene induces the expression of

GST and MATE transporters and appears to regulate other transcription factors involved in the strawberry maturation. Thus, our results indicate that the *FaMYB10* transcription factor plays a key role in the strawberry fruit ripening acting as an important part of the signal transduction cascade during this process.



## FUNCTIONAL CHARACTERIZATION OF STRAWBERRY (*FRAGARIA* x *ANANASSA*) FRUIT-SPECIFIC AND RIPENING- RELATED GENES INVOLVED IN AROMA AND ANTHOCHYANINS BIOSYNTHESIS

Durante el desarrollo de esta tesis doctoral, se ha procedido al estudio de los cambios transcriptómicos que se producen en el receptáculo de fruto de fresa (*Fragaria x ananassa* cv Camarosa) durante su maduración empleando una plataforma de microarrays de oligos de fruto de fresa. Este análisis nos permitió seleccionar varios genes diana potencialmente implicados en el proceso de maduración del fruto y con gran importancia biotecnológica, ya que son determinantes de algunas de las propiedades organolépticas que influyen directamente en la calidad final del fruto de fresa.

Uno de los genes seleccionados (*FaAAT2*) presentó homología significativa de secuencia con genes de plantas superiores que codifican alcohol aciltransferasas (AATs), proteínas implicadas en la generación del aroma característico del fruto de fresa maduro. Estas enzimas participan en el último paso de la biosíntesis de ésteres volátiles, catalizando la esterificación de un resto acilo de acil-CoA con un alcohol. En este trabajo hemos determinado que existe una clara correlación entre el incremento de expresión del gen *FaAAT2* y el aumento de la biosíntesis de ésteres volátiles a lo largo de la maduración de la fresa. Además, se ha comprobado que su expresión está regulada negativamente por las auxinas sintetizadas en los achenios.

Por otra parte, se analizó la actividad enzimática de la proteína recombinante FaAAT2 obtenida a partir del ADNc completo del gen *FaAAT2* empleando una amplia variedad de acil-CoA y alcoholes. La enzima recombinante obtenida mostró actividad en presencia de alcoholes de cadena lineal y alcoholes aromáticos combinados con acetil CoA, aunque mostró preferencia por el cinnamil alcohol como aceptor de grupos acilos. El análisis de los posibles sustratos presentes en el fruto de fresa para esta enzima indicó que la proteína FaAAT2 mostró siempre preferencia por alcoholes C6-C10, siendo más activa con hexanol seguida de octanol y heptanol. Por tanto, nuestros resultados sugieren que la proteína FaAAT2 puede producir ésteres como hexil acetato y octil acetato presentes en el fruto de fresa.

Paralelamente y mediante el silenciamiento transitorio de la expresión del gen *FaAAT2*, se observó una reducción significativa de la producción de volátiles en el fruto de fresa, lo que sugiere que la enzima FaAAT2 estaría implicada en la síntesis de compuestos volátiles y contribuiría de forma importante al aroma final del fruto de fresa.

El segundo gen seleccionado para su estudio fue un factor de transcripción perteneciente a la familia MYB (*FaMYB10*) implicado en la regulación del metabolismo de los flavonoides/fenilpropanoides durante la maduración del fruto de fresa. La expresión de dicho gen resultó ser específica de receptáculo de fruto, inducible a lo largo de la maduración de éste y regulada por auxinas y ácido abscísico. Por otra parte, el análisis transcriptómico de frutos transgénicos con la expresión del gen *FaMYB10* silenciada de forma transitoria indicó que muchos de los genes implicados en el metabolismo de flavonoides/fenilpropanoides [*Early-regulated Biosynthesis Genes* (EBGs): *CHS*, *CHI*, *F3H*, *FLS*; *Late-regulated Biosynthesis Genes* (LBGs): *DFR*, *UFGT*; y genes de la ruta

general: *PAL*, *C4H*, *4CL*] podrían estar regulados por este factor de transcripción, mientras que reprimiría genes involucrados en la biosíntesis de las proantocianidinas (PAs) (Glicosiltransferasas, *F3'5'H*, *LDOX* /*ANS*, *LAR*) en receptáculo de frutos inmaduros. Hemos comprobado también que el gen *FaMYB10* activa la expresión de los transportadores *GST* y *MATE* y parece regular muchos factores de transcripción implicados en la maduración de la fresa. Por tanto, nuestros resultados indican que el factor de transcripción *FaMYB10* juega un papel importante en el proceso de maduración del fruto de fresa actuando como parte importante de la cascada de transducción de señales durante este proceso.

## SUMMARY GENERAL INTRODUCTION

The strawberry (*Fragaria x ananassa*) belongs to the family Rosaceae in the genus *Fragaria*. This soft fruit is cultivated in different regions of the world and is part of the diet of millions of people. Spain is the first producer of strawberries in Europe and the third one in the world after United States and China. The main octoploid variety *Fragaria x ananassa* cultivated is the result of crossing two native American species, *F. virginiana* and *F. chiloensis* (Hancock, 1999; Maberley, 2002; Eriksson *et al.*, 2003). The wild diploid species *Fragaria vesca* is also considered as an ancestor of the cultivated octoploid variety. Recently, the genome of the wild species *Fragaria vesca* has been sequenced (Shulaev *et al.*, 2010). This information, together with the ESTs (*expressed sequence tag*) availability from cultivated species and the development of efficient transformation techniques of these varieties, will allow the development of genomics and recombinant DNA studies between different species of Rosaceae in the future (Bombarely *et al.*, 2010).

The strawberry is a herbaceous perennial plant that has a central stem or crown from which leaves, roots, stolons and inflorescences emerge (Hancock, 1999). The development of the strawberry is determined by the interaction between temperature and photoperiod. The strawberry fruit is considered as a false fruit composed by the achenes (true fruits) and the receptacle, which results of the flower receptacle development (Erendorfer, 1983; Hancock, 1999). The receptacle is formed by a pith at the centre, a fleshy cortex, epidermis, and a ring of vascular bundles with branches that connect the receptacle with the achenes embedded in the epidermal layer. Each fruit can have from 20 to 500 achenes, depending on the cultivar and environmental conditions, formed for a combination of seed and ovary tissue.

Strawberry fruit has been classified as non-climacteric, since there is no concomitant burst of respiration and ethylene production that triggers to the ripening process. Thus, all changes related with the fruit ripening occur without a significant increase in ethylene production, which suggests that this process is independent of this hormone (Iwata *et al.*, 1969a and 1969b; Villareal *et al.*, 2009). The strawberry fruit has a maximum respiration at the transition between stages ripe to overripe.

Strawberries are very appreciated by its flavor, aroma and nutritional value. The mature fruit is composed of approximately 90 % water and 10% total soluble solids. Moreover, it contains many important dietary components such as vitamin C, soluble sugars such as glucose and fructose (which constitute over 80 % of total sugars), organic acids such as citric acid (88 % of total acids) and ellagic acid, which has anticancer properties (Green, 1971; Wrolstad and Shallenberger, 1981; Maas *et al.*, 1991; Hemphill and Martin, 1992; Maas *et al.* 1996; Hancock, 1999).

Soft fruits have an initial phase of growth and elongation, followed by a phase of maturity. The growth of the strawberry receptacle depends of the cortex and medulla cells development while the fruit size is mainly determined for the medulla cells development and the fruit position in the inflorescence (Hancock, 1999). Moreover, the fruit development is determined by the number and distribution of achenes, the receptacle area around each achene and the percentage of fertilized carpels. In this sense, the synthesis of auxin, fundamentally indole-3-acetic acid (IAA), which takes

place in the achenes, is considered the main responsible of the receptacle growth while gibberellins, cytokinins and abscisic acid have a limited role in the fruit growth (Nitsch, 1950; Perkins-Veazie, 1995).

The growth kinetic changes with the cultivar. Thus, while some cultivars present a single sigmoidal growth phase, other ones show a two-phase model of growth (Woodward, 1972; Archbold and Dennis, 1984; Forney and Breen, 1985; Stutte and Darnell, 1987; Perkins-Veazie and Huber, 1987). During elongation, cortical cells undergo an isodiametric growth, together with important changes in the cell wall and subcellular structures. The ripening phase is completed in 30-40 days from anthesis and is determined by physical changes (changes of texture and color), chemical changes (production of aromas and flavors) and variation of gene expression patterns (Knee *et al.*, 1977; Dennis, 1984). At cellular level, maturation causes an increase in cell size, the formation of great vacuolar spaces and modifications of the cell wall that cause occlusion of the intercellular spaces with a carbohydrate matrix (Neal, 1965). In any case, the phase of cell elongation of strawberry fruit depends of the temperature, the contribution of assimilates and water balance fruit / plant.

Along the development and ripening processes, the strawberry fruit suffers important molecular changes such the removal of existing polypeptides and the synthesis of new proteins (Manning, 1994). In this sense, three evolution models of the transcripts have been described: mRNA whose concentration increases along the ripening, mRNA whose levels decrease over the ripening, and mRNA whose components exceed their maximum concentration in the intermediate stage, which then declined in stages of maturation (Veluthambi and Poovaiah, 1984; Reddy and Poovaiah, 1990; Reddy *et al.*, 1990; Manning, 1994).

The hormonal regulation of the fruit development and maturation is one of the most studied processes in strawberry. Auxin produced by the achenes inhibits the fruit ripening in the green stage and, when the IAA concentration declines in the receptacle due to the achenes lignification, the fruit development and ripening begin (Dada *et al.*, 1988; Given *et al.*, 1988b). This suggests that the auxin stimulates the elongation of the fruit while repress its maturation. In parallel, a maximum activity of both cytokinins and gibberellins have been detected mainly in achenes 7 days after anthesis. It has been suggested that the GAs could control the induction of cell division in subapical tissues of axillary buds while that variations in the concentration of cytokinins are important in the process of flowering of strawberry plants (Eshghi and Tafazoli, 2007; Hytönen *et al.* (2009). Additionally, GAs also participates in the differentiation of axillary buds regulated by photoperiod (Hytönen *et al.*, 2009). On the other hand, the abscisic acid (ABA) is also very important in the strawberry development. Generally, this phytohormone is involved in seed maturation, acquisition of tolerance to senescence, in vegetative growth, and in the physiological responses that confers tolerance to water and osmotic stress (Mishra *et al.*, 2006). Moreover, the ABA slows down the growth in plants subjected to water stress by the restriction of ethylene production (Sharp, 2002) and acts over the biotic response (Fan *et al.*, 2009). In strawberry fruit, this hormone is accumulated in both achenes and receptacles after 20 days post anthesis. This increase is concomitant with the decrease of IAA level in both tissues, therefore the ratio ABA / IAA might be sufficient to drive genetic changes that occurs during the transition of elongation phase to fruit ripening phase (Perkins-Veazie *et al.*, 1995). The ABA seems to play a crucial role in the regulation of fruit ripening as the application of exogenous

ABA promotes the ripening of strawberry (Jia *et al.*, 2011). The *FaNCED1* gene silencing, which encodes an important protein in ABA biosynthesis, reduced the endogenous ABA levels in the strawberry fruits producing transgenic fruits without colour with the ripening inhibited (Jia *et al.*, 2011). Moreover, the application of exogenous ABA reversed the transgenic phenotype suggesting that ABA promotes maturation of the strawberry fruit (Jia *et al.*, 2011). The ethylene production also has a maximum level in green fruits (G1-G3) that decreases in white fruit (W) and increases again reaching a maximum in the mature stage (R) (Perkins-Veazie *et al.*, 1995). This amount of ethylene produced during the strawberry ripening, although small, might be sufficient to trigger some of the physiological changes associated with this process (Trainotti *et al.*, 2005).

Carbohydrates are one of the main soluble compounds of the soft fruits. In addition to provide energy for metabolic changes, the carbohydrates have an outstanding role in the generation of flavor. Organic acids, besides being compounds determinants of strawberry fruit flavor, also determine its color, inhibit activity of certain enzymes and change the texture of the fruit (Mussinan and Walradt, 1975). The no-volatile organic acids (citric, malic, etc.) are quantitatively the most important in determining the acidity of the fruit, while volatile organic acids contribute significantly to the aroma of fruit (Mussinan and Walradt, 1975). On the other hand, the phenolic acids provide the fruit acidity and tannins are responsible of the astringency of the fruit as result of its interaction with proteins and mucopolysaccharides of the spit (Ozawa *et al.*, 1987; Ferrer, 1997). The flavones provide the characteristic bitter flavor of the development green stages (Hobson, 1993). These compounds are usually stored in the vacuole and its concentration varies during ripening depending on the variety and the environmental conditions of the plant.

The flavor of strawberry fruit is determined by the complex mixture of volatile compounds and other constituents (such as sugars, organic acids, phenolics and tannins), although esters are one of the most important groups of volatile compounds associated with the aroma of strawberry. Of all these compounds, about one hundred different types have been identified but only some of them contribute decisively to determine the final fruit aroma (Zabetakis and Holden, 1997). In ripe strawberry fruit, the most abundant volatile esters are ethyl butanoate, 2-methyl-ethyl butanoate and ethyl hexanoate. One of enzymes involved in the formation of these esters is the alcohol acyl transferase (AAT) that catalyzes the transfer of the acyl group from acyl-CoA to an alcohol. The AAT expression begins in the white stage of fruit and continues increasing in the intermediate stage to its maximum expression in the red stage, coinciding with the highest levels of volatile esters in the fruit (Pérez *et al.*, 1996; Aharoni *et al.*, 2000). On the other hand, terpenoids are other compounds that also seem to be involved in the aroma of strawberry (Loughrin and Kasperbauer, 2002). Linalool, nerolidol,  $\alpha$ -pinene and limonene are predominant volatile terpenes in strawberries that can be up to 20 % of total volatile fruit (Loughrin and Kasperbauer, 2002). The recombinant enzyme *FaNES1* synthesized (S)-linalool and trans-(S)-nerolidol of GDP and FDP respectively. This gene is expressed strongly and specifically in fruits of cultivated varieties (octoploid) but not in wild varieties. Thus, the linalool and nerolidol are part of the final composition of the fruit aroma in strawberry cultivated varieties. Therefore, the aroma of strawberry is the result of the combination of odors "fruity" (ethyl butanoate, ethyl hexanoate and methyl 2-methylbutanoate), green (Z-3-hexenal), "sweet" (acid butanoic acid and 2-methylbutane), "peach" (decalactone), "Candy" (4-hydroxy-2,5-dimethyl-3

(2H)-furanone (HDMF, furaneol) and 2,5-diethyl-4-methoxy-3 (2H)-furanone (DMMF)) (Aharoni *et al.*, 2004). From these volatile compounds, the HDMF shows a high concentration and a low odor threshold.

Along the development process and strawberry fruit ripening, there is a color transition from the initial green color to red color characteristic of fully mature fruit. This color change is due both to degradation of chlorophyll and the synthesis of anthocyanins located in the vacuoles (Timberlake, 1981; Perkin-Veazie, 1995). Anthocyanin biosynthesis begins in the white fruit from phenylpropanoid and flavonoid by the shikimic acid pathway. The predominant anthocyanin in strawberries is pelargonidin-3-glucoside, which represents 88% of the anthocyanin in the fruit (Perkin-Veazie, 1995). The total concentration of anthocyanins varies about 16 times in the different cultivars and also in its composition. Recently, all these secondary metabolites have gained considerable importance due to its ability to prevent and protect against degenerative and cardiovascular diseases.

The formation of flowers on the strawberry plant is induced at low temperatures and short photoperiods while the floral bud development depends of the temperature and day length. Auxins and cytokinins also play an important role in this process. To improve the strawberry crop, adaptability and disease resistance are studying the effect on the development and fruiting of plants changing their hormonal regulation. These changes can be achieved by introducing genes able to alter the endogenous regulation of plant growth. Other tool used for manipulating endogenous phytohormones is the transformation of strawberry plants with oncogenes from *A. rhizogenes* or *A. Tumefaciens* (Zuker *et al.*, 2001; Casanova *et al.*, 2005).

The strawberry plants are exposed to different abiotic agents (water deficit, high temperature, salinity, heavy metals and mechanical damage), in its natural habitat and these stress conditions can reduce crop yields by up to 50 %. Recently, physiological, biochemical and molecular studies have been performed to improve the plant tolerance to these stresses. Genes as *Fcor1*, 2 and 3 showed a differential expression at low temperatures (NDong *et al.*, 1997) that was accompanied by an accumulation of the glycine betaine in different strawberry cultivars (Rajashekar *et al.*, 1999). The synthesis of a specific group of proteins called heat shock proteins (HSP) has also been observed under high temperatures conditions (Medina-Escobar *et al.*, 1998). On the other hand, Methionine sulfoxide reductase (PMSR) is a relevant peptide in the protection of cells against oxidative damage caused by salt stress and pathogen infection (López *et al.*, 2006).

The strawberry is also susceptible to many diseases and plagues that cause significant economic losses due to expenditure on plant treatments and reducing production. Therefore, the improvement of the strawberry natural resistance by genetic manipulation is an important research objective. For instance, the loci *Rfp1* is associated with the resistance to *Phytophthora fragaria* (Haymes *et al.*, 1997). Moreover, polygenic factors present additive effects against *Verticillium dahliae* (Zebrowska *et al.*, 2006). The strawberry plants produce volatile organic compounds (VOC), which have antifungal activity against *C. acutatum* (Arroyo *et al.*, 2007). In addition, *Fragarina* is a small molecule that responses to stress processes (Filippone *et al.*, 1999). Finally, transgenic strawberry plants with high levels of chitinase reduce the harm effects caused by the oidium fungus (Asao *et al.*, 1997; Asao *et al.*, 2003).

In general, the programs of biotechnology and breeding of berries have as priority the improvement of the fruit quality. For these fruits, the taste (result of the combination of sweetness, acidity and aroma), and firmness are of great economic importance and, therefore, the genes involved in these processes are being studied by transgenesis. However and, although the evaluation of the transgenic gene function can be a valuable tool for the selection of genes, is quite slow.

# INTRODUCCIÓN GENERAL

## 1. LA PLANTA DE FRESA: GENERALIDADES

### 1.1. Origen, especiación y evolución

La fresa, perteneciente al género *Fragaria* L., es un fruto de tipo baya con gran importancia económica en todo el mundo. Este género está incluido dentro de la familia Rosaceae, subfamilia Potentilloideae (anteriormente clasificados dentro de la familia Rosidaeae), teniendo como parientes cercanos a *Duchenea* y *Potentilla* (Mabberley, 2002; Eriksson *et al.*, 2003).

La variedad *Fragaria x ananassa* Duchesne ex Rozier nothosubsp. *ananassa* forma parte regular de la dieta de millones de personas y se cultiva en diferentes regiones del mundo, desde el Ártico hasta los Trópicos. Más de 75 países en el mundo presentan una producción significativa de fresa (FAO, 2007) que ha alcanzado en los últimos 20 años más de 3,6 millones de toneladas métricas (Fig.1). La mayor parte de la producción tiene lugar en el hemisferio norte (98%), aunque no existen barreras genéticas ni climáticas que impidan la expansión hacia el sur. España representa el primer productor de fresa fresca de Europa y el tercero del mundo, tras Estados Unidos y China (FAOSTAT, 2005). De las 295.000 Tm que representan la producción media anual española, el 95% se concentra en la provincia de Huelva (Freshuelva, 2005), la mitad de la cual es exportada a otros países europeos (Infoagro, 2002). No obstante, se estima que entre el 5 y el 25 % de la producción, dependiendo de la variedad, se pierde debido al reblandecimiento que sufre el fruto a lo largo de su maduración, a la infección por diferentes patógenos (infecciones favorecidas por el sistema de cultivo de la planta y por la siembra sucesiva sobre el mismo sustrato), así como por otros factores que afectan a la calidad del fruto (López-Aranda, 1997).

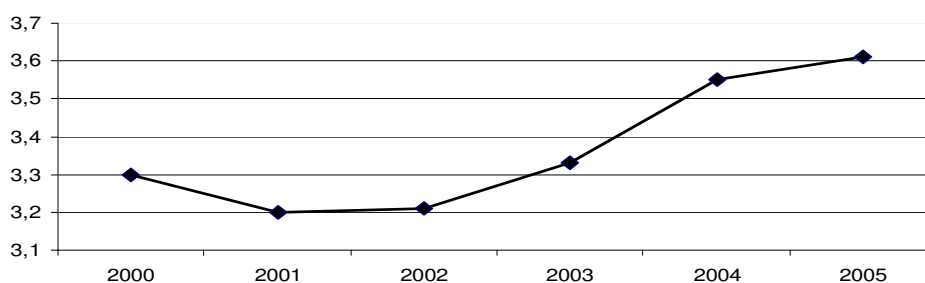


Fig. 1. Producción de fresa en el mundo (FAO, 2007), Tm por año.

El género *Fragaria* incluye 21 especies (Tabla 1) distribuidas en la zona norte, templada y zona holártica (Staudt, 1989, 1999a, b; Rousseau-Gueutin *et al.*, 2008). Actualmente, se han caracterizado las especies europeas, americanas (Staudt *et al.*, 1989; 1999a) y asiáticas (Staudt 1999b, 2003, 2005; Staudt y Dickoré., 2001) de *Fragaria* y están bajo estudio las especies



chinas aunque su caracterización requiere la recopilación y el análisis taxonómico mundial (Dai *et al.*, 2007; Lei *et al.*, 2005). En general, la distribución de los niveles de ploidía específicos en determinados continentes refleja la historia y evolución de estas especies (Staudt, 1999).

En el caso de *Fragaria x ananassa*, los cultivos actuales de esta especie son el resultado del cruzamiento entre dos especies americanas nativas, *F. chiloensis* y *F. virginiana* Duch. (Hancock, 1999). Estas dos especies fueron introducidas en Europa en el siglo XVIII y, posteriormente, fueron cruzadas entre sí.

<i>Especies</i>	<i>Ploidía</i>	<i>Distribución geográfica</i>
<i>F. bucarica</i>	2x	Oeste del Himalaya
<i>F. daltoniana</i> J. Gay		Himalayas
<i>F. gracilis</i> A. Los.		Norte de China
<i>F. innumae</i> Makino		Japón
<i>F. mandshurica</i> Staudt		Norte de China
<i>F. nilgerrensis</i> Schlect.		Sureste de Asia
<i>F. nipponica</i> Lindl.		Japón
<i>F. nubicola</i> Lindl.		Himalaya
<i>F. pentaphylla</i> Lozinsk		Norte de China
<i>F. vesca</i> L.		Europa, Oeste de Asia (Urales), Norte de America
<i>F. viridis</i> Duch.		Europa y Asia
<i>F. yezoensis</i>		Japón
<i>F. corymbosa</i>	4x	Norte de China
<i>F. gracilis</i>		Noroeste de Cina
<i>F. moupinensis</i> (French.) Card		Norte de China
<i>F. orientalis</i> Losinsk syn.= <i>F. corymbosa</i> Lozinsk		Región extremo oriental de Rusia/China
<i>F. tibetica</i> spec. Nov. Ataudt		China
<i>F. x bringhurstii</i> Staudt	5x	California
<i>F. moschata</i> Duch.	6x	Euro-Siberia
<i>F. chiloensis</i> (L.) Miller	8x	Oeste de Norte América, Hawaii y Chile
<i>F. virginiana</i> Miller		Norte America
<i>F. x ananassa</i> Duch. Ex Lamarck		Cultivado en todo el mundo
<i>F. iturupensis</i> Staudt	10x	Isla Iturup, islas Kurile

**Tabla 1. Distribución de las especies de fresa en el mundo (*Fragaria* L.)** (Hummer K.E. and Hancock J., 2009).

La especie diploide *Fragaria vesca* también ha sido considerada como un antepasado de la variedad cultivada octoploide. Recientemente, se ha secuenciado el genoma de la especie silvestre *Fragaria vesca* (Shulaev *et al.*, 2010) y esta información, junto con la disponibilidad de ESTs (*expressed sequence tag*) de especies cultivadas y el desarrollo de técnicas de transformación de estas variedades, permitirán en un futuro el desarrollo de estudios de ADN recombinante y genómica entre diferentes especies de rosáceas (Bombarely *et al.*, 2010).

## 1.2. Citología e interfertilidad

El género *Fragaria* tiene un número cromosómico básico de siete ( $x = 7$ ) (Ichijima, 1926) pero se han identificado cuatro grupos principales de fertilidad: los diploides ( $2n = 2x = 14$ ) que incluyen el género *F. vesca* (Oosumi *et al.*, 2006); los tetraploides ( $2n = 4x = 28$ ) dentro del cual está *F. orientalis*; la especie hexaploide, donde solamente encontramos a *F. moschata* ( $2n = 6x = 42$ ); y cuatro especies octoploides ( $2n = 8x = 56$ ), *F. chiloensis*, *F. iturupensis*, *F. virginiana* y el híbrido cultivado *Fragaria x ananassa*. Las especies octoploides están compuestas por un genoma AAA'A'BBB'B' que implica la contribución de al menos cuatro genomas diploides ancestrales distintos (Bringhurst, 1990). Sin embargo, otros modelos previamente descritos para la composición del genoma (AAAABBCC) (Fedorova, 1946) y (AAA'A'BBBB) (Senanayake y Bringhurst, 1967) respectivamente, indicaron la posibilidad de un componente autoploide dentro del genoma, por lo que su composición en las especies octoploides aún no ha sido rigurosamente establecido.

Se han propuesto numerosos progenitores diploides para las especies octoploides, incluyendo *F. vesca* y la especie japonesa endémica *F. iinumae* (Hancock, 1999), pero se están utilizando otras especies diploides para la investigación genómica de *Fragaria*, incluyendo *F. iinumae* (Folta y Davis, 2006), *F. viridis* (Sargent *et al.*, 2003; Nier *et al.*, 2006) y *F. nubicola* (Sargent *et al.*, 2004a; Sargent *et al.*, 2006; Sargent *et al.*, 2007; Vilanova *et al.*, 2008).

Los cromosomas de *Fragaria* son más bien pequeños, variando entre 0,9 a 1,7 micras de longitud (Yarnell, 1928), y muestran muy poca variación morfológica entre diferentes especies (Iwatsubo y Naruhashi, 1989, 1991). Ichijima (1926) realizó estudios sobre la citología de los cromosomas de *Fragaria* en diversos niveles de ploidía. En las especies diploides estudiadas, no se observó ningún comportamiento cromosómico irregular en el curso de divisiones heterotópicas, conservándose los 14 cromosomas somáticos previamente observados en metafase. En el caso de especies octoploides de *Fragaria*, fue difícil contar los cromosomas somáticos porque su empaquetamiento fue irregular y sólo pudieron ser cuantificados en fase de diacinesis tardía. Así, el número definitivo de cromosomas en estos experimentos no se pudo determinar aunque se estimó que pudieran ser 56, lo que era esperable para una especie octoploide que posee un número haploide de cromosomas  $x = 7$ . Por otra parte, Lim (2004) empleó en *F. vesca* la técnica de hibridación *in situ* fluorescente (FISH) usando los genes de ARNr 45S y 5S. Los resultados revelaron, dentro de los 14 cromosomas somáticos de *F. vesca*, seis sitios 45S y dos sitios 5S lo que permitió la construcción de un cariotipo de esta variedad que incluía tres pares de cromosomas marcadores. A pesar de los resultados obtenidos con esta técnica, aún no se ha extendido su aplicación para mejorar el conocimiento de la genética y citología de genomas octoploides de la especie *Fragaria* (Hummer K.E. y Hancock J., 2009).

## 1.3. Análisis filogenético

A partir de ADN procedente del cloroplasto (cpDNA) y secuencias ITS (espaciadores de transcripción interna) de la región nuclear, se han determinado las relaciones filogenéticas entre las diferentes especies de *Fragaria* (Harrison *et al.*, 1997a; Potter *et al.*, 2000). Dentro de esta filogenia, se ha encontrado un grupo formado por varias especies monofiléticas (ej: *F. viridis* y *F. nilgerrensis*) y otro mayor formado por *F. vesca*, *F. bucharica* (antes *F. nubicola*) y los poliploides de *Fragaria*.

Sargent (2005) estudió con mayor profundidad las relaciones filogenéticas entre muchos de los diploides de *Fragaria* utilizando datos de secuencias ITS y cuatro regiones cpDNA. De esta manera, se determinó una filogenia que agrupaba los diploides en tres clases: la primera contenía una sola especie, *F. iinumae*; otra que contenía muchas de las especies asiáticas diploides, y una tercera que contenía a *F. vesca*, *F. bucharica* y *F. viridis*. Sin embargo, este estudio no incluyó en su análisis ninguna de las especies poliploides existentes, por lo que no proporcionó pruebas acerca de los orígenes de las especies octoploides de *Fragaria*.

Un estudio realizado sobre la región que contiene el intrón de los genes que codifican una alcohol deshidrogenasa (ADH) (Dimeglio y Davis, datos no publicados), y que abarca la mayoría de los diploides de *Fragaria* y de las especies poliploides, sugiere que los diploides *F. vesca*, *F. bucharica*, *F. mandshurica* y *F. iinumae* son posibles donantes de genoma de las especies octoploides, proporcionando una aclaración sobre el origen de estas especies.

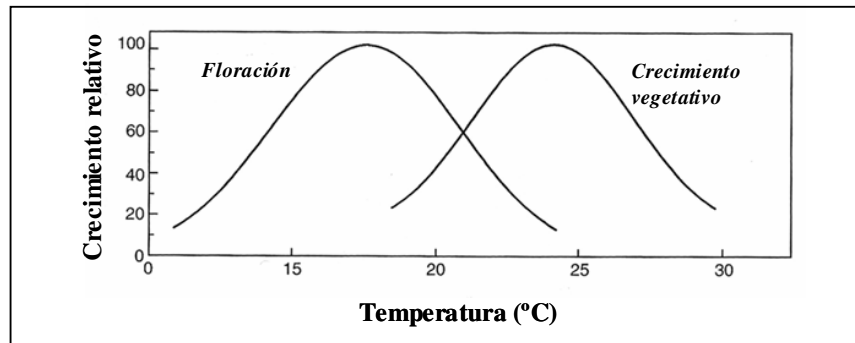
## 2. MORFOLOGÍA DEL FRUTO DE FRESA

La fresa es una planta herbácea perenne compuesta por diferentes meristemos y cuyo desarrollo viene controlado por la interacción entre la temperatura y el fotoperiodo. La planta de fresa posee un tallo central a partir del cual emergen las hojas trifoliadas y las raíces, que son de tipo fasciculado.

Temperatura (°C)	<i>Día corto</i>		<i>Día neutro</i>	
	Inflorescencias	Estolones	Inflorescencias	Estolones
18/14	2,1	0,0	3,3	1,7
22/18	0,3	0,0	1,3	2,3
26/22	0,0	0,8	0,0	2,2
30/26	0,0	2,4	0,0	3,3

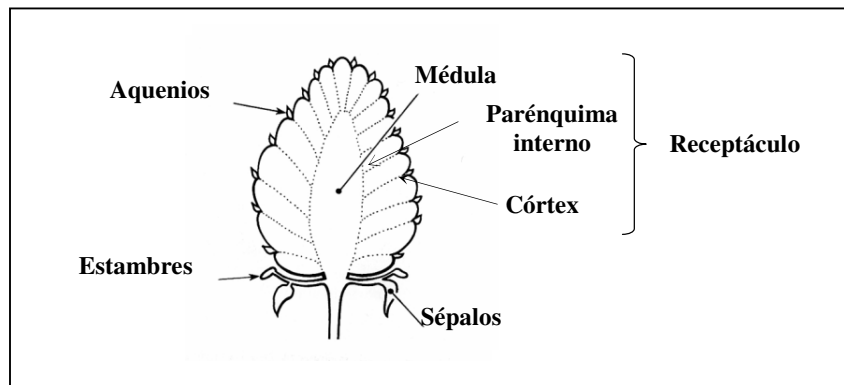
**Tabla 2.** Número medio de inflorescencias y estolones presentes en plantas de fresa de día corto y neutro sometidas a cuatro temperaturas diferentes a lo largo de tres meses (Durner *et al.*, 1984) (Adaptado de Hancock, 1999).

En la axila de cada hoja existe una yema auxiliar a partir de la cual pueden desarrollarse estolones o inflorescencias dependiendo de las condiciones medioambientales. En los cultivares de día corto, las inflorescencias se generan cuando los días son cortos y las temperaturas frías, mientras que los estolones se producen en condiciones de día largo y temperaturas templadas. En los cultivares de día neutro, las flores se producen siguiendo un patrón cíclico sin que influya la duración de los días pero a temperaturas relativamente frías (Tabla 2 y Fig. 2).



**Fig. 2.** Perfil de floración y crecimiento vegetativo de la planta de fresa a diferentes temperaturas. (Adaptado de Hancock, 1999).

Bajo la definición de “frutos blandos” se agrupan varios tipos de bayas. Se trata de frutos pequeños cuyas semillas se encuentran incluidas en un receptáculo. Como ejemplos más representativos de este tipo de frutos, nos encontramos con las grosellas y las fresas.



**Fig. 3.** Estructura típica del fruto de fresa. (Adaptado de Hancock, 1999).

La fresa se desarrolla a partir de una flor con un gineceo coricárpico (donde cada carpelo representa un carpido) y en la que el androceo se ha multiplicado de modo secundario por intercalación. A partir de los carpelos se forman frutos monocarpelares indehiscentes (aquenios) que se disponen sobre la superficie del eje floral, el cual adopta un aspecto cónico y una textura carnosa (receptáculo) para dar lugar a un fruto múltiple (Erendorfer, 1983) (Fig. 3). Por tanto, la fresa es un fruto que posee una estructura de falso fruto constituido por un receptáculo carnoso en cuyo exterior se encuentran los aquenios (verdaderos frutos).

## 2.1. Los aquenios

Los aquenios son una combinación de tejido de la semilla y tejido ovárico y se originan en la base de cada pistilo (Darrow, 1966). Se encuentran embebidos en la capa epidérmica del receptáculo y conectados con el interior de éste mediante haces fibrovasculares a través de los cuales obtienen los nutrientes necesarios para su desarrollo y el de las células parenquimáticas del receptáculo circundante. En función del cultivar del que se trate y de las condiciones de

crecimiento del mismo, pueden existir entre 20 y 500 aquenios en cada receptáculo (Darrow, 1966). Estructuralmente, los aquenios maduros se caracterizan por presentar un grueso pericarpo, una delgada testa, una única capa endospermática y un embrión que completa su desarrollo diez días después de la antesis (Thompson, 1963).

## 2.2. El receptáculo

En el receptáculo, el tejido vascular forma un eje central en torno al cual se disponen los tejidos parenquimatoso y epidérmico del córtex (Havis, 1943). Los haces vasculares se extienden desde el pedicelo, atravesando el tejido parenquimatoso y el córtex, hasta alcanzar a los aquenios localizados en la superficie del receptáculo. Su epidermis es ligeramente pubescente y está formada por una o dos capas delgadas de células. El receptáculo presenta estomas protuberantes y abiertos, relacionados con la transpiración y respiración del fruto (Perkins-Veazie, 1995).

## 3. COMPOSICIÓN DEL FRUTO DE FRESA

El fruto de fresa es el tejido sumidero más importante de la planta, acumulando entre el 20-40% del total del peso seco de ésta. La fructificación inhibe la producción de estolones, coronas e inflorescencias, sin embargo, no afecta generalmente a los niveles totales de peso seco en la planta salvo en raíz, donde se produce una reducción de la biomasa durante dicho proceso (Hancock, 1999).

La fresa es muy apreciada por su delicado sabor, aroma y por su valor nutricional. El fruto maduro se compone aproximadamente en un 90% de agua y en un 10% de sólidos solubles que incluye numerosos componentes importantes de la dieta (Hemphill y Martin, 1992).

Son ricas en vitamina C (o ácido ascórbico). Una cantidad estándar de fresas (10 frutas) suministra el 95 % de los requerimientos dietéticos diarios recomendados de vitamina C (Maas *et al.* 1996). En la naturaleza, la vitamina C se sintetiza a partir de D-glucosa-6-fosfato (D-Glu-6-P) a través de diferentes vías: en animales, la D-Glu-6-P se sintetiza a través de la ruta del ácido *D*-glucurónico para formar el precursor gulono-1,4-lactona; en plantas, existe una ruta más compleja que involucra diferentes compuestos del azúcar (fructosa, manosa) hasta llegar a la síntesis de galactono-1,4-lactona (Wheeler *et al.*, 1998). Recientemente, se ha propuesto una vía alternativa para la síntesis de vitamina C en plantas (Agius *et al.*, 2003). Esta ruta sugiere que la síntesis de la vitamina C se produce a partir de la degradación de componentes pectínicos de la pared celular, principalmente de ácido galacturónico (GalUA). La clonación del gen *GalUA reductasa* de fresa y la correlación de su expresión con el proceso de maduración, parece indicar una relación entre este proceso y el aumento del contenido de vitamina C en el fruto de fresa.

Nutriente	Contenido	Nutriente	Contenido
Agua	92 g	<i>Vitaminas</i>	
Proteínas	0,6g	Vitamina C	56,7 mg
Ácido elálgico <sup>a</sup>	0,09-0,4 mg	Otras	<0,5 mg
Carbohidratos totales	7,0 g	<i>Lípidos</i>	
Fibra	0,5 g	Saturados	0,02 mg
<i>Minerales</i> (mg)		Monoinsaturados	0,052 mg
Ca	14 mg	Poliinsaturados	0,186 mg
Fe	0,4 mg	Colesterol	0
P	19 mg	Fitoesteroles	12 mg
Mg	10 mg	<i>Aminoácidos</i>	
K	166 mg	Todos (n=18)	522 mg
Na	1 mg		
Zn, Cu, Mn	<0,5 mg		

**Tabla 3. Composición del fruto de fresa (por 100 g de peso fresco)** (Maas *et al.*, 1996; Hollman y Venema, 1993). Extraído de Hancock (1999).

Los principales azúcares solubles de la fresa son la glucosa y fructosa, que constituyen más del 80 % de los azúcares totales y el 40 % del peso total seco (Wrolstad y Shallenberger, 1981). La glucosa, la fructosa y la sacarosa son los azúcares solubles que están presentes en el fruto de fresa en todas las etapas de maduración. La glucosa y la fructosa se encuentran casi a concentraciones iguales (Maas *et al.*, 1996), incrementando de forma continua durante el desarrollo de la fruta y pasando de un 5% en frutas verdes pequeñas a un 6,9% en las bayas de color rojo (Kader, 1991). Los niveles de sacarosa son generalmente mucho más bajos y muestran una pequeña acumulación cerca del desarrollo de la fruta (Forney y Breen, 1985). Las invertasas probablemente desempeñan un papel importante en la regulación de la dulzura del fruto mediante el control de sus niveles de sacarosa y hexosas (Ranwala *et al.*, 1992; Manning, 1998).

Por otra parte, el ácido orgánico principal del fruto de fresa es el ácido cítrico, que constituye un 88 % de los ácidos totales (Green, 1971). La fresa contiene también importantes niveles de ácido elálgico, que posee propiedades anticancerígenas (Maas *et al.*, 1991).

## 4. FISIOLÓGÍA DEL FRUTO DE FRESA

A lo largo de su desarrollo, los frutos blandos comparten algunas características que son generales en una amplia diversidad de frutos carnosos. Así, encontramos una fase inicial de crecimiento y elongación, seguida de una fase de maduración caracterizada por determinados cambios físicos (cambios de textura y color), cambios químicos (producción de aromas y sabores) y variación de patrones de expresión génica característicos de cada tipo de fruto.

### 4.1. Cambios macroscópicos

Dentro de los frutos blandos, el género *Fragaria* quizá sea el más estudiado en términos de fisiología y bioquímica, debido a su estructura de falso fruto constituido por un receptáculo

carnoso en cuyo exterior están anclados los verdaderos frutos mediante conexiones vasculares (aquenios).

#### 4.1.1. Crecimiento

El crecimiento del receptáculo de la fresa depende muy directamente del desarrollo de las células del córtex y de la médula, siendo esta última la principal responsable del tamaño del fruto (Hancock, 1999).

El desarrollo del fruto viene determinado por numerosos factores como son el número y distribución de los aquenios en el receptáculo, el área de receptáculo alrededor de cada aquenio y el porcentaje de carpelos fertilizados. Estos factores condicionan la síntesis de auxinas que tiene lugar en los aquenios y que se translocan por el floema basipétalmente desde ellos hasta el pedúnculo, siendo las responsables primarias del crecimiento del receptáculo (Nitsch, 1950). Se ha comprobado que la separación parcial de aquenios en frutos verdes de estadio de desarrollo temprano da lugar a un receptáculo maduro expandido sólo en las proximidades de los aquenios presentes. Además, la aplicación de auxinas sintéticas de forma exógena restaura el crecimiento del receptáculo en frutos a los que se les habían retirado los aquenios (Nitsch, 1950). Debido a esto, gran parte del crecimiento de la fresa ha sido atribuido a la capacidad de las auxinas para estimular el transporte de asimilados. Por ello, las variaciones en el tamaño del fruto entre los distintos cultivares podrían estar determinadas en parte por la actividad promotora del crecimiento que ejerce de manera individualizada cada uno de los aquenios. Por otra parte, las giberelinas, citoquininas y ácido abscísico parecen tener también un papel limitado en el crecimiento del fruto (Perkins-Veazie, 1995).

El tamaño del fruto también está influenciado por la posición que éste ocupa en la inflorescencia, de manera que su tamaño es menor según se trate de frutos primarios, secundarios o terciarios (Moore *et al.*, 1970). Este hecho podría estar relacionado con un periodo de retraso tras la polinización, más largo en el caso del crecimiento del fruto secundario y terciario (Moore *et al.*, 1970). La eliminación de los frutos primarios de la planta motiva un incremento del peso de los frutos secundarios, lo cual parece indicar que se produce una competencia entre los frutos semejante a la dominancia apical en el vástago (Stutte y Darnell, 1987). Se sabe que las diferencias en el tamaño final del fruto están determinadas genéticamente y que éstas están relacionadas con el número y tamaño de los aquenios viables desarrollados en el mismo (Moore *et al.*, 1970).

El fruto de fresa crece rápidamente y, dependiendo de las condiciones medioambientales, alcanza su tamaño total y definitivo aproximadamente 30 días después de la antesis. La cinética de su crecimiento parece variar con el cultivar, presentando algunos de ellos una única fase de crecimiento sigmoideal (Woodward, 1972; Forney y Breen, 1985; Stutte y Darnell, 1987), mientras que otros presentan modelos bifásicos de crecimiento (Archbold y Dennis, 1984; Perkins-Veazie y Huber, 1987). Se ha sugerido que el crecimiento bimodal del receptáculo está relacionado con el desarrollo del endospermo y del embrión dentro de los aquenios (Perkins-Veazie y Huber, 1987), de manera que el segundo periodo de crecimiento acelerado coincide con la maduración del embrión en los aquenios, fenómeno que acompaña a la maduración del receptáculo. Hasta el décimo día tras la polinización, se puede observar un crecimiento logarítmico del peso fresco del receptáculo debido a un aumento de la división y alargamiento celular. A partir del día 20 después de la polinización, aparece una segunda fase

de incremento rápido del peso fresco. Posteriormente, a los 25 días, comienza a observarse cambio de color, quedando completada la maduración a los 30 días tras la polinización. Se ha descrito que hay un incremento en la división celular de hasta tres veces durante los primeros 7 días después de la polinización, mientras que todo el crecimiento posterior es debido a la expansión celular (Knee *et al.*, 1977).

#### 4.1.2. Elongación

En la fase de elongación celular del fruto de fresa se produce un crecimiento isodiamétrico de las células corticales, acompañado de importantes cambios en la pared celular y en la estructura subcelular (Cheng y Breen, 1992). Esta etapa podría estar condicionada por los efectos directos de la temperatura, del aporte de asimilados (tanto para el crecimiento como para el almacenamiento), y del balance hídrico fruto/planta. Existe una correlación lineal directa entre el aporte hídrico y el crecimiento del fruto, ya que el estrés hídrico causado por déficit de agua o por incremento de irradiancia influye en la disminución de la tasa de crecimiento (Pearce *et al.*, 1993). Sin embargo, a corto plazo, los efectos de estos factores abióticos pueden ser diferentes. La temperatura acelera la velocidad de división y elongación celular así como el proceso de maduración del fruto. Lo mismo ocurre con la irradiancia, que regula la tasa de fotosíntesis foliar y por tanto el aporte de carbono al fruto; del mismo modo actúa la transpiración, condicionando la elongación celular (Cockshull *et al.*, 1992).

#### 4.1.3. Maduración

En la mayoría de los frutos blandos, la maduración es un proceso fisiológico de corta duración que sucede rápidamente y en la que los frutos desarrollan una serie de propiedades organolépticas que los hacen aptos para el consumo. En el caso del fruto de fresa, la maduración se completa en 30-40 días desde la antesis (Dennis, 1984) e invariablemente viene determinada por cambios simultáneos en el color, sabor y textura del mismo. A nivel celular, la maduración produce un aumento del tamaño de la célula, la formación de grandes espacios vacuolares, y una modificación de la pared celular que provoca la oclusión del espacio intercelular con una matriz glucídica (Neal, 1965). En cualquier caso, para que el proceso de maduración transcurra adecuadamente, el fruto debe estar unido a la planta ya que, si es separado de ella, sus propiedades organolépticas se reducen de forma significativa.

La firmeza de la fruta es una de las propiedades más importantes a la hora de determinar el grado de madurez y la calidad del fruto y ésta viene determinada por la turgencia celular y por las características y composición de la pared celular. De hecho, el reblandecimiento del fruto comienza con la modificación de la pared celular primaria debida a la solubilización y despolimerización de los polisacáridos que forman parte de ella. Rosli *et al.* (2004) estudió la composición y estructura de los polisacáridos de la pared celular del fruto de fresa durante su desarrollo y maduración en tres cultivares con diferente firmeza (“Camarosa” la más firme, “Toyonaka” de firmeza media y “Pájaro” la más blanda), y comprobó que las principales diferencias entre ellas radicaba en el contenido de polisacáridos de la pared. En general, se observó que la cantidad de hemicelulosa y celulosa disminuyó durante la maduración del fruto en los tres cultivares evaluados, pero no hubo diferencias en su contenido en etapas maduras. Esto sugiere que este polisacárido no tiene un papel fundamental en el reblandecimiento del fruto de fresa (Rosli *et al.*, 2004; Palomer *et al.*, 2006).



Las expansinas están íntimamente implicadas en el proceso de reblandecimiento de la fresa. Su actividad se ha detectado a lo largo de la maduración del fruto, identificándose siete genes diferentes que codifican expansinas (*FaExp 1-7*) (Civello *et al.*, 1999; Harrison *et al.*, 2001; Salentijn *et al.*, 2003; Dotto *et al.*, 2006). Un estudio sobre su expresión en varias variedades con diferente firmeza, mostró una correlación directa entre la firmeza del fruto y los niveles de expresión en tres de los siete genes *FaExp* de fresa identificados. Además, los niveles de expresión de las expansinas estudiadas fueron mayores en los frutos procedentes de la variedad más blanda (“Toyonaka”) que en las variedades más duras (“Camarosa” y “Selva”) (Dotto *et al.*, 2006), lo que indica una correlación clara entre la expresión de estos genes y el proceso de maduración. Por otra parte, también se ha detectado un incremento de expresión de las expansinas justo al principio del comienzo de la maduración en el cultivar más blando, lo que apoya directamente la intervención de estas enzimas en el proceso de maduración de la fresa (Dotto *et al.*, 2006). Salentijn *et al.* (2003) analizaron la existencia de diferencias transcriptómicas relacionadas con la firmeza del fruto en diferentes variedades empleando la tecnología de microarrays de ADN. A partir de los datos obtenidos, seleccionaron varios genes candidatos que mostraron expresión diferencial en las variedades estudiadas, todos ellos relacionados con la degradación de la pared celular, lo que indica que este proceso es clave en la maduración del fruto. También observaron un incremento de expresión de la *FaExp2* y la poligalacturonasa (*FaPG*), ambas implicadas en el reblandecimiento del fruto a través de la degradación de la pared celular, y de genes que codifican enzimas que participan en la biosíntesis de la lignina (*Faccr* y *Facad*). Así, dos clones diferentes de *Faccr* incrementaron su expresión más de 20 veces en frutos más blandos (variedad “Gorella”), mientras que los niveles de expresión de los genes *Facad* (cinamil alcohol deshidrogenasa) fueron tan sólo 2 ó 3 veces más elevados en variedades más firmes (“Holiday”). Ambas enzimas, CCR y CAD, catalizan etapas sucesivas en la ruta de biosíntesis de la lignina y sus diferencias de expresión podrían dar lugar a diferencias en la composición de la lignina en ambos cultivares. Dado que la lignina es un componente básico del tejido vascular (Aharoni *et al.*, 2002b) y que éste se asocia con la textura del fruto (Jewell *et al.*, 1973), diferencias en el contenido y la composición de la lignina pueden ser importantes para determinar el grado de firmeza del fruto. Por lo tanto, se considera que la *Facad* y la *Faccr* participan en el control de la firmeza del fruto de fresa (Aharoni *et al.*, 2002b).

Por otra parte, el fruto de fresa genera cantidades muy pequeñas de etileno debido a la baja concentración de ACC sintasa que presenta (Perkins-Veazie *et al.*, 1995; Perkins-Veazie *et al.*, 1996). Además, se ha observado que la aplicación exógena de etileno no acelera la maduración del fruto ni induce la producción autocatalítica de esta hormona salvo aplicada a grandes dosis, cuando es capaz de incrementar ligeramente la tasa respiratoria del fruto (Janes *et al.*, 1978; Sas *et al.*, 1992; Villareal *et al.*, 2009). Estos datos parecen indicar que el etileno no juega un papel decisivo en el proceso de maduración de la fresa, lo que se ajusta perfectamente con su carácter de fruto no climatérico (Villareal *et al.*, 2009).

## 4.2. Cambios microscópicos

Durante el desarrollo del fruto de fresa y tras la caída de los pétalos, se produce un crecimiento inicial del receptáculo que se debe a una combinación de división y expansión celular (Knee *et al.*, 1977). La extensión celular aparece acompañada de importantes cambios en la pared celular y en las estructuras subcelulares. Así, en el momento de la caída de los pétalos, las células del receptáculo poseen paredes celulares densas y vacuolas pequeñas, los plastos contienen granos de almidón, y tanto el complejo de Golgi como los ribosomas son

abundantes. Por el contrario, durante el desarrollo, las paredes celulares se engrosan, existe una mayor difusión a través de ellas, y el almidón cloroplastidial es hidrolizado completamente, probablemente para ser utilizado como sustrato metabólico durante las fases de proliferación y elongación celular (Knee *et al.*, 1977). Seguidamente, durante la etapa de maduración, los plastos llegan a degenerar, lo que podría considerarse una característica propia de la senescencia, los cloroplastos no se transforman en cromoplastos (Knee *et al.*, 1977), y las mitocondrias permanecen perfectamente normales en los frutos maduros. El proceso de maduración también se caracteriza por la creciente hidratación y desorganización de la pared celular, así como la mayor solubilidad de la lamela media y de la matriz de la pared celular, lo que provoca el reblandecimiento del fruto (Knee *et al.*, 1977).

#### **4.2.1. Cambios organolépticos: desarrollo del olor y sabor**

El sabor del fruto de fresa tiene su origen en la interacción de una mezcla compleja de compuestos volátiles y otros constituyentes mayoritarios del fruto, especialmente azúcares reductores y no reductores, ácidos orgánicos, compuestos fenólicos y taninos.

##### ***Carbohidratos***

Los carbohidratos son uno de los principales compuestos solubles de los frutos blandos. Además de suministrar la energía necesaria para los cambios metabólicos, tienen un papel determinante en la generación del sabor.

A partir del sexto día después de la polinización, los asimilados fotosintéticos comienzan a almacenarse en el receptáculo (Manning, 1993; Darnell y Martin, 1988). El principal producto asimilado que se exporta al receptáculo es la sacarosa, empleándose como sustrato metabólico y/o para la generación de otros glúcidos de almacenamiento (Lis y Antoszewski, 1979). La entrada de sacarosa al fruto se produce a través del apoplasto (Ofosu-Anim y Yamaki, 1994), y la mayoría es hidrolizada en fructosa y glucosa antes de su asimilación por acción de la invertasa (EC 3.2.1.26) (Forney y Breen, 1986). Durante los primeros 10 días después de la antesis, la sacarosa se encuentra presente en el fruto a concentraciones muy bajas, aumentando rápidamente hasta alcanzar un máximo en el estadio intermedio de maduración y disminuyendo bruscamente de nuevo en frutos rojos (Forney y Breen, 1986). Tras la hidrólisis de la sacarosa, la glucosa y fructosa resultantes constituyen los azúcares más abundantes en el fruto de fresa (Forney y Breen, 1986). Así, en frutos maduros de fresa, la glucosa y fructosa aparecen en concentraciones equivalentes (2,3 y 2,2 g/100g de peso fresco, respectivamente), constituyendo cerca del 83% de los azúcares totales (Wrolstad y Shallenberger, 1981). No obstante, con el comienzo de la maduración la sacarosa también empieza a almacenarse como azúcar de reserva (Forney y Breen, 1986). En el fruto de fresa maduro se han detectado también sorbitol, xilitol y xilosa en cantidades trazas (Makinen y Söderling, 1980). En general, durante el proceso de maduración del fruto se produce la acumulación de azúcares en el apoplasto de las células (Ofosu-Anim y Yamaki, 1994).

Con respecto a la regulación de la captación de azúcares, tanto el ácido abscísico (ABA) como el indolacético (IAA) estimulan la incorporación de azúcares en los frutos de fresa (Ofosu-Anim *et al.*, 1996). El ABA promueve el incremento de los procesos de difusión, mientras que el IAA produce la incorporación de azúcares tanto por mecanismos de transporte activo como por procesos de difusión (Ofosu-Anim *et al.*, 1996). Estos datos subrayan la

importancia del ABA y del IAA en la estimulación del proceso de captación de azúcares a lo largo del proceso de maduración del fruto de fresa.

El almidón, principal materia de reserva de hidratos de carbono en plantas, se sintetiza a partir de glucosa en una reacción catalizada por la ADP-glucosa pirofosforilasa (AGPasa). Park y Kim (2007) aislaron las secuencias de las subunidades mayores (FagpL1 y FagpL2) y pequeña (FagpS) de la AGPasa. Comprobaron que la expresión de FagpL1 y FagpS fue elevada y constante durante todo el desarrollo del fruto, mientras que FagpL2 se expresa débilmente sólo en hojas, lo que sugiere un control de la expresión de los genes de la AGPasa tanto a nivel transcripcional como post-transcripcional. Con el fin de modificar el azúcar contenido en la fresa, Park *et al.* (2006a) silenciaron la expresión de FagpS mediante antisentido y consiguieron disminuir el contenido de almidón y aumentar el contenido de sólidos solubles en las plantas transgénicas generadas. En otro trabajo reciente, se ha analizado la actividad de cinco enzimas claves (la invertasa ácida soluble (IASI), la sacarosa sintasa (SS), la sacarosa fosfato sintasa (SPS), la hexoquinasa (HK) y la fructoquinasa (FK)) en la biosíntesis de azúcar durante la maduración de frutas, destacando diferentes patrones en la actividad enzimática y en la acumulación de azúcar (Xie *et al.*, 2007). Por otra parte, Duangsrirai *et al.* (2007) llevaron a cabo la clonación y el análisis de la expresión de dos genes implicados en el metabolismo del sorbitol en fresa, la sorbitol deshidrogenasa NAD-dependiente (FaSDH) y la sorbitol deshidrogenasa-6-fosfato (FaS6PDH). Los niveles de transcripción de ambos genes fueron cuantificados en frutas y hojas, detectándose sólo actividad enzimática correspondiente a la enzima FaSDH.

### ***Ácidos orgánicos***

Los ácidos orgánicos son compuestos determinantes del sabor del fruto de fresa, de tal modo que la relación azúcares/ácidos es un factor utilizado como índice de aceptación del fruto por el consumidor. Además de determinar el pH tisular del fruto, los ácidos orgánicos condicionan la estabilidad de su color, inhiben la actividad de ciertas enzimas y modifican la textura del fruto ya que afectan a las propiedades gelificantes de las pectinas. La mayoría están relacionados con el ciclo de los ácidos tricarbóxicos (cítrico, málico) y se acumulan en las vacuolas.

Los ácidos orgánicos no-volátiles (cítrico, málico, etc.) son cuantitativamente los más importantes en la determinación de la acidez del fruto, mientras que los ácidos orgánicos volátiles pueden contribuir de forma más importante en el aroma del fruto (p.ej. 2-metilol-acetato) (Mussinan y Walradt, 1975). La acidez total del fruto, expresada en base al peso fresco, experimenta un modesto incremento a lo largo del desarrollo del fruto, con un máximo detectado en frutos verdes maduros, seguido por un rápido descenso durante la maduración (Spayd y Morris, 1981). Se ha demostrado que la pérdida de acidez total en el fruto muy maduro se debe, principalmente, a un descenso en el contenido total de ácido málico (Reyes *et al.*, 1982).

### ***Compuestos fenólicos***

Los fenoles engloban a un grupo muy diverso de sustancias entre los que se encuentran metabolitos secundarios tales como los polifenoles, las proantocianidinas (taninos condensados) y los ésteres de los ácidos hidroxibenzoicos e hidroxicinámicos. En frutos de

fresa inmaduros, los compuestos fenólicos están presentes a altos niveles, produciéndose un descenso en su concentración a lo largo del proceso de maduración (Spayd y Morris, 1981).

Los ácidos fenólicos proporcionan acidez al fruto y derivan de la fenilalanina por la vía de los ácidos cumárico y cinámico. Los taninos son los responsables de la astringencia del fruto como consecuencia de su interacción con las proteínas y mucopolisacáridos de la saliva (Ozawa *et al.*, 1987; Ferrer, 1997), y las flavonas dan lugar al amargor característico de los estadios verdes de desarrollo. En general, todos estos compuestos están almacenados en las vacuolas y su concentración varía durante la maduración dependiendo de la variedad y condiciones ambientales de la planta (Hobson, 1993). De hecho, se ha propuesto que la pérdida de astringencia que se produce durante la maduración puede deberse a la interacción de las pectinas solubilizadas con los polifenoles, lo que evitaría que éstos se unieran a las proteínas salivares (Ozawa *et al.*, 1987).

### **Compuestos volátiles**

La mezcla de compuestos volátiles en el fruto de fresa es compleja (Tressl *et al.*, 1969), aunque los ésteres son uno de los grupos de compuestos volátiles más importantes relacionados con el aroma de la fresa. De éstos, más de cien tipos diferentes han sido identificados (Zabetakis y Holden, 1997). A pesar de ello, sólo algunos de estos compuestos contribuyen de forma determinante al aroma del fruto (Tabla 4).

El aroma del fruto de fresa es extremadamente conocido no sólo como una característica del fruto fresco, sino que también es utilizado como aditivo de otros productos (Hancock, 1999). La abundancia relativa de cada uno de los componentes volátiles es una “huella dactilar” de cada cultivar y especie, lo que ha sido motivo de numerosas investigaciones (Douillard y Guichard, 1990; Larsen y Poll, 1992; Larsen *et al.*, 1992). Las especies silvestres *F. vesca* y *F. virginiana* tienen un aroma mucho más fuerte que las variedades cultivadas (Hirvi y Honkanen, 1982). *F. vesca* contiene grandes cantidades de acetato de etilo, pero pequeñas cantidades de metil-butirato, etil-butirato y furanona. *Fragaria nilgerrensis* contiene altos niveles de etil-acetato y furanona, pero niveles bajos de metil-butirato y etil-butirato. Los híbridos entre *F. vesca* y *F. x ananassa* tienen niveles intermedios de fragancia y aroma, mientras que los cruces entre *F. nilgerrensis* y *F. x ananassa* se parecen más a los de *F. nilgerrensis*. Aunque cada uno de estos compuestos difiere en sus propiedades organolépticas, probablemente sólo un pequeño número de ellos contribuyen de manera significativa en el aroma. De hecho, la aplicación del concepto de “valor aromático” u olor umbral, que refleja la concentración necesaria para producir olor, indica que únicamente 15 de estos compuestos participan significativamente en el olor característico de la fresa (Shieberle y Hofmann, 1997).

En frutos de fresa maduros, los ésteres volátiles más abundantes son el butanoato de etilo, el 2-metil-butanoato de etilo y el hexanoato de etilo. Una de las enzimas implicadas en la formación de estos ésteres es la alcohol acil transferasa (AAT) que cataliza la transferencia del grupo acilo desde un acil-CoA a un alcohol. La AAT de fresa ha sido parcialmente purificada y caracterizada, y se ha demostrado que puede utilizar como sustrato acil-CoA tanto al acetil-CoA (100%), como al butil-CoA (70%) y propil-CoA (20%); y, como sustrato alcohol preferido, al hexanol (Pérez *et al.*, 1993; Olías *et al.*, 1995). Recientemente, mediante el análisis de su expresión cuantitativa por técnicas de *microarrays*, se ha demostrado que la SAAT de fresa (AF193789) se expresa 16 veces más en fruto rojo que en fruto verde, lo que

sugiere que cataliza los pasos finales de la síntesis de ésteres volátiles en este fruto (Aharoni *et al.*, 2000). Así, la expresión del gen de la SAAT, que es específica de receptáculo, sólo se detecta en frutos en proceso de maduración, alcanzando el valor máximo de actividad en frutos completamente maduros (Pérez *et al.*, 1996). La expresión del gen comienza en el estadio blanco del fruto, antes de la formación de ésteres volátiles detectables por cromatografía, y continúa aumentando en el estadio intermedio hasta alcanzar su máximo de expresión en el estadio rojo, lo que coincide con los niveles mayores de ésteres volátiles presentes en el fruto (Aharoni *et al.*, 2000).

La enzima SAAT utiliza preferentemente alcoholes alifáticos de cadena media en combinación con diferentes acil-CoA como sustrato, de hecho su actividad resultó insignificante con alcoholes aromáticos y monoterpenol linalol como sustratos. En *Fragaria vesca* se ha aislado e identificado una proteína AAT (VAAT) (Beekwilder *et al.*, 2004) cuya expresión heteróloga muestra una actividad muy distinta a la SAAT. VAAT es mucho más activa cuando utiliza como sustrato alcoholes de cadena corta, al contrario que la SAAT. En general, todos los datos disponibles sugieren que los volátiles presentes en cada especie están determinados en gran medida por el suministro de precursores.

También, se ha propuesto la participación de la enzima piruvato descarboxilasa, codificada por el gen *FaPDC1* (AF333772), en la generación del aroma del fruto maduro a través de su participación en la fermentación etanólica. Se ha comprobado, que la expresión de este gen está asociada al proceso de maduración y está regulada por auxinas (Moyano *et al.*, 2004).

Otros compuestos que parecen intervenir en el aroma de la fresa son los terpenoides. Derivan de la vía del mevalonato y/o de la vía plastidial 2-C-metil-D-eritritol-4-fosfato. Ambas rutas producen compuestos de 5 C que pueden ser empleados por prenil transferasas en reacciones de condensación para producir geranilo difosfato (PIB), precursor de los monoterpenos, y farnesil difosfato (FDP), precursor de diterpenos y de carotenoides. El linalool, nerolidol,  $\alpha$ -pineno y limoneno son terpenos volátiles predominantes en la fresa que pueden suponer hasta un 20% de los volátiles totales del fruto (Loughrin y Kasperbauer, 2002). Recientemente, se ha clonado y expresado una nerolidol sintasa (NES1) que genera como productos mono y sesquiterpenos (Aharoni *et al.*, 2004). La enzima recombinante FaNES1 (AX529067) forma (S)-linalol y trans-(S)-nerolidol del PIB y del FDP respectivamente. Este gen se expresa de forma específica y fuertemente en frutos de variedades cultivadas (octoploides) pero no en las silvestres, por lo que el linalool y nerolidol participan únicamente en la composición final del aroma del fruto de las variedades de fresa cultivadas (Aharoni *et al.*, 2004).

Así, se ha propuesto que el aroma de la fresa es el resultado de la combinación de los olores “afrutado” (etil-butanoato, etil-hexanoato y metil 2-metilbutanoato), “verde” (Z-3-hexenal), “dulce” (ácido butanoico y ácido 2-metilbutanoico), “melocotón” (decalactona), “caramelo” [4-hydroxy-2,5-dimetil-3(2H)-furanona (HDMF, furaneol)], y 2,5-dietil-4-metoxi-3(2H)-furanona (DMMF)) (Pyysalo *et al.*, 1979; Larsen *et al.*, 1992). Entre todos estos compuestos volátiles destaca el HDMF por su elevada concentración y bajo olor umbral (Larsen *et al.*, 1992; Schwab y Roscher, 1997). Así, el HDMF aumenta su concentración a lo largo de la maduración alcanzando sus valores más elevados en frutos muy maduros (Pérez *et al.*, 1996). Sin embargo, el HDMF es rápidamente metabolizado a  $\beta$ -D-glucopiranosido y, por tanto, a su derivado HDMF-glucósido (Roscher *et al.*, 1998).

Se ha comprobado también que genes que codifican una terpeno sintasa (sintasa pineno, PINS) en variedades silvestres de fresa presentan una expresión reducida en especies cultivadas, probablemente debido a la presencia de una mutación por inserción (Aharoni *et al.*, 2004). Así, en *Fragaria vesca*, la enzima FvPINS produce  $\alpha$ -pineno que actúa como sustrato de una hidroxilasa pineno que cataliza la hidroxilación del C 10 del  $\alpha$ -pineno para obtener mirtenol. Por el contrario, en *Fragaria x ananassa*, la ausencia de  $\alpha$ -pineno que se pueda utilizar como sustrato para la obtención de mirtenol y acetato de myrtenyl, produce cambios en el sabor de la fruta (Aharoni *et al.*, 2004), lo que demuestra que mutaciones simples pueden ser determinantes del sabor del fruto entre los diferentes cultivares de fresa.

Otros compuestos, como los ácidos grasos volátiles (2-metilol acetato) que incrementan su concentración durante la maduración, juegan un papel importante en el aroma de la fresa (Dirinck *et al.*, 1981; Yamashita *et al.*, 1977). Además, se han descrito varios compuestos sulfurados relacionados con el aroma del fruto a pesar de encontrarse a concentraciones inferiores a la de otros compuestos volátiles (Dirinck *et al.*, 1981).

Familia Química	Compuestos representativos
Ésteres de bajo peso molecular	Etil butanoato Etil hexanoato Hexil acetato Isoamil acetato
Cetonas	2-Heptanona 3-Hidroxibutanoato
Terpenoides	Linalool $\alpha$ -Terpineol
Furanonas	Furaneol
Dionas de bajo peso molecular	Diacetil
Derivados bencénicos	Benzaldehído
Aldehídos insaturados	<i>t</i> -2-Hexenal
Aldehídos saturados	Hexanal
Alcoholes insaturados	<i>t</i> -2-Hexen-1-ol
Ésteres insaturados	<i>t</i> -2-Hexenil acetato
Furaldehídos	Furfural
Acidos grasos volátiles	2-Metilol acetato
Ésteres tiólicos	Metiltiol acetato
Varios	Etil cinamato Naftaleno

**Tabla 4. Compuestos más representativos que intervienen en el aroma del fruto de fresa** (Adaptado de Hancock, 1999).

El elevado número de compuestos relacionados con el aroma en el fruto de fresa sugiere que las enzimas involucradas podrían ser multifuncionales, lo que evitaría un gasto extra de energía para la síntesis de proteínas nuevas. No obstante, esto también podría ser un reflejo de la falta de especificidad de enzimas como reductasas, esterasas, oxidasas, etc., implicadas en la producción de numerosos compuestos involucrados en el aroma del fruto. En general, los principales componentes del aroma del fruto de fresa no han sido completamente

identificados, pero se cree que es resultado de una mezcla compleja de ésteres, alcoholes, aldehídos y compuestos de azufre (Dirinck *et al.*, 1981; Pérez *et al.*, 1996).

#### 4.2.2. Metabolismo de los fenilpropanoides: aparición del color

A lo largo del proceso de desarrollo y maduración del fruto de fresa, se observa una transición desde el color verde inicial al color rojo propio de frutos completamente maduros. Este cambio de coloración se debe tanto a la degradación de clorofilas como a la síntesis *de novo* de antocianinas responsables de la coloración de los frutos maduros y localizadas en las vacuolas (Timberlake, 1981; Perkin-Veazie, 1995). La biosíntesis de antocianinas comienza en el fruto blanco (Woodward, 1972) y se produce a partir de fenilpropanoides y de flavonoides por la vía del ácido siquímico (Harbone, 1973). Mediante la unión de azúcares en diferentes posiciones a la molécula de antocianina se sintetizan los antocianos que, además, pueden acetilarse con distintos ácidos fenólicos para dar lugar a diferentes pigmentos. Así, en un fenómeno denominado co-pigmentación, las antocianinas forman complejos con las flavononas produciendo un efecto crómico que cubre el rango desde el rojo al azul (Asen *et al.*, 1972). La antocianina predominante en fresa es la pelargonidina-3-glucósido (Wrolstad *et al.*, 1970; Green, 1971; Kalt *et al.*, 1993), que constituye el 88% de las antocianinas presentes en el fruto, aunque también se han detectado pelargonidina-glucósido y cianidina-3-glucósido (Perkins-Veazie, 1995). La concentración total de antocianinas varía unas 16 veces en los diferentes cultivares, observándose también una cierta variación en su composición (Bakker *et al.*, 1994). Recientemente, todos estos metabolitos secundarios han adquirido mucha importancia debido a su capacidad de prevenir y proteger de enfermedades degenerativas y cardiovasculares (Hannum, 2004; Seeram, 2008).

Por otra parte, los fenilpropanoides se sintetizan a partir de fenilalanina por la acción secuencial de la fenilalanina amonio-liasa (PAL), la ácido cinámico 4-hidroxilasa (C4H) y la *p*-cumarato:CoA ligasa (4CL). Estos compuestos actúan como sustratos en la síntesis de flavonoides y/o precursores de la lignina. En etapas tempranas de maduración, la actividad PAL también se ha asociado con la síntesis de proantocianidinas (PA) (Cheng y Breen, 1991). Un ejemplo de enzimas multifuncionales involucradas en la biosíntesis de los fenilpropanoides corresponde a la cinamil alcohol deshidrogenasa (CAD) y la cumarílico CoA reductasa (CCR), implicadas ambas en la biosíntesis de monolignoles y en la lignificación del sistema vascular, lo que repercute directamente en la firmeza de la fruta (Anterola y Lewis, 2002; Blanco Portales *et al.*, 2002). Otros compuestos descritos recientemente en frutos de fresa han sido los isómeros *cis* y *trans*-resveratrol (estilbenos) (Wang *et al.*, 2007). Se ha comprobado que se acumulan preferentemente en receptáculo y que sus niveles podrían verse afectados tanto por el genotipo como por las condiciones ambientales (Wang *et al.*, 2007).

Los niveles y la composición cualitativa de los flavonoides en frutos de fresa dependen de factores genéticos, ambientales y de desarrollo, así como de la manipulación que sufren los frutos tras su recogida (Bakker *et al.*, 1994; Häkkinen y Törrönen, 2000; Wang y Lin, 2000; Anttonen *et al.*, 2006; Da Silva *et al.*, 2007; Tulipani *et al.*, 2008). Debido al cambio de color asociado a la biosíntesis de antocianinas, la vía de los flavonoides se utiliza para estudios funcionales en receptáculo de fruto de fresa. Así, entre los 10-12 días después de la antesis, se observa un primer pico de expresión y actividad enzimática asociado a la síntesis de compuestos derivados del flavan-3-ol y, unos 15-20 días más tarde, se aprecia un segundo pico de expresión que está relacionado con el incremento de la síntesis de antocianos en frutos

completamente desarrollados, principalmente pelargonidina-3-glucósido (Perkins-Veazie, 1995).

Las primeras reacciones de la ruta de biosíntesis de flavonoides son catalizadas por la chalcona sintasa (CHS) y la chalcona isomerasa (CHI). Debido a su posición clave en el inicio de la ruta, la CHS ha sido objeto de un amplio estudio en el fruto de fresa. Así, se ha comprobado que la inhibición de la expresión de la FaCHS bloquea la biosíntesis de flavonoides. Además, plantas transgénicas y agroinfiltradas, muestran niveles reducidos de antocianinas y de flavonoides lo que indica un papel clave de esta enzima en la biosíntesis de estos compuestos (Lunkenbein *et al.*, 2006b; Hoffmann *et al.*, 2006). Por otro lado, se ha descrito un incremento de la actividad de otras enzimas implicadas en la biosíntesis de antocianinas tales como la dihidroflavonol reductasa (DFR) (Moyano *et al.*, 1998; Hirner *et al.*, 2001), la O-metil transferasa (OMT) (Lunkenbein *et al.*, 2006c), la flavonoide 3-hidroxilasa (F3H) o la chalcona reductasa (CHR) (Manning, 1998). La expresión de estos genes está regulada negativamente por la acción de las auxinas (Wilkinson *et al.*, 1995; Manning, 1998; Moyano *et al.*, 1998). Además, los genes correspondientes a la CHS, la F3H y la DFR presentan niveles elevados de expresión en los estadíos verdes inmaduros (Manning, 1998; Moyano *et al.*, 1998), lo que sugiere una implicación adicional de los mismos en el metabolismo de otros compuestos fenólicos, como por ejemplo los taninos.

A pesar de la cantidad de información disponible sobre los genes implicados en la biosíntesis de flavonoides, hasta ahora sólo ha sido descrito en fresa un factor de transcripción (TF) implicado en el control de esta ruta. Así, Aharoni *et al.*, (2001) identificó y caracterizó el factor de transcripción (TF) *Famyb1* cuya sobreexpresión en tabaco dio lugar a la supresión de antocianinas. Esto sugiere que el *Famyb1* actúa como un represor de la transcripción y no como un activador transcripcional. Además, se han identificado en fresa otros TFs relacionados con la biosíntesis de flavonoides: tres de la familia de genes *myb*, cuatro de la familia del gen *myc* (bHLH) y un factor de transcripción WD-40 (Baudry *et al.*, 2004). Estos genes son homólogos a otros TFs implicados en la biosíntesis de flavonoides en otras especies y muestran un patrón de expresión paralelo a la acumulación de flavonoides durante el desarrollo del fruto de fresa (Baudry *et al.*, 2004).

### 4.3. Respiración

Los frutos se clasifican en climatéricos y no-climatéricos, dependiendo del modelo de respiración que presentan durante su proceso de maduración. En el modelo de respiración climatérico aparece un pico típico de respiración cuando éstos se tratan con etileno exógeno, mientras que este fenómeno no sucede en frutos no-climatéricos. Además, en el caso de frutos climatéricos, el aumento de la biosíntesis de etileno endógeno está asociado a cambios típicos del proceso de maduración tales como el reblandecimiento, síntesis de pigmentos y/o degradación de clorofilas (Alexander y Grierson, 2002). Por ello, se considera que el etileno es la hormona que inicia y coordina todos estos procesos (Iwata *et al.*, 1969a y 1969b). Sin embargo, en frutos no-climatéricos, todos los cambios asociados a la maduración del fruto suceden sin que se detecte un incremento significativo de la producción de etileno, lo que parece indicar que este proceso es independiente de dicha hormona (Villareal *et al.*, 2009).

Por consiguiente, con respecto al modelo de respiración, el proceso de maduración del fruto puede pertenecer a tres tipos de modelo (Iwata *et al.*, 1969a y 1969b):



- Frutos en los que la respiración desciende gradualmente durante la maduración, como en el caso de la naranja.
- Frutos en los que los índices de respiración aumentan continuamente hasta la maduración completa, incluso después del pico de respiración típico de frutos climatéricos, como en el caso del tomate.
- Frutos en los que la respiración es máxima en la transición entre los estadios maduros a sobre-maduros, como en el caso de la fresa.

Se ha propuesto que la respiración climatérica aporta energía metabólica adicional. Sin embargo, la fresa, un fruto no climatérico, muestra una intensa fase de maduración que no presenta un requerimiento aparente de energía metabólica adicional. No obstante, en frutos de fresa se ha descrito un aumento de la actividad ATPasa (EC 3.6.1.3) de tres veces en base al peso fresco entre los estadios verde y rojo maduro, lo que sugiere que podría requerirse energía extra para los procesos de transporte que se producen durante esta fase de desarrollo (Ben-Arie y Faust, 1980).

#### 4.4. Choque oxidativo

Mediante la utilización de *microarrays* aplicados al estudio del proceso de maduración del fruto de fresa, se ha observado un incremento de la expresión de genes relacionados con la respuesta a estrés oxidativo durante este proceso y viceversa (Aharoni *et al.*, 2002a). Por ello, se ha propuesto que el programa transcripcional asociado a la maduración del fruto de fresa podría ser parcialmente inducido por el estrés oxidativo generado durante la lignificación de los haces vasculares del fruto en los estadios de maduración del mismo (Aharoni *et al.*, 2002a).

En tomate, se ha observado que durante su proceso de maduración y, concretamente en el estadio blanco-intermedio, se incrementan los índices indicativos de procesos oxidativos como el contenido en peróxido de hidrógeno, la peroxidación de lípidos y la oxidación de proteínas (Jiménez *et al.*, 2002). En otros frutos, como pera y piña, se ha descrito durante la maduración un incremento del nivel de transcrito correspondiente a un gran número de genes que codifican proteínas antioxidantes y enzimas de la ruta de detoxificación de especies reactivas de oxígeno (ROS), lo que apoya la hipótesis de que durante este proceso se produce un fenómeno oxidativo que requiere un equilibrio entre la producción y eliminación de ROS por los sistemas antioxidantes (Fonseca *et al.*, 2004; Moyle *et al.*, 2005). En fresa, también se ha observado un incremento de la producción de anión superóxido ( $O_2^-$ ) a lo largo del proceso de maduración del fruto (López-Ráez *et al.*, 2003). Sin embargo, no se ha observado ninguna modificación en los niveles de transcrito de genes involucrados en estrés oxidativo durante la maduración del fruto de la uva (Terrier *et al.*, 2005).

## 5. REGULACIÓN HORMONAL DEL DESARROLLO Y MADURACIÓN DEL FRUTO DE FRESA

La regulación hormonal del desarrollo y maduración de la fresa es uno de los procesos más estudiados en los frutos blandos. La estructura única de este fruto, con los aquenios en el exterior del receptáculo, lo han hecho un sistema muy útil para estudiar el papel de éstos en el desarrollo, ya que se pueden eliminar fácilmente causando poco daño físico al resto del fruto.

### 5.1. Auxinas

Durante la etapa de desarrollo del fruto, en los aquenios tiene lugar la síntesis de la auxina ácido 3-indol acético (IAA), que es exportada al receptáculo (Nitsch, 1950). El análisis de los niveles de IAA en el fruto de fresa constató que el IAA libre, considerado como la forma activa de la hormona, era la forma predominante en aquenios y presentaba un nivel máximo de 3 µg/g de peso seco a los diez días post-antesis (Dreher y Poovaiah, 1982). De esta cantidad, menos del 1% estaba presente en el receptáculo en el mismo estadio de desarrollo. Por otra parte, se encontró que el IAA conjugado por enlaces tipo amida era la principal forma de IAA presente en el receptáculo. Sin embargo, otros estudios encontraron en el tejido del receptáculo niveles sustancialmente mayores de IAA libre y conjugado que los descritos por Dreher y Poovaiah (1982) (Archbold y Dennis, 1984; Park *et al.*, 2006b). Además, se ha descrito que los niveles de IAA unido por enlace tipo amida presentan una distribución bimodal con un pico de concentración en el receptáculo a los 11 días seguido de un descenso y una posterior acumulación en los últimos estadios de maduración del fruto (Archbold y Dennis, 1984).

Aunque el crecimiento del receptáculo aún no ha podido relacionarse totalmente con los niveles endógenos de auxinas en el propio receptáculo ni en aquenios, sí se sabe que éstos juegan un papel fundamental en el desarrollo del fruto. Los niveles elevados de IAA conjugado tipo éster presentes en aquenios jóvenes pueden servir como fuente de IAA durante el desarrollo del aquenio, suplementando al IAA sintetizado *de novo*. La acumulación en los aquenios de IAA conjugado tipo amida podría ser debido a un producto final del metabolismo del IAA o bien a una forma de almacenamiento del mismo para ser utilizado como una fuente de IAA libre durante la germinación de las semillas. Los estudios realizados con IAA marcado y suministrado exógenamente han demostrado que el IAA libre es capaz de conjugarse en glucosa-IAA y aspartato-IAA (Lis, 1974).

Given *et al.* (1988b) propusieron que las auxinas producidas por los aquenios inhiben la maduración en los frutos en estadio verde. A medida que el fruto se desarrolla, el nivel de las auxinas en los aquenios va declinando, lo que implica que en el receptáculo se produce un descenso en la concentración de IAA hasta un nivel crítico que permite que se desencadene el proceso de maduración. Por lo tanto, las auxinas estimularían la elongación del fruto mientras que reprimirían la maduración del mismo.

Se han descrito numerosos genes involucrados en los procesos metabólicos asociados a la maduración del fruto de fresa y cuya expresión se ve inducida en frutos verdes tras la retirada de los aquenios, como por ejemplo los genes que codifican las enzimas dihidroflavonol reductasa (*FaDFR*) (Moyano *et al.*, 1998; Halbwirth *et al.*, 2006; Almeida *et al.*, 2007), pectato liasas (*Fapl*) (Medina-Escobar *et al.*, 1997b; Benítez-Burraco *et al.*, 2003),

endoglucanasas (*FaEGs*) (Hapster *et al.*, 1998; Manning, 1998; Llop-Tous *et al.*, 1999; Trainotti *et al.*, 1999; Woolley *et al.*, 2001; Spolaore *et al.*, 2003; Palomer *et al.*, 2006), así como los genes *Famyb2*, *FaQR*, *FaHyPRP*, *Fapmsr*, *Faufgt* y *Fa4cl* (López-Ráez *et al.*, 2003; Blanco-Portales *et al.*, 2003; Raab *et al.*, 2006; López *et al.*, 2006; Lunkenbein *et al.*, 2006a), y otros (Manning, 1994 y 1998). No obstante, hay genes relacionados con la maduración que no se ven afectados por las auxinas, por ejemplo, el gen *FaExp2* que codifica una expansina de pared celular. (Aharoni *et al.*, 2002b).

La sugerencia de que la concentración de auxinas podría ser el principal factor hormonal que influye en la maduración del fruto de fresa se ve apoyada por la ausencia de cualquier tipo de relación del etileno con este proceso. Esta falta de relación se deduce de la pobre producción de etileno endógeno (Knee *et al.*, 1977; Abeles y Takeda, 1990), la falta de respuesta a la aplicación de etileno exógeno (Hoad *et al.*, 1971; Iwata *et al.*, 1969b), y por la falta de sensibilidad mostrada frente a inhibidores de la síntesis del etileno. Todo esto no excluye la existencia de otros factores que intervengan en la maduración, ya que se conoce el efecto enrojecedor sobre el fruto de fresa de compuestos como el ácido fumárico, ácidos de frutas y monofenoles (Guttridge *et al.*, 1977).

## 5.2. Giberelinas y citoquininas

Aunque las auxinas son las hormonas que dominan el proceso de crecimiento y maduración de la fresa, sus efectos pueden ser modificados por otras fitohormonas presentes también en el fruto (Lis *et al.*, 1978).

La giberelina GA<sub>3</sub> no estimula el crecimiento del fruto cuando se aplica a frutos a los que se les han retirado los aquenios (Archbold y Dennis, 1985); sin embargo, se ha comprobado que actúa de forma sinérgica con la 1-naftalenacetamida (1-NAAm) en frutos intactos cultivados *in vitro* promoviendo su crecimiento y maduración (Kano y Asahira, 1978). También se ha demostrado que la citoquinina N<sup>6</sup>-benciladenina (BA) suprime el crecimiento y maduración en conjunción con 1-NAAm. La actividad máxima de citoquininas y giberelinas ha sido detectada 7 días después de la antesis, concentrándose principalmente en aquenios. Transcurrido este tiempo, la concentración de citoquininas disminuye en aquenios y receptáculos manteniendo unos niveles basales hasta que el fruto está maduro (Lis *et al.*, 1978). Por otro lado, se ha comprobado que la kinetina no induce crecimiento en tejidos cultivados de fresa ni aplicada a frutos intactos (Lis y Antoszewski, 1979). Por lo tanto, las auxinas son las hormonas que dominan el proceso de crecimiento y maduración, aunque dichos efectos pueden ser modificados por otras sustancias presentes también en el fruto.

Hytönen *et al.* (2009) han propuesto que las GAs podrían controlar la inducción de la división celular en los tejidos subapicales de las yemas axilares y actuar como una señal para determinar el destino del brote. Además, también han observado que las GAs parecen intervenir en la diferenciación de las yemas axilares regulada por el fotoperíodo.

Por otra parte, se ha considerado que el efecto de la temperatura en el desarrollo de los aquenios podría estar relacionado con la actividad de las citoquininas sintetizadas en éstos. De esta forma, la maduración de los frutos que crecen a temperaturas bajas estaría retrasada debido a la alta concentración de citoquininas presente en los aquenios y por un desarrollo ralentizado de los mismos (Kano y Asahira, 1979). También, se ha demostrado que las variaciones de la concentración de citoquininas durante el proceso de inducción floral son

importantes en el proceso de floración en plantas de fresa (Eshghi y Tafazoli, 2007). Yamasaki y Yamashita (1990) estudiaron los cambios en la concentración de citoquininas endógenas en la corona de flores de fresa inducidos en condiciones de noche fría y día corto. Observaron que un aumento del nivel de zeatina y una disminución de la zeatina ribósido justo antes de la iniciación floral, junto con el incremento específico de ribósido zeatina justo después de la iniciación, producía la inducción de flores en plantas de fresa. Estos resultados sugieren que los cambios en la actividad de ribósido zeatina y zeatina juegan un papel importante en la iniciación y el desarrollo floral (Yamasaki y Yamashita, 1990).

### 5.3. Ácido abscísico

El ABA es una fitohormona relacionada con el crecimiento y desarrollo de las plantas. Se ha descrito su participación en el proceso de maduración de la semilla, en la adquisición de tolerancia a la senescencia y en la dominancia. Además, durante el crecimiento vegetativo, el ABA es la hormona clave en las respuestas fisiológicas que confieren tolerancia al estrés hídrico (sequía) y osmótico (altos niveles de salinidad) (Mishra *et al.*, 2006), permitiendo que las plantas puedan colonizar nichos ecológicos donde la disponibilidad de agua está limitada o es esporádica. De hecho, se ha comprobado en varias especies de plantas que la concentración endógena de ABA incrementa más de 10 veces a pocas horas de producirse situaciones de estrés hídrico y que decrece a sus niveles basales con la posterior rehidratación de la planta (Gómez-Cadenas *et al.*, 1996). Parece ser que el incremento de los niveles de ABA durante situaciones de estrés hídrico estimula el cierre de los estomas e inhibe su apertura, lo que resulta vital para evitar la pérdida de agua y el mantenimiento del estado de hidratación de la planta (Mishra *et al.*, 2006). Con el problema medioambiental de escasez de agua que se prevé para el siglo XXI, la modificación de la biosíntesis y del proceso de captación de ABA se presenta como un objetivo de estudio de gran interés para potenciar la resistencia de los cultivos a la sequía (Shinokazi y Yamaguchi-Shinozaki, 2007).

Por otra parte, el ABA también parece estar involucrado en el retraso del crecimiento detectado en plantas sometidas a condiciones de estrés hídrico a través de la restricción de la producción de etileno. Es muy probable que esta interacción hormonal sea relevante en otras respuestas a estreses de plantas en las que se encuentre envuelto el etileno (Sharp, 2002). Además, el ABA controla ciertas funciones fisiológicas o de desarrollo en situaciones normales de la planta. Así, se ha descrito que las plantas deficientes en ABA muestran un fenotipo anormal, incluso en condiciones de buen riego (Wasilewska *et al.*, 2008). Paralelamente, estudios recientes han relevado que esta hormona es también activa es respuesta a estreses bióticos dependientes de patógenos (Fan *et al.*, 2009).

En fresa, se ha observado que el ácido abscísico (ABA) se acumula tanto en aquenios como en receptáculos a los 20 días postantesis (Archbold y Dennis, 1984). Este aumento es simultáneo al descenso del nivel de IAA en ambos tejidos, por ello se ha propuesto que la relación ABA/IAA podría ser suficiente para dirigir el cambio genético que ocurre durante la transición de elongación a maduración del fruto (Perkins-Veazie *et al.*, 1995). Además, se ha comprobado que la aplicación de ABA exógeno acelera la maduración en receptáculos cultivados *in vitro* (Kano y Asahira, 1981). No obstante, estos resultados obtenidos *in vitro* deben ser interpretados con precaución puesto que los frutos cortados no llegan a alcanzar el tamaño total y su crecimiento es mucho más lento que cuando se produce en la planta.

Mediante el uso de diferentes tratamientos y técnicas como el silenciamiento génico, recientemente se han aportado pruebas que apoyan la idea de que el ABA desempeña un papel

crucial en la regulación de la maduración del fruto de fresa. La aplicación de ABA exógeno promovió la maduración del fruto de fresa, mientras que la administración de un inhibidor de la biosíntesis de ABA la retrasó (Jia *et al.*, 2011). Además, se comprobó que el silenciamiento del gen *FaNCE1*, que codifica una proteína clave en la biosíntesis de ABA, redujo la concentración de ABA endógeno del fruto de fresa generando frutos transgénicos con una reducción evidente del color debido a la inhibición de su maduración. No obstante, dicho fenotipo se revertió mediante la aplicación de ABA exógeno lo que parece sugerir que el ABA promueve la maduración del fruto de fresa (Jia *et al.*, 2011).

## 5.4. Etileno

En el fruto de fresa, la producción de etileno presenta un máximo en el estadio verde descendiendo su nivel hasta el día 20 tras la antesis. Dicho descenso se correlaciona con la transición del fruto de estadio verde hasta el estadio blanco de maduración. A continuación se observa un nuevo aumento de su producción, alcanzando un máximo en el estadio maduro (Perkins-Veazie *et al.*, 1995). Este descenso transitorio en la producción de etileno al comienzo del proceso de maduración del fruto podría deberse a la compartimentización del 1-aminociclopropano-1-ácido carboxílico (ACC), precursor del etileno. No obstante, también podría ser debido a un descenso en las actividades ACC sintasa o ACC oxidasa (ACO), responsables de la síntesis de esta fitohormona (Perkins-Veazie *et al.*, 1995). Recientemente se ha descrito que el patrón de expresión del gen *FaACO1* (AJ851828) coincide con la acumulación de esta fitohormona durante el proceso de maduración (Trainotti *et al.*, 2005). Por otra parte, aunque en frutos escindidos y tratados con ACC se incrementó la producción de etileno junto con el peso fresco y la acumulación de antocianinas, no se observó ningún cambio en la respiración (Perkins-Veazie *et al.*, 1996).

Se ha propuesto que la pequeña cantidad de etileno producida durante el proceso de maduración de la fresa podría ser suficiente para desencadenar algunos de los procesos fisiológicos relacionados con la maduración de este fruto (Trainotti *et al.*, 2005); de hecho, se ha observado la presencia de receptores de etileno de tipo-II codificados por el gen *FaEtr2* (AJ297513) en el fruto de fresa (Perkins-Veazie *et al.*, 1996; Leshem y Pinchsov, 2000; Iannetta *et al.*, 2000). Por otra parte, en un fruto no climatérico como el pimiento, se ha observado que el etileno puede tanto acelerar la maduración (Armitage, 1989) como incrementar el nivel de expresión de genes específicos del proceso (Ferrarese *et al.*, 1995; Harpster *et al.*, 1997). Igualmente, en pera se ha descrito que la actividad reguladora del etileno puede tener efectos negativos y/o positivos sobre la expresión de diferentes genes (Trainotti *et al.*, 2003). En uva, se ha descrito un aumento de la expresión de genes involucrados en la maduración en respuesta al tratamiento con etileno (El-Kereamy *et al.*, 2003; Tesniere *et al.*, 2004). Sin embargo, en fresa se ha observado que el etileno reprime la expresión de los genes que codifican una pectín metilesterasa (*FaPE1*) (Castillejo *et al.*, 2004) y una galactosidasa (*FaEG3*) (Trainotti *et al.*, 2001; Balogh *et al.*, 2005), mientras que no se modifica la expresión de otros genes también relacionados con la degradación de la pared celular como es el caso del *FaExp2* y *FaCell* que codifican una expansina y una celulasa respectivamente (Civello *et al.*, 1999). Además, se han clonado tres genes de fresa diferentes que codifican receptores de etileno (Trainotti *et al.*, 2005) y cuya expresión es inducida por esta hormona de forma diferencial durante la maduración del fruto (Trainotti *et al.*, 2005), lo que podría indicar un posible papel del etileno en la maduración del fruto de fresa.

El etileno actúa también acelerando el proceso de senescencia de las hojas en *Arabidopsis*, aunque no es esencial para que este proceso ocurra (Pandey *et al.*, 2000). Además, se ha observado que es necesaria la presencia de señales indicadoras de la edad del tejido para que el etileno precipite la senescencia, al igual que con el ácido salicílico y el metiljasmonato (Pandey *et al.*, 2000; Buchanan-Wollaston *et al.*, 2003). En este sentido, se ha descrito que la aplicación exógena de etileno en frutos de fresa acelera su proceso de senescencia (El-Kazzaz *et al.*, 1983), mientras que el inhibidor de la percepción del etileno, el 1-metil ciclopropeno (1-MPC), mantiene la firmeza del fruto y reduce la acumulación de antocianinas y del contenido en compuestos fenólicos del fruto en postcosecha (Jiang *et al.*, 2001). En general, el etileno juega un papel importante en la maduración de los frutos climatéricos aunque su función en frutos no climatéricos como la fresa no está clara.

## 6. CONTROL DE LA FLORACIÓN

La formación de flores en la planta de fresa es inducida a bajas temperaturas y con fotoperíodos cortos. Aunque, todas las especies de *Fragaria* muestran una gran variedad de respuesta a la temperatura y a la longitud del día a la hora del desarrollo de yemas florales (Heide y Sønsteby, 2007), también las auxinas y citoquininas juegan un papel importante en este proceso (Hou y Huang, 2005; Eshghi y Tafazoli, 2007). Así, es probable que las auxinas se produzcan en las hojas más jóvenes y posteriormente se transporten a los meristemas de los brotes apicales a través de los tejidos vasculares. Esta teoría se ve apoyada por el aislamiento en fresa del gen *ABPI* que codifica una proteína de unión a auxinas (ABP1) (Lazarus y MacDonald, 1996). En cualquier caso, existen cultivares de día corto, de día largo y de fotoperíodo insensible (día neutro o “Everbearing”).

Por otra parte, durante la búsqueda de genes diferencialmente expresados en frutos de fresa, se identificó un ADNc correspondiente al gen *FaGAST1* (ácido giberélico de transcripción estimulada) (de la Fuente *et al.*, 2006). Este gen está altamente expresado en frutos en estadio blanco, rojo maduro y en raíces, donde su expresión se relaciona con el proceso de elongación de las células del extremo apical. Líneas transgénicas de *Fragaria vesca* sobre-expresando el gen *FaGAST1* mostraron un retraso en el crecimiento de la planta, tamaño reducido de los frutos, floración tardía y sensibilidad baja a giberelinas. Por ello, los genes *FaGAST* se han asociado con eventos como la división celular, la elongación celular y la floración (Wisemann y Turnbull, 1999).

Ya que el crecimiento de los meristemas a menudo se convierte en un factor determinante de la transición de la floración, el gen *AGAMOUS* (*AG*) (relacionado con el desarrollo del meristemo, con la formación de los estambres y la iniciación del carpelo) (Battey y Tooke, 2002), juega un papel importante en el proceso de floración. En el caso de la fresa, la expresión de un gen homólogo del *AG* (*FaAG1*) está limitada a los estambres, carpelos y a frutos en desarrollo, en consonancia con su papel regulador del desarrollo de los órganos florales (Rosin *et al.*, 2003). Por otra parte, la histona H4, implicada en el mantenimiento de la estructura de la cromatina en células eucariotas, incrementó su expresión en plantas de fresa bajo condiciones de inducción de la floración (Kurokura *et al.*, 2006).

Actualmente, las investigaciones están centradas en la identificación de genes reguladores de la floración en variedades de día neutro, ya que son las plantas que se adaptan mejor a los climas continentales (Weebadde *et al.*, 2008). Se cree que es un alelo dominante de un sólo

gen el que determina que la floración sea continua (“Everbearing”) en *F. vesca* y en algunas especies de *Fragaria x ananassa* (Battey y Tooke, 2002; Albani *et al.*, 2004; Sugimoto *et al.*, 2005). De hecho, en estudios realizados sobre la sensibilidad de la floración al fotoperiodo en *F. virginiana* y *Fragaria x ananassa*, se ha comprobado que la neutralidad del día está regulada por un solo gen dominante (Hancock *et al.*, 2002). Sin embargo, sólo especies de día neutro de *F. virginiana* se ajustan al modelo de un gen único dominante cuando son cruzadas con especies de día corto de *Fragaria x ananassa*. Así, estos resultados sugieren que la neutralidad del día probablemente esté regulada por diferentes genes según la especie de *Fragaria* y/o que su regulación sea una herencia poligénica de las especies implicadas (Hancock *et al.*, 2002).

## 7. EXPRESIÓN GÉNICA DURANTE EL DESARROLLO Y LA MADURACIÓN DEL FRUTO DE FRESA

El proceso de desarrollo y maduración del fruto de fresa ha sido analizado mediante tres aproximaciones moleculares.

En primer lugar, se compararon los productos de traducción *in vitro* de dos poblaciones de ARNm procedentes de receptáculo de fruto en estadio blanco y estadio rojo de maduración respectivamente. La separación de ambas poblaciones mediante electroforesis bidimensional mostró numerosas diferencias entre ambos. Así, se observó que el estadio intermedio de maduración (fruto blanco) está precedido por numerosos cambios a nivel molecular reflejados en variaciones en ciertos grupos de ARNm (Manning, 1993). Se han descrito tres modelos de evolución de los transcritos: un primer grupo de ARNm cuya concentración aumenta a lo largo de la maduración; un segundo grupo constituido por ciertas poblaciones de ARNm cuyos niveles disminuyen a lo largo del proceso; y un tercer grupo de ARNm cuyos componentes alcanzan su máxima concentración en el estadio intermedio para posteriormente declinar (Veluthambi y Poovaiah, 1984; Reddy y Poovaiah, 1990; Reddy *et al.*, 1990; Manning, 1994). Estos modelos de expresión podrían indicar que el proceso de maduración de la fresa incluye tanto la desaparición de polipéptidos existentes en los estadios de elongación del fruto, como la síntesis de nuevas proteínas. Mediante este sistema de traducción *in vitro* de ARNm, también se han identificado alrededor de 50 polipéptidos que presentan cambios importantes de concentración a lo largo de los diferentes estadios de desarrollo del fruto (Manning, 1994). Además, se ha comprobado que varias enzimas específicas asociadas a membrana (Civello *et al.*, 1995), con la producción de antocianinas (Given *et al.*, 1988a), y con el metabolismo de la sacarosa (Hubbard *et al.*, 1991) también aumentan su actividad durante el proceso de maduración de la fresa.

El proceso de maduración del fruto de fresa también ha sido ampliamente estudiado mediante la caracterización individual de los genes que intervienen en el proceso. De este modo, se ha profundizado, por ejemplo, en la función que desarrollan genes que codifican enzimas degradadoras de la pared celular durante el proceso de maduración de la fresa.

La reestructuración de la pared celular es una de las modificaciones más importantes que sufre el fruto durante su maduración y afecta, fundamentalmente, a su composición pectínica. En nuestro grupo, se han aislado y caracterizado varios genes que codifican pectato liasas (*plA*, *plB* and *plC*) relacionadas con la pérdida de firmeza del fruto durante su proceso de maduración (Medina-Escobar *et al.*, 1997b; Benítez-Burraco *et al.*, 2003). De hecho, su

silenciamiento en frutos transgénicos se tradujo en un incremento de la firmeza de éstos y en un retraso en su proceso de maduración (Jiménez-Bermúdez *et al.*, 2002). Paralelamente, también han sido aislados y caracterizados varios genes que codifican endoglucanasas (*Cel2*, AF054615) (Llop-Tous *et al.*, 1999; Trainotti *et al.*, 1999; Palomer *et al.*, 2006), (*FaEG3*; AJ006349) (Trainotti *et al.*, 1999), (*Cell*, AF07492) (Harpster *et al.*, 1998; Llop-Tous *et al.*, 1999; Woolley *et al.*, 2001), una poligalacturonasa (*spG*, AF380299) (Redondo-Nevado *et al.*, 2001; Quesada *et al.*, 2009; García-Gago *et al.*, 2009) y una xilosidasa (*FaXyl1*, AY486104) (Lee *et al.*, 2003; Minic *et al.*, 2004; Martínez *et al.*, 2004; Bustamante *et al.*, 2006), cuyas características de expresión las relaciona directamente con la maduración de la fresa.

También se han identificado en fresa siete expansinas (*FaEXPI* a *FaEXP7*) (Harrison *et al.*, 2001) que participan en el reblandecimiento de la pared celular utilizando para ello como sustrato al xiloglucano presente en ella. De las siete descritas, sólo dos de ellas son específicas de fruto y aumentan su expresión a lo largo de la maduración [*FaEXP2* (AF159563) y *FaEXP5* (AR226702)] (Harrison *et al.*, 2001). De hecho, se ha encontrado una correlación entre la *FaEXP2* y la *FaEXP5* y los niveles de expresión y firmeza del fruto. Así, estudios en diferentes variedades de fresa indican que ambas expansinas muestran una mayor expresión en las variedades más blandas (Toyonaka y Gorella) que en otros cultivares más firmes (Selva, Camarosa, Holiday y Elsanta) (Salentijn *et al.*, 2003; Dotto *et al.*, 2006). Estos resultados sugieren que las expansinas contribuyen a la maduración de la fruta y pueden ser responsables del grado de reblandecimiento en los distintos cultivares de fresa (Dotto *et al.*, 2006).

Asimismo, se han aislado y caracterizado cuatro genes que codifican pectin metil esterases en el fruto de fresa (*FaPE1* a *FaPE4*). Las PE (CE 3.1.1.11) catalizan la hidrólisis de los grupos metil éster de las pectinas dando lugar a una desesterificación de la pared celular (Prasanna *et al.*, 2007). Su acción consiste en eliminar los grupos metoxilo y, por tanto, catalizan la desmetilación de las pectinas (Castillejo *et al.*, 2004; Prasanna *et al.*, 2007). Así, el grado de esterificación de la pectina es muy importante y puede influir en la actividad de otras enzimas asociadas a la pared como son la poligalacturonasa y las pectato liasas (Prasanna *et al.*, 2007). En fresa, se ha detectado la actividad de seis isoformas diferentes a partir de una muestra de extracto de pared, observándose como la expresión de la *FaPE1* es específica de fruto y está relacionada con la maduración de la fresa. En cambio, las otras isoformas son específicas de hojas (*FaPE2*) y otros tejidos vegetativos (*FaPE3* y *FaPE4*) (Castillejo *et al.*, 2004). En este sentido, la aparición de múltiples isoformas de PE en fresa indican que los diferentes genes codifican proteínas con diferentes funciones en la pared celular a lo largo del proceso de maduración (Castillejo *et al.*, 2004). Además, se ha demostrado que la expresión de la *FaPE1* es inducida por auxinas, al contrario de otros genes de fresa como la PL (Medina-Escobar *et al.*, 1997; Benítez-Burraco *et al.*, 2002), la PG (Quesada *et al.*, 2009) o EGases (Trainotti *et al.*, 1999). La regulación de la *FaPE1* por etileno durante la senescencia del fruto indica que su expresión puede ser un factor determinante en la cosecha de la fresa (Castillejo *et al.*, 2004). Recientemente, se han analizado plantas transgénicas de fresa silvestre (*Fragaria vesca*) con expresión ectópica de la *FaPE1* procedente de *Fragaria x ananassa*. Los frutos obtenidos mostraron cambios en el grado y patrón de esterificación de sus pectinas y también un incremento de la expresión de SA y PR5 (Osorio *et al.*, 2008). Esto sugiere que la *FaPE1* podría participar en la metilación de derivados pectínicos oligogalacturónidos (OGA) envueltos en procesos de defensa. De hecho, los frutos transgénicos de fresa obtenidos fueron más resistentes a *Botrytis cinerea* que los frutos control procedentes de *F. vesca* (Osorio *et al.*, 2008).



Por otra parte, existen evidencias de que la biosíntesis del ácido L-ascórbico en fresa podría realizarse a partir de ácido *D*-galacturónico, principal componente de las pectinas de la pared celular, y estaría catalizada, al menos parcialmente, por una *D*-galacturonato reductasa dependiente de NADPH (GalUR) (Agius *et al.*, 2003). Así, el máximo de expresión del gen *FaGalUR* (AF039182) en el estadio rojo de maduración coincide con el aumento de solubilidad de las pectinas debido a la acción de las pectato liasas y con el máximo contenido de ácido ascórbico que se observa en el fruto maduro, lo que apoya la ruta propuesta por Agius *et al.* (2003) para la biosíntesis del ácido *L*-ascórbico en el fruto de fresa.

El proceso de maduración viene acompañado también de un aumento de las antocianinas presentes en el fruto. Esto supone un incremento de la expresión de genes involucrados en su síntesis, como la PAL, CHS, F3H y DFR (Gong *et al.*, 1997; Moyano *et al.*, 1998; Mori *et al.*, 2001). Concretamente, y teniendo en cuenta que la síntesis de antocianinas se produce dentro de la ruta de biosíntesis de los fenilpropanoides, se ha detectado una inducción general de los genes envueltos en ella (Anterola *et al.*, 2002). Igualmente, la síntesis de antocianinas durante la maduración parece estar regulada por la síntesis *de novo* de la enzima PAL (EC 4.3.1.5) (Hirner *et al.*, 2001; Mori *et al.*, 2001) que es inhibida por la aplicación de auxinas (Given *et al.*, 1988a). La actividad de esta enzima parece presentar dos picos de expresión durante el proceso de desarrollo y maduración del fruto. Así, un primer pico aparece en el fruto verde cinco días después de la antesis y cuando existe un nivel muy alto de fenoles solubles; y el segundo pico aparece 27 días después de la antesis, cuando el fruto está maduro (Cheng y Breen, 1991). Por otro lado, se ha aislado y caracterizado el gen *FaDFR* (AF029685), que presenta una expresión específica de fruto de fresa, y que codifica una dihidroflavonol 4-reductasa (DFR), potencialmente involucrada en el último paso de la ruta común a la biosíntesis de antocianinas y taninos condensados (Moyano *et al.*, 1998). Aunque el máximo de expresión de este gen se observa en los estadios de maduración del fruto, su expresión también se detecta en frutos en desarrollo (verdes), lo que sugiere una posible implicación de este gen no sólo en la producción de color en el fruto, sino también en la síntesis de los taninos condensados que se producen en los estadios iniciales de desarrollo. Por último, se ha propuesto que el gen *FaMYB1* (AF401220), que codifica un factor de transcripción de tipo MYB, podría desempeñar una función reguladora de la síntesis de antocianinas y flavonoles durante la maduración del fruto de fresa (Aharoni *et al.*, 2001) (*Introducción general, apartado 4.2.2*).

Se ha estudiado también la función que desarrollan otros genes en diferentes procesos específicos de la maduración del fruto de fresa, como la producción de compuestos volátiles que participan destacadamente en la generación del aroma del fruto maduro (*FaOMT*, *FaNES1*, *SAAT*, *FaPDC1*) (*Introducción general, apartado 4.2.1*). También, se han analizado los perfiles de expresión de genes involucrados en la síntesis de etileno (*FaACO1*), así como de genes que codifican receptores para esta fitohormona (*FaEtr2*) (*Introducción general, apartado 4.2.1*).

En relación al proceso de lignificación, la caracterización de los patrones de expresión del gen *Facad1* (AF320110) (que codifica una cinamil alcohol deshidrogenasa) y la inmunolocalización del polipéptido que codifica, sugiere su participación en el proceso de lignificación del tejido vascular de los tejidos vegetativos, del receptáculo y de los aquenios del fruto de fresa durante su maduración (Blanco-Portales *et al.*, 2002). En este mismo contexto, se ha identificado una proteína híbrida rica en prolina codificada por el gen

*FaHyPRP* (AY530533) relacionada con el anclaje de polifenoles (ligninas y taninos condensados) a la membrana de las vacuolas y de las células parenquimáticas del receptáculo (Blanco-Portales *et al.*, 2004). La expresión de este gen es específica de fruto y sus niveles de transcrito se incrementan en la etapa de maduración. Estos datos de expresión junto con su localización en los mismos tipos celulares que la enzima *FaCAD1*, parecen indicar que la función de ambas proteína podría ser complementaria (Blanco-Portales *et al.*, 2002).

En general, se ha observado que la mayoría de los genes implicados en el proceso de maduración del fruto de fresa se encuentran regulados negativamente por las auxinas sintetizadas en los aquenios. Este es el caso de los genes *FaDFR* (Moyano *et al.*, 1998), *Fapl* (Medina-Escobar *et al.*, 1997b; Benítez-Burraco *et al.*, 2003;), genes *Cell* y *FaEG3* que codifican endoglucanasas (Harpster *et al.*, 1998; Trainotti *et al.*, 1999), el gen *FaXyl1* (Martínez *et al.*, 2004), y los genes *FaQR*, *Fapmsr*, *Faufgt* (Raab *et al.*, 2006; López *et al.*, 2006; Lunkenbein *et al.*, 2006a), *Fa4cl* (López-Ráez *et al.*, 2003), *FaHyPRP* (Blanco-Portales *et al.*, 2004), y otros (Manning, 1994; Manning, 1998).

## 8. GENES IMPLICADOS EN LA MEJORA DE LA FRESA

La familia de las Rosáceas presenta una gran diversidad fenotípica ya que está compuesta por muchas especies diferentes. Dentro de sus miembros se incluyen árboles de gran interés, como el melocotón y la manzana, así como zarzas, rosas, almendras y fresas. En la actualidad, existe escasa información acerca del desarrollo de sistemas transgénicos eficientes para evaluar la función de genes entre las diferentes especies. A pesar de ello, recientemente se han identificado genes implicados en procesos importantes relacionados con la producción y la calidad de las frutas mediante transgénesis. No obstante, la evaluación de la función de genes transgénicos es bastante lenta aunque proporciona una herramienta muy valiosa para la selección de genes que puedan determinar una mejora del fruto de la fresa.

### 8.1. Mejora de la planta de fresa frente a plagas y enfermedades

#### 8.1.1. Resistencia a agentes abióticos

En su hábitat natural, las plantas de fresa están expuestas a diferentes agentes abióticos como el déficit de agua, altas temperaturas, salinidad, metales pesados y daños mecánicos. Se estima que estas condiciones de estrés pueden reducir el rendimiento de los cultivos hasta un 50% (Vij y Tyagi, 2007). Por ello, se han realizado estudios fisiológicos, bioquímicos y moleculares acerca de la tolerancia de las plantas al estrés y aclarar así cuales son los mecanismos intrínsecos de éstas para poder minimizarlos.

Se sabe que las plantas anuales y perennes de invierno que crecen a bajas temperaturas desarrollan tolerancia frente a la congelación. Así, mediante la utilización de una genoteca de ADNc de plantas de fresa aclimatadas al frío (*Fragaria cold-regulated*, *Fcor*) se consiguieron identificar varios genes (*Fcor1*, 2 y 3) que presentaban expresión diferencial a bajas temperaturas (NDong *et al.*, 1997). Mientras que *Fcor1* y *Fcor2* se expresaron en todos los tejidos analizados, la expresión de *Fcor3* fue específica de hojas. También, se ha aislado una proteína quinasa calcio-dependiente (CDPK) que parece estar involucrada en la tolerancia al frío en fresa (Llop-Tous *et al.*, 2002). Así, *FaCDPK1* se expresa en raíces, estolones,

meristemos, flores, hojas y en frutos a partir del estadio blanco. Además, también se ha observado un incremento significativo de los niveles de transcrito del gen *FaCDPK1* después de 10 h de tratamiento en frío (4 °C) lo que sugiere para esta proteína un papel tanto a nivel de desarrollo de la fruta como en respuesta a bajas temperaturas. Por otra parte, también ha sido clonado en fresa el factor de transcripción CBF1 que participa en la aclimatación de *Arabidopsis thaliana* a bajas temperaturas (Owens *et al.*, 2002). Sin embargo, el análisis de los frutos obtenidos a partir de dos líneas transgénicas de fresa sobre-expresando el gen *FaCBF1*, no mostró cambios significativos en la tolerancia de estas plantas a la congelación (Owens *et al.*, 2002).

Para conferir resistencia al frío en plantas de fresa, también se han utilizado genes foráneos. Así, el gen de trigo *Wcor410a dehidrina ácida*, cuyo nivel de expresión se correlaciona con el grado de tolerancia a la congelación de diferentes genotipos de trigo (Houde *et al.*, 2004), se empleó para obtener líneas transgénicas de fresa con altos niveles de expresión de este gen. Las plantas transgénicas obtenidas presentaron un mayor grado de aclimatación al frío y de tolerancia a la congelación. Otro sistema empleado para incrementar la resistencia de las plantas de fresa a las heladas es mediante la transferencia de la proteína AFP codificada por genes anticongelantes de peces antárticos (AFP). De esta manera, se han obtenido plantas transgénicas de fresa aunque no hay información concluyente sobre su tolerancia al frío (Khammuang *et al.*, 2005). No obstante, a partir de fresa y otros cultivos, se han aislado e identificado un gran número de genes que son inducidos por el frío, aunque aún se conoce poco sobre su función en la resistencia al frío.

La glicina betaína se acumula durante el proceso de aclimatación al frío de la planta de fresa en diferentes cultivares. Un incremento de concentración de dos veces de glicina betaína en fresa incrementa su tolerancia al frío de -5,8 °C a -17 °C (Rajashekar *et al.*, 1999). Del mismo modo, la aplicación exógena de ácido abscísico, que desencadena la síntesis de betaína o glicina betaína, aumenta la supervivencia de las plantas en condiciones de congelación mejorando su crecimiento. Igualmente, en condiciones de estrés osmótico o de sequía también se produce una acumulación significativa de este aminoácido en muchas plantas lo que ha llevado a proponer a algunos autores que la acumulación de este soluto en plantas es un mecanismo de adaptación al medio ambiente.

La osmotina es una proteína relacionada con la patogénesis que inicialmente fue identificada en cultivos celulares de tabaco en condiciones de estrés salino. Muchos estudios han demostrado que la expresión de este tipo de proteínas puede inducirse tanto en condiciones de estrés abiótico como también por infecciones microbianas. En fresa, se ha clonado el gen *OLP2 (osmotin like protein)* que se expresa en hojas, corona, raíces, frutos verdes y frutos rojos con diferente intensidad (Zhang y Shih, 2007). Este gen responde a tres estímulos abióticos (ácido abscísico, ácido salicílico y heridas mecánicas) lo que sugiere que podría ayudar a proteger a la planta frente a estreses ambientales e infecciones por patógenos. Esta teoría parece haber sido confirmada con los datos obtenidos a partir de plantas transgénicas de fresa portadoras del gen osmotina de tabaco, ya que su análisis mostró un incremento de su tolerancia al estrés salino (Husaini y Abdin, 2008). Del mismo modo, el gen de fresa de transferencia no específica de lípidos (*Fxaltp*) también es inducido por el ácido abscísico, ácido salicílico y heridas mecánicas, aunque es reprimido por el estrés al frío (Yubero-Serrano *et al.*, 2003).

Las temperaturas elevadas constituyen otro de los estreses abióticos más frecuentes a los que

se ven sometidas las plantas. Los organismos responden a ellas mediante la síntesis de un grupo específico de proteínas denominadas proteínas de choque térmico (HSP). En fresa, se ha aislado, a partir de una genoteca substractiva de ADNc, el gen *HSP* que muestra una homología significativa de secuencia con la proteína HSPI citoplasmática de bajo peso molecular (Medina-Escobar *et al.*, 1998). No obstante, los datos de expresión del gen *HSP* obtenidos sugieren que esta clase de proteínas no sólo tienen un papel en la respuesta de la planta al estrés sino también en su desarrollo, incluyendo la maduración del fruto. Otro estudio realizado en plantas de fresa expuestas a estrés térmico gradual ha permitido observar un aumento de la actividad peroxidasa con respecto a las plantas control, lo que se ha asociado con los procesos de aclimatación de la planta al calor (Gülen y Eris, 2004). Esto parece indicar que la transcripción de algunos genes peroxidasa es dependiente de la temperatura.

Otro péptido importante en la protección de las células frente al daño oxidativo causado por el estrés salino y por la infección de patógenos es la metionina sulfóxido reductasa (PMSR). Recientemente, se ha aislado el gen *Fapmsr* a partir de frutos de fresa y se ha comprobado que su expresión es específica de receptáculo de frutos rojos maduros (López *et al.*, 2006). La proteína recombinante FaPMSR expresada en *E. coli* redujo el sulfóxido de metionina libre a metionina, protegiendo así a su hospedador frente al daño producido por la adición de H<sub>2</sub>O<sub>2</sub>. Por consiguiente, los resultados obtenidos coinciden con la hipótesis de que el programa de transcripción durante la maduración de la fresa induce estrés oxidativo (Aharoni *et al.*, 2002b).

### 8.1.2. Resistencia a agentes bióticos

Como la mayoría de plantas cultivadas, la fresa es susceptible a muchas enfermedades y plagas que producen importantes pérdidas económicas debido al gasto que suponen los tratamientos fitosanitarios y la reducción de la producción de la cosecha. Además, la eliminación gradual del bromuro de metilo en muchos países desarrollados, aumenta las dificultades para obtener rendimientos aceptables en suelos no fumigados. Por ello, un objetivo muy importante en la investigación actual es la mejora de la resistencia natural de la planta de fresa mediante su manipulación genética.

La antracnosis es una de las principales enfermedades fúngicas de la fresa. Es causada por tres especies de *Colletotrichum* (*C. acutatum*, *C. fragariae* y *C. gloeosporioides*), las cuales se caracterizan por dañar los órganos vegetativos de la planta y el fruto. Estudios realizados sobre la segregación de poblaciones de *Fragaria x ananassa* mostraron que la resistencia a la antracnosis puede ser tanto poligénica como mendeliana (Giménez y Ballington, 2002; Denoyes-Rothan *et al.*, 2005). Independientemente de esto, se han podido seleccionar variedades resistentes de fresa mediante programas de cultivos (Smith *et al.*, 1996).

El loci monogénico dominante *Rfp1*, vinculado a marcadores SCAR (desarrollado a partir de los RAPD), está asociado a la resistencia a *Phytophthora fragariae* (Haymes *et al.*, 1997). Además, se ha analizado un amplio rango de genotipos de *F. x ananassa* con otro loci dominante *Rfp*. Paralelamente y, mediante el estudio genético de poblaciones segregantes, también se ha estudiado la variación genética asociada a la resistencia a *Phytophthora cactorum* (Shaw *et al.*, 2008). Para ello, ha sido de gran ayuda la caracterización molecular y bioquímica del péptido fitotóxico extracelular PcF producido por *Phytophthora cactorum*. Esto ha ayudado a conocer las características del proceso de patogenicidad y está permitiendo

asentar las bases para realizar bioensayos e identificar genotipos resistentes de fresa (Orsomando *et al.*, 2001).

Otro patógeno que infecta a la fresa es *Verticillium dahliae*. Este organismo es transmitido desde el suelo a la planta y ataca a los tejidos vasculares causando graves pérdidas. Estudios de la resistencia frente a este patógeno en diferentes variedades de fresa indican que ésta se basa en factores poligénicos con efecto aditivo, aunque no se ha descartado la herencia mendeliana (Zebrowska *et al.*, 2006). Por otra parte, estudios similares realizados en varias variedades de fresa y sus correspondientes poblaciones F1, indicaron que tanto factores monogénicos como poligénicos están involucrados en la resistencia a la marchitez causada por *Fusarium* (Mori *et al.*, 2005). En cualquier caso, hasta ahora no se han desarrollado marcadores moleculares asociados a locus específicos implicados en la resistencia de la planta a estos hongos patógenos. Actualmente, se están desarrollando tecnologías cada vez más efectivas de secuenciación de ADN que nos permitirán el análisis de los genomas de plantas y microorganismos, permitiendo el desarrollo de nuevos marcadores que permitirán el descubrimiento y mapeo fino de nuevos genes y compuestos vinculados al fenómeno de la resistencia. En este sentido, la secuenciación de genotecas de ADN genómico y ADNc del género *Fragaria* ha permitido identificar genes *RGA* (*Resistance Gene Analogs*) y microsatélites polimórficos relacionados con el fenómeno de la resistencia (Cipriani y Testolin, 2004; Lewers *et al.*, 2005; Folta *et al.*, 2005; Gil-Ariza *et al.*, 2006; Keniry *et al.*, 2006; Monfort *et al.*, 2006). Además, mediante el empleo de cebadores degenerados, recientemente se han amplificado y caracterizado varios tipos de genes *RGA* en tres especies diferentes de *Fragaria* (Martínez-Zamora *et al.*, 2004).

Otra variante poco estudiada en el género *Fragaria* es la resistencia contra enfermedades bacterianas y plagas de artrópodos. No obstante, se han identificado factores de resistencia contra *Xanthomonas fragariae* en *Fragaria virginiana*, *Fragaria virginiana* x *Fragaria x ananassa* y genotipos octoploides de *Fragaria* (Maas *et al.*, 2000; Xue *et al.*, 2006). Por otra parte, Barritt y Shanks (1980, 1981) investigaron poblaciones segregantes de *Fragaria chiloensis* x *Fragaria x ananassa* para identificar genes relacionados con la resistencia a pulgones y ácaros. Así, mediante el estudio de plantas de fresa modificadas genéticamente, se han obtenido resultados importantes frente a estas infecciones. Sin embargo, la aplicación de estos resultados está limitada por la falta de una normativa que regule el uso de cultivos transgénicos en Europa.

Paralelamente, también se está llevando a cabo el análisis de algunos péptidos y productos naturales con propiedades antibióticas aislados a partir de la planta de fresa. Recientemente, se ha evaluado la actividad antifúngica de compuestos orgánicos volátiles (COV) producidos por la planta de fresa frente a *C. acutatum*, lo que abre nuevas perspectivas en el control biológico de patógenos. Así, se ha observado una inhibición del crecimiento del micelio y de la germinación de las esporas de este hongo debido a los COV producidos por una lipoxigenasa a través de la degradación de ácidos grasos de 18 C (Arroyo *et al.*, 2007). Además, se ha aislado de hojas de fresa una molécula pequeña de 316 Da con actividad antibiótica denominada Fragarina que parece participar en respuesta a procesos de estrés (Filippone *et al.*, 1999). Por otra parte, se ha mostrado un incremento de expresión del gen *Cyfl* en tejidos vegetativos de fresa, excepto en receptáculo, indicando que la proteína fitocistatina que codifica este gen podría resultar activa frente a varias proteinasas de cisteína de *Botrytis cinerea* y *Fusarium oxysporum*, favoreciendo así la resistencia de la planta frente a estos patógenos (Martínez *et al.*, 2005).

El moho gris, enfermedad causada por *Botrytis cinerea*, es muy común en todas las regiones productoras de fresa del mundo y una de las más destructivas. La infección primaria aparece en flores pero, el desarrollo de los síntomas típicos, se produce después de que la fruta se ha desarrollado y haya comenzado a madurar. Los pétalos y los estambres son los órganos florales que se infectan principalmente mientras que el receptáculo se infecta normalmente a partir del hongo que crece por el filamento, aunque la infección a través de los pétalos también es posible. Actualmente no hay variedades de *Fragaria x ananassa* resistentes a *B. cinerea*. Si se ha observado diferencias de susceptibilidad, pero probablemente se pueden atribuir a las características morfológicas de la planta. Recientemente, en experimentos realizados en California, el uso de genes heterólogos *PGIP* (polygalacturonase-inhibiting protein) ha dado buenos resultados para controlar la infección por *B. cinerea* en tomates transgénicos. Igualmente, se han obtenido resultados positivos en plantas de fresa del cultivar “Pegasus” transformadas con el gen *PGIP* (de pera) frente a la enfermedad causada por *B. cinerea* tras rociar cada flor con una suspensión de conidios del hongo ( $1 \times 10^4$  / ml) (Schaart *et al.*, 2005).

Otros estudios realizados con plantas transgénicas de fresa han mostrado que altos niveles de quitinasa reducen los daños causados por el hongo oidio en la planta (Asao *et al.*, 1997; Asao *et al.*, 2003). En este sentido, Chalavi *et al.* (2003) aislaron un gen de quitinasa (*pcht28*) de *Solanum chilense* que, tras ser transferido a plantas de fresa de la variedad “Joliette”, incrementó significativamente la resistencia de las plantas transgénicas obtenidas frente a *Verticillium dahliae*. Paralelamente, Ricardo *et al.* (2006) obtuvieron líneas transgénicas de fresas expresando independientemente tres genes de defensa: *ch5B* [que codifica una proteína quitinasa de frijol (*Phaseolus vulgaris*)], *gln2* [que codifica una proteína glucanasa de tabaco (*Nicotiana tabacum*)], y *ap24* (que codifica la proteína taumatina de tabaco). Los principales resultados obtenidos en este estudio indicaron que la expresión del gen *ch5B* en frutos de fresa transgénicos incrementó la resistencia de éstos al moho gris, aunque no tuvo ningún efecto significativo en su resistencia a la antracnosis (Ricardo *et al.*, 2006).

## 8.2. Mejora de la floración y fructificación de la planta de fresa

La modificación de la época de floración y fructificación de un cultivo puede mejorar su producción de manera cuantitativa y cualitativa. Debido a ello, actualmente se está estudiando el efecto que tiene sobre el desarrollo de las plantas y su fructificación la modificación de su regulación hormonal para conseguir una mejora del cultivo de la fresa, de su capacidad de adaptación y de su resistencia a las enfermedades. Estas modificaciones pueden lograrse fácilmente mediante la introducción de genes capaces de alterar la regulación endógena del crecimiento vegetal (PGRs).

Otra herramienta empleada para la manipulación endógena de las fitohormonas es la transformación de plantas de fresa con oncogenes procedentes de *A. tumefaciens* o *A. rhizogenes*. Un ejemplo de esta metodología son los genes *rol*, que se han utilizado en la mejora de ciertas características agronómicas e incluso para la obtención de plantas con una morfogénesis alterada. Estos genes tienen una gran importancia en floricultura (Zuker *et al.*, 2001; Casanova *et al.*, 2005) y, concretamente, el gen *rol C* ha sido especialmente estudiado en frutos (Welander y Zhu, 2006). Bajo el control del promotor constitutivo CaMV-35S, el gen *rol C* ha provocado importantes alteraciones fenotípicas en la mayoría de las plantas estudiadas (Schmülling *et al.*, 1988; Nilsson *et al.*, 1996; Gardner *et al.*, 2006) y, en algunos

casos, modificaciones importantes en la productividad de la planta y en la arquitectura de la flor (Winefield *et al.*, 1999; Mitiouchkina y Dolgov, 2000). En fresa, la expresión del gen *rol C* ha conducido a una mejora del fenotipo de la planta y, como consecuencia, también de su calidad, de su capacidad de adaptación y producción. Su función en fresa se ha estudiado en plantas transgénicas de la variedad “Calypso” (Mazzara *et al.*, 1998), comprobándose la existencia de alteraciones en el desarrollo *in vitro* de raíces frente a las plantas control. Además, las líneas con mayor nivel de expresión del gen *rol C* presentaron hojas de menor dimensión y una disminución del tamaño de la planta (Mezzetti *et al.*, 2004b). Por otra parte, los ensayos agronómicos mostraron que la sobreexpresión del gen *rol C* en fresa modificaron características de interés económico como son la adaptabilidad de la planta, la productividad y la tolerancia al tipo de suelo, así como la calidad de la fruta (Landi y Mezzetti, 2006).

### **8.3. Mejora de la calidad del fruto de fresa mediante la modificación de sus propiedades organolépticas**

Los principales programas de biotecnología y reproducción de bayas tienen como prioridad la mejora de la calidad de la fruta. Para estos frutos tanto el sabor (resultado de la combinación de dulzura, acidez y aroma), como la firmeza son de gran importancia económica. Todos estos aspectos son controlados por procesos asociados al desarrollo y a la maduración de la fruta, lo que implica cambios específicos en la expresión génica y metabolismo celular (Manning, 1994). En frutos climatéricos, todos estos eventos son coordinados por el etileno sintetizado en las etapas tempranas de desarrollo del fruto, mientras que en frutos no climatéricos, aunque estos sufren los mismos cambios fisiológicos y bioquímicos, ninguno de los procesos responden a etileno.

#### **8.3.1. Manipulación del proceso de reblandecimiento**

La maduración de muchos frutos va acompañada de un reblandecimiento del tejido que termina con el deterioro irreversible de éstos. Este deterioro se debe fundamentalmente a la despolimerización y solubilización de la pared celular por la acción de numerosas proteínas, fundamentalmente hidrolasas de pared. Uno de los grupos de enzimas que intervienen en este proceso son las expansinas, que participan en la extensión de la pared celular. Así, se ha propuesto que estas proteínas *in vivo* interrumpen puentes de hidrógeno entre las microfibrillas de celulosa y hemicelulosa dando como resultado una relajación de la pared celular que permite el movimiento de los polímeros durante el crecimiento (McQueen-Mason y Cosgrove, 1994; Civello *et al.*, 1999; Brummell y Harpster, 2001). Su función, por tanto, explica la expresión de estos genes en tejidos vegetales como hipocotilos (McQueen-Mason *et al.*, 1992), coleóptilos (Cosgrove *et al.*, 1993), entrenudos (Cho y Kende., 1997), hojas (Keller y Cosgrove, 1995), raíces (Wu *et al.*, 1996), y frutas (Rose *et al.*, 1997; Brummell *et al.*, 1999; Civello *et al.*, 1999; Harrison *et al.*, 2001; Hiwasa *et al.*, 2003), ya que todos ellos presentan una pared celular en crecimiento. Por otra parte, el estudio de frutos transgénicos de tomate donde se reprime y sobreexpresa el gen *LeExpl*, mostró un incremento de su firmeza y de su reblandecimiento respectivamente. Esto apoya la idea de que estas proteínas participan activamente en el proceso de degradación de la pared celular del fruto (Brummell *et al.*, 1999; Brummell y Harpster., 2001).

En tomate (*Solanum lycopersicum*), se ha observado la expresión de varias expansinas que se han relacionado con la hidrólisis de polímeros de la pared celular y, por lo tanto, con el

reblandecimiento del fruto (McQueen-Mason y Cosgrove, 1994; Civello *et al.*, 1999; Brummell and Harpster, 2001; Li *et al.*, 2003). Igualmente, y a pesar de ser un fruto no climatérico, en fresa se han identificado varias expansinas cuya expresión varía a lo largo de la maduración y, una de las cuales (*FaExp2*) tiene una elevada homología de secuencia con una expansina expresada en el desarrollo temprano del tomate (Civello *et al.*, 1999). Aunque generalmente los genes expresados durante la maduración en fresa son regulados negativamente por auxinas, la expresión del gen *FaExp2* es independiente de estas hormonas. En general, todos los resultados descritos anteriormente sugieren que las expansinas participan en el proceso de maduración de los frutos y que, en frutos no climatéricos como la fresa, existen otros factores distintos a las auxinas que puede coordinar el inicio del proceso de maduración (Civello *et al.*, 1999).

El reblandecimiento del fruto también se está estudiando mediante el silenciamiento de la expresión de genes involucrados en la degradación de la pared celular (Mathews *et al.*, 1995; Woolley *et al.*, 2001; Jimenez-Bermúdez *et al.*, 2002; Palomer *et al.*, 2006; Sesmero *et al.*, 2007). De este modo, dos EGases, también llamadas celulasas, han sido aisladas y estudiadas en fresa (*Facell* y *Facel2*), estando implicados ambos genes en la maduración del fruto (Hapster *et al.*, 1998; Manning, 1998; Llop-Tous *et al.*, 1999; Trainotti *et al.*, 1999; Woolley *et al.*, 2001; Spolaore *et al.*, 2003; Palomer *et al.*, 2006). La expresión del ARNm de *Facell* muestra un aumento gradual durante la maduración y un pico de expresión con la aparición del color rojo en los frutos maduros (Hapster *et al.*, 1998; Llop-Tous *et al.*, 1999). Por el contrario, la expresión de *Facel2* se ha observado en frutos verdes y en tejidos verdes vegetativos (Llop-Tous *et al.*, 1999; Trainotti *et al.*, 1999), por lo que este gen podría estar implicado en las modificaciones iniciales de la pared celular para facilitar tanto el crecimiento celular como la expansión (Woolley *et al.*, 2001). Además, existen diferencias en las estructuras secundaria y terciaria de ambas proteínas EGAsas sugiriendo que podría haber una especificidad de sustrato diferente (Llop-Tous *et al.*, 1999). De hecho, un dominio celulosa dentro de la estructura de *Facel2* podría indicar que esta EGasa puede ser especialmente activa frente a los xiloglucanos que cubren las microfibrillas de celulosa presente en la pared celular (Trainotti *et al.*, 1999). Por lo tanto, se ha propuesto que *Facel2* podría hidrolizar la red de xiloglucanos de la pared celular haciéndola más susceptible a la actividad hidrolítica de la *Facell* (Trainotti *et al.*, 1999; Woolley *et al.*, 2001). Para determinar el verdadero papel de ambos genes en el reblandecimiento del fruto de fresa durante la maduración, se han realizado estudios con el antisentido del gen *Facell* (Woolley *et al.*, 2001) en combinación con *Facel2* (Palomer *et al.*, 2006). Los frutos transgénicos obtenidos mostraron una reducción parcial de la actividad EGasa y cambios en la firmeza de la fruta (Woolley *et al.*, 2001; Palomer *et al.*, 2006). Así, se observó como la regulación de *Facel2* podría compensar la baja expresión de *Facell*, sugiriendo además que ambos genes no son los únicos responsables de la despolimerización de los xiloglucanos durante la maduración de la fresa (Palomer *et al.*, 2006). No obstante, debido a la especificidad de expresión del gen *Facell* en fruto, su promotor es un buen candidato para ser utilizado como herramienta biotecnológica.

Por otra parte, también se han aislado y caracterizado en fresa varias poligalacturonasas (PG1, PG2 y PG3) (Introducción general, apartado 7) (Nogata *et al.*, 1993; Salentijn *et al.*, 2003; Quesada *et al.*, 2009) y, mediante análisis transcriptómicos en varios cultivares de fresa con diferentes firmezas, se ha comprobado su importancia en el proceso de maduración (Salentijn *et al.*, 2003). Recientemente, para aclarar la función de los genes *PGs* en el proceso de reblandecimiento de la fresa, se han generado plantas transgénicas con la expresión del gen *PG1* silenciada (Quesada *et al.*, 2009). La mitad de las líneas transgénicas obtenidas



mostraron frutos significativamente más firmes y una disminución de su reblandecimiento durante la postcosecha frente a los frutos control (Quesada *et al.*, 2009). En este sentido, los análisis indicaron que el silenciamiento del gen *FaPG1* se tradujo en una reducción de la solubilidad y despolimerización de las pectinas de la pared celular que condujo a una mayor integridad del tejido y una mayor firmeza de la fruta (García-Gago *et al.*, 2009).

Paralelamente, también se han realizado en fresa estudios de expresión de varios genes que codifican pectato liasas (PL) (*Introducción general, apartado 7*), observándose un incremento de su expresión durante el proceso de maduración del fruto (Medina-Escobar *et al.*, 1997; Benítez-Burraco *et al.*, 2002.). Este comportamiento junto con su localización, determinada mediante estudios de inmunolocalización, parece indicar que los genes PGs tendrían una función importante en el proceso de despolimerización de la pared celular (Medina-Escobar *et al.*, 1997). Este dato fue confirmado mediante el análisis de los frutos transgénicos obtenidos a partir de 33 líneas transgénicas independientes con la expresión del gen *plC* silenciada. Así, los frutos transgénicos analizados mostraron un incremento significativo de su firmeza y una disminución de su reblandecimiento durante la postcosecha comparados con los frutos control sin mostrar diferencias en su color, tamaño, forma y peso (Jiménez-Bermúdez *et al.*, 2002). Recientemente, se han analizado de forma independiente tres líneas transgénicas con una reducción superior al 90% en el nivel de transcrito correspondiente a pectato liasas (Doménech *et al.*, 2008). El análisis de estos frutos transgénicos mostraron diferencias cuantitativas y cualitativas de los polímeros de pectina de la pared celular del fruto que se tradujo en un incremento de su grado de firmeza (Doménech *et al.*, 2008). Estos resultados indican que los genes *pl* juegan un papel muy importante en la degradación de la pared primaria y lámina media durante la maduración del fruto de fresa lo que los hace muy atractivos como herramientas biotecnológicas para retrasar y/o regular el reblandecimiento del fruto durante y tras su cosecha.

Otras enzimas implicadas también en la maduración del fruto de fresa son las pectín esterases (*Introducción general, apartado 7*). En fresa, se ha aislado la *FaPEI* que muestra un incremento de expresión durante el proceso de maduración paralelo al de los genes PE, PL y PGs. De hecho, se ha propuesto que las modificaciones de la pared celular relacionadas con su reblandecimiento dependen de la actividad PG y PL, aunque la acción de la PE sería un requisito previo para que dichas enzimas hidrolíticas accedieran a la pectina de la pared (Prasanna *et al.*, 2007).

### 8.3.2. Mejora del sabor

El contenido y tipo de carbohidratos presentes en el fruto de fresa juega un papel importante en la determinación de su sabor y calidad. Así, en frutos maduros, los azúcares predominantes son las hexosas, glucosa y fructosa lo que influye en el potencial osmótico de las células y da lugar a un ajuste de la importación del agua y del crecimiento del fruto. En otras muchas especies frutales, la invertasa ( $\beta$ -fructofuranosidasa) es responsable de catalizar el desglose de la sacarosa. Concretamente, una invertasa localizada en pared celular es la encargada de regular la descarga de sacarosa al floema, mientras que una invertasa localizada en vacuola se encarga de regular el almacenamiento de sacarosa y hexosas. En dos cultivares de fresa diferentes (Sinfónica y Senga Sengana) se introdujeron los genes correspondientes a la invertasa vacuolar y de pared celular de patata. El análisis posterior de las plantas transgénicas obtenidas mostró modificaciones en el crecimiento, en la composición de azúcares, en el sabor y en la calidad del fruto (Graham *et al.*, 1997b).

Recientemente, también se han obtenido plantas transgénicas con la expresión de la pirofosforilasa ADP-glucosa (*AGPasa*) silenciada para evaluar los efectos de este gen sobre el contenido de carbohidratos en el fruto en desarrollo (Park *et al.*, 2006). Los resultados mostraron una reducción drástica de los niveles de ARNm correspondientes al gen *AGPasa* en frutos rojos, un incremento (16-37%) del contenido total de azúcares solubles y una disminución (27-47%) del contenido de almidón en la fruta madura. Estos resultados sugieren que el gen *AGPasa* podría ser empleado como herramienta biotecnológica para mejorar el contenido de azúcares solubles y disminuir el contenido de almidón en frutos de fresa, sobre todo teniendo en cuenta que no modifica ninguna otra característica organoléptica importante del fruto (Park *et al.*, 2006).

## 9. ALÉRGENOS DE LA FRESA

Al igual que otras frutas, las fresas contienen proteínas que producen reacciones alérgicas. En fresa, la familia de proteínas Fra a1 presenta homología con el alérgeno Bet v1 de abedul, el cual incluye varios péptidos de unión a la IgE (Karlsson *et al.*, 2004; Musidlowska-Persson *et al.*, 2007; Muñoz *et al.*, 2010). Se han realizado estudios de proteómica en fresa donde se compara variedades de fruto blanco con variedades de fruto rojo. Los resultados obtenidos indican que las proteínas Fra a1 están asociadas con un contenido bajo de alérgenos y con una biosíntesis reducida de antocianinas en genotipos blancos (Hjernø *et al.*, 2006; Alm *et al.*, 2007; Muñoz *et al.*, 2010). Otros alérgenos de fresa son las profilinas y las proteínas de transferencia de lípidos (LTP), que se encuentran muy expresadas en el fruto y se acumulan, principalmente, en situaciones de estrés abiótico (Yubero-Serrano *et al.*, 2003). No obstante, la expresión en levaduras de LTPs y profilinas de fresa aisladas a partir de una genoteca de ADNc, mostró una menor alergenicidad de estas proteínas frente a sus homólogos de manzana y/o melocotón, por lo que podrían ser empleadas en tratamientos de inmunoterapia (Zuidmeer *et al.*, 2006).

## 10. IMPORTANCIA ECONÓMICA DEL FRUTO DE FRESA

EE.UU es el país líder en producción de fresa, con aproximadamente un 25% de la producción mundial, seguido por España, Japón, Polonia, Italia y República de Corea. En Estados Unidos, la industria de la fresa se centra en California, con más del 80% de la producción total. La producción ha crecido de forma constante durante las dos últimas décadas en España, República de Corea y EE.UU, mientras que se ha reducido en los diez últimos años en Japón, Italia y Polonia, después de un aumento espectacular en los años 1970 y 1980.

Debido al coste de la investigación, la aplicación rentable de la biotecnología al cultivo de muchas frutas, verduras, árboles frutales y frutos secos está limitada. Además, la experimentación con cultivos perennes como árboles frutales, bayas y frutos secos es relativamente cara, ya que la unidad experimental es más grande y no es fácil sembrar plantaciones con nuevas variedades. De entre todos los frutos, la fresa es un cultivo especialmente interesante para la aplicación y para el desarrollo de biotecnología avanzada (incluyendo la clonación de genes y la tecnología recombinante) debido a su producción a gran escala y por su cultivo anual (Mezzetti, 2003). En general, las nuevas herramientas y

sistemas de transgénicos desarrollados pueden ayudar a la industria de la fresa mediante su estudio a nivel molecular. Sin embargo, aún no se ha desarrollado una transformación rápida de alto rendimiento que permita estudiar de manera eficiente la genómica funcional de este fruto. Así, y a pesar de los estudios realizados sobre la transformación de la fresa octoploide (Liu y Sanford, 1988; Nehra *et al.*, 1990.; Barcélo *et al.*, 1998; Passey *et al.*, 2003), la eficiencia de transformación varía entre diferentes cultivares, ya que se requieren de 40 a 112 días para la aparición de los primeros brotes visibles. No obstante, la disponibilidad de algunos genotipos, la regeneración eficiente y la transformación de este cultivo se considera un modelo interesante para el desarrollo de la genómica y de estudios de ADN recombinante entre las diferentes especies de Rosáceas.

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## OBJECTIVES

The objectives of this thesis were the following:

1. Identification and selection of genes with specific expression of strawberry fruit receptacle and inducible during its ripening using an oligo microarray.
2. Identification and characterization of strawberry *FaAAT2* gene by the analysis of its expression in fruits, in vegetative plant tissues and under different experimental conditions to determine the behavior of its expression and regulation.
3. Determination of the enzymatic activity of the recombinant *FaAAT2* protein and transitory silencing of the *FaAAT2* gene expression for determining the role of the protein that this gene encodes in strawberry fruit.
4. Determination of *FaMYB10* gene expression along the ripening process of strawberry, in vegetative tissues and in response to the removal of achenes in developing fruits.
5. Evaluation of the role that ABA plays in the regulation of *FaMYB10* gene expression.
6. Determination of the *FaMYB10* gene function in the expression regulation of genes involved in the biosynthetic pathway of flavonoids / phenylpropanoids during the strawberry fruit ripening by the transcriptomic analysis of transgenic fruit with the *FaMYB10* expression transiently silenced.

## OBJETIVOS

Los objetivos de esta Tesis fueron los siguientes:

1. Identificación y selección de genes con expresión específica de fruto de fresa e inducibles durante su maduración a partir de un microarray de oligos de fresa.
2. Identificación y caracterización del gen *FaAAT2* de fresa mediante el análisis de su expresión en frutos, tejidos vegetativos de la planta y en diferentes condiciones experimentales para determinar el comportamiento de su expresión y la regulación de ésta.
3. Determinación de la actividad enzimática de la proteína recombinante FaAAT2 y silenciamiento transitorio en fruto de fresa de la expresión del gen que la codifica para determinar la función del gen *FaAAT2* en el fruto de fresa.
4. Determinación de los perfiles de expresión del gen *FaMYB10* a lo largo del proceso de maduración del fruto de fresa, en tejidos vegetativos y en respuesta a la retirada de achenios en frutos en desarrollo.
5. Determinación del papel que juega el ABA en la regulación de la expresión del gen *FaMYB10*.
6. Determinación de la implicación del gen *FaMYB10* en la regulación de la expresión de los genes que intervienen en la ruta de biosíntesis de flavonoides/fenilpropanoides a lo largo del proceso de maduración del fruto de fresa mediante el análisis transcriptómico de frutos transgénicos con la expresión del gen *FaMYB10* silenciada transitoriamente.

# MATERIALES Y MÉTODOS

## I. MATERIALES

### I.1. MATERIAL QUÍMICO

#### I.1.1. Productos químicos

Todos los productos y reactivos utilizados fueron de alta calidad y se adquirieron en las casas comerciales que aparecen entre paréntesis:

#### A

Acetato amónico ( $\text{NH}_4\text{C}_2\text{H}_3\text{O}_2$ ) (Sigma)  
 Acetato sódico ( $\text{NaCH}_3\text{COO}$ ) (Merck)  
 Acetato potásico ( $\text{KCH}_3\text{COO}$ ) (Merck)  
 Acetil coenzima A, sal sódica ( $\text{C}_{23}\text{H}_{38}\text{N}_7\text{O}_{17}\text{P}_3\text{S}$ ) (Sigma)  
 Acetosiringona (3'5'-Dimethoxy-4'-hydroxyacetophenona) ( $\text{C}_{10}\text{H}_{10}\text{O}_4$ ) (Aldrich)  
 Ácido acético ( $\text{C}_2\text{H}_4\text{O}_2$ ) (Panreac)  
 Ácido benzoico ( $\text{C}_6\text{H}_5\text{COOH}$ ) (Sigma)  
 Ácido bórico ( $\text{H}_3\text{BO}_3$ ) (Sigma)  
 Ácido cafeico ( $\text{C}_9\text{H}_8\text{O}_4$ ) (Sigma)  
 Ácido cinnámico ( $\text{C}_9\text{H}_8\text{O}_2$ ) (Sigma)  
 Ácido clorhídrico (HCl) (Panreac)  
 Ácido etilen-diamino-tetraacético, sal disódica (EDTA- $\text{Na}_2$ ) ( $\text{C}_{10}\text{H}_{14}\text{N}_2\text{O}_8\text{Na}_2 \cdot 2\text{H}_2\text{O}$ ) (Sigma)  
 Ácido indol-3-butírico (IBA) ( $\text{C}_{12}\text{H}_{13}\text{NO}_2$ ) (Sigma)  
 Ácido 1-naftalenacético (1-NAA) (Sigma)  
 Ácido nítrico ( $\text{HNO}_3$ ) (Merck)  
 Ácido salicílico ( $\text{C}_7\text{H}_7\text{NO}_3$ ) (Sigma)  
 Ácido sulfúrico ( $\text{H}_2\text{SO}_4$ ) (Panreac)  
 ADN de fago  $\lambda$  digerido con Hind III (Pharmacia)  
 Agar (Promega)  
 Agarosa (Promega)  
 Alcohol isoamílico ( $\text{C}_6\text{H}_{11}\text{OH}$ ) (Sigma)  
 Azul de Coomassie

#### B

Bacto-triptona (Difco)  
 Bencil acetato ( $\text{C}_9\text{H}_{10}\text{O}_2$ ) (Sigma)  
 Bencil alcohol ( $\text{C}_7\text{H}_7\text{OH}$ ) (Sigma)  
 6-bencil aminopurina (BA) ( $\text{C}_{12}\text{H}_{13}\text{NO}_2$ ) (Sigma)  
 Bencil butirato ( $\text{C}_{11}\text{H}_{14}\text{O}_2$ ) (Sigma)  
 Bencil hexanoato ( $\text{C}_{13}\text{H}_{18}\text{O}_2$ ) (Sigma)  
 Bencil propanoato ( $\text{C}_{10}\text{H}_8\text{O}_2$ ) (Sigma)  
 Bicarbonato sódico ( $\text{NaHCO}_3$ ) (Sigma)  
 Bifosfato potásico ( $\text{KH}_2\text{PO}_4$ ) (Panreac)  
 5-bromo-4-cloro-3-indolil- $\beta$ -D-galactopiranosido (X-gal) ( $\text{C}_{14}\text{H}_{15}\text{BrClNO}_6$ ) (Sigma)  
 Bromuro 2,7-diamino-10-etil-9-fenilfenantridio (Bromuro de etidio) ( $\text{C}_{21}\text{H}_{20}\text{N}_3\text{Br}$ ) (Sigma)

1-Butanol (C<sub>4</sub>H<sub>9</sub>OH) (Sigma)  
2-Butanol (C<sub>4</sub>H<sub>9</sub>OH) (Sigma)  
1-Butil acetato (C<sub>6</sub>H<sub>12</sub>O<sub>2</sub>) (Sigma)  
2-Butil acetato (C<sub>6</sub>H<sub>12</sub>O<sub>2</sub>) (Sigma)  
1-Butil butirato (C<sub>8</sub>H<sub>16</sub>O<sub>2</sub>) (Sigma)  
1-Butil hexanoato (C<sub>10</sub>H<sub>20</sub>O<sub>2</sub>) (Sigma)  
1-Butil propanoato (C<sub>7</sub>H<sub>14</sub>O<sub>2</sub>) (Sigma)  
Butiril coenzima A lithium salt hydrate (C<sub>25</sub>H<sub>42</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>S) (Sigma)

## C

Carbenicilina (C<sub>26</sub>H<sub>25</sub>N<sub>2</sub>NaO<sub>6</sub>S) (Duchefa)  
Carbonato de sodio (Na<sub>2</sub>CO<sub>3</sub>) (Sigma)  
Cinnamil acetato (C<sub>11</sub>H<sub>12</sub>O<sub>2</sub>) (Sigma)  
Cinnamil alcohol (C<sub>9</sub>H<sub>9</sub>OH) (Sigma)  
Cinnamil butirato (C<sub>13</sub>H<sub>16</sub>O<sub>2</sub>) (Sigma)  
Cinnamil hexanoato (C<sub>15</sub>H<sub>20</sub>O<sub>2</sub>) (Sigma)  
Cinnamil propanoato (C<sub>12</sub>H<sub>14</sub>O<sub>2</sub>) (Sigma)  
Cis-3-hexen-1-ol (C<sub>6</sub>H<sub>11</sub>OH) (Sigma)  
Citrato trisódico (Na<sub>3</sub>C<sub>6</sub>H<sub>5</sub>O<sub>7</sub>·H<sub>2</sub>O) (Panreac)  
Cloroformo (CHCl<sub>3</sub>) (Merck)  
Cloruro cálcico (CaCl<sub>2</sub>·2H<sub>2</sub>O) (Sigma)  
Cloruro de litio (LiCl) (Merck)  
Cloruro de magnesio (MgCl<sub>2</sub>) (USB)  
Cloruro potásico (KCl) (Merck)  
Cloruro sódico (NaCl) (Panreac)  
Cloruro de zinc (ZnCl<sub>2</sub>) (Panreac)  
CTAB (Bromuro de hexadecil trimetil amonio) (Sigma)

## D

1-Decanol (C<sub>10</sub>H<sub>21</sub>OH) (Sigma)  
Decil acetato (C<sub>12</sub>H<sub>25</sub>O<sub>2</sub>) (Sigma)  
Deoxiadenosina 5´-trifosfato (dATP) (Farmacia)  
Deoxinucleótidos trifosfato (dNTPs) (Farmacia)  
Dietil pirocarbonato (C<sub>6</sub>H<sub>10</sub>O<sub>5</sub>) (DEPC) (Sigma)  
Dihidrógenofosfato de potasio (KH<sub>2</sub>PO<sub>4</sub>) (Sigma)  
N-N-dimetilformamida (C<sub>3</sub>H<sub>7</sub>NO) (Merck)  
Dimetil sulfóxido (DMSO) (C<sub>2</sub>H<sub>6</sub>SO) (Sigma)  
DNasa I RNasa free (Farmacia)  
Ditiotreitol (DTT) (C<sub>4</sub>H<sub>10</sub>O<sub>2</sub>S<sub>2</sub>) (Sigma)  
Dodecil sulfato sódico (SDS) (C<sub>12</sub>H<sub>25</sub>O<sub>4</sub>SNa) (Sigma)

## E

Espermidina (Sigma)  
Estreptomicina sulfato (C<sub>21</sub>H<sub>39</sub>N<sub>7</sub>O<sub>12</sub>) (Sigma)  
Etanol absoluto (CH<sub>2</sub>OH) (Merck)  
Etil acetato (C<sub>4</sub>H<sub>8</sub>O<sub>2</sub>) (Sigma)  
Etil butirato (C<sub>8</sub>H<sub>16</sub>O<sub>2</sub>) (Sigma)  
Etil hexanoato (C<sub>6</sub>H<sub>12</sub>O<sub>2</sub>) (Sigma)  
Etil propanoato (C<sub>5</sub>H<sub>10</sub>O<sub>2</sub>) (Sigma)

Etilenglicol monobutil éter (2-BE) (C<sub>6</sub>H<sub>14</sub>O<sub>2</sub>) (Sigma)  
Eugenol (C<sub>10</sub>H<sub>11</sub>OH) (Sigma)  
Eugenil acetato (C<sub>12</sub>H<sub>14</sub>O<sub>2</sub>) (Sigma)  
Eugenil butirato (C<sub>12</sub>H<sub>14</sub>O<sub>2</sub>) (Sigma)  
Eugenil hexanoato (C<sub>12</sub>H<sub>14</sub>O<sub>2</sub>) (Sigma)  
Eugenil propanoato (C<sub>12</sub>H<sub>14</sub>O<sub>2</sub>) (Sigma)  
Extracto de levadura (Difco)

**F**

Farnesil acetato (C<sub>17</sub>H<sub>25</sub>O<sub>2</sub>) (Sigma)  
1-Farnesol (C<sub>15</sub>H<sub>22</sub>OH) (Sigma)  
2-Fenil etanol (C<sub>8</sub>H<sub>9</sub>OH) (Sigma)  
2-Feniletil acetato (C<sub>10</sub>H<sub>12</sub>O<sub>2</sub>) (Sigma)  
2-Feniletil butirato (C<sub>12</sub>H<sub>16</sub>O<sub>2</sub>) (Sigma)  
2-Feniletil propanoato (C<sub>11</sub>H<sub>14</sub>O<sub>2</sub>) (Sigma)  
Fenol (C<sub>6</sub>H<sub>5</sub>OH) (Merck)  
Fosfato monosódico diácido (NaH<sub>2</sub>PO<sub>4</sub>) (Panreac)  
Fosfato disódico monoácido (Na<sub>2</sub>HPO<sub>4</sub>) (Panreac)  
Fosfato potásico monobásico (KH<sub>2</sub>PO<sub>4</sub>) (Sigma)  
Formamida desionizada (Sigma)  
Furfuril acetato (C<sub>7</sub>H<sub>10</sub>O<sub>2</sub>) (Sigma)  
Furfuril alcohol (C<sub>5</sub>H<sub>5</sub>OH) (Sigma)

**G**

Gelatina (BioRad)  
Geranil acetato (C<sub>12</sub>H<sub>20</sub>O<sub>2</sub>) (Sigma)  
Geranil butirato (C<sub>14</sub>H<sub>24</sub>O<sub>2</sub>) (Sigma)  
Geranil hexanoato (C<sub>16</sub>H<sub>28</sub>O<sub>2</sub>) (Sigma)  
Geranil propanoato (C<sub>13</sub>H<sub>22</sub>O<sub>2</sub>) (Sigma)  
Geraniol (C<sub>10</sub>H<sub>17</sub>OH) (Sigma)  
Glicerol (C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>) (Panreac)  
Glicina (H<sub>2</sub>NCH<sub>2</sub>COOH) (Merck)  
Glucosa (C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>) (Sigma)  
Glutation reducido (Sigma)

**H**

Hexadeciltrimetil-amonio bromido (CTAB) (C<sub>19</sub>H<sub>42</sub>NBr) (Sigma)  
Hexano (C<sub>6</sub>H<sub>14</sub>) (Sigma)  
Hexanoil acetato (C<sub>8</sub>H<sub>16</sub>O<sub>2</sub>) (Sigma)  
Hexanoil CoA trlithium salt hydrate (C<sub>27</sub>H<sub>43</sub>Li<sub>3</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>S · H<sub>2</sub>O)  
Hexanoil butirato (C<sub>10</sub>H<sub>20</sub>O<sub>2</sub>) (Sigma)  
Hexanoil hexanoato (C<sub>12</sub>H<sub>24</sub>O<sub>2</sub>) (Sigma)  
Hexanoil propanoato (C<sub>9</sub>H<sub>18</sub>O<sub>2</sub>) (Sigma)  
1-Hexanol (C<sub>6</sub>H<sub>11</sub>OH) (Sigma)  
Hidrolizado de caseína (NZ amina) (Sigma)  
Hidróxido sódico (NaOH) (Panreac)  
Hidróxido potásico (KOH) (Panreac)

**I**

Isoamil acetato (C<sub>8</sub>H<sub>14</sub>O<sub>2</sub>) (Sigma)

Isopropanol ( $C_3H_7OH$ ) (Merck)  
Isopropil- $\beta$ -D-tiogalactósido (IPTG) ( $C_9H_{18}O_5S$ ) (Pharmacia)

**K**

Kanamicina monosulfato ( $C_{18}H_{36}N_4O_{117}H_2SO_{47}H_2O$ ) (Duchefa)  
Kinetina (6-furfuril-aminopurina) (Sigma)

**L**

Lanolina (Sigma)  
Linaloil acetato ( $C_{12}H_{20}O_2$ ) (Sigma)  
Linalool ( $C_{10}H_{17}OH$ ) (Sigma)

**M**

Maltosa ( $C_{12}H_{22}O_{11} \cdot H_2O$ ) (USB)  
Marcador de peso molecular 1 Kb (Pharmacia)  
Marcador de peso molecular 100 pb (Pharmacia)  
Marcador de proteínas (Broad Range 2-212 kDa) (BioLabs)  
2-Mercaptoetanol ( $\beta$ -mercaptoetanol) ( $C_2H_6OS$ ) (Sigma)  
Metanol ( $CH_3OH$ ) (Panreac)  
Metil acetato ( $C_3H_6O_2$ ) (Fluka)  
Metil butirato ( $C_5H_{10}O_2$ ) (Fluka)  
Metil hexanoato ( $C_7H_{14}O_2$ ) (Fluka)  
Metil-jasmonato ( $C_{13}H_{20}O_3$ ) (Sigma)  
Metil propanoato ( $C_4H_8O_2$ ) (Fluka)  
Mioinositol ( $C_6H_{12}O_6$ ) (Sigma)  
Monohidrógenofosfato sódico ( $Na_2HPO_4$ ) (Panreac)

**N**

Neril acetato ( $C_{12}H_{20}O_2$ ) (Sigma)  
Nerol ( $C_{10}H_{17}OH$ ) (Sigma)  
Nerolidol ( $C_{15}H_{25}OH$ ) (Sigma)  
Nerolidil acetato ( $C_{17}H_{28}O_2$ ) (Sigma)  
Nitrato amónico ( $NH_4NO_3$ ) (Sigma)  
Nitrato de calcio ( $Ca(NO_3)_2 \cdot 4H_2O$ ) (Sigma)  
Nitrato potásico ( $KNO_3$ ) (Panreac)  
1-Nonanol ( $C_9H_{19}OH$ ) (Sigma)  
Nonil acetato ( $C_{11}H_{22}O_2$ ) (Sigma)  
NZ Amina (Merck)

**O**

Octanoil acetato ( $C_{10}H_{17}O_2$ ) (Sigma)  
Octanoil butanoato ( $C_{12}H_{24}O_2$ ) (Sigma)  
Octanoil hexanoato ( $C_{14}H_{28}O_2$ ) (Sigma)  
Octanoil propanoato ( $C_{11}H_{22}O_2$ ) (Sigma)  
1-Octanol ( $C_8H_{17}OH$ ) (Sigma)  
1-Octen-3-il acetato ( $C_{10}H_{16}O_2$ ) (Sigma)  
1-Octen-3-ol ( $C_8H_{13}OH$ ) (Sigma)

**P**

Pentanol (C<sub>5</sub>H<sub>11</sub>OH) (Sigma)  
 Pentil acetato (C<sub>7</sub>H<sub>14</sub>O<sub>2</sub>) (Sigma)  
 Peróxido de hidrógeno (H<sub>2</sub>O<sub>2</sub>) (Merck)  
 Piridoxina (vitamina B<sub>6</sub>) (C<sub>8</sub>H<sub>11</sub>NO<sub>3</sub>) (Sigma)  
 Polietilenglicol 8000 (PEG-8000) (Panreac)  
 1-Propanol (C<sub>3</sub>H<sub>7</sub>OH) (Merck)  
 Propanoil acetato (C<sub>3</sub>H<sub>7</sub>O) (Sigma)  
 Propionil coenzima A lithium salt (C<sub>24</sub>H<sub>40</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>S) (Sigma)

**R**

Reactivo de Bradford (“Protein Assay”) (BioRad)  
 Rifampicina (C<sub>43</sub>H<sub>58</sub>N<sub>4</sub>O<sub>12</sub>) (Duchefa)  
 RNasa OUT<sup>TM</sup> (Invitrogen)  
 RNasa pancreática (Farmacia)  
 Roti Load (Roth)

**S**

Sacarosa (C<sub>12</sub>H<sub>22</sub>O<sub>11</sub>) (Sigma)  
 Sepharose GST-Bind<sup>TM</sup> Resin (Novogen)  
 Seroalbúmina bovina (BSA) (Sigma)  
 Sulfato de magnesio (MgSO<sub>4</sub>·7H<sub>2</sub>O) (Panreac)  
 Sulfato de manganeso (MnSO<sub>4</sub>·H<sub>2</sub>O) (Sigma)  
 Sulfato de zinc (ZnSO<sub>4</sub>·7H<sub>2</sub>O) (Panreac)  
 Sulfato ferroso (FeSO<sub>4</sub>·7H<sub>2</sub>O) (Sigma)  
 SYBR-Green I (Molecular Probes)

**T**

Terpenil acetato (C<sub>12</sub>H<sub>20</sub>O<sub>2</sub>) (Sigma)  
 Terpeneol (C<sub>10</sub>H<sub>17</sub>OH) (Sigma)  
 Trans-2-hexen-1-il acetato (C<sub>8</sub>H<sub>14</sub>O<sub>2</sub>) (Sigma)  
 Trans-2-hexen-1-ol (C<sub>6</sub>H<sub>11</sub>OH) (Sigma)  
 Tritón X-100 (Sigma)  
 Tween-20 (poliexylen-sorbitan-monolaurato) (BioRad)

**X**

Xilen cianol FF (C<sub>25</sub>H<sub>27</sub>N<sub>2</sub>O<sub>6</sub>S<sub>2</sub>Na) (Sigma)

**Y**

Yoduro potásico (KI) (Panreac)  
 Yoduro sódico (NaI) (Sigma)

**I.1.2. Antibióticos utilizados**

Los antibióticos empleados fueron disueltos en agua destilada y esterilizados por filtración a través de un filtro de 0,22 µm de diámetro de poro. Una vez esterilizados, se repartieron en alícuotas de 1 ml y se mantuvieron almacenados a -20 °C hasta su uso. La concentración de almacenamiento de los antibióticos se recoge en la Tabla 1.



Antibiótico	Solvente	Concentración de almacenamiento	Concentración final
Ampicilina (Sigma)	H <sub>2</sub> O	100 mg/ml	100 µg/ml
Kanamicina (Duchefa)	H <sub>2</sub> O	50 mg/ml	50-100 µg/ml (microorganismos) 25-100 mg/l (plantas)
Rifampicina (Duchefa)	DMSO	100 mg/ml	100 µg/ml
Carbenicilina (Duchefa)	H <sub>2</sub> O	100 mg/ml	250-500 mg/l
Cloranfenicol (Sigma)	EtOH	15 mg/ml	15 µg/µl
Estreptomina (Sigma)	H <sub>2</sub> O	100 mg/ml	100 µg/ml
Espectinomicina (Sigma)	H <sub>2</sub> O	100 mg/ml	100 µg/ml

**Tabla 1. Antibióticos empleados en este trabajo.**

### I.1.3. Kits de biología molecular

*Aurum<sup>TM</sup> Total RNA mini kit* (BioRad)

*Quantum prep Aquapure Genomic DNA Kit* (BioRad)

*QIAGEN<sup>®</sup> Plasmid Mini Kit* (Qiagen)

*QIAquick<sup>®</sup> Gel Extraction Kit* (Qiagen)

*Quantum Prep<sup>®</sup> Plasmid Miniprep Kit* (BioRad)

*WIZARD<sup>®</sup> Plus Minipreps DNA Purification System* (Promega)

*Superscript<sup>TM</sup> II RNase H* (Invitrogen)

*iScript<sup>TM</sup> cDNA Sintesis Kit* (BioRad)

*CLONTECH PCR-Select cDNA Subtraction Kit* (BD Biosciences)

*SuperScript<sup>TM</sup> Double Stranded cDNA Síntesis Kit* (Invitrogen)

*Advantage 2 PCR Enzyme System* (BD Biosciences)

*Marathon<sup>TM</sup> cDNA Amplification Kit* (BD Biosciences)

*MessageAmp<sup>TM</sup> II aRNA Amplification Kit* (Ambion)

*RNeasy<sup>®</sup> Mini Kit* (Quiagen)

*iQ<sup>TM</sup> SYBR<sup>®</sup> Green Supermix* (Biorad)

## I.2. MATERIAL BIOLÓGICO

### I.2.1. Material vegetal

Todo el material vegetal empleado procede de plantas de fresa (*Fragaria x ananassa*) del cultivar Camarosa, recolectados en la Finca Experimental “El Cebollar” en Moguer, Huelva (CIFA, Junta de Andalucía). El material vegetativo utilizado para la experimentación fueron hojas, coronas, estolones y raíces. Las muestras biológicas se congelaron en nitrógeno líquido inmediatamente después de su recolección y se conservaron a -80 °C hasta el momento de su utilización.

Para la transformación por agroinfiltración (*Materiales y Métodos, Apartado II.10.4*) y para los experimentos realizados para la determinación de ABA se utilizaron plantas de fresa (*Fragaria x ananassa*) del cultivar Elsanta (*Materiales y Métodos, Apartados I.1.2.1.2 y I.1.2.1.3*). Las plantas utilizadas se mantuvieron a una temperatura de 25 °C, con un fotoperiodo de 16 h de luz/8 h de oscuridad y bajo una irradiancia de 120  $\mu\text{mol}\cdot\text{m}^{-2}\cdot\text{sec}^{-1}$  proporcionada por lámparas Osram Fuora (München, Germany).

Los estadios de desarrollo y maduración de los frutos se establecieron en función de los siguientes parámetros (Fig. 1):

- Verde-1 (V1): fruto pequeño con color verde en primera fase de crecimiento, con aquenios muy juntos y verdes.
- Verde-2 (V2): fruto elongado con color verde, aquenios muy juntos y verdes.
- Verde-3 (V3): fruto verde de mayor tamaño, con aquenios separados y verdes.
- Blanco-1 (B1): fruto de color blanco que ha alcanzado su tamaño definitivo y con aquenios de color verde.
- Blanco-2 (B2): el fruto conserva el mismo tamaño y color que en el estadio anterior, pero los aquenios se presentan lignificados y de color marrón.
- Rojo (R): fruto completamente rojo y maduro y con aquenios lignificados.
- Sobremaduro (SM): fruto rojo intenso de textura blanda y aquenios rojos lignificados.
- Senescente (SN): fruto de color vino tinto, opaco, aquenios del mismo color.

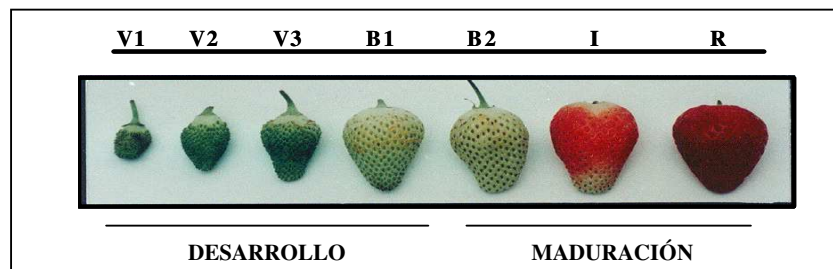


Fig. 1. Estadios de desarrollo y maduración del fruto de fresa (*Fragaria x ananassa* cv. Camarosa).

### I.2.1.1. Retirada de aquenios y tratamiento con auxinas

Con el objeto de determinar si los genes estudiados se encuentran regulados por auxinas, se procedió, sin separar el fruto de la planta madre, a la retirada cuidadosa de los aquenios en frutos de estadio de desarrollo V2 mediante un bisturí. Posteriormente, se aplicó sobre algunos de estos frutos desaquenizados una pasta de lanolina (preparada al 50% en H<sub>2</sub>O y licuada a 65 °C) y, sobre otros frutos también desaquenizados, la misma pasta de lanolina conteniendo la hormona sintética ácido 1-naftalenacético (NAA) 2 mM, disuelta en DMSO al 2% (p/v). Ambos procesos se realizaron a temperatura ambiente. A continuación, los frutos tratados exclusivamente con la pasta de lanolina se recolectaron a las 0, 24, 48, 72 y 96 horas del tratamiento, mientras que los frutos tratados con lanolina más NAA se recogieron después de 96 horas de la desaquenización y del tratamiento con la hormona. En todos los casos, los

frutos tratados se congelaron inmediatamente después de su recolección en nitrógeno líquido y posteriormente se almacenaron a -80 °C hasta su uso.

### **I.2.1.2. Frutos inyectados**

Se recogieron frutos en el estadio de desarrollo V3/B1 e, inmediatamente y mediante una jeringa y aguja hipodérmica, se les inyectó cuidadosamente en el espacio intercelular 1-2 ml de solución estéril. Para ello, se hicieron varias inyecciones sucesivas de 300 µl de la solución elegida en diferentes partes del fruto para cada situación experimental. Los frutos así tratados se conservaron durante el período de experimentación a 25 °C y, posteriormente, se congelaron en nitrógeno líquido y se mantuvieron a -80 °C hasta su procesamiento. Generalmente, este tipo de experimento se llevó a cabo a tiempos cortos (2, 4, 8 h) para evitar la contaminación y deterioro de los frutos tratados. Paralelamente, se trataron frutos control mediante la inyección de H<sub>2</sub>O estéril, que se recolectaron a los mismos tiempos que los frutos problema.

#### ***Tratamiento con NDGA exógeno***

Con el objetivo de bloquear la biosíntesis de ABA, se inyectaron frutos de fresa (*Fragaria x ananassa* cv. Elsanta) en estadios verde-blanco con ácido nordihidroguaiarético (NDGA) (Creelman *et al.*, 1992). El NDGA es un inhibidor de la enzima 9-cis-epoxycarotenoide dioxigenasa (NCED) que actúa bloqueando completamente la biosíntesis de ABA. Los frutos de fresa seleccionados para el experimento fueron inyectados con 1-2 ml de NDGA 100 µM, como previamente había sido descrito para tomate (Zhang *et al.*, 2009), o agua destilada (frutos control). Para cada tratamiento se realizaron tres repeticiones. En general, todos los frutos sometidos a tratamiento fueron cosechados tras 8 días de experimentación y empleados para la determinación de su contenido de ABA y la extracción de ARN. Para ello, los frutos recolectados fueron congelados con nitrógeno líquido inmediatamente y almacenados a -80 °C hasta su uso.

### **1.2.1.3. Tratamiento de estrés hídrico**

Para los experimentos de estrés hídrico, se emplearon tanto frutos de *Fragaria x ananassa* cv. Elsanta en estadio verde-blanco como plantas completas de este mismo cultivar a las que se les retiró el riego.

Los frutos seleccionados para el experimento se mantuvieron con los pedicelos al aire mientras que los frutos control se mantuvieron con los pedicelos sumergidos en medio MS enriquecido con sacarosa. En ambos casos, los pedicelos de los frutos fueron cortados diariamente para eliminar su extremo necrosado y facilitar la absorción del medio correspondiente. Tras cuatro días de tratamiento, los frutos fueron recolectados, congelados en nitrógeno líquido y almacenados a -80 °C hasta la extracción de su ARN.

En el caso del experimento con plantas completas, tanto las sometidas a estrés hídrico como las control se mantuvieron a una temperatura de 25 °C, con un fotoperíodo de 16 h de luz/8 h de oscuridad y bajo una irradiancia de 120 µmol.m<sup>-2</sup>.sec<sup>-1</sup> proporcionada por lámparas Osram Fuora (München, Germany). A las plantas control se les mantuvo el riego diario mientras que a las plantas problema se les retiró hasta presentar un fenotipo claro de estrés hídrico. Llegado este momento se recolectaron frutos, se congelaron en nitrógeno líquido y se almacenaron a -80 °C hasta la extracción de su ARN.

## I.2.2. Estirpes bacterianas

- ***Escherichia coli* XLI-Blue MRA:**  $\Delta(mcrA)183 \Delta(mcrCB-hsdRMS-mrr)173 endA1 supE44 thi-1 gyrA96 recA1 lac^-$ . Estirpe deficiente en la Endonucleasa I no específica (*endA1*) y deficiente en los sistemas de recombinación (*recA1*), lo que aumenta la calidad del ADN plasmídico purificado y la estabilidad del inserto respectivamente. Aunque el ADN transfectado se modifica, no resulta digerido por la acción de restrictasas. Estirpe empleada para la infección con el fago  $\lambda$ -FIX II (Stratagene), en el cual se almacenan genotecas de ADN genómico. Las mutaciones *mcrA*, *mcrCB* y *mrr* previenen la rotura del ADN clonado y que presente adeninas o metioninas metiladas, lo cual es frecuente en ADN eucariótico. Presenta una elevada eficiencia de transformación con ADN no metilado obtenido por PCR (*hsdRMS*).
- ***Escherichia coli* XLI-Blue MRF':**  $\Delta(mcrA)183 \Delta(mcrCB-hsdSMR-mrr)173 endA1 supE44 thi-1 gyrA96 recA1 relA1 lac [F' proAB lacI^qZAM15 Tn10 (Tet^r)]$ . Estirpe empleada para el almacenamiento de ADN plasmídico ya que es deficiente de la Endonucleasa I no específica (*endA1*) y deficiente en los sistemas de recombinación (*recA1*). Se emplea para la infección con el fago  $\lambda$ -ZAP Express, en el cual se almacenan genotecas de ADNc. El episoma F' es requerido para la selección por actividad  $\beta$ -galactosidasa y para la represión del promotor del gen LacZ en ausencia de IPTG. Las mutaciones *mcrA*, *mcrCB* y *mrr* previenen la rotura del ADN clonado.
- ***Escherichia coli* DH5 $\alpha$ :**  $F' supE44 DlacU169 (\Phi80lacZAM15) hsdR17 recA1 endA1 gyrA96 thi-1 relA1$ . Esta estirpe presenta varias mutaciones que favorecen la estabilidad del ADN clonado, se emplea generalmente para la replicación de plásmidos y la multiplicación de cósmidos. La delección  $\Phi80lacZAM15$  permite la  $\alpha$ -complementación con el extremo aminoterminal de la  $\beta$ -galactosidasa codificada por vectores del tipo pUC (entre ellos *pBluescript*).
- ***Escherichia coli* BL21 (DE3) pLysS** (Invitrogen):  $F', ompT, hsdS (rB-, mB-), gal (53, 54)$ . Cepa deficiente en las proteasas *lon* y *ompT*, con expresión nula de la proteína cuando no está inducida por IPTG y con expresión de la lisozima T7 que, entre otras cosas, facilita la rotura de las paredes celulares bacterianas en la extracción de proteínas. Resistente a Cloranfenicol (*Cam*).
- ***Escherichia coli* BL21 (TOP10)** (Invitrogen):  $F' mcrA \Delta(mrr-hsdRMS-mcrBC) \Phi80lacZAM15 \Delta lacZ74 recA1 araD139 \Delta(ara-leu)7697 galU galK rpsL (Str^R) endA1 nupG$ . Estirpe comercializada en forma de células químicamente competentes para la transformación con el vector plasmídico *pCR8/GW/TOPO* (Invitrogen). Permite la obtención de un ADN plasmídico de calidad ya que es una estirpe deficiente de la Endonucleasa I no específica (*endA1*) y deficiente en los sistemas de recombinación (*recA1*). Presenta una elevada eficiencia de transformación con ADN no metilado obtenido por PCR (*hsdRMS*).
- ***Agrobacterium tumefaciens* LBA4404** (Hoekema *et al.*, 1983):  $TiAch5 Rif^r Str^r Thi^+$ . Estirpe bacteriana resistente a rifampicina y empleada para la transformación y obtención de plantas transgénicas de fresa. Contiene el plásmido *Ti* desarmado *pAL4404* que confiere resistencia a estreptomomicina y espectinomomicina pero que no porta los genes de síntesis de opinas. No obstante, se mantiene intacta la región *vir* que aporta en trans las funciones de virulencia necesarias para la transferencia del T-DNA del vector binario correspondiente al genoma de la planta.

- ***Agrobacterium tumefaciens* AGLO** (Lazo *et al.*, 1991): *EHA101pTibO542  $\Delta T$ -region Mop<sup>+</sup>*. Estirpe bacteriana resistente a rifampicina y empleada en la transformación y obtención de plantas transgénicas de fresa. Contiene el plásmido *Ti* desarmado *pTibO542 $\Delta T$*  que posee una región correspondiente a los genes de síntesis de monopinás, y una región *vir* que aporta en *trans* las funciones de virulencia necesarias para la transferencia del T-DNA presente en un vector binario al genoma de la planta

### I.2.2.1. Condiciones de cultivo de los microorganismos

Los cultivos líquidos de *E. coli* se crecieron siempre a 37 °C entre 12-14 horas, en agitación (150-200 rpm) y asegurando que la aireación del cultivo fuera la adecuada. Para ello, el volumen de medio utilizado nunca superó la quinta parte del volumen de aire del recipiente empleado. En el caso de *A. tumefaciens*, los cultivos líquidos se crecieron a 28 °C entre 18-48 horas dependiendo de la estirpe, en agitación (150-250 rpm) y asegurando, igualmente, una aireación elevada. En ambos casos, el medio de cultivo empleado fue generalmente LB suplementado con los antibióticos adecuados.

#### Apéndice I: Composición de los medios de cultivo bacterianos

##### LB (Luria-Bertani) (Autoclave)

Bactotripton	10 g/l
Extracto de levadura	10 g/l
NaCl	10 g/l
H <sub>2</sub> O destilada hasta alcanzar el volumen final. Ajustar a pH 7,5 con NaOH.	

##### LB sólido (Autoclave)

Medio LB
Agar 1,5% (p/v)

### I.2.2.2. Conservación de las estirpes bacterianas

Las estirpes bacterianas se conservaron a -80 °C en el mismo medio nutritivo utilizado para su crecimiento suplementado con glicerol estéril hasta una concentración final del 20% (v/v).

## I.2.3. Vectores de clonación y expresión

### I.2.3.1. Vectores de clonación

- ***pBluescript*** (Stratagene) (Fig. 2). Generalmente, este vector se ha empleado para la subclonación, secuenciación y almacenamiento de fragmentos de ADN. Contiene la secuencia génica del fragmento aminoterminal ( $\alpha$ ) de la  $\beta$ -galactosidasa, que puede ser  $\alpha$ -complementado por el fragmento  $\omega$  presente en el genoma de la célula hospedadora. La secuencia de este fragmento se encuentra interrumpida por la presencia de un sitio de clonación múltiple que contiene 21 dianas únicas para endonucleasas de restricción, ello facilita la selección de recombinantes mediante IPTG y X-Gal. También, contiene secuencias de unión para los cebadores universales *T3*, *T7*, *Forward (M13)* y *Reverse (M13)*, además de conferir resistencia a ampicilina a las células bacterianas que lo contienen.

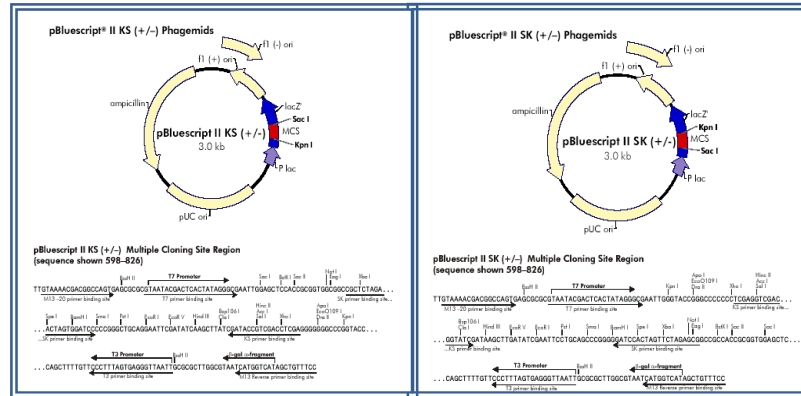


Fig. 2. Vector de clonación *pBluescript*

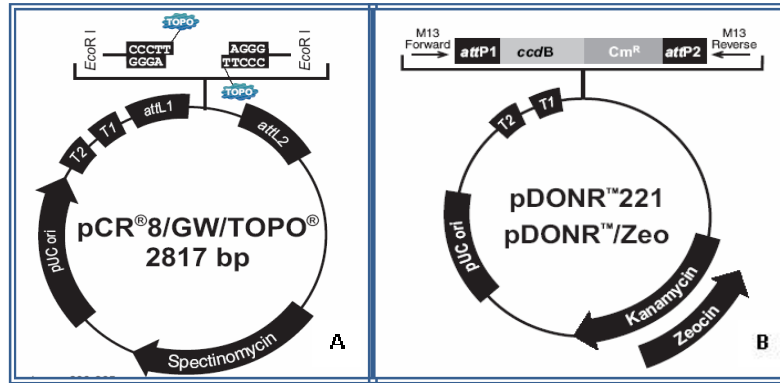
▪ *pCR8/GW/TOPO* (Invitrogen). Este vector ha sido empleado para el subclonaje de fragmentos de ADN amplificados mediante la reacción en cadena de la polimerasa (PCR). Se comercializa en forma linealizada con extremos protuberantes 3' de timidina unida covalentemente a Topoisomerasa I del virus *Vaccinia* (Shuman, 1991). La unión de la topoisomerasa al ADN es eliminada durante el subclonaje de cualquier producto de PCR que presente un residuo de deosiadenosina en su extremo 3' adicionado por la acción inespecífica de la *Taq* polimerasa durante la obtención del amplicón. La presencia de estos residuos aumenta la eficiencia de subclonaje en el vector plasmídico.

Junto al sitio de subclonaje del producto de PCR en el plásmido, existen los sitios *attL Gateway* (Invitrogen). Ello permite que el vector *pCR8/GW/TOPO* pueda ser empleado como un *Entry vector* en el sistema de subclonaje *Gateway* (Invitrogen) (Fig. 3A). El sistema *Gateway* es una metodología de clonaje universal que emplea el sistema de recombinación específica del bacteriófago lambda (Landy, 1989). De este modo, el fragmento de ADN subclonado en este vector puede ser transferido eficazmente mediante recombinación a otro vector que contenga los sitios *attR Gateway* (Invitrogen).

El fragmento subclonado en este vector puede ser secuenciado empleando los cebadores universales *Forward* (M13) y *Reverse* (M13); o escindido mediante digestión enzimática con *EcoRI*. Además, este vector confiere resistencia a espectinomomicina a las células bacterianas que lo contienen.

▪ *pDNOR221<sup>TM</sup>* (*Gateway<sup>®</sup> Vector*, Invitrogen). Este vector (Fig. 3B) se empleó para la clonación de fragmentos de ADN amplificados mediante la reacción en cadena de la polimerasa (PCR). Está diseñado para generar sitios *attL* que flanqueen al producto de PCR subclonado dentro de él y así poder ser empleado posteriormente como *Entry vector* en la recombinación basada en la metodología *Gateway*.

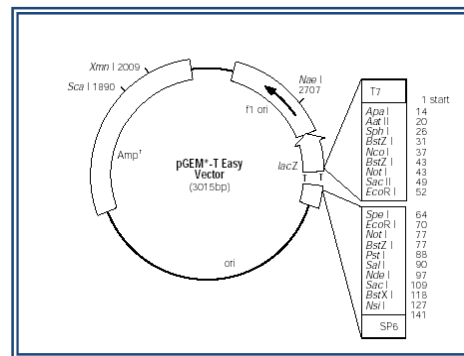
El fragmento clonado en este vector puede ser secuenciado empleando los cebadores universales *Forward* (M13) y *Reverse* (M13). Además, este vector confiere resistencia a kanamicina a las células bacterianas que lo contienen.



**Fig. 3. A) Vector de clonación *pCR<sup>®</sup>8/GW/TOPO<sup>®</sup>*. B) Vector de clonación *pDONR<sup>TM</sup>221***

▪ *pGEM-T Easy* (Promega). El vector *pGEM-T Easy* (Fig. 4) se ha utilizado para la clonación de fragmentos de ADN amplificados mediante PCR. Es un plásmido de alto número de copias que se comercializa en forma linealizada después de haber sido digerido enzimáticamente mediante la endonucleasa de restricción *EcoRV*. Además, la posición 3' de los extremos romos resultantes de la actuación de la restrictasa han sido modificados químicamente adicionando dos restos de deositimidina. Estos residuos incrementan la eficiencia de la ligación de los productos de PCR debido a que numerosas ADN polimerasas termoestables añaden sistemáticamente un residuo de deosiadenosina a los extremos 3' de los fragmentos amplificados, independientemente de la secuencia del ADN utilizado como molde.

El sitio de inserción se encuentra flanqueado por un lugar de clonación múltiple que contiene dianas únicas para 12 endonucleasas de restricción diferentes y puntos de corte duplicados, a ambos lados del lugar de inserción, para tres restrictasas distintas. En los extremos del mismo, aparecen cuatro secuencias promotoras diferentes (cebadores *Reverse (M13)*, *Forward(M13)*, *T3* y *T7*). El sitio de clonación múltiple interrumpe la secuencia génica del fragmento aminoterminal  $\alpha$  de la  $\beta$ -galactosidasa susceptible de ser  $\alpha$ -complementado por el fragmento  $\omega$  existente en el genoma de la célula hospedadora, lo que facilita la selección de recombinantes mediante IPTG y X-Gal. Además, el plásmido *pGEM-T Easy* confiere resistencia al antibiótico ampicilina a las células bacterianas que lo contienen.



**Fig. 4. Vector de clonación *pGEM-T Easy***

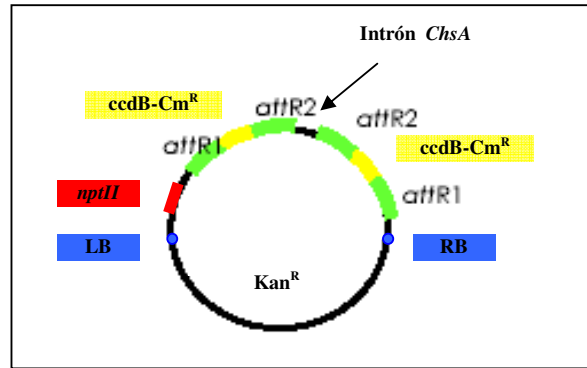
### I.2.3.2. Vectores de expresión

- *pFRN* (Cedido por el Dr. Marten Denekamp del Departamento de Biología Celular y Molecular, Universidad de Utrecht, Países Bajos). Este es un vector binario que se emplea como *Destination vector* en la metodología *Gateway* (Invitrogen) (Fig. 5). Se utiliza en la transformación de plantas ya que produce moléculas de ARN interferente (ARNi) en las plantas transgénicas resultantes, lo que conlleva al silenciamiento génico postranscripcional de los genes clonados.

Este vector es una modificación del vector *pFGC5941* (GhromDB) en el que se ha sustituido el gen *bar* que confiere resistencia a basta, por el gen *nptII* que confiere resistencia a kanamicina en la planta transgénica que lo contiene. Posee además cuatro sitios *attR Gateway* en posiciones invertidas (*attR1-attR2* y *attR2-attR1*), de manera que el inserto es subclonado en orientación antisentido y sentido simultáneamente (Fig. 5). De este modo, se produce la formación de moléculas de ARN de doble cadena (ARNds) desencadenantes del silenciamiento génico por ARNi. Entre las dos regiones *attR Gateway* y separándolas entre sí, se encuentra la secuencia correspondiente al intrón del gen *ChsA* (gen que codifica una chalcona sintasa) y que da lugar a un bucle en la estructura secundaria del ARNds, necesario para la formación del ARNi. La síntesis del ARNds está dirigida por el promotor 35S CaMV.

Este vector incluye además dos genes *ccdB* flanqueados por cada pareja de extremos *attR* (*attR1-ccdB-Cm<sup>R</sup>-attR2* y *attR2-ccdB-Cm<sup>R</sup>-attR1*) (Bernard y Couturier, 1992; Bernard *et al.*, 1993). La proteína codificada por este gen interfiere con la ADN girasa de *E. coli*, inhibiendo el crecimiento de la mayoría de estirpes de *E. coli* (ej. *DH5α* y *TOP10*). Por ello, se almacena en la estirpe de *E. coli* *DB3.1* que contiene la mutación (*gyrA462*) que la hace insensible a los efectos de la proteína CcdB. De esta manera, este gen permite la selección negativa de las células que lo contienen tras el proceso de recombinación con la LR clonasa *Gateway* (*Materiales y Métodos, apartado II.10.1.*). Además, contiene un gen que confiere resistencia al antibiótico cloranfenicol junto al gen *ccdB*, por lo que la presencia de este antibiótico en el medio favorece la estabilidad del gen *ccdB* en el ADN plasmídico. Para la selección en células de *E. coli*, este vector contiene además un gen marcador de resistencia al antibiótico kanamicina.





**Fig. 5. Estructura del vector binario *pFRN* empleado para el silenciamiento génico postranscripcional mediante ARNi en plantas transgénicas de fresa.** RB, right border. LB, left border. La región situada entre los extremos LB y RB es transferida al genoma de la planta durante la transformación mediada por *Agrobacterium*. *attR1* y *attR2*: regiones *att* donde se produce la recombinación mediante el sistema *Gateway* (Invitrogen); *ccdB*: gen empleado en la selección negativa de recombinantes; *Cm<sup>R</sup>*: gen de resistencia a cloranfenicol; *Kan<sup>R</sup>*: gen de resistencia a kanamicina para la selección de bacterias positivas; *nptII*, gen de resistencia a kanamicina para la selección de plantas transgénicas; **intrón *ChsA***: intrón del gen *ChsA*.

- ***pGEX-4T-1*** (Amersham) (Fig. 6): Este vector se emplea en la expresión heteróloga de proteínas en *E. coli* mediante el subclonaje del correspondiente ADNc en el sitio de clonaje múltiple. La expresión de la proteína está bajo control del promotor *tac* que se induce en presencia del análogo de la lactosa isopropyl  $\beta$ -D thiogalactosido (IPTG). Todos los vectores *pGEX* incluyen el gen interno *lacI<sup>f</sup>* cuyo producto es una proteína represora que se une al operador del gen *tac* evitando la expresión del inserto hasta la adición de IPTG y, controlando así, su expresión.

Este vector contiene además el gen de fusión glutatión S-transferasa (*GST*) que lo convierte en un sistema muy versátil de expresión, purificación y detección de proteínas producidas en *Escherichia coli*. El sistema se basa en la expresión inducible de altos niveles de proteína recombinante, que conserva siempre su actividad enzimática, fusionada a la *GST* en el extremo amino terminal. Posteriormente, la proteína de fusión obtenida se purifica a partir de lisados bacterianos mediante cromatografía de afinidad utilizando glutatión reducido, lo que nos permite la captura específica de la proteína y la eliminación de impurezas presentes en la muestra mediante varios lavados sucesivos. Este proceso de purificación preserva tanto la antigenicidad como la actividad de la proteína lo que facilita su posterior análisis. Si es necesario, la *GST* se puede eliminar mediante digestión con la proteasa trombina y liberar así la proteína recombinante de interés para usos posteriores. En general, cualquier proteína de fusión puede ser detectada mediante colorimetría o empleando métodos inmunológicos.

En cualquier caso, las construcciones *pGEX-4T-1*-ADNc obtenidas se transforman preferentemente en la estirpe bacteriana *E.coli BL21 (DE3)* pLysS, resistente a cloranfenicol (Cam). Además, la selección de células de *E. coli* portadoras de este vector se hace en presencia de ampicilina. Por otra parte, para el análisis mediante PCR de los clones de interés se emplean los cebadores *pGEX 5'* y *pGEX 3'* (Tabla 2).

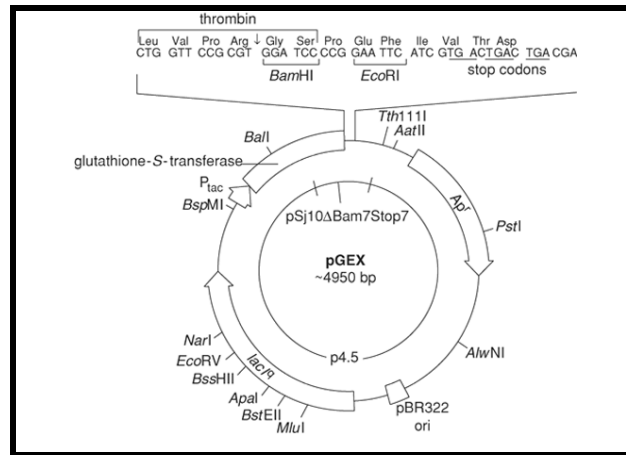


Fig. 6. Vector de expresión *pGEX-T4-1*

## II. MÉTODOS

### II.1. AISLAMIENTO DE ÁCIDOS NUCLEICOS

#### II.1.1. Extracción de ARN

##### II.1.1.1. Tratamiento del material y soluciones utilizadas en la extracción de ARN

El material de vidrio utilizado en la extracción de ARN fue cuidadosamente lavado con agua bidestilada y esterilizado mediante su calentamiento a 180 °C en un horno durante un periodo de cinco a seis horas. El material plástico no desechable, como las cubetas de electroforesis, se trató por inmersión en solución alcalina de NaOH 50 mM durante un periodo de entre tres y doce horas, lavándose seguidamente con agua bidestilada. El resto del material fue esterilizado a 121 °C durante 20 minutos en autoclave.

Las soluciones acuosas fueron tratadas con DEPC a una concentración final de 0,1% (v/v). Tras una agitación vigorosa, se dejaron reposar en una campana de extracción de gases durante 16 horas y posteriormente se esterilizaron en autoclave. Los tampones que contenían Tris en su composición fueron preparados con agua estéril previamente tratada con DEPC y posteriormente se esterilizaron de nuevo. El DEPC es una sustancia tóxica y un potente inhibidor de las RNasas, no obstante, a las condiciones de presión y temperatura que se alcanzan durante la esterilización en autoclave, éste se descompone en CO<sub>2</sub> y CH<sub>2</sub>OH.

## II.1.1.2. Obtención y purificación de ARN

### II.1.1.2.1. Preparación de solventes orgánicos

#### *Preparación de solventes orgánicos (I): neutralización de fenol*

Antes de utilizarse, el fenol se equilibró a pH ~7,8 ya que los ácidos nucleicos se fragmentan en un solvente orgánico a pH ácido. Para ello, el fenol se calentó en un baño a 50 °C hasta que estuvo completamente líquido y se trasvasaron 200 ml a un recipiente de vidrio, marcando el volumen alcanzado. Se añadieron 100 ml de H<sub>2</sub>O destilada y se mezcló en un agitador magnético hasta que se formó una única fase, añadiendo entonces 10 g de Tris de la máxima pureza posible. Una vez disuelto el Tris, se comprobó que el pH de la mezcla era cercano a 8. En este punto, se volvieron a añadir 100 ml de H<sub>2</sub>O destilada y, tras mezclar bien por agitación, la solución se dejó reposar a 4 °C y en oscuridad 16 horas hasta que se formaron de nuevo dos fases. Transcurrido este tiempo, se observó que la fase inferior presentaba un volumen superior a los 200 ml marcados inicialmente. Se retiraron 100 ml de la fase acuosa superior y se añadieron 100 ml de H<sub>2</sub>O destilada. La nueva mezcla se agitó y se dejó reposar para permitir la separación de las dos fases. Este proceso se repitió hasta que la fase orgánica alcanzó el volumen inicial de 200 ml. El fenol neutro se almacenó en partes alícuotas de 20 ml, a -20 °C y en oscuridad, conservando siempre parte de la fase acuosa.

#### *Preparación de solventes orgánicos (II): Fenol: cloroformo: isoamílico (25:24:1; v/v)*

Se empleó para eliminar proteínas presentes en las muestras de ácidos nucleicos. El cloroformo de la mezcla desnaturaliza las sustancias proteicas y facilita la separación de las fases acuosa y orgánica. El alcohol isoamílico reduce la formación de espuma durante el proceso de extracción. Se mezcló un volumen de fenol neutro con un volumen de una mezcla 24:1 de cloroformo: alcohol isoamílico. La mezcla se almacenó a 4 °C protegido de la luz.

### II.1.1.2.2. Método de purificación de ARN empleando cloroformo: isoamilalcohol (Asif *et al.*, 2000)

El tejido congelado (1g) se homogenizó en presencia de N<sub>2</sub> líquido. El polvo obtenido se transfirió a un tubo Beckman estéril de 50 ml que contenía 10 ml de tampón de extracción precalentado a 65 °C y se incubó a esa misma temperatura durante 1 hora con agitación ocasional. Tras la incubación, el tubo se dejó enfriar a temperatura ambiente y se añadió un volumen de cloroformo: isoamilalcohol (24:1). Dicha mezcla se agitó vigorosamente hasta la aparición de una única fase, y posteriormente se centrifugó a 15.000 g durante 15 minutos a temperatura ambiente. La fase acuosa se recuperó en un tubo nuevo y se repitió el lavado con cloroformo: isoamilalcohol como anteriormente. Finalmente, la fase acuosa recuperada se trasvasó a un tubo nuevo, se añadió LiCl hasta una concentración de 3 M, y se incubó durante 16 horas a 4 °C. El ARN se recuperó mediante centrifugación durante 30 minutos a 17.000 g y 4 °C. El precipitado obtenido se resuspendió en 200 µl de H<sub>2</sub>O-DEPC y se lavó con fenol, fenol: cloroformo (1:1) y cloroformo secuencialmente.

Para precipitar los polisacáridos presentes, se procedió de la siguiente forma: a la fase acuosa obtenida se le añadieron 1/30 volúmenes de acetato de sodio 3 M pH 5,2 y 0,1 volúmenes de etanol. La mezcla se incubó en hielo durante 30 minutos y posteriormente se centrifugó a 4 °C en una microfuga a máxima velocidad. Por último, el ARN se precipitó con acetato de sodio 0,3 M pH 5,2 y 3 volúmenes de etanol. La mezcla se incubó durante 3 horas a -80 °C, y

posteriormente el ARN se recuperó mediante centrifugación a 14.000 g durante 45 minutos a 4 °C.

El ARN obtenido se lavó sucesivamente con 1 ml de etanol 70% y 100%, y finalmente se resuspendió en 100 µl de H<sub>2</sub>O-DEPC. La concentración de ARN se determinó mediante espectrofotometría, midiendo su absorbancia a 260 nm (*Materiales y Métodos, apartado II.2.1*). El ARN se almacenó a -80 °C hasta su uso.

**Apéndice 2: Soluciones utilizadas para la obtención y purificación de ARN**

**Tampón de extracción empleando cloroformo: isoamilalcohol (aptdo. II.1.1.2.2)**

Tris-HCl pH 8,2	100 mM
EDTA-Na <sub>2</sub> pH 8	20 mM
NaCl	1,4 M
CTAB	2% (p/v)
β-mercaptoetanol	1% (v/v)

## II.1.2. Extracción de ADN

### II.1.2.1. Obtención y purificación de ADN plasmídico

Las extracciones rutinarias de ADN plasmídico se realizaron siempre empleando *kits* comerciales especialmente diseñados para la purificación de pequeñas cantidades de ADN (miniprep). Cuando la cantidad de ADN plasmídico requerido para experimentación fue mayor, se emplearon otros kits comerciales diseñados para mejorar el rendimiento del ADN obtenido basándose, principalmente, en un aumento del volumen de partida del cultivo en cuestión (midiprep). Siempre se siguieron los protocolos suministrados por las casas comerciales. La integridad del ADN obtenido fue comprobada mediante electroforesis de una parte alícuota de la muestra (*Materiales y Métodos, apartado II.2.2.1*).

**Apéndice 3: Kits de biología molecular empleados para la purificación de ADN plasmídico**

- *CONCERT High Purity Plasmid Miniprep System* (Gibco BRL)
- *Quantum Prop Plamid Miniprep* (BioRad)
- *Accuprep Plasmid Extraction Kit* (BioNeer)

## II.2. CUANTIFICACIÓN Y VISUALIZACIÓN DE ÁCIDOS NUCLEICOS MEDIANTE ELECTROFORESIS

### II.2.1. Cuantificación de ácidos nucleicos

La concentración de ácidos nucleicos se determinó mediante espectrofotometría midiendo su absorbancia a 260 nm y considerando un coeficiente de extinción para el ADN bicatenario de

50  $\mu\text{g}^{-1}\text{cm}^{-1}\text{ml}$  y para el ARN de 40  $\mu\text{g}^{-1}\text{cm}^{-1}\text{ml}$ . Generalmente, se utilizó un espectrofotómetro NanoDrop (*ND-100 Spectrophotometer*).

En el caso de muestras de ARN, paralelamente se realizaron medidas a 230 y 280 nm para determinar el grado de contaminación de la muestra por polisacáridos y proteínas respectivamente. La relación  $\text{Abs}_{260\text{nm}}/\text{Abs}_{230\text{nm}}$  nos indica la presencia de polisacáridos frente a ácidos nucleicos y su valor recomendado es  $\sim 2$ . La relación  $\text{Abs}_{260\text{nm}}/\text{Abs}_{280\text{nm}}$  indica la presencia de proteínas frente a ácidos nucleicos y su valor recomendado es también  $\sim 2$ . Fue absolutamente imprescindible tener en cuenta estos valores en experimentos de RT-PCR para que las muestras de ARN empleadas fueran retrotranscribibles.

De forma más grosera, la concentración de ácidos nucleicos también se estimó por comparación visual de una parte alícuota de la muestra problema frente a un patrón de ADN de concentración conocida (ADN de fago  $\lambda$  digerido con *HindIII*, Pharmacia) separadas electroforéticamente de forma simultánea. Este sistema también nos permitió determinar el grado de pureza de las muestras analizadas.

## II.2.2. Separación electroforética de ácidos nucleicos

### II.2.2.1. Electroforesis de ADN

La separación electroforética del ADN se llevó a cabo de forma horizontal empleando geles de agarosa en tampón TBE [1X]. El porcentaje de agarosa empleado osciló entre 0,8% y 2% (p/v) en función del tamaño de los fragmentos de ADN a separar. Al gel siempre se le añadió bromuro de etidio (BrEt) a una concentración final de 0,5  $\mu\text{g}/\text{ml}$ , el cual permite visualizar las moléculas de ADN con luz ultravioleta ( $\lambda \leq 400 \text{ nm}$ ) al intercalarse en ellas.

El ADN, mezclado con tampón de carga [6X], fue sometido a un campo eléctrico generado mediante una corriente continua de un voltaje comprendido entre 30 y 120 V en función del tamaño y concentración del gel, así como del tamaño de las moléculas de ADN a separar. El tiempo empleado para la separación varió y fue inversamente proporcional al voltaje empleado en cada caso. La visualización de las moléculas de ADN se consiguió por la exposición del gel correspondiente a luz ultravioleta de rango de emisión entre 260 y 302 nm (onda corta-media). En el caso de fragmentos que posteriormente iban a ser purificados, clonados o secuenciados, se empleó luz UV de un rango de emisión de 365 nm (onda larga).

Con objeto de estimar la cantidad y/o tamaño de las moléculas de ADN, en los geles siempre se incluyó un patrón de ADN de concentración y tamaños moleculares conocidos. Los marcadores de peso molecular más utilizados fueron el ADN de fago  $\lambda$  digerido con *HindIII* (Pharmacia) y *IKb* (Pharmacia).

### II.2.2.2. Electroforesis de ARN

Con objeto de determinar la calidad e integridad de las muestras de ARN aisladas, siempre se llevó a cabo una electroforesis de ARN en geles de agarosa al 1,2% (p/v) en tampón TBE [1X] estéril, y en cubetas tratadas con NaOH 50 mM durante al menos 3 horas (el resto del material utilizado se trató antes de entrar en contacto con el ARN como se indica en el apartado II.1.1.1). La muestra de ARN se aplicó al pocillo del gel junto con tampón de carga

[6X] tratado con DEPC, y se sometió a electroforesis a 80 V durante el tiempo necesario para que las bandas de ARN ribosómico (ARNr) se separaran suficientemente.

La visualización de las moléculas de ARN se consiguió por la exposición del gel correspondiente a luz ultravioleta de rango de emisión entre 260 y 302 nm (onda corta-media). Se consideró que el ARN presentaba una integridad adecuada cuando se observaron al menos dos bandas correspondientes al ARNr 28S y 18S, siendo óptima una relación de intensidad dos veces superior para el ARNr 28S con respecto al ARNr 18S.

Al igual que en electroforesis de ADN, en los geles se incluyeron marcadores de peso molecular (ADN de fago  $\lambda$  digerido con *HindIII* y *I K<sub>b</sub>*, ambos de Pharmacia), con objeto de estimar la cantidad y tamaño de las moléculas de ARN.

<b>Apéndice 5: Soluciones empleadas en la electroforesis de ácidos nucleicos</b>			
<b>Tampón TBE [1X]</b>		<b>Tampón de carga [10X]</b>	
H <sub>3</sub> BO <sub>3</sub>	90 mM	Glicerol	50%
EDTA-Na <sub>2</sub>	2,2 mM	Azul de bromofenol	0,25% (p/v)
Ajustar a pH 8		Xilen-cianol (opcional)	0,25% (p/v)
<b>Tampón TAE [1X]</b>		Para las muestras de ARN se utilizó el mismo	
Tris-acetato	40 mM	tampón de carga tratado con DEPC al 0,1% (v/v)	
EDTA-Na <sub>2</sub> pH 8,0	2 mM	y autoclavado posteriormente	
Ajustar a pH 8,5 con ácido acético glacial			

## II.3. MANIPULACIÓN DE MOLÉCULAS DE ADN

### II.3.1 Purificación de fragmentos de ADN

#### II.3.1.1. Purificación de ADN a partir de geles de agarosa

Independientemente del método de purificación empleado, la muestra de ADN problema siempre se separó mediante electroforesis en gel de agarosa. A continuación, el fragmento de ADN de interés se escindió con un bisturí estéril directamente desde el gel mientras éste se visualizaba con luz ultravioleta de longitud de onda larga (365nm). Cuando el objetivo de la purificación fue la obtención de ADN de alta calidad a partir del gel, se empleó el kit *QIAquick® Gel Extraction Kit* (Qiagen), siguiendo las instrucciones suministradas por la casa comercial ([www.qiagen.com](http://www.qiagen.com)). Ocasionalmente y cuando el tamaño de las moléculas a purificar eran inferiores a 500 pb, se empleó también el método de purificación por electroelución.

#### *Electroelución de ADN*

La muestra de ADN elegida se sometió a electroforesis en tampón TBE [1X]. El fragmento de agarosa que contenía el ADN de interés se cortó con un bisturí estéril y se introdujo en una bolsa de diálisis a la que se le añadieron al menos 400  $\mu$ l de TE. La electroelución se llevó a cabo durante 1 hora a 80 V en tampón TBE [1X] cuidando que la orientación de la bolsa

respecto a los polos fuera la adecuada. Transcurrido este tiempo, se invirtió la polaridad durante 30 segundos para facilitar la separación de las moléculas de ADN de las paredes de la bolsa de diálisis. La solución contenida en la bolsa se recogió en un tubo y el ADN se precipitó con etanol y acetato sódico (*Materiales y Métodos, apartado II.3.2*) durante, al menos, 1 hora.

Las membranas de diálisis utilizadas para la electroelución fueron previamente tratadas hirviéndolas durante 10 minutos en una solución de bicarbonato sódico 2% (p/v) y EDTA- $\text{Na}_2$  1 mM. Se lavaron con  $\text{H}_2\text{O}$  bidestilada y se volvieron a hervir durante 10 minutos en EDTA- $\text{Na}_2$  1 mM. Después de un nuevo lavado con  $\text{H}_2\text{O}$  bidestilada, se conservaron a 4 °C en etanol al 20% hasta su uso.

**Apéndice 6: Soluciones empleadas en la purificación de fragmentos de ADN contenidos en agarosa**

**Tampón TE (Autoclave)**

Tris-HCl pH 7,5      10 mM

EDTA- $\text{Na}_2$  pH 8      0,1 mM

**Tampón TAE [10X]**

Ver Apéndice 5

**Tampón TBE [10X]**

Ver Apéndice 5

### II.3.1.2. Purificación de ADN a partir de una solución acuosa

El uso del sistema *CONCERT™ Rapid PCR Purification System* (GibcoBRL) permitió una eficaz purificación de fragmentos de ADN presentes en soluciones acuosas (productos de PCR, fragmentos resultantes de digestiones con endonucleasas, moléculas marcadas, etc). El proceso se llevó a cabo siguiendo las recomendaciones suministradas por la casa comercial ([www.invitrogen.com](http://www.invitrogen.com)). El ADN se recuperó directamente en  $\text{H}_2\text{O}$  estéril.

### II.3.2. Concentración de muestras de ADN

#### *Precipitación con etanol y acetato sódico*

Las muestras de ADN disueltas en  $\text{H}_2\text{O}$  o tampón se precipitaron adicionando 2,5 volúmenes de etanol absoluto y 0,1 volúmenes de acetato sódico 3 M pH 5,6 a la muestra. Seguidamente, la mezcla se incubó a -80 °C durante, al menos, 30 minutos y el precipitado se recuperó por centrifugación a 15.000 g durante 30 minutos. El ADN recuperado se lavó sucesivamente con etanol al 70%, para eliminar sales residuales, y con etanol absoluto, centrifugando cada vez a 15.000 g durante 5 minutos para recuperar la muestra. El etanol residual se evaporó incubando la muestra en una estufa a 37 °C. Finalmente, el ADN se resuspendió en el volumen deseado de tampón o  $\text{H}_2\text{O}$  estéril.

#### *Concentración por desecación*

El ADN en disolución también se concentró por desecación al vacío a temperatura ambiente o a 50 °C, en un secador de vacío *SpeedVac SVC100* (Savant). Ocasionalmente, las muestras también fueron concentradas por desecación en estufa a 37 °C hasta conseguir la evaporación de la fase líquida de la muestra.

### II.3.3. Digestión de moléculas de ADN con endonucleasas de restricción

Las digestiones con endonucleasas de restricción se realizaron de acuerdo con las recomendaciones de las casas comerciales correspondientes y durante un período comprendido entre 2 y 12 horas a 37 °C (salvo excepciones indicadas por las casas comerciales). Generalmente, en cada digestión se añadieron 5 U de enzima/ $\mu\text{g}$  de ADN para asegurar una digestión completa. Las digestiones se comprobaron mediante electroforesis en gel de agarosa en tampón TBE [1X] (*Materiales y Métodos, apartado II.2.2.1.*) de una parte alícuota de dicha muestra junto a la misma muestra sin digerir.

En el caso de digestiones de ADN genómico, el período de incubación a 37 °C siempre se prolongó durante 12 horas añadiéndose a la mezcla, además, espermidina a una concentración final de 0,01 M. Este compuesto se une a sustancias contaminantes cargadas negativamente y facilita la actuación de las endonucleasas de restricción.

#### Apéndice 7. Mezcla de digestión enzimática

ADN (0,5-1 $\mu\text{g}$ )	x $\mu\text{l}$
Tampón [10X]	2 $\mu\text{l}$
Enzima de restricción (5U)	0,5 $\mu\text{l}$
H <sub>2</sub> O bidestilada hasta	20 $\mu\text{l}$

### II.3.4. Ligación de moléculas de ADN

Para que se lleve a cabo la ligación de dos moléculas de ADN (vector e inserto) es necesario digerir ambas previamente con la misma endonucleasa de restricción para generar extremos cohesivos capaces de unirse entre sí.

#### *Desfosforilación del vector*

Durante la ligación, el vector digerido con una única enzima de restricción puede religarse generando clones que sólo contendrían el plásmido empleado. Por tanto, es recomendable la desfosforilación del vector en cuestión para evitar un alto número de falsos positivos en los transformantes generados posteriormente. De esta manera, aumenta la garantía de que el vector sólo pueda recircularizarse una vez incluya el inserto que se quiere clonar.

El proceso de desfosforilación se realizó añadiendo 1U de *fosfatasa alcalina* de timo de ternera (*CIAP*) (Invitrogen) por cada volumen inferior o igual a 100  $\mu\text{l}$  de vector digerido. La mezcla se incubó 15 minutos a 37 °C. En el caso de extremos protuberantes 3', se realizó una incubación adicional a 56 °C durante 15 minutos. Para inactivar la enzima, la mezcla se incubó 5 minutos a 70 °C y se fenolizó. El vector desfosforilado se recuperó por precipitación con etanol y acetato sódico (*Materiales y Métodos, apartado II.3.2.*).



**Reaccion de ligación**

Las concentraciones de vector e inserto utilizadas para la ligación de fragmentos de ADN fueron proporcionales a los tamaños de las moléculas que se deseaba ligar. Se aplicó la relación:

$$\frac{\text{ng vector} \times \text{tamaño del inserto (Kb)}}{\text{tamaño del vector (Kb)}} \times \text{relación vector/inserto} = \text{ng de inserto}$$

En el caso de ligaciones con el vector *pGEM-T Easy* (Promega), se siguieron las instrucciones indicadas por la casa comercial que recomienda que la relación vector:inserto sea 1:3 para conseguir la mayor eficiencia. Cuando el vector empleado fue *pGEX-4T-1* (Amershan), se utilizó una relación 1:5 entre el tamaño del vector y el inserto aplicando la relación:

$$\frac{2 \times \text{ADN (gramos)}}{\text{tamaño del inserto(pb)} \times 649(\text{Dalton/pb})} \times \text{relación vector/inserto} = \text{moles del vector}$$

En cualquier caso, la mezcla de ligación se realizó como se indica en el *Apéndice 8* y ésta se incubó rutinariamente a 16 °C durante 14-16 horas antes de proceder a la transformación de células de *E. coli*.

**Apéndice 8: Reacción de ligación**

Vector	x µl
Inserto	y µl
Tampón ligación (Invitrogen) [5X]	1 µl
T4 ligasa (Invitrogen) 1U/µl	1 µl
H <sub>2</sub> O destilada estéril hasta	10 µl

Cuando empleamos el vector *pGEM-T Easy* (Promega), tanto la mezcla de ligación como el periodo de incubación fueron los recomendados por la casa comercial.

**Apéndice 9: Enzimas empleadas en la desfosforilación y ligación de moléculas de ADN**

*T4 DNA ligasa* (Invitrogen): 1 U/µl  
*Fosfatasa alcalina de timo de ternera (CIAP)* (Invitrogen): 1U/ml

**II.3.5. Amplificación por PCR de fragmentos de ADN**

La reacción en cadena de la polimerasa (PCR) se utilizó con varios fines: a) en la comprobación de la orientación de los insertos correspondientes a los genes *FaAAT2* y *FaMYB10* cuando fueron incluidos en vectores de clonación; b) en la identificación de

transformantes positivos (*Materiales y Métodos, apartado II.4.4.3*); c) y en estudios de expresión de los genes *FaAAT2* y *FaMYB10* mediante QRT-PCR (*Materiales y Métodos, apartado II.6.3*).

### II.3.5.1. Cebadores universales empleados en la amplificación por PCR

Los cebadores universales se emplearon para la amplificación y, en algunos casos, para la secuenciación de fragmentos de ADN incluidos en los vectores *pBluescript*, *pGEM-Teasy*, *pGEX-4T-1* y *pCR8/GW/TOPO* (*Materiales y Métodos, apartado I.2.3.1*) (Tabla 2). La temperatura de anillamiento siempre fue 55 °C y el programa de PCR empleado el que se detalla en la Tabla 4.

Cebadores universales	
<i>T7</i>	5'-GTAATACGACTCACTATAGGGC-3'
<i>T3</i>	5'-AATTAACCCTCACTAAAGGG-3'
<i>Reverse (M13)</i>	5'-GGAAACAGCTATGACCATG-3'
<i>Forward (M13)</i>	5'-GTAAAACGACGGCCAGT-3'
<i>Sp6</i>	5'-GATTTAGGTGACACTATAG-3'
<i>pGEX 5'</i>	5'-GGGCTGGCAAGCCACGTTTGGTG-3'
<i>pGEX 3'</i>	5'-CCGGGAGCTGCATGTGTCAGAGG-3'

Tabla 2. Cebadores universales empleados.

Los cebadores *T3*, *T7*, *Forward (M13)* y *Reverse (M13)* se utilizaron para la detección y secuenciación de insertos específicos en el vector *pBluescript*<sup>®</sup> (*Materiales y Métodos, apartado I.2.3.1* y *apartado II.3.6*), mientras que los cebadores *Sp6* y *T7* se emplearon con el mismo objetivo cuando el vector portador del inserto fue el *pGEM T-Easy*. Cuando el vector empleado fue el *pGEX-4T-1*, los cebadores utilizados para la amplificación y secuenciación fueron el *pGEX5'* y *pGEX3'*. En el caso del vector *pCR8/GW/TOPO* se empleó siempre el cebador *Forward (M13)* para la determinación de la orientación del inserto que portaba y para su secuenciación.

### II.3.5.2. Cebadores específicos empleados en la amplificación por PCR

Los cebadores específicos utilizados en todos los casos para la amplificación de secuencias conocidas se diseñaron empleando el programa *Oligo 5.0* (Tabla 3).

Los oligonucleótidos empleados en QRT-PCR (Tabla 3) fueron diseñados específicamente, generalmente en el extremo 3', a partir de la secuencia conocida de cada uno de los genes. El amplicón obtenido fue siempre entre 100 y 200 pb, tamaño recomendado para que la concentración de reactivos disponibles en la mezcla no sea limitante, no viéndose afectada ni la reacción de PCR ni la emisión de fluorescencia (*Materiales y Métodos, apartado II.6.3*).

Gen	Oligonucleótidos específicos		Tamaño amplicón
<i>FaPAE</i>	<i>PAE1</i>	5'- CAT TCA CCG GTG ATG TGG AAG CAG TAA ACC -3'	156 pb
	<i>PAE2</i>	5'- GAA GCC AAT CCT CCA GCT GAA CAA CCA GA -3'	
<i>NDR1</i>	<i>NDR1 up</i>	5'- CGG AAT TGT GGT CGG AGA AAA CGC TGT -3'	149 pb
	<i>NDR1 low</i>	5'- TCC TCA TGG ATT GCT CCC CCT TTC ATT -3'	
<i>FaAAT2</i>	<i>FaSAAT2 up</i>	5'- TGT GGA GGT GAG AGG ACG ACC CC -3'	147 pb
	<i>FaSAAT2 low</i>	5'- TGG CAA GCA TAC TGG CAC CAA GAT TTC -3'	
<i>Famyb3</i>	<i>Famyb3 up</i>	5'- TGC CGG ACG ATT GCC AGG AAG -3'	129 Pb
	<i>Famyb3 low</i>	5'- TGA AGG TCC GTG GTC GA -3'	
<i>FaAAT2</i>	<i>FLAAT Forward</i>	5'- TGT CCC ATT CAT CAT GTC TTA CAA GAA -3'	1326 pb
	<i>FLAAT Reverse</i>	5'- TGC CAT CTA AAT AGC CTC CAA AAG AA -3'	
<i>FaAAT2</i>	<i>FaAATprotForward</i>	5'- CG GAA TTC TCT TAC AAG AAC AAT C 3'	1170 pb
	<i>FaAATprotReverse</i>	5'- CTA CTA ACCA GAG CTC ACT GAG CTC AAA G -3'	
<i>FaAAT2</i>	<i>GWFaAAT2 up</i>	5'- GTA ACA GTC CGC TGG GAT ATG CAG -3'	444 pb
	<i>GWFaAAT2 low</i>	5'- GTG AAG AAG TAA AAC GTG ATT GCC ATC TAA A -3'	
<i>Famyb3</i>	<i>GWFamyb3 up</i>	5'- AGA TGA CTA GAT GAT TGC TTG CCG -3'	407 pb
	<i>GWFamyb3 low</i>	5'- TGC CGG ACG ATT GCC AGG AAG -3'	
<i>SAAT</i>	<i>SAATup</i>	5'- GGA GGA CAT CAT GGA TTG GAG TTG C -3'	147 pb
	<i>SAATlow</i>	5'- GGG GAT CTT GTT CTA GCA TAG CC -3'	
<i>PAL</i>	<i>FaPAL FW</i>	5'- GAT GCA AAG GCT AAG GCA AG -3'	176 pb
	<i>FaPAL RV</i>	5'- AGC CCT AAC GCT CTC AAC CT -3'	
<i>C4H</i>	<i>FaC4H FW</i>	5'- TGC CCT TGG CTT CAT GAC T -3'	136 pb
	<i>FaC4H RV</i>	5'- GCT TGA CAC TAC GGA GAA AGG -5'	
<i>4CL</i>	<i>4-CL 2</i>	5'- GAT GAC GGA GGC GAC CCA TTT GAT G -3'	330 pb
	<i>4-CL 3</i>	5'- GGC ACG ATT TGA TCA CCT CCA CGG -3'	
<i>CHI</i>	<i>FaCHI Fw</i>	5'-GTCAATGTACCCTATATCACC-3'	135 pb
	<i>FaCHI Rv</i>	5'-GCTCAGTTTCATGCCTTGAC-3'	
<i>CHS</i>	<i>FaCHS FW</i>	5'- GCC TTT GTT TGA GCT GGT CT -3'	154 pb
	<i>FaCHS RV</i>	5'- CCC AGG AAC ATC TTT GAG GA -3'	
<i>GST</i>	<i>FaGST up</i>	5'- GGC GAC TTG GCC TTG GTG CGC CGC TC -3'	138 pb
	<i>FaGST low</i>	5'- TCG CCG GAA GAT GGC TCA GAT CAG C -3'	
<i>ANS</i>	<i>ANS FW</i>	5'- GAC TTG TCC ATT TGG CCT C -3'	102 pb
	<i>ANS RV</i>	5'- CCC CCT CAG TTC CTT AGC ATA CTC -3'	
<i>FRAA 2</i>	<i>FRAA-2 FW</i>	5'- CGT GGA GAT CAA GGA AGA GC -3'	153 pb
	<i>FRAA-2 RV</i>	5'- GGA ACA TCA GCG GAA CAA AT -3'	
<i>DFR-1</i>	<i>DFRT1 Cab</i>	5'- TTG TTG AGA ATT TCA AAT AAG TTG TTG -3'	115 pb
	<i>DFRT2 Col</i>	5'- TCC TTA AGC ACA AAT TAC ATC ATC A -3'	
<i>DFR-2</i>	<i>CI01-D2a</i>	5'- GGC TTA TTA ATC TAT CTT CTG -3'	132 pb
	<i>CI01-D2b</i>	5'- TGA GAC ATC CTA CTA TTT CAT T -3'	
<i>UFGT</i>	<i>UFGTA</i>	5'- GGC TGC ACT TGC TGG TGG TTC TAC -3'	160 pb
	<i>UFGTB</i>	5'- GCT TCA CCA GAT GGG ACA GAT GC -3'	
<i>FLS</i>	<i>FLS up</i>	5'- AGT GCA ACT TCT CCT TTC TGA TAG C -3'	162 pb
	<i>FLS low</i>	5'- CAT GAG GCA CAA TGG GGA CTC TAA -3'	
<i>MADS</i>	<i>MADS2-1</i>	5'- AGA AAT GGG GAG GGG GAG AGT AGA -3'	149 pb
	<i>MADS2-2</i>	5'- GAG AAG ATG ATG AGA GCA ACC TCG -3'	
<i>PYR</i>	<i>BetVI up</i>	5'- CGA ACC CTC GCC CAA CAA CAC ATG CA -3'	133 pb
	<i>BetVI low</i>	5'- GCC ACC GTC GCC GAT CAT GTT -3'	
<i>NCEDI</i>	<i>FaNCEDI FW</i>	5'- CGG CCA CTC CGG AAT CGC ACG TCT -3'	172 pb
	<i>FaNCEDI3 REV</i>	5'- GGT GTC CGC CGA CTC AAC CCA GA -3'	
<i>MATE</i>	<i>FaMATE up</i>	5'-TCTCGGGCCTGTCACTTACCACGC-3'	154 pb
	<i>FaMATE low</i>	5'-GCCCGATTCCAGGCCTTGCAC-3'	

Tabla 3 . Cebadores específicos empleados en la amplificación, clonación y secuenciación de fragmentos de los genes de secuencia conocida indicados. En negrita se indican las secuencias diana de varias enzimas de restricción incluídas en algunos de los cebadores empleados.

Aunque todos los cebadores específicos fueron diseñados para trabajar con un rango de temperatura de anillamiento amplio (52-60 °C), generalmente se utilizó una temperatura de 55 °C para trabajar simultáneamente con varias parejas de cebadores. Cuando se observó la aparición de dímeros de cebadores o de bandas de amplificación inespecífica a esta temperatura, se determinó individualmente la temperatura óptima de anillamiento para cada pareja de cebadores. En ocasiones, algunos de estos oligonucleótidos también fueron empleados en la secuenciación de fragmentos de ADN o para la amplificación de fragmentos que posteriormente fueron subclonados en vectores plasmídicos.

Concretamente, los cebadores específicos FLAAT diseñados a partir de la secuencia conocida del gen *FaAAT2* fueron empleados para la obtención del ADNc completo correspondiente a dicho gen (*Apartado II.7.1*), los cebadores *FaAATprot* (*Apartado II.7.2.*) se diseñaron para la obtención de la construcción *pGEX-4T-1-FaAAT2*, y los cebadores *GWFaAAT2* se emplearon para la generación de la construcción *pFRN-FaAAT2*. Por otra parte, para la generación de la construcción *pFRN-FaMYB10* se diseñaron los cebadores específicos *GWFaMYB10* (*Apartado II.10.*).

En general, las amplificaciones se llevaron a cabo en un volumen final de 25 µl. La mezcla de reacción incluyó:

Tampón de PCR	[10X]	2,5 µl
MgCl <sub>2</sub>	25 mM	1,5 µl
Mezcla de dNTPs	5 mM cada uno	1 µl
ADN molde	20-50 ng	x µl
Cebador 3'	2 µM	2,5 µl
Cebador 5'	2 µM	2,5 µl
Taq polimerasa	2 U	y µl
H <sub>2</sub> O bidestilada estéril	hasta	25 µl

En todas las amplificaciones rutinarias, salvo excepciones, se utilizó el mismo programa básico recogido en la Tabla 4. La temperatura de anillamiento de los cebadores se determinó en función de sus secuencias y de la región de ADN que se iba a amplificar, pudiendo variar en un rango de 50-65 °C según la pareja de cebadores empleada.

	Temperatura	Duración	Repeticiones
1	95 °C	2-5 min	1
2	95 °C	30 seg- 1 min	35-40 ciclos
3	T <sup>a</sup> anillamiento	30 seg - 1 min.	
4	72 °C	1-2 min	
5	72 °C	5-10 min	1
7	10 °C	Mantenido	1

**Tabla 4. Programa para la amplificación por PCR de fragmentos de ADN.**

Invariablemente, siempre se comprobó que las reacciones de amplificación habían transcurrido de manera adecuada analizando una alícuota del volumen total de la mezcla de PCR mediante electroforesis en gel de agarosa (*Materiales y Métodos, apartado II.2.2.1*).

**Apéndice 10: Soluciones empleadas en la amplificación por PCR de fragmentos de ADN****Tampón de PCR [10X]**

Tris-HCl pH 9,0	100 mM
KCl	500 mM
Autoclavar y añadir posteriormente Tritón X-100 al 15% (v/v)	

**II.3.6. Secuenciación**

La secuenciación se llevó a cabo con un secuenciador *ABI PRISM™ 3130 XL Genetic Analyzer* de *Applied Biosystems* en el Servicio Central de Apoyo a la Investigación de la Universidad de Córdoba (SCAI). Las muestras a analizar se prepararon siguiendo fielmente las instrucciones indicadas en el protocolo del *ABI PRISM™ Dye Terminator V 3.1 Cycle Sequencing Ready Reaction Kit*.

La obtención de ADN de alta calidad resultó ser un parámetro crítico del proceso de secuenciación, por ello el ADN se obtuvo utilizando distintos *kits* comerciales (*Materiales y Métodos, apartado I.1.4*). Generalmente, los cebadores empleados para la secuenciación de insertos en *pBluescript®* fueron *T3*, *T7*, *M13 forward* y *M13 reverse*. Adicionalmente, se empleó el cebador *SP6* para la secuenciación de insertos incluidos en *pGEM-T Easy* y los cebadores *pGEX3* y *pGEX5* para los insertos incluidos en el vector *pGEX-4T-1*.

**II.4. OBTENCIÓN DE CÉLULAS COMPETENTES Y TRANSFORMACIÓN DE *Escherichia coli*****II.4.1. Preparación de células competentes permanentes de *E. coli* DH5α y BL21**

Una colonia aislada de la estirpe deseada de *E. coli* se creció en medio LB a 37 °C y en agitación durante toda la noche. A la mañana siguiente, se tomó 1 ml de este cultivo y se inoculó en 100 ml de medio LB fresco y estéril contenido en un matraz de 250 ml y se incubó de nuevo a 37 °C y en agitación hasta alcanzar una  $D.O_{550nm} = 0,48$ .

Después de enfriar el cultivo en hielo, las células se recolectaron por centrifugación durante 10 minutos a 4.000 rpm y a 4 °C y, posteriormente, se resuspendieron en 2 ml de solución TfbI. Las células se incubaron nuevamente en hielo durante 5 minutos y se volvieron a recoger por centrifugación en las mismas condiciones anteriores. A continuación, se resuspendieron en 2 ml de solución TfbII y se mantuvieron en hielo durante 15 minutos. Finalmente, se distribuyeron en tubos Eppendorf estériles en partes alícuotas de 100 µl y se conservaron a -80 °C hasta su uso.

Las células competentes *E.coli* DH5α así preparadas se utilizaron para transformaciones convencionales, mientras que las células competentes *E.coli* BL21 se emplearon en la transformación con el plásmido *pGEX-4T-1* (*Materiales y Métodos, apartado II.7.2*). En el

caso de la transformación de células de *E. coli* con el vector plasmídico *pCR8/GW/TOPO* empleado como *entry vector* en el sistema Gateway, siempre se emplearon las células competentes comerciales *One Shot TOP10 Chemically competent E. coli* (Invitrogen) (*Materiales y Métodos, apartado II.10.1.*).

## **II.4.2. Transformación de células de *E. coli* químicamente competentes**

En todos los casos, salvo cuando usamos las células *One Shot TOP10* comerciales que se dispensan en alícuotas de 50  $\mu$ l, se mezcló una parte alícuota de células competentes (100  $\mu$ l) con la muestra de ADN (~ 45 ng) que se deseaba transformar, y la mezcla se incubó en hielo durante 30 minutos. Seguidamente, las células se sometieron a un choque térmico de 42 °C durante 1,5 minutos e inmediatamente se enfriaron en hielo durante 2 minutos. A continuación, se añadieron 0,7 ml de medio LB estéril y la muestra se incubó a 37 °C en agitación durante, al menos, 1 hora para reactivar el metabolismo celular. Una vez transcurrido este tiempo, las células se recogieron por centrifugación rápida a 15.000 g a temperatura ambiente y se volvieron a resuspender en 150  $\mu$ l de LB. A continuación, las células se sembraron en medio LB sólido conteniendo los antibióticos adecuados para la selección de los transformantes obtenidos y éstos se dejaron crecer a 37 °C durante 12 horas.

## **II.4.3. Selección e identificación de transformantes de *E. coli* positivos**

La selección de transformantes positivos se realizó en función de los marcadores de selección contenidos en los vectores plasmídicos empleados para la transformación. Se consideraron transformantes positivos aquellas células que, además de crecer en las condiciones de selección, también portaban el vector plasmídico con el inserto correcto utilizado en la ligación original.

### **II. 4.3.1. Selección por antibióticos**

Inicialmente, la selección de los transformantes positivos se realizó en medio selectivo LB sólido suplementado con los antibióticos a los que confería resistencia el vector introducido. En el caso del vector plasmídico *pCR8/GW/TOPO*, portador del gen de resistencia a espectinomicina, la selección de los transformantes positivos se llevó a cabo en medio LB-agar suplementado con espectinomicina (100  $\mu$ g/ml). Cuando el vector empleado en la transformación fue el vector plasmídico *pGEX-4T-1*, la selección de los transformantes positivos se realizó en presencia de ampicilina (100  $\mu$ g/ml), mientras que los transformantes portadores del vector *pDNOR<sup>TM</sup>22* y del vector binario *pFRN* se seleccionaron en presencia de kanamicina (100  $\mu$ g/ml).

### **II. 4.3.2. Selección por antibióticos, IPTG y X-gal**

En el caso de las construcciones derivadas de los vectores *pBluescript* y *pGEM-T Easy* (que portan como marcadores el gen de resistencia a ampicilina y el gen de la  $\beta$ -galactosidasa), la selección de transformantes positivos se realizó sembrando las células transformadas en placas de LB sólido suplementadas con ampicilina (100  $\mu$ g/ml), 40  $\mu$ l de solución de IPTG (0,1 M en H<sub>2</sub>O, esterilizado por filtración y almacenado a -20 °C) y 40  $\mu$ l de solución de X-gal

(20% p/v en N-N-dimetilformamida, almacenado a 4 °C), y se incubaron a 37 °C durante 12 horas. Una vez crecidas las colonias, se seleccionaron aquellas que presentaron un color blanco, lo que significaba que se había producido la inserción del fragmento de ADN exógeno en el sitio de clonación múltiple del vector provocando la interrupción del gen de la  $\beta$ -galactosidasa, e impidiendo así la síntesis correcta de la enzima que capacitaría a la bacteria para hidrolizar el X-gal y producir el compuesto (5-bromo-4-cloro-3-indol) que colorea la colonia de azul.

### II.4.3.3. Identificación de transformantes positivos

#### II.4.3.3.1. Identificación de transformantes positivos mediante análisis de restricción

A fin de comprobar que las supuestas colonias positivas incluían los vectores de clonación con el inserto de interés en cada caso, se aisló ADN plasmídico de cada transformante positivo seleccionado y se digirió con la enzima de restricción adecuada para liberar el inserto o un fragmento de éste (*Materiales y Métodos, apartado II.3.3*). Posteriormente éste se visualizó electroforéticamente en gel de agarosa (*Materiales y Métodos, apartado II.1.1.1*)

#### II.4.3.3.2. Identificación de transformantes positivos mediante PCR

Para comprobar que los vectores de clonación con el inserto de interés de los supuestos transformantes positivos correspondían a nuestro gen de interés, se procedió a su amplificación mediante PCR a partir de ADN plasmídico previamente aislado o bien directamente a partir de la colonia seleccionada empleando cebadores universales (*T3, T7, Forward M13 y Reverse M13*) y/o específicos diseñados a partir de la secuencia interna del inserto. La reacción de PCR se realizó como se indica en *Materiales y Métodos, apartado II.3.5*. Cuando la PCR se hizo directamente a partir de colonia, fue necesario siempre realizar una réplica de la colonia seleccionada en una nueva placa de LB-agar con el antibiótico de selección para mantener la línea celular.

#### **Apéndice 11: Soluciones empleadas en la obtención de células competentes y transformación de *E. coli***

##### **Medios LB líquido y LB sólido**

Ver Apéndice 1

##### **Medio SOC (Autoclave)**

Tryptona	2%
Extracto de levadura	0,5%
NaCl	10 mM
KCl	2,5 mM
MgCl <sub>2</sub>	10 mM
MgSO <sub>4</sub>	10 mM
Glucosa	20 mM

## **II.5. OBTENCIÓN DE CÉLULAS COMPETENTES Y TRANSFORMACIÓN DE *Agrobacterium tumefaciens*.**

### **II.5.1. Preparación de células competentes de *A. tumefaciens* y transformación por choque térmico**

Este protocolo se empleó para generar células químicamente competentes de *A. tumefaciens* que posteriormente se transformaron mediante un choque de frío.

Se creció una colonia aislada de *A. tumefaciens* LBA4404 o AGLO a 28 °C en 50 ml de LB suplementado con estreptomicina (50 µg/ml) o rifampicina (100 µg/ml) respectivamente. Una vez alcanzada una D.O.<sub>600 nm</sub> de 0,5, el cultivo se centrifugó 10 minutos a 3.500 rpm y las células recogidas se resuspendieron en 10 ml de NaCl 0.15 M. Nuevamente, las células en suspensión se sometieron a una nueva centrifugación en las mismas condiciones descritas anteriormente pero, en esta ocasión, el pellet obtenido se resuspendió en 1 ml de CaCl<sub>2</sub> 20 mM frío que, posteriormente, se distribuyó en alícuotas de 200 µl.

La transformación de las células competentes obtenidas se llevó a cabo añadiendo entre 0.5-1 µg del ADN plasmídico de interés a una o varias alícuotas de células y dejándolas incubar en hielo durante 30 minutos. Transcurrido este tiempo, las células se sometieron a un cambio brusco de temperatura congelándolas en nitrógeno líquido durante 1 minuto e inmediatamente después incubándolas a 37 °C durante 5 minutos. Se les añadió entonces 1 ml de LB a cada una de las muestras transformadas y se mantuvieron a 28 °C en agitación suave entre 2-4 h para su recuperación. Posteriormente, las células se precipitaron mediante una centrifugación rápida, se resuspendieron en 100 µl de LB fresco, y se sembraron en placas de LB-agar suplementadas con los antibióticos correspondientes. Las placas se depositaron en una estufa a 28 °C y las células se dejaron crecer entre 48-72 horas.

### **II.5.2. Selección e identificación de transformantes positivos de *A. tumefaciens***

La selección de transformantes positivos se realizó en función de los marcadores de selección contenidos en los vectores plasmídicos empleados para la transformación. Se consideraron transformantes positivos aquellas células que, además de crecer en las condiciones de selección, también portaban el vector plasmídico con el inserto correcto utilizado en la ligación original.

#### **II. 5.2.1. Selección por antibióticos**

Las células de *A. tumefaciens* transformadas con el vector binario *pFRN*, portador del gen de resistencia a kanamicina, se seleccionaron en presencia de este antibiótico a una concentración de 50 µg/ml. No obstante, como las cepas de *A. tumefaciens* empleadas presentan resistencia a estreptomicina y/o rifampicina, simultáneamente también se añadieron estos antibióticos (100 µg/ml) para la selección de los transformantes positivos de la cepa LBA4404 y AGLO respectivamente. Ocasionalmente, la adición simultánea de ambos antibióticos (kanamicina/estreptomicina o kanamicina/rifampicina) al medio de cultivo retrasó excesivamente la aparición de colonias transformantes. En estos casos, se optó por suplementar inicialmente el medio LB únicamente con kanamicina y, posteriormente, realizar



réplicas de las supuestas colonias transformantes en placas de LB suplementadas con ambos antibióticos.

### II.5.2.2. Identificación de transformantes positivos mediante PCR

La comprobación de las colonias positivas de *A. tumefaciens* crecidas en medio selectivo, se llevó a cabo mediante PCR empleando oligonucleótidos específicos y siguiendo el protocolo descrito en *Materiales y Métodos*, apartado II.3.5.

## II.6. ESTUDIOS DE EXPRESIÓN GÉNICA

### II.6.1. Tratamiento del ARN con *DNasa I*

Previo a su retrotranscripción, cualquier muestra de ARN se trató con *DNasa I* libre de *RNasas* (Pharmacia) para eliminar cualquier residuo de ADN genómico arrastrado durante la extracción y así evitar amplificaciones inespecíficas en posteriores reacciones de amplificación. El tratamiento con *DNasa I* se aplicó a muestras de 40-50 µg de ARN total (Apéndice 12).

#### Apéndice 12: Tratamiento de ARN con *DNasa I*

Muestra de ARN total (40-50 mg)	x µl
Tris-HCl [1M] pH 7,5	4 µl
MgCl <sub>2</sub> [0,1M]	6 µl
<i>DNasa I</i> ( <i>RNasa free</i> ) (Pharmacia) [7,5U/ml]	1 µl
H <sub>2</sub> O-DEPC hasta	100 µl

La mezcla de reacción se incubó a 37 °C durante 1-1,5 horas, teniendo cuidado de no sobrepasar este tiempo (un aumento del tiempo de incubación produce cierta degradación y menor recuperación de ARN). Posteriormente, la muestra fue tratada con igual volumen (1:1) de mezcla fenol: cloroformo (v/v) y cloroformo sucesivamente, y la fase acuosa recuperada se precipitó con 0,1 volúmenes de acetato sódico [3M] pH 5,2 y 2,5 volúmenes de etanol 100%, a -20 °C durante, al menos, 3 horas. El ARN precipitado se recuperó por centrifugación y se resuspendió en 20 ml de H<sub>2</sub>O estéril tratada con DEPC. Todas las soluciones empleadas se trataron con DEPC y se esterilizaron antes de su uso. La cuantificación y el grado de pureza del ARN tratado y precipitado se determinó con un espectrofotómetro *NanoDrop* (*ND-100 Spectrophotometer*). La integridad de las muestras se determinó mediante su visualización en gel de agarosa al 1% (p/v).

### II.6.2. Comprobación de la pureza del ARN total

Antes de proceder a la retrotranscripción del ARN tratado con *DNasa I*, siempre se estimó el grado de pureza de las muestras correspondientes mediante la determinación de su grado de contaminación por polisacáridos y proteínas. Para ello se determinó la relación  $Abs_{260nm}/Abs_{230nm}$  como se indica en el apartado II.2.1. de *Materiales y Métodos*. Finalmente, y una

vez comprobada la calidad de la muestra, el volumen total se diluyó hasta una concentración de trabajo de 1µg/ml.

### II.6.3. RT-PCR cuantitativa en tiempo real

La técnica de PCR cuantitativa en tiempo real (“*quantitative real-time PCR*”; QRT-PCR), permite cuantificar la cantidad de ARNm correspondiente a un gen determinado en una muestra. Esta cuantificación se consigue mediante la medida del incremento de fluorescencia emitida por el amplicón correspondiente a ese gen en cada ciclo de amplificación.

La cuantificación basada en medidas a tiempo final son inexactas debido a que pueden verse seriamente afectadas por la limitación de reactivos, posibles diferencias en los componentes de la reacción o por el número de ciclos. Sin embargo, la cuantificación en tiempo real del número de copias inicial de un gen se basa en el ciclo umbral (Ct), que se define como el número de ciclos al cual la fluorescencia es estadísticamente significativa sobre el ruido de fondo. Este valor de Ct es inversamente proporcional al logaritmo del número de copias iniciales de un gen y, por tanto, a menor valor de Ct mayor cantidad de moléculas iniciales existen.

La información cuantitativa basada en el Ct es más exacta que la información basada en las determinaciones a tiempo final debido a que están basadas en medidas tomadas a lo largo de la fase exponencial de amplificación por PCR, cuando la eficiencia de ésta no se ha visto afectada todavía por la limitación de reactivos, diferencias en la composición de la reacción o en los ciclos de la PCR.

Aunque existen varias estrategias de emisión de fluorescencia detectable en la PCR cuantitativa en tiempo real, en este trabajo se optó por el uso del fluoróforo *SYBR-Green I* (Molecular Probes) en dilución 1/150.000. Este compuesto es una molécula similar al bromuro de etidio que se intercala en la doble cadena de ADN emitiendo entonces su señal de fluorescencia. Debido a que su unión se produce a moléculas de doble cadena, en este caso fue más conveniente detectar la señal fluorescente emitida en el paso de extensión de la PCR (72 °C). Por esta misma razón, fue también necesario optimizar la temperatura de anillamiento de los cebadores que se iban a emplear para seleccionar una temperatura que redujera o eliminara completamente la formación de dímeros de cebadores y así evitar una interferencia en la señal de emisión. Posteriormente, y en caso de aparición de dímeros de cebadores, siempre se seleccionó la temperatura de medida de emisión de fluorescencia ligeramente por encima de la temperatura de disociación de los dímeros de cebadores. Esta temperatura se calculó a partir de las curvas de “*melting*” (ver más adelante). No obstante, los dímeros de cebadores, cuando aparecieron, lo hicieron en los ciclos finales de la PCR, donde no interfirieron con el valor de Ct del amplicón que apareció en los primeros ciclos de la reacción.

#### II.6.3.1. Reacción de retrotranscripción

La retrotranscripción de las muestras a analizar se llevó cabo empleando el kit *iScript<sup>TM</sup> cDNA Sintesis Kit* (BioRad) que, además de facilitar todo el proceso, incrementa la sensibilidad y el rendimiento de éste. La enzima *iScript* es una transcriptasa reversa modificada derivada de *MMLV* y optimizada para ser capaz de sintetizar cDNA a partir de un amplio rango de mRNA. La síntesis de la cadena de ss-ADNc se realizó siguiendo las

instrucciones de la casa comercial y empleando la mezcla de reacción y el programa de retrotranscripción detallados en el *apéndice 13*.

<i>Apéndice 13. Mezcla de reacción de retrotranscripción</i>		Programa empleado
ARN total [1µg/ml]	1 µl	1 ciclo de : 25 °C, 5 minutos 42 °C, 30 minutos 85 °C, 5 minutos 4 °C (mantenido)
Tampón iScript [5X]	4 µl	
<i>Transcriptasa reversa</i> (BioRad)	1 µl	
H <sub>2</sub> O tratada con DEPC	14 µl	
Volumen final	20 µl	

### II.6.3.2. Reacción de amplificación por PCR a partir de ADNc

A partir de los ADNc sintetizados previamente, se llevaron a cabo amplificaciones en tiempo real que permitieron comparar los niveles de transcrito correspondientes a los genes en estudio en condiciones experimentales frente a condiciones control. La reacción de amplificación en tiempo real se realizó en un *iCycler iQ system* (Bio-Rad) con capacidad para amplificar 96 muestras independientes de forma simultánea a las que se les asignó unas coordenadas individuales e identificables tanto por el ordenador como por el experimentador durante todo el proceso.

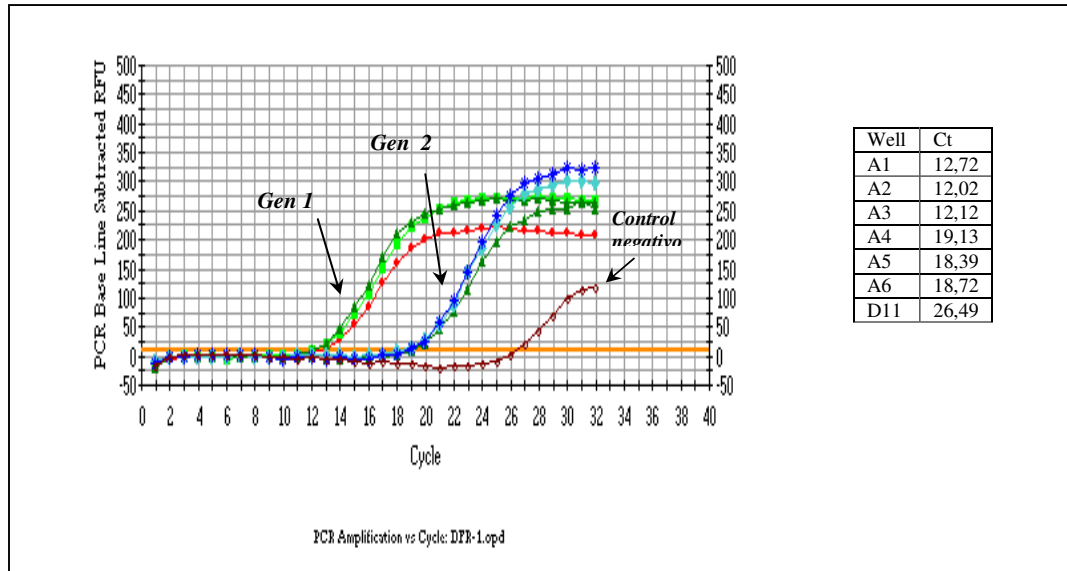
En primer lugar, se diseñó la distribución de las muestras en cada uno de los 96 pocillos de la placa de experimentación. En cada placa, se incluyeron por triplicado tanto las muestras correspondientes al gen control constitutivo, que sirvieron para normalizar los datos obtenidos en la PCR cuantitativa, como las correspondientes a los genes en estudio. Así, para cada gen, se realizaron tres reacciones independientes de PCR cuantitativa a partir de la misma muestra de ADNc en cada una de las situaciones experimentales analizadas que nos proporcionó una media del valor de Ct para cada muestra. Obligatoriamente, en cada placa de experimentación también se incluyó una muestra con 20 ng de ADN plasmídico correspondiente a cada uno de los genes en estudio incluidos en la placa, y dos muestras control sin ADN.

La mezcla de reacción de la PCR se preparó en hielo y estuvo compuesta por:

ADNc	3 µl
Tampón de PCR (Biotools) [10X]	3 µl
dNTPs (5 mM cada uno)	1,2 µl
Cebador 3' (2 µM)	3 µl
Cebador 5' (2 µM)	3 µl
<i>Taq polimerasa</i> (Biotools) (1 U/µl)	0,5 µl
<i>SYBR-Green I</i> (Molecular Probes) (1/150.000)	3 µl
H <sub>2</sub> O estéril hasta	30 µl

Para minimizar los errores por pipeteo, se preparó una mezcla madre para el total de muestras, tanto experimentales como control. Puesto que cada muestra se amplificó por triplicado (30 µl x 3), de la mezcla madre se tomaron 81 µl para cada muestra, a los que posteriormente se añadieron 9 µl de ADNc correspondiente a cada situación experimental (volumen final 90 µl). A continuación, se repartieron 25 µl de cada mezcla de reacción en cada uno de los pocillos manteniendo el orden previamente establecido para cada muestra y evitando la formación de

burbujas que impidieran una correcta detección de la fluorescencia emitida. Posteriormente, la placa se cubrió con una lámina transparente de plástico (Bio-Rad), evitando dejar alguna huella sobre la misma que pudiera interferir en la emisión de fluorescencia. Al sufrir esta lámina de plástico el primer calentamiento en el termociclador, la placa se sella completamente evitando la pérdida de muestra por evaporación. En general, en todas las amplificaciones realizadas se empleó el mismo programa básico recogido en la Tabla 4 de *Materiales y Métodos* y el resultado de cada amplificación se visualizó directamente para cada ciclo durante el transcurso de la reacción (Fig. 7).



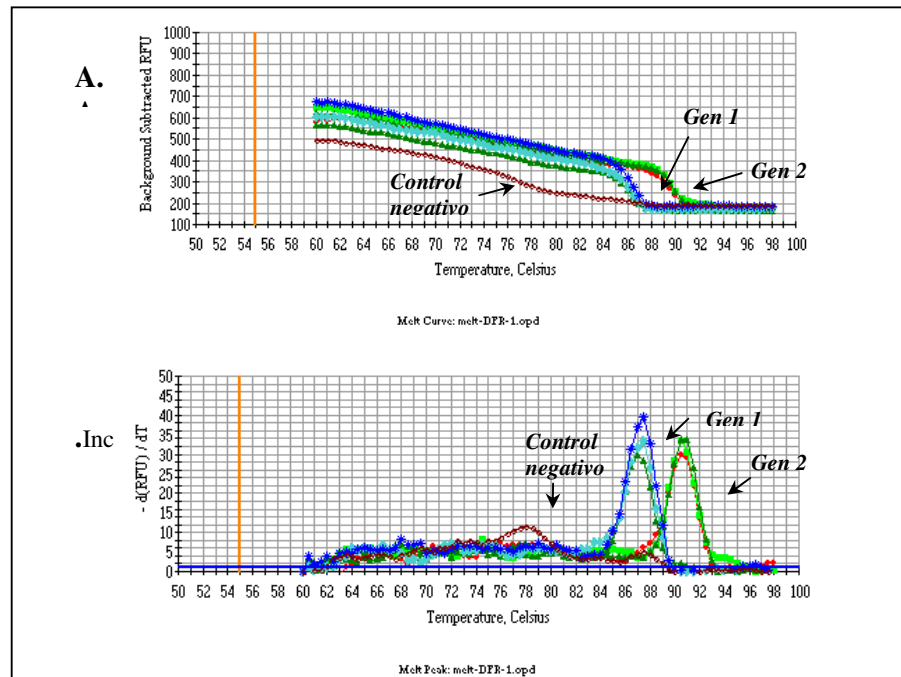
**Fig. 7. Ejemplo de curvas de amplificación en un *iCycler iQ* system (Bio-Rad).** Se muestran las curvas correspondientes a un gen problema (gen 1) y al gen espaciador 26S-18S (gen 2). También se representa la curva de amplificación correspondiente al control negativo (sin ADNc), cuya señal de fluorescencia corresponde a la formación de los dímeros de cebadores. En la tabla, se muestran los valores de Cts correspondientes a cada curva.

Una vez terminada la PCR, la placa con las muestras amplificadas se guardó a 4 °C y, posteriormente, se empleó para comprobar la coincidencia de los datos obtenidos en el análisis cuantitativo con los visualizados electroforéticamente en gel de agarosa al 1,2% (p/v) (*Materiales y Métodos*, apartado II.2.2.1).

### II.6.3.3. Curva de fusión de las muestras amplificadas

Terminada la amplificación de las muestras, éstas se sometieron a un programa de desnaturalización progresiva (“programa de *melting*”) (Tabla 5) que nos proporcionó una curva de fusión independiente (*curva de melting*) para cada muestra amplificadas (Fig. 8). Este programa se basa en el aumento progresivo de 0,5 °C de temperatura por ciclo, desde una temperatura inicial de 60 °C hasta una final de 95 °C. De esta manera, las moléculas de menor tamaño y con menos puentes de hidrógeno intercatenarios se disociarán antes que las de tamaño superior, que poseen un mayor número de puentes, detectándose una curva de fusión diferente para cada una de las especies moleculares existentes en la muestra. Por tanto, las curvas de “*melting*” se emplearon para detectar la presencia de diferentes amplicones en una

misma reacción de PCR, potencialmente pertenecientes a contaminantes (Fig. 8). También, fueron útiles para normalizar la reacción y eliminar el ruido de fondo de los dímeros de cebadores.



**Fig. 8.** Curva de *melting* correspondiente a los amplicones generados por QRT-PCR en el sistema *iCycler iQ system* (Bio-Rad). Se muestran las curvas de fusión correspondientes a un gen problema (gen 1) y al gen interespaciador 26S-18S (gen 2). **A**, señal de fluorescencia frente a temperatura; **B**, derivada de la señal de fluorescencia  $[-d(\text{RFU})/dT]$  frente a temperatura. No se observa la aparición de contaminantes, ya que sólo aparece un pico por muestra. Además, comprobamos que la temperatura de *melting* ( $T_m$ ) es constante para el amplicón correspondiente a cada gen.

	Temperatura	Duración	Repeticiones
1	95 °C	3 min	1
2	60 °C	30 seg	1
3	60 °C + 0,5 °C/ciclo	10 seg	78
4	4 °C	mantenido	

**Tabla 5.** Programa de “*melting*” empleado para la generación de curvas de fusión

#### II.6.3.4. Análisis de los datos

Invariablemente, siempre se analizaron en primer lugar las curvas de fusión obtenidas para todas las muestras incluidas en la placa en estudio y determinar así la existencia o no de dímeros de cebadores y de una o varias especies moleculares. Estos datos nos permiten confirmar que las amplificaciones cuantificadas se han realizado de forma específica y que los valores de  $C_t$  obtenidos corresponden únicamente al transcrito del gen en estudio.

Los valores de Ct se obtuvieron automáticamente a partir de una línea base que el programa define por defecto, aunque estos valores pudieron ser modificados para ajustar el análisis adecuadamente. Se estudió el comportamiento individualizado de cada curva obtenida a fin de desechar las curvas alteradas. El hecho de poseer tres datos por muestra permitió comparar los valores de Ct obtenidos en todos los casos y hacer una media de los valores fiables.

### II.6.3.5. Normalización y representación de los datos

Los valores de Ct obtenidos para cada una de las muestras analizadas fueron normalizados frente a los valores de Ct de un gen control constitutivo. La normalización permite corregir la concentración de ARN inicial por muestra en la RT y la eficiencia de la reacción de PCR de cada muestra.

En este trabajo se emplearon varios genes como control: el gen NDR1 y el gen que codifica la región interespaciadora 26S-18S, ambos de expresión constitutiva y constante en todas las condiciones experimentales analizadas. La secuencia de los cebadores empleados para la amplificación de los genes control se recoge en *Materiales y Métodos, apartado II.3.5.2*

En general, la normalización se llevó a cabo según la siguiente fórmula (Pedersen, 2001):

<p style="text-align: center;">Incremento de la expresión = <math>2^{-\Delta(\Delta Ct)}</math></p> <p>donde <math>\Delta Ct = Ct \text{ gen problema} - Ct \text{ gen constitutivo}</math>  y <math>\Delta(\Delta Ct) = \Delta Ct \text{ gen inducido} - \Delta Ct \text{ control}</math></p>
--

Una vez normalizados los datos, éstos se expresaron respecto al control del experimento o respecto a la muestra con menor valor de expresión, al que se le asignó un valor igual a la unidad. El resto de valores se representaron por comparación con éste. Para el análisis estadístico de los datos mediante la *t* de Student, se empleó el programa *GraphPad InStat* considerando un valor de confianza de  $p < 0.01$ , lo que nos permitió identificar diferencias estadísticamente significativas entre ellos.

#### **Apéndice 14: Soluciones, enzimas y kits empleados en RT-PCR**

*DNasa I* libre de *RNasas* (Pharmacia): 10 U/ $\mu$ l

Tampón de PCR [10X] (Ver Apéndice 10)

iScript cDNA Synthesis Kit (Bio-Rad)

## II.7. OBTENCIÓN Y ANÁLISIS DE LA PROTEÍNA RECOMBINANTE FaAAT2

### II.7.1. Aislamiento mediante RACE del ADNc completo correspondiente al gen *FaAAT2*

Se empleó el kit *Marathon<sup>TM</sup> cDNA Amplification Kit* (BD Biociences), siguiendo siempre el manual suministrado por la casa comercial ([www.clontech.com](http://www.clontech.com)). Así, a partir de una mezcla de *dsADNc Marathon* previamente obtenida, se realizó una amplificación selectiva empleando el cebador *API* (contenido en el ADNc) combinado independientemente con los oligonucleótidos específicos *FaSAAT-up* y *FaSAAT-low*, ambos diseñados a partir de la EST de secuencia parcial correspondiente al gen *FaAAT2*. De esta forma, se aislaron e identificaron dos fragmentos del ADNc del gen *FaAAT2*, uno hacia el extremo 3' y otro hacia el 5', que cuando se solaparon bioinformáticamente, dieron lugar a la secuencia teórica correspondiente al ADNc completo de dicho gen. La enzima empleada para la amplificación fue la *Taq Advantage* de alta fidelidad recomendada por la casa comercial. La mezcla de reacción y el programa de PCR utilizados se describen en el *Apéndice 15*.

<i>Apéndice 15. Mezcla de reacción de PCR</i>	Programa utilizado
Advantage buffer 2xPCR                      5 µl dNTPs (10 mM)                                    2 µl Cebador <i>API</i> (10 µM)                            1 µl Cebador <i>FaSAAT up o low*</i> (10 µM)        8 µl Advantage Polimerasa                            1 µl Marathon cDNA                                    5 µl H <sub>2</sub> O    35µl	94 °C, 30 segundos 94 °C, 5 segundos 60 °C, 20 segundos 68 °C, 3 minutos 78 °C, 10 minutos 4 °C mantenido  } 30 ciclos
*Ver secuencia en la Tabla 3 ( <i>apartado II.3.5.2</i> )	

El producto de la reacción de amplificación se fraccionó mediante electroforesis en gel de agarosa al 1% (p/v) y los fragmentos resultantes se purificaron a partir del gel utilizando el kit comercial *QIAquick® Gel Extraction Kit* (Qiagen), siguiendo las instrucciones de la casa comercial. La cantidad de ADNc obtenida se cuantificó mediante un espectrofotómetro *Nanodrop*. Los distintos fragmentos de *dsADNc-FaAAT2* amplificados se clonaron directamente en el vector comercial *pGEM T-Easy* mediante una reacción de ligación (*Materiales y Métodos, apartado II.3.4*).

La mezcla de ligación se incubó durante toda la noche a 4 °C y, posteriormente, a temperatura ambiente durante aproximadamente 2 horas. Del volumen total de la mezcla de ligación, se emplearon 10 µl para transformar una alícuota de células competentes de *E.coli DH5a*. A continuación, las células transformadas se sembraron en medio sólido LB suplementado con ampicilina (100 mg/ml), IPTG (20 mM) y X-Gal (80 mg/ml) y se dejaron crecer durante 12

horas a 37 °C. De los transformantes positivos obtenidos, se seleccionaron 25 colonias (blancas) que se comprobaron mediante PCR empleando oligonucleótidos específicos del gen *FaAAT2*. Paralelamente, para determinar la secuencia y orientación del inserto dentro del vector de clonación, se secuenciaron varios de los clones recombinantes positivos previamente analizados por PCR. Para ello, se utilizaron los cebadores universales *T7* y *SP6*. Mediante el ensamblaje de las secuencias de los diferentes fragmentos secuenciados, se obtuvo el ADNc teórico completo del gen *FaAAT2*. Éste sirvió como molde para diseñar cebadores específicos del extremo 5' (*FLAAT-up*) y 3' (*FLAAT-low*) (Tabla 3, *Materiales y métodos, apartado II.3.5.2*), que se emplearon para aislar físicamente el ADNc completo real correspondiente al gen *FaAAT2* a partir de una población de ADNc de estadio rojo (Fig. 9). Para todo el proceso de amplificación, se empleó la enzima de alta fidelidad *iProof DNA polimerasa*. La mezcla de reacción y el programa de PCR utilizados se describen en el Apéndice 16.

Apéndice 16. Mezcla de reacción de PCR	Programa utilizado
5XiProof HF Buffer                      10 µl dNTPs (5mM)                              2 µl <i>FLAAT-Forward*</i> (2 µM)                12,5 µl <i>FLAAT-Reverse*</i> (2 µM)                12,5 µl <i>iProof DNA polimerasa</i> 0,5 µl ADNc                                        2 µl H <sub>2</sub> O    10,5 µl  *Ver secuencia en la Tabla 3 ( <i>apartado II.3.5.2</i> )	98 °C, 1 minutos 98 °C, 10 segundos 55 °C, 30 segundos 72 °C, 50 segundos 72 °C, 5 minutos 4 °C mantenido <div style="display: inline-block; vertical-align: middle; margin-left: 10px;">             } 35 ciclos           </div>

El producto de la reacción de amplificación se fraccionó mediante electroforesis en un gel de agarosa al 1% (p/v) y el fragmento de ds-ADNc se extrajo y se purificó del gel utilizando el kit comercial *QIAquick® Gel Extraction Kit* (Qiagen). Tras su poliadenilación (Apéndice 17), el ADNc completo correspondiente al gen *FaAAT2* se volvió a purificar como se indica previamente y, a continuación, se subclonó en el vector de clonación *pGEM T-easy* (*Materiales y Métodos, apartado II.3.4*). Nuevamente, se transformó una lúcuota de células *E.coli DH5α* con la construcción obtenida, se seleccionaron transformantes positivos en medio sólido LB suplementado con ampicilina (100 mg/ml), IPTG (20 mM) y X-Gal (80 mg/ml), y varios de ellos fueron comprobados mediante PCR y secuenciación.

Apéndice 17. Mezcla de reacción de poliadenilación	Programa utilizado
10XPCR                                      5 µl Cl <sub>2</sub> Mg (50 mM)                            1,5 µl dATP (2 mM)                                1 µl <i>DNA polimerasa</i> 1 µl ADN    27 µl H <sub>2</sub> O    14,5 µl	72 °C, 20 minutos



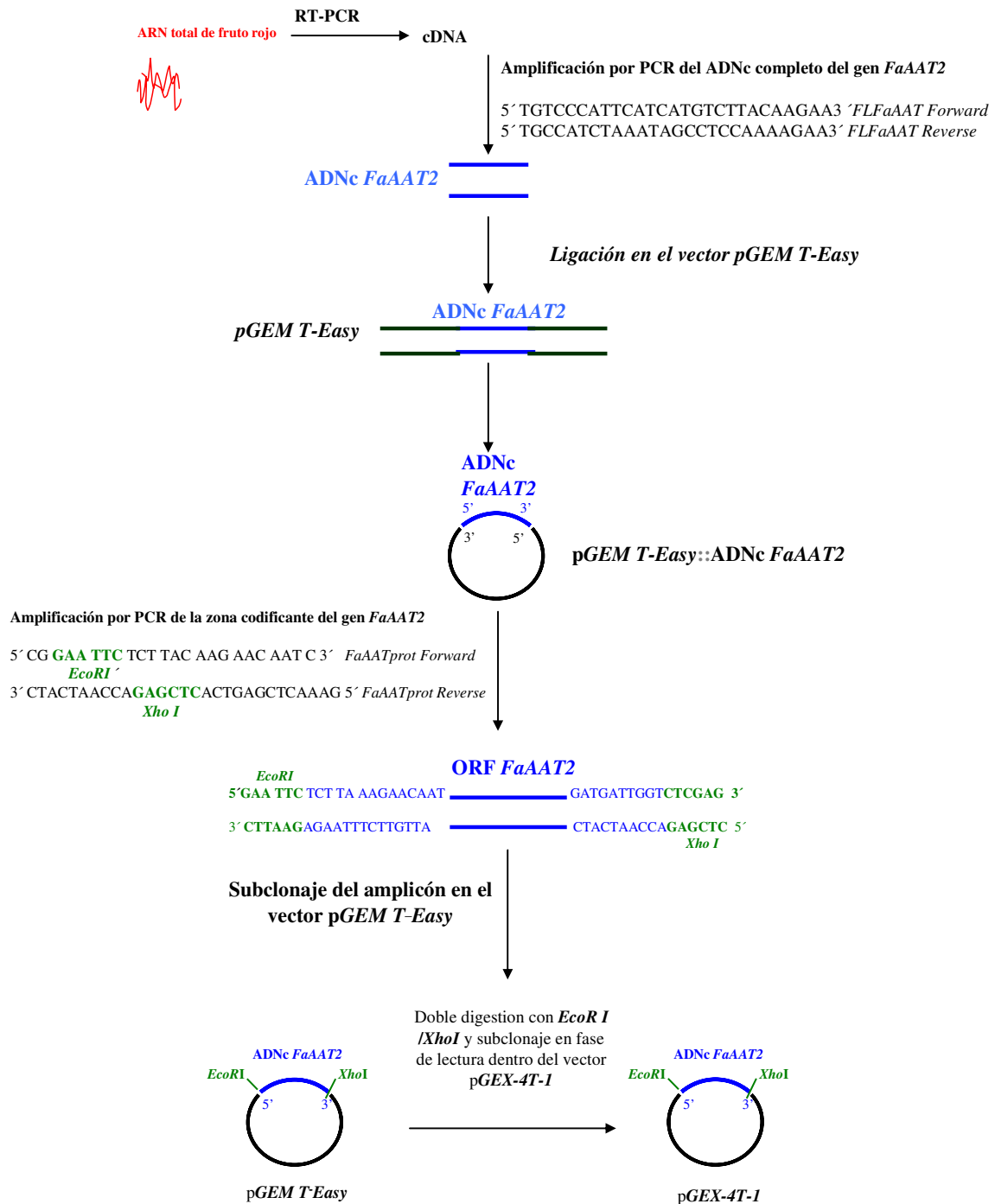


Fig. 9: Proceso de subclonaje del ADNc del gen *FaAAT2* en el vector de expresión *pGEX-4T-1*.

## II.7.2. Clonación del ADNc correspondiente al gen *FaAAT2* en el vector *pGEX-4T-1* (Amersham)

El ADNc completo correspondiente al gen *FaAAT2* se subclonó en fase de lectura dentro del vector de expresión *pGEX-4T-1* (Fig. 9) para obtener la proteína recombinante FaAAT2. Para ello, y para asegurarnos la amplificación de la región codificante completa del gen *FaAAT2*, se diseñaron dos cebadores específicos: uno en el extremo 5' en el cual se eliminó el codón ATG de la proteína y se incluyó un sitio de reconocimiento para la endonucleasa *EcoRI* (*FaAAT-prot-Forward*); y otro en el extremo 3' en el cual se eliminó el codón TGA de la proteína y se incluyó un sitio de reconocimiento para *XhoI* (*FaAAT-prot-reverse*). La amplificación del ADNc completo con ambos cebadores facilitó posteriormente su subclonaje en fase de lectura dentro del vector de expresión. Para dicha amplificación, se empleó *iProof DNA polimerasa* de alta fidelidad. La mezcla de reacción y el programa de PCR empleados se detallan en el Apéndice 18.

Apéndice 18. Mezcla de reacción de amplificación		Programa utilizado	
5XiProof HF Buffer	10 µl	98 °C, 1 minutos	} 35 ciclos
dNTPs (5 mM)	2 µl	98 °C, 10 segundos	
<i>FaAATproForward</i> * (2 µM)	12,5 µl	55 °C, 30 segundos	
<i>FaAATprotReverse</i> * (2 µM)	12,5 µl	72 °C, 50 segundos	
<i>iProof DNA polimerasa</i>	0,5 µl	72 °C, 5 minutos	
ADNc	2 µl	4 °C mantenido	
H <sub>2</sub> O	10,5 µl		
*Ver secuencia en la Tabla 3 (apartado II.3.5.2)			

El producto de la reacción de amplificación se visualizó electroforéticamente. El fragmento de ds-ADNc correspondiente al gen *FaAAT2* se extrajo y se purificó del gel utilizando el kit comercial *QIAquick® Gel Extraction Kit* (Qiagen) siguiendo las instrucciones de la casa comercial. A continuación, el fragmento de ADN purificado se poliadeniló (Apéndice 17), se volvió a purificar con *QIAGEN® Plasmid Mini Kit* (Qiagen), y finalmente se subclonó en el vector *pGEM T-Easy* (Materiales y Métodos, apartado II.3.4).

Seguidamente, se procedió al subclonaje de la región codificante completa correspondiente al gen *FaAAT2* en el vector de expresión *pGEX-4T-1*. Para ello, tanto el *dsADNc-FaAAT2* (previamente clonado en *pGEM T-Easy*), como el propio vector *pGEX-4T-1* se digirieron con las enzimas de restricción *EcoRI* y *XhoI* para generar extremos cohesivos complementarios. Para evitar la recircularización del vector digerido y aumentar así el rendimiento de la ligación, se procedió a su desfosforilación con *CIAP* (Materiales y Métodos, apartado II.3.4). Una vez que vector e inserto estuvieron digeridos y purificados con el kit comercial *QIAquick® Gel Extraction Kit* (Qiagen), ambos se sometieron a una reacción de ligación con una relación vector:inserto de 1:5 (Materiales y Métodos, apartado II.3.4). La reacción se incubó a 4 °C toda la noche y, transcurrido este tiempo, a temperatura ambiente aproximadamente 2 horas. A continuación, se transformó una alícuota de células competentes *E.coli DH5α* con el total de la reacción de ligación y éstas, una vez transformadas, se sembraron en medio LB suplementado con ampicilina (100 mg/ml) y se dejaron crecer al menos 12 horas a 37 °C. Del total de colonias positivas obtenidas, se seleccionaron 10 para

determinar si la construcción *pGEX-4T-1::FaAAT2* estaba bien. Se purificó ADN plasmídico de todas las colonias positivas seleccionadas y, mediante digestión con *EcoRI* y *XhoI*, se liberó el inserto de *ADNc-FaAAT2* para comprobar el tamaño del mismo mediante electroforesis. Así mismo, para confirmar que el fragmento de *ADNc-FaAAT2* estaba en la fase de lectura correcta (“*frame*”) dentro del vector de expresión *pGEX-4T-1*, se procedió a la secuenciación del ADN plasmídico procedente de varios clones recombinantes independientes empleando los cebadores específicos *pGEX5'* y *pGEX3'*. Las secuencias obtenidas confirmaron que el gen *FaAAT2* había entrado en el marco de lectura adecuado e inmediatamente después del gen que codifica la proteína *GST* dentro del vector de expresión *pGEX-4T-1*. De todos los clones positivos analizados y secuenciados, se seleccionó uno para su uso en experimentos posteriores de inducción de la proteína recombinante de fusión. Previamente, hubo que transformar con la construcción correspondiente células competentes *E.coli BL21* (*Materiales y Métodos, apartado II.4.2*). Los transformantes positivos, en esta ocasión, se seleccionaron en medio LB suplementado con ampicilina (100 mg/ml) y cloranfenicol (100 mg/ml).

### **II.7.3. Inducción de la proteína recombinante de fusión GST-FaAAT2**

Para la inducción de la proteína de fusión GST-FaAAT2, se crecieron a 37 °C en medio LB suplementado con ampicilina y cloranfenicol (ambos a 100 mg/ml) durante 12 horas, varios cultivos de células de *E.coli BL21* conteniendo la construcción *pGEX4T-1::FaAAT2*. Al día siguiente, empleando como inóculo 3 ml de los cultivos anteriores, se crecieron nuevos cultivos en presencia de ampicilina y cloranfenicol en matraces de 300 ml para permitir una correcta aireación del medio. Éstos se mantuvieron a 37 °C en agitación hasta alcanzar una D.O.~0,6, momento en el que se procedió a la inducción de la proteína recombinante mediante la adición de IPTG a una concentración final de 1 mM. El cultivo inducido se dejó crecer a 16 °C y 150 rpm durante unas 12 horas, parámetros óptimos para la obtención de una concentración apropiada de proteína recombinante.

### **II.7.4. Purificación de la proteína recombinante FaAAT2**

Una vez inducida la proteína recombinante, las células se recogieron mediante centrifugación a 5.000 rpm durante 15 minutos a 4 °C. El pellet obtenido se congeló a -80 °C durante 15 minutos y, una vez transcurrido ese tiempo, se resuspendió en 8 ml de tampón de lavado 1X. La suspensión se transfirió a un tubo Falcon y, siempre en hielo, se sonicó 30 segundos con un 10% de energía, al menos 3 veces. A continuación, la muestra se centrifugó nuevamente a 18.000 rpm durante 20-30 minutos a 4 °C para recuperar la proteína total soluble, incluida la proteína recombinante, liberada tras la sonicación y en suspensión en el sobrenadante de la muestra.

La purificación de la proteína recombinante FaAAT2 se llevó a cabo mediante el empleo de *GST-Sepharose* (Novogen). Previamente a la purificación se dispuso una alícuota de *GST-Sepharose* (Novogen) (500 µl) en un tubo Falcon de 15 ml y ésta se lavó varias veces con 4 ml de tampón de lavado 1X frío. A continuación, el sobrenadante con la proteína recombinante en suspensión se incubó a 4 °C en agitación con la resina durante, al menos, 30 minutos para favorecer la interacción de la GST fusionada a la proteína recombinante FaAAT2 con la resina. Transcurrido el periodo de incubación, la mezcla se centrifugó en frío a 800 g durante 3 minutos y el pellet obtenido se lavó varias veces con 8 ml de tampón de

lavado. Posteriormente, la muestra se incubó 5 minutos a temperatura ambiente en 200  $\mu$ l de tampón de elución y, tras centrifugarla a 800 g durante 5 minutos, recogimos el sobrenadante (Fracción 1 de la proteína total). La muestra se volvió a incubar durante 5 minutos en 200  $\mu$ l de tampón de elución en las mismas condiciones anteriores y, nuevamente, recogimos el sobrenadante (Fracción 2 de la proteína total).

**Apéndice 19. Soluciones empleadas para la inducción y purificación de la proteína recombinante**

**Medio LB** (Apéndice 1)

**10X Tampón de lavado, pH 7.3**

43 mM  $\text{Na}_2\text{HPO}_4 \times 7 \text{ H}_2\text{O}$   
 14,7 mM  $\text{KH}_2\text{PO}_4$   
 1,37 M NaCl  
 27 mM KCl

**10X Tampón de reconstitución, pH 8.0**

500 mM Tris-HCl

**1X Tampón de elución:** 1X Tampón de reconstitución + 10 mM Glutathion

## II.7.5. Análisis de la proteína recombinante FaAAT2

### II.7.5.1. Cuantificación de la proteína recombinante

La concentración de proteína recombinante obtenida en la inducción se determinó por el método de *Bradford* (Bradford, 1976). Para ello, se hicieron por duplicado medidas de cada muestra añadiendo un volumen variable de muestra (100  $\mu$ l como máximo) y 900  $\mu$ l de reactivo *Bradford* (“Protein Assay”, BioRad) diluido cinco veces con  $\text{H}_2\text{O}$  destilada. La medida espectrofotométrica se realizó a una longitud de onda de 595 nm y el valor de la proteína total final se expresó en  $\mu$ g de proteína/ml de extracto. El cálculo de la concentración de proteína problema final se realizó a partir de una recta de calibrado realizada con concentraciones conocidas de BSA.

### II.7.5.2. Separación electroforética de la proteína recombinante en SDS-PAGE

La identificación y el aislamiento de la proteína recombinante FaAAT2-GST se llevó a cabo en geles de acrilamida. Previamente a la electroforesis, las muestras fueron tratadas con *ROTI LOAD* (Roth), tampón de carga especial que estabiliza y protege los enlaces péptidicos de las proteínas evitando su degradación. Así, a cada 10  $\mu$ l de muestra se añadieron 3.3  $\mu$ l de *ROTI LOAD* y la mezcla se incubó 3 minutos a 95 °C. Paralelamente, se polimerizó el gel *Tris-Glycin-SDS* (*Progel Tris-Glycin 12% 1.0 mm, ANAMED*) y se introdujo en un tanque con tampón 1X Tris/Glicina. La electroforesis se realizó a 30 mA, 40 W y 150 V durante 1h. Finalizado este tiempo, el gel se tiñó durante 30 minutos en una solución de azul de *Coomassie G250* al 0,25% (p/v) (Apéndice 20). El exceso de colorante se eliminó posteriormente con solución de lavado en agitación suave durante el tiempo necesario para visualizar las bandas correspondientes a las proteínas.

**Apéndice 20. Soluciones empleadas para la electroforesis de geles de poliacrilamida**

**Tampón 10X Tris/Glicina** (no es necesario ajustar el pH)  
30,29 g (0,25 M) Tris-Base (121,14 g/mol) (RT); 144,13 g (1,92 M) Glicina (75,07 g/mol) (RT). Hasta 1 l con H<sub>2</sub>O MQ

**Apéndice 21. Soluciones empleadas para la coloración/decoloración de geles de poliacrilamida**

**Solución de tinción**

0,33 g Coomassie en 120 ml Metanol  
24 ml CO<sub>2</sub>COOH  
120 ml H<sub>2</sub>O

**Solución de lavado**

7% CH<sub>3</sub>COOH  
10% Metanol

## II.7.6. Determinación de la actividad enzimática FaAAT2

### II.7.6.1. Ensayo de la actividad enzimática *in vivo*

A varios cultivos de *E.coli* (20 ml) con la proteína recombinante FaAAT2 inducida, se les añadió diferentes alcoholes (10  $\mu$ M) que, utilizando los acil-CoA endógenos de *E.coli*, podrían dar lugar a las correspondientes reacciones de esterificación. Como controles, se empleó un cultivo bacteriano portador del vector *pGEX-4T-1* vacío y otro portador de la construcción *pGEX4T-1::FaAAT2* sin inducir. Todos los cultivos sometidos a análisis, tanto los controles como el problema, fueron incubados a 16 °C y 120 rpm durante 18 h. Transcurrido ese tiempo, se llevó a cabo la extracción de volátiles añadiendo 5 ml de hexano a cada cultivo. Para asegurar la extracción, la muestra se mantuvo en agitación a temperatura ambiente durante 15 minutos. Transcurrido este tiempo se separó el hexano del cultivo y, a continuación, se concentró con nitrógeno gaseoso hasta un volumen de 200  $\mu$ l. De este volumen se inyectaron 3  $\mu$ l en el equipo de cromatografía de gases-espectrometría de masas (GC-MS), procediendo de este modo a la cuantificación de los diferentes compuestos volátiles obtenidos. Se utilizaron dos tipos de columna para su análisis, dependiendo del número de carbonos de los alcoholes empleados en los ensayos. Así, para alcoholes de C1-C4 se utilizó una columna ZB-WAX [Zebron/phenomenex, (60 m X 0,32 mm i.d., 0,25  $\mu$ m), mientras que para alcoholes de C5-C10 se empleó una columna HP-5MS [J&WScientific, (30 m X 0,25 mm i.d., 0,5  $\mu$ m). En todos los casos, la temperatura del inyector y del detector fue de 250 °C. La temperatura del programa oscilaba de 40 °C (1 minuto) a 60 °C (1 minuto) en un rango de 2 °C min<sup>-1</sup> y mantenido a 190 °C (5 minutos) en un rango de 10 °C min<sup>-1</sup>. Los compuestos fueron identificados comparando su tiempo de retención con el de los productos estándares.

### II.7.6.2. Ensayo de la actividad enzimática *in vitro*

Tras el proceso de inducción y purificación, la actividad de la proteína recombinante FaAAT2 fue ensayada en un volumen total de 500  $\mu$ l para determinar su especificidad tanto por distintos grupos acil-CoA, como por diferentes alcoholes (*Apéndice 22*). En general, el ensayo se llevó a cabo incubando la mezcla de reacción durante 20 minutos a 30 °C en agitación y añadiendo, inmediatamente después, 1-Nonanol 1mM como compuesto estándar (alcohol que no utiliza la proteína FaAAT2 como sustrato). A continuación, a la mezcla de reacción se le añadió 1 ml de hexano. La muestra se mantuvo en agitación durante 15 minutos a temperatura ambiente y, finalmente, se recuperó el hexano portando los compuestos volátiles extraídos junto con el compuesto estándar. Esta muestra se concentró con nitrógeno gaseoso hasta 200  $\mu$ l y, mediante GC-MS, se procedió a su análisis de la misma manera que en el *apartado II.7.6.1 de Materiales y Métodos*.

<i>Apéndice 22</i>	Determinación de la especificidad por el grupo acil-CoA	Determinación de la especificidad por diferentes alcoholes
Tampón Tris-HCl 50mM pH 7,5, 10% glicerol, 1mM DTT	X	X
Alcohol	Concentración de saturación 20 mM	Varias concentraciones (1 mM, 5 mM, 10 mM, 20 mM, 60 mM)
Acil-CoA	Varias concentraciones (0,01 mM, 0,1 mM, 0,25 mM, 1 mM, 2,5 mM)	Concentración de saturación 0,1 mM
FaAAT2 recombinante	2 $\mu$ g	2 $\mu$ g
Volumen final	500 $\mu$ l	500 $\mu$ l

Los diferentes compuestos obtenidos se identificaron a través de su espectro de masas tomando como referencia la biblioteca *NIST MS* y los tiempos de retención de los diferentes compuestos estándares empleados (Sigma o Fluka) (*Apéndice 23*).

### II.7.7. Estudios cinéticos de la actividad enzimática FaAAT2

Los parámetros cinéticos de la actividad enzimática correspondiente a la proteína recombinante FaAAT2 se determinaron mediante el programa informático *HYPER32.exe* (*Version 1.0.0, 2003 de MS Windows*).

**Apéndice 23. Compuestos estándares utilizados para identificar los diferentes compuestos volátiles**

Bencil acetato (Sigma)	Etil hexanoato (Sigma)	Metil acetato (Fluka)
Bencil propanoato (Sigma)	Eugenil acetato (Sigma)	Isoamil acetato (Sigma)
Bencil butirato (Sigma)	Eugenil butirato (Sigma)	Linaloil acetato (Sigma)
Bencil hexanoato (Sigma)	Eugenil propanoato (Sigma)	Metil propanoato (Fluka)
1-Butil acetato (Sigma)	Farnesil acetato (Sigma)	Metil butirato (Fluka)
1-Butil propanoato (Sigma)	2-Feniletil acetato (Sigma)	Metil hexanoato (Fluka)
1-Butil butirato (Sigma)	2-Feniletil propanoato (Sigma)	Neril acetato (Sigma)
1-Butil hexanoato (Sigma)	2-Feniletil butirato (Sigma)	Nerolidil acetato (Sigma)
2-Butil acetato (Sigma)	Furfuril acetato (Sigma)	Nonil acetato (Sigma)
Cinnamil acetato (Sigma)	Geranil acetato (Sigma)	Octanoil acetato (Sigma)
Cinnamil propanoato (Sigma)	Geranil propanoato (Sigma)	Octanoil propanoato (Sigma)
Cinnamil butirato (Sigma)	Geranil butiarto (Sigma)	Octanoil butanoato (Sigma)
Cinnamil hexanoato (Sigma)	Geranil hexanoato (Sigma)	Octanoil hexanoato (Sigma)
Decil acetato (Sigma)	Hexanoil acetato (Sigma)	1-octen-3-il acetato (Sigma)
Etil acetato (Sigma)	Hexanoil propanoato (Sigma)	Pentil acetato (Sigma)
Etil propanoato (Sigma)	Hexanoil butirato (Sigma)	Propanoil acetato (Sigma)
Etil butirato (Sigma)	Hexanoil hexanoato (Sigma)	Terpenil acetato (Sigma)

**II.8. MICROARRAYS****II.8.1. Análisis bioinformático de secuencias ESTs**

Mediante el uso de programas informáticos incluidos en la página web *EGassembler* (<http://egassembler.hgc.jp/>) (Masoudi-Nejad *et al.*, 2006), se procesaron un total de 42960 ESTs de fresa. La aplicación de estos programas elimina las colas poli-T, el vector, adaptadores de secuencias, repeticiones simples, repeticiones intercaladas, pequeños ARN, secuencias de baja complejidad y secuencias con menos de 100 pb de longitud y que contienen más de un 3 % de N. Después de esta primera filtración, se excluyeron las secuencias componentes de la librería de *Arabidopsis RepBase* (en su mayoría retroelementos y secuencias de transposones de ADN) empleando el método *slow* (0-5 % más sensible). Además, se eliminaron las secuencias correspondientes al vector y a orgánulos mediante la aplicación de las bases de datos *Core NCBI's vector* y *Arabidopsis plastid* respectivamente. Una vez que las secuencias fueron procesadas, las ESTs se ensamblaron y se agruparon utilizando el programa *CAP3*, incluido en el *EGassembler service*, con un solapamiento máximo de 20 bases, un punto de corte de identidad mayor al 75% y un valor umbral de similitud de 700. Además, *EGassembler service* proporciona las secuencias de los *contigs* completamente alineadas como un archivo de texto, y esto fue comprobado visualmente para tener una idea aproximada de la calidad de las secuencias obtenidas. Se obtuvieron 8640 *contigs* y 26574 *singletons*, lo que genera un total de 35214 secuencias ESTs analizadas.

Mediante el programa *JAVA Blast2GO* (ejecutado en el sistema Windows) se realizaron búsquedas y anotaciones funcionales similares de las secuencias ensambladas que contenían *contigs* y *singletons* (Götz *et al.*, 2008). Este procedimiento se hizo en varios pasos consecutivos para intentar asignar una función al mayor número de secuencias posible. Inicialmente, se realizó una búsqueda con BlastX, usando la base de datos de proteínas de NCBI, y considerando 1.0 E-05 como valor umbral de una similitud significativa. Todas las secuencias que se obtuvieron mediante BlastX se emplearon para obtener Ontología de Genes

(GO), en InterPro, Enzimas y anotaciones funcionales adicionales KEGG. Sin embargo, para el análisis y generación de tablas y gráficos se excluyeron aquellas secuencias con valores de  $e$  superiores a  $1.0 \times 10^{-15}$ . Las anotaciones de Ontología de Genes (GO) se realizaron utilizando la base de datos *GO Blast2GO* depositados en el servidor español desde mayo de 2010.

Finalmente, el conjunto de secuencias que no aparecieron en el BlastX se analizaron mediante BlastN y tBlastX independientemente con el propósito de asignar secuencias ausentes de las bases de datos de proteínas. Debido a que las bases BlastN y tBlastX se usan para el análisis de secuencias de ADN, dichas secuencias no pudieron ser anotadas mediante GO e InterPro como el resto.

## II.8.2. Generación y análisis de *Microarrays*

En este trabajo, los diferentes análisis transcriptómicos realizados se llevaron a cabo con un microarray de oligos (60 *mer length*) diseñado por *Nimblegen Systems Inc.* a partir de secuencias no redundantes de *Fragaria x ananassa* y *Fragaria vesca*. Se imprimieron un mínimo de 4-6 oligos por cada sonda en cuatro bloques independientes. Las muestras de ARN total fueron tratadas con *DNaseI* (Apéndice 12) y después se purificaron mediante columnas de *Qiagen* de acuerdo con el protocolo suministrado en el *kit*. Tanto el marcaje de las muestras (con Cy3), como la hibridación con cuatro sondas y la normalización de datos se realizaron por *Nimblegen Systems Inc.* siguiendo el procedimiento de análisis de expresión descrito en <http://www.nimblegen.com/>. En resumen, 10  $\mu\text{g}$  de ARN total de receptáculo fueron procesados usando el sistema de síntesis de ADNc de *Roche*, optimizado para la obtención de ADNc de doble cadena. Dicho ADNc fue purificado mediante el *kit High Pure PCR Product Purification* y las muestras obtenidas fueron sometidas a retrotranscripción. Se realizaron tres réplicas de las reacciones para cada muestra de ARN total. Cada muestra de ADNc fue marcada con Cy3 de acuerdo al protocolo de *Roche NimbleGen's* empleando el *kit NimbleGen One-Color DNA Labeling*. Siempre se empleó 1  $\mu\text{g}$  de cDNA para las reacciones de marcaje. Mediante una asignación aleatoria, cada muestra de ADNc marcada con Cy3 se aplicó al array de fresa diseñado con formato *12x135K* (cada porta contenía 12 matrices independientes con 140.856 sondas cada una que cubrieron 35.214 genes, 4 sondas/genes diana). La matriz se hibridó durante 16 horas a 42 °C, se lavó, se secó y se escaneó con un *NimbleGen MS 200 Microarray Scanner* (*Roche NimbleGen*) a una resolución de 2  $\mu\text{m}$ . El software *NimbleScan v2.6* (*Roche NimbleGen*) se usó para la normalización de las señales de intensidad de fluorescencia de las imágenes escaneadas y, posteriormente, se llevó a cabo un análisis *Robust Multi-Array* (RMA) para generar los valores de expresión génica. El RMA se realizó a través de réplicas del array en cada condición testada y de la muestra.

El análisis de los datos de expresión obtenidos se llevó a cabo con el software de análisis de expresión génica *ArrayStar* (DNASTAR). Finalmente, el análisis estadístico de los datos mediante la  $t$  de Student y FDR (Benjamini-Hochberg, 1995) se llevó a cabo con un valor de confianza de  $p < 0.01$ , lo que nos permitió identificar diferencias estadísticamente significativas entre ellos.



## II.9. EXTRACCIÓN DE COMPUESTOS VOLÁTILES Y ANTOCIANINAS DEL FRUTO DE FRESA.

### II.9.1. Extracción de compuestos volátiles

El tejido de fruto de fresa congelado (1g) se trituró en presencia de N<sub>2</sub> líquido y el polvo obtenido se sometió a la extracción de compuestos volátiles mediante SPME (Solid phase microextraction) y empleando 50 µl de 1,2-dimetoxietano (0,965 nmol/l) como estándar. La homogenización de la muestra se realizó con un vortex, aproximadamente durante 30 segundos, para asegurar la mezcla completa de los reactivos. A continuación, se añadió a la mezcla 1 ml de NaCl 35% (p/v) y, tras una nueva homogenización, la muestra se incubó a 30 °C durante 30 minutos en SPME con una fibra de 85 µm de polidimetilsiloxano/carboxeno (Carboxen/PDMS) (Supelco; 57295-U). Finalizada la extracción de los compuestos volátiles, se procedió a su desorción en una columna ZB-WAX [Zebron/phenomenex, (60 m X 0,32 mm i.d., 0,25 µm)] mediante GC-MS (Cromatografía de gases-espectrometría de masas) durante 10 minutos a 220 °C. La temperatura del programa empleado fue entre 40 °C (1min) a 60 °C (1 min) en un rango de 2 °C min<sup>-1</sup> y mantenido a 190 °C (5 min) en un rango de 10 °C min<sup>-1</sup>. En el caso del inyector y del detector, las temperaturas empleadas fueron 200 y 250 °C respectivamente. Finalmente, el espectro de masas se obtuvo por una ionización del electrón de 70 eV con un rango de espectro de 29-400 *m/z*.

Los diferentes compuestos obtenidos se identificaron a través de su espectro de masas, tomando como referencia la biblioteca *NIST MS* y los tiempos de retención de los diferentes compuestos estándar que se emplearon para los ensayos *in vitro* de la proteína recombinante FaAAT2 (Sigma o Fluka) (Apéndice 23). Por otra parte, la concentración de los compuestos volátiles obtenidos se calculó tomando como referencia el sustrato estándar 1,2-dimetoxietano (0,965 nmol/l), y teniendo en cuenta tanto el área de los diferentes compuestos volátiles y sus concentraciones, como el área del estándar. En general, se aplicó la fórmula:

$$\text{Concentración volátil} = \text{Concentración Estándar} / \text{Área estándar} \times \text{Área volátil}.$$

### II.9.2. Extracción de antocianinas y flavonoides

Para la determinación del contenido de antocianinas totales en fruto de fresa (Bustamante *et al.*, 2009), los frutos seleccionados (0,3 g de tejido) se homogenizaron en presencia de N<sub>2</sub> líquido hasta obtener un polvo fino. Este polvo se transfirió a un tubo estéril que contenía 3 ml de ácido clorhídrico:metanol (v/v) al 1% y la mezcla se incubó a 0 °C durante 10 minutos. Transcurrido este tiempo, la muestra se centrifugó a 1.500 g durante 10 minutos a 4 °C y al sobrenadante recuperado se le midió la absorbancia a una longitud de onda de 515 nm. La concentración de antocianinas presente en la solución obtenida se determinó empleando el valor 36,000 L.mol<sup>-1</sup>.cm<sup>-1</sup> como coeficiente de extinción molar (Woodward, 1972). Cada experimento se repitió tres veces.

Para la determinación de flavonoides, se emplearon 50 mg de fruto de fresa liofilizado. La extracción se llevó a cabo con 250  $\mu\text{l}$  de metanol conteniendo 4-metilumbeliferil o D-glucuronido (0.2 mg/mL) como estándar interno. La mezcla obtenida fue sonicada durante 5 minutos en un baño de ultrasonidos (Bandelin Sonopuls GM 2017) y centrifugada a 13.200 rpm durante 10 minutos. Al sobrenadante obtenido se le añadió de nuevo 500  $\mu\text{l}$  de metanol y se sometió a un nuevo proceso de sonicación y centrifugación como el descrito anteriormente. Finalmente, la muestra obtenida fue concentrada al vacío durante 2 horas aproximadamente y resuspendida en 35  $\mu\text{l}$  de agua para su análisis posterior mediante LC-ESI-MSN (sistema compuesto por un espectrómetro de masas Bruker Daltonics 3000 plus (Agilent 1100 HPLC, Agilent Technologies), equipado con un detector de longitud de onda variable). Los diferentes componentes de la muestra se separaron mediante una columna Phenomenex Luna C-18 (150 mm de largo x 2,0 mm id, tamaño de partícula 5  $\mu\text{m}$ ) a 25 °C. El gradiente lineal utilizado fue de 100 % tampón A (0,1 % ácido fórmico en agua) hasta 100 % de tampón B (0,1 % ácido fórmico en metanol) durante 30 minutos con un flujo de 0,2 mL / min. Los parámetros de LC utilizados fueron 0-50 % de B durante 0-30 minutos después de 35-50 minutos de 50 % a 100 % de B volviendo a 100-0 % de B durante 50-65 minutos. La longitud de onda utilizada osciló entre 520 nm (antocianidinas) y 280 nm (análisis de otros metabolitos y sustratos). El ESI del capilar se fijó de -4000 V a -500 V. Como gas seco se empleó nitrógeno a una temperatura de 330 °C y un flujo de 9 L / min. Los espectros de masas oscilaron entre 100 y 800 m / z. Las medidas en el MS se llevaron a cabo utilizando helio como gas de colisión ( $3.56 \times 10^{-6}$  mbar) con 1V de voltaje de colisión. Los espectros fueron adquiridos en el modo de ionización positiva y negativa y los datos fueron analizados empleando el software 5.1 DataAnalysis (Bruker Daltonics).

### II.9.3. Extracción de ABA

Para la extracción de ácido abscísico a partir de frutos de fresa, se empleó como estándar interno ácido abscísico deuterado (dABA). Durante su preparación, los protones del anillo del ABA (5 mg) se intercambiaron durante al menos 48 horas en 10 ml de agua pesada (Sigma: pureza isotópica 99,96%) a temperatura ambiente y en presencia de hidróxido de sodio 1M deuterado (Sigma: pureza isotópica 99%) (Rock and Zeevaart, 1990). El medio se acidificó con ácido clorhídrico a pH 3. La solución ácida se mezcló con éter dietílico (50:50 v/v), se centrifugó a 5000 g durante 10 minutos a temperatura ambiente y se desecó a 35 °C. Las muestras que contenían [H] se disolvieron en metanol. La pureza del [ $^2\text{H}_6$ ]-ABA fue evaluada mediante HPLC en las condiciones indicadas a continuación.

En la extracción de ABA se empleó 1 g de fruto de fresa (*Materiales y Métodos, apartados II.2.1.2 y II.2.1.3*) que fue homogenizado en  $\text{N}_2$  líquido hasta obtener un polvo fino. La muestra triturada fue colocada en un vaso de vidrio de 50 ml y se mezcló con 1,26 nmol del estándar interno (40  $\mu\text{l}$  de 31,5 nmol  $\text{mL}^{-1}$ ) mediante agitación durante 5 minutos. La mezcla obtenida se extrajo dos veces con 10 ml de metanol / agua pH 5.5 (50:50 v / v) en agitación durante 30 minutos y posteriormente fue centrifugada a 5000 g durante 5 minutos a temperatura ambiente. El sobrenadante fue recogido y extraído por duplicado con 10 ml de diclorometano. Los extractos de diclorometano obtenidos fueron centrifugados a 5000 g durante 5 minutos a temperatura ambiente y la fase inferior se dejó evaporar a 40 °C. El residuo se disolvió en 100  $\mu\text{l}$  de acetona 100% y en 250  $\mu\text{l}$  de agua / acetonitrilo (70:30 v / v) (0,1% ácido fórmico). Finalmente, la muestra se centrifugó a velocidad máxima durante 5 minutos utilizando el sobrenadante recuperado para su medida por HPLC-MS (1200 L Triple Quadrupole). El volumen de inyección fue 8  $\mu\text{l}$  y la columna empleada fue C18 Phenomenex, con una i.d. 150x2.1 mm y un tamaño de partícula de 3  $\mu\text{m}$ . La fase móvil empleada estuvo

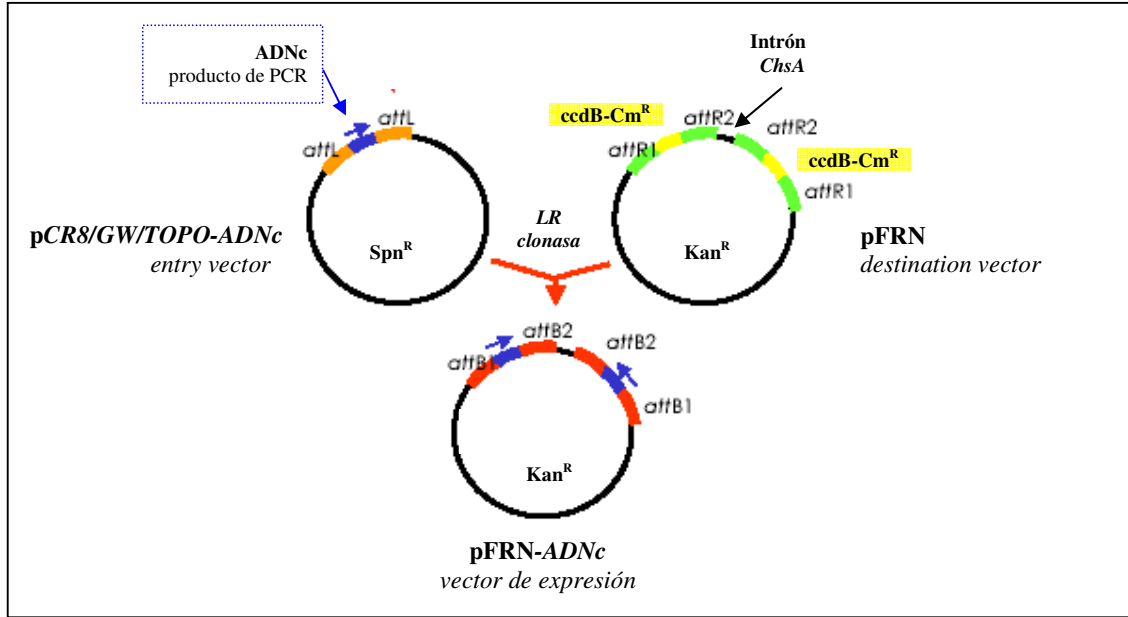
compuesta de agua / acetonitrilo (70:30 v / v) (0,1% ácido fórmico), con un flujo de 0.2 mL min<sup>-1</sup>. La MS constó de un sistema SIM (Selecting Ion Monitoring) y el flujo de N<sub>2</sub> empleado (calidad LCMS) fue de 50 L/h. La tensión del capilar fue de 5,5 kV. El tiempo de permanencia elegido fue de 1 s/scan. El ABA fue detectado a una longitud de onda de 263 nm y el dABA a 268-269. Para procesar los datos cuantitativos obtenidos a partir de los estándares de calibración y las muestras de las plantas se empleó el software 5.1 DataAnalysis (Bruker Daltonics).

## II.10. GENERACIÓN DE PLANTAS TRANSGÉNICAS

### II.10.1. Introducción a la metodología *Gateway*

La tecnología Gateway<sup>®</sup> es un método de clonación universal que aprovecha las propiedades específicas de recombinación del bacteriófago  $\lambda$  (Landy, 1989). Este sistema utiliza una mezcla de enzimas de recombinación constituida por la *Integrasa (Int)*, una *Excionasa (Xis)* y la proteína IHF (*Integration Host Factor*) codificada por *E. coli*. Esta mezcla cataliza la recombinación *LR clonasa Gateway in vitro* entre un *Entry vector* (pCR8/GW/TOPO<sup>®</sup>) que contiene el ADN de interés flanqueado por las regiones *attL*, y un *Destination vector* (pFRN) que incluye las regiones *attR*. Mediante esta recombinación específica entre los sitios *att* (*attR* x *attL* ↔ *attB* x *attP*) se genera un vector de expresión destinado a la obtención de plantas transgénicas (Fig. 10).

Para optimizar al máximo la obtención de clones positivos tras la recombinación LR, los vectores Gateway<sup>®</sup> contienen entre los dos sitios *att*, además de un gen que confiere resistencia a cloranfenicol (Cm<sup>R</sup>), el gen *ccdB*, que permite una selección negativa del *Destination vector* en *E. coli* siempre que la recombinación haya transcurrido adecuadamente. La proteína *CcdB* interfiere con la ADN girasa de *E. coli* (Bernard y Couturier, 1992), inhibiendo así el crecimiento de la mayoría de las cepas de *E. coli* (por ejemplo, DH5a<sup>™</sup>, TOP10). Cuando se produce la recombinación LR entre el *Destination vector* y el *Entry vector*, el cassette que contiene al gen *ccdB* es reemplazado por el gen de interés generando así el vector de expresión. La selección del vector de expresión obtenido (pFRN-ADN) se realiza en células de *E. coli* carentes del episoma F' y en presencia de kanamicina, seleccionando así solamente aquellas células que incorporan un vector carente del gen *ccdB* y con resistencia a kanamicina.



**Fig. 10.** Reacción de recombinación mediante el sistema *LR clonasa Gateway* (Invitrogen) para la obtención de una construcción ARNi. *Kan<sup>R</sup>*, resistencia a kanamicina. *Spn<sup>R</sup>*, resistencia a espectinomicina. *Cm<sup>R</sup>*, resistencia a cloranfenicol.

### II.10.1.1. Subclonaje de moléculas de ADN en el vector *pCR8/GW/TOPO* (Invitrogen)

El vector *pCR8/GW/TOPO* (Invitrogen) se empleó como *Entry vector* para el subclonaje de productos de PCR procedentes de la amplificación de una región previamente seleccionada (~400 pb) de los genes *FaAAT2* y *FaMYB10*. Posteriormente, el fragmento amplificado fue transferido desde el vector *pCR8/GW/TOPO* mediante recombinación de las regiones *att* al vector binario *pFRN* mediante la metodología *Gateway* (Invitrogen) (*Materiales y Métodos, apartado I.2.3*). Obtuvimos así un vector de expresión que se empleó para el silenciamiento de los genes elegidos mediante la generación de moléculas de ARN interferente en las plantas transgénicas obtenidas.

El subclonaje de los fragmentos generados por PCR dentro del vector *pCR8/GW/TOPO* se realizó siempre siguiendo las indicaciones de la casa comercial. La mezcla de reacción empleada, así como el programa de PCR utilizado se recogen en *Materiales y Métodos, apartado II.3.5.2*. Rutinariamente, al programa general de PCR se le adicionó, tras el último ciclo de amplificación, un paso de extensión final a 72 °C de 30 minutos de duración para asegurar la presencia de un residuo de deosiadenosina protuberante en el extremo 3', imprescindible para el subclonaje del amplicón obtenido dentro del vector *pCR8/GW/TOPO*. En cualquier caso, tanto la amplificación del fragmento de ADN correspondiente al gen *FaMYB10* como del gen *FaAAT2* se realizó empleando oligonucleótidos diseñados específicamente para cada gen (*Materiales y Métodos, apartado II.3.5.2*).

Tras la amplificación, se procedió a la purificación del producto de PCR obtenido empleando el kit comercial *CONCERT<sup>TM</sup> Rapid PCR Purification System* (Gibco BRL). Una vez

determinada la concentración del ADN recuperado mediante espectrofotometría, se procedió a su subclonaje dentro el vector *pCT8/GW/TOPO* utilizando la mezcla de reacción que se detalla en el *Apéndice 24* e incubando la misma durante toda la noche a temperatura ambiente. Transcurrido este tiempo, se procedió a la transformación de una alícuota de células competentes *One Shot TOP10 Chemically Competent E. coli* (Invitrogen) empleando 2-6  $\mu\text{l}$  de la mezcla de reacción (*Materiales y Métodos, apartado II.4.2*).

**Apéndice 24: Mezcla de reacción para el subclonaje de fragmentos de ADN en el vector *pCT8/GW/TOPO* (Invitrogen)**

Amplicón purificado	2 $\mu\text{l}$
Solución salina (Invitrogen)	1 $\mu\text{l}$
H <sub>2</sub> O milliQ	2 $\mu\text{l}$
<i>pCT8/GW/TOPO</i> (Invitrogen)	1 $\mu\text{l}$

### II.10.1.2. Subclonaje de moléculas de ADN en el vector *pFRN* mediante la reacción *LR clonasa Gateway* (Invitrogen)

Una vez generado el *Entry vector pCR8/GW/TOPO* conteniendo independientemente el fragmento de ADN correspondiente a los genes *FaAAT2* y *FaMYB10*, se procedió a su transferencia al vector binario *pFRN* mediante la recombinación de ambos vectores mediada por la *LR clonasa Gateway* (Invitrogen) (Fig. 10).

La recombinación se realizó empleando la siguiente mezcla de reacción y adicionando los reactivos en el orden indicado:

pCR8/GW/TOPO::ADNc (300 ng)	1-10 $\mu\text{l}$
pFRN (300 ng)	2 $\mu\text{l}$
Tampón de reacción de la LR Clonasa [5X]	4 $\mu\text{l}$
Tampón TE pH 8 hasta	16 $\mu\text{l}$
<i>LR Clonase enzyme mix</i>	4 $\mu\text{l}$

La mezcla se incubó a 25 °C durante 16 horas y, transcurrido este periodo, se incubó nuevamente a 37 °C durante 10 minutos en presencia de 2  $\mu\text{l}$  de *Proteinasa K*. A continuación, se procedió a la transformación con 5  $\mu\text{l}$  del total de la reacción de una alícuota de células competentes *One Library Efficiency DH5a Chemically Competent Cells* (Invitrogen) como se describe en *Materiales y Métodos, apartado II.4.2*.

### II.10.2. Principios básicos de la transformación genética mediada por *Agrobacterium*

Uno de los métodos más extendidos para la transformación genética de plantas es el empleo de *Agrobacterium* como vector biológico portador del ADN que será transferido a la planta. Esta metodología se basa en la condición natural que posee esta bacteria para insertar genes

de manera estable en una célula vegetal. *Agrobacterium tumefaciens* es una bacteria Gram-negativa del suelo que produce la enfermedad de “agalla de corona” en una amplio rango de especies de plantas dicotiledóneas. Esta enfermedad se produce por la infección de *Agrobacterium* a través de heridas preexistentes. Así, la bacteria responde con quimiotactismo positivo a las moléculas de naturaleza fenólica que la planta libera al sufrir una herida. La utilización de esta bacteria como vector ha sido posible gracias a la eliminación mediante ingeniería genética de los genes responsables de la formación del tumor, dejando intacto el resto de los mecanismos moleculares implicados en el proceso de colonización (Hoekema *et al.*, 1983; Potrykus, 1991; Hooyakaas y Beijersbergen, 1994; Christie, 1997; de la Riva *et al.*, 1998; Gelvin, 2003).

En el plásmido binario desarmado contenido en *Agrobacterium*, se sitúa la región denominada T-DNA (*Transfer DNA*), que es la porción de ADN de dicho plásmido que será integrada en el genoma de la planta. En este fragmento de ADN, se localiza un gen de selección (resistencia a antibióticos, herbicidas, etc.), así como el fragmento de interés correspondiente al gen que se desea integrar en la planta. En estas construcciones, los genes están incluidos en casetes que contienen promotores y terminadores reconocibles por la célula vegetal y que son necesarios para la expresión de los genes introducidos. Además, el T-DNA está delimitado por los extremos derecho (RB, *right border*) e izquierdo (LB, *left border*), imprescindibles para la transferencia de éste desde el plásmido binario al genoma de la planta (Caballero *et al.*, 2001).

La metodología de transformación mediada por *Agrobacterium* consiste básicamente en la incubación del explanto vegetal (protoplastos, discos de hoja, callos embriogénicos, etc) con un cultivo de la bacteria que porta el plásmido adecuado. Para aumentar el número de células del explanto que sean competentes para la infección y posterior regeneración, el explanto se somete a daño físico mediante la producción de heridas, lo que predispone a las células a la infección con *Agrobacterium* y a la incorporación del T-DNA. Este proceso se denomina *inducción*. Tras la *infección*, se realiza un *cocultivo* del explanto con la bacteria en medio no selectivo para permitir la expresión de los genes foráneos en las células vegetales que hayan incorporado el T-DNA. Finalmente, en medio selectivo suplementado con los antibióticos adecuados, se realiza simultáneamente la *selección* de las células transformadas y la eliminación de la bacteria empleada en la transformación (El Mansouri *et al.*, 1997; Caballero *et al.*, 2001).

## II.10.3. Transformación de *Fragaria x ananassa* cv. Chandler

### II.10.3.1. Obtención y mantenimiento de plántulas de *Fragaria x ananassa* cv. Chandler *in vitro*.

Las plántulas de *Fragaria x ananassa* cv. Chandler empleadas en este trabajo fueron cedidas por el Dr. F. Pliego Alfaro (Universidad de Málaga) y se obtuvieron mediante la regeneración de ápices caulinares (López-Aranda *et al.*, 1994; El Mansouri *et al.*, 1997). Las plántulas se mantuvieron en medio de multiplicación durante cuatro semanas antes de ser subcultivadas (*Materiales y Métodos*, apéndice 25). En cada subcultivo, siempre se eliminaron las raíces y se separaron las plántulas aparecidas en yemas axiales para multiplicar el *stock* de plántulas. En general, las plántulas se crecieron con un fotoperiodo de 16 h de luz/8 h de oscuridad, con una irradiación de  $25 \mu\text{mol m}^{-2} \text{s}^{-1}$  (lámparas Sylvania Gro-lux), y con una humedad relativa en el interior de la cámara de 60-70% (El Mansouri *et al.*, 1997).

### II.10.3.2. Transformación de plantas de *Fragaria x ananassa* cv. Chandler mediante infección con la cepa LBA4404 de *A. tumefaciens*.

La transformación de *Fragaria x ananassa* cv. Chandler mediada por *A. tumefaciens* se llevó a cabo según el método descrito por Barceló *et al.* (1998), que adaptó a fresa la técnica de transformación previamente descrita por Horsch *et al.* (1985).

El proceso de transformación consta de cuatro fases diferenciadas:

- Precultivo. Durante esta etapa se obtuvieron los explantos foliares a usar posteriormente en el proceso de transformación. Para ello, a partir de plántulas *in vitro* de 3-5 semanas de edad, se seleccionaron hojas trifoliadas jóvenes, de mayor potencial regenerativo (Raviv *et al.*, 1987), que se cortaron en secciones de 5 mm<sup>2</sup>. Los explantos obtenidos se colocaron, siempre con el haz hacia abajo, en placas de Petri con medio de organogénesis (*Materiales y Métodos*, apéndice 25). El precultivo se mantuvo durante 8 días a 25 °C y siempre en oscuridad para reducir la exudación fenólica y favorecer la morfogénesis de los explantos (Liu y Standford, 1988; George, 1993; Barceló *et al.*, 1998).

- Infección. Durante esta etapa, se llevó a cabo la infección de los explantos foliares obtenidos en la etapa anterior con el cultivo de *Agrobacterium* LBA4404 portador del vector binario que contenía nuestra construcción de interés. Para ello, inicialmente se cultivó la estirpe de *Agrobacterium* portadora de nuestra construcción en 5 ml de medio LB líquido suplementado con rifampicina (100 µg/ml) y kanamicina (50 µg/ml) a 28 °C y 200 rpm durante 16 h. Transcurrido este tiempo, se refrescaron varios cultivos empleando como inóculo 200 µl del cultivo anterior. En esta ocasión, los cultivos se crecieron en 5 ml de medio LB líquido (pH 5,4) suplementado con los antibióticos anteriores y con acetosiringona (100 µM), que incrementa la virulencia de *Agrobacterium*, y se incubaron a 28 °C y 200 rpm durante 16 h. Una vez alcanzada una D.O.<sub>600 nm</sub> entre 0,6-1 unidades, se diluyeron con H<sub>2</sub>O hasta ajustar su D.O. a 0,2 en un volumen final de 50 ml y se procedió a la infección propiamente dicha. Así, a cada uno de los cultivos diluidos se les añadió ~40 explantos de hoja (una vez finalizado el precultivo), que se mantuvieron sumergidos en la solución mediante agitación suave durante 20 minutos. Finalmente, los explantos se recogieron y se secaron sobre dos papeles secantes estériles para eliminar el exceso de medio de cultivo e, inmediatamente después, se dispusieron nuevamente sobre medio de organogénesis manteniendo el haz en contacto con éste.

- Selección. Terminado el periodo de cocultivo, durante esta etapa, los explantos se subcultivaron durante 4 días a 25 °C y en oscuridad en nuevo medio de organogénesis suplementado con carbenicilina (500 mg/l), para eliminar a *Agrobacterium*, y kanamicina (25 mg/l), para seleccionar los explantos transformados. Transcurrido este tiempo, los explantos se mantuvieron con un fotoperiodo de 16 h de luz/ 8 h de oscuridad a 25 °C en la cámara de cultivo. Durante el periodo de organogénesis y regeneración, que puede variar entre 4 y 6 meses dependiendo de la construcción transformada, los explantos se subcultivaron a nuevo medio de organogénesis selectivo cada 4 semanas. Tras cuatro subcultivos, la concentración de carbenicilina añadida al medio se redujo a 250 mg/l, retirándose completamente en el sexto subcultivo. Simultáneamente, en el cuarto subcultivo, la concentración de kanamicina se incrementó hasta 50-100 µg/ml para reducir los eventos con inestabilidad genética (Houde *et al.*, 2004). Cuando aparecieron plántulas de 2 cm de longitud, éstas se aislaron del resto del explanto y se subcultivaron en medio de multiplicación suplementado con el antibiótico

correspondiente, generalmente kanamicina (100 µg/ml). Cada planta obtenida a partir de un explanto se consideró un evento independiente de transformación.

- Cocultivo. Durante esta etapa, los explantos infectados se mantuvieron durante 2 días en ausencia de antibióticos de selección en medio de organogénesis a 25 °C y en oscuridad en una cámara de cultivo.

**Apéndice 25: Medios y soluciones empleadas en la transformación mediada por *Agrobacterium tumefaciens* de *Fragaria x ananassa* cv. Chandler.**

**Medio LB.** Ver Apéndice 1

**Acetosiringona** (100 mM)

19,6 mg/ml en EtOH 70%. Almacenar a 4 °C

**Medio MS** (Murashige y Shoog, 1962)

para *Fragaria x ananassa* cv. Chandler

*Sales minerales*

NH <sub>4</sub> NO <sub>3</sub>	0,47 g/l
KNO <sub>3</sub>	1,31 g/l
MgSO <sub>4</sub> ·7H <sub>2</sub> O	0,24 g/l
KH <sub>2</sub> PO <sub>4</sub>	0,13 g/l
KCl	0,074 g/l
Ca(NO <sub>3</sub> ) <sub>2</sub> ·4H <sub>2</sub> O	0,59 g/l
NaFe-EDTA	10 ml/l

(de una solución compuesta por 3,724 g/l de Na<sub>2</sub>EDTA Titriplex) y 2,78 g/l de FeSO<sub>4</sub>)

*Micronutrientes*

Añadir 10 ml/l de una solución compuesta por:

MnSO <sub>4</sub> ·H <sub>2</sub> O	1,690 g/l
ZnSO <sub>4</sub> ·7H <sub>2</sub> O	0,860 g/l
CuSO <sub>4</sub> ·5H <sub>2</sub> O	0,0025 g/l
KI	0,0830 g/l
CoCl <sub>2</sub> ·6H <sub>2</sub> O	0,0025 g/l
H <sub>3</sub> BO <sub>3</sub>	0,620 g/l
Na <sub>2</sub> MoO <sub>4</sub> ·2H <sub>2</sub> O	0,025 g/l

*Stock de vitaminas*

Añadir 10 ml/l de una solución compuesta por:

Tiamina.HCl	0,1 g/ml
Piridoxina.HCl	0,05 g/ml
Ácido nicotínico	0,05 g/ml
Glicina	0,2 g/ml

*Otros componentes*

Sacarosa	20 g/l
Myo-Inositol	100 mg/l
Agar (A-1296; Sigma)	7 g/l

**Medio MS de organogénesis**

Añadir al medio MS las hormonas:

Ácido Indol-3-butírico (IBA)	0,5 mg/l
6-benzyl aminopurina (BA)	2 mg/l

**Medio MS de multiplicación**

Añadir al medio MS la hormona Kinetina 0,47 mg/l

*Otros componentes*

Sacarosa	20 g/l
Myo-Inositol	100 mg/l
Agar (A-1296; Sigma)	7 g/l

Las hormonas se prepararon a una concentración de almacenamiento de 0,1 mg/l. Para disolverlas, se añadieron unas gotas de NaOH 1N hasta su disolución y luego se completó el volumen con H<sub>2</sub>O destilada.

Los antibióticos se añadieron al medio estéril templado antes de solidificar. Posteriormente, éste se distribuyó en frascos previamente esterilizados.

### II.10.3.3. Aclimatación y multiplicación de las plantas transgénicas

Se aclimató una única plántula crecida en medio LB suplementado con kanamicina (50 mg/l) por cada evento independiente de transformación. Siempre se sembraron en macetas de 250 ml con turba y arena (1:1). Las plantas seleccionadas, que siempre tuvieron un sistema radicular bien desarrollado, se extrajeron del medio de cultivo y sus raíces se lavaron con agua abundante para eliminar restos de medio y evitar contaminaciones. A continuación, las raíces se introdujeron en la turba humedecida y, para mantener una humedad elevada, la maceta se cubrió con una bolsa de plástico transparente. Las macetas se mantuvieron a temperatura ambiente con iluminación natural y siempre humedecidas. La aclimatación de la



planta se realizó mediante la realización de una abertura de ~1 cm en la bolsa cada dos días hasta retirarla completamente.

Una vez finalizada la aclimatación, las plántulas se multiplicaron mediante propagación vegetativa en invernaderos en el CIFA de Churriana, Málaga. La temperatura, humedad y fotoperiodo del invernadero fueron las ambientales. Cuando fue necesario, las plantas se abonaron y fueron sometidas a distintos tratamientos fitosanitarios.

#### **II.10.3.4. Selección y análisis de plantas transgénicas**

La primera selección de las plantas transgénicas se realizó a nivel fenotípico en base a su resistencia frente a kanamicina. Así, todos los explantos resistentes a kanamicina que mostraron un aspecto sano y proliferación de microcallos, se subcultivaron periódicamente manteniendo la presión de selección hasta la generación de plántulas. Cuando éstas presentaron un tamaño suficiente, se crecieron en medio de multiplicación suplementado con kinetina y, posteriormente, fueron trasvasadas a maceta. Este periodo tuvo una duración aproximada de 6-8 meses. Por otro lado, las plántulas necrosadas, etioladas o deformes fueron desechadas.

Las plantas que presentaron resistencia a kanamicina fueron analizadas posteriormente mediante QRT-PCR (*Materiales y Métodos, apartado 6.3.*). Para ello se realizó la extracción del ADN genómico de la planta como se indica en el *apartado II.1.2.2. de Materiales y Métodos*. Este ADN se cuantificó espectrofotométricamente y se visualizó en gel de agarosa al 0,9% para comprobar su pureza e integridad (*apartado II.2.2. de Materiales y Métodos*).

#### **II.10.4. Transformación mediante agroinfiltración de plantas *Fragaria x ananassa* cv. Elsanta.**

##### **II.10.4.1. Obtención y mantenimiento de plantas de *Fragaria x ananassa* cv. Elsanta**

El cultivar *Fragaria x ananassa* cv. Elsanta se empleó para la transformación de frutos de fresa mediante agroinfiltración. Las plantas se mantuvieron a una temperatura de 25 °C, con un fotoperiodo de 16 h de luz/8 h de oscuridad, y bajo una irradiancia de 120  $\mu\text{mol}\cdot\text{m}^{-2}\cdot\text{sec}^{-1}$  proporcionada por lámparas Osram Fuora (München, Germany).

##### **II.10.4.2. Transformación de plantas de *Fragaria x ananassa* cv. Elsanta a través de agroinfiltración con *A. tumefaciens* AGL0**

La transformación de *Fragaria x ananassa* cv. Elsanta mediada por *A. tumefaciens* AGL0 (Lazo *et al.*, 1991) se llevó a cabo según el método descrito previamente por Hoffmann *et al.* (2006), que adecúa a esta especie la técnica de transformación previamente descrita por Spolaore *et al.* (2001).

La estirpe AGL0 de *A. tumefaciens*, conteniendo las construcciones *pFRN::FaAAT2* y *pFRN::FaMYB10* de forma independiente, fue cultivada a 28 °C en 50 ml de medio LB suplementado con los antibióticos adecuados. Cuando el cultivo alcanzó una  $\text{D.O.}_{600\text{nm}} \sim 0.8$ , las células de *Agrobacterium* fueron recolectadas mediante centrifugación a 4.000 g durante

10 minutos y, posteriormente, resuspendidas en 10 ml de medio agar MacConkey modificado (MMA) (*Materiales y Métodos, apéndice 26*) (Spolaore *et al.*, 2001). A continuación, esta suspensión celular se inyectó en frutos en un estadio intermedio entre verde y blanco, generalmente alcanzado 14 días después de la polinización. La suspensión se inyectó uniformemente en el fruto usando una jeringuilla hipodérmica estéril de 1 ml y procurando pinchar una o dos veces solamente para evitar dañar el fruto en exceso. Tras la inyección, las plantas se dejaron nuevamente en la cámara de cultivo en las mismas condiciones de cultivo descritas previamente. Aunque se hizo un seguimiento diario de la evolución de los frutos inyectados para comprobar la existencia o no de cambios fenotípicos evidentes, los frutos no se recolectaron hasta 14 días después de la inyección (estadio rojo). En paralelo y de forma simultánea, también se inyectaron frutos sin transformar (control) con un cultivo de la cepa *AGLO* de *A. tumefaciens*. En cualquier caso, los frutos inyectados una vez recolectados se congelaron a -80 °C hasta su uso. Paralelamente, se hizo lo mismo con la estirpe utilizada como control positivo que contenía la construcción pBI-Intrón (Hoffmann *et al.*, 2006). Como control negativo de utilizaron frutos inyectados con el plasmido vacío pFRN.

**Apéndice 26: Medios y soluciones empleadas en la transformación transitoria de *Fragaria x ananassa* cv. Elsanta con *Agrobacterium tumefaciens* *AGLO*.**

**Medio Luria-Bertani** (Ver Apéndice 1)

**Medio MMA** (Spolaore *et al.*, 2001)

*Medio MS* (Murashige y Shoog, 1962) (Ver Apéndice 30)

10 mmol l<sup>-1</sup> MES (morfolina etanosulfónico) a pH 5,6

20 g l<sup>-1</sup> de Sacarosa

200 µmol l<sup>-1</sup> de Acetosiringona

### II.10.4.3. Análisis de frutos transgénicos

El grado de silenciamiento de los genes en estudio (*FaAAT2* y *FaMYB10*) se determinó mediante QRT-PCR en los frutos transgénicos obtenidos en ambas transformaciones. En el caso de los frutos transgénicos *FaAAT2*, también se realizaron extracciones de volátiles que posteriormente fueron analizados mediante GC-MS (*Materiales y Métodos, apartado II.7.6*). Por otra parte, en el caso de los frutos transgénicos *FaMYB10*, se determinaron mediante HPLC los niveles antocianinas y flavonoides frente a frutos control (*Materiales y Métodos, apartado II.9.2*).

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## **CHAPTER 1: USING OF A CUSTOM MADE OLIGO MICROARRAY PLATFORM TO DISCOVER NEW CANDIDATE GENES WITH POTENTIAL BIOTECHNOLOGICAL ROLES IN STRAWBERRY FRUIT DEVELOPMENT AND RIPENING**

### **1. ABSTRACT**

Strawberry is one of most important fruit crop in the world. Several genetic, genomic, proteomic, metabolomic and functional studies by reverse-genetic have been developed in recent years to address the molecular basis of the strawberry (*Fragaria x ananassa*) fruit ripening process. However, the molecular information regarding this important physiological process is still scarce. In this work, we have used a custom-made oligo microarray platform to perform high-throughput analysis of gene expression in strawberry fruit receptacle. The aims of this study is to select target genes potentially involved in the fruit ripening process and to produce valuable information that might eventually lead to discovery of genes implicated in the physiological pathways that could render fruits with improved organoleptic and quality characteristics.

### **2. INTRODUCTION**

In flowering plants, fruits ripening is a developmental and biochemical process that involves numerous metabolic changes that confer selective advantages by aiding seed maturation and dispersal. The cultivated strawberry (*Fragaria x ananassa*) is one of the most economically important small fleshy fruits and is rich in flavor compounds, fiber, vitamins and antioxidants (Reganold *et al.*, 2010). Today, it represents the third most valuable crop in the non citrus fruit category, behind grapes and apples, within the United States (Sjulin, 2003). This biological, dietary and economical significance has made the molecular dissection of the metabolic and regulatory pathways supporting the strawberry fruit growth and ripening an area of considerable research interest.

The cultivated strawberry is a hybrid octoploid species (*Fragaria xananassa* Duchesne ex. Rozier) that belongs to the family *Rosaceae* in the genus *Fragaria*. The strawberry fruits have a high nutrient content and are highly appreciated for human consumption due to their organoleptic properties and health benefits (Seeram, 2008). Thus, the benefits that the strawberry fruit consumption on cardiovascular, neurodegenerative and other diseases like aging, obesity, and cancer have been object of study during the last years (Hannum, 2004; Mink *et al.*, 2007; Seeram, 2008).

Strawberry is considered a typical non-climacteric fruit, based on the fact that do not increase its respiration at ripening and have no clear requirement of ethylene to complete the fruit maturation (Giovannoni, 2007). Thus, to classify the strawberry as a non-climacteric fruit did not differ between the receptacle and the achenes or true fruits. In climacteric fruit, ethylene provides the signal for ripening by activation of many genes involved in fruit ripening (Alexander and Grierson, 2002; Giovannoni, 2007). The auxins, which are supplied by the achenes, are considered as an important key regulator of ripening (Bombarely *et al.*, 2010).

During the strawberry fruit ripening, the hormones regulation, the synthesis of anthocyanins

and flavonoids, and the changes occurring in the cell wall play an important role. Thus, the flavor, odor and firmness of strawberry fruit are of great economic importance. All these features are controlled by processes associated with the development and fruit ripening, which involves specific changes in gene expression and cellular metabolism (Manning *et al.*, 1994). Therefore, growth and ripening of strawberry fruits is an important field of research.

In the strawberry fruit receptacle occur structural, biochemical and physiological events. Thus, the strawberry fruit has four sequential stages during development and ripening (Gillaspy *et al.*, 1993). First phase includes organogenesis that involves fertilization and development of the ovary (fruit set). The second phase is characterized by an active process of cell division accompanied by seed and early embryo formation. In the third phase, fruit growth is produced by cell expansion due to an increase in cell volume. This phase is accompanied of an embryo maturation. The four phases is the ripening phase, which is initiated after seed maturation and is characterized by a rise in the content of soluble solids in the receptacle, the production of natural aroma and flavour compounds and alterations to fruit shape, size, texture and pigmentation. Therefore, the molecular and functional characterization of those genes expressed in strawberry fruit receptacle and potentially related with fruit quality properties could be an approach of biotechnological interest.

The strawberry (*Fragaria x ananassa*, Dutch) is one of the most consumed fruits worldwide. The variety and content of polyphenolic constituents of strawberries, represented mainly by non-flavonoid, flavonoids, anthocyanins and condensed tannins (ellagitannins), have recently attracted increasing attention (Clifford, 2000; Halbwirth *et al.*, 2006). Anthocyanins exhibit cytoprotective activities across multitude of biochemical mechanisms (Hwang *et al.*, 2011) and seem to provide indirect antioxidant protection by activation of cellular antioxidant enzymes, which are crucial components of the antioxidant defense system in the body. Aharoni *et al.*, (2001) identified and characterized the transcription factor (TF) *Famyb1*, which plays a regulatory role in the synthesis of anthocyanins and flavonols during fruit ripening strawberry. Volatile acyl esters are important metabolites in strawberry fruit flavour. Using microarrays has been identified an alcohol acyl transferase (*SAAT*) involved in the biosynthesis of volatile (Aharoni *et al.*, 2000). Furanol (HDMF) is the main volatile compound responsible for the aroma of strawberry (Roscher *et al.*, 1997). The genes of two enzymes involved in the HDMF biosynthesis have been cloned (Raab *et al.*, 2006; Lunkenbein *et al.*, 2006). Given the importance of the cell wall in the integrity of the strawberry fruit, genes coding modifying enzymes of the cell wall have been analyzed. Among these genes are expansins (Civello *et al.*, 1999), cellulases (Trainotti *et al.*, 2006),  $\beta$ -galactosidase (Trainotti *et al.*, 2001), pectate lyases (Medina-Escobar *et al.*, 1997b; Benítez-Burraco *et al.*, 2003), and pectinmethylesterases (Osorio *et al.*, 2008).

The aim of this study was to expand the knowledge about the molecular mechanisms involved in strawberry fruit receptacle ripening in order to identify genes with biotechnological relevance for strawberry fruit quality. For this purpose, the microarray platform was utilized to examine transcriptomic changes produced along developmental (growth), ripening and senescence stages of fruit receptacle. Thus, the changes in the expression corresponding to these genes were analyzed in two receptacle growth stages (G1 and G3), two ripening stages (W and R) and two senescent stages (OR and SN). The comparative microarray analysis identified 2575 genes whose expression was significantly ( $p < 0.05$ ) differentially regulated trough the growth, ripening and senescence stages of fruit receptacle.

### **3. RESULTS AND DISCUSSION**

#### **3.1. Validation of the microarray data by QRT-PCR**

Microarrays analyses are very productive approaches to select target genes differentially expressed through a physiological process. However, once the fold of expression change of a set of genes has been determined and statistical analysis of the data performed to identify significantly differently expressed genes, the changes in expression for these candidates targets should be verified by other techniques such as quantitative RT-PCR (QRT-PCR) (Wurmbach, 2009). Although, the ranking of regulated genes is often similar, the fold changes obtained from microarrays analysis differs from the fold changes measured by QRT-PCR. This discrepancy appears to be more pronounced the more strongly a gene is regulated (Wurmbach, 2009). However, although there are quantitative differences between data generated by both methods, qualitatively correlate (Wurmbach, 2009). In general, the fold changes for differential gene expression measured by microarray methods are lower than the corresponding fold changes for the same genes measured by QRT-PCR (Wurmbach, 2009). That is due to the fact that cDNA microarrays display a saturation effect, which explains the low correlation between microarrays and QRT-PCR data for higher regulated genes (Wurmbach, 2009). Furthermore, the broad range of linearity of QRT-PCR reactions, higher than seven orders of magnitude, results in more accurate measurements, compared to microarrays as far as the dynamic range for microarrays is only up to four orders of magnitude. It can be concluded that analyses of changes in gene expression performed by QRT-PCR are more accurate to estimate the fold-change of differential expression than microarray determination (Wurmbach, 2009).

Usually, QRT-PCR analysis performed on genes identified as differentially expressed in microarrays experiments provides a more accurate estimation of the fold-change of gene expression. Moreover, in the case of low abundance genes, microarrays analysis may result in undetectable changes of gene expression due to the lower sensitivity of this technique. However, these levels of expression by QRT-PCR could still measure changes in gene expression (Wurmbach, 2009).

For the above described considerations, we have proceeded to validate the gene expression changes observed in microarray experiment by QRT-PCR methodologies. As expected, a clear qualitative positive relationship for changes in gene expression between both methodologies was observed although the highest values of differential expression were obtained by the QRT-PCR methodology (Table 12).

#### **3.2. Specific strawberry fruit receptacle gene expression**

Receptacle fruit ripening requires the orchestration of many different, seemingly disparate physiological and biochemical changes. These changes are, at least in part, mediated through the differential expression of many genes. Some of these genes code for proteins that participate directly in the ripening process while others code for proteins involved in signal transduction or transcription factors that control the expression of further banks of genes. It is far from the scope of this chapter to discuss all the genes whose level of transcripts changes significantly in fruit receptacle along the ripening process or in the different physiological conditions studied. Besides, many of the pattern expression profiles observed for the genes



included in our microarray are coincident with those stated in a previous strawberry ripening-related microarray study (Aharoni and O'Connell, 2002). We will discuss in this chapter the more relevant genes potentially involved in key metabolic processes related with the most important characteristics of receptacle fruit quality.

Changes that are important for fruit quality, like anthocyanins and flavour content, as well as fruit softening are expected to be produced by methabolic pathways quite specific or over activated in fruit receptacle, whereas hormone control of this process might be supported by the achenes.

The functional analysis of the 2575 genes whose expression was up-regulated in ripen fruit receptacle showed that 340 of them had not yet assigned physiological role (uncharacterized protein) (Table 10), while 811 genes did not present any homology of sequence with those of genes whose sequences are deposited in the databases (no homology) (Table 11).

### **3.3. Main genes differentially expressed along fruit receptacle ripening**

#### **3.3.1. Transcription factors**

Transcription factors (TFs) control cellular processes by activating or repressing the expression of downstream target genes. As regulatory proteins, they play key roles in many biological processes as cell growth and differentiation, physiological and developmental processes (including fruit growth and ripening), signalling process and in the regulation of multiple biochemical pathways steps producing metabolite accumulation (Qu and Zhu, 2006). These functional characteristics offer much promise for manipulating methabolic pathways in higher plants (Qu and Zhu, 2006). Within the *Fragaria vesca* genome, 1616 transcription factors have been putatively indentified (Shulaev *et al.*, 2011). In our microarrays we have observed that only 134 of them increased their expression along the receptacle ripening process. The low amount of genes coding TFs whose expression levels changed along the fruit receptacle growth and ripening indicated that these transcription factors could play important key transcriptional roles in the regulation of the expression of genes related with physiological and metabolic processes involved in the receptacle growth and ripening. In our microarray study, the vast majority of the genes that code enzymes involved in the biochemical pathways that determine the organoleptics properties of the fruit presented a common expression pattern (expression induced in ripen receptacles and fruit specific). Thus, probably the TFs that display the same expression pattern could be implicate in the transcriptional regulation of genes belonging to these metabolic pathways.

#### ***Helix-Loop-Helix (bHLH) transcription factors***

Overall, *Fragaria vesca* genome has 226 genes coding basic helix-loop-helix (*bHLH*) TFs. The expression profiling analysis of our microarray platform have shown that only the transcript amount of eight of them (*UCOESTup41*, *161*, *366*, *477*, *1461*, *1606*, *1652*, *1708*, *1813*) increased in comparison between the transcriptomes corresponding to mature red *versus* small green immature fruit receptacles (Table 1). *UCOESTup477* and *UCOESTup161* showed higher levels of expression which may be probably involved in the ripening process of red fruit receptacle (Table 1). These TFs have been related with multitude of physiological and metabolic processes as cell proliferation and development, phenylpropanoid, flavonoid and anthocyanin biosynthesis, hormone signaling,

photomorphogenesis, etc. (Qu and Zhu, 2006). *UCOESTup477* gene potentially encode a helix-loop-helix TF that is homologous to members of the *Arabidopsis* PRE (Paclobutrazol resistance) family, rice (*Oryza sativa*) IL11 and mammalian Id protein (Lee *et al.*, 2006; Zhang *et al.*, 2009). The *Arabidopsis PRE1* gene has been implicated in gibberelic acid (GA) responses as elongation of hypocotyls and petioles (Lee *et al.*, 2006). Recently, it has been proposed that *IL11* and *PRE1* play a functional role in the transition from growth of young organs to growth arrest (Zhang *et al.*, 2009). In *Arabidopsis* and rice, *PRE1*-like genes interact by heterodimerization with inhibitory basic helix-loop-helix TFs inactivating them (Zhang *et al.*, 2009). In tomato, has been shown that the gene *Style 2.1*, a homologous gene of *PRE1*, also promotes the elongation of distal style cells that causes an increase in style length (Chen *et al.*, 2007). At present, there are not any studies that determine the physiological role of these TFs in fruit growth and ripening process.

Thus, it is known that the action of the bHLH TFs is mediated through the interaction, by heterodimerization, with different TFs as bHLHs, MYBs or MADS, or with regulators proteins as photoreceptors or WD40. This fact indicates that this TF could play an important regulatory role of the molecular mechanisms that support the receptacle fruit ripening process.

### ***Dof transcription factors***

Also, the *F. vesca* genome contains 15 genes that potentially code C2C2-*Dof* transcription factors (Shulaev *et al.*, 2011) all of them are represented in our microarray platform. Only one of these *Dof* TFs represented in our microarray platform was up-regulated in strawberry ripen receptacles (*UCOESTup76*) (Table 1). *DOF* genes constitute one of the largest TFs families in plants. These TFs have been related with very different biological functions as photosynthetic carbon assimilation, accumulation of storage proteins in seeds, germination, dormancy, response to phytohormones (auxins or giberellins mediated responses), flowering time, guard cell specific gene expression, salicylic acid mediated responses (Yanagisawa, 2004; Moreno-Risueno *et al.*, 2007; Fornara *et al.*, 2009). Recently, the involvement of an *Arabidopsis* DOF transcription factor (*AtDOF4;2*) in the regulation of the phenylpropanoid and the auxins transport metabolism has been proposed (Skyrycz *et al.*, 2007).

The correlation between the expression characteristics of the *FaDOF* genes and those coding enzymes of the phenylpropanoid metabolic pathway, in both fruit growth and ripening, could suggest that these transcriptional factors could play a regulatory role potentially related with the modulation of expression of genes encoding enzymes of the phenolic metabolism in strawberry fruits. Additionally, we cannot discard, for *UCOESTup76* gene, a specific functional role in those responses mediated by hormones as auxins and giberellins during the developmental stages of the fruit.

### ***NAC transcription factors***

There are 150 members of the *NAC* TFs family in the *F. vesca* genome. The *NAC* transcription factors are plant-specific transcriptional regulators and are important in plant growth, development and stress responses (Olsen *et al.*, 2004). Different members of this transcription factor family have been described and are involved in a very wide range of functions such as flower development, meristem formation, lateral root formation, auxins signalling, biotic and abiotic stress response (Olsen *et al.*, 2004; Ya-Ni *et al.*, 2008). However, the regulatory roles that play these TFs in the fruit ripening process are very

scarce. In our array only eleven *NAC* TFs were up-regulated in ripen receptacle (*UCOESTup558, 580, 766, 794, 1071, 1243, 1270, 1325, 1366, 154, 2422*) (Table 1). In tomato a mutation in a gene encoding a *NAC* (*NOR*)-type transcription factor led to fruit incapable of maturing (Giovannoni, 2007). However, the strawberry *NAC* TFs does not present significant homology of sequence with the tomato *NOR* sequence, indicating that both genes are not orthologous of the tomato *NOR* gene. One of the functions of these transcriptions factors has been related with the reduction of cell division, increase in cell size (fruit size), signalling under osmotic stress (fruit turgor) and senescence processes (Ya-Ni *et al.*, 2008). The expression features of these genes throughout fruit development and ripening and their relatively fruit specific expression could suggest a putative relationship with these processes. However, recent molecular studies have suggested that in vascular plants, some *NAC* TFs are master regulators of secondary cell wall biosynthesis by regulating a cascade of downstream transcription factors that leads to activation of the biosynthetic genes that promote secondary wall deposition (Zhong *et al.*, 2010). Thus an additional functional role for the strawberry *NAC* TFs could be the reinforcement of the secondary cell wall of the receptacle vascular cells enabling tracheary and vascular elements to withstand the negative pressure generated in the ripen receptacle during transpiration (Zhong *et al.*, 2010). A relationship in vascular cells between the regulatory role of *NAC* TFs and lignin biosynthesis through the regulation of lignin-specific *MYB* TFs has been also reported (Zhong *et al.*, 2010). In this sense, it is noteworthy that the amount of transcript corresponding to two sets of lignin biosynthetic genes as caffeic acid O-methyltransferase (*FaOMT*), cinnamoyl-CoA reductase (*FaCCR*), cinnamyl alcohol dehydrogenase (*FaCAD1*) and several laccases increased and/or decreased their expression in ripen fruits in parallel with the expression profiles of *FaNAC* genes. These correlations suggest that *FaNAC* genes could be regulating the expression of genes coding enzymes that determine the deposition of lignin in the cell wall of vascular cells. Alternatively, these *NAC* TFs could act as master regulatory TFs that would control the transcriptional network that governs the expression of all TFs and biosynthetic genes involved in the biosynthesis of secondary cell wall compounds that are necessary for the development of the vascular tissue during the developing receptacle. In this sense, it is noteworthy that previous studies have shown the presence of lignin in immature xylem cells of the fibrovascular strands of the receptacle of all stages of development (Aharoni *et al.*, 2002). These studies have also demonstrated that the *FaCAD1* protein was immunolocalized during all stages of fruit growth and development to immature xylems cells undergoing active lignification (Aharoni *et al.*, 2002).

### ***MADs transcription factors***

In our microarray platform are also represented 31 *MADS* TFs detected in the whole *F. vesca* genome. Only the expression of four of them (*UCOESTup525, 529, 2231* and *2333*) was induced in ripen fruit receptacle (Table 1). An increase in gene expression for *MADS box* genes along fruit ripening has been reported in fruits as banana (Friedman *et al.*, 2007), peach (Martin *et al.*, 2006; Trainotti *et al.*, 2006), pear (Yamame *et al.*, 2007), Satsuma mandarina (Endo *et al.*, 2006), pineapple (Moyle *et al.*, 2005), grape (Boss *et al.*, 2002) and apple (Sung *et al.*, 2000). The *MADS-box* genes cloned in these species show sequence homology to *Arabidopsis MADS-box* ones. However, there is not much evidence regarding their function during fruit ripening or about the target genes regulated for them. In tomato, the function of a *MADS box* transcriptional factor (RIPENING-INHIBITOR (*RIN*) *MADS-box*) expressed in fruit have been recently elucidated. *RIN* encodes a partially deleted *MADS-box* protein of the *SEPALLATA* clade whose expression is necessary for the progression of ripening process in tomato (Giovannoni, 2007).

The sequences corresponding to strawberry *MADS box* genes have not significant homology with those of *RIN* genes of tomato. That probably suggest that this *MADS* transcription factor regulates gene expression patterns that are ripening-related but different to those reported in tomato for *RIN* genes.

### ***MYBs transcription factors***

Of the 187 myb TFs found in the *F. vesca* genome (Shulaev *et al.*, 2011), only 15 genes were up-regulated in ripen receptacles (Table 1). Of them, *UCOESTup51* gene codes a R2R3 myb transcription factor (*FaMyb10*) functionally characterized in strawberry (Lin-Wang *et al.*, 2010). Thus, we have observed that the expression of this gene is fruit-specific and is strongly up-regulated in red ripen receptacles (Chapter 3). The *FaMyb10* expression pattern is very coincident with those observed for the vast majority of genes coding enzymes involved in the biosynthesis of anthocyanins. In this sense, it has been demonstrated that this gene regulates the production of anthocyanin in strawberry ripen fruits (Lin-Wang *et al.*, 2010).

### ***WRKY transcription factors***

On the other hand, 90 different WRKY transcription factors are present in the whole genome of *F. vesca*. Out of them, 9 of these transcription factors increased its expression in ripen receptacle (Table 1). WRKY proteins are key transcription regulators that can act as activators as well as repressors of the gene transcription (Rushton *et al.*, 2010). The function of these transcription factors has been related with the plant immune response in biotic stresses but also with abiotic stresses as drought and cold (Rushton *et al.*, 2010), senescence and/or in metabolic pathway as tannin biosynthesis (Rushton *et al.*, 2010).

Our expression profiling studies have shown that the expression of *UCOESTup61* is highly up regulated in ripen fruit receptacle (Table 1). WRKY transcription factor was shown to be an activator of ABA signaling in processes as salt and drought stresses. The ratio ABA/auxins has been proposed as the hormonal clue that initiates the molecular processes involved in the strawberry fruit ripening process (Perkins-Veazie, 1995). Besides, transcriptomic profiling analysis have shown that the expression of members of the WRKY family strongly up-regulated during senescence. Thus, the ripening-related WRKY transcription factor (*UCOESTup61*) could be involved in the regulation of ripening related processes mediated by ABA. Furthermore, a potential key regulatory role of the receptacle senescence process can not be discarded and should be considered for this transcription factor.

### ***Yabby transcription factors***

Of the five C2C2-*Yabby* genes found within the *F. vesca* genome (Shulaev *et al.*, 2011) only one of them is represented in our microarray platform (*UCOESTup770*) and increased its expression in ripen receptacles (Table 1). The *YABBY* TFs constitute a family of transcription factors which are unique to seed plants. In the domestication of tomatoes, a mutation in the transcription factor *fasciated* (a *Yabby* transcription factor) has led to the extreme fruit size phenotype being its expression restricted to the carpel and stamen primordia and also to the placental tissue, which surrounds the ovules (Cong *et al.*, 2008). Except for this *YABBY* gene described and characterized in tomato, no functions have been described for homologous

genes in another fruits such as strawberry. The involvement of the strawberry *Yabby* gene in molecular process related with receptacle fruit size must be elucidated through genetic reverse approaches.

### 3.3.2. Genes related to primary metabolism

#### *Glycogenins*

In our microarrays analysis, we observed the up-regulation of different plant glycogenins (*UCOESTup19*, 1881 and 2317) in red ripen fruit receptacles. Among them, *UCOESTup19* had higher levels of expression in ripe fruits so it could be related to maturation processes (Table 2). Sequence analysis of *UCOESTup19* showed that this gene belongs to the *GT8* family of plant glycogenins-like genes. Although *Arabidopsis* *GT8* genes are annotated as plant glycogenin-like starch initiation proteins (PGSIPs) (Yin *et al.*, 2010), the *GT8* family is a protein family consisting of enzymes with very distinct proven and proposed functions. Indeed, a suggestion has been made to split the *GT8* family into two groups (Sterling *et al.*, 2006): the cell wall biosynthesis-related genes (*GAUTs* and *GATLs*) and the non-cell wall synthesis-related genes (*GolSs* and *PGSIPs*). Additionally, it was described that a glycogenin-like gene (*OsGGT*) induced its expression by submergence stress. The expression of this gene also increased in response to ethylene, gibberellin, abscisic acid, drought and salt treatment (Qi *et al.*, 2005). The relationship of these putative glicogenins with the strawberry ripening process is unkonwn. However, the high expression of *UCOESTup 19* and its clear up-regulation in ripen fruits indicate that a relationship with receptacle drought stress or with processes produced in the cell wall along the maturation of the fruit cannot be discarded.

#### *$\beta$ -hydroxyisobutyryl-CoA hydrolase*

Our expression profiling studies have shown that the expression of *UCOESTup10* is highly up-regulated in ripen fruit receptacle (Table 2). This gen encodes a  $\beta$ -hydroxyisobutyryl-CoA hydrolase needed for valine catabolism and fatty acid beta-oxidation. Studies with *CHY1* mutant from *Arabidopsis*, which encodes a peroxisomal beta-hydroxyisobutyryl (HIBYL)-CoA hydrolase, revealed that this enzyme has a important role in cold stress signalling within peroxisomal metabolism, and in tolerance to cold stress and darkness-induced starvation (Dong *et al.*, 2009). Previous studies with *CHY1* have provided information about the mechanism of Val catabolism in plants (Zolman *et al.*, 2001; Lange *et al.*, 2004). Moreover, the disruption of this enzyme results with accumulation of a toxic intermediate, methacrylyl-CoA, which inhibits 3-ketoacyl-CoA thiolase activity and blocks peroxisomal  $\beta$ -oxidation (Lange *et al.*, 2004). Further examination of the *chyl* mutant have allowed a better understanding of the timing of Val catabolism, the intracellular localization of this process, and the overall contribution of Val catabolism in *Arabidopsis* metabolism (Zolman *et al.*, 2001). More recently, Ibdah *et al.* (2009) have proposed *chyl* mutant has a deficiency of benzoic acid-containing glucosinolates in the seeds suggesting that this gene is involved in the synthesis of benzoic acid.

#### *Valine, leucine and isoleucine metabolism*

Interestingly, four genes represented in our microarray platform and whose expression was up-regulated in ripen receptacles, presented high homology of sequence with genes putatively coding for 3-hydroxyisobutyryl-Coenzyme A hydrolases (*UCOESTup10*, 113, 675

and 1710) (Table 2). Furthermore, the amount of transcript corresponding to two of them was very high in receptacle, suggesting an important role for these enzymes in the physiology of ripening process. It has been demonstrated that 3-hydroxyisobutyryl-Coenzyme A hydrolase converts 3-hydroxyisobutyryl-Coenzyme A to 3-hydroxyisobutyric acid. Thus, this enzyme plays an important metabolic role related with the degradation of the branched amino acid valine. Finally, the valine degradative pathway renders propionyl-CoA that can be used as energy source or utilized for biosynthetic purposes (Wanders *et al.*, 2012). At present, any 3-hydroxyisobutyryl-Coenzyme A hydrolase has been characterized in higher plants yet. Gene silencing genetic reverse approaches must be used to elucidate the physiological function that these interesting enzymes play in the maturation of the strawberry fruit receptacle.

### ***Nitrate reductase***

Nitrogen assimilation is a vital process controlling plant growth and development. In high plants, nitrate is the major nitrogen source, after taken up into plant cells, and it must be reduced to ammonia for further usage. As the first enzyme in nitrate reduction pathway, the nitrate reductase (NR, NIA) is critical for regulation of the nitrogen assimilation (Campbell *et al.*, 1999). In our microarray analysis, we have observed the overexpression of a nitrate reductase in ripen receptacle (*UCOESTup373*) (Table 2). This gene exhibited high level of expression so that it could have an important role in the fruit ripening processes. It is well documented that the amount and activity of NR is strongly controlled at transcriptional and post-transcriptional levels by nitrate, light and CO<sub>2</sub> levels, circadian rhythms, nitrogen and carbon metabolites, phytohormones, etc. (Wang *et al.*, 2011). Posttranslational mechanisms could reversibly modulate NR activity and permit quick responses to environmental and cellular metabolism changes, being the dominant regulation mechanism of NR activity (Wang *et al.*, 2011). Previous studies have showed that the phosphorylation may rapidly inactivate NR in response to several signals, including dark, decrease in CO<sub>2</sub> levels or increase in cytosolic pH (Su *et al.*, 1996; Campbell *et al.*, 1999). On the other hand, application of exogenous reactive oxygen species (ROS) or accumulation endogenous ROS in some conditions, causes the rapid activation of NR via phosphorylation (Wang *et al.*, 2010). For example, during light-to-dark transitions, release of single oxygen is coupled with activation of NR (Cookson *et al.*, 2005). Application of exogenous salicylic acid or accumulation of endogenous salicylic acid induced the ROS generation, also could activate MPK6 and increase total NR activity (Overmyer *et al.*, 2000; Umebese *et al.*, 2009). Phosphorylation at S627 of NR by MPK6 may represent a rapid activation mechanism when plants need excessive nitrate reduction (Wang *et al.*, 2011).

### **3.3.3. Organoleptic properties of the fruit receptacles**

#### ***Aroma related genes***

The volatile compounds emitted by strawberry fruits contribute to the flavor of the fruit. More than 360 volatiles are produced by the strawberry fruit but not all are equally important for the overall aroma. Aliphatic esters contribute to the aroma of nearly all fruits, being some of them responsible for a particular fruit aroma. These flavor esters are biosynthesized by enzymatic reactions catalyzed by alcohol acyltransferases (AATs), which link alcohols to CoA-activated acyl moieties. Numerous *AAT* genes have been isolated and characterized in fruits indicating their physiological key role in the production of aliphatic esters components of the fruit aroma (Aharoni *et al.*, 2000; Beekwilder *et al.*, 2004; El-Sharkawy *et al.*, 2005).

Our array studies have detected in ripen fruits a strong increase of the expression of two genes *UCOESTup90* and *UCOESTup134* (Table 3), both code two different AATs proteins (*FaAAT1* and *FaATT2*). *FaAAT1* gene corresponds to the strawberry *SAAT* gene, previously identified by Aharoni *et al.*, (2000), and whose recombinant enzyme catalyzes the formation of esters using aliphatic medium chain alcohols in combination with various chain length acyl-CoA as substrates (Aharoni *et al.*, 2000). On the other hand, *FaAAT2* gene presents a high homology of sequence with a gene coding a putative alcohol acyltransferase of *Malus domestica* and has been functionally characterized in this study (Chapter 2). Both enzymes play different or synergistic physiological roles related to the production of volatiles in ripen fruits.

Similarly a gene encodes a quinone oxidoreductase (*FaQR*, *UCOESTup131*) increased its expression level in ripen fruits (Table 3). This enzyme is related to the biosynthesis of 4-Hydroxy-2,5-dimethyl-3(2H)-furanone (HMDF), one of the most important volatiles of the overall strawberry flavor (Raab *et al.*, 2006). As in the case of the two *FaAAT* genes, the *FaQR* expression was mainly detected in strawberry receptacle. These data suggest that the expression of all genes involved in strawberry fruit flavor are probably under the control of the same developmental ripen-related regulatory developmental program.

#### ***Fatty acids-derived and other lipophilic flavor compounds***

Specifically, flavors ester production relies upon the supply of alcohols and acyl-CoA formed during  $\beta$ -oxidation.

In plants, the majority of volatiles on a quantitative and qualitative basis originate from the degradation of saturated and unsaturated straight-chain fatty acids by  $\alpha$ - and  $\beta$ -oxidation processes (Schwab *et al.*, 2008). Additionally, de novo synthesis and hydrolysis of acyl carrier protein (acyl ACP) can also provide volatile acids (Schwab *et al.*, 2008). In fruits, alcohols can also be formed by hydrogenation of aldehydes through the action of flavor-related alcohol dehydrogenases (ADHs) (e.g. Manriquez *et al.*, 2006). In our microarray study, the expression of genes putatively coding a stearyl ACP desaturase (*UCOESTup1377*), an enoyl-CoA hydratase (*UCOESTup1621*), an Acyl-CoA thioesterase (*UCOESTup2450*) and a malonyl-CoA decarboxylase (*UCOESTup642*) were up-regulated in ripen fruit receptacle (Table 2). These genes seem to be involved in fatty acid metabolism related to the production of volatiles along the fruit ripening process and/or constitute structural components of the lipid bodies that are involved in the cell lipid storage. Cells store triacylglycerides (TAGs) in organelles termed oil bodies (OBs) (Poxleitner *et al.*, 2006). Thus, upon ripening, TAGs present in the OBs could catabolize to release free fatty acids in order to provide substrates for volatiles production.

The expression of these genes were also strongly expressed in ripen fruit receptacles in comparison with the expression observed in vegetative tissues. These expression profiles match with the expression profiles of the strawberry alcohol acyltransferases and quinone reductase genes represented in the array, which could implicate these genes in the process of volatile ester formation in strawberry (Aharoni *et al.*, 2000). Besides, these entire expression patterns were also coincident with those observed for genes related to the physiological clues involved in the determination of the main characteristics related to the receptacle fruit quality characteristics, indicating a probably common regulatory network for these metabolic processes.

### ***Carboxylesterases***

The sequences of three up-regulated genes represented in our array (*UCOESTup143*, *643* and *965*) presented a high homology of sequence with those of genes of *Malus* encoding CXE carboxylesterases (Table 3). In addition, two of them (*UCOESTup143* and *643*) showed high expression levels in fruit receptacle. Carboxylesterases (CXE, EC.3.1.1.1) are metabolic enzymes that catalyze the hydrolysis of carboxylic esters into their corresponding alcohols and carboxylic acids. Recently, it has been demonstrated that two ripening-related CXE carboxylesterases genes from *Malus domestica* (*MdCXE1* and *MdCXE16*) are involved in the production of alcohols, as hexanol or butanol, from their corresponding esters. Perhaps, carboxylesterases contribute to the production of these increased alcohols through the hydrolysis of increasingly abundant esters during ripening (Souleyre *et al.*, 2011).

## **3.3.4. Flavonoid and phenylpropanoid metabolism**

### **3.3.4.1. Genes of shikimate pathway**

The shikimate pathway converts these sugar phosphates to aromatic amino acids such as phenylalanine, which becomes the precursor for the phenylpropanoid, flavonoid and anthocyanin biosynthesis pathways. Shikimate dehydrogenase (SKDH) is one of the crucial enzymes of the shikimate pathway. Our transcriptomic studies have shown a clear up-regulation of the expression corresponding to a gene coding a SKDH in mature red fruit receptacle (*UCOESTup1134*) (Table 3). Thus, SKDH gene could be involved in the increase of anthocyanins in strawberry fruit after harvest (Cao *et al.*, 2010).

### **3.3.4.2. Genes of phenylpropanoids, anthocyanins and flavonoids pathways**

Phenylpropanoids biosynthetic pathway is well understood and is conserved among seed plants (Tanaka *et al.*, 2008). In *Fragaria x ananassa*, the phenylpropanoid and flavonoid pathways have been the object of enzymological, metabolomic and molecular studies (Almeida *et al.*, 2007). In our microarrays studies, we have detected genes involved in the general pathway of synthesis of phenylpropanoids, anthocyanins and flavonoids metabolites. Between the genes identified are two phenylalanine ammonia lyases (*UCOESTup1333*; *UCOESTup755*), one cinnamate-4-hydroxylase (*UCOESTup677*) and two 4-Coumarate-CoA ligases (*UCOESTup116*; *UCOESTup2205*) (Table 3).

### ***Phenylpropanoids biosynthesis pathway***

The biosynthesis of monolignols requires two enzymatic steps that branch off the general phenylpropanoid pathway and are catalyzed by cinnamoyl-CoA reductase (CCR) and cinnamyl alcohol dehydrogenase (CAD). We have observed that two CCR genes (*UCOESTup583*; *UCOESTup1780*) and several CAD genes (*UCOESTup60*; *UCOESTup194*; *UCOESTup397*; *UCOESTup1065*) increased its expression in red-ripen fruit receptacle (Table 3). These expression profiles may be related to an increase of the vascular bundles lignifications, as previously it has been described by Aharoni *et al.* (2002). Additionally, both genes could provide to the receptacle cells with precursor of the volatile eugenol and their expression pattern could be related to vascular bundle formation, which occurs principally during the green stages of receptacle fruit growth.



Eugenol is a phenylpropene derived from *p*-coumaryl, sinapyl and coniferyl alcohols. It is considered one of the compounds that are part of the aroma of both *F. x ananassa* and *F. vesca* fruits (Pyysalo *et al.*, 1979). Treatments of strawberry with eugenol increased the antifungal and antibacterial activity of the fruit and enhanced the free radical scavenging capacity as well as the antiproliferative activity in fruit (Wang *et al.*, 2007). In our microarray study, we have detected changes in the expression of a putative gene that coding a eugenol synthases (*PCEBER*, *UCOESTup32*), enzyme responsible of the eugenol biosynthesis (Table 3). Its expression was strongly up-regulated in ripen fruit receptacles and was practically receptacle fruit specific. This expression pattern profile, similar to those found for other aroma related genes, suggests the involvement of this gene in ripen-related eugenol biosynthesis. This physiological role is also supported by a parallel increment of the cinnamyl alcohol dehydrogenase genes expression, enzymes responsible of the sinapyl and coniferyl alcohols production during the receptacle fruit ripening process (Blanco-Portales *et al.*, 2002).

### ***Flavonols, isoflavonols and anthocyanidin biosynthesis pathway***

In ripe strawberry fruit receptacle, anthocyanins are the major flavonoids compounds compared to flavonols, flavan-3-ols and simple phenols. The vast majority of genes involved in these metabolic pathways are represented in our microarray. Thus, the studies carried out in this chapter showed that the expression of genes coding two UDP glucose:flavonoid-3-O-glucosyltransferase genes [*UCOESTup12* (*FaUFGT*); *UCOESTup694* (*UFGT1*) and *UCOESTup695* (*UFGT2*)], several UDP-glucosyl transferases genes [*UCOESTup14* (*FaGT1*); *UCOESTup628* (*FaGT2*); *UCOESTup43* (*FaGT3*); *UCOESTup34* (*FaGT4*); *UCOESTup135* (*FaGT6*) and *UCOESTup1003* (*FaGT7*)] and different dihydroflavonol-4-reductases (*UCOESTup435*; *UCOESTup838*; *UCOESTup1507* and *UCOESTup2528*) (Table 3), was up-regulated in ripen receptacles as has been previously reported (Lunkenbein *et al.*, 2006; Almeida *et al.*, 2007; Griesser *et al.*, 2008). These fruit specific glucosyl transferases have been functionally characterized and its involvement in the glucosylation of anthocyanidins and flavonols has been well established (Lunkenbein *et al.*, 2006; Griesser *et al.*, 2008).

Besides, we have been identified in our microarray studies two chalcones syntases [*UCOESTup1434* (*FrCHS5*); *UCOESTup1441* (*FrCHS2*)], two chalcones isomerases [*UCOESTup2572* (*CHI*); *UCOESTup2573* (*CHI*)] one anthocyanidin synthase [*UCOESTup1230* (*FaANS*)] and a flavanone 3 $\beta$ -hydroxylase [*UCOESTup1565* (*FrF3H1*)] (Table 3). These results indicate that the major regulatory points for the phenylpropanoids biosynthesis in ripen receptacles of *Fragaria x ananassa* cv Camarosa are the metabolic reactions catalyzed by FaCLs and did not support that FaCHS plays a regulatory role in this metabolic pathway. In fact, in the experiments reported by Almeida *et al.* (2007), the high transcript levels of FaCHS gene detected in T/R stages were in contrast with the low FaCHS activity found in other studies (Halbwirth *et al.*, 2006). The high up-regulation of the expression corresponding to different genes as *FaUFGTs* and *FaDFRs* in ripen receptacles suggests that these genes are regulatory key point of the high anthocyanins biosynthesis observed in ripen fruits (Almeida *et al.*, 2007). Similarly, the up-regulation of *FaCADs* gene would indicate a similar important regulatory point for these genes in the biosynthesis pathways leading to the production of monolignols and flavonols compounds, as it has been detected in strawberry fruits (Almeida *et al.*, 2007).

As in the case of genes related with flavor or firmness characteristics, the expression of the genes related with phenylpropanoid pathway presented very high transcript levels in receptacle than those found in vegetative tissues.

### ***Transport of flavonoids***

Flavonoids glycosides, including anthocyanins, are water soluble compounds that are transported and accumulated in large central vacuoles of most plants (Pourcel *et al.*, 2009). Transport mechanism is scarcely understood though may be redundant. The first established flavonoid transporter mechanism involves a glutathione S-transferase (GST)-like protein, however the molecular mechanism whereby these proteins achieve the transport has not yet been clarified (Tanaka *et al.*, 2008). Recently, it have been demonstrated that a membrane protein of the multidrug and toxic efflux transporter family (TT12) is involved in the vacuolar accumulation of glycosilated anthocyanidin and proanthocyanidin in *Arabidopsis* and *Medicago sativa* plants (Marinova *et al.*, 2007; Zhao and Dixon, 2009). In this sense, our microarrays studies have detected several genes encoding putative TT12 transporters (*UCOESTup29*, 123, 257, 403, 450, 622, 1605, 1802) and several GST-like proteins (*UCOESTup5*, 47, 201, 520, 547, 645, 813, 1322, 1402, 1619, 1635) strongly up-regulated in ripen receptacle fruits and whose expression patterns are identical to those found for genes involved in flavonoid biosynthesis (Table 3). This correlation indicates that the proteins coded for both genes must be involved in flavonoid vacuolar accumulation in receptacle cells along fruit development and ripening. Interestingly, intact flavonoid exerts control of the TT12 transporter in barley (Tanaka *et al.*, 2008).

### ***Other proteins related to the phenylpropanoids, anthocyanins and flavonoids pathways***

#### ***Fra a***

Recent functional analyses have identified other genes related to the phenylpropanoids, anthocyanins and flavonoids pathways. Thus, the *Fra a* genes have been identified as essential genes for the colour formation in strawberry fruits (Muñoz *et al.*, 2010). In our microarrays studies, we detected an increase of *Fra a 2* allergen gene expression (*UCOESTup787*) in ripen fruits (Table 3). This gene is homologous to the pollen allergen gene *Bet VI* (Alm *et al.*, 2007). Transitory down regulation of *Fra a* genes expression in strawberry ripen fruits produced colorless fruit consistent with the parallel down-regulation of the phenylalanine ammonia lyase (*FaPAL*) and to a lesser extent of the chalcone synthase (*FaCHS*) transcript levels (Muñoz *et al.*, 2010). So, a potential function as carrier of pathway intermediates or as (co-)transporter of anthocyanins into the vacuole has been suggested for *Fra a* gene (Muñoz *et al.*, 2010).

#### ***Ketone/ziringone syntase***

Other interesting gene detected in the analysis of our microarray showed homology with a raspberry ketone/ziringone syntase 1 (*RZS1*, *UCOESTup665*) (Table 3) (Koeduka *et al.*, 2011). This gene participates in the biosynthetic pathway of raspberry ketones synthesized with a reaction similar to that catalyzed by chalcone synthase and stilbene synthase (Abe *et al.*, 2001). The *RZS1* transcript level was high in the mature stage of raspberry fruits, which was the predominant tissue to produce raspberry ketone (Koeduka *et al.*, 2011).

### 3.3.5. Genes of alkaloids metabolism

Alkaloids are physiologically active secondary metabolites containing heterocyclic nitrogen in their structures. These complex molecules are widespread in the plant kingdom and it is estimated that about 30 % of all plants contain alkaloids (Facchini *et al.*, 2001; Ziegler and Facchini, 2008). Most theories propose a role for alkaloids in the interaction of plants with their environment, either by providing a chemical defense against pathogens or by participating in different plant-insect interactions (Grayer and Harborne, 1994; Rhodes, 1994; Ziegler and Facchini, 2008). The contributions of alkaloids to plant fitness to their surroundings may be modulated by the rate and type of alkaloids produced in response to biotic and abiotic factors (Bennet and Wallsgrove, 1994; Kutchan, 1995; Ziegler and Facchini, 2008).

#### *Anthranilate synthases*

Two genes represented in our array platform (*UCOESTup552* and *561*) code for anthranilate synthases (Table 3). The expression of both genes was up-regulated and its levels of transcript were also high in red ripen receptacles. Anthranilate synthase (AS), composed of  $\alpha$  and  $\beta$  subunits, is a branch-point enzyme converting chorismate to anthranilate, leading to the synthesis of Trp and other indole alkaloid derivatives. In higher plants, genes encoding the  $\alpha$  subunit of anthranilate synthase have two or more copies, which differentiate into two major groups: genes associated with steady-state functions of the cell and genes that are induced by stress (Mobley *et al.* 1999; Tozawa *et al.* 2001; Matsukawa *et al.* 2002).

#### *Vindoline*

Vindoline constitutes the main terpenoid indole alkaloid accumulated in leaves of *Catharanthus roseus* (Guirimand *et al.*, 2011). The desacetoxyvindoline 4-hydroxylase (D4H) (*UCOESTup33*), which catalyzes the last reaction in vindoline biosynthesis, was highly up-regulated in ripen fruit receptacle (Table 3). Previously studies have shown as the expression of D4H appears to be under complex, multilevel developmental and light regulation (Vazquez-Flota *et al.*, 1998). Recently, Guirimand *et al.* (2011) have proved that *D4H* gene plays a regulatory role during the vindoline biosynthesis in *Catharanthus roseus*. Our microarray study has also identified a set of genes implicated in alkaloid biosynthesis that is up-regulated in fruits ripening (Table 3). The vinorine synthases are member of the BAHD acyl transferase family, which play a central role enzyme in the biosynthesis of alkaloids (Ma *et al.*, 2004; Ma *et al.*, 2005), however the productions of alkaloids in fruits have not been characterized. The amino acid sequences correspondent to *UCOESTup73*, *UCOESTup574* and *UCOESTup761* showed us that the three proteins contain the BAHD domain. Among then, *UCOESTup574* shows both a strong up-regulation of its expression and the highest amount of transcripts in ripen receptacle. Thus, probably this gene plays has an important physiological role related with the metabolic processes that are produced along the fruit ripening process (Table 3). Thus, the functional role played by this putative strawberry and ripening-related vinorine-synthase gene should be clarified by reverse genetic experiments.

### 3.3.6. Other genes related to secondary metabolism

#### *Aldo keto reductases*

Our microarrays studies have also identified several aldo keto reductases genes (*UCOESTup364*; *UCOESTup1124*; *UCOESTup1928*) (Table 3). Recently, a gene that encodes an aldo keto reductase (*FaGALUR*) has been characterized in strawberry (Cruz-Rus *et al.*, 2011). This gene is involved in the Vitamin C biosynthesis (Cruz-Rus *et al.*, 2011) although the production of this compound in strawberry fruits is not completely clarified by the expression of this gene (Zorrilla-Fontanesi *et al.*, 2011). In fact, it has suggested the existence of a homologue gene to *FaGALUR* that would be also involved in the production of Vitamin C in strawberry (Zorrilla-Fontanesi *et al.*, 2011).

#### *Cytochrome P450*

Plant cytochromes P450 (CYPs) are involved in a wide range of biosynthetic reactions, leading to various fatty acid conjugates, plant hormones, defensive compounds, or medically important drugs (Bolwell *et al.*, 1994). We have observed the expression of several cytochromes P450, which some of them are strongly up-regulated in red ripen receptacles (Table 3). Plant P450s catalyze a vast diversity of monooxygenation/hydroxylation reactions in secondary metabolism and some of them are involved in reactions such as methylenedioxy-bridge formation, phenol coupling reactions, oxidative rearrangement of carbon skeletons and oxidative C-C bond cleavage. Terpenoids, which represent the largest class of characterized natural plant compounds, are often substrates for plant CYPs (Mizutani *et al.*, 2011). In addition, in our microarray platform, we have observed the expression of CYP86B (*UCOESTup305*), which is a subfamily of cytochrome P450 monooxygenases (Table 9). In *Arabidopsis thaliana*, CYP86B1 is a very long chain fatty acid hydroxylase specifically involved in polyester monomer biosynthesis during the plant development (Compagnon *et al.*, 2009).

#### *S-adenosyl-L-methionine-dependent methyltransferase*

Plant S-Adenosyl-L-methionine-dependent methyltransferases are a large family of enzymes with broad biological functions. These enzymes are involved in the O-methylation of many secondary metabolites of plants, as pectins, phenylpropanoids, flavonoids, lipids, proteins, polysaccharides, polynucleotides, etc. These modifications result in a myriad of crucial biological functions (Andersen and Markham, 2006; Huguene *et al.*, 2009)

In our transcriptomic study, we have detected several genes encoding these types of proteins (*UCOESTup197*, *500*, *655* and *1457*) whose expression was up-regulated in ripen-receptacles (Table 3). Two of them (*UCOESTup197* and *500*) showed the highest levels of up-regulation and of amount of transcripts, indicating the O-methylation of abundant metabolites in ripen fruits as for instance flavonoids and phenylpropanoids. However, reverse genetic approaches combined with non-target metabolomic analysis, should be necessary to determine the functional role played for these genes along the ripening process.

### 3.3.7. Hormone metabolism and signaling

#### 3.3.7.1 Hormonal regulation of the strawberry receptacle ripening process

A number of plant regulators including auxin, ethylene, gibberellins and abscisic acid (ABA) have been proposed as implicated in the control of berry development and ripening. However, the role played by these plant hormones in the strawberry fruit receptacle development and ripening processes remains very poorly understood. Our microarrays analysis may shed light regarding the physiological role played by these hormones in these important fruit processes.

#### *Auxins*

In strawberry fruits, it was proposed that the expansion of the receptacle cells during the early stages of fruit development that promotes the growth of the receptacle is mediated by the auxins synthesized by the achenes (Perkins-Veazie, 1995). The auxins are exported from the achenes to the receptacle through the vascular bundles promoting the fruit growth and inhibiting the ripening process by activation of fruit growth related genes while repress ripening-related genes (Perkins-Veazie, 1995). The declining of receptacle auxin content during the fruit development trigger receptacle fruit ripening through the induction of the expression of ripening-related genes (Given *et al.*, 1988b).

The IAA levels in plants are modulated by a specific group of amidohydrolases (ILL2 amidohydrolases) that release the active hormone from its auxin-amino acid conjugated storage forms (Bitto *et al.*, 2009). We have detected that the expression of two genes coding iaa-amino acid hydrolases was up-regulated in ripen receptacle (*UCOESTup1303* and *UCOESTup2085*). Similarly, the expression of two different indole-3-acetic acid-amido synthetase (GH3) genes (*UCOESTup831* and *UCOESTup2520*) were up-regulated in ripen receptacle (Table 4). *GH3* genes code IAA-amido synthetase which conjugates IAA to amino acids regulating the free auxin content in plants (Staswick *et al.*, 2005; Wang *et al.*, 2008). Involvement of these genes with ripening-associated process has been proposed in non-climacteric fruits as pepper or grape (Liu *et al.*, 2005; Böttcher *et al.*, 2010). Also, it has been proposed that these enzymes could participate in IAA degradation through the biosynthesis of IAA-conjugates that may inactivate the IAA function which enables ripening (Staswick 2009; Böttcher *et al.*, 2010). Auxin-response factors (ARFs) are transcription factors acting on the auxin signaling pathway as activator or repressor of the expression of auxin regulated genes (Tiwari *et al.*, 2003; Benjamins and Scheres, 2008). They can heterodimerize with Aux/IAA proteins modulating the expression of auxin-responsive genes (Wang *et al.*, 2011). Our study also shows the transcript level increase of a gene that code ARF regulators (*UCOESTup1428*) in red ripen receptacle (Table 4). Besides, genes presenting a high sequence homology with *germin-like* genes (*UCOESTup727*) exhibited higher levels of expression in ripen strawberry fruit receptacle (Table 4). The expression of *germin-like* genes has been related with the evolution of the auxin content during the fruit development in plum (El-Sharkawy *et al.*, 2010). Similarly, in our transcriptomic analyses, we have found six *SAUR* genes whose expression was strongly up-regulated in ripen fruits (*UCOESTup173*, *182*, *206*, *928*, *977* and *1136*) (Table 2). *SAUR* (small auxin-up RNA) genes constitute a large auxin-responsive gene family whose function is largely unknown.

It has been indicated that the auxins content in the receptacle decreases in red ripen fruits (Given *et al.*, 1988b). Our microarray study detected different set of genes coding auxins

related proteins whose expression was down-regulated in ripen fruit receptacle (data not shown). The decreased expression of many auxin-related genes in ripen receptacles showed by our transcriptomic studies supports the clear relationship, previously reported, between a declining in the auxins content of the fruit receptacle and the fruit ripening. However, the increased expression of a different set of auxin-related genes in ripen receptacles also indicates that these hormones could play an additional physiological role in the ripening process, probably related with the secondary expansion of the cell of the fruit receptacle along the ripening (Medina-Escobar *et al.*, 1997b; Benítez-Burraco *et al.*, 2003; Palomer *et al.*, 2006). The results indicate that auxins use apparently different signaling pathways along the growth and ripening processes of fruit receptacles and open new perspectives that suggest that, similarly to those previously demonstrated for climacteric fruits (El-Sharkawy *et al.*, 2010), the auxins seem also to be involved in some of the mechanisms that control the physiological processes involved in receptacle fruit ripening of this non-climacteric fruits.

### ***Gibberellins***

In strawberry, there is very scarce information related with the functional physiological roles that play the gibberelins (GAs) during the strawberry fruit growth and ripening process. It was observed that GA<sub>3</sub> did not stimulate growth when applied to fruits from which achenes had been removed (Dreher and Povaiah, 1982). In addition, it was demonstrated that the exogenous application of giberellic acid (GA<sub>3</sub>) to strawberry fruits delayed the development of red color (Martínez, 1996). Later, Bustamante *et al.* (2009) described a reduction of the protein and mRNA levels of the ripen-related and fruit-specific enzyme  $\beta$ -xylosidase after the application of GA<sub>3</sub> to strawberry white fruits. Recently, a preliminary study has proposed that gibberellins could be involved in the development and ripening of the fruit receptacle (Csukasi *et al.*, 2011). These studies suggest that gibberellins could play a dual regulatory physiological role, first promoting receptacle growth in combination with the auxins produced in the achenes, and afterwards playing a relevant role related with the receptacle ripening process. Supporting this proposal, our microarrays studies have shown a clear induction in ripe fruit receptacle of two genes that coding enzymes involved in the biosynthesis of gibberellins, such as a Giberellin 2 oxidase (*UCOESTup266*) and a Giberellin 3 beta-dioxygenases (*UCOESTup1835*) (Table 4).

The role played for GAs probably could be related with the differentiation of cambial meristem cells to xylem tissue and with an increase of xylem lignification in receptacle vascular tissue during the ripening process. Experiments in poplar, aspen and tobacco have demonstrated that transgenic plants which over-expression of these genes exhibit significantly increased levels of xylem lignification (Biemelt *et al.*, 2004). In accordance with this suggestion, our microarray studies have also shown the up-regulation of genes coding key enzymes of the lignin biosynthesis pathway, as cinnamyl CoA reductase and cinnamyl alcohol dehydrogenase in ripen fruit receptacles (*UCOESTup583*, *1780*, *60*, *194*, *397* and *1065*) (Table 4).

### ***Absciscic acid (ABA) metabolism and signaling***

There are only scarce studies relating the absciscic acid (ABA) with the strawberry fruit ripening process. However, it has been reported that ABA is present in both receptacle and achene tissues, with amounts changing during the berry development (Lis *et al.*, 1978; Archbold and Dennis, 1984). Besides, it has been indicated that ABA treatments through fruits peduncles for three days stimulate anthocyanin accumulation (Bustamante *et al.*, 2009).

It was proposed that the increase in the receptacle abscisic acid (ABA) content could promote the strawberry ripening process (Perkins-Veazie, 1995). In plants, ABA biosynthesis proceeds through the plastid-localized 2-C-methyl-D-erythritol 4-phosphate (MEP) pathway (Cazzonelli and Pogson, 2010). Our microarray analyses have shown the expression of genes that coding an enzyme involved in crucial steps of ABA biogenesis pathway. One of these genes coding a 9-cis-epoxycarotenoid dioxygenase 3 (*UCOESTup1120*) which was induced in ripen fruit receptacle (Table 4). This gene has large amount of expression in ripe fruit receptacle which suggests that it could be involved in the ripening processes (Table 4). It has been shown that the silencing of this gene avoid anthocyanin production in ripen strawberry fruits (Jia *et al.*, 2011). These results indicate that this metabolic pathway is operative in fruit receptacle probably to produce ABA in ripen receptacles and support that this hormone could play important physiological role in the strawberry fruit ripening process. Besides, we observed the up-regulation in red ripen fruit receptacles of the *FaPYR/RCAR/PYL* (*UCOESTup888* and *UCOESTup1025*) gene (Table 4) that presents a significant sequence homology with putative ABA receptors containing the START domain (Weiner *et al.*, 2010). The presence of the signatures SGLP ('cap' loop) and HRL ('lock' loop), always conserved in these proteins cDNA (Weiner *et al.*, 2010), in the deduced protein sequence derived of the *FaPYR* supports even more that this gene codes an ABA receptor. Recently, studies showed that the down-regulation a similar but not identical *FaPYR1* gene delayed the fruit ripening and also decreased the anthocyanin content in receptacle of strawberry ripen fruits. This expression silencing also showed that a set of ABA-responsive gene transcripts, including *AB11* and *SnRK2*, was altered (Chai *et al.* 2011). Furthermore, the loss of red colouring in *FaPYR1* RNAi fruits could not be rescued by exogenously applied ABA, which could promote the ripening of wild-type fruits. These results demonstrate that the putative ABA receptor *FaPYR1* acts as a positive regulator in strawberry fruit ripening (Chai *et al.* 2011). Additionally, we have also observed an increased amount of transcripts corresponding to a *FaASR* gene (*UCOESTup262*) encoding an ABA stress and ripening-induced protein (ASR) in receptacle of ripen fruits. These results indicated that *FaASR* gene has an important role in ripening process of ripen fruits. The ASR proteins have been reported to act as a downstream component involving in ABA signal transduction in both grape berry and tomato (Cakir *et al.*, 2003; Shkolnik and Bar-Zvi, 2008). The grape and tomato ASR proteins have been proposed to regulate the transcription of sugar- and abiotic stress-regulated genes in fruit and vegetative tissues (Cakir *et al.*, 2003; Saumonneau *et al.*, 2008; Shkolnik and Bar-Zvi, 2008). Recently, Chen *et al.* (2011) showed that *FaASR* may be involved in strawberry fruit ripening. They observed that an increase in the content of endogenous ABA might increase *FaASR* expression partially contributing to the acceleration of strawberry fruit ripening (Chen *et al.*, 2011). However, the functional mechanism through ASR protein regulates the ABA responses are not fully understood. Taken together, these results show that both *FaPYR2/FaASR* genes probably regulate the gene expression of ABA-dependent genes whose responses are not related with the organoleptics properties of the ripen fruit.

The sequences of genes *UCOESTup162* and *1400* present a high homology of sequence with those that code HVA22 proteins of higher plants. In our transcriptomic analysis, we have found that the expression of both genes was up-regulated in strawberry ripen fruits (Table 4). Homologs of HVA22 have been identified in diverse eukaryotes, including plants, fungi, mammals, flies and worms, but not in any prokaryotes (Guo and Ho, 2008). In several vegetative tissues of plants, the expression of *HVA22* genes is dramatically up-regulated by abscisic acid and abiotic stress, as cold, drought, extreme temperatures and salt stresses (Shen *et al.*, 1993; Shen *et al.*, 2001; Chen *et al.*, 2002). In barley (*Hordeum vulgare*), it was proposed that ABA induces the accumulation of HVA22 proteins capable of negatively

regulating GA-mediated vacuolation/programmed cell death in barley aleurone. These proteins could inhibit vesicular trafficking involved in nutrient mobilization to delay coalescence of protein storage vacuoles as part of its role in regulating seed germination and seedling growth (Guo *et al.*, 2008). Recently, it has been proposed that HVA22 proteins play a physiological role as suppressors of autophagy in both plants and yeast (Chen *et al.*, 2009). Curiously, several studies have shown that the HVA22 promoter could be regulated by WRKY transcriptional factors in response to those conditions where increases in the ABA production proceed (Zhang *et al.*, 2009). In this sense, it is noteworthy that several genes coding WRKYs TFs increased its expression along the ripening process in strawberry fruit receptacle. The existence of a relationship between WRKY and HVA22 expression must be clarified through functional studies based in reverse genetic approaches.

In opposition to those found for other hormones, we have not observed genes related with the biogenesis of ABA whose expressions are up-regulated in immature green receptacles (data not shown). So, our results could be in accordance with the proposal that ABA plays a physiological role only in the ripening process.

### ***Abscisic acid (ABA) and Isoprenoid metabolism***

Isoprenoids are functionally and structurally the most diverse group of plant metabolites (Thulasiram *et al.*, 2007). They can operate as primary metabolites, participating in essential plant cellular processes, and as secondary metabolites, of which many have substantial commercial, pharmacological, and agricultural value. Isoprenoid end products participate in a wide range of physiological processes in plants acting in them both synergistically, such as chlorophyll and carotenoids during photosynthesis, or antagonistically, such as gibberellic acid and abscisic acid during seed germination (Vranova *et al.*, 2012).

The function of isoprenoid compounds during environmental challenge is diverse. Some of them are involved in protection of the photosynthetic apparatus, the amount and composition of carotenoid compounds, particularly xanthophylls, with roles in detoxification of the cell from free radicals and reactive oxygen species (ROS) caused by high light intensity during drought stress (Demming-Adams and Adams, 1996; Niyogi *et al.*, 1997; Munne-Bosch *et al.*, 1999; Munne-Bosch and Alegre, 2000a,b). Others, as  $\alpha$ -tocopherol, are also important antioxidant agents (Abbasi *et al.*, 2007). Sterols have been reported as protectors of biological membranes during drought and cold stress (Nakamura *et al.*, 2001), while the isoprene seems to increase the thermotolerance in leaves of some plant species (Singsaas *et al.*, 1997). In our studies microarrays, we showed different genes involved in the biosynthesis of isoprenoid, which were up-regulated in strawberry ripen fruits (*UCOESTup922*, *1670*, *854*, *1727*, *2192*, *1610*, *72*, *2169* and *208*) (Table 4).

The phytohormone abscisic acid (ABA) is involved in the response to cold, salt and drought stress (Loyola *et al.*, 2012). Water deficit triggers the production of ABA, which in turn causes stomatal closure and induces the expression of drought stress-related genes, whose products allow temporary acclimatisation of diverse plant species (Seki *et al.*, 2007). Our study detected high transcript levels of a Phytoene synthase (*UCOESTup1573*) in red-ripen receptacle (Table 4). This enzyme is directly involved in the ABA biosynthesis, so that high expression levels of *UCOESTup1573* gene might be involved in the ripening processes of red fruit receptacle (Table 4).



## ***Ethylene***

*AP2/ERF* (Ethylene Response Element) gene family encodes putative transcription factors (Shigyo *et al.*, 2006). These families of transcription factors are mostly associated with response to biotic and environmental stress or acts as key regulators in developmental process (Zhang *et al.*, 2009). In our microarrays platform, we have detected 10 *AP2/ERF* genes whose expressions were up-regulated (Table 1). The *UCOESTup889* and *UCOESTup752* exhibited large levels of expression in red fruit which suggest that it could be involved in ripening processes. Recently, an *AP2/ERF* gene (*SIAP2a*) has been identified and functionally characterized through transcriptional profiling of fruit maturation (Chung *et al.*, 2010). This ripening related gene, in contrast to previously described transcription factors, is a negative regulator of ripening (Chung *et al.*, 2010).

## ***Methyl Jasmonate (MeJA)***

MeJA and its free jasmonic acid (JA), both referred as jasmonates, are lipid-derived signals that mediate plant stress responses and development processes such as seed germination, flower and fruit development, leaf abscission and senescence (Avanci *et al.*, 2010; Wasternack *et al.*, 2010). In our study, we have identified an enzyme S-Adenosyl-L-methionine:jasmonic acid carboxyl methyltransferase (*UCOESTup69*) that catalyzes the methylation of JA to form MeJA (Table 4). The S-adenosyl-L-methionine:jasmonic acid carboxyl methyltransferase (JMT) have been functionally characterized corresponding to an enzyme of *Arabidopsis thaliana* (Seo *et al.*, 2001). These studies suggest that this enzyme is a key for the jasmonate-regulated plant responses (Seo *et al.*, 2001). Activation of JMT expression leads to production of methyl jasmonate that could act as an intracellular regulator, a diffusible intercellular signal transducer, and an airborne signal mediating intra- and inter- plant communications (Seo *et al.*, 2001).

### **3.3.7.2. Signaling**

#### ***Receptors***

Plants contain a large family of receptor-like kinases (RLKs) that regulate various growth and developmental processes, phytohormone perception and biotic and abiotic stress responses (Nurnberger *et al.*, 2006; Chae *et al.*, 2009; Lehti *et al.*, 2009). The adaptive responses of plants to extracellular or intracellular ligands and stimuli are governed by a functional continuum between the plant cell wall (CW) and the plasma membrane (PM) in which RLKs, with CW-bound extracellular domains, probably function as cell wall integrity sensors (Humphrey *et al.*, 2007; Chinchilla *et al.*, 2009). As numerous RLKs share conserved structural features within the extracellular domains, they can be grouped into protein subfamilies (Shiu *et al.*, 2004). A group of RLKs that are regarded as potential CW-PM linkers are the lectin receptor kinases. This receptor contains extracellular lectin motifs that are known to bind various carbohydrates. Based on the extracellular lectin motifs three types can be distinguished G, C, and L (Bouwmeester and Govers, 2009). We have observed an increased amount of transcripts corresponding to three G-type lectin receptor kinases (*UCOESTup431*, *1732* and *2230*) in receptacle of strawberry ripen fruit when compared with immature green receptacle (Table 4). G-type lectin receptor kinases are also called S-locus receptor kinases, historically known as S-domain RLKs. In Brassicaceae, the S-locus receptor kinase SRK acts as the stigmatic determinant of the self-incompatibility response and possibly functions as a receptor for the pollen ligand SCR/SP11 (Paetsch *et al.*, 2006). G-

type lectin receptor kinases were also shown to play roles in plant defence. The rice gene *Pid2*, for example, confers resistance to the fungal pathogen *Magnaporthe grisea* whereas *NgRLK1* from *Nicotiana glutinosa* was selected in a yeast two-hybrid screen as a putative interactor with capsicein, an elicitor from *Phytophthora capsici* (Kim *et al.*, 2010). Besides the G-type lectin motifs the extracellular domains of these proteins contain cysteine-rich EGF-like (epidermal growth factor) and PAN (plasminogen-appnenematode) motifs that both function in protein homodimerization (Naithani *et al.*, 2007). As yet, the role of the G-lectin motif is unknown and there is also no evidence for a function in ligand binding.

Besides, we observed the up-regulation in red ripen fruit receptacles of different legume-like or L-type lectin receptor kinases (LecRKs) genes (*UCOESTup121, 292, 434, 482, 732, 760* and *1675*) (Table 4). The LecRKs have extracellular domains resemble soluble legume lectins which are ubiquitous in leguminous seeds (Andre *et al.*, 2005). Although LecRKs are implied to function in diverse biological processes, their exact biological role has not yet been clarified. LecRKs that have been described to function during plant development include the SGC lectin RLK of *Arabidopsis*, which is required for proper pollen development (Wan *et al.*, 2008). More recently, Xin *et al.* (2009) showed that a specific subfamily of LecRKs is responsible for negatively regulating the abscisic acid (ABA) response during seed germination and hypothesized that these genes directly or indirectly affect defence. Lately, several reports have presented data linking ABA-signalling with defence responses (Asselbergh *et al.*, 2008). NbLRK1, a legume-like lectin receptor kinase from *Nicotiana benthamiana* was reported to interact intracellularly with the *Phytophthora infestans* elicitor INF1 and seems to be involved in the subsequent INF1-induced cell death (Kanzaki *et al.*, 2008). Another LecRK with a potential link to plant defence and pathogen response is LecRK79 in *Arabidopsis* (Gouget *et al.*, 2006). LecRK79 mediates CW-PM adhesions and hence the continuum between the cell wall and the plasma membrane (Gouget *et al.*, 2006). Its role in plant defence is, furthermore, supported by the observation that LecRK79 expression is induced upon inoculation with several nonhost and avirulent pathogens (Bouwmeester *et al.*, 2009). Taken together, these data suggests that LecRKs play crucial roles in both developmental and adaptive processes.

Other receptors are leucine-rich repeat receptor-like kinases (LRR-RLKs), which contain LRRs in their extracellular domain. These receptors are involved in many developmental processes and in host responses to biotic and abiotic stresses (Chinchilla *et al.*, 2009; Dievart *et al.*, 2011). Our microarray analysis have shown in ripen receptacle the over expression of genes that coding different leucine rich repeat-receptor like kinase (LRR-RLKs) (*UCOESTup196, 205, 286, 432, 456, 1435* and *2542*) (Table 4). Among them, *UCOESTup432* showed higher level of expression so that this receptor could have an important role in the fruit ripening processes (Table 4). Recently, a vast number studies have demonstrated major roles played by LRR-RLKs in plants during almost all developmental processes and in defense/resistance against a large range of pathogens (Dievart *et al.*, 2011). Forward and reverse genetic approaches have revealed various physiological functions of *Arabidopsis* LRR-RLKs (Morillo and Tax, 2006). Brassinosteroid insensitive1 (BRI1), the receptor for the plant steroid hormone, brassinolide (BL), constitutes one of the best studied plant LRR-RLK, and was shown to regulate stem elongation, vascular differentiation, seed size, fertility, flowering time, and senescence (Li *et al.*, 2002; Nam and Li, 2002; Wang *et al.*, 2005). Binding of brassinolide to an island domain that folds back between LRR repeat 21 and 22 was suggested to provide a docking platform for the formation of heteromeric complexes with another LRR-RLK, BAK1 (BRI1-associated receptor kinase1). Recently studies have showed as BAK1 and BAK1-interacting LRR-RLKs in plant immunity

(Kemmerling *et al.*, 2011). Another subset of plant LRR-RLKs has been shown to function as pattern recognition receptors mediating their cognition of microbial surface structures (pathogen or microbe associated molecular patterns, PAMPs/MAMPs) and plant innate immunity to microbial infection (Nürnberg and Kemmerling, 2006). For example, *Arabidopsis* FLS2 (Flagellin Sensing 2) and EFR (EF-Tu Receptor) sense bacterial flagellin and elongation factor EF-Tu, and thereby confer basal immunity to microbial pathogens displaying the respective cognate ligand (Zipfel *et al.*, 2006; Chinchilla *et al.*, 2007). The large number of LRR-RLK that are encoded by the *A. thaliana* genome and the proven role of FLS2 in plant immunity have prompted us to undertake a systematic survey for additional LRR-RLKs that mediate plant-pathogen encounters (Kemmerling *et al.*, 2007).

Our study has also showed the expression the cysteine-rich RLKs (CRKs) (*UCOESTup26* and *1425*) (Table 4), which represent a prominent subfamily of transmembrane-anchored RLKs. Acharya *et al.* (2007) characterized the gene CRK13 suggesting that up regulation of CRK13 leads to hypersensitive response-associated cell death, and induces defense against pathogens by causing increased accumulation of salicylic acid. In *Arabidopsis thaliana* has been shown that a CRK is transcriptionally induced by pathogens, salicylic acid and ozone (O<sub>3</sub>). However, its role in responses to biotic and abiotic stresses remains to be elucidated (Ederli *et al.*, 2011).

The wall-associated kinases (WAKs) are receptor-like kinases that are linked to the pectin fraction of the cell wall, and have a cytoplasmic protein kinase domain (Kohorn *et al.*, 2012). In our microarrays platform, we have detected a wall-associated receptor kinase (*UCOESTup765*) whose expression was up-regulated in red ripen fruit receptacles (Table 4). WAKs are clearly involved for cell expansion, so that WAKs are required for cell elongation (Anderson *et al.*, 2001; Wagner and Kohorn, 2001; Kohorn *et al.*, 2012). A WAK2 null allele, *wak2-1*, causes a loss of cell expansion roots, but only under limiting sugar and salt conditions (Kohorn *et al.*, 2006b). WAKs are also implicated in the pathogen response, and their expression is activated by numerous environmental stimuli (Denoux *et al.*, 2008; Brutus *et al.*, 2010; Kohorn *et al.*, 2012). Recent works supports the idea that WAKs are receptors for both pectin in the cell wall, and for pectin fragments, oligogalacturonic acids (OGs), generated during some pathogen attacks (Denoux *et al.*, 2008; Mohnen, 2008; Harholt *et al.*, 2010; Brutus *et al.*, 2010; Kohorn *et al.*, 2012).

The proline-rich, extensin-like receptor kinase (PERK) family is characterized by a putative extracellular domain related to cell wall proteins, followed by a transmembrane domain and kinase domain (Nakhamchik *et al.*, 2004). In our array platform, we observed the up-regulation in red ripen fruit receptacles of a proline-rich extensin-like receptor kinase (PERK) (*UCOESTup1103*) (Table 4). The isolation and characterization of PERK1 from *Brassica napus* displayed that this receptor respond to a wound and/or pathogen stimulus (Silva *et al.*, 2002). Haffani *et al.* (2006) showed as PERK receptor kinases from *Arabidopsis* are involved in growth and floral organ formation. Recently studies in *Arabidopsis* have demonstrated that a member of the proline-rich extensin-like receptor kinase family, *PERK4*, acts at an early stage of the ABA signaling pathway to inhibit root growth through intracellular calcium signaling (Bai *et al.*, 2009).

### ***Kinases***

Mitogen-activated protein kinase (MAPK or MPK) cascades are common mechanisms to translate external stimuli into cellular responses in all eukaryotes, including higher plants.

These protein kinase cascades consist of three subsequently acting protein kinases, a MAPK kinase kinase (MAPKKK), a MAPK kinase (MAPKK or MKK), and finally the MAPK (Menges *et al.*, 2008). Several genes that coding different mitogen-activated protein kinase kinase kinase (MAP3K) (*UCOESTup281*, *722*, *1263*, *1285*, *1725* and *1966*) and a mitogen-activated protein kinase (MAPK) (*UCOESTup2133*) were up-regulated in ripen fruit receptacle (Table 4). MAP3Ks are serine/threonine kinases that activate MAP2Ks through phosphorylation on two serine/threonine residues in a conserved S/T-X3-5-S/T motif. Likewise, MAP2Ks are dual-specificity kinases that phosphorylate MAPKs on threonine and tyrosine residues in the T-X-Y motif (Nakagami *et al.*, 2005). In plants, MAPK signaling appears to involve cross-talk with a variety of stress responses and developmental processes forming complex interconnected networks within cells. Traditional genetic and biochemical methods have identified MAP3K/MAP2K/MAPK signaling modules with overlapping roles in controlling diverse cellular functions (Taj *et al.*, 2010; Sörensson *et al.*, 2012). These include cell division, development, hormone signaling (abscisic acid-ABA, auxin and ethylene) and synthesis and response to abiotic stress (wounding, high and low temperature, high salinity, UV radiation, ozone, ROS, drought and high and low osmolarity, heavy metals) and pathogens (Nakagami *et al.*, 2005; Fernández-Pascual *et al.*, 2006; Colcombet *et al.*, 2008; Jammes *et al.*, 2009; Taj *et al.*, 2010). The first complete MAPK cascade in regulating plant defense against bacterial pathogen, MAP3K1-MAP2K4/MAP2K5-MAPK3/MAPK6-WRKY22/ WRKY29, was proposed as being downstream of the flagellin receptor kinase (FLS2 LRR), which potentially activates the MAP3K1 by phosphorylating the Ser/ Thr residues (Asai *et al.*, 2002). The role of MAPKs has been seen during symbiotic association between plant and pathogenic organism (Fernández-Pascual *et al.*, 2006). This suggests that activation of MAPK pathways is a specific response of the host cells to live bacteria which may lead to a successful symbiotic interaction, suggesting that MAPKs may take part in the recognition of compatible partners. Beside this symbiotic association, host MAPK cascades are also activated by fungal pathogens (Izumitsu *et al.*, 2009). Infection by plant fungal pathogen *Phytophthora infestans* led to the rapid transcriptional induction of *MAP3K19*, *MAP2K9* and *MAP2K4*, while with that of *Botrytis cinerea* infection led to the rapid transcriptional induction of *MAP3K18*, *MAP3K19* and *MAP3K20*, *Raf43*, *ZIK2*, *ZIK8*, suggesting that signaling to bacterial and fungal pathogen attack is distinct (Menges *et al.*, 2008). Beside this, the MAPK cascade comprising MAP3K-YODA-MAP2K4/MAP2K5-MAPK3/MAPK6, plays an important role in regulating stomatal development (Popescu *et al.*, 2009; Bayer *et al.*, 2009; Sörensson *et al.*, 2012). MPK3 and MPK6 have been shown to play important roles in plant development, such as during regulation of stomatal patterning (Wang *et al.*, 2007; Sörensson *et al.*, 2012). The hormones abscisic acid, salicylic acid, jasmonic acid, auxin and ethylene may interact with one another in regulating stress signaling and plant stress tolerance. Another MAPK cascade, MAP3K1-MAPKK1/MAPKK2-MAPK4-MKS1 mediates jasmonate and salicylate dependent defense responses (Qiu *et al.*, 2008). MAPKs may have role in ABA signaling, which mediates responses to environmental stress, chiefly water stress. MAPK9 and MAPK12, which are preferentially activated in guard cells, share functional redundancy and serve as positive regulators acting downstream of reactive oxygen species and calcium signaling, but upstream of anion channels in guard cell ABA signalling (Jammes *et al.*, 2009).

Other serine/threonine protein kinase detected in our array studies was *96 Pto kinase interactor 1* (*UCOESTup1364*) (Table 4). Probably this gene plays a relevant role in the fruit ripening processes, showing higher amount of expression in red fruits (Table 4). *Pto* was the first disease-resistance gene cloned from a plant that confers recognition of a specific pathogen (Martin *et al.*, 1993). The intracellular protein kinase that it encodes activates an

immune response in tomato (*Solanum lycopersicum*) to bacterial speck disease by interacting with either the AvrPto or AvrPtoB type III effector proteins that are delivered into the plant cell by *Pseudomonas syringae* pathovar *tomato* (Pedley and Martin, 2003; Xing *et al.*, 2007). This recognition event triggers signaling pathways leading to effector-triggered immunity (ETI), which inhibits pathogen growth (Oh and Martin, 2011). In cultivated and wild strawberries have been isolated Pto-like serine/threonine kinases which were in disease resistance (Martínez-Zamora *et al.*, 2008). Strawberry Pto-like clones presented sequences that were clearly identified as the activation segments contained in the Pto, and some of them showed residues previously identified as being required for binding to AvrPto resistance (Martínez-Zamora *et al.*, 2008).

### 3.3.8. Cell wall related-genes

One of the most important quality traits of strawberry fruit is its firmness. Moreover, the inverse correlation ship between fruit firmness and flavor (Salentjin *et al.*, 2003) makes important, for molecular breeding or transgenic approaches, the discovering of the genetic clues related with fruit firmness. Cell wall constituents contain pectic polysaccharides and xyloglucans. Along the strawberry fruit ripening, a degradation of the cell wall pectinate components has been described. In our array studies, we have detected that a set of genes coding cell wall hydrolases, as polygalacturonases (*UCOESTup18*, 218, 518, 791 and 1151), pectin-methylesterases (*UCOESTup411* and 1354), pectin esterases (*UCOESTup698*, 767, 1013 and 2210), pectate lyases (*UCOESTup1162*, 1603, 2138 and 2139), endo-polygalacturonases (*UCOESTup59* and 397), endo- $\beta$ -1,4-glucanases (*UCOESTup59*, 232, 365, 370, 481, 649 and 750),  $\beta$ -glucosidases (*UCOESTup151*, 1730, 2154, 2159 and 1096) and  $\beta$ -xylosidases (*UCOESTup709* and 1996) increased its expression in ripen fruit receptacle (Table 5). Moreover, we have also observed an increase in the mRNA abundance for three genes coding xyloglucan endotransglucosylase/hydrolase genes (XTH) enzymes (*UCOESTup653*, 858 and 1387) in ripen fruits (Table 5). Our results are coincident with those previously reported for these genes along strawberry fruit development and ripening where a functional role related with the depolymerization of pectic polysaccharides of the cell walls related with fruit softening have been proposed or demonstrated (Jiménez-Bermúdez *et al.*, 2002; Salentjin *et al.*, 2003; Bustamante *et al.*, 2006).

These expression profiles indicate that the transcriptional regulation of these cell wall hydrolases respond to different physiological clues to those observed for ripen related cell wall hydrolases and indicate their relationship with the molecular events related with the cell wall modifications that allow cell expansion process characteristic of the fruit growth and development. At this respect, it has been suggested that xyloglucan endotransglucosylase/hydrolase (XTH) and expansin genes are associated with petal growth and development (Harada *et al.*, 2011).

The expansins play important roles in cell wall loosening through non-enzymatic mechanisms. Besides, they are also involved in molecular events as cell expansion, wherein cell-wall modification occurs (Sampedro and Cosgrove, 2005). In this sense, we have observed that genes coding  $\alpha$  or  $\beta$  expansins (*UCOESTup303*, 855, 2226, 777 and 1527) up-regulated their expression in ripen fruit receptacle (Table 5).

During the fruit softening, there is a loss of galactose that might be related with the  $\beta$ -galactosidase activity detected in red strawberry fruit (Trainotti *et al.*, 2001). In our microarrays studies have detected a  $\beta$ -galactosidase gene (*UCOESTup77*), which were also

up-regulated in ripen fruit receptacle (Table 5). Previous studies showed as *Faβgal1* gene had an expression increment during the ripening stages, with a maximum of expression at the red stages, indicating that this gene might be to related with the softening process (Trainotti *et al.*, 2001).

We have also detected an increase of the amount of transcripts corresponding to several genes putatively coding different rhamnogalacturonate lyases (*UCOESTup55*, 263 and 2337) in ripen fruits (Table 5). The *UCOESTup263* gene displays high expression level, therefore it has probably an important role in the fruit ripening process. Additionally, the genes were predominantly expressed in fruit receptacle in respect to vegetative tissues. These expression patterns were identical to those found for other coding cell wall hydrolases included in our microarray platform. These results suggest a common regulatory mechanism for all ripening-related modifying enzymes. The cell wall pectic polysaccharides are composed by different pectins, homogalacturonans, rhamnogalacturonans type I (RG-I) and rhamnogalacturonan type II (RG-II). In plants, it has been proposed that rhamnogalacturonate lyases are able to cleave the main chain of the rhamnogalacturonan I (RG-I), a cell wall pectic polysaccharide (Deng *et al.*, 2006). However, there are scarce studies regarding the physiological roles of these enzymes in plant cell wall modifications. In this sense, some studies suggest that the disruption of the RG-I backbone could influence cell-cell interactions (Vicente *et al.*, 2007). Thus, this enzyme could be implicated in the decrease of the cell-cell interactions in fruit ripen receptacle.

The involvement of rhamnogalacturonate lyase in the degradation of plant cell wall pectins has not been still clarified. However, these groups of enzymes are components of the battery of enzymes that constitute the secretome of plant pathogenic bacterium (Kazemi-Pour, 2004). Functional studies by RNAi related with the role of this ripening-specific gene could play in fruit softening is actually being performed in our laboratory.

### 3.3.9. Stresses related genes

#### *Biotic stress*

During the strawberry culture and post-harvest, the fruit is susceptible to diseases caused by pathogens. The strawberry plant responds to the infection by pathogenesis-related protein accumulation. PR proteins were first observed in tobacco plants infected with tobacco mosaic virus (TMV) (van Loon and van Kammen, 1970), and they were subsequently identified in many other plants species. In strawberry ripen fruit, we detected an increase of PR proteins transcripts (*UCOESTup13*, 248, 251 and 712) (Table 6). The PR-3, -4, -8 and -11 families consists of chitinases belonging to various chitinase classes (I-VII). In our microarrays, we have observed the expression of several chitinases (*UCOESTup239*, 447, 335, 391, 1174 and 1241) in ripe fruit receptacle (Table 6). Chitin is a structural component of the cell wall of many fungi, as well as insects and nematodes, which are major pathogens and pests of crop plants (Collinge *et al.*, 1993). Chitinases are ubiquitously distributed in bacteria, fungi, animals and plants. They hydrolyze the  $\beta$ -1,4-linkage between N- acetylglucosamine residues of chitin (Zhang, 2006). Genes encoding a class III chitinase and two class II chitinases (designated as *FaChi2-1* and *FaChi2-2*) were cloned and their complete nucleotide sequences were obtained from strawberry (Khan, 2002). After fungal inoculation of plants with *C. fragariae* or *C. acutatum*, the *FaChi2-1* and *FaChi2-2* expression were observed (Khan, 2002). Several class I chitinases have been show to inhibit fungal growth *in vitro* (Sela-Buurlage *et al.*, 1993). On the other hand, a class II from tobacco (Sela-Buurlage *et al.*,

1993) showed no detectable *in vitro* inhibitory activity. However, transgenic tobacco (Jach *et al.*, 1995) and wheat plant (Oldach *et al.*, 2001) expressing a barley class II chitinase also showed enhanced resistance to fungal infection.

The PR-5 family consists of thaumatin-like proteins and osmotin-like proteins. In the microarray platform were represented two thaumatin-like proteins (*UCOESTup64* and *712*) and two osmotin-like proteins (*UCOESTup308* and *984*) (Table 6). Previously, an osmotin-like protein (*FaOLP2*) has been isolated and sequenced from strawberry (Zhang and Shih, 2007). The positive responses of *FaOLP2* to abscisic acid, salicylic acid and mechanical wounding, suggested that strawberry *FaOLP2* may help to protect against osmotic-related environmental stresses and it may also be involved in plant defence system against pathogens (Zhang and Shih, 2007). Other PR, such as a lipid transfer protein (*UCOESTup616*) and several peroxidases (*UCOESTup958*, *1223* and *2051*), were also up regulated in ripen fruit receptacle (Table 6). Recently studies have demonstrated the gene *Faprox-1* (peroxidase) from strawberry is expressed in response to *Colletotrichum* infection (Casado-Díaz *et al.*, 2006).

Our study shown also as a gene that code BOP/NPR1/NIM1-like regulatory protein (*UCOESTup56*) accumulated their transcript level in red-ripen receptacle (Table 6). BOP belongs to a BTB/POZ domain and ankyrin repeat-containing proteins family that includes the plant defense response regulator NPR1 and are expressed in a small group of proximal, adaxial lateral organ cells adjacent to the meristem-organ boundary (Ha *et al.*, 2004; Hepworth *et al.*, 2005; Jun *et al.*, 2010). NPR1 is known to be a transcriptional regulator that mediates salicylic acid (SA)-induced gene expression in association with TGA family transcription factors. Thus, *NPR1* is required for the development of systemic acquired resistance and induction of pathogenesis related genes (Mou *et al.*, 2003; Zhang, 2006; Zhang, 2012).

### ***Abiotic stress***

Heat-shock proteins are an important adaptation to heat stress in plants. In our microarrays, we have observed the expression of three heat-shock proteins (*UCOESTup901*, *1478* and *1481*) in ripe fruit receptacle (Table 6). Medina-Escobar *et al.* (1998) isolated *njjs4* gene (class-I LMW heat-shock protein-like gene) from strawberry. Those results showed a specific relationship of this gene with the seed maturation and fruit ripening processes. Furthermore, *njjs4* gene has a heat-stress-independent role in plant development, including fruit ripening (Medina-Escobar *et al.*, 1998).

Many studies on fruit ripening have focused on the analysis of aquaporin gene expression and their participation at different stages of fruit development (Chervin *et al.*, 2008; Fouquet *et al.*, 2008). We have identified the nodulin 26-like intrinsic protein (*NIP2;1*, *UCOESTup23*) gene that shows sequence homology with aquaporins family (Table 6). In addition, the aquaporin *NIP1;2* gene was also up-regulated in strawberry ripen fruit receptacle (*UCOESTup1659*) (Table 6). In a previous work, a full-length sequence of a *PIP1* subtype aquaporin was cloned (*FaPIP1;1*). Its expression increased during fruit ripening and was negatively regulated by auxins (Mut *et al.*, 2008). Alleva *et al.* (2010) cloned and characterized a novel aquaporin (*FaPIP2;1*) from strawberry fruit. The co-expression of both *FaPIP* subtypes resulted in an enhancement of water permeability although the expression pattern of *FaPIP1;1* and *FaPIP2;1* in two cultivars with contrasting fruit firmness showed that the firmer cultivar (Camarosa) has a higher accumulation of *FaPIP1* and

*FaPIP2* mRNAs during fruit ripening against to the softer cultivar (Toyonoka). These results suggest that a complex regulation of water transport depending on the *PIP1* and *PIP2* rate expression profile could play a role in fruit physiology. Thus, aquaporins involved in the maturation and softening process fruit (Alleva *et al.*, 2010).

### 3.3.10. Transporters and permeases

In plants, ABC proteins were originally identified as transporters involved in the final detoxification process (Martinoia *et al.*, 1993). Since this finding, numerous reports have shown that the functions of this class of transporters extend far beyond detoxification. ABC transporters have frequently been shown to be involved in such diverse processes as pathogen response, surface lipid deposition, phytate accumulation in seeds, and transport of the phytohormones auxin and abscisic acid (Kang *et al.*, 2011). Thus, we have observed as different family members belonging to the ABC transporters have increased their expression in strawberry ripe fruit (*UCOESTup169, 444, 913, 1296, 1904, 1931* and *2479*) (Table 7). Therefore, ABC transporters play an important role in organ growth, plant nutrition, plant development, response to abiotic stress, and in the interaction between the plant with its environment (Kang *et al.*, 2011).

Plant anion channels allow the efflux of anions from cells. They are involved in turgor pressure control, changes in membrane potential, organic acid excretion, tolerance to salinity and inorganic anion nutrition (Kollist *et al.*, 2011). Different genes that coding anion transporters (*UCOESTup228, 1861* and *2112*) accumulated also their transcript level in red-ripen receptacle (Table 7). The recent molecular identification of anion channel genes in guard cells and in roots allows a better understanding of their function and of the mechanisms that control their activation (Kollist *et al.*, 2011).

Other transporters detected in our studies were sulphate transporters (*UCOESTup241* and *2240*) (Table 7). Plants, as autotrophic organisms, have a set of transporters and enzymes that mediate uptake and assimilation of inorganic sulfate and subsequent metabolic conversion to organic sulfur compounds. Thus, sulfate transporters play significant roles in coordinating the assimilatory functions to adapt with varying sulfur nutritional status that fluctuates in the environment (Takahashi, 2010).

Our microarrays have also detected different genes implicated with peptides transporters. In plants, the PTR/NRT1 gene family is much larger than in other kingdoms and consists of 53 genes in *Arabidopsis* (Tsay *et al.*, 2007). Functional di-/tripeptide transport has been shown for members from *Arabidopsis* (*AtPTR1, AtPTR2, AtPTR3, and AtPTR5* (Rentsch *et al.*, 2007; Tsay *et al.*, 2007; Komarova *et al.*, 2008), faba bean [*VfPTR1* (Miranda *et al.*, 2003)], barley [*HvPTR1* (West *et al.*, 1998)], and *Hakea actites* [*HaPTR4* (Paungfoo-Lonhienne *et al.*, 2009)]. We have observed the gene expression those coding peptides transporters PTR1 (*UCOESTup253, 1383* and *1636*) (Table 7). Experiments using antisense repression of *AtPTR2* showed the importance of peptide transport for flowering and seed development (Song *et al.*, 1997). Furthermore, work with knock-out mutants (*atptr1* and *atptr5*) and overexpression lines (*35S-AtPTR5*) demonstrated that *AtPTR5* facilitates peptide transport into germinating pollen and possibly into maturing pollen, ovules and seeds and provided evidence that peptide transporters facilitate uptake of nitrogen from the rhizosphere (Komarova *et al.*, 2008).



Two genes that encoding oligopeptide transporter OPT (*UCOESTup17* and *1763*) were also up-regulated in strawberry fruit ripen (Table 7). Studies about members of the OPT (oligopeptide transporter) family have showed that these family mediate the transport of oligopeptides and derivatives that contain three to six amino acids (Stacey *et al.*, 2002).

Ammonium and nitrate are the prevalent nitrogen sources for growth and development of higher plants. Several genes that coding nitrate transporters (*UCOESTup377*, *778* and *1482*) and ammonium transporters (*UCOESTup701* and *1240*) increased their levels of transcript in ripen fruits receptacle (Table 7). A two-component system for nitrate transport including NRT2s with a partner protein (*NAR2* or *NRT3.1*) has been identified in *Arabidopsis* (Laugier *et al.*, 2012). *OsNAR2.1* from rice has been recently characterized (Yan *et al.*, 2011). *OsNAR2.1* was mainly expressed in roots and induced by nitrate and suppressed by ammonium and some amino acids. Silencing of *OsNAR2.1* by RNA interference showed that *OsNAR2.1* plays a key role in enabling the plant to cope with variable nitrate supply (Yan *et al.*, 2011).

The amino acid distribution in plants includes apoplasmic transport steps which require import as well as export processes (Okumoto and Pilot, 2011) and consequently the presence of amino acid exporters has been postulated for a number of intercellular transport steps (Bush, 1993; Rentsch *et al.*, 2007). We have identified different genes that coding different amino acids transporters whose expression was up-regulated in strawberry ripen fruit receptacle (*UCOESTup745*, *861*, *1008*, *1142*, *1508*, *1093* and *2502*) (Table 7). Developing seeds are strong sink organs and need to be supplied with large amounts of assimilates. Nutrients arriving through the vasculature of the funiculus are delivered into the chalazal region of ovules and developing seeds. The import of amino acids into the developing seed is at least in part mediated by members of the AAP (Amino acid permease) family, which are described as unidirectional, proton-coupled amino acid symporters (Hirner *et al.*, 1998; Schmidt *et al.*, 2007; Sanders *et al.*, 2009).

### **3.3.11. Miscellaneous**

#### ***Redox related proteins***

The mitochondrial respiratory chain consists of a series of sequentially acting electron carriers, most of which are integral membrane proteins with prosthetic groups capable of accepting and donating one or two electrons. The transfer of two electrons from NADH through the respiratory chain to molecular oxygen generates a proton-motive force across the inner mitochondrial membrane that drives the synthesis of ATP (Hatefi *et al.*, 1985; Eubel *et al.*, 2004). Higher-plant mitochondria are interesting systems for the study of supercomplex formation due to its indirect participation in the photosynthesis (Douce *et al.*, 2001). These supercomplex are composed by a NADH dehydrogenase (complex I), a succinate dehydrogenase (complex II), a cytochrome c reductase (complex III), a cytochrome c oxidase (complex IV), and an ATP synthase (complex V) (Eubel *et al.*, 2004; Bultema *et al.*, 2009). In our microarray platform, we have detected several genes implicated in mitochondrial respiratory chain (Table 9). Between them were up regulated different NADH dehydrogenases, four cytochrome c oxidases (*UCOESTup551*, *1014*, *1614* and *2293*) and a cytochrome c reductase (*UCOESTup2532*) in ripen fruit receptacle (Table 9).

The chloroplast NAD(P)H dehydrogenase (NDH) complex is involved in photosystem I cyclic electron transport and chlororespiration in higher plants (Peng *et al.*, 2010). Previous studies identified in *Arabidopsis* a chlororespiratory reduction 6 (*crr6*) mutant lacking NDH activity. These results showed that CRR6 was a novel specific factor necessary for the assembly or stabilization of the NDH complex (Munshi *et al.*, 2006). In our microarray, studies have identified a gene that has sequence homology to *chlororespiratory reduction 6* gene (*UCOESTup640*) (Table 9). Other identified gene involved in photosynthesis was a Ferredoxin (*Fds*) (*UCOESTup1952*) (Table 9). In higher plants, *Fds* are mainly distributed in photosynthetic organs and occupy key positions for partitioning photo-reducing power to many metabolic processes (Arnon, 1987). They are also present in nonphotosynthetic organs such as roots (Suzuki *et al.*, 1991), and it is generally assumed that nonphotosynthetic *Fds* are probably involved in electron transfer from pyridine dinucleotides to some Fd linked enzymes (Suzuki *et al.*, 1991). Recent studies have shown the involvement of ferredoxin in the oxygen reduction in the photosynthetic electron transport chain of thylakoids isolated from pea (Kozuleva and Ivanov, 2010). Also, Ferredoxins are proteins involved in other processes that require reducing equivalents, such as reduction of nitrogen or desaturation of fatty acids (Venegas-Calderon *et al.*, 2009). Thus, photosynthetic ferredoxin could promote desaturase activity in sunflower cotyledons (Venegas-Calderon *et al.*, 2009).

Thioredoxins (Trxs) are a multigenic family of proteins in plants that plays a critical role in redox balance. We have detected three thioredoxins (*UCOESTup625*, *1438* and *1948*) that increased their expression in ripen receptacle (Table 9). In plants, Trxs are involved in a variety of cellular processes in two manners. Thus, they can regulate the redox status of target proteins through thiol-disulfide exchange reactions. For example, Trxs catalyze the conversion of the salicylic acid-induced nonexpresser of PR genes1 (*NPRI*) to a monomer upon pathogen challenge (Tada *et al.*, 2008) and regulate cytosolic, chloroplastic, and mitochondrial enzyme activities in plant cells (Balmer *et al.*, 2003; Yamazaki *et al.*, 2004). In addition, Trxs can enhance heat shock resistance in plants through redox-independent modes (Park *et al.*, 2009).

Glutaredoxins (Grxs) are ubiquitous oxidoreductases which are similar to thioredoxins and possess a typical glutathione-reducible CxxC or CxxS active site (Fomenko *et al.*, 2002). In our microarrays, we have observed five glutaredoxin (*UCOESTup489*, *543*, *780*, *815* and *950*) (Table 9). Thioredoxins and glutaredoxins are probably involved in similar physiological events (Meyer *et al.*, 1999). In *Arabidopsis* only eight out of the 31 predicted Grxs have been functionally characterized by genetic approaches: three monothiol CGFS-type (GRXS14, GRXS15, and GRXS17), two dithiol CPYC-type (GRXC1 and GRXC2), and only three of the most numerous CC-type (GRXC7/ROXY1, GRXC8/ROXY2 and GRXC9). Genetic studies indicate that these GRX are involved in protection against protein oxidative damage produced by H<sub>2</sub>O<sub>2</sub> treatment (Cheng *et al.*, 2006; Bandyopadhyay *et al.*, 2008; Cheng, 2008), in protection against oxidative cellular (Meyer *et al.*, 2009), in plant defence responses against pathogens (Ndamukong *et al.*, 2007) and in flower development and salicylic acid signalling (Rouhier *et al.*, 2008).

### **SCF complex**

SCF complexes are the largest family of E3 ubiquitin-protein ligases and mediate the ubiquitination of diverse regulatory and signalling proteins (Zheng *et al.*, 2002). The SCF core components consist of the RING-finger protein Rbx1, the scaffold Cull1 and a linker protein Skp1 that associates with different F-box proteins to form a range of SCF ligases

(Cardozo and Pagano, 2004; Willems *et al.*, 2004; Petroski and Deshaies, 2005). F-box proteins directly bind substrates and determine substrate selectivity of the various SCF complexes (Jin *et al.*, 2004; Hua *et al.*, 2011). Substrate binding to SCF ligases is generally initiated by phosphorylation and other post-translational modifications on target proteins and has been considered the most important regulatory step in ubiquitylation (Petroski and Deshaies, 2005). We have also detected an increase of the amount of transcripts corresponding to several putative genes that code three SKP1 (*UCOESTup52*, 839 and 2238) and different F-box proteins in ripen fruits (Table 9). The *UCOESTup52* and *UCOESTup1238* genes display high level of expression and, therefore, they seem to play an important role in the fruit ripening process. Recently, it has been shown that a ubiquitin-ligase complex SCF<sup>TIR1/AFB</sup> (for Skp1-Cul1-F-box protein), which includes the Transport Inhibitor Response1/Auxin Signaling F-box (TIR1/AFB) auxin receptor family, acts as a major regulator of diverse aspects of plant growth and development (Takahashi *et al.*, 2012; Pérez-Henríquez *et al.*, 2012). On the other hand, it has been proved that SKP1 is involved in abscisic acid signalling to regulate seed germination, stomatal opening and root growth in *Arabidopsis thaliana* (Li *et al.*, 2012). Therefore, SKP1 is involved in ABA signalling and may positively regulate ABA signalling by SCF-mediated protein degradation (Li *et al.*, 2012). Other studies with *SKP1-like* genes from *Lilium longiflorum* (*LSK1-LSK3*) are specifically expressed in late pollen developmental stages and the elongating pollen tube (Chang *et al.*, 2009). Thus, the ubiquitin-proteasome pathway mediates protein degradation and is involved in diverse aspects of plant development and differentiation, including pollen tube elongation and self-incompatibility (Chang *et al.*, 2009).

### ***Exocyst complex component 7***

The exocyst, a complex of eight proteins, contributes to the morphogenesis of polarized cells in a broad range of eukaryotes. In these organisms, the exocyst appears to facilitate vesicle docking at the plasma membrane during exocytosis (Cole *et al.*, 2005). Our transcriptomic studies have shown a clear up-regulation of the expression corresponding to a gene that coding an exocyst complex (EXO70H6) (*UCOESTup27*) in mature red fruit receptacle (Table 9). Orthologs of genes encoding all components of the exocyst have been identified in *Arabidopsis thaliana* and *Oryza sativa* suggesting the existence of a plant exocyst (Jurgens and Geldner, 2002; Elias *et al.*, 2003). Exocyst complex is involved in the tip growth observed in root hairs and pollen tubes (Fowler and Quatrano, 1997; Feijó *et al.*, 2004) making of these places likely sites for exocyst activity. Tip growth requires the rapid delivery of secretory vesicles to the specific region on the membrane where growth of new membrane is focused. Pollen tube tip growth also involves the localization and recycling of membrane components, such as ion channels and possibly receptors, to the tip via endocytosis and exocytosis (Wen *et al.*, 2005). Orthologs of two different exocyst components in two widely divergent plant species, SEC8 in *Arabidopsis* (Cole *et al.*, 2005) and SEC3 in maize (Wen *et al.*, 2005) have been shown to be important for the proper development of the polarly growing pollen tube and root hair, respectively.

### ***Syntaxin-24***

Syntaxin-related protein KNOLLE, a multifunctional protein family belonging to the SNARE superfamily, plays an important role in many physiological processes in plants. In our microarrays, we have observed the expression of a *Syntaxin-24* (*UCOESTup290*) in ripe fruit receptacle (Table 9). In plant cytokinesis, Golgi/trans-Golgi network-derived vesicles are targeted to the plane of cell division where they fuse with another one to form the

partitioning membrane (cell plate). This fusion of membrane requires a specialised syntaxin (Qa-SNARE) (Touihri *et al.*, 2011). Ul-Rehman *et al.* (2011) demonstrated in normal growing pollen tubes that the asymmetric distribution of syntaxins helps to define exocytic sub-domains but requires the involvement of additional signaling and functional mechanisms, namely phosphoinositides, and small GTPases. The localization of syntaxins at different membrane domains likely depends of the interaction with specific partners not yet identified (Ul-Rehman *et al.*, 2011). Studies in rice transformants (OsKNOLLE) suggested that this protein could play a crucial role in responses to abiotic stresses such as salt, Cu<sup>2+</sup>, H<sub>2</sub>O<sub>2</sub>, Cd<sup>2+</sup>, and Hg<sup>2+</sup> (Wang *et al.*, 2011).

### ***Rossmann-fold NAD(P)-binding domain-containing protein***

The Rossmann fold, or mononucleotide-binding motif, was first identified in dinucleotide-binding proteins (Rossmann *et al.*, 1974) and it is a single βαβαβ motif that binds a mononucleotide (Murzin *et al.*, 1995). We have observed the expressions of a Rossmann-fold NAD(P)-binding domain-containing protein (*UCOESTup347*), which are up-regulated in red ripen receptacles (Table 9). In plant, the Rossmann fold has not been documented yet.

### ***Tetratricopeptide repeat motifs***

Proteins containing tetratricopeptide repeat (TPR) motifs control the specific interactions with partner proteins, either forming active multiprotein complexes or acting as co-chaperones involved in the folding of a growing set of substrates (D'Andrea and Regan, 2003; Davies and Sánchez, 2005). Previous studies have shown that TPR proteins are involved in plant hormonal regulation, such as ethylene biosynthesis (Yoshida *et al.*, 2005) and GA and cytokinin responses (Greenboim-Wainberg *et al.*, 2005). In our array studies, we have detected that two genes encoding tetratricopeptide repeat domain-containing protein (*UCOESTup379* and *1363*) increased its expression in ripen fruit receptacle (Table 9). Rosado *et al.* (2006) demonstrated that *Tetratricopeptide-repeat thioredoxin-like 1* (TTL1) regulates responses to osmotic stress and ABA during germination and seedling development in *Arabidopsis* plants. A detailed study of TTL family members in *Arabidopsis* could give more information into plant hormonal regulation controlled by proteins containing TPRs (Rosado *et al.*, 2006).

### ***Early nodulin-like protein***

Early nodulin-like proteins (ENODLs) are chimeric arabinogalactan proteins (AGPs) related to the phytocyanin family (Seifert *et al.*, 2007). Although they show similarities with other phytocyanins, they lack amino acid residues for copper binding. Despite the existence of other phytocyanins, information about the function of ENODLs is largely lacking in plants (Greene *et al.*, 1998). We have detected an increase of the amount of transcripts corresponding to two genes that encoding early nodulin-like proteins (*UCOESTup414* and *478*) in ripen fruits (Table 9). In legumes, ENODLs are expressed during early stages of root nodule development and could have a role in cell differentiation and cell wall reorganization during nodulation (Vijn *et al.*, 1995; Greene *et al.*, 1998). Recently, 22 members of *ENODL* genes have been characterized in *Arabidopsis thaliana*. These studies showed that ENODLs might be involved in plant development under altered conditions including stress or pathogen response (Mashiguchi *et al.*, 2009).

### ***DVL11***

In our studies, we have identified a gene that belongs to the family of plant peptides DVL. Thus, the *DVL1* gene (*UCOESTup608*) increased level of transcription in ripen red receptacle (Table 9). Wen *et al.* (2004) showed that these polypeptides could have a role in plant development. Recent studies have suggested that these genes play a role in local signalling, specifically in the coordination of socket cell recruitment and differentiation (Valdivia *et al.*, 2011).

### ***Blue copper proteins***

Blue copper proteins, which are also known as cupredoxins, are small and soluble proteins (10–14 kDa) whose active site contains a type-I copper. These proteins are involved in various biological redox systems, such as bacterial and plant photosynthesis (Baker, 1994; Sykes, 1994; DeRiezo *et al.*, 2004). In our microarrays, we have observed two genes those encoding blue copper proteins (*UCOESTup773* and *2334*) are up-regulated in red-ripen receptacle (Table 9). Other studies have suggested that blue copper proteins may participate in the regulation of fiber development and in response to high-salinity and heavy metal stresses in cotton (Ruan *et al.*, 2011).

### ***BURP domain proteins***

The BURP domain-containing proteins are a large family of evolutionarily conserved proteins only found in plants. Some members of this family had been reported to be involved in the reproductive development and stress resistance of plants (Hattori *et al.*, 1998). A gene that encoding BURP domain protein (*UCOESTup799*) accumulated their transcript level in strawberry ripen fruits (Table 9). On the other hand, recently studies have suggested that BURP genes showed no tissue specificity and respond to stress treatments in Soybean. This may indicate that this subfamily specifically acted as a defence against stress in soybean and could likely play similar roles in other plant species (Xu *et al.*, 2010).

### ***LOB domain proteins***

In our microarray study, we have detected changes in the expression of a putative gene that coding a LOB domain protein (*UCOESTup1308*) (Table 9). These proteins are conserved in a variety of evolutionarily divergent plant species and constitute a large plant-specific family of largely unknown function. *LBD* genes have been implicated in a variety of developmental processes in plants, although to date, relatively few members have been assigned functions (Husbands *et al.*, 2007). LBD proteins have previously been predicted to be transcription factors. Thus, Husbands *et al.* (2007) demonstrated that members of the basic helix-loop-helix (bHLH) family of transcription factors are capable of interacting with LOB. The expression patterns of bHLH048 and LOB overlap at lateral organ boundaries, suggesting that bHLH048 post-translationally regulates the function of LOB at lateral organ boundaries (Husbands *et al.*, 2007).

### ***Circadian clock-associated FKF1***

In higher plants, a circadian clock controls hypocotyl elongation, daily leaf movements, flowering time, and the rhythm of CO<sub>2</sub> fixation in Crassulacean acid metabolism (McClung, 2001). Other genes have been also implicated in the *Arabidopsis thaliana* clock (McWatters

*et al.*, 2000). In strawberry ripen fruit, we detected an increase of transcript of a gene that encoding a Circadian clock-associated FKF1 (*UCOESTup106*) (Table 9). The *FLAVIN-BINDING KELCH REPEAT F-BOX1 (FKF1)* seems to play a role in circadian clock function, regulating the transition to flowering (Nelson *et al.*, 2000). The FKF1 LOV domain can bind to a flavin mononucleotide chromophore and undergo light-induced photochemistry, suggesting that FKF1 could directly sense blue light (Imaizumi *et al.*, 2003).

#### ***Tonoplast intrinsic protein (FavRB7)***

Tonoplast intrinsic proteins (TIPs) are associated with the water transport via transcellular pathway (Chrispeels and Maurel, 1994). We observed the up-regulation of a *tonoplast intrinsic protein* expression (*UCOESTup333*) (Table 9) in red ripen fruit receptacles. This gene presents a significant sequence homology with *FaRB7* gene from *Fragaria x ananassa* Duch whose promoter was used, as alternative to CaMV 35S promoter, to achieve near-root-specific transgene expression in strawberry (Vaughan *et al.*, 2006). Thus, the use of a root-specific promoter to express resistance genes in a targeted manner benefits the genetic improvement of commercial strawberry varieties (Vaughan *et al.*, 2006).

#### ***Actin binding calponin homology domain-containing protein***

Our transcriptomic studies have shown an up-regulation of the expression corresponding to a gene coding an *Actin binding calponin homology domain-containing protein* (*UCOESTup1235*) in mature red fruit receptacle (Table 9). Plant kinesins, with a calponin-homology domain (KCHs), were recently identified and associated with a putative role in microtubule–microfilament crosslinking (Tamura *et al.*, 1999; Preuss *et al.*, 2004). KCHs belong to a distinct branch of the minus end-directed kinesin subfamily and so far have only been identified in land plants, including the mosses (Richardson *et al.*, 2006). Recently studies in rice (*Oryza sativa*) have indicated that OsKCH1 could play a role as linkers between actin filaments and microtubules in both cell elongation and division (Frey *et al.*, 2009).

#### ***Stay green 1 (SGR1)***

Our transcriptomic analysis also detected a gene putatively encoding a stay green protein (SGR1) that increased its transcript levels in ripen fruit receptacles (*UCOESTup1289*) (Table 9). The SGR1 gene is required for the dismantling of photosynthetic chlorophyll–protein complexes during senescence (Hörtensteiner, 2009), degrading chlorophyll to colorless linear tetrapyrroles that are stored in the vacuole of senescing cells although its exact role remains still elusive (Sakuraba *et al.*, 2012).

The involvement of the strawberry *FaSGR1* gene in processes related with fruit receptacle growth, ripening and senescence are unknown.

#### ***Flotillins***

The sequences of two ripening-related genes (*UCOESTup93* and *UCOESTup1027*) are homologs to those corresponding to plant flotillins genes (Table 9). The expression of one of them (*UCOESTup93*), was strongly up-regulated in ripen receptacles. Besides, the amount of transcript corresponding to this gene was high. Flotillins are membrane proteins that form microdomains in the plasma membrane of all cell types studied to date in bacteria, fungi,

plants and metazoans, which suggests that they perform important and, probably conserved, functions. Flotillins have been implicated in myriad processes that include endocytosis, signal transduction and regulation of the cortical cytoskeleton, although the molecular mechanisms that underlie flotillin function in these different cases are still poorly understood. In plants, the physiological role played for flotillins genes is scarcely known. Microscopy data suggest that two flotillins-like genes (*FLOT2* and *FLOT4*) localize to membrane microdomains in *M. truncatula* (Haney and Long, 2010). Besides, both genes have been proposed to be involved in symbiotic interactions. Thus, *FLOT4* and *LYK3* (lysin motif receptor-like kinase) are genes that mediated bacterial infection (Haney *et al.*, 2011). Both genes have increased co-localization after bacterial inoculation of plants with *M. truncatula* (Haney and Long, 2010; Haney *et al.*, 2011). Besides, *FLOT4* and *LYK3* genes have similar RNA interference phenotypes and gene expression patterns (Haney and Long, 2010). This implies that the both genes may function cooperatively to mediate symbiotic infection. The most parsimonious explanation for increased proximity and similarity of dynamics of *FLOT4* and *LYK3* after bacterial treatment is that both are components of a shared complex. An alternative is that *FLOT4* and *LYK3* co-localization arises because they occupy the same compartment (but do not necessarily interact), whether it be a plasma membrane-tethered vesicle or a microdomain in the plasma membrane (Haney *et al.*, 2011). In opposition, *M. truncatula FLOT2* also localizes to membrane associated puncta and is required for symbiosis but not for infection thread elongation (Haney and Long, 2010).

The functions that these proteins could play in fruit ripening are unknown, however the strong up-regulation of *UCOESTup93* gene expression with the maturation of the fruit receptacle and the high levels of transcript in ripen fruits indicate that this gene plays a relevant role in this physiological process.

### ***Cyclo-DOPA 5-O-glucosyltransferase***

Another ripening-related gene that presents very high amount of transcript in ripen receptacles putatively codes for a Cyclo-DOPA 5-O-glucosyltransferase (*UCOESTup415*) (Table 9). UDP-glucose:cyclo-DOPA 5-O-glucosyltransferase represents a single subclade distinct from those of other phenylpropanoid and flavonoid glucosyltransferases. It has been proposed that these enzymes are involved in another pathway of betacyanin biosynthesis via glucosylation at the cyclo-DOPA step rather than at the betanidin step (Sasaki *et al.*, 2005). However the main color pigment in strawberry fruits are anthocyanins and the occurrence of betalains and anthocyanins is mutually exclusive (Harris *et al.*, 2012). The anthocyanins metabolism is very strong in strawberry ripen fruits, for that, it is quite intriguing the potential physiological role played for this enzyme along receptacle maturation.

### ***Cystinosins***

Two genes expressed in strawberry receptacles (*UCOESTup93* and *UCOESTup598*) potentially coding for cystinosins-like proteins (Table 9). Both genes up-regulate its expression in ripen receptacles. Besides, one of them (*UCOESTup93*) also presented high levels of transcript, indicating that the protein coded could play important roles in the ripening process.

Cystinosins are PQ-loop repeat containing proteins whose biological functions have not been still elucidated. In mammals, a physiological role as protein cargo receptors involved in vesicle formation and protein trafficking has been proposed (Saudek, 2012). Preliminary

results indicate that cystinosin plays a role in the vesicular trafficking and membrane fusion. Cystinosin would not serve directly as membrane transporters but rather as receptor proteins bringing their cargo to lysosome via endosome. Cystinosin is not confined just to the lysosomes, it has been observed to move from phagosome to lysosome in *C. elegans* (Saudek, 2012).

These PQ-loop genes are associated with an important phenotype although the molecular mechanism of their function is not clear even for the most studied ones (cystinosin, MPDU1). The function of most of the others remains to be discovered. The largest group, plant PQ-loop set of *SWEETs* or nodulin *MtN3* genes (Saudek, 2012), remained enigmatic until they were hit recently in a high throughput search for a specific physiological function (Saudek, 2012).

In the fruit ripening process, cystosinin as a putative cargo receptor could transport products released from the cell wall along it degradation to lysosomes in order to use them as carbon source for metabolic purposes. Genomic functional studies must be carried out to test this proposal.

### ***2-Nitropropane dioxygenase***

Other gene whose expression was up-regulated and presenting high expression levels in matured receptacle was *UCOESTup918* (Table 9). This gene potentially encodes a 2-nitropropane dioxygenase. In fungus, this enzyme catalyses the oxidative denitrification of nitroalkanes to the corresponding aldehydes, while producing H<sub>2</sub>O<sub>2</sub> and NO<sub>2</sub> (Daubner *et al.*, 2002).

In higher plants, this enzyme has not been functionally characterized yet. However, the expression of genes potentially coding for 2-nitropropane dioxygenases was up-regulated in roots from *Arabidopsis thaliana* and *Brassica juncea* Cd-treated plants (Roth *et al.*, 2006; Alvarez *et al.*, 2009). A possible relationship between these genes and detoxifying nitro-compounds that accumulate in response to Cd was proposed (Roth *et al.*, 2006; Alvarez *et al.*, 2009). However, very recently it was demonstrated that in facultative anaerobic, as *Neisseria gonorrhoeae*, 2-nitropropane dioxygenases are involved in the unsaturated fatty acids (UFA) synthesis anaerobically (Vincent and Clark, 2011). The functional role played for this enzyme along fruit ripening is unknown but could be related with the oxidative stress produced in the fruit along the ripening process or may be involved in the anaerobic biosynthesis of unsaturated fatty acids, probably for the production of volatiles compounds.

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## UP REGULATED GENES

GENE REGULATION (1/4)		Fruit ripen receptacles Up regulated					
GENES	Putative function	Fold	p-value	u.a.e	Species	e-value	Best Match BlastX
<b>TRANSCRIPTION FACTORS</b>							
<b>MYB transcription factors</b>							
<i>UCOESTup51</i>	MYB transcription factor 10 (MYB10)	62.013	0.00007	16282.90	<i>Fragaria x ananassa</i>	1.00E-41	EU155162.1
<i>UCOESTup53</i>	MYB transcription factor 160 (MYB160)	58.178	0.00055	1677.32	<i>Medicago truncatula</i>	4.00E-52	XM_003601151.1
<i>UCOESTup67</i>	MYB transcription factor 26 (MYB26)	46.063	0.00005	8801.50	<i>P.sativum</i>	5.00E-82	Y11105.1
<i>UCOESTup105</i>	MYB transcription factor 10 (MYB10)	30.720	0.00040	1825.55	<i>Rosa rugosa</i>	6.00E-46	FR828543.1
<i>UCOESTup368</i>	MYB transcription factor	8.966	0.00172	7937.65	<i>Glycine max</i>	2e -58	DQ822914.1
<i>UCOESTup505</i>	MYB transcription factor 161 (MYB161)	7.061	0.00379	209.61	<i>Glycine max</i>	2.00E-87	DQ822965.1
<i>UCOESTup857</i>	MYB transcription factor 4 (MYB4)	4.443	0.00046	4279.79	<i>Rosa rugosa</i>	8.00E-153	GU967443.1
<i>UCOESTup1667</i>	MYB transcription factor 59-2 (MYB59-2)	2.625	0.00584	1631.64	<i>Arabidopsis thaliana</i>	4.00E-74	DQ075253.1
<i>UCOESTup1760</i>	MYB transcription factor 5 (MYB5)	2.531	0.00203	3628.30	<i>Humulus lupulus</i>	2.00E-70	FR751555.1
<i>UCOESTup1766</i>	MYB transcription factor 1 (MYB1)	2.529	0.00117	2816.64	<i>Malus x domestica</i>	1.00E-124	EF016490.1
<i>UCOESTup1819</i>	MYB transcription factor 3 (MYB3)	2.474	0.02830	154.84	<i>Pinus taeda</i>	4.00E-64	DQ399059.1
<i>UCOESTup1850</i>	MYB4R1 transcription factor	2.451	0.00237	1300.84	<i>Arabidopsis lyrata</i>	2.00E-158	XM_002883063.1
<i>UCOESTup1869</i>	MYB transcription factor	2.440	0.00654	189.20	<i>Cucumis sativus</i>	4.00E-44	EU284118.1
<i>UCOESTup1962</i>	c-MYB transcription factor (MYB3R3)	2.361	0.00773	489.91	<i>Arabidopsis thaliana</i>	8.00E-66	AF214117.2
<i>UCOESTup2151</i>	MYB transcription factor 23 (MYB23)	2.239	0.03900	1115.38	<i>Arabidopsis thaliana</i>	1.00E-52	NM_123397.2
<b>bHLH transcription factors</b>							
<i>UCOESTup41</i>	Transcription factor bHLH75	74.046	0.00017	1780.78	<i>Arabidopsis thaliana</i>	7.00E-43	NM_102343.4
<i>UCOESTup161</i>	Transcription factor HEC2 (bHLH88)	49.922	0.00010	8020.40	<i>Medicago truncatula</i>	2.00E-39	XM_003611682.1
<i>UCOESTup366</i>	Transcription factor bHLH78	8.969	0.00020	3219.03	<i>Glycine max</i>	1.00E-144	XM_003532209.1
<i>UCOESTup477</i>	Transcription factor bHLH135	7.461	0.00016	8056.17	<i>Glycine max</i>	4.00E-20	NM_001254137.1
<i>UCOESTup1461</i>	Transcription factor bHLH25	2.881	0.00816	201.11	<i>Glycine max</i>	3.00E-89	NM_001252914.1
<i>UCOESTup1606</i>	Transcription factor bHLH149	2.708	0.02280	4573.24	<i>Glycine max</i>	1.00E-33	XM_003535991.1
<i>UCOESTup1652</i>	Transcription factor bHLH66	2.652	0.00114	1784.79	<i>Medicago truncatula</i>	5.00E-32	XM_003590628.1
<i>UCOESTup1813</i>	Transcription factor bHLH87	2.480	0.00674	94.25	<i>Glycine max</i>	2.00E-52	XM_003529695.1
<b>WRKY transcription factors</b>							
<i>UCOESTup61</i>	WRKY transcription factor 6 (WKKY6)	49.875	0.00011	354.47	<i>Vitis vinifera</i>	1.00E-76	XM_002269660.2
<i>UCOESTup130</i>	WRKY transcription factor	24.423	0.00007	14288.60	<i>Medicago truncatula</i>	5.00E-62	XM_003617375.1
<i>UCOESTup399</i>	WRKY transcription factor 15 (WRKY15)	8.479	0.00743	2448.93	<i>Malus x domestica</i>	1e -82	HM122718.1
<i>UCOESTup544</i>	WRKY transcription factor 47 (WRKY47)	6.496	0.00044	211.38	<i>Arabidopsis thaliana</i>	8.00E-50	AF480165.1
<i>UCOESTup575</i>	WRKY transcription factor 48 (WRKY48)	6.249	0.00060	2094.08	<i>Nicotiana tabacum</i>	4.00E-81	AB041520.1
<i>UCOESTup691</i>	WRKY-type DNA binding protein	5.360	0.00027	5047.51	<i>Solanum tuberosum</i>	1e -47	AB061245.1

(Table continues on following page)

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<b>UCOESTup1395</b>	WRKY transcription factor 36 (WRKY36)	2.992	0.00142	10211.97	<i>Glycine max</i>	5.00E-80	XM_003541905.1
<b>UCOESTup1853</b>	WRKY transcription factor 14-1	2.449	0.00478	1418.16	<i>Dimocarpus longan</i>	5.00E-95	JF708964.1
<b>UCOESTup2365</b>	WRKY DNA binding protein	2.113	0.00568	1467.31	<i>Fragaria x ananassa</i>	3.00E-101	EU727547.1
<b>NAC transcription factors</b>							
<b>UCOESTup558</b>	NAC transcription factor 19 (NAC19)	6.383	0.00058	5903.56	<i>Malus x domestica</i>	7.00E-100	HM122660.1
<b>UCOESTup766</b>	NAC transcription factor 89 (NAC089)	4.906	0.00277	26.96	<i>Populus trichocarpa</i>	3e -66	XM_002314042.1
<b>UCOESTup794</b>	NAC transcription factor 73 (NAC73)	4.744	0.00953	327.65	<i>Populus trichocarpa</i>	4e -71	XM_002307527.1
<b>UCOESTup1071</b>	NAC transcription factor 12 (NAC012)	3.724	0.00562	220.11	<i>Populus trichocarpa</i>	1.00E-79	XM_002316844.1
<b>UCOESTup1243</b>	NAC transcription factor 10 (NAC10)	3.302	0.04850	136.66	<i>Malus x domestica</i>	1.00E-80	HM122652.1
<b>UCOESTup1270</b>	NAC transcription factor 75 (NAC075)	3.223	0.02000	189.16	<i>Populus trichocarpa</i>	3.00E-76	XM_002300830.1
<b>UCOESTup1325</b>	NAC transcription factor 157 (NAC157)	3.105	0.00220	1719.00	<i>Populus trichocarpa</i>	6.00E-117	XM_002305738.1
<b>UCOESTup1954</b>	NAC transcription factor 22 (NAC22)	2.366	0.00201	18930.96	<i>Malus x domestica</i>	7.00E-107	HM122664.1
<b>Dof zinc finger protein</b>							
<b>UCOESTup76</b>	Dof zinc finger protein	41.029	0.00011	5497.86	<i>Glycine max</i>	1.00E-45	XM_003537068.1
<b>Zinc finger proteins</b>							
<b>UCOESTup42</b>	RING-H2 finger protein	73.506	0.00032	1548.83	<i>Medicago truncatula</i>	1.00E-44	XM_003638616.1
<b>UCOESTup172</b>	C3HC4 RING finger protein	18.280	0.00217	356.74	<i>Arabidopsis thaliana</i>	2.00E-73	NM_115335.3
<b>UCOESTup191</b>	C2H2L zinc finger protein (C2H2L23)	16.369	0.00215	14309.16	<i>Malus x domestica</i>	3.00E-38	HM122497.1
<b>UCOESTup192</b>	RING-H2 finger protein	16.344	0.00013	11276.37	<i>Medicago truncatula</i>	8.00E-23	XM_003590265.1
<b>UCOESTup223</b>	C2H2L zinc finger protein	13.895	0.00042	274.15	<i>Arabidopsis thaliana</i>	2.00E-93	NM_122195
<b>UCOESTup258</b>	Superman protein (FRASUP5)	12.154	0.00261	179.50	<i>Fragaria virginiana</i>	0.0	GU830923.1
<b>UCOESTup1416</b>	Superman protein (FRASUP5)	2.969	0.01110	159.77	<i>Fragaria virginiana</i>	3.00E-106	GU830920.1
<b>UCOESTup267</b>	Zinc finger protein	11.793	0.00024	1871.30	<i>Medicago truncatula</i>	4.00E-63	XM_003609219.1
<b>UCOESTup275</b>	HIT-type Zinc finger family protein	11.571	0.00013	3761.98	<i>Arabidopsis thaliana</i>	4.00E-36	NM_001197981.1
<b>UCOESTup602</b>	Zinc finger protein	6.032	0.00267	1006.35	<i>Medicago truncatula</i>	3.00E-41	XM_003621753.1
<b>UCOESTup627</b>	RING-H2 finger protein ATL20	5.823	0.00057	1006.35	<i>Arabidopsis thaliana</i>	3e -41	NM_102569.2
<b>UCOESTup680</b>	C2H2 zinc finger protein (ZPT3-1)	5.426	0.00071	916.02	<i>Silene latifolia</i>	3e -51	DQ017764.1
<b>UCOESTup820</b>	RING zinc finger protein	4.588	0.00049	242.11	<i>Arabidopsis thaliana</i>	9.00E-41	AK221570.1
<b>UCOESTup843</b>	Zinc finger protein	4.499	0.00271	140.48	<i>Arabidopsis lyrata</i>	3.00E-77	XM_002877889.1
<b>UCOESTup899</b>	Zinc finger protein CONSTANS-LIKE 10	4.289	0.00501	1366.30	<i>Arabidopsis thaliana</i>	2.00E-115	NM_124200.2
<b>UCOESTup908</b>	C2H2 zinc finger protein (C2H2L15)	4.254	0.00047	150.45	<i>Malus x domestica</i>	1.00E-51	HM122488.1
<b>UCOESTup1006</b>	Ring-H2 finger A2A	3.906	0.01650	6726.72	<i>Arabidopsis lyrata</i>	8.00E-32	XM_002892803.1
<b>UCOESTup1092</b>	C2H2 zinc finger protein	3.652	0.00284	3654.80	<i>Malus x domestica</i>	7.00E-179	HM122505.1
<b>UCOESTup1097</b>	RING finger family protein	3.631	0.00119	11250.62	<i>Medicago truncatula</i>	1.00E-34	XM_003601970.1
<b>UCOESTup1125</b>	Ring zinc finger protein (ZFP1)	3.566	0.00125	3568.11	<i>Artemisia desertorum</i>	0.0	AY928808.1
<b>UCOESTup1198</b>	Zinc finger protein (C2H2L5)	3.420	0.04340	141.06	<i>Brassica rapa</i>	3.00E-65	HM579879.1
<b>UCOESTup1224</b>	RING finger protein	3.350	0.00226	8851.91	<i>Medicago truncatula</i>	2.00E-73	XM_003637350.1
<b>UCOESTup1292</b>	Zinc finger protein	3.171	0.00214	800.81	<i>Arabidopsis lyrata</i>	4.00E-24	XM_002892312.1
<b>UCOESTup1300</b>	C2H2L zinc finger protein	3.156	0.00105	608.30	<i>Arabidopsis thaliana</i>	4.00E-78	NM_102423.2
<b>UCOESTup1320</b>	Zinc finger CCCH domain-containing protein	3.116	0.00207	3046.07	<i>Medicago truncatula</i>	1.00E-64	XM_003629294.1
<b>UCOESTup1488</b>	Zinc finger protein	2.845	0.00799	3492.56	<i>Medicago truncatula</i>	4.00E-29	XM_003599611.1
<b>UCOESTup1665</b>	RING finger protein (RFP1)	2.628	0.00111	1042.24	<i>Glycine max</i>	4.00E-83	EU786799.1
<b>UCOESTup1814</b>	Zinc finger and SCAN domain-containing protein	2.479	0.00235	7654.78	<i>Medicago truncatula</i>	1.00E-72	XM_003604615.1
<b>UCOESTup1854</b>	Zinc finger protein	2.449	0.01250	660.48	<i>Glycine max</i>	2.00E-111	XM_003555211.1

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<b>UCOESTup2158</b>	Zinc finger protein	2.236	0.00203	8801.10	<i>Medicago truncatula</i>	3.00E-118	XM_003630975.1
<b>UCOESTup2160</b>	C4C4-type RING finger protein (RFP1)	2.227	0.02820	4939.02	<i>Vitis pseudoreticulata</i>	8.00E-71	GU446678.1
<b>UCOESTup2174</b>	Zinc finger protein	2.176	0.01620	58.61	<i>Medicago truncatula</i>	9.00E-31	XM_003621753.1
<b>UCOESTup2219</b>	Zinc finger protein	2.194	0.00320	267.22	<i>Arabidopsis thaliana</i>	8.00E-175	NM_104378.1
<b>UCOESTup2385</b>	RING finger protein	2.100	0.00460	11992.59	<i>Medicago truncatula</i>	7.00E-75	XM_003592665.1
<b>UCOESTup2421</b>	RING finger family protein	2.079	0.00955	72.95	<i>Medicago truncatula</i>	2.00E-27	XM_003636043.1
<b>UCOESTup2452</b>	Zinc finger SWIM domain-containing protein	2.064	0.01730	88.40	<i>Medicago truncatula</i>	7.00E-52	XM_003605654.1
<b>UCOESTup2524</b>	Zinc finger protein	2.026	0.00954	221.81	<i>Medicago truncatula</i>	7.00E-58	XM_003615443.1
<b>Homeobox</b>							
<b>UCOESTup519</b>	WUSCHEL-related homeobox 9 (HB-3)	6.774	0.00053	1197.10	<i>Arabidopsis thaliana</i>	2.00E-61	NM_128948.3
<b>UCOESTup2554</b>	Homeobox-leucine zipper protein HAT5	2.009	0.02070	3998.13	<i>Arabidopsis thaliana</i>	4.00E-78	NM_111013.4
<b>MADS Transcription factors</b>							
<b>UCOESTup525</b>	Agamous-like MADS-box protein AGL21	6.711	0.00460	274.11	<i>Glycine max</i>	7.00E-56	XM_003534204.1
<b>UCOESTup529</b>	Agamous-like MADS-box protein AGL61	6.645	0.00336	551.35	<i>Glycine max</i>	3.00E-28	XM_003555262.1
<b>UCOESTup2231</b>	MADS-box family transcription factor	2.187	0.03240	447.05	<i>Medicago truncatula</i>	4.00E-29	XM_003593246.1
<b>UCOESTup2333</b>	MADS-box protein	2.133	0.00671	11522.52	<i>Rosa rugosa</i>	3.00E-157	AB025643.1
<b>Ethylene responsive transcription factors</b>							
<b>UCOESTup371</b>	AP2/ERF domain-containing transcription factor	8.949	0.00171	1516.02	<i>Populus trichocarpa</i>	7e -37	XM_002327017.1
<b>UCOESTup452</b>	AP2 domain class transcription factor (AP2D26)	7.653	0.00059	1660.78	<i>Malus x domestica</i>	4.00E-43	GU732450.1
<b>UCOESTup860</b>	AP2/ERF domain-containing transcription factor (DREB14)	4.438	0.00084	1354.28	<i>Populus trichocarpa</i>	6.00E-63	XM_002304518.1
<b>UCOESTup889</b>	AP2 domain class transcription factor (AP2D38)	4.319	0.00265	5256.91	<i>Malus x domestica</i>	1.00E-45	GU732462.1
<b>UCOESTup935</b>	AP2/ERF domain-containing transcription factor (ERF19)	4.149	0.02450	165.20	<i>Populus trichocarpa</i>	6.00E-39	XM_002314598.1
<b>UCOESTup1051</b>	AP2/ERF domain-containing transcription factor (ERF18)	3.777	0.00179	219.36	<i>Populus trichocarpa</i>	2.00E-29	XM_002307604.1
<b>UCOESTup1631</b>	AP2/ERF domain-containing transcription factor (DREB13)	2.676	0.00228	158.80	<i>Populus trichocarpa</i>	2.00E-60	XM_002323948.1
<b>UCOESTup1752</b>	AP2 domain class transcription factor (AP2D15)	2.538	0.00574	20207.83	<i>Malus x domestica</i>	3.00E-74	GU732439.1
<b>UCOESTup2181</b>	Ethylene-responsive transcription factor RAP2-6	2.224	0.04700	116.71	<i>Medicago truncatula</i>	3.00E-23	XM_003602699.1
<b>SCL domain class transcription factors</b>							
<b>UCOESTup272</b>	SCL domain class transcription factor 29	11.721	0.00076	279.45	<i>Malus x domestica</i>	0.0	HM122678.1
<b>UCOESTup915</b>	SCL domain class transcription factor	4.229	0.00204	14966.33	<i>Malus x domestica</i>	3.00E-54	HM122682.1
<b>UCOESTup892</b>	GRAS family transcription factor	4.313	0.00621	12961.60	<i>Populus trichocarpa</i>	2.00E-156	XM_002305878.1
<b>Others transcription factors</b>							
<b>UCOESTup186</b>	Basic leucine-zipper 70	16.632	0.00010	1901.42	<i>Arabidopsis thaliana</i>	1.00E-26	NM_125476.1
<b>UCOESTup449</b>	Global transcription factor group (GTB902)	7.723	0.00073	446.80	<i>Populus trichocarpa</i>	3.00E-48	XM_002307913.1
<b>UCOESTup455</b>	Nuclear transcription factor Y subunit B-5	7.623	0.01090	2008.63	<i>Arabidopsis thaliana</i>	1.00E-33	NM_130348.2
<b>UCOESTup495</b>	PLATZ transcription factor	7.193	0.00049	443.73	<i>Arabidopsis thaliana</i>	5.00E-75	NM_115931.2
<b>UCOESTup770</b>	Protein YABBY	4.900	0.00085	1290.40	<i>Medicago truncatula</i>	8.00E-46	XM_003608713.1
<b>UCOESTup1594</b>	Transcriptional activator DEMETER	4.406	0.00078	204.79	<i>Arabidopsis thaliana</i>	3.00E-101	NM_001085058.1
<b>UCOESTup1135</b>	CAMTA domain class transcription factor	3.541	0.00150	5639.46	<i>Malus x domestica</i>	0.0	HM122523.1
<b>UCOESTup1219</b>	Nuclear transcription factor Y subunit B-3	3.363	0.03300	552.12	<i>Medicago truncatula</i>	1.00E-67	XM_003625527.1
<b>UCOESTup1396</b>	Nuclear transcription factor Y-alpha (NFYA)	2.991	0.00221	411.06	<i>Populus euphratica</i>	4.00E-64	HQ161880.1
<b>UCOESTup1469</b>	TCP family transcription factor	2.87	0.00981	591.91	<i>Medicago truncatula</i>	8.00E-53	XM_003592291.1

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UCOESTup1515	Transcription factor DYSFUNCTIONAL TAPETUM 1	2.808	0.03410	157.71	<i>Glycine max</i>	1.00E-24	XM_003528371.1
UCOESTup1650	GATA transcription factor	2.653	0.00289	1983.54	<i>Medicago truncatula</i>	2.00E-84	XM_003608354.1
UCOESTup1771	Transcription factor tau subunit sfc4	2.525	0.01330	398.72	<i>Medicago truncatula</i>	1.00E-126	XM_003607185.1
UCOESTup2467	Transcription factor tau subunit sfc4	2.058	0.01640	1016.28	<i>Medicago truncatula</i>	2.00E-171	XM_003607495.1
UCOESTup825	bZIP domain class transcription factor	4.558	0.00040	8697.40	<i>Malus x domestica</i>	0.0	HM122472.1
UCOESTup1678	bZIP transcription factor 52 (bZIP52)	2.613	0.00987	1891.07	<i>Glycine max</i>	3.00E-172	NM_001251358.1
UCOESTup1826	bZIP protein	2.467	0.03340	7180.79	<i>Oryza sativa</i>	2.00E-23	AY333186.1
UCOESTup1883	GATA transcription factor	2.429	0.00577	318.52	<i>Medicago truncatula</i>	3.00E-30	XM_003610792.1
UCOESTup1965	Global transcription factor group	2.357	0.00243	12118.32	<i>Populus trichocarpa</i>	1.00E-129	XM_002300050.1
UCOESTup1216	WD-40 repeat family	3.368	0.00203	1513.79	<i>Medicago truncatula</i>	1.00E-39	XM_003638731.1
UCOESTup1862	WD repeat-containing protein	2.445	0.04420	4296.24	<i>Medicago truncatula</i>	1.00E-149	XM_003590588.1
UCOESTup1971	WD repeat-containing protein 74	2.356	0.01250	1491.23	<i>Glycine max</i>	0.0	XM_003528796.1
UCOESTup355	LuxR family transcriptional regulator	9.290	0.00044	1253.09	<i>Schiedea adamantis</i>	3e -44	GU831097.1
UCOESTup795	Knotted-like homeobox KNOX4	4.741	0.00815	247.84	<i>Fragaria vesca</i>	0.0	HQ413777.1
<b>EPISTATIC CHANGES RELATED PROTEINS</b>							
UCOESTup103	Nucleosome/chromatin assembly factor group	30.873	0.00308	291.93	<i>Populus trichocarpa</i>	7.00E-55	XM_002308247.1
UCOESTup1840	Nucleosome/chromatin assembly factor group	2.458	0.00274	540.44	<i>Populus trichocarpa</i>	2.00E-55	XM_002323809.1
UCOESTup617	Nucleosome assembly protein 1;2 (NAP1;2)	5.914	0.00470	165.29	<i>Arabidopsis thaliana</i>	3e -55	NM_001202624.1
UCOESTup439	Histone H2B.2	7.837	0.00162	4348.29	<i>Camellia sinensis</i>	2.00E-52	HM003233.1
UCOESTup560	Methyl-CpG-binding domain protein 4	6.354	0.00043	119.05	<i>Arabidopsis thaliana</i>	4.00E-66	NM_202524.1
UCOESTup810	Bromodomain protein	4.66	0.00079	1079.22	<i>Populus trichocarpa</i>	2.00E-29	XM_002303992.1
UCOESTup936	Knotted 1-binding protein 36 (KNB36)	4.148	0.00139	3376.49	<i>Nicotiana tabacum</i>	3.00E-30	DQ303421.1
UCOESTup932	Nucleic acid binding / methyltransferase	4.161	0.00075	3579.82	<i>Arabidopsis thaliana</i>	3.00E-80	NM_115709.1
UCOESTup1183	GCN5-related N-acetyltransferase (GNAT)	3.446	0.04970	211.26	<i>Arabidopsis thaliana</i>	2.00E-99	NM_128564.1
UCOESTup1213	JmjC domain-containing protein D	3.380	0.00116	2652.09	<i>Medicago truncatula</i>	0.0	XM_003590525.1
UCOESTup1211	SNF5-type chromatin-remodeling complex protein	3.384	0.00068	5440.68	<i>Glycine max</i>	7.00E-115	HM068618.1
UCOESTup1464	N-Acetyltransferase	2.877	0.00735	88.27	<i>Medicago truncatula</i>	3.00E-72	XM_003630075.1
UCOESTup2037	DRM-type cytosine DNA-methyltransferase	2.308	0.01170	1178.63	<i>Fragaria x ananassa</i>	0.0	FJ804062.1
UCOESTup277	Chromodomain-helicase-DNA-binding protein	11.547	0.00110	207.92	<i>Medicago truncatula</i>	9.00E-32	XM_003625680.1
UCOESTup2045	Chromodomain helicase-DNA-binding protein	2.304	0.04700	159.61	<i>Medicago truncatula</i>	2.00E-29	XM_003615661.1
UCOESTup2371	Histone deacetylase	2.109	0.00727	574.30	<i>Populus trichocarpa</i>	5.00E-32	XM_002328042.1

**Table 1. Up-regulated genes implicated in regulation in fruit ripen receptacles.**

Magnitudes of relative induction to fruit ripen receptacles,  $p$ -value ( $\leq 0.05$ ) and u.a.e (arbitrary units of expression) in red fruit are given. Mean value of u.a.e is 1771.57. Columns show the best annotated matches from the search results of tBlastX analysis, species, putative function and match  $e$ - value.



PRIMARY METABOLISM (1/5)		Fruit ripen receptacles <i>Up regulated</i>					
GENES	Putative function	Fold	p-value	u.a.e.	Species	e-value	Best Match BlastX
<b>CARBOHYDRATE METABOLISM</b>							
<b>Glycolysis</b>							
<i>UCOESTup1055</i>	Hexokinase 1	3.768	0.00057	2347.71	<i>Eriobotrya japonica</i>	0.0	<a href="#">JF414121.1</a>
<i>UCOESTup1919</i>	Glyceraldehyde-3-phosphate dehydrogenase	2.395	0.00133	9326.29	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003595990.1</a>
<i>UCOESTup973</i>	Phosphoglycerate mutase	4.009	0.00799	1804.77	<i>Arabidopsis thaliana</i>	2.00E-101	<a href="#">NM_102067.2</a>
<i>UCOESTup517</i>	Enolase	6.783	0.00045	3017.42	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002274298.1</a>
<i>UCOESTup2364</i>	Enolase	2.115	0.00383	10306.99	<i>Zea mays</i>	0.0	<a href="#">EU959614.1</a>
<i>UCOESTup1893</i>	Pyruvate kinase	2.418	0.00159	8632.59	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_124670.2</a>
<i>UCOESTup2194</i>	Pyruvate dehydrogenase	2.214	0.00199	18138.84	<i>Glycine max</i>	6.00E-175	<a href="#">XM_003533767.1</a>
<b>Gluconeogenesis</b>							
<i>UCOESTup1175</i>	Phosphoenolpyruvate carboxykinase	3.465	0.02650	923.21	<i>Flaveria pringlei</i>	1.00E-53	<a href="#">AB050473.1</a>
<b>Pentose phosphate pathway</b>							
<i>UCOESTup1955</i>	Glucose-6-phosphate dehydrogenase 2	2.366	0.00274	6794.18	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_121314.3</a>
<i>UCOESTup1145</i>	6-Phosphogluconolactonase 2	3.532	0.00070	2179.62	<i>Glycine max</i>	3.00E-138	<a href="#">XM_003516359.1</a>
<i>UCOESTup1815</i>	6-Phosphogluconate dehydrogenase	2.479	0.01830	1133.14	<i>Cucumis sativus</i>	2.00E-72	<a href="#">FJ610345.1</a>
<b>Starch and sucrose metabolism</b>							
<i>UCOESTup242</i>	Sucrose phosphate synthase	12.98	0.00012	1733.51	<i>Pyrus pyrifolia</i>	0.0	<a href="#">AB334114.1</a>
<i>UCOESTup380</i>	Trehalose-phosphate synthase	8.701	0.00015	3854.67	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_106505.4</a>
<i>UCOESTup1457</i>	Starch synthase isoform 1	2.890	0.00198	3408.95	<i>Manihot esculenta</i>	0.0	<a href="#">EF667960.1</a>
<i>UCOESTup1721</i>	Alpha.alpha-trehalose-phosphate synthase [UDP-forming] 1	2.566	0.03020	1051.47	<i>Arabidopsis thaliana</i>	8.00E-35	<a href="#">NM_106505.4</a>
<i>UCOESTup1909</i>	Alpha.alpha-trehalose-phosphate synthase [UDP-forming] 9	2.404	0.01610	1063.43	<i>Glycine max</i>	0.0	<a href="#">XM_003519657.1</a>
<i>UCOESTup1943</i>	Beta-amylase 3	2.376	0.00438	39.88	<i>Arabidopsis thaliana</i>	3.00E-25	<a href="#">NM_117813.2</a>
<b>Glucoen metabolism</b>							
<i>UCOESTup19</i>	Glycogenin	139.311	0.00012	6795.11	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003608665.1</a>
<i>UCOESTup1881</i>	Glycogenin	2.430	0.00678	2903.64	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_106363.4</a>
<i>UCOESTup2317</i>	Glycogenin	2.143	0.00970	678.40	<i>Glycine max</i>	4.00E-171	<a href="#">XM_003555744.1</a>
<b>Others genes related with carbohydrate metabolism</b>							
<i>UCOESTup593</i>	Beta-1.4-mannosyl-glycoprotein	6.114	0.00112	2159.58	<i>Arabidopsis thaliana</i>	3.00E-71	<a href="#">NM_101170.3</a>
<i>UCOESTup635</i>	Alpha-1.2-fucosyltransferase 1	5.797	0.00527	66.31	<i>Populus tremula</i>	0.0	<a href="#">EU024129.1</a>
<i>UCOESTup662</i>	O-fucosyltransferase	5.565	0.02250	94.61	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_121579.3</a>
<i>UCOESTup733</i>	O-fucosyltransferase	5.082	0.00034	1685.89	<i>Arabidopsis thaliana</i>	1e -145	<a href="#">NM_111405.3</a>
<i>UCOESTup2010</i>	O-fucosyltransferase	2.329	0.00153	6154.19	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_126209.2</a>
<i>UCOESTup1118</i>	Nucleotide pyrophosphatase/phosphodiesterase	3.578	0.00428	419.20	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003628604.1</a>
<i>UCOESTup1355</i>	Glycosyl hydrolase	3.054	0.04160	120.56	<i>Arabidopsis thaliana</i>	1.00E-80	<a href="#">NM_118101.3</a>
<i>UCOESTup1523</i>	UDP-glucose 4-epimerase	2.796	0.00321	3709.08	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003610933.1</a>
<i>UCOESTup1745</i>	UDP-Arabinose 4-epimerase 1	2.542	0.00257	14697.34	<i>Glycine max</i>	0.0	<a href="#">XM_003524972.1</a>
<i>UCOESTup1804</i>	Isomerase	2.494	0.00304	2318.47	<i>Medicago truncatula</i>	9.00E-117	<a href="#">XM_003590624.1</a>

(Table continues on following page)



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<i>UCOESTup1986</i>	Isoamylase isoform 3	2.341	0.00185	14250.59	<i>Solanum tuberosum</i>	0.0	<a href="#">AY132998.1</a>
<i>UCOESTup2167</i>	Nucleotide-diphospho-sugar transferase	2.231	0.00516	770.05	<i>Arabidopsis thaliana</i>	2.00E-127	<a href="#">NM_001084385.1</a>
<i>UCOESTup2267</i>	Trehalase	2.169	0.02170	687.31	<i>Nicotiana tabacum</i>	0.0	<a href="#">AB501123.1</a>
<i>UCOESTup2331</i>	Xylose isomerase	2.133	0.00245	6819.79	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003610131.1</a>
<i>UCOESTup2416</i>	Phosphorylated carbohydrates phosphatase	2.082	0.01040	4017.13	<i>Medicago truncatula</i>	1.00E-151	<a href="#">XM_003600990.1</a>
<b>LIPID METABOLISM</b>							
<b>Synthesis and <math>\beta</math> Oxidation of fatty acyds</b>							
<i>UCOESTup1623</i>	Beta-ketoacyl-CoA synthase	2.688	0.01140	274.76	<i>Populus trichocarpa</i>	6.00E-73	<a href="#">XM_002325994.1</a>
<i>UCOESTup2084</i>	Beta-ketoacyl-ACP synthase II-1	2.279	0.04340	1235.41	<i>Arachis hypogaea</i>	0.0	<a href="#">EU823327.1</a>
<i>UCOESTup2313</i>	Beta-ketoacyl-CoA synthase	2.146	0.01200	1841.89	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002312526.1</a>
<i>UCOESTup2356</i>	Beta-ketoacyl-CoA synthase	2.120	0.00256	298.34	<i>Populus trichocarpa</i>	4.00E-72	<a href="#">XM_002327169.1</a>
<i>UCOESTup433</i>	Delta-9 desaturase	7.987	0.00016	917.37	<i>Rosa hybrid</i>	2.00E-130	<a href="#">D49383.1</a>
<i>UCOESTup613</i>	3-ketoacyl-CoA reductase	5.933	0.00037	8466.37	<i>Gossypium hirsutum</i>	2e -96	<a href="#">AY902468.1</a>
<i>UCOESTup1621</i>	Enoyl-ACP reductase	2.689	0.00461	274.76	<i>Malus x domestica</i>	1.00E-162	<a href="#">DQ266044.1</a>
<i>UCOESTup970</i>	Acyl carrier protein	4.019	0.00462	4046.94	<i>Arachis hypogaea</i>	5.00E-32	<a href="#">FJ768733.1</a>
<i>UCOESTup1533</i>	Acyl carrier protein	2.783	0.00103	28323.33	<i>Fragaria vesca</i>	1.00E-94	<a href="#">AJ001446.1</a>
<i>UCOESTup1164</i>	Delta-9 fatty acid desaturase	3.494	0.00792	308.47	<i>Vernicia fordii</i>	7.00E-118	<a href="#">GU564349.1</a>
<i>UCOESTup1377</i>	Stearoyl-ACP desaturase (SAD)	3.019	0.00090	404.48	<i>Vernicia montana</i>	0.0	<a href="#">EU072353.1</a>
<i>UCOESTup1357</i>	Acyl-Coenzyme A oxidase 2	3.052	0.00102	6775.45	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_125910.5</a>
<i>UCOESTup1426</i>	Sphingolipid delta-4 desaturase	2.941	0.00119	9705.15	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_116731.3</a>
<i>UCOESTup1789</i>	3-Oxoacyl-[acyl-carrier-protein] reductase	2.506	0.02700	5146.84	<i>Glycine max</i>	3.00E-125	<a href="#">XM_003518929.1</a>
<i>UCOESTup2035</i>	Omega-3 desaturase	2.310	0.00147	8253.29	<i>Prunus persica</i>	0.0	<a href="#">AF517831.2</a>
<i>UCOESTup2031</i>	Acyl-CoA synthetase family member 3	2.314	0.00740	1259.62	<i>Glycine max</i>	0.0	<a href="#">XM_003530106.1</a>
<i>UCOESTup2404</i>	Acyl-coenzyme A synthetase	2.089	0.00361	10692.02	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003629663.1</a>
<i>UCOESTup2243</i>	2,4-Dienoyl-CoA reductase	2.181	0.00200	10118.32	<i>Glycine max</i>	3.00E-142	<a href="#">NM_001253332.1</a>
<b>Was synthesis</b>							
<i>UCOESTup367</i>	Long-chain-alcohol O-fatty-acyltransferase 5	8.969	0.00040	23454.17	<i>Arabidopsis thaliana</i>	3e -67	<a href="#">NM_124916.1</a>
<i>UCOESTup1391</i>	CER1 protein	2.997	0.01810	415.08	<i>Arabidopsis thaliana</i>	5.00E-71	<a href="#">NM_180601.2</a>
<i>UCOESTup1757</i>	Protein WAX2	2.536	0.00182	1591.75	<i>Glycine max</i>	0.0	<a href="#">XR_136391.1</a>
<b>Glycerophospholipid metabolism</b>							
<i>UCOESTup793</i>	1-Acylglycerone phosphate reductase	4.746	0.04190	6780.72	<i>Arabidopsis thaliana</i>	3e -63	<a href="#">NM_121043.2</a>
<i>UCOESTup1653</i>	Glycerol-phosphate acyltransferase	2.650	0.00262	164.45	<i>Glycine max</i>	2.00E-150	<a href="#">XM_003552182.1</a>
<b>Lipid transporters</b>							
<i>UCOESTup638</i>	Polyketide cyclase/dehydrase and lipid transport	5.785	0.00103	309.33	<i>Arabidopsis thaliana</i>	1e -132	<a href="#">NM_105147.3</a>
<i>UCOESTup1393</i>	Glycolipid transfer protein domain-containing protein 1	2.996	0.03150	496.73	<i>Glycine max</i>	1E-86	<a href="#">NM_001253330.1</a>
<b>Steroids</b>							
<i>UCOESTup319</i>	UDP-glucose:sterol 3-O-glucosyltransferase	10.131	0.00052	1126.26	<i>Withania somnifera</i>	0.0	<a href="#">EU342378.2</a>
<i>UCOESTup502</i>	Acyl-CoA sterol acyl transferase 1 (ASAT1)	7.123	0.00028	5437.13	<i>Arabidopsis thaliana</i>	4.00E-100	<a href="#">NM_115056.3</a>
<i>UCOESTup1077</i>	Oxysterol-binding family protein	3.693	0.00188	2469.43	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002283398.1</a>
<i>UCOESTup2034</i>	Oxysterol-binding family protein	2.311	0.00402	3547.13	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002872324.1</a>
<b>GDSL esterases/lipases</b>							
<i>UCOESTup313</i>	GDSL esterase/lipase	10.377	0.00052	1432.06	<i>Arabidopsis thaliana</i>	6e -118	<a href="#">NM_202420.2</a>
<i>UCOESTup337</i>	GDSL motif-lipase	9.753	0.00418	298.22	<i>Zea mays</i>	1e -76	<a href="#">EU964074.1</a>

(Table continues on following page)

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<i>UCOESTup419</i>	GDSL esterase/lipase	8.245	0.00215	503.57	<i>Arabidopsis thaliana</i>	5.00E-152	<a href="#">NM_123554.2</a>
<i>UCOESTup429</i>	GDSL esterase/lipase	8.098	0.00034	7728.70	<i>Arabidopsis thaliana</i>	8.00E-103	<a href="#">NM_102626.3</a>
<i>UCOESTup903</i>	GDSL esterase/lipase 5	4.277	0.00206	3760.29	<i>Arabidopsis thaliana</i>	8.00E-103	<a href="#">NM_104270.2</a>
<i>UCOESTup1873</i>	GDSL esterase/lipase	2.436	0.02250	118.66	<i>Medicago truncatula</i>	4.00E-87	<a href="#">XM_003627369.1</a>
<b>Hydrolysis of fats (lipids)</b>							
<i>UCOESTup410</i>	Thioesterase	8.337	0.01680	1451.54	<i>Arabidopsis thaliana</i>	7.00E-64	<a href="#">NM_105497.4</a>
<i>UCOESTup2450</i>	Acyl-protein thioesterase	2.065	0.01840	6524.33	<i>Medicago truncatula</i>	7.00E-126	<a href="#">XM_003610452.1</a>
<i>UCOESTup952</i>	Lipase 3	4.103	0.00063	787.07	<i>Arabidopsis lyrata</i>	2.00E-157	<a href="#">XM_002867939.1</a>
<i>UCOESTup2407</i>	Lipase	2.088	0.00629	2410.84	<i>Glycine max</i>	2.00E-128	<a href="#">XM_003523711.1</a>
<i>UCOESTup1825</i>	Esterase/lipase/thioesterase family protein	2.468	0.00729	963.79	<i>Arabidopsis thaliana</i>	8.00E-147	<a href="#">NM_116151.3</a>
<i>UCOESTup1559</i>	Esterase PIR7A	2.760	0.01380	1094.80	<i>Glycine max</i>	7.00E-63	<a href="#">XM_003538777.1</a>
<b>Others genes related with lipid metabolism</b>							
<i>UCOESTup642</i>	Malonyl-CoA decarboxylase	5.723	0.00027	24069.56	<i>Arabidopsis lyrata</i>	2e -162	<a href="#">XM_002872641.1</a>
<i>UCOESTup1078</i>	Acyl:CoA ligase acetate-CoA synthetase	3.690	0.00339	15379.83	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002307166.1</a>
<i>UCOESTup1418</i>	Acyl:CoA ligase 2	2.959	0.00505	590.74	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002322437.1</a>
<i>UCOESTup1254</i>	Omega-hydroxypalmitate O-feruloyl transferase	3.271	0.00084	7670.71	<i>Glycine max</i>	4.00E-85	<a href="#">XM_003519156.1</a>
<i>UCOESTup2236</i>	Omega-hydroxypalmitate O-feruloyl transferase	2.185	0.02640	352.62	<i>Medicago truncatula</i>	1.00E-50	<a href="#">XM_003611325.1</a>
<i>UCOESTup1345</i>	Myristoyl-acyl carrier protein thioesterase	3.068	0.03490	33.83	<i>Glycine max</i>	2.00E-176	<a href="#">XM_003555217.1</a>
<i>UCOESTup2065</i>	1-Phosphatidylinositol phosphodiesterase	2.289	0.04660	918.92	<i>Arabidopsis thaliana</i>	4.00E-54	<a href="#">NM_120030.3</a>
<i>UCOESTup2173</i>	Membrane bound O-acyl transferase family protein	2.228	0.03220	5699.63	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002892654.1</a>
<b>AMINO ACIDS METABOLISM</b>							
<b>Proline and arginine metabolism</b>							
<i>UCOESTup1663</i>	Pyrroline-5-carboxylate reductase	2.631	0.00129	5424.97	<i>Actinidia deliciosa</i>	2.00E-143	<a href="#">U92287.1</a>
<i>UCOESTup2106</i>	Delta-1-pyrroline-5-carboxylate dehydrogenase	2.264	0.04270	4818.16	<i>Malus x domestica</i>	0.0	<a href="#">EU925831.1</a>
<b>Lysine, alanin and aspartate metabolism</b>							
<i>UCOESTup180</i>	L-Aspartate oxidase (AO)	17.26	0.00013	3107.36	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_121480.3</a>
<i>UCOESTup2388</i>	Alanine aminotransferase 2 (ALAT2)	2.098	0.00286	16119.50	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_105892.4</a>
<i>UCOESTup2269</i>	Lysine ketoglutarate reductase	2.168	0.00208	5106.26	<i>Zea mays</i>	0.0	<a href="#">NM_001156498.1</a>
<b>Glycine, serine, cysteine, threonine and methionine metabolism</b>							
<i>UCOESTup145</i>	Cysteine synthase	21.94	0.00296	41.38	<i>Nicotiana plumbaginifoli</i>	1.00E-89	<a href="#">AY450295.1</a>
<i>UCOESTup469</i>	Cysteine synthase	7.536	0.00150	1778.14	<i>Glycine max</i>	6.00E-43	<a href="#">EF433422.1</a>
<i>UCOESTup688</i>	Adenosylhomocysteinase (AHC2)	5.373	0.00089	20088.29	<i>Medicago truncatula</i>	1e -160	<a href="#">AY224189.1</a>
<i>UCOESTup797</i>	Phosphoglycerate dehydrogenase	4.722	0.00752	5191.18	<i>Gossypium hirsutum</i>	0.0	<a href="#">FJ415190.1</a>
<i>UCOESTup1193</i>	Homocysteine s-methyltransferase	3.425	0.00577	1162.82	<i>Medicago truncatula</i>	8.00E-167	<a href="#">XM_003614594.1</a>
<i>UCOESTup1934</i>	L-allo-threonine aldolase	2.381	0.00220	13778.10	<i>Glycine max</i>	0.0	<a href="#">XM_003521724.1</a>
<i>UCOESTup1740</i>	Serine hydroxymethyltransferase 4	2.545	0.00337	8814.79	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002300986.1</a>
<i>UCOESTup2012</i>	Glycine decarboxylase complex H-protein	2.327	0.00193	4330.93	<i>Populus tremuloides</i>	4.00E-43	<a href="#">AY229875.1</a>
<i>UCOESTup2009</i>	Serine acetyltransferase	2.330	0.03980	6654.50	<i>Citrullus vulgaris</i>	4.00E-141	<a href="#">D49535.1</a>
<i>UCOESTup2471</i>	Homoserine dehydrogenase	2.057	0.00695	6364.97	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003629571.1</a>
<i>UCOESTup2570</i>	S-Methyl-5-thioribose kinase	2.000	0.00303	13424.92	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_103869.3</a>
<b>Biosynthesis of L-leucine and pyruvate metabolism</b>							
<i>UCOESTup1349</i>	Phosphatidylserine decarboxylase	3.061	0.03900	32.35	<i>Triticum monococcum</i>	4.00E-41	<a href="#">AY485644.1</a>

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<b>UCOESTup1874</b>	2-Isopropylmalate synthase 2	2.435	0.00205	8602.77	<i>Arabidopsis thaliana</i>	2.00E-69	NM_106063.2
<b>Valine, leucine and isoleucine metabolism</b>							
<b>UCOESTup10</b>	Beta-hydroxyisobutyryl-CoA hydrolase 1	218.298	0.00006	10370.93	<i>Arabidopsis lyrata</i>	5.00E-111	XM_002865047.1
<b>UCOESTup113</b>	3-Hydroxyisobutyryl-CoA hydrolase	28.161	0.00009	11276.44	<i>Arabidopsis thaliana</i>	8.00E-127	NM_128618.3
<b>UCOESTup675</b>	Beta-hydroxyisobutyryl-CoA hydrolase	5.442	0.00037	471.37	<i>Arabidopsis lyrata</i>	1e -102	XM_002865047.1
<b>UCOESTup1710</b>	3-Hydroxyisobutyryl-CoA hydrolase 1	2.575	0.00588	98.70	<i>Arabidopsis thaliana</i>	3.00E-117	NM_125991.3
<b>Others genes related with amino acids metabolism</b>							
<b>UCOESTup221</b>	Pyridoxal phosphate-dependent transferase	14.058	0.00022	1436.55	<i>Arabidopsis thaliana</i>	4.00E-167	NM_124571.2
<b>UCOESTup1149</b>	Pyridoxal-5'-phosphate-dependent enzyme	3.527	0.00057	1078.21	<i>Arabidopsis lyrata</i>	0.0	XM_002894491.1
<b>UCOESTup1095</b>	Acetylornithine transaminase	3.647	0.00775	4562.94	<i>A. glutinosa</i>	0.0	Y08680.1
<b>UCOESTup1299</b>	GMP synthase [glutamine-hydrolyzing]	3.157	0.00122	616.62	<i>Glycine max</i>	3.00E-89	XM_003531426.1
<b>UCOESTup1436</b>	Acetolactate synthase small subunit	2.917	0.00073	20088.29	<i>Medicago truncatula</i>	0.0	XM_003629897.1
<b>UCOESTup1807</b>	Branched-chain-amino-acid aminotransferase 6	2.492	0.00519	358.11	<i>Arabidopsis thaliana</i>	2.00E-115	NM_103897.3
<b>UCOESTup1906</b>	Amine oxidase	2.407	0.01130	127.50	<i>Medicago truncatula</i>	0.0	XM_003592356.1
<b>UCOESTup1592</b>	Amine oxidase	2.726	0.04000	120.24	<i>Glycine max</i>	1.00E-60	XM_003555291.1
<b>UCOESTup2283</b>	N-terminal glutamine amidohydrolase	2.162	0.01140	1102.13	<i>Arabidopsis thaliana</i>	1.00E-86	NM_129740.3
<b>NITROGEN METABOLISM</b>							
<b>UCOESTup373</b>	Nitrate reductase	8.859	0.00029	5611.10	<i>Prunus persica</i>	0.0	AB061670.1
<b>UCOESTup693</b>	L-Asparaginase	5.350	0.00124	22561.54	<i>Glycine max</i>	0.0	NM_001249677.1
<b>UCOESTup1167</b>	Nodulin-specific glutamine synthetase	3.487	0.01620	189.82	<i>Vigna aconitifolia</i>	0.0	M94765.1
<b>UCOESTup1849</b>	Allantoinase (ALN)	2.451	0.00155	5785.63	<i>Robinia pseudoacacia</i>	0.0	AY466437.1
<b>OTHERS GENES RELATED WITH PRIMARY METABOLISM</b>							
<b>Krebs cycle</b>							
<b>UCOESTup600</b>	2-Oxoglutarate dehydrogenase	6.061	0.02240	93.38	<i>Arabidopsis thaliana</i>	2.00E-42	NM_115399.2
<b>UCOESTup2074</b>	Citrate synthase 1	2.283	0.00207	12376.09	<i>Prunus persica</i>	0.0	AF367444.1
<b>Aldehyde dehydrogenases</b>							
<b>UCOESTup291</b>	Aldehyde dehydrogenase family 2 member C4	11.133	0.00051	617.51	<i>Glycine max</i>	0.0	XM_003530446.1
<b>UCOESTup741</b>	Aldehyde dehydrogenase family 2 member C4	5.043	0.00343	424.27	<i>Glycine max</i>	0.0	XM_003528864.1
<b>Epoxide hydrolases</b>							
<b>UCOESTup914</b>	Epoxide hydrolase	4.230	0.00120	5938.70	<i>Arabidopsis thaliana</i>	1.00E-78	NM_114960.3
<b>UCOESTup1168</b>	Epoxide hydrolase 2	3.485	0.00584	402.25	<i>Glycine max</i>	4.00E-139	NM_001253205.1
<b>UCOESTup1715</b>	Epoxide hydrolase 3	2.571	0.00134	994.64	<i>Prunus persica</i>	5.00E-170	FN430418.1
<b>UCOESTup2039</b>	Epoxide hydrolase 3	2.307	0.01010	28.56	<i>Prunus persica</i>	6.00E-126	FN430418.1
<b>UCOESTup2048</b>	Epoxide hydrolase 2	2.301	0.00530	2953.51	<i>Glycine max</i>	2.00E-133	XM_003542718.1
<b>UCOESTup2147</b>	Epoxide hydrolase	2.243	0.00470	7996.66	<i>Arabidopsis thaliana</i>	1.00E-155	NM_116467.4
<b>Others</b>							
<b>UCOESTup198</b>	Carbonic anhydrase	15.783	0.00015	574.84	<i>Arabidopsis lyrata</i>	9.00E-97	XM_002892388.1
<b>UCOESTup1012</b>	Alcohol dehydrogenase-like 1	3.898	0.00372	321.81	<i>Vitis vinifera</i>	5.00E-122	XM_003632103.1
<b>UCOESTup731</b>	Epimerase	5.087	0.00062	3407.89	<i>Arabidopsis thaliana</i>	4e -121	NM_116078.3
<b>UCOESTup853</b>	Polyamine oxidase	4.448	0.00192	1794.30	<i>Malus x domestica</i>	0.0	AB250235.1
<b>UCOESTup1070</b>	NADP-dependent malic enzyme	3.724	0.00051	8422.61	<i>Phaseolus vulgaris</i>	0.0	J03825.1
<b>UCOESTup1161</b>	Alpha-carboxyltransferase	3.496	0.00067	12756.62	<i>Jatropha curcas</i>	0.0	GQ845013.1

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<i>UCOESTup1283</i>	Dienelactone hydrolase	3.196	0.00073	12190.76	<i>Arabidopsis thaliana</i>	5.00E-42	<a href="#">NM_113263.3</a>
<i>UCOESTup1362</i>	S-Adenosylmethionine synthetase	3.040	0.00069	26480.46	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003625634.1</a>
<i>UCOESTup1492</i>	Lipoyl synthase	2.839	0.00594	6335.46	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_120926.2</a>
<i>UCOESTup1719</i>	D-Inositol-3-phosphate glycosyltransferase	2.568	0.01380	466.87	<i>Glycine max</i>	0.0	<a href="#">XM_003548657.1</a>
<i>UCOESTup1964</i>	O-acyltransferase	2.358	0.01570	225.37	<i>Arabidopsis thaliana</i>	2.00E-160	<a href="#">NM_114779.2</a>
<i>UCOESTup2180</i>	Dolichyl-phosphate mannosyltransferase polypeptide 3	2.224	0.00470	3225.91	<i>Arabidopsis thalian</i>	3.00E-44	<a href="#">NM_103710.2</a>
<i>UCOESTup2470</i>	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase	2.058	0.04580	53.76	<i>Arabidopsis thaliana</i>	1.00E-131	<a href="#">NM_129224.3</a>

**Table 2. Up-regulated genes corresponding to primary metabolism in fruit ripen receptacles.**

Magnitudes of relative induction to fruit ripen receptacles,  $p$ -value ( $\leq 0.05$ ) and u.a.e (arbitrary units of expression) in red fruit are given. Mean value of u.a.e is 1771.57. Columns show the best annotated matches from the search results of tBlastX analysis, species, putative function and match e- value.

SECONDARY METABOLISM (1/4)		Fruit ripen receptacles <i>Up regulated</i>					
GENES	Putative function	Fold	p-value	u.a.e.	Species	e-value	Best Match BlastX
<b>SHIKIMATE METABOLISM</b>							
<i>UCOESTup1134</i>	Shikimate dehydrogenase	3.545	0.00186	4753.16	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002319546.1</a>
<b>PHENYLPROPANOIDS, ANTHOCYANINS AND FLAVONOIDS METABOLISM</b>							
<b>General pathway</b>							
<i>UCOESTup755</i>	Phenylalanine ammonia-lyase 2	4.987	0.00032	19382.11	<i>Rubus idaeus</i>	0.0	<a href="#">AF237955.1</a>
<i>UCOESTup1333</i>	Phenylalanine ammonia-lyase 6	3.087	0.00103	20852.50	<i>Fragaria x ananassa</i>	0.0	<a href="#">HM641823.1</a>
<i>UCOESTup677</i>	Cinnamate-4-hydroxylase	5.436	0.00025	17109.34	<i>Rubus occidentalis</i>	0.0	<a href="#">FJ554629.1</a>
<i>UCOESTup116</i>	4-Coumarate-CoaA ligase 7	27.161	0.00008	19750.94	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_116755.4</a>
<i>UCOESTup2205</i>	4-Coumarate-CoA ligase	2.204	0.01940	912.02	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003612611.1</a>
<b>Phenylpropanoids pathway</b>							
<i>UCOESTup583</i>	Cinnamoyl CoA reductase 2 (CCR2)	6.188	0.000265	7357.27	<i>Populus trichocarpa</i>	1.00E-158	<a href="#">XM_002314016.1</a>
<i>UCOESTup1780</i>	Cinnamoyl CoA reductase 1 (CCR1)	2.516	0.001550	26101.36	<i>Fragaria x ananassa</i>	0.0	<a href="#">AY285922.1</a>
<i>UCOESTup60</i>	Cinnamyl alcohol dehydrogenase (CAD)	50.572	0.000589	9849.51	<i>Fragaria x ananassa</i>	0.0	<a href="#">U63534.1</a>
<i>UCOESTup194</i>	Cinnamyl alcohol dehydrogenase 3	16.266	0.000144	7024.28	<i>Camellia sinensis</i>	4.00E-176	<a href="#">GQ438848.1</a>
<i>UCOESTup397</i>	Cinnamyl alcohol dehydrogenase 1	8.497	0.000524	835.51	<i>Arabidopsis thaliana</i>	8e -41	<a href="#">NM_105927.3</a>
<i>UCOESTup1065</i>	Cinnamyl alcohol dehydrogenase	3.740	0.01100	321.98	<i>Populus trichocarpa</i>	8.00E-163	<a href="#">XM_002322537.1</a>
<i>UCOESTup32</i>	Isoflavone reductase	207.001	0.000115	9021.06	<i>Populus trichocarpa</i>	2.00E-98	<a href="#">XM_002313752.1</a>
<i>UCOESTup499</i>	Putative Eugenol syntase (PCBER)	7.142	0.000366	4149.85	<i>Pyrus communis</i>	1.00E-170	<a href="#">AF071477.1</a>
<b>Flavonols, isoflavonoids and anthocyanins pathway</b>							
<i>UCOESTup1434</i>	Chalcone synthase (FrCHS5)	2.926	0.00443	29375.63	<i>Fragaria x ananassa</i>	0.0	<a href="#">AB201758.1</a>
<i>UCOESTup1441</i>	Chalcone synthase (FrCHS2)	2.914	0.00507	29987.35	<i>Fragaria x ananassa</i>	0.0	<a href="#">AB201756.1</a>
<b>Flavonols</b>							
<i>UCOESTup2573</i>	Chalcone isomerase	6.132	0.04550	14512.76	<i>Glycyrrhiza echinata</i>	2.00E-116	<a href="#">AB154414.1</a>
<i>UCOESTup2572</i>	Chalcone isomerase	3.725	0.01590	16676.87	<i>Medicago truncatula</i>	1.00E-108	<a href="#">AY278228.1</a>
<i>UCOESTup1575</i>	Flavanone 3-hydroxylase (FrF3H1)	2.749	0.00113	36215.99	<i>Fragaria x ananassa</i>	0.0	<a href="#">AB201760.1</a>
<b>Anthocyanins</b>							
<i>UCOESTup1230</i>	Anthocyanidin synthase (FaANS)	3.336	0.00084	16509.73	<i>Fragaria x ananassa</i>	0.0	<a href="#">AY695817.1</a>
<i>UCOESTup12</i>	Flavonoid glucosyltransferases (FaUGFT)	202.079	0.00011	18695.43	<i>Fragaria x ananassa</i>	0.0	<a href="#">AY575056.1</a>
<i>UCOESTup405</i>	Flavonoid C- glucosyltransferases	8.381	0.00116	706.85	<i>Oryza sativa Japonica</i>	3.00E-60	<a href="#">FM179712.1</a>
<i>UCOESTup694</i>	Flavonoid glucosyltransferases (UGFT1)	5.345	0.00029	3636.03	<i>Hieracium pilosella</i>	2e -138	<a href="#">EU561020.1</a>
<i>UCOESTup695</i>	Flavonoid glucosyltransferases (UGFT2)	5.343	0.00060	804.57	<i>Hieracium pilosella</i>	2e -144	<a href="#">EU561019.1</a>
<i>UCOESTup14</i>	UDP-glucose glucosyltransferase (FaGT1)	170.167	0.00007	25165.04	<i>Fragaria x ananassa</i>	0.0	<a href="#">AY663784.1</a>
<i>UCOESTup34</i>	UDP-rhamnose:rhamnosyltransferase (FaGT4)	85.215	0.00012	7953.91	<i>Fragaria x ananassa</i>	2.00E-82	<a href="#">AY663787.1</a>
<i>UCOESTup43</i>	UDP-glucose glucosyltransferase (FaGT3)	72.097	0.00007	3449.83	<i>Fragaria x ananassa</i>	0.0	<a href="#">AY663786.1</a>
<i>UCOESTup135</i>	UDP-glucose glucosyltransferase (FaGT6)	23.120	0.00007	7602.22	<i>Fragaria x ananassa</i>	0.0	<a href="#">DQ289587.1</a>

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<i>UCOESTup628</i>	UDP-glucose glucosyltransferase (FaGT2)	5.822	0.00029	37479.91	<i>Fragaria x ananassa</i>	0.0	<a href="#">AY663785.1</a>
<i>UCOESTup1003</i>	UDP-glucose glucosyltransferase (FaGT7)	3.907	0.00092	2433.23	<i>Fragaria x ananassa</i>	3.00E-165	<a href="#">DQ289588.1</a>
<i>UCOESTup2432</i>	UDP-glucose glucosyltransferase (FaGT5)	2.072	0.00871	22064.80	<i>Fragaria x ananassa</i>	0.0	<a href="#">DQ289586.1</a>
<i>UCOESTup435</i>	Dihydroflavonol-4-reductase	7.914	0.00023	2702.18	<i>Medicago truncatula</i>	3.00E-172	<a href="#">XM_003614592.1</a>
<i>UCOESTup838</i>	Dihydroflavonol reductase (DFR)	4.517	0.00120	6231.56	<i>Vitis vinifera</i>	1.00E-146	<a href="#">XM_003633468.1</a>
<i>UCOESTup1507</i>	Dihydroflavonol-4-reductase	2.817	0.03040	5087.71	<i>Medicago truncatula</i>	4.00E-123	<a href="#">XM_003612824.1</a>
<i>UCOESTup2528</i>	Dihydroflavonol -4-reductase	2.021	0.00484	28535.21	<i>Rosa hybrida</i>	1.00E-161	<a href="#">AY780885.1</a>
<b>Isoflavonoids</b>							
<i>UCOESTup175</i>	Isoflavone 3'-hydroxylase	17.949	0.00014	2326.08	<i>Medicago truncatula</i>	1.00E-108	<a href="#">AY278228.1</a>
<i>UCOESTup388</i>	Malonyl-CoA:isoflavone 7-O-glucoside-6"-O-malonyltransferase	8.618	0.00063	409.96	<i>Glycine max</i>	3e -73	<a href="#">AB291059.1</a>
<i>UCOESTup1229</i>	2-Hydroxyisoflavanone dehydratase	3.338	0.00350	2933.90	<i>Glycyrrhiza echinata</i>	2.00E-116	<a href="#">AB154414.1</a>
<b>Transporters phenylpropanoids</b>							
<i>UCOESTup2</i>	Glutathione S-transferase (FaGST1)	1226.608	0.000052	23444.91	<i>Malus x domestica</i>	1.00E-114	<a href="#">JN573600.1</a>
<i>UCOESTup47</i>	Glutathione S-transferase (FaGST2)	67.591	0.000065	18187.51	<i>Glycine max</i>	6.00E-82	<a href="#">NM_001248057.1</a>
<i>UCOESTup203</i>	Glutathione S-transferase (FaGST3)	15.304	0.000378	1849.48	<i>Lycopersicon esculentum</i>	7.00E-79	<a href="#">AY007561.1</a>
<i>UCOESTup520</i>	Glutathione S-transferase (FaGST4)	6.770	0.000523	1974.71	<i>Pyrus communis</i>	3.00E-123	<a href="#">DQ901400.1</a>
<i>UCOESTup597</i>	Glutathione S-transferase (FaGST5)	6.081	0.000221	10177.87	<i>Glycine max</i>	2.00E-68	<a href="#">NM_001251730.1</a>
<i>UCOESTup645</i>	Glutathione S-transferase (FaGST6)	5.708	0.001570	7096.10	<i>Populus trichocarpa</i>	3e -99	<a href="#">GU065689.1</a>
<i>UCOESTup813</i>	Glutathione S-transferase (FaGST7)	4.630	0.000364	19749.03	<i>Rheum australe</i>	2.00E-114	<a href="#">EU931209.1</a>
<i>UCOESTup1321</i>	Glutathione S-transferase (FaGST8)	3.111	0.008180	35.12	<i>Populus trichocarpa</i>	7.00E-56	<a href="#">GU065677.1</a>
<i>UCOESTup1402</i>	Glutathione S-transferase (FaGST9)	2.983	0.033400	190.49	<i>Glycine max</i>	2.00E-71	<a href="#">NM_001251779.1</a>
<i>UCOESTup1619</i>	Glutathione S-transferase (FaGST10)	2.691	0.001070	31809.84	<i>Carica papaya</i>	1.00E-113	<a href="#">AJ000923.1</a>
<i>UCOESTup1635</i>	Glutathione S-transferase (FaGST11)	2.671	0.001140	428.87	<i>Populus trichocarpa</i>	3.00E-75	<a href="#">GU065697.1</a>
<i>UCOESTup29</i>	Multidrug and toxin extrusion protein (MATE 1)	106.577	0.000077	15774.51	<i>Arabidopsis thaliana</i>	1.00E-160	<a href="#">NM_124290.2</a>
<i>UCOESTup123</i>	Multidrug and toxin extrusion protein (MATE 3)	25.751	0.000338	4776.78	<i>Arabidopsis thaliana</i>	1.00E-130	<a href="#">NM_101384.1</a>
<i>UCOESTup238</i>	Multidrug and toxin extrusion protein (MATE 2)	13.141	0.000445	443.12	<i>Medicago truncatula</i>	2.00E-114	<a href="#">HM856605.1</a>
<i>UCOESTup257</i>	Multidrug and toxin extrusion protein (MATE4)	12.176	0.000385	3258.25	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_103646.3</a>
<i>UCOESTup403</i>	Multidrug and toxin extrusion protein (MATE5)	8.406	0.005190	2066.29	<i>Arabidopsis lyrata</i>	2.00E-91	<a href="#">XM_002890044.1</a>
<i>UCOESTup450</i>	Multidrug and toxin extrusion protein (MATE6)	7.702	0.002640	531.91	<i>Arabidopsis thaliana</i>	1.00E-134	<a href="#">NM_104614.4</a>
<i>UCOESTup622</i>	Multidrug and toxin extrusion protein (MATE7)	5.872	0.000338	1723.24	<i>Glycine max</i>	2e -162	<a href="#">JN316209.1</a>
<i>UCOESTup1605</i>	Multidrug and toxin extrusion protein (MATE8)	2.708	0.019800	975.29	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003615351.1</a>
<i>UCOESTup1802</i>	TRANSPARENT TESTA 12	2.498	0.025300	4155.87	<i>Glycine max</i>	0.0	<a href="#">XM_003517662.1</a>
<b>Others proteins related with flavonols, isoflavonoids and anthocyanins</b>							
<i>UCOESTup665</i>	Ketone/zingerone synthase 1 (ZS1)	5.521	0.00641	1067.01	<i>Rubus idaeus</i>	8e -157	<a href="#">JN166691.1</a>
<i>UCOESTup787</i>	Fra a 2 allergen (Fraa2)	4.807	0.00195	16070.76	<i>Fragaria x ananassa</i>	1.00E-102	<a href="#">GQ148818.1</a>
<i>UCOESTup2249</i>	NAD(P)H-dependent 6'-deoxychalcone synthase	2.178	0.02160	2738.35	<i>Medicago truncatula</i>	2.00E-117	<a href="#">XM_003607060.1</a>
<b>VOLATILE ORGANIC COMPOUNDS</b>							
<b>Esters</b>							
<i>UCOESTup134</i>	Alcohol acyl transferase (FaAAT2)	64.976	0.00005	19277.12	<i>Fragaria x ananassa</i>	5.00E-98	<a href="#">JN089766.1</a>
<i>UCOESTup90</i>	Alcohol acyl transferase (SAAT)	35.287	0.00034	22927.96	<i>Fragaria x ananassa</i>	1.00E-25	<a href="#">AF193789.1</a>
<i>UCOESTup154</i>	Alcohol acyl transferase	20.614	0.00096	907.44	<i>Fragaria vesca</i>	0.0	<a href="#">AF193790.1</a>
<i>UCOESTup327</i>	HXXXD-type acyl-transferase-like protein	9.988	0.00240	359.63	<i>Arabidopsis thaliana</i>	2e -44	<a href="#">NM_102288.6</a>

(Table continues on following page)

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Quinones							
<i>UCOESTup131</i>	Quinone oxidoreductase (FaQR)	24.311	0.00571	1201.50	<i>Fragaria x ananassa</i>	7.00E-102	<a href="#">AY048861.1</a>
Other genes related with volatile organic compounds							
<i>UCOESTup1257</i>	Pyruvate decarboxylase	3.264	0.00052	26601.16	<i>Fragaria x ananassa</i>	0.0	<a href="#">AF193791.1</a>
<i>UCOESTup2405</i>	Pyruvate decarboxylase	2.089	0.00421	6537.34	<i>Citrus sinensis</i>	0.0	<a href="#">DQ001726.1</a>
<i>UCOESTup508</i>	Short chain dehydrogenase/reductase	6.945	0.00034	16553.98	<i>Nandina domestica</i>	3.00E-98	<a href="#">FJ789568.1</a>
<i>UCOESTup1374</i>	Short chain dehydrogenase	3.021	0.00209	829.03	<i>Solanum tuberosum</i>	3.00E-87	<a href="#">AB192882.1</a>
<i>UCOESTup143</i>	CXE carboxylesterase 6	22.123	0.00017	6556.58	<i>Malus pumila</i>	3.00E-141	<a href="#">DQ279907.1</a>
<i>UCOESTup643</i>	CXE carboxylesterase 8	5.722	0.00032	5326.00	<i>Malus pumila</i>	1e -112	<a href="#">DQ279909.1</a>
<i>UCOESTup965</i>	CXE carboxylesterase	4.036	0.01320	2200.11	<i>Malus pumila</i>	2.00E-149	<a href="#">DQ279906.1</a>
ALKALOIDS METABOLISM							
<i>UCOESTup33</i>	Desacetoxyvindoline 4-hydroxylase	86.126	0.00006	795.07	<i>Catharanthus roseus</i>	1.00E-87	<a href="#">U71605.1</a>
<i>UCOESTup925</i>	Reticuline oxidase	4.182	0.00366	834.55	<i>Arabidopsis thaliana</i>	4.00E-165	<a href="#">AY140079.1</a>
<i>UCOESTup1451</i>	Hyoscyamine 6-dioxygenase	2.897	0.00740	685.52	<i>Glycine max</i>	3.00E-115	<a href="#">XM_003552560.1</a>
<i>UCOESTup2005</i>	Polyneuridine-aldehyde esterase	2.331	0.02200	86.54	<i>Glycine max</i>	8.00E-53	<a href="#">NM_001252849.1</a>
<i>UCOESTup1829</i>	Strictosidine synthase	2.466	0.03080	42.48	<i>Arabidopsis thaliana</i>	2.00E-58	<a href="#">NM_115562.3</a>
<i>UCOESTup2077</i>	Secologanin synthase	2.282	0.00408	507.99	<i>Glycine max</i>	0.0	<a href="#">XM_003546704.1</a>
<i>UCOESTup73</i>	Vinorine synthase	43.609	0.00006	25247.58	<i>Medicago truncatula</i>	3.00E-95	<a href="#">XM_003601793.1</a>
<i>UCOESTup574</i>	Vinorine synthase	6.254	0.00458	105.51	<i>Medicago truncatula</i>	5.00E-71	<a href="#">XM_003616797.1</a>
<i>UCOESTup761</i>	Vinorine synthase	4.946	0.00954	307.34	<i>Glycine max</i>	4e -67	<a href="#">XM_003536970.1</a>
<i>UCOESTup552</i>	Anthranilate synthase	6.454	0.00058	9836.85	<i>Populus trichocarpa</i>	2.00E-122	<a href="#">XM_002314725.1</a>
<i>UCOESTup561</i>	Anthranilate synthase	6.340	0.00047	6001.56	<i>Arabidopsis thaliana</i>	0.0	<a href="#">M92353.1</a>
OTHERS GENES RELATED WITH SECONDARY METABOLISM							
Glycosyltransferases							
<i>UCOESTup140</i>	UDP-glucose glucosyltransferase	22.532	0.00011	2018.47	<i>Arabidopsis thaliana</i>	2.00E-69	<a href="#">AY062579.1</a>
<i>UCOESTup287</i>	Glycosyltransferase 61	11.206	0.00055	489.80	<i>Arabidopsis thaliana</i>	5.00E-111	<a href="#">NM_001124784.1</a>
<i>UCOESTup460</i>	C-Glucosyltransferase	7.589	0.00812	1128.35	<i>Oryza sativa Japonica</i>	3.00E-48	<a href="#">FM179712.1</a>
<i>UCOESTup713</i>	Glycosyltransferase 47	5.173	0.02560	171.70	<i>Populus tremula</i>	0.0	<a href="#">AY935507.1</a>
<i>UCOESTup1022</i>	Glycosyltransferase	3.868	0.00117	474.26	<i>Arabidopsis thaliana</i>	1.00E-114	<a href="#">NM_126388.2</a>
<i>UCOESTup1102</i>	Glucosyltransferases	3.619	0.00103	3060.50	<i>Pyrus communis</i>	0.0	<a href="#">FJ854495.1</a>
<i>UCOESTup1259</i>	Glycosyltransferase 1	3.259	0.01690	113.63	<i>Withania somnifera</i>	5.00E-60	<a href="#">HM030823.1</a>
<i>UCOESTup1722</i>	Glycosyltransferase 29	2.563	0.00129	3433.43	<i>Arabidopsis thaliana</i>	9.00E-172	<a href="#">NM_114741.4</a>
<i>UCOESTup1549</i>	Beta-1,3-glucosyltransferase	2.765	0.00191	3020.61	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003610832.1</a>
<i>UCOESTup2315</i>	Hydroquinone glucosyltransferase	2.144	0.00507	5065.07	<i>Medicago truncatula</i>	2.00E-161	<a href="#">XM_003626508.1</a>
Methyltransferases							
<i>UCOESTup197</i>	S-adenosyl-L-methionine-dependent methyltransferase	15.864	0.00013	14581.23	<i>Medicago truncatula</i>	3.00E-107	<a href="#">XM_003624980.1</a>
<i>UCOESTup500</i>	S-adenosyl-L-methionine-dependent methyltransferase	7.138	0.00028	15292.13	<i>Arabidopsis thaliana</i>	7.00E-105	<a href="#">NM_121121.3</a>
<i>UCOESTup655</i>	S-adenosyl-L-methionine-dependent methyltransferase	5.609	0.00316	779.96	<i>Arabidopsis thaliana</i>	1e -91	<a href="#">NM_129701.3</a>
<i>UCOESTup1497</i>	S-Adenosylmethionine-dependent methyltransferase	2.834	0.00788	4244.56	<i>Zea mays</i>	3.00E-136	<a href="#">EU955451.1</a>
<i>UCOESTup1288</i>	Methyltransferase FkbM family	3.182	0.00239	302.42	<i>Medicago truncatula</i>	1.00E-22	<a href="#">XM_003593293.1</a>
<i>UCOESTup1493</i>	Methyltransferase 13	2.838	0.00814	1412.61	<i>Glycine max</i>	9.00E-116	<a href="#">XM_003516435.1</a>
Aldo/keto reductases							
<i>UCOESTup364</i>	Aldo/keto reductase	9.030	0.00148	460.03	<i>Fragaria x ananassa</i>	4e -120	<a href="#">AY703448.1</a>

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<b>UCOESTup1124</b>	Aldo-keto reductase	3.567	0.00091	14140.63	<i>Fragaria x ananassa</i>	0.0	<a href="#">AF039182.1</a>
<b>UCOESTup1928</b>	Aldo-keto reductase 4	2.386	0.00770	1519.43	<i>Glycine max</i>	2.00E-156	<a href="#">NM_001253147.1</a>
<b>Others</b>							
<b>UCOESTup36</b>	Cytochrome P450	83.536	0.00017	5644.60	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002307093.1</a>
<b>UCOESTup39</b>	Cytochrome P450	77.493	9.66E-05	306.29	<i>Populus trichocarpa</i>	5.00E-145	<a href="#">XM_002332289.1</a>
<b>UCOESTup68</b>	Cytochrome P450	45.817	7.31E-05	3131.09	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002319738.1</a>
<b>UCOESTup85</b>	Cytochrome P450	37.336	0.00366	809.14	<i>Arabidopsis thaliana</i>	1.00E-58	<a href="#">NM_148857.2</a>
<b>UCOESTup171</b>	Cytochrome P450	18.743	0.00019	4493.51	<i>Medicago truncatula</i>	1.00E-69	<a href="#">XM_003589612.1</a>
<b>UCOESTup187</b>	Cytochrome P450	16.537	0.00312	338.02	<i>Populus trichocarpa</i>	6.00E-178	<a href="#">XM_002319390.1</a>
<b>UCOESTup213</b>	Cytochrome P450	14.509	0.00090	213.36	<i>Vitis vinifera</i>	7.00E-168	<a href="#">XM_002280933.1</a>
<b>UCOESTup233</b>	Cytochrome P450	13.431	0.00108	1021.34	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002319405.1</a>
<b>UCOESTup240</b>	Cytochrome P450	13.085	0.00213	316.80	<i>Nicotiana tabacum</i>	6.00E-156	<a href="#">GU590869.1</a>
<b>UCOESTup305</b>	CYP86B1	10.578	0.00016	11684.92	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002874068.1</a>
<b>UCOESTup324</b>	Cytochrome P450	10.016	0.00016	24491.45	<i>Ricinus communis</i>	1e-147	<a href="#">XM_002511248.1</a>
<b>UCOESTup375</b>	Cytochrome P450	8.779	0.00110	1442.25	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002315974.1</a>
<b>UCOESTup601</b>	Cytochrome P450	6.034	0.00081	1730.38	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002315974.1</a>
<b>UCOESTup832</b>	Cytochrome P450	4.538	0.01360	711.96	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002297912.1</a>
<b>UCOESTup907</b>	Cytochrome P450	4.265	0.01550	87.14	<i>Populus trichocarpa</i>	1.00E-59	<a href="#">XM_002299543.1</a>
<b>UCOESTup1004</b>	Cytochrome P450	3.907	0.00781	241.33	<i>Sesamum radiatum</i>	4.00E-48	<a href="#">AB194715.1</a>
<b>UCOESTup1062</b>	Cytochrome P450	3.750	0.03230	127.68	<i>Gossypium arboreum</i>	1.00E-145	<a href="#">AF332974.1</a>
<b>UCOESTup1067</b>	Cytochrome P450	3.731	0.00483	336.82	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003618306.1</a>
<b>UCOESTup1110</b>	Cytochrome P450	3.598	0.02830	26.52	<i>Populus trichocarpa</i>	4.00E-85	<a href="#">XM_002303510.1</a>
<b>UCOESTup1140</b>	Cytochrome P450	3.539	0.00575	197.61	<i>Populus trichocarpa</i>	8.00E-154	<a href="#">XM_002317036.1</a>
<b>UCOESTup1200</b>	Cytochrome P450	3.417	0.02770	40.58	<i>Arabidopsis thaliana</i>	5.00E-60	<a href="#">NM_001203102.1</a>
<b>UCOESTup1217</b>	Cytochrome P450	3.368	0.00629	40.55	<i>Glycine max</i>	6.00E-148	<a href="#">Y10982.1</a>
<b>UCOESTup1267</b>	Cytochrome P450	3.236	0.00140	54.55	<i>Glycine max</i>	1.00E-62	<a href="#">XM_003533152.1</a>
<b>UCOESTup1611</b>	Cytochrome P450	2.705	0.02330	144.56	<i>Glycine max</i>	3.00E-77	<a href="#">XM_003529262.1</a>
<b>UCOESTup1616</b>	Cytochrome P450	2.697	0.00281	15592.10	<i>Citrus sinensis</i>	2.00E-78	<a href="#">AF426451.1</a>
<b>UCOESTup2063</b>	Cytochrome b5 isoform Cb5-D	2.289	0.01170	1767.79	<i>Vernicia fordii</i>	3.00E-47	<a href="#">AY578730.1</a>
<b>UCOESTup117</b>	Flavoprotein monooxygenase	27.155	0.00007	9371.83	<i>Arabidopsis lyrata</i>	4.00E-90	<a href="#">XM_002868137.1</a>
<b>UCOESTup1981</b>	Flavin-containing monooxygenase	2.346	0.00843	141.03	<i>Arabidopsis lyrata</i>	2.00E-176	<a href="#">XM_002887968.1</a>
<b>UCOESTup204</b>	Isopenicillin N epimerase	15.254	0.00091	3025.44	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003633567.1</a>
<b>UCOESTup585</b>	Molybdopterin biosynthesis protein CNX2	6.170	0.00024	2339.65	<i>Arabidopsis thaliana</i>	1.00E-125	<a href="#">NM_001202723.1</a>
<b>UCOESTup606</b>	Alliin lyase	6.000	0.00050	1602.51	<i>Arabidopsis thaliana</i>	1e-104	<a href="#">AY050779.1</a>
<b>UCOESTup2477</b>	Alliin lyase	2.054	0.01070	429.36	<i>Medicago truncatula</i>	5.00E-173	<a href="#">XM_003601163.1</a>
<b>UCOESTup1087</b>	Bifunctional monodehydroascorbate reductase and carbonic anhydrase nectarin-3	3.665	0.00052	777.88	<i>Medicago truncatula</i>	5.00E-79	<a href="#">XM_003625055.1</a>
<b>UCOESTup1163</b>	O-methyltransferase (OMT2)	3.495	0.02920	400.23	<i>Vitis vinifera</i>	1.00E-133	<a href="#">GQ357168.1</a>
<b>UCOESTup1723</b>	4,5-DOPA dioxygenase extradiol	2.563	0.01530	777.88	<i>Medicago truncatula</i>	2.00E-124	<a href="#">XM_003619657.1</a>
<b>UCOESTup1785</b>	Holocarboxylase synthetase hcs2	2.508	0.00192	518.86	<i>Medicago truncatula</i>	2.00E-156	<a href="#">XM_003601050.1</a>

**Table 3. Up-regulated genes corresponding to secondary metabolism in fruit ripen receptacles.**

Magnitudes of relative induction to fruit ripen receptacles,  $p$ -value ( $\leq 0.05$ ) and u.a.e (arbitrary units of expression) in red fruit are given. Mean value of u.a.e is 1771.57. Columns show the best annotated matches from the search results of tBlastX analysis, species, putative function and match  $e$ - value.



SIGNALING (1/5)		Fruit ripen receptacles <i>Up regulated</i>					
GENES	Putative function	Fold	p-value	u.a.e.	Species	e-value	Best Match BlastX
<b>RECEPTORS</b>							
<b>Lectin receptor kinase</b>							
<i>UCOESTup121</i>	L-Lectin receptor kinase	25.962	0.00687	596.93	<i>Medicago truncatula</i>	5.00E-137	<a href="#">XM_003608319.1</a>
<i>UCOESTup292</i>	L-Lectin receptor kinase	11.063	0.00046	3019.42	<i>Vitis vinifera</i>	2.00E-94	<a href="#">XM_002262712.1</a>
<i>UCOESTup434</i>	L-Lectin receptor kinase	7.980	0.00057	2323.49	<i>Populus nigra</i>	0.0	<a href="#">AB030083.1</a>
<i>UCOESTup482</i>	L-Lectin receptor kinase	7.389	0.00199	56.85	<i>Gossypium hirsutum</i>	0.0	<a href="#">HQ630672.1</a>
<i>UCOESTup732</i>	L-Lectin receptor kinase	5.085	0.00193	1784.41	<i>Medicago truncatula</i>	4e -179	<a href="#">AY358030.1</a>
<i>UCOESTup760</i>	L-Lectin receptor kinase	4.963	0.03840	619.13	<i>Arabidopsis thaliana</i>	3e -115	<a href="#">NM_121091.1</a>
<i>UCOESTup1675</i>	L-Lectin receptor kinase	2.615	0.00324	1903.55	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003588829.1</a>
<i>UCOESTup431</i>	G-Lectin receptor kinase	8.025	0.00193	138.61	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002270658.2</a>
<i>UCOESTup1732</i>	G-Lectin receptor kinase	2.551	0.00193	550.03	<i>Arabidopsis thaliana</i>	2.00E-167	<a href="#">NM_104818.1</a>
<i>UCOESTup2230</i>	G-Lectin receptor kinase	2.187	0.02850	106.87	<i>Arabidopsis thaliana</i>	4.00E-115	<a href="#">NM_104829.2</a>
<b>Leucine-rich repeat-containing protein</b>							
<i>UCOESTup196</i>	Leucine-rich repeat-containing protein	16.044	0.00614	182.61	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_179207.2</a>
<i>UCOESTup205</i>	Leucine-rich repeat-containing protein	15.224	0.00260	93.59	<i>Arabidopsis thaliana</i>	0.0	<a href="#">FJ708744.1</a>
<i>UCOESTup286</i>	Leucine-rich repeat-containing protein	11.239	0.01880	161.58	<i>Vitis vinifera</i>	2.00E-69	<a href="#">XM_003633734.1</a>
<i>UCOESTup432</i>	Leucine-rich repeat-containing protein	8.023	0.00014	15658.40	<i>Glycine max</i>	3.00E-126	<a href="#">FJ014728.1</a>
<i>UCOESTup456</i>	Leucine-rich repeat-containing protein	7.622	0.00684	95.77	<i>Arabidopsis thaliana</i>	7.00E-26	<a href="#">NM_122117.3</a>
<i>UCOESTup1435</i>	Leucine-rich repeat-containing protein	2.920	0.00067	1921.25	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003608576.1</a>
<i>UCOESTup2542</i>	Leucine-rich repeat-containing protein	2.015	0.01180	678.31	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002889451.1</a>
<b>Cysteine-rich receptor-like protein kinase</b>							
<i>UCOESTup26</i>	Cysteine-rich receptor-like protein kinase	116.3	0.00032	580.84	<i>Medicago truncatula</i>	4.00E-42	<a href="#">XM_003628806.1</a>
<i>UCOESTup1425</i>	Cysteine-rich receptor-like protein kinase	2.946	0.00271	1165.18	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003613856.1</a>
<b>Wall-associated receptors kinases</b>							
<i>UCOESTup765</i>	Wall-associated receptor kinase	4.924	0.02710	53.96	<i>Arabidopsis thaliana</i>	4e -12	<a href="#">NM_001198080.1</a>
<b>Proline-rich extensin-like receptor kinase</b>							
<i>UCOESTup1103</i>	Proline-rich extensin-like receptor kinase (PERK)	3.615	0.00053	1195.97	<i>Glycine max</i>	0.0	<a href="#">XM_003547220.1</a>
<b>Others receptors</b>							
<i>UCOESTup125</i>	Receptor protein kinase	25.258	0.00007	2471.52	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003629955.1</a>
<i>UCOESTup565</i>	Receptor protein kinase	6.313	0.00109	180.29	<i>Medicago truncatula</i>	6.00E-61	<a href="#">XM_003621082.1</a>
<i>UCOESTup762</i>	Receptor protein kinase	4.935	0.00040	1234.80	<i>Arabidopsis thaliana</i>	0.0	<a href="#">AF084035.1</a>
<i>UCOESTup1967</i>	Receptor protein kinase	2.357	0.02040	31.86	<i>Arabidopsis thaliana</i>	7.00E-114	<a href="#">NM_103687.1</a>
<i>UCOESTup2292</i>	Receptor protein kinase	2.156	0.00239	1338.14	<i>Glycine max</i>	0.0	<a href="#">XM_003532181.1</a>
<i>UCOESTup418</i>	Glutamate-gated kainate-type ion channel receptor	8.252	0.00034	718.55	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002305057.1</a>
<i>UCOESTup636</i>	Glutamate-gated kainate-type ion channel receptor	5.793	0.00104	579.69	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002305056.1</a>
<i>UCOESTup739</i>	Glutamate-gated kainate-type ion channel receptor	5.055	0.02300	56.27	<i>Populus trichocarpa</i>	4e -180	<a href="#">XM_002324332.1</a>

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UCOESTup1304	MAM4 receptor	3.150	0.00300	80.76	<i>Malus micromalus</i>	6.00E-37	JN006152.1
UCOESTup2287	ER lumen protein retaining receptor protein	2.158	0.00422	12726.25	<i>Arabidopsis lyrata</i>	1.00E-159	XM_002888996.1
<b>KINASES</b>							
<b>Serine/threonine-protein kinase</b>							
UCOESTup281	Mitogen-activated protein kinase kinase kinase A	11.397	0.00038	596.93	<i>Medicago truncatula</i>	4.00E-109	XM_003611744.1
UCOESTup722	Mitogen-activated protein kinase kinase kinase 1	5.149	0.00057	3019.42	<i>Arabidopsis thaliana</i>	1e -71	NM_116919.3
UCOESTup1263	Mitogen-activated protein kinase kinase kinase 1	3.245	0.00335	2323.49	<i>Glycine max</i>	1.00E-94	XM_003544724.1
UCOESTup1285	Mitogen-activated protein kinase kinase kinase 1	3.193	0.04860	56.85	<i>Glycine max</i>	8.00E-28	XM_003520761.1
UCOESTup1725	Mitogen-activated protein kinase kinase kinase 1	2.561	0.00160	1784.41	<i>Glycine max</i>	7.00E-36	XM_003517256.1
UCOESTup1966	Mitogen-activated protein kinase kinase kinase 1	2.357	0.01440	619.13	<i>Glycine max</i>	0.0	XM_003524601.1
UCOESTup2133	Mitogen-activated protein kinase	2.254	0.01100	1903.55	<i>Medicago truncatula</i>	8.00E-150	XM_003617923.1
UCOESTup1364	96 Pto kinase interactor 1	3.036	0.00735	5006.42	<i>Capsicum annuum</i>	0.0	EU560904.1
UCOESTup1184	Serine/threonine-protein kinase	3.442	0.00134	4329.88	<i>Glycine max</i>	4.00E-135	XR_137280.1
UCOESTup473	Serine/threonine-protein kinase	7.520	0.00155	4410.55	<i>Arabidopsis thaliana</i>	3.00E-117	NM_113431.5
UCOESTup929	Serine/threonine-protein kinase	4.175	0.00470	505.76	<i>Arabidopsis thaliana</i>	2.00E-25	NM_179039.3
UCOESTup1379	Serine/threonine-protein kinase	3.015	0.00575	348.56	<i>Glycine max</i>	0.0	XM_003524514.1
UCOESTup1827	Serine/threonine protein kinase	2.466	0.00265	701.19	<i>Medicago truncatula</i>	0.0	XM_003604077.1
UCOESTup1885	Serine/threonine protein kinase	2.427	0.00155	9204.70	<i>Arabidopsis thaliana</i>	0.0	NM_180212.1
UCOESTup2057	Serine/threonine-protein kinase	2.293	0.00177	9204.70	<i>Glycine max</i>	0.0	XM_003555999.1
UCOESTup2144	Serine/threonine-protein kinase	2.244	0.00269	3476.85	<i>Glycine max</i>	0.0	XM_003539055.1
UCOESTup2153	Serine/threonine protein kinase	2.238	0.02340	335.66	<i>Medicago truncatula</i>	0.0	XM_003608235.1
UCOESTup2208	Serine/threonine-protein kinase	2.203	0.00736	18801.98	<i>Glycine max</i>	0.0	XM_003549582.1
UCOESTup2495	Serine/threonine protein kinase	2.046	0.00532	1668.77	<i>Medicago truncatula</i>	0.0	XM_003607671.1
<b>Others kinases proteins</b>							
UCOESTup314	Kinase protein	10.331	0.00040	692.89	<i>Arabidopsis thaliana</i>	0.0	NM_127822.2
UCOESTup402	Kinase protein	8.412	0.03110	140.00	<i>Platanus x acerifolia</i>	1.00E-61	EU722860.1
UCOESTup423	Kinase protein	8.236	0.00044	459.39	<i>Arabidopsis thaliana</i>	0.0	NM_121238.4
UCOESTup426	Kinase protein	8.186	0.00030	4197.98	<i>Arabidopsis thaliana</i>	2.00E-106	NM_128240.3
UCOESTup504	Avr9/Cf-9 induced kinase 1 (ACIK1)	7.083	0.00019	3217.46	<i>Nicotiana tabacum</i>	5.00E-158	AY220481.2
UCOESTup587	Kinase protein	6.170	0.00418	276.76	<i>Populus trichocarpa</i>	4.00E-158	DQ997693.1
UCOESTup724	Kinase protein	5.142	0.00187	216.52	<i>Zea mays</i>	92 -142	NM_001111954.1
UCOESTup819	Kinase protein	4.600	0.00050	594.03	<i>Arabidopsis thaliana</i>	3.00E-109	NM_117528.1
UCOESTup891	Kinase protein	4.315	0.00044	8592.72	<i>Arabidopsis thaliana</i>	0.0	NM_111649.4
UCOESTup1132	Kinase protein	3.548	0.00104	1850.29	<i>Arabidopsis thaliana</i>	7.00E-124	NM_120844.1
UCOESTup2023	Kinase protein	2.318	0.02350	2152.62	<i>Glycine max</i>	0.0	NM_001248100.1
UCOESTup2518	Kinase protein	2.030	0.03900	101.76	<i>Arabidopsis thaliana</i>	0.0	AF370599.1
UCOESTup2276	Kinase protein	2.165	0.03290	228.99	<i>Populus trichocarpa</i>	1.00E-120	DQ997692.1
UCOESTup817	D-glycerate 3-kinase	4.608	0.00045	5938.70	<i>Arabidopsis thaliana</i>	4.00E-175	NM_179581.2
UCOESTup1248	Hydroxyethylthiazole kinase family protein	3.282	0.02500	7905.67	<i>Arabidopsis lyrata</i>	2.00E-76	XM_002883451.1
UCOESTup1917	Pantothenate kinase	2.397	0.00216	2583.06	<i>Medicago truncatula</i>	1.00E-160	XM_003601211.1
UCOESTup2107	Casein kinase II subunit alpha-1	2.263	0.01590	1097.55	<i>Glycine max</i>	1.00E-162	XM_003549971.1
UCOESTup1499	Phosphatidylinositol-4-phosphate 5-kinase	2.830	0.00217	17882.82	<i>Glycine max</i>	4.00E-94	XM_003517865.1
UCOESTup2007	Phosphatidylinositol-4-phosphate 5-kinase	2.330	0.00329	1380.88	<i>Arabidopsis lyrata</i>	0.0	XM_002891047.1
UCOESTup2332	Phosphatidylinositol-4-phosphate 5-kinase	2.133	0.00351	5607.79	<i>Arabidopsis thaliana</i>	0.0	NM_001202923.1

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<b>HORMONES</b>							
<b>Auxins</b>							
<i>UCOESTup40</i>	Auxin-binding protein	75.155	0.00012	1008.00	<i>Prunus persica</i>	5.00E-94	<a href="#">U79114.2</a>
<i>UCOESTup1029</i>	Auxin-induced protein	3.852	0.00457	233.18	<i>Medicago truncatula</i>	4.00E-22	<a href="#">XM_003607072.1</a>
<i>UCOESTup1034</i>	Auxin-induced protein	3.843	0.01290	414.98	<i>Glycine max</i>	4.00E-53	<a href="#">XM_003544345.1</a>
<i>UCOESTup1093</i>	Auxin-induced protein	3.650	0.00040	16951.92	<i>Glycine max</i>	0.0	<a href="#">XM_003531870.1</a>
<i>UCOESTup1386</i>	Auxin-induced protein	3.005	0.00110	457.66	<i>Medicago truncatula</i>	3.00E-97	<a href="#">XM_003593066.1</a>
<i>UCOESTup2304</i>	Auxin-induced protein	2.150	0.02370	31.35	<i>Glycine max</i>	2.00E-111	<a href="#">XM_003541297.1</a>
<i>UCOESTup2359</i>	Auxin-induced protein	2.118	0.01570	5523.34	<i>Medicago truncatula</i>	5.00E-152	<a href="#">XM_003626384.1</a>
<i>UCOESTup2090</i>	Auxin-responsive protein	2.276	0.04670	3003.51	<i>Arabidopsis thaliana</i>	8.00E-41	<a href="#">NM_125125.2</a>
<i>UCOESTup2140</i>	Auxin-responsive protein	2.246	0.00196	11301.43	<i>Glycine max</i>	2.00E-63	<a href="#">XM_003541323.1</a>
<i>UCOESTup1428</i>	Auxin response factor	2.938	0.00344	521.23	<i>Malus x domestica</i>	0.0	<a href="#">FJ177422.1</a>
<i>UCOESTup173</i>	SAUR family protein	17.994	0.00017	7595.48	<i>Populus trichocarpa</i>	4.00E-45	<a href="#">XM_002310820.1</a>
<i>UCOESTup182</i>	SAUR family protein	17.085	0.00405	288.18	<i>Populus trichocarpa</i>	7.00E-44	<a href="#">XM_002309385.1</a>
<i>UCOESTup206</i>	SAUR family protein	15.204	0.00193	260.76	<i>Populus trichocarpa</i>	4.00E-27	<a href="#">XM_002306121.1</a>
<i>UCOESTup928</i>	SAUR family protein	4.177	0.02320	350.73	<i>Populus trichocarpa</i>	4.00E-37	<a href="#">XM_002312960.1</a>
<i>UCOESTup977</i>	SAUR family protein	4.003	0.03230	3770.37	<i>Populus trichocarpa</i>	1.00E-60	<a href="#">XM_002320012.1</a>
<i>UCOESTup1136</i>	SAUR family protein	3.541	0.00351	6006.44	<i>Populus trichocarpa</i>	8.00E-28	<a href="#">XM_002318429.1</a>
<i>UCOESTup727</i>	Germin-like protein (glp)	5.102	0.00084	1292.31	<i>Chimonanthus praecox</i>	1e -75	<a href="#">EU116342.1</a>
<i>UCOESTup831</i>	Indole-3-acetic acid-amido synthetase	4.543	0.01460	422.04	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_124831.2</a>
<i>UCOESTup2520</i>	Indole-3-acetic acid amido synthetase	2.029	0.00729	1622.70	<i>Zea mays</i>	1.00E-69	<a href="#">FJ223130.1</a>
<i>UCOESTup1303</i>	IAA-amino acid hydrolase	3.151	0.00282	2554.00	<i>Populus trichocarpa</i>	1.00E-90	<a href="#">XM_002308417.1</a>
<i>UCOESTup2085</i>	IAA-amino acid hydrolase	2.278	0.01920	97.05	<i>Populus tomentosa</i>	0.0	<a href="#">FJ851363.1</a>
<b>Abscisic acid</b>							
<i>UCOESTup262</i>	ABA-stress- and ripening-induced protein (ASR)	12.050	0.00029	18468.68	<i>Fragaria x ananassa</i>	7.00E-106	<a href="#">JN006160.1</a>
<i>UCOESTup1120</i>	9-Cis-epoxycarotenoid dioxygenase (NCED)	3.576	0.00307	9271.14	<i>Fragaria x ananassa</i>	0.0	<a href="#">HQ399498.1</a>
<i>UCOESTup888</i>	Abscisic acid receptor PYR1	4.326	0.00643	3478.54	<i>Fragaria x ananassa</i>	1.00E-61	<a href="#">JF268669.1</a>
<i>UCOESTup1025</i>	Abscisic acid receptor PYL2	3.856	0.00217	1793.92	<i>Glycine max</i>	4.00E-36	<a href="#">XM_003545324.1</a>
<i>UCOESTup162</i>	HVA22 protein	19.521	0.00011	5215.88	<i>Medicago truncatula</i>	9.00E-69	<a href="#">XM_003635810.1</a>
<i>UCOESTup1400</i>	HVA22 protein	2.985	0.00197	3086.39	<i>Arabidopsis thaliana</i>	1.00E-66	<a href="#">NM_119836.2</a>
<i>UCOESTup1589</i>	SnRK2 calcium sensor (SCaS)	2.727	0.00795	8456.54	<i>Nicotiana glauca</i>	1.00E-175	<a href="#">FJ882981.1</a>
<b>Abscisic acid and Isoprenoid metabolism</b>							
<i>General pathway</i>							
<i>UCOESTup948</i>	3-Hydroxy-3-methylglutaryl-CoA reductase	4.118	0.01880	7355.54	<i>Malus x domestica</i>	0.0	<a href="#">EF580921.1</a>
<i>UCOESTup1670</i>	Farnesyl diphosphate synthase (FPS)	2.622	0.00108	2161.88	<i>Panax quinquefolium</i>	0.0	<a href="#">GQ401664.1</a>
<i>UCOESTup854</i>	Terpene synthase	4.446	0.00426	5249.79	<i>Populus trichocarpa</i>	2.00E-140	<a href="#">JF449453.1</a>
<i>UCOESTup1727</i>	Terpene synthase	2.561	0.03110	11873.28	<i>Populus trichocarpa</i>	0.0	<a href="#">JF449452.1</a>
<i>UCOESTup2192</i>	Diphosphomevelonate decarboxylase	2.215	0.00351	9422.09	<i>Hevea brasiliensis</i>	0.0	<a href="#">AB294695.1</a>
<i>Monoterpenoids</i>							
<i>UCOESTup1610</i>	Linalool synthase	2.705	0.02320	8966.61	<i>Actinidia arguta</i>	1.00E-168	<a href="#">GQ338153.1</a>
<i>Sesquiterpenoids</i>							
<i>UCOESTup72</i>	(-)-Germacrene D synthase	44.029	0.00007	1246.26	<i>Vitis vinifera</i>	2.00E-145	<a href="#">AY561842.1</a>

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<b>UCOESTup2169</b>	(E)-Beta-caryophyllene synthase	2.231	0.03220	27.48	<i>Vitis vinifera</i>	0.0	<a href="#">JF808010.1</a>
<b>Triterpenoids</b>							
<b>UCOESTup208</b>	Beta-amyrin synthase	15.142	0.00253	911.92	<i>Malus x domestica</i>	0.0	<a href="#">AB055512.1</a>
<b>Tetraterpenoids (carotenoids)</b>							
<b>UCOESTup1573</b>	Phytoene synthase	2.745	0.00114	21305.42	<i>Fragaria x ananassa</i>	0.0	<a href="#">FJ784889.1</a>
<b>Gibberelins</b>							
<b>UCOESTup266</b>	Gibberellin 2-oxidase (GA2ox2)	11.972	0.00150	1319.09	<i>Populus trichocarpa</i>	3.00E-127	<a href="#">XM_002301494.1</a>
<b>UCOESTup1835</b>	Gibberellin 3-beta-dioxygenase 4	2.461	0.00520	364.00	<i>Glycine max</i>	0.0	<a href="#">XM_003521839.1</a>
<b>Cytokinins</b>							
<b>UCOESTup737</b>	Cytokinin riboside 5'-monophosphate phosphoribohydrolase	5.061	0.00086	2788.80	<i>Petunia x hybrida</i>	4e -107	<a href="#">AB588038.1</a>
<b>UCOESTup2246</b>	Cytokinin riboside 5'-monophosphate phosphoribohydrolase	2.179	0.00842	2086.46	<i>Arabidopsis thaliana</i>	2.00E-66	<a href="#">NM_119685.2</a>
<b>UCOESTup528</b>	Cytokinin oxidase	6.696	0.00185	1197.59	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002307645.1</a>
<b>UCOESTup1433</b>	Cytokinin oxidase	2.927	0.02160	110.20	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002308894.1</a>
<b>UCOESTup1783</b>	Cytokinin oxidase	2.512	0.00679	187.02	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002304737.1</a>
<b>UCOESTup2104</b>	Cytokinin-O-glucosyltransferase 1	2.266	0.03400	603.76	<i>Arabidopsis thaliana</i>	1.00E-164	<a href="#">NM_129230.2</a>
<b>UCOESTup2115</b>	Cytokinin-O-glucosyltransferase	2.260	0.00322	10200.06	<i>Medicago truncatula</i>	2.00E-152	<a href="#">XM_003615784.1</a>
<b>UCOESTup589</b>	Adenylate isopentenyltransferase (IPT1b)	6.153	0.01370	252.01	<i>Malus x domestica</i>	9.00E-110	<a href="#">HQ585952.1</a>
<b>UCOESTup661</b>	Adenylate isopentenyltransferase (IPT3a)	5.570	0.00126	694.58	<i>Malus x domestica</i>	1e -145	<a href="#">HQ606061.1</a>
<b>UCOESTup1227</b>	Adenylate isopentenyltransferase	3.348	0.00126	785.60	<i>Malus x domestica</i>	1.00E-108	<a href="#">HQ585950.1</a>
<b>UCOESTup785</b>	Histidine-containing phosphotransfer protein 4	4.812	0.03350	105.51	<i>Arabidopsis thaliana</i>	5e -48	<a href="#">NM_001202983.1</a>
<b>Ethylene</b>							
<b>UCOESTup325</b>	Ethylene-forming-enzyme-like dioxygenase	10.005	0.000624	16212.50	<i>Prunus armeniaca</i>	5e -86	<a href="#">U97530.1</a>
<b>UCOESTup533</b>	1-Aminocyclopropane-1-carboxylate oxidase-1	6.626	0.00060	1746.46	<i>Arabidopsis thaliana</i>	3.00E-126	<a href="#">NM_100539.2</a>
<b>UCOESTup1837</b>	1-Aminocyclopropane-1-carboxylate oxidase	2.460	0.01250	1436.67	<i>Pelargonium hortorum</i>	3.00E-118	<a href="#">U07953.1</a>
<b>Jasmonic acid</b>							
<b>UCOESTup69</b>	S-Adenosyl-L-methionine;jasmonic acid carboxyl methyltransferas	44.644	0.00059	857.26	<i>Arabidopsis lyrata</i>	7.00E-94	<a href="#">XM_002893011.1</a>
<b>UCOESTup969</b>	12-Oxophytodienoate reductase 3	4.020	0.00054	1629.13	<i>Solanum lycopersicum</i>	0.0	<a href="#">NM_001246944.1</a>
<b>UCOESTup2290</b>	2-Oxophytodienoate reductase 3	2.158	0.03800	196.39	<i>Glycine max</i>	0.0	<a href="#">XM_003542309.1</a>
<b>OTHER SIGNALING RELATED PROTEINS</b>							
<b>Calcium signaling</b>							
<b>UCOESTup846</b>	Calcium binding motif-containing protein	4.491	0.00053	357.55	<i>Arabidopsis thaliana</i>	2.00E-26	<a href="#">NM_117418.1</a>
<b>UCOESTup1291</b>	Calcineurin-like phosphoesterase	3.177	0.00136	7763.12	<i>Arabidopsis thaliana</i>	3.00E-72	<a href="#">NM_101705.1</a>
<b>UCOESTup1983</b>	Calcium-binding protein BBP1	2.345	0.04630	213.00	<i>Glycine max</i>	1.00E-46	<a href="#">XM_003545755.1</a>
<b>UCOESTup2248</b>	Calmodulin	2.179	0.02750	356.43	<i>Nicotiana tabacum</i>	4.00E-72	<a href="#">AB050849.1</a>
<b>Transducin proteins</b>							
<b>UCOESTup548</b>	Transducin/WD-40 repeat-containing protein	6.477	0.00040	8164.03	<i>Arabidopsis thaliana</i>	3.00E-135	<a href="#">NM_102297.2</a>
<b>UCOESTup992</b>	Transducin family protein / WD-40 repeat family	3.951	0.00076	2794.60	<i>Arabidopsis thaliana</i>	9.00E-164	<a href="#">NM_130366.3</a>
<b>UCOESTup1369</b>	Transducin	3.031	0.00129	3203.17	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002892822.1</a>

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Phospholipase D							
UCOESTup88	Phospholipase D	36.321	0.00040	2950.75	<i>Cucumis sativus</i>	0.0	<a href="#">EF363796.2</a>
UCOESTup1316	Phospholipase D	3.130	0.00083	649.97	<i>Glycine max</i>	0.0	<a href="#">XM_003534784.1</a>
UCOESTup1465	Phospholipase D	2.877	0.03070	133.81	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003603794.1</a>
Phosphatases							
UCOESTup315	Phosphatase	10.331	0.00044	811.07	<i>Brassica rapa</i>	7e -143	<a href="#">GQ906447.1</a>
UCOESTup837	Phosphatase 2C 40	4.518	0.00036	3315.67	<i>Arabidopsis thaliana</i>	3.00E-157	<a href="#">NM_112529.2</a>
UCOESTup942	Phosphatase 2C ABI1	4.129	0.04100	300.03	<i>Zea mays</i>	2.00E-63	<a href="#">NM_001158117.1</a>
UCOESTup988	Phosphatase type 2C	3.966	0.00056	8144.71	<i>Lotus japonicus</i>	1.00E-74	<a href="#">AF092431.1</a>
UCOESTup1054	Phosphatase	3.769	0.00409	734.04	<i>Lycopersicon esculentum</i>	2.00E-84	<a href="#">AF305968.1</a>
UCOESTup1056	Pyrophosphatase 2	3.766	0.00485	1009.79	<i>Glycine max</i>	4.00E-86	<a href="#">XM_003531579.1</a>
UCOESTup1155	Phosphatase	3.514	0.00418	11428.61	<i>Arabidopsis thaliana</i>	4.00E-64	<a href="#">DQ503426.1</a>
UCOESTup1779	Phosphatase 2C 22	2.517	0.00138	2903.32	<i>Glycine max</i>	1.00E-156	<a href="#">XM_003522584.1</a>
UCOESTup2430	Phosphatase 2C 80	2.073	0.03240	857.78	<i>Arabidopsis thaliana</i>	1.00E-34	<a href="#">NM_126070.3</a>
UCOESTup2521	Phosphatase 2C 4	2.027	0.00325	561.99	<i>arabidopsis thaliana</i>	0.0	<a href="#">NM_100636.2</a>
Others							
UCOESTup235	Two-component response regulator	13.269	0.00022	3949.24	<i>Medicago truncatula</i>	2.00E-145	<a href="#">XM_003602339.1</a>
UCOESTup1749	Two-component response regulator	2.539	0.00179	12058.93	<i>Glycine max</i>	0.0	<a href="#">XM_003529498.1</a>
UCOESTup976	Phytoalexin-deficient 4-1 protein	4.004	0.00110	2734.78	<i>Solanum tuberosum</i>	3.00E-138	<a href="#">AY753546.1</a>
UCOESTup968	Small GTP-binding protein	4.025	0.00743	7880.85	<i>L.japonicus</i>	8.00E-99	<a href="#">Z73954.1</a>
UCOESTup1679	Small G protein family protein	2.609	0.00347	1181.96	<i>Arabidopsis lyrata</i>	2.00E-151	<a href="#">XM_002864690.1</a>
UCOESTup1237	ADP-ribosylation factor	3.319	0.01350	305.28	<i>Medicago truncatula</i>	1.00E-89	<a href="#">XM_003613171.1</a>
UCOESTup1463	Septum-promoting GTP-binding protein 1	2.88	0.00981	1844.09	<i>Glycine max</i>	1.00E-93	<a href="#">XM_003539821.1</a>
UCOESTup1701	Multiple inositol polyphosphate phosphatase	2.584	0.00178	3627.60	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003600923.1</a>
UCOESTup2130	Ras-related protein RHN1	2.256	0.00487	15493.79	<i>Glycine max</i>	1.00E-97	<a href="#">XM_003524342.1</a>
UCOESTup2223	RAB GTPase H1E (RABH1e)	2.192	0.00260	3465.21	<i>Arabidopsis thaliana</i>	5.00E-122	<a href="#">NM_121064.3</a>
UCOESTup2271	RAB GTPase homolog A4C	2.168	0.00386	8766.41	<i>Arabidopsis thaliana</i>	1.00E-115	<a href="#">NM_124170.2</a>
UCOESTup2436	Nitric oxide synthase-interacting protein	2.071	0.04970	2026.50	<i>Arabidopsis thaliana</i>	2.00E-36	<a href="#">NM_104844.2</a>

**Table 4. Up-regulated genes implicated in signaling in fruit ripen receptacles.**

Magnitudes of relative induction to fruit ripen receptacles, *p*-value ( $\leq 0.05$ ) and u.a.e (arbitrary units of expression) in red fruit are given. Mean value of u.a.e is 1771.57. Columns show the best annotated matches from the search results of tBlastX analysis, species, putative function and match *e*-value.

CELL WALL (1/2)		Fruit ripen receptacles <i>Up regulated</i>					
GENES	Putative function	Fold	p-value		Species	e-value	Best Match BlastX
<b>Polygalacturonases</b>							
<i>UCOESTup18</i>	Polygalacturonase 2 (PG2)	143.225	6.48E-05	4140.41	<i>Fragaria x ananassa</i>	0.0	<a href="#">DQ458990.1</a>
<i>UCOESTup218</i>	Polygalacturonase	14.391	0.00363	178.03	<i>Fragaria x ananassa</i>	0.0	<a href="#">AF380299.1</a>
<i>UCOESTup518</i>	Polygalacturonase (PcPG2)	6.779	0.00617	368.93	<i>Pyrus communis</i>	2.00E-97	<a href="#">AB067641.1</a>
<i>UCOESTup791</i>	Polygalacturonase 1 (XOPG1)	4.752	0.00061	298.56	<i>Solanum lycopersicum</i>	7e -92	<a href="#">NM_001247327.1</a>
<i>UCOESTup1151</i>	Polygalacturonase	3.517	0.00280	11102.19	<i>Fragaria x ananassa</i>	0.0	<a href="#">AY280662.1</a>
<b>Polygalacturonase inhibiting protein</b>							
<i>UCOESTup1253</i>	Polygalacturonase-inhibiting protein (PGIP)	3.276	0.0350	57.58	<i>Fragaria x ananassa</i>	0.0	<a href="#">EU117213.1</a>
<b>Pectinesterase inhibitor</b>							
<i>UCOESTup24</i>	Pectinesterase inhibitor	117.101	6.43E-05	20277.76	<i>Medicago truncatula</i>	5.00E-39	<a href="#">XM_003590090.1</a>
<b>Pectin methylesterases</b>							
<i>UCOESTup411</i>	Pectin methylesterases	8.326	0.00239	748.81	<i>Pyrus communis</i>	0.0	<a href="#">AB067683.1</a>
<i>UCOESTup1354</i>	Pectin methylesterases	3.054	0.00103	21142.44	<i>Arabidopsis thaliana</i>	0.0	<a href="#">U25649.1</a>
<b>Pectinesterase</b>							
<i>UCOESTup698</i>	Pectinesterase 35 (PME35)	5.318	0.00164	1716.81	<i>Arabidopsis thaliana</i>	7e -161	<a href="#">NM_115763.2</a>
<i>UCOESTup767</i>	Pectinesterase 31 (PME31)	4.904	0.02080	198.72	<i>Arabidopsis thaliana</i>	1e -155	<a href="#">NM_113832.3</a>
<i>UCOESTup1013</i>	Pectinesterase 41 (PME41)	3.893	0.00307	2011.24	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_116466.3</a>
<i>UCOESTup2210</i>	Pectinesterase	2.203	0.03360	253.79	<i>Medicago truncatula</i>	2.00E-147	<a href="#">XM_003609888.1</a>
<b>Rhamnogalacturonate lyases</b>							
<i>UCOESTup55</i>	Rhamnogalacturonate lyase	54.247	0.00057	1399.79	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_127827.3</a>
<i>UCOESTup263</i>	Rhamnogalacturonate lyase	12.019	0.00012	13774.31	<i>Medicago truncatula</i>	1.00E-30	<a href="#">XM_003603661.1</a>
<i>UCOESTup2337</i>	Rhamnogalacturonate lyase	2.132	0.04150	19.96	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_100863.6</a>
<b>Beta-1,4-glucanases</b>							
<i>UCOESTup59</i>	Beta-1.4-glucanase (FaEG1)	50.796	0.00094	16787.68	<i>Fragaria x ananassa</i>	2.00E-55	<a href="#">AJ414709.1</a>
<i>UCOESTup232</i>	Beta-1.3-glucanase	13.436	0.00057	1110.14	<i>Vitis riparia</i>	4.00E-118	<a href="#">EU676805.1</a>
<i>UCOESTup365</i>	Beta-1.4-glucanase (Cel1)	8.972	0.00022	36340.19	<i>Fragaria x ananassa</i>	0.0	<a href="#">AF074923.1</a>
<i>UCOESTup370</i>	Beta-1.3-glucanase	8.955	0.00190	714.38	<i>Citrus sinensis</i>	2e -31	<a href="#">J000081.1</a>
<i>UCOESTup481</i>	Beta-1.3-glucanase	7.396	0.00021	913.27	<i>Fragaria x ananassa</i>	0.0	<a href="#">AB106651.1</a>
<i>UCOESTup649</i>	Beta-1.3-glucanase (BG2-1)	5.650	0.00025	1159.32	<i>Fragaria x ananassa</i>	0.0	<a href="#">AY170375.1</a>
<i>UCOESTup750</i>	Beta-1.3-glucanase	5.020	0.00207	11575.52	<i>Ziziphus jujuba</i>	0.0	<a href="#">DQ093571.1</a>
<b>Beta-galactosidase</b>							
<i>UCOESTup77</i>	Beta-galactosidase	40.868	7.63E-05	9909.66	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003630403.1</a>
<b>Beta-glucosidase</b>							
<i>UCOESTup151</i>	Beta-glucosidase D7	20.930	0.00018	12309.51	<i>Lotus japonicus</i>	1.00E-143	<a href="#">EU710846.1</a>
<i>UCOESTup1730</i>	Beta-glucosidase	2.557	0.00337	6714.37	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003601302.1</a>

(Table continues on following page)

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<i>UCOESTup2154</i>	Beta-glucosidase D4	2.238	0.04550	43.74	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003593097.1</a>
<i>UCOESTup2159</i>	Beta-glucosidase D4	2.236	0.00629	1813.98	<i>Medicago truncatula</i>	2.00E-144	<a href="#">XM_003620155.1</a>
<i>UCOESTup1096</i>	Glucan endo-1,3-beta-glucosidase	3.646	0.00124	64.38	<i>Glycine max</i>	9.00E-168	<a href="#">XM_003541468.1</a>
<b>Glycosyl hydrolase</b>							
<i>UCOESTup1375</i>	Glycosyl hydrolase 9	3.021	0.00373	411.89	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002301451.1</a>
<i>UCOESTup1762</i>	Glycosyl hydrolase 9	2.531	0.00371	3296.31	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002867654.1</a>
<i>UCOESTup1105</i>	Glycoside hydrolase 28	3.612	0.00330	3919.71	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_119498.3</a>
<b>Expansin</b>							
<i>UCOESTup303</i>	Expansin 2 (Exp2)	10.606	0.00016	34267.13	<i>Fragaria x ananassa</i>	0.0	<a href="#">AF159563.1</a>
<i>UCOESTup855</i>	Expansin 3 (Exp3)	4.445	0.00462	8278.69	<i>Populus tremula</i>	3.00E-125	<a href="#">AY435101.1</a>
<i>UCOESTup2226</i>	Expansin B1	2.191	0.00859	64.90	<i>Vitis vinifera</i>	6.00E-136	<a href="#">XM_002278881.1</a>
<i>UCOESTup777</i>	Expansin 1 (RhEXPA1)	4.864	0.00090	10409.62	<i>Rosa hybrid</i>	2e -135	<a href="#">AB370116.1</a>
<i>UCOESTup1527</i>	Beta-Expansin	2.786	0.00263	617.99	<i>Solanum lycopersicum</i>	8.00E-103	<a href="#">NM_001247930.1</a>
<b>Pectate lyase</b>							
<i>UCOESTup1162</i>	Pectate lyase (PL)	3.496	0.00126	19890.53	<i>Fragaria x ananassa</i>	0.0	<a href="#">U63550.1</a>
<i>UCOESTup1633</i>	Pectate lyase	2.674	0.01210	73.21	<i>Prunus persica</i>	2.00E-154	<a href="#">GU462127.1</a>
<i>UCOESTup2138</i>	Pectate lyase B	2.247	0.00225	18684.67	<i>Fragaria x ananassa</i>	0.0	<a href="#">AF339024.1</a>
<i>UCOESTup2139</i>	Pectate lyase (pIA and pIB)	2.247	0.00242	25021.01	<i>Fragaria x ananassa</i>	0.0	<a href="#">AF339025.1</a>
<b>Xyloglucan transferases</b>							
<i>UCOESTup555</i>	Xyloglucan galactosyltransferase KATAMARI1	6.428	0.00237	2065.07	<i>Medicago truncatula</i>	1.00E-78	<a href="#">XM_003617783.1</a>
<i>UCOESTup653</i>	Xyloglucan:xyloglucosyl transferase (XTH30)	5.630	0.00454	5390.19	<i>Arabidopsis thaliana</i>	2e -132	<a href="#">NM_102950.3</a>
<b>Xyloglucan endotransglucosylase/hydrolase</b>							
<i>UCOESTup858</i>	Xyloglucan endotransglucosylase/hydrolase (XTH8)	4.440	0.03700	285.03	<i>Malus x domestica</i>	1.00E-137	<a href="#">EU494967.1</a>
<i>UCOESTup1387</i>	Xyloglucan endotransglycosylase hydrolase (XTH1)	3.005	0.00119	8079.87	<i>Apium graveolens</i>	8.00E-114	<a href="#">DQ204724.1</a>
<b>Xyloglucanase-specific endoglucanase inhibitor</b>							
<i>UCOESTup1380</i>	Xyloglucanase-specific endoglucanase inhibitor protein	3.015	0.02450	25.71	<i>Petunia x hybrida</i>	8.00E-105	<a href="#">FJ606762.1</a>
<b>Beta xylosidase</b>							
<i>UCOESTup709</i>	Beta xylosidase (Xyl1)	5.218	0.00040	2210.86	<i>Fragaria x ananassa</i>	0.0	<a href="#">AY486104.2</a>
<i>UCOESTup1996</i>	Beta-xylosidase/alpha-L-arabinofuranosidase 9	2.334	0.00574	1667.60	<i>Medicago truncatula</i>	0.0	<a href="#">XM_002867654.1</a>
<b>Proline-rich protein</b>							
<i>UCOESTup1860</i>	Hydroxyproline-rich glycoprotein	2.446	0.00853	1460.78	<i>Arabidopsis lyrata</i>	2.00E-39	<a href="#">XM_002864076.1</a>

**Table 5. Up-regulated genes corresponding to the cell wall in fruit ripen receptacles.**

Magnitudes of relative induction to fruit ripen receptacles, *p*-value ( $\leq 0.05$ ) and u.a.e (arbitrary units of expression) in red fruit are given. Mean value of u.a.e is 1771.57. Columns show the best annotated matches from the search results of tBlastX analysis, species, putative function and match *e*- value.

STRESSES (1/3)		Fruit ripen receptacles Up regulated					
GENES	Putative function	Fold	p-value	u.a.e.	Species	e-value	Best Match BlastX
<b>BIOTIC STRESS</b>							
<b>Disease resistance response protein</b>							
<i>UCOESTup8</i>	Disease resistance response protein	328.340	0.00011	1855.77	<i>Medicago truncatula</i>	4.00E-36	<a href="#">XM_003609731.1</a>
<i>UCOESTup579</i>	Disease resistance response protein	6.207	0.00957	76.46	<i>Vitis vinifera</i>	6.00E-28	<a href="#">XM_002263505.2</a>
<i>UCOESTup1301</i>	Disease resistance response protein (DIR2-1)	3.156	0.01260	1493.66	<i>Populus balsamifera</i>	4.00E-85	<a href="#">GU129170.1</a>
<i>UCOESTup1129</i>	NB-LRR type disease resistance protein	3.553	0.00379	5158.86	<i>Medicago truncatula</i>	3.00E-79	<a href="#">XM_003593619.1</a>
<i>UCOESTup1344</i>	NBS-LRR type disease resistance protein	3.068	0.00960	973.65	<i>Glycine max</i>	5.00E-34	<a href="#">NM_001248742.1</a>
<i>UCOESTup422</i>	Tir-nbs-lrr resistance protein	8.237	0.00174	177.48	<i>Populus trichocarpa</i>	3.00E-36	<a href="#">XM_002325460.1</a>
<i>UCOESTup526</i>	Nbs-lrr resistance protein	6.701	0.00137	24.37	<i>Populus trichocarpa</i>	2.00E-41	<a href="#">XM_002334218.1</a>
<i>UCOESTup764</i>	Cc-nbs-lrr resistance protein	4.932	0.00099	654.36	<i>Populus trichocarpa</i>	7e -126	<a href="#">XM_002297715.1</a>
<i>UCOESTup840</i>	Nbs-lrr resistance protein	4.511	0.00343	220.96	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002326530.1</a>
<i>UCOESTup2545</i>	Nbs-lrr resistance protein	2.014	0.03840	84.95	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003612644.1</a>
<i>UCOESTup2568</i>	Cc-nbs-lrr resistance protein	2.002	0.03700	358.69	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002310708.1</a>
<b>Pathogenesis-related protein (PR)</b>							
<b>PR-5</b>							
<i>UCOESTup64</i>	Thaumatococcal protein (FcPR5)	47.481	0.00156	1829.19	<i>Fragaria chiloensis</i>	9.00E-152	<a href="#">HM197717.1</a>
<i>UCOESTup712</i>	Thaumatococcal patogenesis related protein	5.176	0.02270	487.65	<i>Arabidopsis thaliana</i>	9e -93	<a href="#">NM_120027.3</a>
<i>UCOESTup712</i>	Thaumatococcal protein	3.698	0.02810	643.70	<i>Arabidopsis thaliana</i>	2.00E-111	<a href="#">AF360165.1</a>
<i>UCOESTup308</i>	Osmotin -like protein	10.513	0.00022	4448.13	<i>Ricinus communis</i>	1e -123	<a href="#">XM_002509703.1</a>
<i>UCOESTup984</i>	Osmotin - like protein (olp2)	3.980	0.01730	612.42	<i>Fragaria x ananassa</i>	6.00E-163	<a href="#">DQ325524.1</a>
<b>PR-3, -4, -8 and -11 families</b>							
<i>UCOESTup239</i>	IV Chitinase (CHI4-2)	13.115	0.00013	1041.83	<i>Fragaria x ananassa</i>	2.00E-176	<a href="#">JN415653.1</a>
<i>UCOESTup447</i>	IV Chitinase	7.742	0.00148	779.23	<i>Corylus heterophylla</i>	2.00E-118	<a href="#">JF428141.1</a>
<i>UCOESTup335</i>	III Chitinase (chi3)	9.783	0.00119	1000.29	<i>Fragaria x ananassa</i>	2e -167	<a href="#">AF134347.1</a>
<i>UCOESTup391</i>	V Chitinase	8.590	0.00151	892.61	<i>Pyrus pyrifolia</i>	5e -47	<a href="#">FJ589787.1</a>
<i>UCOESTup1174</i>	III Chitinase (ChiFIII)	3.468	0.04970	124.65	<i>Vitis vinifera</i>	2.00E-133	<a href="#">EU935006.1</a>
<i>UCOESTup1241</i>	I Chitinase	3.305	0.00052	234.56	<i>Casuarina equisetifolia</i>	1.00E-158	<a href="#">HQ414236.1</a>
<b>Other PR proteins</b>							
<i>UCOESTup13</i>	Pathogenesis-related protein	191.982	0.00011	1367.84	<i>Arabidopsis thaliana</i>	2.00E-73	<a href="#">NM_001084372.2</a>
<i>UCOESTup248</i>	Pathogenesis-related protein PAR-1b	12.712	0.00954	451.98	<i>Nicotiana tabacum</i>	5.00E-74	<a href="#">X83851.1</a>
<i>UCOESTup251</i>	Pathogenesis-related protein 4B	12.672	0.00597	1356.43	<i>Nicotiana tabacum</i>	2.00E-72	<a href="#">X60282.1</a>
<i>UCOESTup616</i>	Protease inhibitor/seed storage/lipid transfer protein	5.917	0.00030	7163.16	<i>Arabidopsis thaliana</i>	5e -22	<a href="#">NM_112712.1</a>
<i>UCOESTup958</i>	Peroxidase ATP14a	4.075	0.00988	68.84	<i>Arabidopsis thaliana</i>	5.00E-79	<a href="#">X98803.1</a>
<i>UCOESTup1223</i>	Peroxidase	3.351	0.00081	698.06	<i>Bruguiera gymnorhiza</i>	2.00E-163	<a href="#">GU478979.1</a>
<i>UCOESTup2051</i>	Peroxidase 10	2.298	0.02100	970.57	<i>Arabidopsis thaliana</i>	3.00E-63	<a href="#">AY142591.1</a>
<b>Others proteins related with biotic stress</b>							

(Table continues on following page)



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<i>UCOESTup21</i>	Elicitor responsive gene 3 (ERG3)	119.736	0.00006	25857.53	<i>Oryza sativa</i>	1.00E-25	<a href="#">AF090698.1</a>
<i>UCOESTup2143</i>	Elicitor-responsive protein	2.244	0.00203	4920.98	<i>Medicago truncatula</i>	1.00E-54	<a href="#">XM_003616359.1</a>
<i>UCOESTup56</i>	BOP/NPR1/NIM1-like regulatory protein	52.835	0.00016	6774.68	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002308869.1</a>
<i>UCOESTup184</i>	Alpha-amylase/subtilisin inhibitor	16.829	0.00102	2263.44	<i>Medicago truncatula</i>	1.00E-62	<a href="#">XM_003638347.1</a>
<i>UCOESTup225</i>	C1 Kunitz-type trypsin inhibitor	13.736	0.00085	443.91	<i>Populus nigra</i>	8.00E-47	<a href="#">HQ630655.1</a>
<i>UCOESTup342</i>	Pleiotropic drug resistance protein	9.610	0.00044	1197.63	<i>Populus trichocarpa</i>	3e -91	<a href="#">XM_002298087.1</a>
<i>UCOESTup443</i>	Respiratory burst oxidase (RBOH F)	7.773	0.00131	462.15	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_105079.2</a>
<i>UCOESTup1509</i>	Major cherry allergen Pru av 1.0202	2.815	0.00309	822.74	<i>Prunus avium</i>	1.00E-81	<a href="#">AY540508.1</a>
<i>UCOESTup2321</i>	Allergen profilin (pf-1 gene)	2.139	0.04150	18752.19	<i>Malus x domestica</i>	1.00E-75	<a href="#">AJ507457.1</a>
<i>UCOESTup1660</i>	Plastid lipid associated protein CHRC	2.636	0.00276	6226.20	<i>Solanum lycopersicum</i>	8.00E-118	<a href="#">NM_001247254.1</a>
<i>UCOESTup1775</i>	Hypersensitive reaction associated Ca <sup>2+</sup> -binding protein (HRA32)	2.522	0.03890	225.38	<i>Phaseolus vulgaris</i>	3.00E-50	<a href="#">AF145386.1</a>
<i>UCOESTup1342</i>	Wound-induced protein	3.077	0.00711	71.89	<i>Prunus dulcis</i>	1.00E-28	<a href="#">EF640697.1</a>
<i>UCOESTup2016</i>	Wound-induced protein 1	2.324	0.03180	25857.53	<i>Glycine max</i>	3.00E-41	<a href="#">XM_003537278.1</a>
<b>ABIOTIC STRESS</b>							
<b>Heat stress</b>							
<i>UCOESTup901</i>	DNAJ heat shock protein	4.283	0.00721	177.95	<i>Arabidopsis thaliana</i>	6.00E-21	<a href="#">NM_122265.4</a>
<i>UCOESTup1478</i>	Heat stress transcription factor A-6b	2.859	0.00610	428.65	<i>Glycine max</i>	3.00E-84	<a href="#">XM_003555303.1</a>
<i>UCOESTup1481</i>	Heat shock protein (SB100)	2.856	0.04030	72.33	<i>Glycine max</i>	0.0	<a href="#">NM_001251193.1</a>
<b>Drought stress</b>							
<i>UCOESTup23</i>	Nodulin 26-like intrinsic protein (NIP2;1)	117.482	0.00028	4234.91	<i>Fragaria chiloensis</i>	1.00E-137	<a href="#">GQ869535.1</a>
<i>UCOESTup1659</i>	Aquaporin NIP1-2	2.637	0.00199	23643.85	<i>Medicago truncatula</i>	3.00E-122	<a href="#">XM_003593738.1</a>
<i>UCOESTup299</i>	Stress-related protein 1 (SRP1)	10.759	0.00240	9538.38	<i>Capsicum annuum</i>	2.00E-74	<a href="#">GU373985.1</a>
<i>UCOESTup746</i>	Drought-stressed leaves	5.029	0.00625	3304.96	<i>Populus</i>	3e -30	<a href="#">CU229384.1</a>
<i>UCOESTup844</i>	Dehydration-responsive element-binding protein	4.498	0.00233	315.71	<i>Arabidopsis thaliana</i>	8.00E-42	<a href="#">NM_121850.1</a>
<i>UCOESTup1358</i>	Desiccation-related protein PCC13-62	3.052	0.00137	3206.11	<i>Brachypodium distachyon</i>	9.00E-42	<a href="#">XR_137870.1</a>
<i>UCOESTup2503</i>	Desiccation-related protein PCC13-62	2.039	0.02090	4835.98	<i>Medicago truncatula</i>	2.00E-38	<a href="#">XM_003594648.1</a>
<i>UCOESTup2391</i>	Salt tolerance protein	2.097	0.04600	74.26	<i>Medicago truncatula</i>	2.00E-48	<a href="#">XM_003603941.1</a>
<b>Others proteins related with abiotic stress</b>							
<i>UCOESTup1206</i>	Heavy-metal-associated protein	3.396	0.03020	52.34	<i>Arabidopsis thaliana</i>	7.00E-35	<a href="#">NM_102148.3</a>
<i>UCOESTup1867</i>	Heavy metal transport/detoxification protein	2.441	0.00137	15053.53	<i>Arabidopsis thaliana</i>	6.00E-90	<a href="#">NM_122366.3</a>
<i>UCOESTup1337</i>	Methionine sulfoxide reductase	3.083	0.00415	12290.25	<i>Populus trichocarpa</i>	3.00E-76	<a href="#">XM_002313915.1</a>
<i>UCOESTup2339</i>	Hypoxia-responsive family protein	2.130	0.00330	9241.85	<i>Citrus sinensis</i>	5.00E-21	<a href="#">DQ001729.1</a>

**Table 6. Up regulated genes implicated in stresses in fruit ripen receptacles.**

Magnitudes of relative induction to fruit ripen receptacles, *p*-value ( $\leq 0.05$ ) and u.a.e (arbitrary units of expression) in red fruit are given. Mean value of u.a.e is 1771.57. Columns show the best annotated matches from the search results of tBlastX analysis, species, putative function and match *e*- value.

TRANSPORTERS AND PERMEASES (1/3)		Fruit ripen receptacles <i>Up regulated</i>					
GENES	Putative function	Fold	p-value	u.a.e.	Species	e-value	Best Match BlastX
<b>ABC transporters</b>							
<i>UCOESTup169</i>	ABC transporter G	18.809	0.00010	322.51	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003612901.1</a>
<i>UCOESTup444</i>	ABC transporter	7.768	0.00131	120.39	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002298204.1</a>
<i>UCOESTup913</i>	ABC transporter (pdr3 gene)	4.236	0.00040	2552.08	<i>Nicotiana tabacum</i>	0.0	<a href="#">AJ831379.1</a>
<i>UCOESTup1296</i>	ABC transporter A	3.162	0.00063	2909.70	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_114646.3</a>
<i>UCOESTup1904</i>	ABC transporter 1	2.409	0.02300	3415.15	<i>Arabidopsis thaliana</i>	1.00E-85	<a href="#">NM_116396.3</a>
<i>UCOESTup1931</i>	ABC transporter 1	2.382	0.00218	2692.63	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_122390.3</a>
<i>UCOESTup2479</i>	ABC transporter G family member 29 (PDR1)	2.053	0.01750	370.50	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_112505.3</a>
<b>Anion transporters</b>							
<i>UCOESTup228</i>	Anion transporter 5	13.641	0.00053	241.48	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_123804.3</a>
<i>UCOESTup1861</i>	Organic anion transporter	2.445	0.00430	405.22	<i>Arabidopsis lyrata</i>	9.00E-159	<a href="#">XM_002884794.1</a>
<i>UCOESTup2112</i>	Anion-transporting ATPase	2.261	0.00241	8324.00	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002882617.1</a>
<b>Sulfate transporters</b>							
<i>UCOESTup241</i>	Sulfate transporter	12.983	0.00012	4068.85	<i>Arabidopsis thaliana</i>	4.00E-124	<a href="#">AK229248.1</a>
<i>UCOESTup2240</i>	Sulfate transporter	2.183	0.00446	5547.05	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003621739.1</a>
<b>Peptide transporters</b>							
<i>UCOESTup253</i>	Peptide transporter PTR1	12.393	0.00112	832.21	<i>Medicago truncatula</i>		<a href="#">XM_003591218.1</a>
<i>UCOESTup1383</i>	Peptide transporter PTR1	3.010	0.00112	923.19	<i>Medicago truncatula</i>	1.00E-73	<a href="#">XM_003627785.1</a>
<i>UCOESTup1636</i>	Peptide transporter PTR1	2.671	0.02530	537.86	<i>Medicago truncatula</i>	5.00E-149	<a href="#">XM_003613510.1</a>
<i>UCOESTup339</i>	Peptide transporter	9.743	0.00230	345.47	<i>Hakea actites</i>	3e -31	<a href="#">EF608214.1</a>
<i>UCOESTup704</i>	Proton-dependent oligopeptide transport family	5.281	0.00032	350.27	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002877903.1</a>
<i>UCOESTup917</i>	Oligopeptide transporter OPT family	4.218	0.00055	4587.18	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002303648.1</a>
<i>UCOESTup1763</i>	Oligopeptide transporter OPT family	2.530	0.02240	3646.21	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003625124.1</a>
<i>UCOESTup2549</i>	Transporter protein	2.012	0.02890	149.44	<i>Trifolium pratense</i>	4.00E-21	<a href="#">AB236746.1</a>
<b>Nitrate transporters</b>							
<i>UCOESTup377</i>	Nitrate transporter	8.761	0.00024	5306.26	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_105653.4</a>
<i>UCOESTup678</i>	Nitrate transporter	5.435	0.00049	1976.52	<i>Cucumis sativus</i>	1e -100	<a href="#">HM772992.1</a>
<i>UCOESTup1482</i>	Nitrate transporter	2.854	0.00825	121.89	<i>Populus trichocarpa</i>	9.00E-168	<a href="#">XM_002321586.1</a>
<b>Exportins</b>							
<i>UCOESTup488</i>	Exportin-2	7.305	0.00030	1050.30	<i>Arabidopsis thaliana</i>	5.00E-111	<a href="#">NM_130217.3</a>

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<b>UCOESTup1841</b>	Exportin-2	2.456	0.00180	6639.53	<i>Glycine max</i>	0.0	<a href="#">XM_003528740.1</a>
<b>UCOESTup2357</b>	Exportin-5	2.118	0.00356	1231.07	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003626316.1</a>
<b>Importins</b>							
<b>UCOESTup1329</b>	Importin subunit beta-4	3.093	0.00082	2873.11	<i>Glycine max</i>	0.0	<a href="#">XM_003532937.1</a>
<b>UCOESTup2124</b>	Importin alpha isoform 9	2.258	0.00936	2882.12	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_120385.3</a>
<b>Ammonium transporters</b>							
<b>UCOESTup701</b>	Ammonium transporter (PtrAMT1-5)	5.310	0.03800	68.14	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002301801.1</a>
<b>UCOESTup1240</b>	Ammonium transporter (PtrAMT4-1)	3.306	0.02220	32.92	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002302048.1</a>
<b>Amino acid transporters</b>							
<b>UCOESTup745</b>	Bidirectional amino acid transporter 1 (BAT1)	5.032	0.00503	281.08	<i>Arabidopsis thaliana</i>	1e -111	<a href="#">NM_126178.3</a>
<b>UCOESTup861</b>	Cationic amino acid transporter	4.435	0.00081	3040.70	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002303678.1</a>
<b>UCOESTup1008</b>	Amino-acid permease	3.905	0.00893	278.27	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003602614.1</a>
<b>UCOESTup1142</b>	Amino acid transporter	2.816	0.04160	5472.70	<i>Populus trichocarpa</i>	5.00E-46	<a href="#">XM_002311440.1</a>
<b>UCOESTup1508</b>	Lysine/histidine transporter	2.409	0.00834	694.22	<i>Populus trichocarpa</i>	3.00E-150	<a href="#">XM_002300627.1</a>
<b>UCOESTup1903</b>	Tryptophan/tyrosine permease	2.039	0.00417	630.51	<i>Arabidopsis thaliana</i>	9.00E-89	<a href="#">NM_121955.2</a>
<b>Calcium transporters</b>							
<b>UCOESTup1626</b>	Calcium-transporting ATPase 2	2.683	0.00222	1406.57	<i>Glycine max</i>	5.00E-46	<a href="#">XM_003549962.1</a>
<b>UCOESTup2052</b>	Ca2+-transporting ATPase (ECA4)	2.298	0.04450	203.03	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_100640.3</a>
<b>UCOESTup2101</b>	Calcium antiporter 1	2.267	0.00309	1595.27	<i>Malus x domestica</i>	0.0	<a href="#">FJ008870.1</a>
<b>Others transporters</b>							
<b>UCOESTup71</b>	Citrate transporter	44.112	0.00015	524.45	<i>Glycine max</i>	0.0	<a href="#">EU971078.1</a>
<b>UCOESTup78</b>	Carbohydrate transporter	40.666	0.00021	7068.93	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003596504.1</a>
<b>UCOESTup155</b>	Cyclic nucleotide-gated ion channel	20.583	0.00015	1175.68	<i>Arabidopsis thaliana</i>	3.00E-45	<a href="#">NM_124692.3</a>
<b>UCOESTup289</b>	Mitochondrial phosphate transporter	11.148	0.00161	2571.67	<i>Zea mays</i>	2.00E-160	<a href="#">NM_001111372.1</a>
<b>UCOESTup334</b>	Ferric reductase defective 3a (FRD3a)	9.783	0.00013	17224.22	<i>Glycine max</i>	0.0	<a href="#">EU591739.1</a>
<b>UCOESTup464</b>	High-affinity K+ transporter (HAK1)	7.569	0.00200	310.77	<i>Capsicum annuum</i>	0.0	<a href="#">AY560009.1</a>
<b>UCOESTup492</b>	Plasma-membrane choline transporter	7.236	0.00022	745.85	<i>Arabidopsis thaliana</i>	4.00E-106	<a href="#">NM_111241.4</a>
<b>UCOESTup689</b>	Nuclear transport factor 2 and RNA recognition motif domain	5.367	0.00265	359.47	<i>Arabidopsis thaliana</i>	4e -57	<a href="#">NM_125491.2</a>
<b>UCOESTup1119</b>	Hexose transporter 4	3.577	0.00629	75.21	<i>Vitis vinifera</i>	0.0	<a href="#">AY538260.1</a>

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<i>UCOESTup910</i>	Equilibrative nucleoside transporter	3.574	0.00084	2734.98	<i>Medicago truncatula</i>	3.00E-170	<a href="#">XM_003605978.1</a>
<i>UCOESTup1122</i>	Cation proton exchanger	3.539	0.00056	4871.46	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002304501.1</a>
<i>UCOESTup1139</i>	Glycerol-3-phosphate transporter	3.432	0.00101	7111.83	<i>Glycine max</i>	0.0	<a href="#">XM_003534317.1</a>
<i>UCOESTup1189</i>	Potassium channel tetramerization domain-containing protein	2.782	0.00103	2839.17	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002878690.1</a>
<i>UCOESTup1535</i>	Porin/voltage-dependent anion-selective channel protein	2.690	0.00986	1704.22	<i>Populus trichocarpa</i>	2.00E-123	<a href="#">XM_002320653.1</a>
<i>UCOESTup1625</i>	UDP-glucose/GDP-mannose transporter	2.686	0.00237	489.03	<i>Medicago truncatula</i>	3.00E-64	<a href="#">XM_003588725.1</a>
<i>UCOESTup1620</i>	Phosphate transporter1-3	2.357	0.04100	274.29	<i>Glycine max</i>	0.0	<a href="#">FJ797403.1</a>
<i>UCOESTup1968</i>	High-affinity nickel-transport family protein	2.249	0.00465	13431.33	<i>Medicago truncatula</i>	1.00E-152	<a href="#">XM_003607123.1</a>
<i>UCOESTup2136</i>	Plasma membrane H+ ATPase	2.186	0.00702	20172.84	<i>Prunus persica</i>	0.0	<a href="#">AJ271438.1</a>
<i>UCOESTup2561</i>	Sugar transport protein 7	2.005	0.02150	6698.79	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_116436.5</a>

**Table 7. Genes implicated in transporters regulated in fruit ripen receptacles.**

Magnitudes of relative induction to fruit ripen receptacles,  $p$ -value ( $\leq 0.05$ ) and u.a.e (arbitrary units of expression) in red fruit are given. Mean value of u.a.e is 1771.57. Columns show the best annotated matches from the search results of tBlastX analysis, species, putative function and match e- value.

CELL CYCLE (1/1)		Fruit ripen receptacles <i>Up regulated</i>					
GENES	Putative function	Fold	p-value	u.a.e.	Species	e-value	Best Match BlastX
<i>UCOESTup1821</i>	Cell division control protein	2.471	0.00155	1823.467	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003592982.1</a>
<i>UCOESTup2360</i>	Cyclin-U4-1 (CYCP4;1)	2.118	0.03110	312.2235	<i>Arabidopsis thaliana</i>	5.00E-38	<a href="#">NM_130038.3</a>
<i>UCOESTup1922</i>	Cyclin-dependent kinase	2.391	0.01040	5213.095	<i>Euphorbia esula</i>	0.0	<a href="#">AF230740.1</a>
<i>UCOESTup2456</i>	Cyclin-dependent kinase C_1 (CDKC_1)	2.062	0.04070	3086.992	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002873402.1</a>
<i>UCOESTup2257</i>	CDK-activating kinase (cak)	2.174	0.00276	4902.452	<i>Medicago sativa</i>	0.0	<a href="#">AF302013.1</a>

**Table 8. Up-regulated genes corresponding to cell cycle in fruit ripen receptacles.**

Magnitudes of relative induction to fruit ripen receptacles,  $p$ -value ( $\leq 0.05$ ) and u.a.e (arbitrary units of expression) in red fruit are given. Mean value of u.a.e is 1771.57. Columns show the best annotated matches from the search results of tBlastX analysis, species, putative function and match e- value.

MISCELANEOUS (1/11)		Fruit ripen receptacles Up regulated					
GENES	Putative function	Fold	p-value	u.a.e.	Species	e-value	Best Match BlastX
<b>REDOX RELATED PROTEINS</b>							
<b>Mitochondrial respiratory chain</b>							
<i>Complex I</i>							
UCOESTup320	NAD(P)H dehydrogenase B2	10.115	0.00013	9861.07	<i>Arabidopsis thaliana</i>	0.0	NM_116741.3
UCOESTup547	NADH dehydrogenase subunit 7	6.480	0.01090	298.21	<i>Cucumis sativus</i>	3.00E-59	FJ007643.1
UCOESTup728	NADH dehydrogenase 1	5.102	0.00182	5819.43	<i>Camellia sinensis</i>	4e -69	AY839917.1
UCOESTup798	NADH:ubiquinone oxydoreductase subunit 7	4.712	0.00069	1712.09	<i>N.sylvestris</i>	5.00E-180	GQ856147.1
UCOESTup849	NADH dehydrogenase subunit 4L	4.476	0.00054	2127.91	<i>Silene latifolia</i>	1.00E-21	HM099809.1
UCOESTup880	NADH dehydrogenase subunit 1	4.366	0.00676	2149.38	<i>Glycine max</i>	0.0	U09988.1
UCOESTup881	NAD(P)H:quinone oxidoreductase	4.361	0.00318	4286.39	<i>Solanum tuberosum</i>	7.00E-78	AB061251.1
UCOESTup987	NAD(P)H dehydrogenase 1	3.970	0.01210	73.57	<i>Arabidopsis thaliana</i>	0.0	NM_100592.4
UCOESTup2066	NADH dehydrogenase I subunit 1	2.288	0.00259	29751.20	<i>Arabidopsis thaliana</i>	3.00E-24	NM_201711.2
UCOESTup2372	NADH dehydrogenase (ubiquinone) 1	2.109	0.02260	3506.60	<i>Arabidopsis thaliana</i>	0.0	NM_127595.3
UCOESTup2525	NADH-quinone oxidoreductase subunit I	2.024	0.03200	8420.30	<i>Medicago truncatula</i>	4.00E-116	XM_003636151.1
UCOESTup2560	NADH-ubiquinone oxidoreductase subunit PSST	2.005	0.00481	17287.16	<i>Lupinus luteus</i>	8.00E-103	AF281035.1
<i>Complex III</i>							
UCOESTup2532	Cytochrome C reductase	2.018	0.00421	254.67	<i>Jatropha curcas</i>	8.00E-35	FJ899656.1
<i>Complex IV</i>							
UCOESTup551	Cytochrome c oxidase subunit VIb	6.455	0.00458	163.50	<i>Arabidopsis thaliana</i>	2.00E-41	NM_125166.4
UCOESTup1014	Cytochrome c-type	3.891	0.01500	3574.32	<i>Glycine max</i>	1.00E-89	XM_003540664.1
UCOESTup1614	Cytochrome c oxidase	2.699	0.00103	2933.32	<i>Glycine max</i>	2.00E-57	NM_001253167.1
UCOESTup2293	Cytochrome c oxidase	2.156	0.00426	4388.02	<i>Arabidopsis lyrata</i>	5.00E-101	XM_002889355.1
<i>Others</i>							
UCOESTup850	Alternative oxidase 2a	4.467	0.00506	4778.27	<i>Daucus carota</i>	5.00E-166	EU286575.2
UCOESTup1214	Alternative oxidase 4	3.380	0.00155	859.04	<i>Arabidopsis thaliana</i>	7.00E-139	NM_118352.3
UCOESTup803	Cytochrome b-c1 synthesis (BCS1)	4.690	0.00165	2182.00	<i>Arabidopsis thaliana</i>	5e -145	NM_114953.2
UCOESTup1121	Cytochrome b-c1 complex subunit 8	3.575	0.00275	8842.42	<i>Jatropha curcas</i>	2.00E-33	FJ899668.1
<b>Photosynthetic electron transport chain plant</b>							
UCOESTup640	Chlororespiratory reduction 6	5.769	0.00075	3597.70	<i>Arabidopsis thaliana</i>	8e -104	NM_130358.3
UCOESTup1952	Chloroplast ferredoxin-3 (FD III-1)	2.369	0.00181	13503.40	<i>Dimocarpus longan</i>	5.00E-65	JF733784.1
<b>Thioredoxin system</b>							
UCOESTup625	H-Type thioredoxin	5.856	0.00029	8591.13	<i>Citrus cv. Shiranuhi</i>	1e -62	EF122401.1
UCOESTup1438	DSBA-like thioredoxin domain containing protein	2.916	0.00083	6208.90	<i>Medicago truncatula</i>	1.00E-78	XM_003621475.1
UCOESTup1948	Thioredoxin	2.371	0.00519	3201.28	<i>Populus trichocarpa</i>	6.00E-53	XM_002304947.1

(Table continues on following page)

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Glutaredoxin system							
UCOESTup489	Glutaredoxin 5	7.251	0.00228	1214.62	<i>Populus trichocarpa</i>	7.00E-41	<a href="#">XM_002320997.1</a>
UCOESTup543	Glutaredoxin 21	6.512	0.00783	1012.83	<i>Populus trichocarpa</i>	7.00E-49	<a href="#">XM_002320609.1</a>
UCOESTup780	Glutaredoxin 18	4.846	0.01810	594.73	<i>Populus trichocarpa</i>	1e -42	<a href="#">XM_002320996.1</a>
UCOESTup815	Glutaredoxin	4.613	0.00264	505.19	<i>Arabidopsis thaliana</i>	3.00E-41	<a href="#">FJ611910.1</a>
UCOESTup950	Monothiol glutaredoxin-S2	4.106	0.00229	1367.65	<i>Arabidopsis thaliana</i>	1.00E-50	<a href="#">NM_121865.3</a>
Others redox related proteins							
UCOESTup436	Oxidoreductase., 2OG-Fe(II) oxygenase	7.914	0.00300	33.14	<i>Arabidopsis thaliana</i>	8.00E-125	<a href="#">NM_001037027.1</a>
UCOESTup496	FAD/NAD(P)-binding oxidoreductase	7.175	0.00034	1591.50	<i>Arabidopsis thaliana</i>	5.00E-72	<a href="#">NM_120614.2</a>
UCOESTup842	Oxidoreductase/ zinc ion binding protein	4.504	0.00865	447.56	<i>Arabidopsis lyrata</i>	5.00E-88	<a href="#">XM_002875415.1</a>
UCOESTup1204	Oxidoreductase	3.402	0.00090	665.75	<i>Arabidopsis lyrata</i>	2.00E-141	<a href="#">XM_002874840.1</a>
UCOESTup1584	2OG-Fe(II) oxidoreductase	2.735	0.01220	9811.58	<i>Populus trichocarpa</i>	8.00E-123	<a href="#">XM_002298446.1</a>
UCOESTup974	2-Alkenal reductase	4.009	0.04840	5846.32	<i>Artemisia annua</i>	1.00E-111	<a href="#">FJ750460.1</a>
UCOESTup1319	Aminocyclopropanecarboxylate oxidase	3.122	0.00698	2371.78	<i>Arabidopsis thaliana</i>	1.00E-157	<a href="#">NM_127517.4</a>
UCOESTup1519	Programmed cell death protein 2	2.801	0.00088	33.14	<i>Medicago truncatula</i>	7.00E-88	<a href="#">XM_003602448.1</a>
ATPases							
AAA-ATPases							
UCOESTup202	AAA-type ATPase like protein	15.455	0.00063	560.82	<i>Solanum tuberosum</i>	0.0	<a href="#">DQ191627.1</a>
UCOESTup668	AAA-type ATPase like protein	5.489	0.00044	1235.47	<i>Arabidopsis thaliana</i>	3e -146	<a href="#">AK175116.1</a>
UCOESTup2378	AAA-type ATPase like protein	2.105	0.00305	7955.51	<i>Arabidopsis thaliana</i>	2.00E-147	<a href="#">AK176580.1</a>
ATP synthase							
UCOESTup1658	ATP synthase protein 9 and NADH dehydrogenase subunit 5 genes	2.638	0.01860	382.9854	<i>Helianthus annuus</i>	5.00E-73	<a href="#">AF258785.1</a>
UCOESTup2014	ATP synthase CF1 alpha subunit (atpA)	2.326	0.01360	2773.768	<i>Sparganium eurycarpum</i>	2.00E-38	<a href="#">HQ180436.1</a>
UCOESTup1666	ATP synthase CF0 subunit III (atpH)	2.625	0.00210	5317.053	<i>Trachelium caeruleum</i>	7.00E-28	<a href="#">EU017218.1</a>
UCOESTup1822	F1 ATPase a-subunit (atpA) gene	2.471	0.00406	4163.52	<i>Panax ginseng</i>	0.0	<a href="#">AF034118.1</a>
UCOESTup1921	ATP synthase CF1 alpha subunit (atpA)	2.393	0.01020	2681.595	<i>Fosterella caulescens</i>	7.00E-36	<a href="#">HQ180415.1</a>
UCOESTup2083	Nuclear control of ATPase protein	2.280	0.00851	7296.86	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003617138.1</a>
DNA/RNA METABOLISM							
RNases							
UCOESTup37	S-Ribonuclease	82.336	0.00043	597.87	<i>Pyrus pyrifolia</i>	3.00E-25	<a href="#">AB545982.1</a>
RNA helicases							
UCOESTup99	DEAD-box RNA helicase	32.554	0.00100	261.08	<i>Prunus persica</i>	1.00E-45	<a href="#">GQ865548.1</a>
UCOESTup99	DEAD box RNA helicase RH2b	4.544	0.00066	250.67	<i>Hevea brasiliensis</i>	0.0	<a href="#">HQ323243.1</a>
UCOESTup1280	DEAD-box ATP-dependent RNA helicase 37	3.200	0.00070	7022.17	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_129813.4</a>
UCOESTup1331	DEAD-box ATP-dependent RNA helicase 53	3.089	0.00165	6053.27	<i>Glycine max</i>	7.00E-94	<a href="#">XM_003518442.1</a>
UCOESTup1343	DEAD-box ATP-dependent RNA helicase 37	3.073	0.00073	5288.23	<i>Glycine max</i>	0.0	<a href="#">XM_003524900.1</a>
UCOESTup1754	DEAD-box ATP-dependent RNA helicase 48	2.537	0.00595	725.69	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_105004.2</a>
UCOESTup2426	DEAD-box ATP-dependent RNA helicase 7	2.078	0.01040	2982.83	<i>Arabidopsis thaliana</i>	7.00E-71	<a href="#">NM_125613.2</a>
UCOESTup979	ATP-dependent RNA helicase	3.989	0.00354	10464.32	<i>Arabidopsis thaliana</i>	1.00E-21	<a href="#">AY059740.1</a>
UCOESTup2336	ATP-dependent RNA helicase eIF4A	2.132	0.02710	366.51	<i>Medicago truncatula</i>	3.00E-41	<a href="#">XM_003611705.1</a>
Transcription							

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<b>Transcription preinitiation complex</b>							
<b>UCOESTup882</b>	Transcription factor TFIIB	4.355	0.00998	298.08	<i>Glycine max</i>	4.00E-88	<a href="#">NM_001251414.1</a>
<b>UCOESTup1714</b>	Transcription initiation factor TFIID subunit 11	2.572	0.00911	2343.90	<i>Zea mays</i>	8.00E-58	<a href="#">NM_001159121.1</a>
<b>UCOESTup2417</b>	Transcription initiation factor TFIID subunit H4	2.082	0.02930	1848.69	<i>Arabidopsis thaliana</i>	4.00E-76	<a href="#">NM_117806.3</a>
<b>UCOESTup2425</b>	Transcription initiation factor TFIID subunit H1	2.078	0.00984	2075.45	<i>Arabidopsis thaliana</i>	1.00E-162	<a href="#">NM_104451.3</a>
<b>Small nuclear ribonucleoproteins</b>							
<b>UCOESTup993</b>	Small nuclear ribonucleoprotein D2	3.951	0.00711	2202.02	<i>Arabidopsis thaliana</i>	1.00E-52	<a href="#">NM_201981.3</a>
<b>UCOESTup1859</b>	U4/U6 small nuclear ribonucleoprotein Prp3	2.446	0.00312	399.01	<i>Glycine max</i>	2.00E-83	<a href="#">XM_003538613.1</a>
<b>UCOESTup2203</b>	U4/U6 small nuclear ribonucleoprotein Prp3	2.206	0.00401	3393.02	<i>Glycine max</i>	0.0	<a href="#">XM_003516688.1</a>
<b>RNA Polymerases Subunits</b>							
<b>UCOESTup981</b>	RNA polymerase beta subunit	3.984	0.00185	1794.38	<i>Sanguisorba sitchensis</i>	9.00E-72	<a href="#">JF317513.1</a>
<b>RNA Polimerase types</b>							
<b>UCOESTup451</b>	5.8S rRNA and 25S rRNA with 18S rRNA fragment	7.669	0.00038	6258.18	<i>Arabidopsis thaliana</i>	0.0	<a href="#">X52320.1</a>
<b>UCOESTup2491</b>	DNA-directed RNA polymerase I subunit A1	2.048	0.00830	70.38	<i>Arabidopsis thaliana</i>	8.00E-61	<a href="#">NM_115626.1</a>
<b>UCOESTup2514</b>	DNA-directed RNA polymerase I subunit rp49	2.031	0.00366	5807.20	<i>Medicago truncatula</i>	6.00E-80	<a href="#">XM_003595009.1</a>
<b>UCOESTup1581</b>	rRNA-processing protein UTP23	2.739	0.00286	1911.94	<i>Medicago truncatula</i>	4.00E-85	<a href="#">XM_003597343.1</a>
<b>UCOESTup2093</b>	Ribosomal RNA-processing protein 8	2.273	0.00304	1944.93	<i>Arabidopsis thaliana</i>	9.00E-113	<a href="#">NM_123417.3</a>
<b>UCOESTup2312</b>	RNA polymerase II second largest subunit (RPB2)	2.146	0.00208	6357.81	<i>Solanum lycopersicum</i>	0.0	<a href="#">NM_001246960.1</a>
<b>UCOESTup2396</b>	RNA polymerase II C-terminal domain phosphatase	2.095	0.00859	103.68	<i>Medicago truncatula</i>	3.00E-45	<a href="#">XM_003620850.1</a>
<b>UCOESTup1690</b>	DNA-directed RNA polymerase II	2.600	0.04360	2138.69	<i>Arabidopsis thaliana</i>	1.00E-69	<a href="#">NM_112574.2</a>
<b>UCOESTup2447</b>	DNA-directed RNA polymerase II	2.066	0.04570	2841.93	<i>Zea mays</i>	3.00E-26	<a href="#">EU973151.1</a>
<b>UCOESTup2412</b>	E11-associated factor Eaf	2.085	0.01970	3695.74	<i>Medicago truncatula</i>	8.00E-95	<a href="#">XM_003630935.1</a>
<b>UCOESTup1781</b>	DNA-directed RNA polymerase III subunit RPC4	2.513	0.00885	1534.7	<i>Medicago truncatula</i>	5.00E-59	<a href="#">XM_003590926.1</a>
<b>UCOESTup1877</b>	DNA-directed RNA polymerase III subunit C2	2.434	0.00977	517.56	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_123882.4</a>
<b>UCOESTup2011</b>	DNA-directed RNA polymerase III subunit RPC2	2.328	0.04300	99.71	<i>Glycine max</i>	6.00E-133	<a href="#">XM_003529012.1</a>
<b>RNA-binding protein</b>							
<b>UCOESTup963</b>	Glycine-rich RNA-binding protein 3	4.044	0.00078	3414.72	<i>Arabidopsis thaliana</i>	3.00E-45	<a href="#">NM_125496.2</a>
<b>UCOESTup1462</b>	RNA-binding protein 8A	2.881	0.01300	5389.36	<i>Glycine max</i>	6.00E-49	<a href="#">XM_003517473.1</a>
<b>UCOESTup2161</b>	RNA-binding ASCH domain protein	2.235	0.00913	2221.28	<i>Arabidopsis thaliana</i>	1.00E-54	<a href="#">NM_111203.2</a>
<b>UCOESTup2368</b>	RNA-binding protein 24-B	2.111	0.00644	9720.91	<i>Medicago truncatula</i>	1.00E-97	<a href="#">XM_003603829.1</a>
<b>UCOESTup2487</b>	RNA-binding protein NOB1	2.049	0.00318	7679.54	<i>Arabidopsis thaliana</i>	4.00E-164	<a href="#">NM_123484.2</a>
<b>mRNA</b>							
<b>UCOESTup1707</b>	Pre-mRNA-processing factor	2.577	0.00309	724.55	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003629846.1</a>
<b>UCOESTup2229</b>	Pre-mRNA-splicing factor ISY1	2.188	0.02910	2203.58	<i>Medicago truncatula</i>	1.00E-122	<a href="#">XM_003617743.1</a>
<b>UCOESTup1587</b>	Enhancer of mRNA-decapping protein 4	2.729	0.01590	194.06	<i>Glycine max</i>	3.00E-110	<a href="#">XM_003530774.1</a>
<b>UCOESTup1729</b>	Enhancer of mRNA-decapping protein	2.558	0.01590	131.68	<i>Medicago truncatula</i>	1.00E-36	<a href="#">XM_003600391.1</a>
<b>UCOESTup323</b>	Cap guanine-N7 methyltransferase	10.050	0.000978	1222.28	<i>Arabidopsis lyrata</i>	2e -38	<a href="#">XM_002885346.1</a>
<b>UCOESTup2550</b>	Splicing factor Prp18	2.011	0.03450	10649.83	<i>Arabidopsis thaliana</i>	2.00E-133	<a href="#">NM_100196.2</a>
<b>UCOESTup619</b>	Splicing factor U2af small subunit A	5.889	0.00035	3361.66	<i>Arabidopsis thaliana</i>	2e -80	<a href="#">NM_102530.3</a>
<b>UCOESTup2503</b>	Polyadenylate-binding protein 2-A	2.750	0.00192	2647.44	<i>Medicago truncatula</i>	1.00E-36	<a href="#">XM_003599075.1</a>
<b>Processing of RNA</b>							

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<i>UCOESTup1220</i>	RNA recognition motif-containing protein	3.361	0.00069	1956.40	<i>Arabidopsis lyrata</i>	2.00E-98	<a href="#">XM_002876250.1</a>
<i>UCOESTup2555</i>	H/ACA ribonucleoprotein complex subunit 4	2.008	0.00421	11031.44	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_115574.2</a>
<b>Others</b>							
<i>UCOESTup1020</i>	DNA-binding protein SMUBP-2	3.871	0.00216	376.65	<i>Glycine max</i>	4.00E-100	<a href="#">XM_003553373.1</a>
<i>UCOESTup1130</i>	DNA-binding protein SMUBP-2	3.551	0.00921	866.54	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003625122.1</a>
<i>UCOESTup2054</i>	RNA (guanine-9-)-methyltransferase domain-containing protein	2.296	0.01200	3948.88	<i>Medicago truncatula</i>	3.00E-106	<a href="#">XM_003594254.1</a>
<i>UCOESTup1458</i>	Mitochondrial transcription termination	2.889	0.00110	3353.38	<i>Arabidopsis thaliana</i>	4.00E-62	<a href="#">XM_002871248.1</a>
<i>UCOESTup2216</i>	Ribosomal RNA methyltransferase 1	2.198	0.01330	8770.67	<i>Glycine max</i>	0.0	<a href="#">XM_003545890.1</a>
<i>UCOESTup2309</i>	RNA-dependent RNA polymerase	2.148	0.00752	1556.51	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002308626.1</a>
<i>UCOESTup2340</i>	Exosome complex exonuclease RRP6	2.130	0.01080	2008.63	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003605886.1</a>
<b>Translation</b>							
<b>Translation factors</b>							
<i>UCOESTup792</i>	Translation initiation factor 3 large subunit	4.751	0.00152	1586.80	<i>Oryza sativa</i>	2e -135	<a href="#">AJ437346.1</a>
<i>UCOESTup1043</i>	Translation initiation factor eIF-1A	3.812	0.01170	905.76	<i>Beta vulgaris</i>	8.00E-51	<a href="#">AJ251896.1</a>
<i>UCOESTup1089</i>	Translation-initiation factor 3	3.661	0.00475	178.15	<i>Prunus avium</i>	0.0	<a href="#">AY050484.1</a>
<i>UCOESTup1268</i>	Translation initiation factor 3 subunit G	3.228	0.01150	144.07	<i>Glycine max</i>	2.00E-87	<a href="#">XM_003551959.1</a>
<i>UCOESTup2189</i>	Translation initiation factor 2B beta subunit	2.217	0.00492	2998.45	<i>Nicotiana tabacum</i>	0.0	<a href="#">AF137288.2</a>
<i>UCOESTup2228</i>	Translation initiation factor 4E type 3	2.188	0.00757	6416.25	<i>Glycine max</i>	1.00E-125	<a href="#">XM_003518212.1</a>
<i>UCOESTup1612</i>	eIF4-gamma/eIF5/eIF2-epsilon domain-containing protein	2.704	0.00506	107.38	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002870010.1</a>
<i>UCOESTup2375</i>	Initiation factor iso4G (eIFiso4G)	2.107	0.00881	107.38	<i>Carica papaya</i>	0.0	<a href="#">HM802937.1</a>
<i>UCOESTup2281</i>	Elongation factor Tu	2.163	0.03190	1571.54	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002270996.1</a>
<b>tRNA</b>							
<i>UCOESTup1252</i>	tRNA (guanine-N(7)-)-methyltransferase	3.276	0.00573	1527.27	<i>Medicago truncatula</i>	1.00E-147	<a href="#">XM_003603537.1</a>
<i>UCOESTup1618</i>	Histidyl-tRNA synthetase	2.696	0.00140	15247.13	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_111144.5</a>
<i>UCOESTup1897</i>	Aspartyl-tRNA synthetase	2.416	0.00274	14142.09	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003588818.1</a>
<i>UCOESTup1990</i>	Peptidyl-tRNA hydrolase ICT1	2.337	0.00888	770.87	<i>Glycine max</i>	2.00E-91	<a href="#">XM_003549838.1</a>
<i>UCOESTup2050</i>	tRNA pseudouridine synthase A	2.299	0.01110	693.68	<i>Medicago truncatula</i>	3.00E-136	<a href="#">XM_003630553.1</a>
<i>UCOESTup2197</i>	tRNA 2-thiolation	2.211	0.00277	4255.64	<i>Glycine max</i>	2.00E-144	<a href="#">XM_003553363.1</a>
<i>UCOESTup1654</i>	Poly(A) polymerase	2.642	0.00231	5620.44	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003627003.1</a>
<b>Others</b>							
<i>UCOESTup453</i>	Pumilio 7 (PUM7)	7.641	0.02690	70.85	<i>Arabidopsis thaliana</i>	3.00E-38	<a href="#">NM_106466.2</a>
<i>UCOESTup1503</i>	Pumilio domain-containing protein PPD1	2.825	0.00187	1166.90	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002266633.1</a>
<i>UCOESTup1569</i>	Pumilio homolog 24	2.746	0.00222	2709.68	<i>Glycine max</i>	0.0	<a href="#">XM_003550391.1</a>
<i>UCOESTup1682</i>	Pumilio 12 (PUM12)	2.607	0.00137	2423.82	<i>Arabidopsis thaliana</i>	3.00E-88	<a href="#">NM_125034.2</a>
<i>UCOESTup1739</i>	Translation machinery-associated protein 22	2.546	0.03500	2294.23	<i>Glycine max</i>	3.00E-73	<a href="#">XM_003533706.1</a>
<i>UCOESTup2389</i>	RNA binding protein	2.098	0.00641	2668.12	<i>Medicago truncatula</i>	9.00E-97	<a href="#">XM_003609204.1</a>
<b>Replication</b>							
<i>UCOESTup408</i>	DNA helicase domain-containing protein	8.346	0.00074	669.70	<i>Arabidopsis thaliana</i>	2.00E-155	<a href="#">NM_105251.1</a>
<i>UCOESTup1060</i>	RNA-directed DNA polymerase gene	3.756	0.00310	155.59	<i>Beta vulgaris</i>	2.00E-68	<a href="#">EF101866.1</a>
<i>UCOESTup1726</i>	Replication factor C1 (RFC1)	2.561	0.00406	318.14	<i>Arabidopsis thaliana</i>	1.00E-52	<a href="#">NM_147883.5</a>
<i>UCOESTup1944</i>	Replication factor A1 (RPA1A)	2.374	0.01040	3425.84	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_126648.3</a>
<i>UCOESTup2278</i>	ATP-dependent DNA helicase 2 subunit KU70	2.163	0.00489	2152.88	<i>Glycine max</i>	0.0	<a href="#">XM_003556532.1</a>

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<i>UCOESTup2490</i>	DNA polymerase III polC-type	2.049	0.00527	669.70	<i>Medicago truncatula</i>	3.00E-63	<a href="#">XM_003626124.1</a>
<b>Mobile genetic elements</b>							
<i>UCOESTup736</i>	LTR retrotransposon RTip1	5.066	0.00137	1147.34	<i>Ipomoea purpurea</i>	2e -22	<a href="#">AB000394.1</a>
<i>UCOESTup1397</i>	LINE-type retrotransposon Belline16_3	2.991	0.01740	24.06	<i>Beta vulgaris</i>	9.00E-36	<a href="#">FR852830.1</a>
<i>UCOESTup2172</i>	LINE-type retrotransposon Belline15_3	2.228	0.01500	29.98	<i>Beta vulgaris</i>	4.00E-33	<a href="#">FR852827.1</a>
<i>UCOESTup2098</i>	Ty1-copia retrotransposon FaRE1	2.269	0.03410	86.05	<i>Fragaria x ananassa</i>	9.00E-78	<a href="#">FJ871121.1</a>
<i>UCOESTup430</i>	Transposase	8.063	0.00527	252.82	<i>Zea mays</i>	8.00E-86	<a href="#">AH008191.2</a>
<i>UCOESTup479</i>	Transposase	7.418	0.00040	868.17	<i>Arabidopsis thaliana</i>	0.0	<a href="#">AK227645.1</a>
<i>UCOESTup824</i>	Transposase	4.573	0.02550	125.52	<i>Arabidopsis thaliana</i>	1.00E-31	<a href="#">AF120335.1</a>
<b>Nucleotide metabolism</b>							
<i>UCOESTup224</i>	Adenine nucleotide alpha hydrolases	13.852	0.00052	205.05	<i>Arabidopsis thaliana</i>	1.00E-34	<a href="#">NM_121745.1</a>
<i>UCOESTup524</i>	Adenine nucleotide alpha hydrolases	6.712	0.00016	16987.62	<i>Arabidopsis thaliana</i>	1.00E-39	<a href="#">NM_111199.1</a>
<i>UCOESTup604</i>	Adenine/guanine permease AZG1	6.029	0.04070	518.93	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_111933.2</a>
<i>UCOESTup344</i>	Quinolinat synthase (QS)	9.563	0.00036	3563.55	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_124400.2</a>
<i>UCOESTup2185</i>	Dimethyladenosine transferase	2.221	0.00365	4717	<i>Arabidopsis thaliana</i>	9.00E-146	<a href="#">AY113864.1</a>
<i>UCOESTup1576</i>	Inosine-uridine preferring nucleoside hydrolase	2.744	0.00325	1113.12	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_121891.3</a>
<i>UCOESTup2507</i>	Nucleoside-triphosphatase (APY1)	2.037	0.00547	6408.06	<i>Arabidopsis thaliana</i>	5.00E-29	<a href="#">NM_111279.4</a>
<i>UCOESTup2562</i>	Nucleoside-triphosphatase	2.005	0.02760	3942.59	<i>Medicago truncatula</i>	1.00E-28	<a href="#">XM_003624531.1</a>
<i>UCOESTup2327</i>	AMP deaminase	2.136	0.03810	397.80	<i>Glycine max</i>	2.00E-29	<a href="#">XR_137561.1</a>
<i>UCOESTup2037</i>	DRM-type cytosine DNA-methyltransferase	2.308	0.01170	1178.63	<i>Fragaria x ananassa</i>	0.0	<a href="#">FJ804061</a>
<b>Others genes related with DNA/RNA metabolism</b>							
<i>UCOESTup904</i>	Cytidine/deoxycytidylate deaminase	4.274	0.00092	8727.66	<i>Zea mays</i>	2.00E-92	<a href="#">EU974505.1</a>
<i>UCOESTup863</i>	Endonuclease	4.425	0.0282	73.99	<i>Beta vulgaris</i>	3.00E-25	<a href="#">FR852830.1</a>
<i>UCOESTup1239</i>	DNA damage-binding protein	3.310	0.0126	67.18	<i>Medicago truncatula</i>	4.00E-28	<a href="#">XM_003638042.1</a>
<i>UCOESTup1326</i>	54-kD signal recognition particle (SRP)	3.105	0.0336	926.79	<i>Solanum lycopersicum</i>	0.0	<a href="#">NM_001247499.1</a>
<i>UCOESTup1334</i>	RNA ligase	3.087	0.0076	46.86	<i>Arabidopsis thaliana</i>	5.00E-110	<a href="#">NM_001160848.1</a>
<i>UCOESTup2343</i>	FACT complex subunit SSRP1	2.127	0.00401	6555.33	<i>Arabidopsis thaliana</i>	2.00E-84	<a href="#">NM_113794.3</a>
<i>UCOESTup2455</i>	Exonuclease	2.062	0.00932	2186.99	<i>Arabidopsis thaliana</i>	2.00E-86	<a href="#">NM_112370.3</a>
<b>PROTEIN METABOLISM</b>							
<b>Ubiquitin-proteins</b>							
<i>UCOESTup31</i>	Ubiquitin-protein ligase	100.492	0.00011	1513.59	<i>Medicago truncatula</i>	4.00E-63	<a href="#">XM_003602578.1</a>
<i>UCOESTup174</i>	E3 ubiquitin-protein ligase	17.967	0.00052	330.23	<i>Arabidopsis thaliana</i>	3.00E-165	<a href="#">NM_001197991.1</a>
<i>UCOESTup201</i>	E3 ubiquitin-protein ligase	15.598	0.00079	204.46	<i>Arabidopsis thaliana</i>	4.00E-147	<a href="#">NM_128708.4</a>
<i>UCOESTup550</i>	E3 ubiquitin-protein ligase RING1	6.474	0.00569	480.14	<i>Vitis vinifera</i>	8.00E-20	<a href="#">XM_002283176.2</a>
<i>UCOESTup778</i>	E3 ubiquitin-protein ligase PUB23	4.860	0.01980	270.99	<i>Arabidopsis thaliana</i>	2e -125	<a href="#">NM_129152.2</a>
<i>UCOESTup845</i>	Ubiquitin-protein ligase RNF1/2 (RING1B)	4.493	0.00590	1106.04	<i>Arabidopsis thaliana</i>	2.00E-67	<a href="#">NM_123795.4</a>
<i>UCOESTup1249</i>	E3 ubiquitin-protein ligase RING1	3.281	0.02980	3584.45	<i>Glycine max</i>	1.00E-123	<a href="#">XM_003539490.1</a>
<i>UCOESTup1443</i>	E3 ubiquitin-protein ligase ARI	2.906	0.00202	366.98	<i>Arabidopsis thaliana</i>	3.00E-125	<a href="#">NM_119602.1</a>
<i>UCOESTup1896</i>	E3 ubiquitin-protein ligase RNF144A	2.418	0.03370	1071.48	<i>Glycine max</i>	5.00E-72	<a href="#">XM_003529805.1</a>
<i>UCOESTup2064</i>	E3 ubiquitin-protein ligase Topors	2.289	0.01620	198.06	<i>Medicago truncatula</i>	3.00E-95	<a href="#">XM_003591044.1</a>
<i>UCOESTup2346</i>	E3 ubiquitin-protein ligase ARI8	2.126	0.00227	4108.01	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_105217.3</a>
<i>UCOESTup2397</i>	E3 ubiquitin-protein ligase MARCH2	2.095	0.01240	685.53	<i>Medicago truncatula</i>	2.00E-83	<a href="#">XM_003592508.1</a>
<i>UCOESTup168</i>	Ubiquitin	18.944	0.00016	4017.13	<i>Arabidopsis thaliana</i>	1.00E-21	<a href="#">U84967.1</a>

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<i>UCOESTup1504</i>	Ubiquitin carboxyl-terminal hydrolase	2.822	0.00085	1812.91	<i>Arabidopsis thaliana</i>	1.00E-135	<a href="#">NM_105843.2</a>
<i>UCOESTup1655</i>	Ubiquitin fusion degradation UFD1	2.640	0.00339	4463.58	<i>Arabidopsis thaliana</i>	3.00E-151	<a href="#">NM_201828.3</a>
<i>UCOESTup1741</i>	Polyubiquitin	2.545	0.00442	54.60	<i>P.sylvestris</i>	3.00E-46	<a href="#">X98063.1</a>
<i>UCOESTup1755</i>	Ubiquitin	2.537	0.00975	1132.40	<i>Arachis hypogaea</i>	1.00E-70	<a href="#">DQ887086.1</a>
<i>UCOESTup2000</i>	Ubiquitin-specific protease 8	2.333	0.02100	470.99	<i>Arabidopsis thaliana</i>	0.0	<a href="#">AK226691.1</a>
<i>UCOESTup2164</i>	Polyubiquitin (ubq10)	2.232	0.03040	11979.62	<i>Arabidopsis thaliana</i>	0.0	<a href="#">L05361.1</a>
<i>UCOESTup2439</i>	Ubiquitin fusion degradation protein	2.069	0.00284	10323.81	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003616928.1</a>
<i>UCOESTup2496</i>	Ubiquitin-conjugating enzyme 22	2.045	0.00365	5911.11	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002886040.1</a>
<b>SCF complex</b>							
<i>UCOESTup52</i>	SKP1	58.768	0.00009	10415.09	<i>Hevea brasiliensis</i>	6.00E-23	<a href="#">HM640272.1</a>
<i>UCOESTup839</i>	SKP1	4.515	0.03310	122.68	<i>Citrus maxima</i>	8.00E-51	<a href="#">FJ851401.1</a>
<i>UCOESTup2238</i>	SKP1	2.184	0.03170	151.66	<i>Petunia integrifolia</i>	1.00E-68	<a href="#">DQ250015.1</a>
<i>UCOESTup54</i>	F-box protein	54.820	0.00120	359.72	<i>Medicago truncatula</i>	8.00E-21	<a href="#">XM_003599569.1</a>
<i>UCOESTup185</i>	F-box protein	16.661	0.01350	2033.68	<i>Populus trichocarpa</i>	4.00E-53	<a href="#">XM_002307964.1</a>
<i>UCOESTup362</i>	F-box protein	9.085	0.01500	505.33	<i>Arabidopsis thaliana</i>	1e -34	<a href="#">NM_124191.3</a>
<i>UCOESTup441</i>	F-box protein	7.797	0.00170	111.58	<i>Populus trichocarpa</i>	3e -23	<a href="#">XM_002298382.1</a>
<i>UCOESTup567</i>	F-box protein	6.306	0.00069	263.09	<i>Vitis vinifera</i>	1.00E-48	<a href="#">XM_002264228.2</a>
<i>UCOESTup596</i>	F-box protein	6.082	0.03140	149.59	<i>Arabidopsis lyrata</i>	3.00E-51	<a href="#">XM_002874796.1</a>
<i>UCOESTup663</i>	F-box protein	5.561	0.01860	112.80	<i>Pyrus pyrifolia</i>	1e -35	<a href="#">AB545981.1</a>
<i>UCOESTup686</i>	F-box protein	5.380	0.01380	162.58	<i>Populus trichocarpa</i>	3e -39	<a href="#">XM_002308681.1</a>
<i>UCOESTup740</i>	F-box protein	5.052	0.00028	732.01	<i>Arabidopsis thaliana</i>	4e -95	<a href="#">NM_102874.3</a>
<i>UCOESTup776</i>	F-box protein	4.866	0.02710	83.90	<i>Pyrus pyrifolia</i>	0.0	<a href="#">AB545981.1</a>
<i>UCOESTup783</i>	F-box protein	4.839	0.01100	30.43	<i>Arabidopsis thaliana</i>	4e -23	<a href="#">NM_101227.2</a>
<i>UCOESTup822</i>	F-box protein	4.582	0.00065	1244.44	<i>Populus trichocarpa</i>	3.00E-26	<a href="#">XM_002301552.1</a>
<i>UCOESTup833</i>	F-box protein	4.534	0.00054	947.75	<i>Prunus avium</i>	1.00E-58	<a href="#">AB360340.1</a>
<i>UCOESTup1094</i>	F-box protein	3.650	0.00057	3630.77	<i>Medicago truncatula</i>	4.00E-88	<a href="#">XM_003589259.1</a>
<i>UCOESTup1146</i>	F-box protein	3.532	0.01040	413.69	<i>Glycine max</i>	9.00E-139	<a href="#">XM_003548370.1</a>
<i>UCOESTup1238</i>	F-box protein	3.312	0.00084	10519.54	<i>Populus trichocarpa</i>	3.00E-70	<a href="#">XM_002308681.1</a>
<i>UCOESTup1339</i>	F-box protein	3.081	0.00565	76.10	<i>Medicago truncatula</i>	9.00E-21	<a href="#">XM_003604991.1</a>
<i>UCOESTup1368</i>	F-box protein	3.031	0.00101	636.70	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_120250.3</a>
<i>UCOESTup1491</i>	F-box protein	2.840	0.00451	1459.29	<i>Glycine max</i>	7.00E-109	<a href="#">XM_003550313.1</a>
<i>UCOESTup1597</i>	F-box protein	2.714	0.00114	1530.58	<i>Arabidopsis thaliana</i>	4.00E-167	<a href="#">NM_104435.2</a>
<i>UCOESTup1647</i>	F-box protein	2.657	0.01040	63.29	<i>Glycine max</i>	1.00E-76	<a href="#">XM_003541621.1</a>
<i>UCOESTup1674</i>	F-box protein	2.615	0.00234	5209.99	<i>Glycine max</i>	0.0	<a href="#">XM_003545134.1</a>
<i>UCOESTup1685</i>	F-box protein	2.604	0.00193	5591.78	<i>Glycine max</i>	0.0	<a href="#">XM_003539780.1</a>
<i>UCOESTup1706</i>	F-box protein	2.579	0.00696	5877.25	<i>Prunus dulcis</i>	5.00E-59	<a href="#">AB101660.1</a>
<i>UCOESTup1776</i>	F-box protein	2.521	0.00353	1388.14	<i>Populus trichocarpa</i>	4.00E-34	<a href="#">XM_002323147.1</a>
<i>UCOESTup1992</i>	F-box protein	2.335	0.00455	3531.57	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003594025.1</a>
<i>UCOESTup1999</i>	F-box protein	2.333	0.01430	458.56	<i>Prunus armeniaca</i>	0.0	<a href="#">AY587565.1</a>
<i>UCOESTup2038</i>	F-box protein	2.307	0.00731	873.31	<i>Medicago truncatula</i>	3.00E-180	<a href="#">XM_003622293.1</a>
<i>UCOESTup2165</i>	F-box protein	2.231	0.00214	3777.42	<i>Glycine max</i>	0.0	<a href="#">XM_003554447.1</a>
<i>UCOESTup2247</i>	F-box protein	2.179	0.01230	5178.68	<i>Populus trichocarpa</i>	8.00E-153	<a href="#">XM_002303460.1</a>
<i>UCOESTup2273</i>	F-box protein	2.167	0.00276	1261.66	<i>Medicago truncatula</i>	1.00E-27	<a href="#">XM_003598053.1</a>
<i>UCOESTup2288</i>	F-box protein	2.158	0.00497	430.32	<i>Arabidopsis thaliana</i>	3.00E-107	<a href="#">NM_115715.2</a>

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UCOESTup2308	F-box protein	2.148	0.00304	3001.35	<i>Glycine max</i>	3.00E-22	<a href="#">XM_003542850.1</a>
UCOESTup2320	F-box protein	2.139	0.00472	747.64	<i>Medicago truncatula</i>	2.00E-21	<a href="#">XM_003598886.1</a>
UCOESTup2350	F-box protein	2.123	0.02300	272.91	<i>Prunus mume</i>	3.00E-58	<a href="#">AB092623.1</a>
UCOESTup2373	F-box protein	2.109	0.04400	3854.89	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003609245.1</a>
UCOESTup2386	F-box protein	2.100	0.00699	1100.15	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003590611.1</a>
UCOESTup2458	F-box protein	2.060	0.00246	3096.51	<i>Arabidopsis thaliana</i>	2.00E-84	<a href="#">NM_179015.2</a>
UCOESTup2565	F-box protein	2.004	0.01120	3764.75	<i>Medicago truncatula</i>	2.00E-71	<a href="#">XM_003629218.1</a>
<b>Ribosomal proteins</b>							
UCOESTup57	Ribosomal protein S26	51.867	0.00059	20230.90	<i>Prunus persica</i>	8.00E-33	<a href="#">AY935820.1</a>
UCOESTup1281	Ribosomal protein S26	3.198	0.00302	21665.49	<i>Humulus lupulus</i>	1.00E-142	<a href="#">AF223066.1</a>
UCOESTup296	Ribosomal protein S18	10.843	0.00013	16272.33	<i>Litchi chinensis</i>	2.00E-89	<a href="#">JF759906.1</a>
UCOESTup361	Ribosomal protein S3	9.152	0.00169	108.00	<i>Helianthus annuus</i>	4e -127	<a href="#">L31645.1</a>
UCOESTup940	Ribosomal protein S60	4.138	0.01390	4612.27	<i>Solanum tuberosum</i>	1.00E-23	<a href="#">DQ191633.1</a>
UCOESTup2184	Ribosomal protein S60	2.223	0.01410	4310.22	<i>Zea mays</i>	2.00E-36	<a href="#">EU953048.1</a>
UCOESTup2349	Ribosomal protein S60	2.123	0.01310	15058.26	<i>Medicago truncatula</i>	2.00E-135	<a href="#">XM_003635722.1</a>
UCOESTup1556	Ribosomal protein S16	2.761	0.00227	407.99	<i>Rosa hybrid</i>	9.00E-65	<a href="#">EU022333.1</a>
UCOESTup1817	Ribosomal protein S12	2.476	0.01920	113.65	<i>Phytolacca americana</i>	5.00E-78	<a href="#">AY237143.1</a>
UCOESTup2110	Ribosomal protein S14	2.262	0.04880	1211.74	<i>Juncus effusus</i>	1.00E-33	<a href="#">DQ380467.1</a>
UCOESTup2117	Ribosomal protein S50	2.260	0.03270	2261.86	<i>Medicago truncatula</i>	8.00E-58	<a href="#">XM_003624419.1</a>
UCOESTup2361	Ribosomal protein S40	2.118	0.04320	6949.92	<i>Arabidopsis thaliana</i>	9.00E-113	<a href="#">NM_129283.3</a>
UCOESTup2535	Ribosomal protein S40	2.018	0.01210	8789.37	<i>Zea mays</i>	1.00E-64	<a href="#">EU957837.1</a>
UCOESTup2410	Ribosomal protein S23	2.087	0.02810	1109.59	<i>S.angustifolia</i>	6.00E-29	<a href="#">HQ183592.1</a>
UCOESTup210	Ribosomal protein L2	14.889	0.00081	135.52	<i>Fragaria x ananassa</i>	0.0	<a href="#">DQ768221.1</a>
UCOESTup1367	Ribosomal protein L2	3.034	0.01080	2498.25	<i>Spiraea tomentosa</i>	2.00E-125	<a href="#">HQ664572.1</a>
UCOESTup2381	Ribosomal protein L2	2.102	0.00314	3397.10	<i>Ceanothus prostratus</i>	1.00E-74	<a href="#">HQ664552.1</a>
UCOESTup312	Ribosomal protein L14	10.392	0.00037	2498.25	<i>Arabidopsis lyrata</i>	6e -25	<a href="#">XM_002886798.1</a>
UCOESTup1083	Ribosomal protein L27	3.676	0.02620	3627.39	<i>Panax ginseng</i>	2.00E-74	<a href="#">AB043975.1</a>
UCOESTup1378	Ribosomal protein L	3.018	0.00339	22477.86	<i>Thottea tomentosa</i>	6.00E-50	<a href="#">DQ008797.1</a>
<b>Protease inhibitor</b>							
UCOESTup468	Serpin	7.539	0.00089	147.70	<i>Citrus x paradisi</i>	2.00E-112	<a href="#">AY158152.1</a>
UCOESTup1947	Serpin	2.372	0.04970	156.35	<i>Medicago truncatula</i>	2.00E-61	<a href="#">XM_003602925.1</a>
UCOESTup1007	Protease inhibitor	3.906	0.04340	60.55	<i>Glycine max</i>	3.00E-22	<a href="#">NM_001251765.1</a>
<b>Proteases</b>							
UCOESTup229	Matrix metalloproteinase (MMP-1)	13.531	0.01460	237.12	<i>Ricinus communis</i>	6.00E-99	<a href="#">XM_002517365.1</a>
UCOESTup384	Nucleoporin autopeptidase	8.661	0.00227	156.72	<i>Daucus carota</i>	0.0	<a href="#">AB326233.1</a>
UCOESTup572	Nucleoporin autopeptidase	6.261	0.00416	240.04	<i>Arabidopsis thaliana</i>	8.00E-31	<a href="#">NM_104659.2</a>
UCOESTup498	Aspartyl protease	7.166	0.00025	5510.12	<i>Populus tremula</i>	4.00E-124	<a href="#">EU752975.1</a>
UCOESTup1275	Aspartic proteinase	3.207	0.00068	16027.70	<i>Vigna unguiculata</i>	0.0	<a href="#">U61396.2</a>
UCOESTup754	Cysteine protease	4.998	0.00058	10419.21	<i>Daucus carota</i>	8e -36	<a href="#">AB098630.1</a>
UCOESTup878	Cysteine proteinase	4.367	0.00104	3925.16	<i>Arabidopsis thaliana</i>	7.00E-73	<a href="#">NM_179959.3</a>
UCOESTup1156	Cysteine protease	3.503	0.00131	3813.53	<i>Actinidia deliciosa</i>	0.0	<a href="#">EF530144.1</a>
UCOESTup1279	Cysteine protease	3.201	0.04070	100.96	<i>Daucus carota</i>	2.00E-42	<a href="#">AB098625.1</a>
UCOESTup2475	Cysteine protease	2.055	0.01780	27.69	<i>Ipomoea batatas</i>	1.00E-67	<a href="#">AF242372.1</a>
UCOESTup1582	Protease Do-like 9	2.737	0.00111	2007.63	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_123384.2</a>

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<i>UCOESTup2021</i>	Protease 2	2.319	0.01660	419.84	<i>Glycine max</i>	0.0	<a href="#">XM_003519868.1</a>
<i>UCOESTup2042</i>	Prenyl-dependent CAAX protease	2.304	0.00905	2734.92	<i>Arabidopsis lyrata</i>	1.00E-67	<a href="#">XM_002879554.1</a>
<i>UCOESTup2088</i>	Metalloendopeptidase	2.276	0.00166	3296.71	<i>Arabidopsis lyrata</i>	2.00E-82	<a href="#">XM_002892318.1</a>
<i>UCOESTup2362</i>	Carboxyl-terminal-processing protease	2.117	0.03210	350.97	<i>Zea mays</i>	0.0	<a href="#">NM_001155275.1</a>
<b>Carboxipeptidases</b>							
<i>UCOESTup356</i>	Serine carboxypeptidase	9.271	0.00021	9000.38	<i>Pisum sativum</i>	0.0	<a href="#">AJ251970.1</a>
<b>Chaperones</b>							
<i>UCOESTup553</i>	Chaperone DnaJ-domain containing protein	6.444	0.00029	6651.45	<i>Arabidopsis thaliana</i>	2.00E-41	<a href="#">NM_105769.4</a>
<i>UCOESTup1131</i>	Chaperone protein DnaJ	3.55	0.00771	1485.07	<i>Glycine max</i>	9.00E-69	<a href="#">XM_003521623.1</a>
<i>UCOESTup2111</i>	Chaperone protein DnaJ 13	2.261	0.00223	1202.76	<i>Arabidopsis thaliana</i>	3.00E-50	<a href="#">NM_129128.3</a>
<i>UCOESTup947</i>	Peptidyl-prolyl cis-trans isomerase	4.122	0.00061	7990.03	<i>Arabidopsis thaliana</i>	1.00E-57	<a href="#">NM_102458.1</a>
<i>UCOESTup1430</i>	Peptidyl-prolyl cis-trans isomerase E	2.938	0.01240	3869.80	<i>Medicago truncatula</i>	1.00E-62	<a href="#">XM_003614064.1</a>
<i>UCOESTup2155</i>	Peptidyl-prolyl cis-trans isomerase	2.237	0.00172	8205.46	<i>Medicago truncatula</i>	3.00E-80	<a href="#">XM_003600842.1</a>
<i>UCOESTup1512</i>	Tubulin-specific chaperone C	2.811	0.00130	3866.44	<i>Glycine max</i>	1.00E-97	<a href="#">XM_003531298.1</a>
<i>UCOESTup2215</i>	Chaperone BCS1	2.198	0.00959	91.02	<i>Glycine max</i>	7.00E-162	<a href="#">XM_003517160.1</a>
<b>OTHERS</b>							
<i>UCOESTup27</i>	Exocyst complex component 7 (EXO70H6)	111.85	0.00028	1137.18	<i>Arabidopsis thaliana</i>	2.00E-95	<a href="#">NM_148445.3</a>
<i>UCOESTup62</i>	RING/U-box domain-containing protein	49.128	0.00029	832.84	<i>Arabidopsis thaliana</i>	2.00E-34	<a href="#">NM_106120.1</a>
<i>UCOESTup1603</i>	U-box domain-containing protein 35	2.708	0.00303	1584.42	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003627163.1</a>
<i>UCOESTup2328</i>	RING/U-box domain-containing protein	2.136	0.04620	63.63	<i>Arabidopsis thaliana</i>	2.00E-40	<a href="#">_NM_128094.1</a>
<i>UCOESTup1191</i>	U-box domain-containing protein	3.431	0.01050	178.48	<i>Medicago truncatula</i>	4.00E-146	<a href="#">XM_003626455.1</a>
<i>UCOESTup93</i>	Cystinosin	33.881	0.00012	5909.89	<i>Arabidopsis thaliana</i>	2.00E-116	<a href="#">NM_123432.3</a>
<i>UCOESTup598</i>	Cystinosin	6.068	0.00252	3197.00	<i>Glycine max</i>	5.00E-45	<a href="#">XM_003547635.1</a>
<i>UCOESTup83</i>	Flotillin	38.227	5.81E-05	8683.89	<i>Medicago truncatula</i>	0.0	<a href="#">GU224281.1</a>
<i>UCOESTup1027</i>	Flotillin	3.859	0.03440	88.32	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003603284.1</a>
<i>UCOESTup106</i>	Circadian clock-associated FKF1	30.704	8.27E-05	2602.26	<i>Populus tremula</i>	0.0	<a href="#">HQ833382.1</a>
<i>UCOESTup146</i>	Annexin	21.577	0.00074	171.81	<i>Gossypium hirsutum</i>	3.00E-158	<a href="#">U89609.1</a>
<i>UCOESTup612</i>	Annexin	5.941	0.00020	27586.06	<i>Fragaria x ananassa</i>	9e -180	<a href="#">AF188832.1</a>
<i>UCOESTup152</i>	Glyoxal oxidase	20.789	0.00081	347.92	<i>Arabidopsis thaliana</i>	3.00E-60	<a href="#">NM_101310.3</a>
<i>UCOESTup960</i>	Glyoxal oxidase	4.064	0.03730	132.25	<i>Arabidopsis thaliana</i>	2.00E-51	<a href="#">NM_101845.2</a>
<i>UCOESTup188</i>	FH protein interacting protein FIP2	16.449	0.00772	135.66	<i>Arabidopsis thaliana</i>	5.00E-67	<a href="#">AF174429.1</a>
<i>UCOESTup222</i>	Pentatricopeptide repeat-containing protein	13.928	0.00040	1091.86	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_120914.2</a>
<i>UCOESTup905</i>	Pentatricopeptide repeat-containing protein	4.271	0.00200	2195.56	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002873600.1</a>
<i>UCOESTup1190</i>	Pentatricopeptide repeat-containing protein	3.432	0.04490	238.44	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003617262.1</a>
<i>UCOESTup1251</i>	Pentatricopeptide repeat-containing protein	3.276	0.00067	1183.92	<i>Glycine max</i>	0.0	<a href="#">XM_003540639.1</a>
<i>UCOESTup1266</i>	Pentatricopeptide repeat-containing	3.239	0.00385	2836.93	<i>Arabidopsis lyrata</i>	1.00E-152	<a href="#">XM_002866952.1</a>
<i>UCOESTup1273</i>	Pentatricopeptide repeat-containing protein	3.217	0.00783	57.39	<i>Glycine max</i>	5.00E-57	<a href="#">XM_003520371.1</a>
<i>UCOESTup1276</i>	Pentatricopeptide repeat-containing protein	3.205	0.01200	294.55	<i>Arabidopsis lyrata</i>	4.00E-174	<a href="#">XM_002864400.1</a>
<i>UCOESTup1388</i>	Pentatricopeptide repeat-containing protein	3.002	0.04490	404.48	<i>Glycine max</i>	0.0	<a href="#">XM_003552915.1</a>
<i>UCOESTup1414</i>	Pentatricopeptide repeat-containing protein	2.969	0.00069	2162.96	<i>Arabidopsis thaliana</i>	2.00E-165	<a href="#">NM_201700.2</a>
<i>UCOESTup1477</i>	Pentatricopeptide repeat-containing protein	2.860	0.00215	1533.05	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002892418.1</a>
<i>UCOESTup1524</i>	Pentatricopeptide repeat-containing protein	2.795	0.00358	204.21	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003597739.1</a>
<i>UCOESTup1570</i>	Pentatricopeptide repeat-containing protein	2.746	0.00265	143.49	<i>Glycine max</i>	0.0	<a href="#">XM_003539446.1</a>
<i>UCOESTup1579</i>	Pentatricopeptide repeat protein 77	2.741	0.00119	369.51	<i>Funaria hygrometrica</i>	2.00E-141	<a href="#">JF501600.1</a>

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UCOESTup1632	Pentatricopeptide repeat-containing protein	2.675	0.00185	2014.95	<i>Glycine max</i>	5.00E-76	<a href="#">XM_003556423.1</a>
UCOESTup1634	Pentatricopeptide repeat-containing protein	2.672	0.01420	2892.93	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_119751.3</a>
UCOESTup1651	Pentatricopeptide repeat-containing protein	2.653	0.04250	213.48	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003610700.1</a>
UCOESTup1669	Pentatricopeptide repeat-containing protein	2.623	0.00338	1192.07	<i>Medicago truncatula</i>	9.00E-176	<a href="#">XM_003626639.1</a>
UCOESTup1831	Pentatricopeptide repeat-containing protein	2.463	0.01510	698.59	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003621562.1</a>
UCOESTup1833	Pentatricopeptide repeat-containing protein	2.461	0.00183	1303.07	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003597935.1</a>
UCOESTup1855	Pentatricopeptide repeat-containing protein	2.448	0.01180	1061.83	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_102412.1</a>
UCOESTup1868	Pentatricopeptide repeat-containing protein	2.441	0.00383	4344.32	<i>Medicago truncatula</i>	5.00E-166	<a href="#">XM_003623482.1</a>
UCOESTup1872	Pentatricopeptide repeat-containing protein	2.439	0.00456	469.63	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_111347.1</a>
UCOESTup1914	Pentatricopeptide repeat-containing protein	2.401	0.00696	151.13	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_127268.3</a>
UCOESTup1923	Pentatricopeptide repeat-containing protein	2.390	0.00227	1324.78	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_113854.4</a>
UCOESTup1929	Pentatricopeptide repeat-containing protein	2.386	0.04680	284.74	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003591931.1</a>
UCOESTup1991	Pentatricopeptide repeat-containing protein	2.337	0.02930	410.04	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_100192.2</a>
UCOESTup2120	Pentatricopeptide repeat-containing protein	2.259	0.00539	15493.80	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002887511.1</a>
UCOESTup2175	Pentatricopeptide repeat-containing protein	2.226	0.00440	164.88	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003589651.1</a>
UCOESTup2209	Pentatricopeptide repeat-containing protein	2.203	0.01490	501.55	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_112291.1</a>
UCOESTup2244	Pentatricopeptide repeat-containing protein	2.181	0.00505	639.74	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_100864.1</a>
UCOESTup2300	Pentatricopeptide repeat-containing protein	2.153	0.00919	2559.87	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003603783.1</a>
UCOESTup2342	Pentatricopeptide repeat-containing protein	2.128	0.01520	143.37	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003607715.1</a>
UCOESTup2393	Pentatricopeptide repeat-containing protein	2.095	0.00312	129.00	<i>Medicago truncatula</i>	5.00E-31	<a href="#">XM_003591238.1</a>
UCOESTup2399	Pentatricopeptide repeat-containing protein	2.094	0.00738	3700.71	<i>Medicago truncatula</i>	4.00E-180	<a href="#">XM_003607940.1</a>
UCOESTup2424	Pentatricopeptide repeat-containing protein	2.078	0.00399	314.18	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003611840.1</a>
UCOESTup2451	Pentatricopeptide repeat-containing protein	2.064	0.00908	376.71	<i>Arabidopsis thaliana</i>	1.00E-139	<a href="#">NM_122593.1</a>
UCOESTup2506	Pentatricopeptide repeat-containing protein	2.038	0.02380	496.03	<i>Arabidopsis thaliana</i>	2.00E-145	<a href="#">NM_128631.3</a>
UCOESTup2526	Pentatricopeptide repeat-containing protein	2.023	0.03480	101.76	<i>Arabidopsis lyrata</i>	7.00E-27	<a href="#">XM_002867926.1</a>
UCOESTup2527	Pentatricopeptide repeat-containing protein	2.022	0.01720	934.47	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_147929.3</a>
UCOESTup2536	Pentatricopeptide repeat protein (PPR1)	2.017	0.00839	2145.09	<i>Gossypium hirsutum</i>	0.0	<a href="#">FJ812359.1</a>
UCOESTup290	Syntaxin-24	11.144	0.00021	4311.39	<i>Glycine max</i>	1.00E-21	<a href="#">XM_003554411.1</a>
UCOESTup326	N-ethylmaleimide sensitive fusion protein	9.994	0.00069	522.21	<i>Nicotiana tabacum</i>	0.0	<a href="#">D86506.1</a>
UCOESTup333	Tonoplast intrinsic protein (FavRB7)	9.851	0.00077	8572.00	<i>Fragaria x ananassa</i>	3e -141	<a href="#">DQ178022.1</a>
UCOESTup347	Rossmann-fold NAD(P)-binding domain-containing protein	9.481	0.00019	17157.49	<i>Arabidopsis thaliana</i>	9e -146	<a href="#">NM_120332.3</a>
UCOESTup372	Phloem protein 2 (pp2)	8.900	0.00090	824.24	<i>Cucurbita moschata</i>	3e -24	<a href="#">AF150627.1</a>
UCOESTup379	Tetratricopeptide repeat -containing protein	8.754	0.00044	770.20	<i>Arabidopsis thaliana</i>	2e -131	<a href="#">NM_125914.4</a>
UCOESTup1363	Tetratricopeptide repeat-containing protein	3.038	0.00064	10877.06	<i>Arabidopsis thaliana</i>	2.00E-120	<a href="#">NM_124262.3</a>
UCOESTup400	Alpha/beta-hydrolase domain-containing protein	8.462	0.00014	21558.98	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_105142.3</a>
UCOESTup415	Cyclo-DOPA 5-O-glucosyltransferase	8.282	0.00028	10126.32	<i>Mirabilis jalapa</i>	2.00E-148	<a href="#">AB182643.1</a>
UCOESTup414	Early nodulin-like protein 20 (ENODL20)	8.299	0.00058	1722.76	<i>Arabidopsis thaliana</i>	7.00E-29	<a href="#">NM_201810.1</a>
UCOESTup478	Early nodulin-like protein 4 (ENODL4)	7.445	0.00028	30970.09	<i>Arabidopsis thaliana</i>	7.00E-39	<a href="#">NM_119401.3</a>
UCOESTup2109	Early nodulin-like protein 1	2.262	0.03990	94.43	<i>Glycine max</i>	3.00E-53	<a href="#">XM_003554961.1</a>
UCOESTup467	FRO1 and FRO2 protein	7.541	0.00051	1525.62	<i>Arabidopsis thaliana</i>	0.0	<a href="#">BT003007.1</a>
UCOESTup545	Dynamin-related protein 1A	6.495	0.00334	82.52	<i>Zea mays</i>	0.0	<a href="#">NM_001158305.1</a>
UCOESTup599	Nudix hydrolase 2 (NUDT2)	6.061	0.00180	610.85	<i>Arabidopsis thaliana</i>	1.00E-107	<a href="#">NM_124139.3</a>
UCOESTup608	DVL11	5.960	0.00067	11829.50	<i>Arabidopsis thaliana</i>	1.00E-20	<a href="#">BK001754.1</a>
UCOESTup631	Signal recognition particle	5.809	0.00069	1826.16	<i>Humulus lupulus</i>	2e -23	<a href="#">AJ236706.1</a>

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UCOESTup638	Polyketide cyclase/dehydrase and lipid transport	5.785	0.00103	496.03	<i>Arabidopsis thaliana</i>	1e -132	<a href="#">NM_105147.3</a>
UCOESTup646	Ankyrin protein	5.702	0.00497	235.23	<i>Zea mays</i>	7e -118	<a href="#">EU957258.1</a>
UCOESTup814	Ankyrin protein	4.624	0.00122	321.52	<i>S. purpuratus</i>	4.00E-23	<a href="#">XM_001181509.1</a>
UCOESTup1717	Ankyrin protein	2.569	0.00256	1873.43	<i>Glycine max</i>	5.00E-45	<a href="#">XM_003536908.1</a>
UCOESTup1823	Ankyrin protein	2.471	0.00422	347.52	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003597649.1</a>
UCOESTup2270	Ankyrin protein	2.168	0.00305	5830.94	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003624606.1</a>
UCOESTup2445	Ankyrin protein	2.066	0.01450	61.60	<i>Medicago truncatula</i>	4.00E-37	<a href="#">XM_003612671.1</a>
UCOESTup618	Photosystem I assembly protein ycf4	5.908	0.00085	1490.10	<i>Fragaria vesca</i>	6e -66	<a href="#">JF345175.1</a>
UCOESTup2533	Photosystem II D2 protein	2.018	0.00565	3800.63	<i>Roystonea princeps</i>	1.00E-51	<a href="#">AY147654.1</a>
UCOESTup726	Light-dependent short hypocotyl 1 (LSH1)	5.121	0.00983	1975.29	<i>Arabidopsis thaliana</i>	2e -66	<a href="#">AY319947.1</a>
UCOESTup773	Blue copper protein	4.868	0.04260	139.75	<i>Triticum aestivum</i>	1e -22	<a href="#">AF031195.1</a>
UCOESTup2334	Blue copper protein	2.132	0.00262	7870.47	<i>Medicago truncatula</i>	2.00E-28	<a href="#">XM_003609318.1</a>
UCOESTup775	Patatin protein 1	4.867	0.00498	177.29	<i>Gossypium hirsutum</i>	2e -40	<a href="#">AY929163.1</a>
UCOESTup953	Patatin protein 3	4.102	0.00058	4116.93	<i>Nicotiana tabacum</i>	3.00E-143	<a href="#">AF158253.1</a>
UCOESTup796	CUP-SHAPED COTYLEDON 2 (CUC2)	4.730	0.00308	4339.78	<i>Carica papaya</i>	4e -97	<a href="#">BK007973.1</a>
UCOESTup799	BURP domain protein (BNM2A)	4.712	0.00211	223.18	<i>Brassica napus</i>	2e -51	<a href="#">FJ204000.1</a>
UCOESTup851	Translocase	4.463	0.03950	2401.06	<i>Arabidopsis thaliana</i>	2.00E-69	<a href="#">AY463970.1</a>
UCOESTup870	Beta amylin synthase	4.403	0.01210	40.55	<i>Malus x domestica</i>	0.0	<a href="#">FJ032007.1</a>
UCOESTup1201	Dihydrofolate reductase	3.416	0.00076	18731.76	<i>Glycine max</i>	2.00E-115	<a href="#">XM_003554028.1</a>
UCOESTup872	SUPPRESSOR OF GENE SILENCING	4.382	0.00104	3705.19	<i>Arabidopsis thaliana</i>	7.00E-135	<a href="#">NM_122263.2</a>
UCOESTup918	2-Nitropropane dioxygenase	4.215	0.00053	5394.16	<i>Arabidopsis lyrata</i>	2.00E-156	<a href="#">XM_002866557.1</a>
UCOESTup1000	Prohibitin 1	3.924	0.00057	4085.46	<i>Arabidopsis thaliana</i>	8.00E-119	<a href="#">NM_118993.3</a>
UCOESTup1063	B3 domain-containing protein	3.748	0.00138	1208.34	<i>Glycine max</i>	1.00E-32	<a href="#">XM_003516732.1</a>
UCOESTup1495	B3 domain-containing protein	2.837	0.00838	56.42	<i>Glycine max</i>	2.00E-24	<a href="#">XM_003518302.1</a>
UCOESTup1068	NEDD8 ultimate buster 1	3.729	0.00535	487.71	<i>Glycine max</i>	1.00E-150	<a href="#">XM_003533810.1</a>
UCOESTup1100	Phosphatidylethanolamine-binding protein	3.625	0.01890	755.17	<i>Arabidopsis thaliana</i>	8.00E-66	<a href="#">NM_120208.4</a>
UCOESTup1147	Vacuolar processing enzyme a (VPEa)	3.530	0.04020	132.84	<i>Populus tomentosa</i>	4.00E-166	<a href="#">FJ461342.1</a>
UCOESTup1137	COBRA-like protein 6	3.540	0.00114	197.77	<i>Arabidopsis thaliana</i>	3.00E-148	<a href="#">NM_100851.2</a>
UCOESTup1676	COBRA- like protein	2.615	0.00440	1382.84	<i>Glycine max</i>	0.0	<a href="#">XM_003518132.1</a>
UCOESTup1172	Bcl-2-associated protein	3.475	0.00055	3879.92	<i>Vitis vinifera</i>	3.00E-56	<a href="#">GU169698.1</a>
UCOESTup1194	Maturase (matR)	3.424	0.00067	3828.51	<i>Geum canadense</i>	1.00E-99	<a href="#">DQ110342.1</a>
UCOESTup1235	Actin binding calponin -containing protein	3.320	0.00194	2620.21	<i>Hordeum vulgare</i>	0.0	<a href="#">AK374831.1</a>
UCOESTup1313	Hypersensitive-induced response protein 4	3.137	0.00167	8191.40	<i>Arabidopsis thaliana</i>	1.00E-164	<a href="#">NM_124536.3</a>
UCOESTup1289	Stay green 1 (SGR1)	3.180	0.00079	8924.01	<i>Pyrus x bretschneideri</i>	1.00E-128	<a href="#">JN168000.1</a>
UCOESTup1308	LOB domain-containing protein 1	3.143	0.00114	4989.46	<i>Glycine max</i>	1.00E-69	<a href="#">XM_003556167.1</a>
UCOESTup1530	LOB domain-containing protein 4	2.785	0.00344	716.73	<i>Glycine max</i>	1.00E-69	<a href="#">XM_003531448.1</a>
UCOESTup1404	Early flowering 6 protein (REF6)	2.982	0.00197	300.13	<i>Arabidopsis thaliana</i>	1.00E-25	<a href="#">NM_148863.3</a>
UCOESTup1405	Nuclease HARBII	2.982	0.03500	1289.43	<i>Glycine max</i>	2.00E-148	<a href="#">XM_003555765.1</a>
UCOESTup1480	Mitochondrial substrate carrier family protein	2.858	0.00660	1315.47	<i>Glycine max</i>	2.00E-171	<a href="#">XM_003528755.1</a>
UCOESTup2539	Mitochondrial substrate carrier family protein	2.016	0.00330	5828.53	<i>Arabidopsis thaliana</i>	1.00E-135	<a href="#">NM_115254.3</a>
UCOESTup1498	Chloroplast channel forming outer membrane	2.832	0.00802	3006.64	<i>Pisum sativum</i>	1.00E-45	<a href="#">AJ009987.1</a>
UCOESTup1519	Programmed cell death protein 2	2.801	0.00088	2371.78	<i>Medicago truncatula</i>	7.00E-88	<a href="#">XM_003602448.1</a>
UCOESTup1562	Nitrile-specifier protein	2.753	0.00981	8842.42	<i>Medicago truncatula</i>	2.00E-168	<a href="#">XM_003596116.1</a>
UCOESTup1588	Anaphase-promoting complex subunit 10	2.728	0.00166	1637.16	<i>Glycine max</i>	1.00E-62	<a href="#">NM_001253078.1</a>
UCOESTup1591	ATP binding microtubule motor family protein	2.726	0.00099	890.24	<i>Arabidopsis thaliana</i>	2.00E-130	<a href="#">NM_180411.2</a>

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UCOESTup1599	Thiamin pyrophosphokinase1	2.713	0.04950	2372.23	<i>Arabidopsis thaliana</i>	7.00E-109	<a href="#">NM_100169.2</a>
UCOESTup1606	Cytosolic Fe-S cluster assembly factor nbp35	2.707	0.00280	8737.00	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003588940.1</a>
UCOESTup1673	Metal tolerance protein	2.617	0.01260	704.26	<i>Populus trichocarpa</i>	2.00E-172	<a href="#">XM_002317622.1</a>
UCOESTup1742	Flowering time control protein FY (FY)	2.545	0.02860	2013.89	<i>Arabidopsis thaliana</i>	4.00E-84	<a href="#">NM_001203373.1</a>
UCOESTup1788	Iron-sulfur protein	2.506	0.00963	2329.78	<i>Glycine max</i>	2.00E-173	<a href="#">XM_003521415.1</a>
UCOESTup1798	Ion binding / oxidoreductase	2.500	0.01160	1130.32	<i>Arabidopsis thaliana</i>	1.00E-90	<a href="#">NM_124567.4</a>
UCOESTup1894	GTPase-activating protein 32	2.418	0.00172	5826.22	<i>Glycine max</i>	1.00E-166	<a href="#">XM_003554732.1</a>
UCOESTup1924	Regulator of Vps4 activity in the MVB pathway	2.389	0.01530	2000.56	<i>Arabidopsis thaliana</i>	3.00E-31	<a href="#">NM_103145.4</a>
UCOESTup1939	VERNALIZATION INSENSITIVE 3	2.379	0.00186	3682.78	<i>Glycine max</i>	0.0	<a href="#">XM_003544200.1</a>
UCOESTup1993	PKHD-type hydroxylase	2.335	0.00472	14610.41	<i>Medicago truncatula</i>	1.00E-128	<a href="#">XM_003620308.1</a>
UCOESTup2081	Notchless protein	2.281	0.01970	1758.78	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_124660.3</a>
UCOESTup2087	Nucleoside-triphosphatase (APY2)	2.277	0.00312	10575.05	<i>Arabidopsis thaliana</i>	8.00E-35	<a href="#">NM_121833.6</a>
UCOESTup2092	Phytochrome and flowering time regulatory protein 1 (PFT1)	2.274	0.04240	26.54	<i>Arabidopsis thaliana</i>	3.00E-46	<a href="#">NM_102365.4</a>
UCOESTup2099	ADP-ribosylation factor GTPase	2.268	0.00509	1758.78	<i>Glycine max</i>	3.00E-91	<a href="#">XM_003534093.1</a>
UCOESTup2116	Carbon catabolite repressor protein	2.260	0.00463	1802.02	<i>Medicago truncatula</i>	2.00E-113	<a href="#">XM_003612498.1</a>
UCOESTup2182	Nuclear factor Y subunit C	2.224	0.04780	1118.91	<i>Phaseolus vulgaris</i>	2.00E-109	<a href="#">GQ913690.1</a>
UCOESTup2188	Fasciclin-like arabinogalactan protein	2.219	0.03990	338.37	<i>Medicago truncatula</i>	2.00E-144	<a href="#">XM_003620155.1</a>
UCOESTup2191	Mitochondrial import receptor subunit TOM20	2.216	0.03100	2484.82	<i>Glycine max</i>	2.00E-69	<a href="#">XM_003551282.1</a>
UCOESTup2207	Peroxisomal biogenesis factor	2.203	0.00254	4263.45	<i>Medicago truncatula</i>	2.00E-89	<a href="#">XM_003608663.1</a>
UCOESTup2556	Peroxisomal biogenesis factor 11	2.008	0.00512	824.01	<i>Arabidopsis thaliana</i>	1.00E-103	<a href="#">XM_002894021.1</a>
UCOESTup2277	Vacuolar sorting protein 9	2.164	0.00334	1287.10	<i>Arabidopsis thaliana</i>	2.00E-73	<a href="#">NM_120968.2</a>
UCOESTup2282	Aminomethyltransferase	2.162	0.00219	6084.24	<i>Arabidopsis lyrata</i>	7.00E-177	<a href="#">XM_002872599.1</a>
UCOESTup2286	ADP, ATP carrier protein	2.159	0.01700	1060.35	<i>Arabidopsis thaliana</i>	7.00E-103	<a href="#">NM_115046.5</a>
UCOESTup2318	Monocopper oxidase	2.140	0.00314	4729.21	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_117312.3</a>
UCOESTup2341	Conserved oligomeric Golgi complex subunit	2.128	0.01510	173.50	<i>Medicago truncatula</i>	1.00E-32	<a href="#">XM_003618143.1</a>
UCOESTup2363	UBX domain-containing protein 1 (PUX1)	2.117	0.03550	30.43	<i>Arabidopsis lyrata</i>	2.00E-29	<a href="#">XM_002876990.1</a>
UCOESTup2401	Zinc ion binding protein	2.094	0.01330	4440.21	<i>Arabidopsis thaliana</i>	4.00E-118	<a href="#">NM_104469.3</a>
UCOESTup2409	PAF1 complex component	2.087	0.00576	737.54	<i>Populus trichocarpa</i>	6.00E-123	<a href="#">XM_002326080.1</a>
UCOESTup2440	Transmembrane and coiled-coil domain	2.068	0.01890	2032.20	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003612064.1</a>
UCOESTup2466	Embryonic flower 2	2.058	0.01050	1931.68	<i>Camellia sinensis</i>	2.00E-43	<a href="#">GQ477137.1</a>
UCOESTup2480	Prohibitin 1	2.053	0.03450	3455.57	<i>Petunia x hybrida</i>	6.00E-137	<a href="#">AY907015.1</a>
UCOESTup2485	Villin-4	2.051	0.01090	2981.72	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003610027.1</a>
UCOESTup2486	AT-hook motif nuclear-localized protein 22	2.051	0.01530	319.69	<i>Arabidopsis thaliana</i>	1.00E-59	<a href="#">NM_130105.3</a>
UCOESTup2493	GLABRA2 expression modulator (GEM)	2.047	0.00457	6279.31	<i>Arabidopsis thaliana</i>	1.00E-101	<a href="#">NM_201781.1</a>

**Table 9. Other genes up regulated in fruit ripen receptacles.**

Magnitudes of relative induction to fruit ripen receptacles,  $p$ -value ( $\leq 0.05$ ) and u.a.e (arbitrary units of expression) in red fruit are given. Mean value of u.a.e is 1771.57. Columns show the best annotated matches from the search results of tBlastX analysis, species, putative function and match e- value.

UNCHARACTERIZED PROTEINS (1/8)		Fruit ripen receptacles <i>Up regulated</i>						
GENES	Putative function	Fold	p-value	U.a.e in green fruits	U.a.e in red fruits	Species	e-value	Best Match BlastX
<b>UCOESTup3</b>	Uncharacterized protein	936.377	0.00005	34.09	20299.05	<b>Clytia hemisphaerica</b>	3.00E-67	FP949155.1
<b>UCOESTup4</b>	Uncharacterized protein	895.643	0.00020	16.11	4850.48	<b>FRA2270 Strawberry</b>	1.00E-41	CO378894.1
<b>UCOESTup22</b>	Uncharacterized protein	119.016	0.00013	15.96	540.73	<i>Prunus avium</i>	4.00E-22	HE643083.1
<b>UCOESTup38</b>	Uncharacterized protein	79.780	0.00301	11.57	240.47	<i>Royal Gala</i>	2.00E-15	CN936174.1
<b>UCOESTup44</b>	Uncharacterized protein	69.374	5.82E-05	364.34	24334.55	<b>Clytia hemisphaerica</b>	1.00E-144	FP967705.1
<b>UCOESTup45</b>	Uncharacterized protein	68.112	8.75E-05	267.67	15913.26	<b>Citrus clementina</b>	2.00E-178	DY287831.1
<b>UCOESTup50</b>	Uncharacterized protein	63.614	0.00022	23.09	633.19	<i>Fragaria x ananassa</i>	1.00E-44	CO380732.1
<b>UCOESTup58</b>	Uncharacterized protein	50.962	0.00006	101.20	4068.67	<b>Prunus avium</b>	2.00E-11	HE643011.1
<b>UCOESTup65</b>	Uncharacterized protein	47.313	0.00062	17.11	217.65	<i>Nicotiana tabacum</i>	5.00E-30	BP134706.1
<b>UCOESTup79</b>	Uncharacterized protein	40.213	0.00017	262.10	10259.24	<b>Prunus avium</b>	2.00E-27	HE644863.1
<b>UCOESTup80</b>	Uncharacterized protein	39.913	0.00009	56.76	1738.81	<b>Malus x domestica</b>	8.00E-24	CN489695.1
<b>UCOESTup84</b>	Uncharacterized protein	37.704	0.00512	21.22	274.85	<i>Prunus persica</i>	2.00E-19	DW345255.1
<b>UCOESTup94</b>	Uncharacterized protein	33.721	0.00114	11.73	128.76	<i>Glycine max</i>	4.00E-92	XM_003525579.1
<b>UCOESTup96</b>	Uncharacterized protein	33.394	0.00023	314.28	10278.43	<b>Clytia hemisphaerica</b>	2.00E-154	FP967817.1
<b>UCOESTup101</b>	Uncharacterized protein	31.811	0.00011	830.18	25966.16	<b>Clytia hemisphaerica</b>	9.00E-82	CU438597.1
<b>UCOESTup104</b>	Uncharacterized protein	30.810	0.00019	43.95	677.82	<i>Fragaria x ananassa</i>	1.00E-40	GW403204.1
<b>UCOESTup108</b>	Uncharacterized protein	29.522	0.00058	17.26	199.76	<i>Fragaria x ananassa</i>	6.00E-47	GW402860.1
<b>UCOESTup109</b>	Uncharacterized protein	29.157	0.00039	15.45	160.26	<i>Ficus elastica</i>	5.00E-10	GW827993.1
<b>UCOESTup110</b>	Uncharacterized protein	28.770	0.00076	44.76	1043.44	<i>Prunus persica</i>	1.00E-28	DN553625.1
<b>UCOESTup112</b>	Uncharacterized protein	28.215	0.00040	50.79	1063.12	<i>Panax ginseng</i>	5.00E-33	JK986067.1
<b>UCOESTup119</b>	Uncharacterized protein	26.650	0.00029	16.98	141.99	<i>Prunus persica</i>	1.00E-25	DW356900.1
<b>UCOESTup122</b>	Uncharacterized protein	25.925	7.44E-05	654.38	15483.60	<b>Lotus japonicus</b>	4.00E-92	FS358096.1
<b>UCOESTup124</b>	Uncharacterized protein	25.522	0.00013	299.66	7420.51	<i>Fragaria x ananassa</i>	7.00E-117	GW403006.1
<b>UCOESTup137</b>	Uncharacterized protein	23.078	0.00012	623.78	13569.57	<b>Clytia hemisphaerica</b>	6.00E-117	FP978675.1
<b>UCOESTup138</b>	Uncharacterized protein	23.004	0.00236	42.88	551.83	<i>Fragaria vesca</i>	2.00E-35	DY674164.1
<b>UCOESTup139</b>	Uncharacterized protein	22.584	0.00011	78.54	1735.93	<b>Populus trichocarpa</b>	2.00E-17	XM_002315445.1
<b>UCOESTup142</b>	Uncharacterized protein	22.352	0.00117	20.36	186.42	<i>Linum usitatissimum</i>	1.00E-16	JG042046.1
<b>UCOESTup148</b>	Uncharacterized protein	21.218	0.00044	346.21	7129.58	<b>Glycine max</b>	2.00E-27	NM_001248525.1
<b>UCOESTup150</b>	Uncharacterized protein	20.966	0.00016	127.25	2347.69	<i>Prunus persica</i>	2.00E-88	FC865179.1
<b>UCOESTup160</b>	Uncharacterized protein	20.044	0.00014	562.42	11526.95	<b>Fragaria vesca</b>	2.00E-171	EX686817.1
<b>UCOESTup176</b>	Uncharacterized protein	17.826	0.00036	141.07	2234.96	<b>Glycine max</b>	7.00E-51	XM_003525025.1
<b>UCOESTup178</b>	Uncharacterized protein	17.521	0.00052	67.98	1022.87	<i>Fragaria vesca</i>	3.00E-112	EX678202.1
<b>UCOESTup181</b>	Uncharacterized protein	17.159	0.00034	30.73	332.23	<i>Ipomopsis aggregata</i>	1.00E-84	GT316411.1
<b>UCOESTup190</b>	Uncharacterized protein	16.388	0.00067	207.85	3354.84	<b>Fragaria vesca</b>	6.00E-65	EX662684.1
<b>UCOESTup207</b>	Uncharacterized protein	15.176	0.00034	42.94	493.40	<i>Phaseolus acutifolius</i>	4.00E-50	HO781690.1
<b>UCOESTup211</b>	Uncharacterized protein	14.687	0.00014	359.56	5126.30	<b>Soybean</b>	2.00E-12	BT092660.1
<b>UCOESTup212</b>	Uncharacterized protein	14.679	0.00226	18.75	162.81	<i>Royal Gala</i>	8.00E-26	CN856637.1
<b>UCOESTup215</b>	Uncharacterized protein	14.479	0.02140	39.00	346.08	<i>Fragaria vesca</i>	7.00E-21	FN562326.1

(Table continues on following page)



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<i>UCOESTup217</i>	Uncharacterized protein	14.407	0.00012	<b>95.55</b>	<b>1246.51</b>	<i>Vitis vinifera</i>	2.00E-72	<a href="#">AM432923.2</a>
<i>UCOESTup220</i>	Uncharacterized protein	<b>14.257</b>	0.00034	<b>334.46</b>	<b>4720.91</b>	<i>Prunus persica</i>	5.00E-33	<a href="#">BU045802.1</a>
<i>UCOESTup227</i>	Uncharacterized protein	13.666	0.00211	<b>19.52</b>	<b>131.77</b>	<i>Vitis vinifera</i>	2.00E-19	<a href="#">AM425022.2</a>
<i>UCOESTup229</i>	Uncharacterized protein	13.531	0.01460	<b>34.58</b>	<b>237.13</b>	<i>Ricinus communis</i>	6.00E-99	<a href="#">XM_002517365.1</a>
<i>UCOESTup234</i>	Uncharacterized protein	13.348	0.00099	<b>46.75</b>	<b>468.11</b>	<i>Prunus persica</i>	3.00E-43	<a href="#">DY641609.1</a>
<i>UCOESTup237</i>	Uncharacterized protein	<b>13.197</b>	0.00027	<b>376.60</b>	<b>5239.34</b>	<i>Euphorbia esula</i>	1.00E-106	<a href="#">DV143350.1</a>
<i>UCOESTup244</i>	Uncharacterized protein	<b>12.948</b>	0.00022	<b>672.49</b>	<b>8859.37</b>	<i>Arabidopsis thaliana</i>	1.00E-151	<a href="#">NM_125986.2</a>
<i>UCOESTup246</i>	Uncharacterized protein	12.848	0.00064	<b>163.77</b>	<b>1628.73</b>	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002285550.2</a>
<i>UCOESTup247</i>	Uncharacterized protein	12.823	0.00204	<b>29.18</b>	<b>147.10</b>	<i>Malus x domestica</i>	9.00E-63	<a href="#">GO520338.1</a>
<i>UCOESTup256</i>	Uncharacterized protein	12.196	0.00043	<b>48.00</b>	<b>113.34</b>	<i>Arabidopsis thaliana</i>	2.00E-99	<a href="#">NM_116932.2</a>
<i>UCOESTup260</i>	Uncharacterized protein	<b>12.064</b>	0.00020	<b>555.63</b>	<b>6645.94</b>	<i>Fragaria vesca</i>	3.00E-177	<a href="#">EX671125.1</a>
<i>UCOESTup269</i>	Uncharacterized protein	<b>11.754</b>	0.00016	<b>247.19</b>	<b>2546.47</b>	<i>Glycine max</i>	0.0	<a href="#">XM_003516356.1</a>
<i>UCOESTup280</i>	Uncharacterized protein	<b>11.499</b>	0.00054	<b>271.05</b>	<b>3028.70</b>	<i>Royal Gala</i>	2.00E-21	<a href="#">CN888789.1</a>
<i>UCOESTup288</i>	Uncharacterized protein	11.152	0.00217	<b>132.57</b>	<b>1439.46</b>	<i>Brassica oleracea</i>	7.00E-17	<a href="#">JF920286.1</a>
<i>UCOESTup307</i>	Uncharacterized protein	<b>10.516</b>	0.00013	<b>443.90</b>	<b>4446.96</b>	<i>Ipomopsis aggregata</i>	6.00E-07	<a href="#">GT316081.1</a>
<i>UCOESTup316</i>	Uncharacterized protein	<b>10.317</b>	0.00166	<b>212.16</b>	<b>2133.25</b>	<i>Castor bean</i>	2.00E-12	<a href="#">EE254649.1</a>
<i>UCOESTup317</i>	Uncharacterized protein	10.285	0.00301	<b>97.11</b>	<b>1017.79</b>	<i>Malus x domestica</i>	4.00E-52	<a href="#">GO543484.1</a>
<i>UCOESTup321</i>	Uncharacterized protein	10.105	0.00020	<b>92.04</b>	<b>846.03</b>	<i>Fragaria vesca</i>	7.00E-153	<a href="#">EX662393.1</a>
<i>UCOESTup322</i>	Uncharacterized protein	10.063	0.00206	<b>37.72</b>	<b>219.99</b>	<i>Fragaria vesca</i>	8.0E-84	<a href="#">EX663735</a>
<i>UCOESTup328</i>	Uncharacterized protein	<b>9.954</b>	0.00028	<b>314.21</b>	<b>3003.75</b>	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_106715.4</a>
<i>UCOESTup332</i>	Uncharacterized protein	<b>9.865</b>	0.00013	<b>688.74</b>	<b>7480.25</b>	<i>Citrus clementina</i>	9.00E-80	<a href="#">DY280804.1</a>
<i>UCOESTup343</i>	Uncharacterized protein	<b>9.601</b>	0.00013	<b>326.26</b>	<b>3014.73</b>	<i>Rosa chinensis</i>	2.00E-13	<a href="#">BI977506.1</a>
<i>UCOESTup346</i>	Uncharacterized protein	9.491	0.00069	<b>65.38</b>	<b>461.10</b>	<i>Populus trichocarpa</i>	7e -77	<a href="#">XM_002317162.1</a>
<i>UCOESTup348</i>	Uncharacterized protein	9.458	0.00228	<b>26.71</b>	<b>149.46</b>	<i>Royal Gala</i>	2.00E-25	<a href="#">CN887486.1</a>
<i>UCOESTup349</i>	Uncharacterized protein	9.440	0.00080	<b>18.53</b>	<b>86.63</b>	<i>Malus hybrid</i>	1.00E-31	<a href="#">GO501297.1</a>
<i>UCOESTup352</i>	Uncharacterized protein	<b>9.404</b>	0.00022	<b>322.75</b>	<b>2918.76</b>	<i>Fragaria vesca</i>	5e -56	<a href="#">JF345175.1</a>
<i>UCOESTup353</i>	Uncharacterized protein	9.321	0.00045	<b>887.48</b>	<b>8168.68</b>	<i>Fragaria vesca</i>	3e -49	<a href="#">GU363535.1</a>
<i>UCOESTup360</i>	Uncharacterized protein	9.176	0.00207	<b>152.41</b>	<b>1388.05</b>	<i>Fragaria vesca</i>	2.00E-99	<a href="#">EX680210.1</a>
<i>UCOESTup363</i>	Uncharacterized protein	9.034	0.00036	<b>902.04</b>	<b>8827.36</b>	<i>Malus x domestica</i>	5.00E-68	<a href="#">CN913096.1</a>
<i>UCOESTup269</i>	Uncharacterized protein	<b>11.754</b>	0.00016	<b>247.19</b>	<b>2546.47</b>	<i>Dioscorea alata</i>	4.00E-160	<a href="#">HO855395.1</a>
<i>UCOESTup389</i>	Uncharacterized protein	8.616	0.00679	<b>80.52</b>	<b>573.35</b>	<i>Quercus petraea</i>	2.00E-20	<a href="#">FN758152.1</a>
<i>UCOESTup392</i>	Uncharacterized protein	<b>8.583</b>	0.00069	<b>3462.67</b>	<b>31326.05</b>	<i>Fragaria vesca</i>	1.00E-109	<a href="#">EX686997.1</a>
<i>UCOESTup393</i>	Uncharacterized protein	8.527	0.00014	<b>245.06</b>	<b>2001.51</b>	<i>Acacia mangium</i>	2.00E-04	<a href="#">FS584383.1</a>
<i>UCOESTup396</i>	Uncharacterized protein	8.502	0.00452	<b>109.48</b>	<b>805.99</b>	<i>Prunus armeniaca</i>	4.00E-42	<a href="#">CB822290.1</a>
<i>UCOESTup381</i>	Uncharacterized protein	8.699	0.00064	<b>54.57</b>	<b>377.06</b>	<i>Fragaria vesca</i>	3e -51	<a href="#">GU363535.1</a>
<i>UCOESTup407</i>	Uncharacterized protein	8.365	0.00426	<b>140.10</b>	<b>1183.68</b>	<i>Populus trichocarpa</i>	2.00E-39	<a href="#">AK328441.1</a>
<i>UCOESTup413</i>	Uncharacterized protein	8.311	0.00057	<b>51.07</b>	<b>236.99</b>	<i>Fragaria vesca</i>	1.00E-40	<a href="#">DV439229.1</a>
<i>UCOESTup417</i>	Uncharacterized protein	8.263	0.00187	<b>14.93</b>	<b>47.13</b>	<i>Solanum lycopersicum</i>	3.00E-11	<a href="#">EU124737.2</a>
<i>UCOESTup428</i>	Uncharacterized protein	8.180	0.00315	<b>175.03</b>	<b>1459.74</b>	<i>Fragaria vesca</i>	1.00E-96	<a href="#">EX672842.1</a>
<i>UCOESTup440</i>	Uncharacterized protein	7.801	0.01660	<b>18.61</b>	<b>69.46</b>	<i>Prunus cerasifera</i>	5.00E-14	<a href="#">FM253563.1</a>
<i>UCOESTup445</i>	Uncharacterized protein	<b>7.766</b>	0.00029	<b>811.38</b>	<b>4944.63</b>	<i>Fragaria x ananassa</i>	2.00E-79	<a href="#">GW403124.1</a>
<i>UCOESTup446</i>	Uncharacterized protein	7.762	0.02130	<b>36.07</b>	<b>137.62</b>	<i>Quercus mongolica</i>	1.00E-12	<a href="#">DB999199.2</a>
<i>UCOESTup448</i>	Uncharacterized protein	<b>7.741</b>	0.00199	<b>487.05</b>	<b>3347.63</b>	<i>Oryza sativa Japonica</i>	1.00E-70	<a href="#">AB512491.1</a>
<i>UCOESTup457</i>	Uncharacterized protein	7.620	0.00442	<b>23.06</b>	<b>111.32</b>	<i>Prunus persica</i>	1.00E-33	<a href="#">DY647357.1</a>

(Table continues on following page)

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<b>UCOESTup458</b>	Uncharacterized protein	<b>7.609</b>	0.00017	<b>585.79</b>	<b>4400.53</b>	<b>Beta vulgaris</b>	2.00E-17	FP885871.1
UCOESTup470	Uncharacterized protein	7.534	0.00065	<b>30.51</b>	<b>147.56</b>	Rosa hybrid	3.00E-56	BQ104989.1
UCOESTup471	Uncharacterized protein	7.530	0.00022	<b>127.65</b>	<b>825.08</b>	Vitis vinifera	8.00E-23	XM_002285309.1
UCOESTup472	Uncharacterized protein	7.527	0.00329	<b>85.08</b>	<b>565.66</b>	Rosa hybrida	3.00E-12	EC587641.1
UCOESTup476	Uncharacterized protein	7.463	0.00043	<b>69.75</b>	<b>401.56</b>	Glycine max	7.00E-58	XM_003533560.1
<b>UCOESTup485</b>	Uncharacterized protein	<b>7.347</b>	0.00133	<b>225.01</b>	<b>1828.37</b>	<b>Arabidopsis thaliana</b>	5.00E-163	NM_102646.4
UCOESTup487	Uncharacterized protein	7.325	0.01040	<b>124.41</b>	<b>994.57</b>	Humulus lupulus	1.00E-37	EX517030.1
UCOESTup491	Uncharacterized protein	7.248	0.00144	<b>100.48</b>	<b>624.33</b>	Arabidopsis thaliana	1.00E-46	NM_102204.2
UCOESTup493	Uncharacterized protein	7.236	0.01310	<b>49.21</b>	<b>259.02</b>	Vitis vinifera	2.00E-16	AM465968.1
UCOESTup501	Uncharacterized protein	7.135	0.00090	<b>31.07</b>	<b>133.68</b>	Fragaria x ananassa	1.00E-17	GT151464.1
UCOESTup503	Uncharacterized protein	7.096	0.02160	<b>72.88</b>	<b>375.79</b>	Malus x domestica	7.00E-02	CN897673
UCOESTup506	Uncharacterized protein	6.981	0.00136	<b>49.66</b>	<b>308.26</b>	Coffea arabica	2.00E-06	EE884570.1
<b>UCOESTup508</b>	Uncharacterized protein	<b>6.945</b>	0.00034	<b>2386.82</b>	<b>16553.98</b>	<b>Nandina domestica</b>	3.00E-98	FJ789568.1
UCOESTup510	Uncharacterized protein	6.878	0.01580	<b>153.92</b>	<b>1170.11</b>	Arabidopsis thaliana	5.00E-65	NM_114531.2
UCOESTup512	Uncharacterized protein	6.851	0.00026	<b>294.20</b>	<b>1.992.87</b>	Fragaria vesca	3.00E-42	EX660289.1
UCOESTup514	Uncharacterized protein	6.839	0.01250	<b>68.69</b>	<b>468.85</b>	Glycine max	1.00E-123	FJ795038.1
UCOESTup516	Uncharacterized protein	6.790	0.00040	<b>152.26</b>	<b>954.26</b>	Fragaria vesca	3.00E-05	EX669563.1
UCOESTup537	Uncharacterized protein	6.606	0.02150	<b>42.17</b>	<b>207.94</b>	Medicago truncatula	1.00E-11	XM_003613312.1
UCOESTup539	Uncharacterized protein	6.591	0.00087	<b>1618.19</b>	<b>10507.91</b>	Fragaria x ananassa	1.00E-67	GW402332.1
UCOESTup554	Uncharacterized protein	6.442	0.04100	<b>72.68</b>	<b>396.95</b>	Vitis vinifera	1.00E-50	XM_002272854.1
UCOESTup559	Uncharacterized protein	6.380	0.00770	<b>50.79</b>	<b>226.81</b>	Citrus clementina	5.00E-84	DY294061.1
UCOESTup562	Uncharacterized protein	6.325	0.00692	<b>30.79</b>	<b>122.44</b>	Brassica napus	1.00E-06	ES984012.1
UCOESTup566	Uncharacterized protein	6.312	0.00029	<b>171.48</b>	<b>774.57</b>	Vitis vinifera	0.0	XM_002270255.1
UCOESTup580	Uncharacterized protein	6.206	0.00893	<b>1916.19</b>	<b>13146.04</b>	Fragaria x ananassa	3.00E-123	GT151981.1
UCOESTup573	Uncharacterized protein	6.260	0.00103	<b>129.71</b>	<b>545.04</b>	Vitis vinifera	2.00E-22	XM_002282226.2
UCOESTup577	Uncharacterized protein	6.245	0.01380	<b>54.71</b>	<b>217.99</b>	Arabidopsis thaliana	4.00E-14	NM_127745.1
UCOESTup584	Uncharacterized protein	6.188	0.00188	<b>19.81</b>	<b>72.20</b>	Fragaria vesca	2.00E-63	GU363535.1
<b>UCOESTup585</b>	Uncharacterized protein	<b>6.177</b>	0.00079	<b>387.11</b>	<b>2480.08</b>	<b>Vitis vinifera</b>	3.00E-27	XM_002279217.2
UCOESTup591	Uncharacterized protein	6.120	0.03320	<b>58.85</b>	<b>281.42</b>	Rosa multiflora	1.00E-44	HQ455834.1
UCOESTup592	Uncharacterized protein	6.114	0.00075	<b>538.57</b>	<b>3048.13</b>	Fragaria x ananassa	2.00E-05	CO379135.1
UCOESTup605	Uncharacterized protein	6.024	0.00089	<b>145.90</b>	<b>894.66</b>	Zea mays	8.00E-13	NM_001152047.1
UCOESTup610	Uncharacterized protein	5.955	0.00102	<b>102.14</b>	<b>586.55</b>	Prunus persica	2e-36	DY640850.1
UCOESTup611	Uncharacterized protein	5.946	0.00167	<b>103.51</b>	<b>482.02</b>	Fragaria vesca	4.00E-58	DY671527
<b>UCOESTup615</b>	Uncharacterized protein	<b>5.923</b>	0.01800	<b>401.02</b>	<b>2328.54</b>	<b>Fragaria vesca</b>	1.00E-09	EX664615.1
UCOESTup629	Uncharacterized protein	5.821	0.00061	<b>26.59</b>	<b>97.46</b>	Arabidopsis thaliana	7e-86	NM_123706.3
UCOESTup637	Uncharacterized protein	5.790	0.02610	<b>72.40</b>	<b>469.05</b>	Malus x domestica	2e-14	FN823234.1
UCOESTup652	Uncharacterized protein	5.630	0.00113	<b>102.31</b>	<b>440.54</b>	Fragaria vesca	1.00E-05	EX663114.1
UCOESTup656	Uncharacterized protein	5.609	0.01520	<b>66.86</b>	<b>363.72</b>	Fragaria vesca	2.00E-117	DV440279.1
UCOESTup659	Uncharacterized protein	5.579	0.00057	<b>48.68</b>	<b>232.13</b>	Arabidopsis thaliana	1e-76	NM_102744.2
UCOESTup670	Uncharacterized protein	5.481	0.02590	<b>16.84</b>	<b>46.05</b>	Gossypium hirsutum	4.00E-14	DW509525.1
UCOESTup672	Uncharacterized protein	5.463	0.00264	<b>20.92</b>	<b>59.90</b>	Rubus idaeus	1.00E-07	EE284359.1
UCOESTup673	Uncharacterized protein	5.456	0.00723	<b>17.22</b>	<b>38.23</b>	Fragaria vesca	8.00E-28	DY674164.1
UCOESTup687	Uncharacterized protein	5.376	0.00065	<b>194.33</b>	<b>1031.64</b>	Fragaria vesca	4.00E-30	EX660250.1
UCOESTup690	Uncharacterized protein	5.362	0.00026	<b>1116.98</b>	<b>6097.52</b>	Arabidopsis thaliana	1e-85	NM_101952.1

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<i>UCOESTup692</i>	Uncharacterized protein	5.355	0.00036	<b>372.33</b>	<b>1986.57</b>	<i>Fragaria vesca</i>	3.00E-52	<a href="#">DY667041.1</a>
<i>UCOESTup696</i>	Uncharacterized protein	5.331	0.02640	<b>50.36</b>	<b>224.93</b>	<i>Prunus avium</i>	1.00E-19	<a href="#">HE643002.1</a>
<i>UCOESTup700</i>	Uncharacterized protein	5.315	0.00069	<b>184.60</b>	<b>938.91</b>	<i>Beta vulgaris</i>	4e -57	<a href="#">BA000009.3</a>
<i>UCOESTup702</i>	Uncharacterized protein	5.295	0.00130	<b>160.77</b>	<b>773.98</b>	<i>Arabidopsis lyrata</i>	5e -137	<a href="#">XM_002870066.1</a>
<i>UCOESTup703</i>	Uncharacterized protein	5.287	0.03620	<b>22.84</b>	<b>67.19</b>	<i>Fragaria x ananassa</i>	3.00E-07	<a href="#">CO817818.1</a>
<i>UCOESTup706</i>	Uncharacterized protein	5.263	0.01370	<b>64.09</b>	<b>289.73</b>	<i>Prunus persica</i>	9.00E-11	<a href="#">DW347755</a>
<i>UCOESTup707</i>	Uncharacterized protein	5.255	0.00641	<b>37.84</b>	<b>114.80</b>	<i>Arabidopsis thaliana</i>	1e -150	<a href="#">NM_126891.3</a>
<i>UCOESTup711</i>	Uncharacterized protein	5.183	0.00595	<b>20.84</b>	<b>58.07</b>	<i>Fragaria vesca</i>	2.00E-49	<a href="#">DY670917.1</a>
<i>UCOESTup715</i>	Uncharacterized protein	5.165	0.01770	<b>424.06</b>	<b>2235.61</b>	<i>Citrus clementina</i>	1.00E-70	<a href="#">DY280804.1</a>
<i>UCOESTup718</i>	Uncharacterized protein	5.158	0.00066	<b>2968.66</b>	<b>16078.48</b>	<i>Arabidopsis thaliana</i>	4e -73	<a href="#">NM_128429.2</a>
<i>UCOESTup723</i>	Uncharacterized protein	5.143	0.00124	<b>98.34</b>	<b>427.08</b>	<i>Arabidopsis thaliana</i>	9e -42	<a href="#">NM_123434.2</a>
<i>UCOESTup730</i>	Uncharacterized protein	5.087	0.00040	<b>1461.55</b>	<b>7091.11</b>	<i>Fragaria vesca</i>	1.00E-162	<a href="#">EX658933.1</a>
<i>UCOESTup734</i>	Uncharacterized protein	5.070	0.03410	<b>50.41</b>	<b>192.02</b>	<i>Ipomopsis aggregata</i>	1.00E-17	<a href="#">GT313569.1</a>
<i>UCOESTup735</i>	Uncharacterized protein	5.069	0.00629	<b>33.02</b>	<b>124.97</b>	<i>Phaseolus vulgaris</i>	1.00E-85	<a href="#">FE710476.1</a>
<i>UCOESTup742</i>	Uncharacterized protein	5.040	0.00437	<b>1487.65</b>	<b>6805.28</b>	<i>Vitis vinifera</i>	5e -56	<a href="#">XM_002273433.1</a>
<i>UCOESTup746</i>	Uncharacterized protein	5.029	0.00625	<b>660.98</b>	<b>3304.96</b>	<i>Populus</i>	3e -30	<a href="#">CU229384.1</a>
<i>UCOESTup757</i>	Uncharacterized protein	4.984	0.03460	<b>16.55</b>	<b>46.12</b>	<i>Venturia inaequalis</i>	1.00E-49	<a href="#">FE969433.1</a>
<i>UCOESTup763</i>	Uncharacterized protein	4.933	0.00107	<b>1886.16</b>	<b>11444.95</b>	<i>Citrus sinensis</i>	4.00E-108	<a href="#">CV714299.1</a>
<i>UCOESTup769</i>	Uncharacterized protein	4.902	0.04320	<b>45.02</b>	<b>161.81</b>	<i>Arabidopsis thaliana</i>	6e -37	<a href="#">NM_124486.2</a>
<i>UCOESTup774</i>	Uncharacterized protein	4.867	0.00407	<b>257.51</b>	<b>1281.01</b>	<i>Fragaria vesca</i>	2e -86	<a href="#">GU363534.1</a>
<i>UCOESTup782</i>	Uncharacterized protein	4.839	0.00028	<b>653.43</b>	<b>3043.18</b>	<i>Fragaria vesca</i>	2e -59	<a href="#">GU363534.1</a>
<i>UCOESTup784</i>	Uncharacterized protein	4.825	0.01450	<b>23.54</b>	<b>56.50</b>	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002272884.1</a>
<i>UCOESTup786</i>	Uncharacterized protein	4.809	0.00512	<b>129.95</b>	<b>568.59</b>	<i>Fragaria vesca</i>	7.00E-35	<a href="#">EX662393.1</a>
<i>UCOESTup788</i>	Uncharacterized protein	4.806	0.00201	<b>272.61</b>	<b>1296.62</b>	<i>Arabidopsis thaliana</i>	2e -28	<a href="#">NM_106325.2</a>
<i>UCOESTup789</i>	Uncharacterized protein	4.788	0.01710	<b>21.25</b>	<b>65.91</b>	<i>Carica papaya</i>	8.00E-108	<a href="#">EX270415.1</a>
<i>UCOESTup800</i>	Uncharacterized protein	4.712	0.00701	<b>84.82</b>	<b>376.26</b>	<i>Fragaria x ananassa</i>	2e -67	<a href="#">DQ768221.1</a>
<i>UCOESTup809</i>	Uncharacterized protein	4.663	0.00117	<b>84.82</b>	<b>376.26</b>	<i>Sorghum bicolor</i>	1.00E-06	<a href="#">XM_002448228.1</a>
<i>UCOESTup811</i>	Uncharacterized protein	4.644	0.00420	<b>162.81</b>	<b>700.42</b>	<i>Vitis vinifera</i>	8.00E-36	<a href="#">FQ384294.1</a>
<i>UCOESTup812</i>	Uncharacterized protein	4.644	0.01590	<b>207.44</b>	<b>936.07</b>	<i>Arabidopsis lyrata</i>	1.00E-04	<a href="#">XM_002882032.1</a>
<i>UCOESTup816</i>	Uncharacterized protein	4.612	0.04570	<b>29.74</b>	<b>98.87</b>	<i>Medicago truncatula</i>	3.00E-27	<a href="#">EX528196.1</a>
<i>UCOESTup818</i>	Uncharacterized protein	4.601	0.01680	<b>47.38</b>	<b>189.76</b>	<i>Phaseolus acutifolius</i>	6.00E-22	<a href="#">HO796103.1</a>
<i>UCOESTup829</i>	Uncharacterized protein	4.547	0.00053	<b>802.44</b>	<b>3662.97</b>	<i>Fragaria x ananassa</i>	2.00E-30	<a href="#">GT149766.1</a>
<i>UCOESTup834</i>	Uncharacterized protein	4.534	0.00166	<b>2798.50</b>	<b>13318.82</b>	<i>Fragaria vesca</i>	1.00E-138	<a href="#">DY669461.1</a>
<i>UCOESTup836</i>	Uncharacterized protein	4.520	0.04770	<b>19.89</b>	<b>52.05</b>	<i>Pyrus pyrifolia</i>	5.00E-133	<a href="#">AB545982.1</a>
<i>UCOESTup847</i>	Uncharacterized protein	4.489	0.00128	<b>248.32</b>	<b>1106.30</b>	<i>Populus trichocarpa</i>	1.00E-56	<a href="#">XM_002304107.1</a>
<i>UCOESTup862</i>	Uncharacterized protein	4.431	0.00559	<b>329.20</b>	<b>1722.86</b>	<i>Vitis vinifera</i>	5.00E-54	<a href="#">XM_002268526.1</a>
<i>UCOESTup865</i>	Uncharacterized protein	4.417	0.00055	<b>840.53</b>	<b>3720.40</b>	<i>Fragaria vesca</i>	8.00E-52	<a href="#">GU363534.1</a>
<i>UCOESTup868</i>	Uncharacterized protein	4.405	0.00404	<b>28.89</b>	<b>111.83</b>	<i>Picea sitchensis</i>	7.00E-04	<a href="#">GH284419.1</a>
<i>UCOESTup866</i>	Uncharacterized protein	4.415	0.00359	<b>883.79</b>	<b>3817.79</b>	<i>Glycine max</i>	1.00E-08	<a href="#">AK245696.1</a>
<i>UCOESTup871</i>	Uncharacterized protein	4.402	0.00052	<b>1067.63</b>	<b>4815.79</b>	<i>Vitis vinifera</i>	4.00E-132	<a href="#">XM_002274858.1</a>
<i>UCOESTup876</i>	Uncharacterized protein	4.371	0.00430	<b>62.26</b>	<b>238.95</b>	<i>Populus trichocarpa</i>	1.00E-15	<a href="#">XM_002298170.1</a>
<i>UCOESTup879</i>	Uncharacterized protein	4.367	0.00484	<b>560.28</b>	<b>2675.56</b>	<i>Fragaria vesca</i>	3.00E-40	<a href="#">GU363534.1</a>
<i>UCOESTup884</i>	Uncharacterized protein	4.337	0.00285	<b>349.63</b>	<b>1546.94</b>	<i>Ipomopsis aggregata</i>	6.00E-31	<a href="#">GT316337.1</a>
<i>UCOESTup886</i>	Uncharacterized protein	4.332	0.01100	<b>74.53</b>	<b>212.50</b>	<i>Prunus persica</i>	2.00E-28	<a href="#">DY636475.1</a>

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UCOESTup894	Uncharacterized protein	4.308	0.00036	<b>2328.57</b>	<b>9950.73</b>	<i>Fragaria vesca</i>	3.00E-81	<a href="#">EX682262.1</a>
UCOESTup895	Uncharacterized protein	4.299	0.04590	<b>47.74</b>	<b>193.61</b>	<i>Prunus persica</i>	6.00E-45	<a href="#">DW342703.1</a>
UCOESTup896	Uncharacterized protein	4.298	0.02950	<b>27.86</b>	<b>89.09</b>	<i>Fragaria x ananassa</i>	4.00E-78	<a href="#">DQ768221.1</a>
UCOESTup897	Uncharacterized protein	4.297	0.00123	<b>47.74</b>	<b>193.61</b>	<i>Phaseolus acutifolius</i>	2.00E-15	<a href="#">HO782409.1</a>
UCOESTup898	Uncharacterized protein	4.291	0.00063	<b>194.52</b>	<b>767.86</b>	<i>Populus trichocarpa</i>	1.00E-28	<a href="#">XM_002300176.1</a>
UCOESTup912	Uncharacterized protein	4.249	0.00107	<b>419.05</b>	<b>1824.46</b>	<i>Populus trichocarpa</i>	2.00E-60	<a href="#">XM_002325000.1</a>
UCOESTup916	Uncharacterized protein	4.222	0.00845	<b>61.84</b>	<b>199.76</b>	<i>Cabernet Sauvignon</i>	9.00E-05	<a href="#">CF207799.1</a>
UCOESTup921	Uncharacterized protein	4.202	0.00069	<b>534.68</b>	<b>2190.56</b>	<i>Fragaria ananassa</i>	5.00E-78	<a href="#">GT149873</a>
UCOESTup926	Uncharacterized protein	4.179	0.00085	<b>2429.29</b>	<b>10207.70</b>	<i>Vitis vinifera</i>	2.00E-49	<a href="#">XM_002285200.1</a>
UCOESTup930	Uncharacterized protein	4.166	0.00103	<b>759.87</b>	<b>3094.73</b>	<i>Fragaria vesca</i>	4.00E-63	<a href="#">EX657432.1</a>
UCOESTup938	Uncharacterized protein	4.143	0.00054	<b>230.84</b>	<b>824.17</b>	<i>Soybean</i>	7.00E-41	<a href="#">BT093812.1</a>
UCOESTup939	Uncharacterized protein	4.141	0.00165	<b>169.18</b>	<b>663.64</b>	<i>Fragaria x ananassa</i>	9.00E-17	<a href="#">DQ768221.1</a>
UCOESTup951	Uncharacterized protein	4.105	0.00079	<b>1042.09</b>	<b>4324.28</b>	<i>Fragaria x ananassa</i>	1.00E-29	<a href="#">DQ768221.1</a>
UCOESTup954	Uncharacterized protein	4.102	0.00832	<b>52.30</b>	<b>140.54</b>	<i>Fragaria vesca</i>	6.00E-65	<a href="#">EX673050.1</a>
UCOESTup956	Uncharacterized protein	4.088	0.00632	<b>78.19</b>	<b>243.51</b>	<i>Oryza sativa Indica</i>	2.00E-05	<a href="#">CX100097.1</a>
UCOESTup959	Uncharacterized protein	4.065	0.01070	<b>486.44</b>	<b>2076.08</b>	<i>Fragaria x ananassa</i>	4.00E-34	<a href="#">DQ768221.1</a>
UCOESTup975	Uncharacterized protein	4.006	0.00058	<b>1757.40</b>	<b>6695.88</b>	<i>Rosa chinensis</i>	5.00E-30	<a href="#">B1978427.1</a>
UCOESTup978	Uncharacterized protein	4.000	0.00134	<b>998.68</b>	<b>3856.12</b>	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002265252.1</a>
UCOESTup1002	Uncharacterized protein	3.913	0.00214	<b>4686.09</b>	<b>18861.64</b>	<i>Nicotiana tabacum</i>	2.00E-16	<a href="#">DQ444223.1</a>
UCOESTup1005	Uncharacterized protein	3.906	0.00058	<b>1231.48</b>	<b>4750.89</b>	<i>Vitis vinifera</i>	3.00E-28	<a href="#">XM_002267695.1</a>
UCOESTup1016	Uncharacterized protein	3.879	0.01100	<b>361.02</b>	<b>1530.92</b>	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002262569.2</a>
UCOESTup1017	Uncharacterized protein	3.877	0.00202	<b>1653.56</b>	<b>6478.04</b>	<i>Nicotiana tabacum</i>	3.00E-111	<a href="#">BA000042.1</a>
UCOESTup1021	Uncharacterized protein	3.870	0.00201	<b>879.39</b>	<b>3252.14</b>	<i>Glycine max</i>	2.00E-07	<a href="#">XM_003555855.1</a>
UCOESTup1026	Uncharacterized protein	3.861	0.00039	<b>517.37</b>	<b>1951.98</b>	<i>Triticum aestivum</i>	8.00E-28	<a href="#">X15225.1</a>
UCOESTup1036	Uncharacterized protein	3.841	0.00260	<b>106.94</b>	<b>375.99</b>	<i>Fragaria vesca</i>	2.00E-35	<a href="#">JF345175.1</a>
UCOESTup1045	Uncharacterized protein	3.802	0.04940	<b>55.24</b>	<b>198.12</b>	<i>Glycine max</i>	3.00E-26	<a href="#">XM_003549665.1</a>
UCOESTup1046	Uncharacterized protein	3.800	0.00631	<b>525.74</b>	<b>2558.75</b>	<i>Medicago truncatula</i>	2.00E-08	<a href="#">XM_003610592.1</a>
UCOESTup1047	Uncharacterized protein	3.796	0.03600	<b>55.27</b>	<b>194.01</b>	<i>Glycine max</i>	3.00E-26	<a href="#">XM_003549665.1</a>
UCOESTup1064	Uncharacterized protein	3.748	0.00815	<b>635.85</b>	<b>2429.04</b>	<i>Arabidopsis thaliana</i>	2.00E-16	<a href="#">NM_125672.2</a>
UCOESTup1073	Uncharacterized protein	3.715	0.00203	<b>2029.34</b>	<b>7128.21</b>	<i>Arabidopsis thaliana</i>	1.00E-100	<a href="#">AY035083.1</a>
UCOESTup1074	Uncharacterized protein	3.714	0.00042	<b>2029.34</b>	<b>7128.21</b>	<i>Glycine max</i>	6.00E-47	<a href="#">XM_003541097.1</a>
UCOESTup1079	Uncharacterized protein	3.686	0.03560	<b>590.65</b>	<b>1953.44</b>	<i>Populus trichocarpa</i>	4.00E-105	<a href="#">XM_002316899.1</a>
UCOESTup1080	Uncharacterized protein	3.683	0.00500	<b>179.39</b>	<b>571.46</b>	<i>Carica papaya</i>	3.00E-106	<a href="#">EU431224.1</a>
UCOESTup1082	Uncharacterized protein	3.676	0.01180	<b>115.16</b>	<b>414.97</b>	<i>Fragaria x ananassa</i>	5.00E-30	<a href="#">DQ768221.1</a>
UCOESTup1104	Uncharacterized protein	3.615	0.00190	<b>68.96</b>	<b>243.72</b>	<i>Vitis vinifera</i>	2.00E-33	<a href="#">XM_002267193.1</a>
UCOESTup1107	Uncharacterized protein	3.609	0.02840	<b>61.20</b>	<b>199.38</b>	<i>Glycine max</i>	3.00E-25	<a href="#">XM_003550563.1</a>
UCOESTup1138	Uncharacterized protein	3.540	0.00657	<b>117.00</b>	<b>344.36</b>	<i>Glycine max</i>	4.00E-130	<a href="#">XM_003556551.1</a>
UCOESTup1141	Uncharacterized protein	3.539	0.00613	<b>88.60</b>	<b>205.49</b>	<i>Vitis vinifera</i>	9.00E-160	<a href="#">XM_002268408.1</a>
UCOESTup1159	Uncharacterized protein	3.501	0.00316	<b>688.23</b>	<b>1542.42</b>	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_100678.2</a>
UCOESTup1182	Uncharacterized protein	3.450	0.00126	<b>1530.24</b>	<b>5186.33</b>	<i>Brassica carinata</i>	0.0	<a href="#">JF920287.1</a>
UCOESTup1210	Uncharacterized protein	3.385	0.00478	<b>108.28</b>	<b>208.83</b>	<i>Vitis vinifera</i>	2.00E-43	<a href="#">XM_002273363.1</a>
UCOESTup1212	Uncharacterized protein	3.383	0.00058	<b>1821.25</b>	<b>5721.55</b>	<i>Glycine max</i>	0.0	<a href="#">XM_003528878.1</a>
UCOESTup1218	Uncharacterized protein	3.363	0.02330	<b>141.31</b>	<b>420.84</b>	<i>Arabidopsis thaliana</i>	3.00E-46	<a href="#">NM_001124057.1</a>
UCOESTup1222	Uncharacterized protein	3.352	0.00057	<b>835.09</b>	<b>2301.87</b>	<i>Medicago truncatula</i>	1.00E-117	<a href="#">XM_003601034.1</a>

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UCOESTup1226	Uncharacterized protein	3.349	0.00562	169.33	525.07	<i>Arabidopsis thaliana</i>	1.00E-66	NM_115829.3
UCOESTup1244	Uncharacterized protein	3.298	0.00926	604.36	2030.02	<i>Glycine max</i>	3.00E-29	XM_003552056.1
UCOESTup1246	Uncharacterized protein	3.290	0.02900	58.60	189.49	<i>Glycine max</i>	7.00E-138	XM_003523772.1
UCOESTup1250	Uncharacterized protein	3.277	0.00378	1191.02	3899.85	<i>Populus trichocarpa</i>	2.00E-117	XM_002302376.1
UCOESTup1255	Uncharacterized protein	3.269	0.00076	4706.40	15546.54	<i>Zea mays</i>	3.00E-37	EU971971.1
UCOESTup1260	Uncharacterized protein	3.256	0.00123	399.99	1296.19	<i>Medicago truncatula</i>	2.00E-22	XM_003605730.1
UCOESTup1265	Uncharacterized protein	3.242	0.00202	250.20	778.21	<i>Vigna radiata</i>	8.00E-06	HM367685.1
UCOESTup1289	Uncharacterized protein	3.180	0.00079	2918.00	8924.01	<i>Pyrus x bretschneideri</i>	1.00E-128	JN168000.1
UCOESTup1293	Uncharacterized protein	3.170	0.00864	3886.52	13141.45	<i>Arabidopsis thaliana</i>	2.00E-93	AY122933.1
UCOESTup1309	Uncharacterized protein	3.143	0.00363	318.62	1001.76	<i>Vitis vinifera</i>	8.00E-89	XM_002285731.1
UCOESTup1330	Uncharacterized protein	3.091	0.00089	1843.94	5243.58	<i>Glycine max</i>	9.00E-89	XM_003532439.1
UCOESTup1332	Uncharacterized protein	3.088	0.01370	174.80	558.29	<i>Fragaria x ananassa</i>	1.00E-48	AY860312.1
UCOESTup1338	Uncharacterized protein	3.081	0.00409	389.14	1170.81	<i>Fragaria vesca</i>	2.00E-41	GU363534.1
UCOESTup1346	Uncharacterized protein	3.064	0.00114	1537.12	4621.76	<i>Glycine max</i>	6.00E-147	XM_003529323.1
UCOESTup1353	Uncharacterized protein	3.056	0.02810	51.76	107.00	<i>Glycine max</i>	2.00E-100	XM_003517628.1
UCOESTup1381	Uncharacterized protein	3.014	0.00222	1319.40	3748.12	<i>Glycine max</i>	0.0	XM_003520978.1
UCOESTup1392	Uncharacterized protein	2.996	0.00087	1478.41	4023.87	<i>Arabidopsis thaliana</i>	4.00E-106	NM_100272.3
UCOESTup1399	Uncharacterized protein	2.987	0.04060	37.48	88.05	<i>Medicago truncatula</i>	4.00E-50	XM_003623867.1
UCOESTup1421	Uncharacterized protein	2.949	0.00406	118.15	323.88	<i>Glycine max</i>	4.00E-124	XM_003522686.1
UCOESTup1423	Uncharacterized protein	2.947	0.00686	1438.78	4219.76	<i>Populus trichocarpa</i>	2.00E-37	XM_002328929.1
UCOESTup1432	Uncharacterized protein	2.928	0.00513	443.92	968.81	<i>Glycine max</i>	0.0	XM_003536648.1
UCOESTup1439	Uncharacterized protein	2.916	0.00305	263.49	736.51	<i>Glycine max</i>	0.0	XM_003535727.1
UCOESTup1449	Uncharacterized protein	2.899	0.00150	408.56	1262.18	<i>Glycine max</i>	2.00E-28	XM_003544412.1
UCOESTup1455	Uncharacterized protein	2.891	0.01040	74.36	179.90	<i>Fragaria x ananassa</i>	3.00E-63	DQ768221.1
UCOESTup1456	Uncharacterized protein	2.890	0.00132	588.52	1542.45	<i>Glycine max</i>	0.0	XM_003517203.1
UCOESTup1459	Uncharacterized protein	2.887	0.00965	584.43	1627.97	<i>Glycine max</i>	0.0	XM_003539776.1
UCOESTup1460	Uncharacterized protein	2.883	0.00090	4132.19	12002.16	<i>Medicago truncatula</i>	6.00E-159	XM_003603370.1
UCOESTup1470	Uncharacterized protein	2.870	0.02930	280.64	824.71	<i>Fragaria x ananassa</i>	3.00E-19	AY860312.1
UCOESTup1468	Uncharacterized protein	2.870	0.00095	1966.82	5603.11	<i>Fragaria x ananassa</i>	2.00E-22	DQ768221.1
UCOESTup1502	Uncharacterized protein	2.828	0.01720	172.54	486.86	<i>Fragaria x ananassa</i>	4.00E-30	AY860312.1
UCOESTup1532	Uncharacterized protein	2.784	0.01980	144.25	393.00	<i>Glycine max</i>	3.00E-30	XM_003533319.1
UCOESTup1531	Uncharacterized protein	2.784	0.01350	521.02	1480.02	<i>Fragaria x ananassa</i>	3.00E-29	DQ768221.1
UCOESTup1534	Uncharacterized protein	2.783	0.00555	2500.08	7270.60	<i>Arabidopsis thaliana</i>	1.00E-51	NM_114640.3
UCOESTup1541	Uncharacterized protein	2.773	0.00240	1030.38	2811.60	<i>Glycine max</i>	4.00E-75	XM_003551188.1
UCOESTup1543	Uncharacterized protein	2.772	0.04820	284.50	846.95	<i>Fragaria x ananassa</i>	1.00E-17	AY860312.1
UCOESTup1553	Uncharacterized protein	2.763	0.01090	30.30	58.40	<i>Arabidopsis thaliana</i>	2.00E-26	NM_121501.3
UCOESTup1560	Uncharacterized protein	2.756	0.00090	226.80	577.78	<i>Fragaria x ananassa</i>	6.00E-50	DQ768221.1
UCOESTup1566	Uncharacterized protein	2.749	0.04360	290.96	862.32	<i>Fragaria x ananassa</i>	2.00E-28	AY860312.1
UCOESTup1571	Uncharacterized protein	2.746	0.00308	686.15	2023.15	<i>Arabidopsis thaliana</i>	0.0	NM_124111.2
UCOESTup1583	Uncharacterized protein	2.736	0.00262	10667.06	29289.81	<i>Glycine max</i>	3.00E-31	XM_003533753.1
UCOESTup1615	Uncharacterized protein	2.698	0.00199	1196.64	3230.49	<i>Fragaria vesca</i>	2.00E-56	JF345175.1
UCOESTup1656	Uncharacterized protein	2.640	0.00699	610.71	1630.37	<i>Glycine max</i>	7.00E-77	XM_003531319.1
UCOESTup1671	Uncharacterized protein	2.621	0.03520	18.90	35.36	<i>Glycine max</i>	1.00E-146	XM_003545460.1
UCOESTup1688	Uncharacterized protein	2.601	0.00224	600.17	1455.50	<i>Glycine max</i>	8.00E-94	XM_003536066.1

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UCOESTup1691	Uncharacterized protein	2.597	0.00210	<b>259.03</b>	<b>652.29</b>	<i>Arabidopsis thaliana</i>	8.00E-35	<a href="#">AY114049.1</a>
UCOESTup1699	Uncharacterized protein	2.585	0.00294	<b>752.67</b>	<b>1917.83</b>	<i>Glycine max</i>	9.00E-83	<a href="#">XM_003555935.1</a>
UCOESTup1698	Uncharacterized protein	2.585	0.00268	<b>815.44</b>	<b>2576.27</b>	<i>Medicago truncatula</i>	7.00E-94	<a href="#">XM_003615136.1</a>
UCOESTup1704	Uncharacterized protein	2.582	0.00211	<b>2251.62</b>	<b>5621.91</b>	<i>Arabidopsis thaliana</i>	3.00E-41	<a href="#">NM_101515.2</a>
UCOESTup1713	Uncharacterized protein	2.572	0.00372	<b>311.36</b>	<b>794.72</b>	<i>Glycine max</i>	7.00E-49	<a href="#">XM_003554650.1</a>
UCOESTup1724	Uncharacterized protein	2.562	0.02060	<b>1088.46</b>	<b>2895.93</b>	<i>Gomystylus bancanus</i>	2.00E-77	<a href="#">EU849490.1</a>
UCOESTup1728	Uncharacterized protein	2.559	0.00208	<b>6723.38</b>	<b>17039.00</b>	<i>Glycine max</i>	2.00E-53	<a href="#">XM_003524648.1</a>
UCOESTup1737	Uncharacterized protein	2.548	0.00672	<b>119.70</b>	<b>281.41</b>	<i>Glycine max</i>	5.00E-68	<a href="#">XM_003544839.1</a>
UCOESTup1738	Uncharacterized protein	2.547	0.01700	<b>54.51</b>	<b>113.99</b>	<i>Glycine max</i>	4.00E-09	<a href="#">XM_003546496.1</a>
UCOESTup1753	Uncharacterized protein	2.538	0.00641	<b>3170.14</b>	<b>7757.51</b>	<i>Arabidopsis thaliana</i>	8.00E-38	<a href="#">NM_114683.4</a>
UCOESTup1772	Uncharacterized protein	2.524	0.01160	<b>2312.80</b>	<b>6010.17</b>	<i>Glycine max</i>	3.00E-22	<a href="#">XR_136676.1</a>
UCOESTup1774	Uncharacterized protein	2.523	0.01740	<b>827.94</b>	<b>2174.35</b>	<i>Glycine max</i>	4.00E-13	<a href="#">XM_003517925.1</a>
UCOESTup1782	Uncharacterized protein	2.512	0.00167	<b>4976.86</b>	<b>12427.75</b>	<i>Medicago truncatula</i>	7.00E-110	<a href="#">XM_003611564.1</a>
UCOESTup1797	Uncharacterized protein	2.500	0.01060	<b>1308.92</b>	<b>3459.16</b>	<i>Glycine max</i>	0.0	<a href="#">NM_001248161.1</a>
UCOESTup1808	Uncharacterized protein	2.488	0.00172	<b>483.97</b>	<b>1270.06</b>	<i>Arabidopsis thaliana</i>	1.00E-90	<a href="#">AF182953.1</a>
UCOESTup1809	Uncharacterized protein	2.487	0.00156	<b>1593.58</b>	<b>4024.87</b>	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003617173.1</a>
UCOESTup1810	Uncharacterized protein	2.485	0.00267	<b>5878.50</b>	<b>14275.14</b>	<i>Populus trichocarpa</i>	2.00E-30	<a href="#">XM_002315839.1</a>
UCOESTup1816	Uncharacterized protein	2.476	0.00484	<b>1333.10</b>	<b>3138.31</b>	<i>Glycine max</i>	4.00E-112	<a href="#">XM_003546624.1</a>
UCOESTup1844	Uncharacterized protein	2.455	0.00656	<b>291.11</b>	<b>702.76</b>	<i>Glycine max</i>	0.0	<a href="#">XM_003524069.1</a>
UCOESTup1856	Uncharacterized protein	2.448	0.02190	<b>278.23</b>	<b>658.91</b>	<i>Carica papaya</i>	9.00E-07	<a href="#">EU431224.1</a>
UCOESTup1865	Uncharacterized protein	2.442	0.03860	<b>149.91</b>	<b>342.46</b>	<i>Medicago truncatula</i>	2.00E-133	<a href="#">XM_003591613.1</a>
UCOESTup1866	Uncharacterized protein	2.442	0.04290	<b>294.30</b>	<b>743.99</b>	<i>Medicago truncatula</i>	8.00E-51	<a href="#">XM_003609808.1</a>
UCOESTup1878	Uncharacterized protein	2.433	0.00215	<b>1430.71</b>	<b>3335.95</b>	<i>Glycine max</i>	4.00E-145	<a href="#">XM_003553997.1</a>
UCOESTup1886	Uncharacterized protein	2.426	0.00396	<b>16.65</b>	<b>25.46</b>	<i>Glycine max</i>	0.0	<a href="#">XM_003534146.1</a>
UCOESTup1895	Uncharacterized protein	2.418	0.00542	<b>3030.03</b>	<b>6536.03</b>	<i>Arabidopsis thaliana</i>	1.00E-101	<a href="#">NM_100889.3</a>
UCOESTup1901	Uncharacterized protein	2.410	0.02830	<b>91.75</b>	<b>192.51</b>	<i>Arabidopsis thaliana</i>	4.00E-86	<a href="#">NM_122113.1</a>
UCOESTup1907	Uncharacterized protein	2.406	0.02690	<b>159.73</b>	<b>379.14</b>	<i>Glycine max</i>	7.00E-22	<a href="#">XM_003548042.1</a>
UCOESTup1910	Uncharacterized protein	2.404	0.04920	<b>53.05</b>	<b>95.34</b>	<i>Medicago truncatula</i>	4.00E-67	<a href="#">XM_003588677.1</a>
UCOESTup1915	Uncharacterized protein	2.400	0.01290	<b>2315.54</b>	<b>5107.49</b>	<i>Glycine max</i>	2.00E-152	<a href="#">XM_003524060.1</a>
UCOESTup1938	Uncharacterized protein	2.380	0.02320	<b>3222.24</b>	<b>8055.43</b>	<i>Glycine max</i>	9.00E-84	<a href="#">XM_003542613.1</a>
UCOESTup1942	Uncharacterized protein	2.377	0.00231	<b>875.16</b>	<b>2085.27</b>	<i>Arabidopsis thaliana</i>	1.00E-28	<a href="#">NM_125730.2</a>
UCOESTup1953	Uncharacterized protein	2.367	0.01670	<b>15.43</b>	<b>26.28</b>	<i>Glycine max</i>	6.00E-52	<a href="#">XM_003530107.1</a>
UCOESTup1977	Uncharacterized protein	2.351	0.01070	<b>65.57</b>	<b>129.97</b>	<i>Glycine max</i>	0.0	<a href="#">XM_003516678.1</a>
UCOESTup1987	Uncharacterized protein	2.341	0.01550	<b>944.63</b>	<b>2244.91</b>	<i>Arabidopsis thaliana</i>	6.00E-11	<a href="#">NM_117836.3</a>
UCOESTup1998	Uncharacterized protein	2.334	0.03660	<b>1249.41</b>	<b>3057.22</b>	<i>Arabidopsis thaliana</i>	1.00E-27	<a href="#">NM_121859.2</a>
UCOESTup2006	Uncharacterized protein	2.331	0.02920	<b>1498.76</b>	<b>3627.15</b>	<i>Glycine max</i>	2.00E-20	<a href="#">XM_003517458.1</a>
UCOESTup2017	Uncharacterized protein	2.323	0.00458	<b>390.76</b>	<b>796.64</b>	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003601827.1</a>
UCOESTup2029	Uncharacterized protein	2.316	0.00337	<b>4132.51</b>	<b>9333.25</b>	<i>Glycine max</i>	0.0	<a href="#">XM_003524697.1</a>
UCOESTup2046	Uncharacterized protein	2.303	0.00250	<b>1003.33</b>	<b>2339.14</b>	<i>Glycine max</i>	5.00E-127	<a href="#">XM_003539969.1</a>
UCOESTup2058	Uncharacterized protein	2.292	0.01620	<b>2364.05</b>	<b>5520.17</b>	<i>Glycine max</i>	3.00E-41	<a href="#">XM_003555975.1</a>
UCOESTup2059	Uncharacterized protein	2.292	0.04220	<b>15.30</b>	<b>24.39</b>	<i>Glycine max</i>	6.00E-75	<a href="#">XM_003536479.1</a>
UCOESTup2071	Uncharacterized protein	2.285	0.00144	<b>1492.45</b>	<b>3403.82</b>	<i>Glycine max</i>	0.0	<a href="#">XM_003534778.1</a>
UCOESTup2078	Uncharacterized protein	2.282	0.01250	<b>823.02</b>	<b>1908.40</b>	<i>Arabidopsis thaliana</i>	6.00E-13	<a href="#">NM_001161112.2</a>
UCOESTup2079	Uncharacterized protein	2.281	0.00379	<b>1025.28</b>	<b>2222.74</b>	<i>Glycine max</i>	0.0	<a href="#">XM_003516340.1</a>

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UCOESTup2086	Uncharacterized protein	2.277	0.00243	<b>618.18</b>	<b>1325.68</b>	<i>Medicago truncatula</i>	8.00E-78	<a href="#">XM_003597719.1</a>
UCOESTup2096	Uncharacterized protein	2.271	0.02270	<b>257.78</b>	<b>480.36</b>	<i>Glycine max</i>	5.00E-41	<a href="#">NM_003517608.1</a>
UCOESTup2100	Uncharacterized protein	2.268	0.00548	<b>807.30</b>	<b>2007.25</b>	<i>Arabidopsis thaliana</i>	6.00E-54	<a href="#">NM_118963.4</a>
UCOESTup2113	Uncharacterized protein	2.261	0.01230	<b>564.87</b>	<b>1080.19</b>	<i>Glycine max</i>	2.00E-117	<a href="#">XM_003518006.1</a>
UCOESTup2114	Uncharacterized protein	2.260	0.00199	<b>3799.20</b>	<b>8281.88</b>	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002280765.1</a>
UCOESTup2131	Uncharacterized protein	2.255	0.00229	<b>7733.14</b>	<b>15961.70</b>	<i>Glycine max</i>	7.00E-150	<a href="#">XM_003524881.1</a>
UCOESTup2132	Uncharacterized protein	2.255	0.00242	<b>990.65</b>	<b>2062.36</b>	<i>Arabidopsis thaliana</i>	1.00E-174	<a href="#">NM_113710.2</a>
UCOESTup2163	Uncharacterized protein	2.232	0.00508	<b>2005.23</b>	<b>4386.23</b>	<i>Glycine max</i>	5.00E-16	<a href="#">XM_003521303.1</a>
UCOESTup2166	Uncharacterized protein	2.231	0.00440	<b>976.65</b>	<b>2112.55</b>	<i>Glycine max</i>	0.0	<a href="#">XM_003539949.1</a>
UCOESTup2195	Uncharacterized protein	2.214	0.03630	<b>176.86</b>	<b>387.30</b>	<i>Arabidopsis thaliana</i>	1.00E-66	<a href="#">NM_121260.2</a>
UCOESTup2204	Uncharacterized protein	2.205	0.01230	<b>2696.51</b>	<b>6026.04</b>	<i>Fragaria x ananassa</i>	1.00E-88	<a href="#">DQ768221.1</a>
UCOESTup2225	Uncharacterized protein	2.191	0.00331	<b>892.69</b>	<b>2104.97</b>	<i>Glycine max</i>	0.0	<a href="#">XM_003538273.1</a>
UCOESTup2237	Uncharacterized protein	2.184	0.01630	<b>443.34</b>	<b>1160.48</b>	<i>Glycine max</i>	2.00E-77	<a href="#">XM_003547522.1</a>
UCOESTup2242	Uncharacterized protein	2.182	0.03370	<b>649.13</b>	<b>1501.59</b>	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003625832.1</a>
UCOESTup2254	Uncharacterized protein	2.176	0.03480	<b>799.50</b>	<b>1752.80</b>	<i>Glycine max</i>	1.00E-11	<a href="#">XR_137284.1</a>
UCOESTup2272	Uncharacterized protein	2.168	0.01120	<b>90.81</b>	<b>176.30</b>	<i>Medicago truncatula</i>	9.00E-38	<a href="#">XM_003590666.1</a>
UCOESTup2274	Uncharacterized protein	2.166	0.00473	<b>881.54</b>	<b>2182.55</b>	<i>Glycine max</i>	1.00E-41	<a href="#">XM_003549878.1</a>
UCOESTup2302	Uncharacterized protein	2.151	0.00671	<b>8280.10</b>	<b>16179.75</b>	<i>Glycine max</i>	0.0	<a href="#">XM_003534047.1</a>
UCOESTup2306	Uncharacterized protein	2.149	0.00656	<b>819.71</b>	<b>1775.54</b>	<i>Glycine max</i>	1.00E-30	<a href="#">XM_003527857.1</a>
UCOESTup2310	Uncharacterized protein	2.148	0.03010	<b>20.52</b>	<b>32.50</b>	<i>Arabidopsis thaliana</i>	5.00E-10	<a href="#">NM_129200.3</a>
UCOESTup2316	Uncharacterized protein	2.143	0.00283	<b>2783.82</b>	<b>5588.06</b>	<i>Glycine max</i>	1.00E-14	<a href="#">XM_003531634.1</a>
UCOESTup2347	Uncharacterized protein	2.125	0.01010	<b>1244.86</b>	<b>2638.63</b>	<i>Arabidopsis thaliana</i>	1.00E-09	<a href="#">NM_122468.3</a>
UCOESTup2351	Uncharacterized protein	2.122	0.00228	<b>678.14</b>	<b>1518.17</b>	<i>Medicago truncatula</i>	1.00E-117	<a href="#">XM_003612114.1</a>
UCOESTup2377	Uncharacterized protein	2.106	0.03030	<b>334.08</b>	<b>693.67</b>	<i>Arabidopsis thaliana</i>	7.00E-60	<a href="#">NM_001125386.1</a>
UCOESTup2383	Uncharacterized protein	2.101	0.00452	<b>4057.54</b>	<b>8320.46</b>	<i>Glycine max</i>	0.0	<a href="#">XM_003543071.1</a>
UCOESTup2390	Uncharacterized protein	2.098	0.02880	<b>268.44</b>	<b>529.91</b>	<i>Zea mays</i>	4.00E-43	<a href="#">NM_001155690.1</a>
UCOESTup2413	Uncharacterized protein	2.084	0.02560	<b>20.52</b>	<b>32.10</b>	<i>Arabidopsis thaliana</i>	3.00E-21	<a href="#">NM_115414.1</a>
UCOESTup2418	Uncharacterized protein	2.081	0.00323	<b>1565.15</b>	<b>3345.16</b>	<i>Glycine max</i>	2.00E-20	<a href="#">XM_003524481.1</a>
UCOESTup2437	Uncharacterized protein	2.070	0.00236	<b>3603.51</b>	<b>7799.50</b>	<i>Arabidopsis thaliana</i>	1.00E-162	<a href="#">NM_203161.2</a>
UCOESTup2438	Uncharacterized protein	2.069	0.00278	<b>6121.04</b>	<b>12686.90</b>	<i>Arabidopsis thaliana</i>	3.00E-96	<a href="#">NM_117839.4</a>
UCOESTup2448	Uncharacterized protein	2.065	0.00598	<b>360.51</b>	<b>731.34</b>	<i>Zea mays</i>	1.00E-45	<a href="#">EU971810.1</a>
UCOESTup2515	Uncharacterized protein	2.030	0.00274	<b>2517.38</b>	<b>5561.77</b>	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_103432.1</a>
UCOESTup2530	Uncharacterized protein	2.020	0.00554	<b>726.04</b>	<b>1511.55</b>	<i>Medicago truncatula</i>	1.00E-150	<a href="#">XM_003620630.1</a>
UCOESTup2531	Uncharacterized protein	2.019	0.02780	<b>1701.56</b>	<b>3499.48</b>	<i>Glycine max</i>	1.00E-115	<a href="#">XM_003543206.1</a>
UCOESTup2553	Uncharacterized protein	2.009	0.00699	<b>444.62</b>	<b>841.74</b>	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_129599.2</a>
UCOESTup2569	Uncharacterized protein	2.001	0.00478	<b>3377.04</b>	<b>6558.96</b>	<i>Glycine max</i>	2.00E-98	<a href="#">XM_003533305.1</a>

**Table 10. Uncharacterized protein up regulated in fruit ripen receptacles analyzed by microarray experiment.**

Magnitudes of relative induction to fruit ripen receptacles,  $p$ -value ( $\leq 0.05$ ) and u.a.e (arbitrary units of expression) in green and red fruits are given. Mean value of u.a.e is 1771.57. Columns show the best annotated matches from the search results of tBlastX analysis, species, putative function and match  $e$ - value.

Interesting genes

NO HOMOLOGY (1/19)		Fruit ripen receptacles <i>Up regulated</i>			
GENES	Putative function	Fold	p-value	U.a.e. in green fruits	U.a.e in red fruits
<i>UCOESTup1</i>	No homology	2303.220	6.15E-05	12.75	6745.23
<i>UCOESTup6</i>	No homology	424.879	6.76E-05	12.56	1300.67
<i>UCOESTup7</i>	No homology	366.841	0.00032	17.12	1695.68
<i>UCOESTup9</i>	No homology	222.637	0.00245	18.89	2654.17
<i>UCOESTup17</i>	No homology	146.744	0.00011	9.79	301.41
<i>UCOESTup20</i>	No homology	135.811	0.00119	22.47	894.55
<i>UCOESTup28</i>	No homology	106.858	0.00018	25.95	951.46
<i>UCOESTup35</i>	No homology	84.701	0.00088	21.41	903.33
<i>UCOESTup48</i>	No homology	65.060	0.00056	30.42	1030.95
<i>UCOESTup63</i>	No homology	49.042	0.00010	57.78	2141.29
<i>UCOESTup66</i>	No homology	47.247	0.00046	28.68	983.47
<i>UCOESTup74</i>	No homology	43.225	0.00012	23.91	530.32
<i>UCOESTup82</i>	No homology	38.440	0.00051	18.12	237.75
<i>UCOESTup86</i>	No homology	36.720	0.00254	43.70	1390.15
<i>UCOESTup89</i>	No homology	35.682	0.00013	39.02	885.85
<i>UCOESTup92</i>	No homology	34.671	0.00012	50.09	970.19
<i>UCOESTup94</i>	No homology	33.721	0.00114	29.37	55.01
<i>UCOESTup95</i>	No homology	33.654	0.00054	23.32	285.88
<i>UCOESTup97</i>	No homology	33.135	0.00108	20.99	349.60
<i>UCOESTup98</i>	No homology	33.000	0.00251	37.18	489.50
<i>UCOESTup107</i>	No homology	29.683	0.04300	19.72	367.75
<i>UCOESTup111</i>	No homology	28.431	0.00187	18.77	251.20
<i>UCOESTup115</i>	No homology	27.624	0.00096	24.03	236.37
<i>UCOESTup118</i>	No homology	27.086	0.00012	115.87	2820.64
<i>UCOESTup120</i>	No homology	26.443	0.00023	127.16	3457.28
<i>UCOESTup126</i>	No homology	25.209	0.00752	62.58	1294.48
<i>UCOESTup127</i>	No homology	25.169	0.00091	69.61	1308.21
<i>UCOESTup128</i>	No homology	24.833	0.00114	16.76	154.29
<i>UCOESTup136</i>	No homology	23.118	0.00023	22.09	232.76
<i>UCOESTup142</i>	No homology	22.352	0.00117	20.36	186.42
<i>UCOESTup147</i>	No homology	21.524	0.00269	68.14	1012.55
<i>UCOESTup148</i>	No homology	21.218	0.00044	346.21	7129.58
<i>UCOESTup153</i>	No homology	20.720	0.00011	330.51	6967.18
<i>UCOESTup156</i>	No homology	20.580	0.00032	65.38	461.10
<i>UCOESTup158</i>	No homology	20.407	0.00577	46.29	581.05
<i>UCOESTup159</i>	No homology	20.089	0.00011	262.67	4433.68
<i>UCOESTup164</i>	No homology	19.275	0.00219	52.50	44328
<i>UCOESTup165</i>	No homology	19.114	0.00044	60.13	94003

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<i>UCOESTup166</i>	No homology	19.091	0.00527	<b>11.80</b>	<b>70.42</b>
<i>UCOESTup167</i>	No homology	19.055	0.00095	<b>17.91</b>	<b>183.49</b>
<i>UCOESTup170</i>	No homology	18.771	0.00288	<b>62.33</b>	<b>935.76</b>
<i>UCOESTup177</i>	No homology	17.614	0.00517	<b>51.76</b>	<b>107.00</b>
<i>UCOESTup193</i>	No homology	16.276	0.00057	<b>47.45</b>	<b>524.47</b>
<i>UCOESTup195</i>	No homology	16.201	0.00094	<b>44.33</b>	<b>418.48</b>
<i>UCOESTup209</i>	No homology	15.097	0.02022	<b>26.63</b>	<b>215.49</b>
<i>UCOESTup214</i>	No homology	14.502	0.00961	<b>19.80</b>	<b>80.92</b>
<i>UCOESTup216</i>	No homology	14.456	0.00153	<b>14.46</b>	<b>106.64</b>
<i>UCOESTup219</i>	No homology	14.346	0.00184	<b>89.76</b>	<b>1312.59</b>
<i>UCOESTup230</i>	No homology	13.474	0.00326	<b>42.00</b>	<b>356.47</b>
<i>UCOESTup243</i>	No homology	12.980	0.00061	<b>70.88</b>	<b>569.54</b>
<i>UCOESTup245</i>	No homology	12.895	0.04350	<b>64.93</b>	<b>837.23</b>
<i>UCOESTup249</i>	No homology	12.708	0.04610	<b>32.89</b>	<b>373.60</b>
<i>UCOESTup250</i>	No homology	12.678	0.00130	<b>380.58</b>	<b>4926.11</b>
<i>UCOESTup252</i>	No homology	12.556	0.01950	<b>28.79</b>	<b>240.63</b>
<i>UCOESTup254</i>	No homology	12.372	0.00040	<b>635.79</b>	<b>7862.63</b>
<i>UCOESTup265</i>	No homology	11.993	0.00572	<b>54.84</b>	<b>427.33</b>
<i>UCOESTup268</i>	No homology	11.793	0.00082	<b>52.53</b>	<b>612.79</b>
<i>UCOESTup270</i>	No homology	11.745	0.00254	<b>14.63</b>	<b>67.82</b>
<i>UCOESTup274</i>	No homology	11.64	0.00019	<b>433.58</b>	<b>4916.56</b>
<i>UCOESTup276</i>	No homology	11.565	0.00214	<b>17.22</b>	<b>87.36</b>
<i>UCOESTup278</i>	No homology	11.534	0.00029	<b>154.58</b>	<b>995.81</b>
<i>UCOESTup279</i>	No homology	11.523	0.00263	<b>24.50</b>	<b>168.30</b>
<i>UCOESTup282</i>	No homology	11.378	0.00121	<b>33.76</b>	<b>247.48</b>
<i>UCOESTup283</i>	No homology	11.375	0.00691	<b>50.04</b>	<b>695.43</b>
<i>UCOESTup294</i>	No homology	11.036	0.00074	<b>18.26</b>	<b>97.07</b>
<i>UCOESTup300</i>	No homology	10.738	0.00064	<b>30.30</b>	<b>202.19</b>
<i>UCOESTup304</i>	No homology	10.589	0.00234	<b>92.60</b>	<b>857.31</b>
<i>UCOESTup309</i>	No homology	10.440	0.00096	<b>114.03</b>	<b>1064.91</b>
<i>UCOESTup310</i>	No homology	10.400	0.00951	<b>24.04</b>	<b>105.82</b>
<i>UCOESTup311</i>	No homology	10.395	0.00305	<b>28.29</b>	<b>180.74</b>
<i>UCOESTup318</i>	No homology	10.175	0.00114	<b>37.65</b>	<b>209.38</b>
<i>UCOESTup329</i>	No homology	9.924	0.00180	<b>346.39</b>	<b>3633.09</b>
<i>UCOESTup331</i>	No homology	9.900	0.00049	<b>774.11</b>	<b>7665.97</b>
<i>UCOESTup336</i>	No homology	9.757	0.00251	<b>15.49</b>	<b>55.63</b>
<i>UCOESTup338</i>	No homology	9.748	0.00570	<b>119.24</b>	<b>917.02</b>
<i>UCOESTup340</i>	No homology	9.687	0.03680	<b>14.98</b>	<b>68.14</b>
<i>UCOESTup341</i>	No homology	9.667	0.00017	<b>176.48</b>	<b>1553.06</b>
<i>UCOESTup350</i>	No homology	9.410	0.00168	<b>51.04</b>	<b>299.64</b>
<i>UCOESTup351</i>	No homology	9.406	0.00548	<b>93.11</b>	<b>797.64</b>
<i>UCOESTup357</i>	No homology	9.193	0.00064	<b>175.88</b>	<b>1414.80</b>
<i>UCOESTup359</i>	No homology	9.184	0.00216	<b>383.92</b>	<b>3592.79</b>
<i>UCOESTup378</i>	No homology	8.760	0.00036	<b>561.44</b>	<b>4598.76</b>
<i>UCOESTup382</i>	No homology	8.676	0.00165	<b>415.87</b>	<b>3805.09</b>

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<i>UCOESTup383</i>	No homology	8.664	0.02040	<b>92.40</b>	<b>780.86</b>
<i>UCOESTup386</i>	No homology	8.641	0.00345	<b>56.34</b>	<b>278.70</b>
<i>UCOESTup387</i>	No homology	8.618	0.00027	<b>28.41</b>	<b>124.28</b>
<i>UCOESTup390</i>	No homology	8.595	0.00057	<b>134.36</b>	<b>1060.55</b>
<i>UCOESTup401</i>	No homology	8.433	0.00385	<b>39.23</b>	<b>188.44</b>
<i>UCOESTup406</i>	No homology	8.375	0.00296	<b>722.42</b>	<b>2111.01</b>
<i>UCOESTup409</i>	No homology	8.344	0.00077	<b>59.16</b>	<b>359.37</b>
<i>UCOESTup412</i>	No homology	8.322	0.01070	<b>27.54</b>	<b>123.10</b>
<i>UCOESTup416</i>	No homology	8.272	0.02570	<b>227.08</b>	<b>2299.89</b>
<i>UCOESTup420</i>	No homology	8.243	0.00061	<b>248.40</b>	<b>1981.97</b>
<i>UCOESTup437</i>	No homology	7.880	0.00027	<b>56.51</b>	<b>301.06</b>
<i>UCOESTup438</i>	No homology	7.854	0.00096	<b>109.87</b>	<b>823.78</b>
<i>UCOESTup442</i>	No homology	7.783	0.00936	<b>81.96</b>	<b>476.02</b>
<i>UCOESTup454</i>	No homology	7.636	0.00300	<b>105.32</b>	<b>771.94</b>
<i>UCOESTup461</i>	No homology	7.584	0.00363	<b>346.92</b>	<b>2950.20</b>
<i>UCOESTup463</i>	No homology	7.571	0.00091	<b>36.21</b>	<b>127.99</b>
<i>UCOESTup465</i>	No homology	7.560	0.01099	<b>73.26</b>	<b>560.36</b>
<i>UCOESTup471</i>	No homology	7.530	0.00022	<b>127.65</b>	<b>825.08</b>
<i>UCOESTup474</i>	No homology	7.510	0.00783	<b>31.26</b>	<b>126.79</b>
<i>UCOESTup476</i>	No homology	7.463	0.00043	<b>69.75</b>	<b>401.56</b>
<i>UCOESTup483</i>	No homology	7.370	0.00148	<b>43.40</b>	<b>243.07</b>
<i>UCOESTup484</i>	No homology	7.367	0.00922	<b>35.59</b>	<b>164.87</b>
<i>UCOESTup486</i>	No homology	7.337	0.00460	<b>55.43</b>	<b>299.60</b>
<i>UCOESTup490</i>	No homology	7.250	0.00787	<b>160.78</b>	<b>1214.63</b>
<i>UCOESTup493</i>	No homology	7.236	0.01310	<b>49.21</b>	<b>259.02</b>
<i>UCOESTup509</i>	No homology	6.923	0.00033	<b>276.70</b>	<b>1583.46</b>
<i>UCOESTup511</i>	No homology	6.861	0.03520	<b>294.20</b>	<b>1992.87</b>
<i>UCOESTup513</i>	No homology	6.842	0.02930	<b>14.11</b>	<b>49.25</b>
<i>UCOESTup521</i>	No homology	6.758	0.00399	<b>36.46</b>	<b>200.11</b>
<i>UCOESTup522</i>	No homology	6.740	0.00711	<b>18.50</b>	<b>57.91</b>
<i>UCOESTup523</i>	No homology	6.735	0.00049	<b>72.29</b>	<b>365.00</b>
<i>UCOESTup527</i>	No homology	6.697	0.00022	<b>111.24</b>	<b>619.17</b>
<i>UCOESTup530</i>	No homology	6.636	0.00045	<b>219.66</b>	<b>1235.06</b>
<i>UCOESTup531</i>	No homology	6.634	0.00090	<b>471.56</b>	<b>2.646.84</b>
<i>UCOESTup535</i>	No homology	6.619	0.00878	<b>127.49</b>	<b>682.62</b>
<i>UCOESTup536</i>	No homology	6.612	0.00306	<b>188.64</b>	<b>1257.36</b>
<i>UCOESTup538</i>	No homology	6.596	0.01820	<b>55.58</b>	<b>350.96</b>
<i>UCOESTup540</i>	No homology	6.554	0.02180	<b>13.74</b>	<b>53.12</b>
<i>UCOESTup541</i>	No homology	6.535	0.00160	<b>361.05</b>	<b>2336.03</b>
<i>UCOESTup542</i>	No homology	6.514	0.00561	<b>222.41</b>	<b>1461.15</b>
<i>UCOESTup554</i>	No homology	6.442	0.04100	<b>72.68</b>	<b>396.95</b>
<i>UCOESTup557</i>	No homology	6.386	0.00119	<b>251.18</b>	<b>1577.06</b>
<i>UCOESTup563</i>	No homology	6.324	0.00081	<b>106.52</b>	<b>673.93</b>
<i>UCOESTup564</i>	No homology	6.313	0.00090	<b>14.53</b>	<b>37.22</b>
<i>UCOESTup568</i>	No homology	6.303	0.00982	<b>16.99</b>	<b>40.97</b>

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<i>UCOESTup569</i>	No homology	6.297	0.01490	<b>46.68</b>	<b>180.72</b>
<i>UCOESTup570</i>	No homology	6.268	0.00034	<b>609.05</b>	<b>4007.93</b>
<i>UCOESTup571</i>	No homology	6.267	0.00235	<b>159.95</b>	<b>946.47</b>
<i>UCOESTup576</i>	No homology	6.248	0.00847	<b>17.56</b>	<b>60.74</b>
<i>UCOESTup581</i>	No homology	6.203	0.00060	<b>133.79</b>	<b>781.87</b>
<i>UCOESTup588</i>	No homology	6.156	0.00082	<b>318.84</b>	<b>1919.28</b>
<i>UCOESTup590</i>	No homology	6.132	0.04550	<b>17.61</b>	<b>51.08</b>
<i>UCOESTup594</i>	No homology	6.095	0.00111	<b>57.20</b>	<b>293.72</b>
<i>UCOESTup609</i>	No homology	5.957	0.00080	<b>146.03</b>	<b>748.15</b>
<i>UCOESTup614</i>	No homology	5.925	0.00059	<b>459.36</b>	<b>2819.79</b>
<i>UCOESTup620</i>	No homology	5.887	0.00860	<b>829.15</b>	<b>5342.41</b>
<i>UCOESTup621</i>	No homology	5.879	0.00529	<b>150.50</b>	<b>910.73</b>
<i>UCOESTup624</i>	No homology	5.857	0.03150	<b>25.76</b>	<b>89.71</b>
<i>UCOESTup626</i>	No homology	5.826	0.00254	<b>55.05</b>	<b>225.97</b>
<i>UCOESTup634</i>	No homology	5.797	0.00096	<b>52.49</b>	<b>240.14</b>
<i>UCOESTup639</i>	No homology	5.778	0.00198	<b>128.49</b>	<b>695.73</b>
<i>UCOESTup641</i>	No homology	5.732	0.00467	<b>67.56</b>	<b>311.85</b>
<i>UCOESTup644</i>	No homology	5.719	0.00062	<b>115.78</b>	<b>598.76</b>
<i>UCOESTup648</i>	No homology	5.655	0.00805	<b>35.20</b>	<b>122.49</b>
<i>UCOESTup651</i>	No homology	5.636	0.00760	<b>58.95</b>	<b>271.00</b>
<i>UCOESTup654</i>	No homology	5.623	0.02530	<b>18.62</b>	<b>67.55</b>
<i>UCOESTup658</i>	No homology	5.597	0.00085	<b>167.24</b>	<b>841.27</b>
<i>UCOESTup657</i>	No homology	5.597	0.00025	<b>309.12</b>	<b>1645.47</b>
<i>UCOESTup660</i>	No homology	5.570	0.00067	<b>150.85</b>	<b>779.13</b>
<i>UCOESTup666</i>	No homology	5.516	0.00739	<b>155.16</b>	<b>838.33</b>
<i>UCOESTup667</i>	No homology	5.490	0.00043	<b>33.68</b>	<b>125.56</b>
<i>UCOESTup669</i>	No homology	5.481	0.00548	<b>32.54</b>	<b>150.12</b>
<i>UCOESTup674</i>	No homology	5.451	0.00051	<b>127.47</b>	<b>661.14</b>
<i>UCOESTup676</i>	No homology	5.441	0.00035	<b>92.68</b>	<b>441.40</b>
<i>UCOESTup681</i>	No homology	5.423	0.01040	<b>25.93</b>	<b>79.24</b>
<i>UCOESTup682</i>	No homology	5.422	0.00030	<b>39.23</b>	<b>188.44</b>
<i>UCOESTup684</i>	No homology	5.383	0.00074	<b>1156.66</b>	<b>5911.06</b>
<i>UCOESTup685</i>	No homology	5.381	0.00230	<b>49.94</b>	<b>158.94</b>
<i>UCOESTup699</i>	No homology	5.317	0.00044	<b>208.76</b>	<b>1069.72</b>
<i>UCOESTup705</i>	No homology	5.267	0.02080	<b>28.24</b>	<b>91.22</b>
<i>UCOESTup710</i>	No homology	5.193	0.00032	<b>113.44</b>	<b>517.24</b>
<i>UCOESTup714</i>	No homology	5.171	0.01550	<b>41.16</b>	<b>180.65</b>
<i>UCOESTup717</i>	No homology	5.161	0.00609	<b>79.13</b>	<b>301.32</b>
<i>UCOESTup719</i>	No homology	5.156	0.00316	<b>388.27</b>	<b>2046.70</b>
<i>UCOESTup720</i>	No homology	5.152	0.00044	<b>770.76</b>	<b>3924.87</b>
<i>UCOESTup721</i>	No homology	5.152	0.01780	<b>21.02</b>	<b>49.69</b>
<i>UCOESTup725</i>	No homology	5.133	0.00298	<b>72.23</b>	<b>238.93</b>
<i>UCOESTup729</i>	No homology	5.090	0.00090	<b>211.19</b>	<b>1003.21</b>
<i>UCOESTup738</i>	No homology	5.057	0.01970	<b>26.85</b>	<b>86.59</b>
<i>UCOESTup743</i>	No homology	5.038	0.04860	<b>75.48</b>	<b>312.77</b>

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<i>UCOESTup744</i>	No homology	5.032	0.00184	<b>228.04</b>	<b>1096.89</b>
<i>UCOESTup747</i>	No homology	5.027	0.00044	<b>334.08</b>	<b>1631.60</b>
<i>UCOESTup748</i>	No homology	5.026	0.00067	<b>164.11</b>	<b>755.12</b>
<i>UCOESTup749</i>	No homology	5.022	0.00149	<b>98.93</b>	<b>419.13</b>
<i>UCOESTup751</i>	No homology	5.018	0.00161	<b>30.26</b>	<b>99.37</b>
<i>UCOESTup752</i>	No homology	5.016	0.02870	<b>20.54</b>	<b>61.99</b>
<i>UCOESTup753</i>	No homology	5.013	0.00198	<b>199.89</b>	<b>1043.77</b>
<i>UCOESTup756</i>	No homology	4.986	0.00825	<b>34.24</b>	<b>124.40</b>
<i>UCOESTup758</i>	No homology	4.971	0.04320	<b>15.17</b>	<b>43.88</b>
<i>UCOESTup759</i>	No homology	4.967	0.00052	<b>267.75</b>	<b>1255.13</b>
<i>UCOESTup771</i>	No homology	4.887	0.00301	<b>64.85</b>	<b>203.00</b>
<i>UCOESTup772</i>	No homology	4.886	0.00458	<b>32.36</b>	<b>105.74</b>
<i>UCOESTup781</i>	No homology	4.843	0.00068	<b>267.79</b>	<b>1211.41</b>
<i>UCOESTup801</i>	No homology	4.703	0.03060	<b>24.03</b>	<b>69.69</b>
<i>UCOESTup802</i>	No homology	4.702	0.00369	<b>187.74</b>	<b>907.84</b>
<i>UCOESTup805</i>	No homology	4.685	0.00037	<b>711.26</b>	<b>3101.11</b>
<i>UCOESTup821</i>	No homology	4.588	0.00640	<b>52.94</b>	<b>178.42</b>
<i>UCOESTup826</i>	No homology	4.558	0.00069	<b>256.35</b>	<b>1153.65</b>
<i>UCOESTup827</i>	No homology	4.554	0.00605	<b>70.16</b>	<b>281.33</b>
<i>UCOESTup828</i>	No homology	4.551	0.00943	<b>169.36</b>	<b>820.31</b>
<i>UCOESTup835</i>	No homology	4.532	0.00461	<b>224.86</b>	<b>1024.96</b>
<i>UCOESTup841</i>	No homology	4.510	0.04250	<b>77.42</b>	<b>373.29</b>
<i>UCOESTup852</i>	No homology	4.457	0.03150	<b>562.90</b>	<b>2923.34</b>
<i>UCOESTup862</i>	No homology	4.431	0.00559	<b>37.72</b>	<b>219.99</b>
<i>UCOESTup864</i>	No homology	4.419	0.01080	<b>130.07</b>	<b>562.83</b>
<i>UCOESTup869</i>	No homology	4.405	0.00511	<b>17.46</b>	<b>37.73</b>
<i>UCOESTup873</i>	No homology	4.379	0.01470	<b>68.21</b>	<b>284.65</b>
<i>UCOESTup883</i>	No homology	4.341	0.00160	<b>34.41</b>	<b>99.47</b>
<i>UCOESTup885</i>	No homology	4.335	0.00065	<b>830.05</b>	<b>3584.13</b>
<i>UCOESTup887</i>	No homology	4.328	0.03400	<b>40.08</b>	<b>134.29</b>
<i>UCOESTup900</i>	No homology	4.288	0.00040	<b>175.88</b>	<b>733.30</b>
<i>UCOESTup911</i>	No homology	4.251	0.00688	<b>20.86</b>	<b>48.62</b>
<i>UCOESTup912</i>	No homology	4.249	0.00107	<b>419.05</b>	<b>1824.46</b>
<i>UCOESTup919</i>	No homology	4.213	0.01630	<b>86.86</b>	<b>364.42</b>
<i>UCOESTup920</i>	No homology	4.207	0.00165	<b>921.18</b>	<b>3896.79</b>
<i>UCOESTup923</i>	No homology	4.199	0.00089	<b>189.74</b>	<b>723.12</b>
<i>UCOESTup931</i>	No homology	4.163	0.04780	<b>63.60</b>	<b>209.88</b>
<i>UCOESTup933</i>	No homology	4.158	0.00409	<b>41.19</b>	<b>131.90</b>
<i>UCOESTup937</i>	No homology	4.148	0.02050	<b>26.50</b>	<b>92.70</b>
<i>UCOESTup941</i>	No homology	4.136	0.00075	<b>476.77</b>	<b>1519.15</b>
<i>UCOESTup943</i>	No homology	4.125	0.01080	<b>225.40</b>	<b>958.81</b>
<i>UCOESTup945</i>	No homology	4.124	0.00052	<b>275.32</b>	<b>1090.41</b>
<i>UCOESTup946</i>	No homology	4.122	0.00051	<b>2373.82</b>	<b>8895.02</b>
<i>UCOESTup955</i>	No homology	4.088	0.00199	<b>42.76</b>	<b>124.23</b>
<i>UCOESTup961</i>	No homology	4.056	0.00179	<b>49.42</b>	<b>174.63</b>

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<i>UCOESTup966</i>	No homology	4.035	0.00954	<b>90.63</b>	<b>359.48</b>
<i>UCOESTup972</i>	No homology	4.009	0.00052	<b>372.12</b>	<b>1357.47</b>
<i>UCOESTup982</i>	No homology	3.984	0.01260	<b>22.64</b>	<b>52.12</b>
<i>UCOESTup983</i>	No homology	3.984	0.03250	<b>39.97</b>	<b>105.12</b>
<i>UCOESTup986</i>	No homology	3.97	0.00413	<b>49.80</b>	<b>158.26</b>
<i>UCOESTup991</i>	No homology	3.952	0.00661	<b>32.08</b>	<b>88.71</b>
<i>UCOESTup995</i>	No homology	3.942	0.00071	<b>234.46</b>	<b>868.15</b>
<i>UCOESTup998</i>	No homology	3.939	0.00505	<b>14.38</b>	<b>29.06</b>
<i>UCOESTup999</i>	No homology	3.937	0.00719	<b>70.00</b>	<b>198.72</b>
<i>UCOESTup1001</i>	No homology	3.921	0.00141	<b>157.13</b>	<b>636.69</b>
<i>UCOESTup1009</i>	No homology	3.904	0.00131	<b>476.77</b>	<b>1519.15</b>
<i>UCOESTup1010</i>	No homology	3.900	0.00043	<b>662.99</b>	<b>2570.55</b>
<i>UCOESTup1011</i>	No homology	3.899	0.00187	<b>304.78</b>	<b>1115.02</b>
<i>UCOESTup1019</i>	No homology	3.871	0.00111	<b>334.69</b>	<b>1071.61</b>
<i>UCOESTup1023</i>	No homology	3.866	0.01150	<b>40.50</b>	<b>116.57</b>
<i>UCOESTup1024</i>	No homology	3.863	0.03130	<b>129.02</b>	<b>477.01</b>
<i>UCOESTup1030</i>	No homology	3.852	0.03170	<b>27.74</b>	<b>68.58</b>
<i>UCOESTup1031</i>	No homology	3.851	0.02080	<b>21.34</b>	<b>43.77</b>
<i>UCOESTup1032</i>	No homology	3.850	0.00058	<b>173.11</b>	<b>603.02</b>
<i>UCOESTup1033</i>	No homology	3.843	0.00867	<b>100.16</b>	<b>375.41</b>
<i>UCOESTup1035</i>	No homology	3.841	0.00057	<b>101.02</b>	<b>351.40</b>
<i>UCOESTup1037</i>	No homology	3.838	0.00119	<b>183.43</b>	<b>651.72</b>
<i>UCOESTup1038</i>	No homology	3.837	0.00178	<b>239.66</b>	<b>536.28</b>
<i>UCOESTup1039</i>	No homology	3.833	0.00732	<b>44.18</b>	<b>123.01</b>
<i>UCOESTup1040</i>	No homology	3.832	0.01250	<b>67.49</b>	<b>218.99</b>
<i>UCOESTup1041</i>	No homology	3.825	0.00126	<b>1109.84</b>	<b>4137.63</b>
<i>UCOESTup1042</i>	No homology	3.821	0.00659	<b>295.40</b>	<b>1017.91</b>
<i>UCOESTup1044</i>	No homology	3.810	0.00321	<b>573.76</b>	<b>2098.10</b>
<i>UCOESTup1045</i>	No homology	3.802	0.04940	<b>55.24</b>	<b>198.12</b>
<i>UCOESTup1048</i>	No homology	3.79	0.03720	<b>52.12</b>	<b>138.91</b>
<i>UCOESTup1049</i>	No homology	3.787	0.00954	<b>197.55</b>	<b>743.99</b>
<i>UCOESTup1052</i>	No homology	3.777	0.01650	<b>18.53</b>	<b>34.53</b>
<i>UCOESTup1053</i>	No homology	3.769	0.00087	<b>123.64</b>	<b>426.66</b>
<i>UCOESTup1057</i>	No homology	3.761	0.03680	<b>53.82</b>	<b>161.47</b>
<i>UCOESTup1058</i>	No homology	3.758	0.00396	<b>194.17</b>	<b>786.47</b>
<i>UCOESTup1059</i>	No homology	3.757	0.00960	<b>65.83</b>	<b>208.76</b>
<i>UCOESTup1066</i>	No homology	3.737	0.00102	<b>466.41</b>	<b>1696.92</b>
<i>UCOESTup1069</i>	No homology	3.726	0.00216	<b>120.33</b>	<b>418.39</b>
<i>UCOESTup1072</i>	No homology	3.72	0.00052	<b>491.00</b>	<b>1846.69</b>
<i>UCOESTup1075</i>	No homology	3.705	0.00311	<b>427.07</b>	<b>1583.48</b>
<i>UCOESTup1079</i>	No homology	3.686	0.03560	<b>590.65</b>	<b>1953.44</b>
<i>UCOESTup1081</i>	No homology	3.678	0.00246	<b>641.85</b>	<b>2368.91</b>
<i>UCOESTup1085</i>	No homology	3.67	0.01890	<b>14.44</b>	<b>25.13</b>
<i>UCOESTup1088</i>	No homology	3.665	0.02300	<b>16.47</b>	<b>35.39</b>
<i>UCOESTup1091</i>	No homology	3.658	0.04300	<b>45.27</b>	<b>117.35</b>

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<i>UCOESTup1101</i>	No homology	3.625	0.01900	<b>35.91</b>	<b>98.47</b>
<i>UCOESTup1106</i>	No homology	3.609	0.00109	<b>134.60</b>	<b>429.29</b>
<i>UCOESTup1109</i>	No homology	3.603	0.03250	<b>62.38</b>	<b>246.38</b>
<i>UCOESTup1111</i>	No homology	3.596	0.02550	<b>65.49</b>	<b>216.88</b>
<i>UCOESTup1112</i>	No homology	3.595	0.00225	<b>310.40</b>	<b>693.76</b>
<i>UCOESTup1113</i>	No homology	3.593	0.00343	<b>1095.63</b>	<b>4041.87</b>
<i>UCOESTup1114</i>	No homology	3.589	0.01990	<b>116.69</b>	<b>375.03</b>
<i>UCOESTup1115</i>	No homology	3.583	0.00869	<b>17.84</b>	<b>35.94</b>
<i>UCOESTup1116</i>	No homology	3.582	0.00732	<b>954.38</b>	<b>2271.80</b>
<i>UCOESTup1123</i>	No homology	3.571	0.00138	<b>28.67</b>	<b>55.73</b>
<i>UCOESTup1126</i>	No homology	3.564	0.01110	<b>42.79</b>	<b>109.94</b>
<i>UCOESTup1127</i>	No homology	3.560	0.00766	<b>406.95</b>	<b>1471.25</b>
<i>UCOESTup1128</i>	No homology	3.556	0.00691	<b>63.79</b>	<b>175.76</b>
<i>UCOESTup1133</i>	No homology	3.547	0.00077	<b>124.33</b>	<b>401.94</b>
<i>UCOESTup1143</i>	No homology	3.538	0.00140	<b>277.14</b>	<b>915.20</b>
<i>UCOESTup1148</i>	No homology	3.528	0.01110	<b>39.53</b>	<b>97.95</b>
<i>UCOESTup1150</i>	No homology	3.521	0.00061	<b>1591.53</b>	<b>5588.89</b>
<i>UCOESTup1152</i>	No homology	3.516	0.00145	<b>640.49</b>	<b>2166.98</b>
<i>UCOESTup1153</i>	No homology	3.516	0.01430	<b>44.81</b>	<b>117.48</b>
<i>UCOESTup1154</i>	No homology	3.515	0.01020	<b>47.77</b>	<b>143.48</b>
<i>UCOESTup1158</i>	No homology	3.502	0.03430	<b>207.57</b>	<b>798.65</b>
<i>UCOESTup1157</i>	No homology	3.502	0.00243	<b>78.97</b>	<b>231.18</b>
<i>UCOESTup1160</i>	No homology	3.497	0.01100	<b>19.84</b>	<b>33.84</b>
<i>UCOESTup1165</i>	No homology	3.488	0.00060	<b>599.25</b>	<b>2093.51</b>
<i>UCOESTup1166</i>	No homology	3.488	0.01900	<b>193.46</b>	<b>624.96</b>
<i>UCOESTup1169</i>	No homology	3.484	0.00066	<b>167.37</b>	<b>580.07</b>
<i>UCOESTup1170</i>	No homology	3.478	0.00539	<b>163.68</b>	<b>548.74</b>
<i>UCOESTup1171</i>	No homology	3.477	0.01510	<b>38.43</b>	<b>78.20</b>
<i>UCOESTup1173</i>	No homology	3.469	0.00424	<b>233.94</b>	<b>784.70</b>
<i>UCOESTup1176</i>	No homology	3.457	0.00065	<b>177.31</b>	<b>587.28</b>
<i>UCOESTup1177</i>	No homology	3.455	0.00057	<b>246.77</b>	<b>852.28</b>
<i>UCOESTup1178</i>	No homology	3.455	0.01450	<b>60.07</b>	<b>182.29</b>
<i>UCOESTup1180</i>	No homology	3.453	0.02490	<b>343.47</b>	<b>1252.34</b>
<i>UCOESTup1179</i>	No homology	3.453	0.00564	<b>93.16</b>	<b>306.07</b>
<i>UCOESTup1181</i>	No homology	3.452	0.00485	<b>214.03</b>	<b>708.35</b>
<i>UCOESTup1186</i>	No homology	3.441	0.01550	<b>1771.65</b>	<b>6324.36</b>
<i>UCOESTup1187</i>	No homology	3.439	0.00062	<b>537.25</b>	<b>1802.30</b>
<i>UCOESTup1192</i>	No homology	3.429	0.02690	<b>39.91</b>	<b>90.41</b>
<i>UCOESTup1195</i>	No homology	3.423	0.00833	<b>16.51</b>	<b>28.44</b>
<i>UCOESTup1199</i>	No homology	3.417	0.00117	<b>372.29</b>	<b>943.29</b>
<i>UCOESTup1202</i>	No homology	3.413	0.02050	<b>99.40</b>	<b>285.50</b>
<i>UCOESTup1203</i>	No homology	3.411	0.00647	<b>32.27</b>	<b>94.34</b>
<i>UCOESTup1207</i>	No homology	3.393	0.00190	<b>164.98</b>	<b>514.04</b>
<i>UCOESTup1208</i>	No homology	3.393	0.00208	<b>548.77</b>	<b>1938.28</b>
<i>UCOESTup1215</i>	No homology	3.377	0.02540	<b>129.56</b>	<b>413.82</b>

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<i>UCOESTup1221</i>	No homology	3.360	0.00960	<b>19.31</b>	<b>46.58</b>
<i>UCOESTup1225</i>	No homology	3.349	0.00215	<b>319.32</b>	<b>1045.10</b>
<i>UCOESTup1228</i>	No homology	3.342	0.01970	<b>55.50</b>	<b>143.82</b>
<i>UCOESTup1231</i>	No homology	3.332	0.02970	<b>110.54</b>	<b>275.11</b>
<i>UCOESTup1232</i>	No homology	3.330	0.03870	<b>620.80</b>	<b>2288.95</b>
<i>UCOESTup1233</i>	No homology	3.322	0.00262	<b>3731.27</b>	<b>12626.72</b>
<i>UCOESTup1236</i>	No homology	3.320	0.04120	<b>27.04</b>	<b>66.07</b>
<i>UCOESTup1242</i>	No homology	3.302	0.00075	<b>346.49</b>	<b>1065.34</b>
<i>UCOESTup1245</i>	No homology	3.290	0.01210	<b>253.70</b>	<b>782.53</b>
<i>UCOESTup1247</i>	No homology	3.288	0.00711	<b>168.03</b>	<b>514.01</b>
<i>UCOESTup1250</i>	No homology	3.277	0.00378	<b>1191.02</b>	<b>3899.85</b>
<i>UCOESTup1256</i>	No homology	3.269	0.00926	<b>2042.54</b>	<b>6878.64</b>
<i>UCOESTup1258</i>	No homology	3.262	0.00148	<b>1462.44</b>	<b>4703.81</b>
<i>UCOESTup1261</i>	No homology	3.255	0.02830	<b>56.62</b>	<b>159.81</b>
<i>UCOESTup1262</i>	No homology	3.246	0.00063	<b>1386.93</b>	<b>4262.04</b>
<i>UCOESTup1264</i>	No homology	3.245	0.01300	<b>209.08</b>	<b>761.38</b>
<i>UCOESTup1271</i>	No homology	3.220	0.00594	<b>42.81</b>	<b>104.84</b>
<i>UCOESTup1272</i>	No homology	3.220	0.01930	<b>501.34</b>	<b>1684.51</b>
<i>UCOESTup1277</i>	No homology	3.203	0.03990	<b>52.92</b>	<b>115.57</b>
<i>UCOESTup1278</i>	No homology	3.202	0.01030	<b>44.86</b>	<b>102.00</b>
<i>UCOESTup1282</i>	No homology	3.198	0.00815	<b>108.24</b>	<b>360.53</b>
<i>UCOESTup1284</i>	No homology	3.196	0.00074	<b>913.23</b>	<b>2885.11</b>
<i>UCOESTup1286</i>	No homology	3.191	0.00110	<b>1226.22</b>	<b>3836.44</b>
<i>UCOESTup1287</i>	No homology	3.183	0.00419	<b>161.50</b>	<b>473.49</b>
<i>UCOESTup1290</i>	No homology	3.180	0.02630	<b>45.64</b>	<b>119.29</b>
<i>UCOESTup1295</i>	No homology	3.165	0.04070	<b>376.12</b>	<b>1348.05</b>
<i>UCOESTup1297</i>	No homology	3.162	0.00813	<b>790.18</b>	<b>2532.87</b>
<i>UCOESTup1298</i>	No homology	3.159	0.01120	<b>54.10</b>	<b>141.79</b>
<i>UCOESTup1305</i>	No homology	3.148	0.00217	<b>13.48</b>	<b>25.69</b>
<i>UCOESTup1306</i>	No homology	3.147	0.01200	<b>52.10</b>	<b>133.50</b>
<i>UCOESTup1307</i>	No homology	3.146	0.00291	<b>3875.82</b>	<b>11735.92</b>
<i>UCOESTup1311</i>	No homology	3.142	0.01120	<b>62.68</b>	<b>141.11</b>
<i>UCOESTup1312</i>	No homology	3.139	0.02140	<b>16.45</b>	<b>28.03</b>
<i>UCOESTup1314</i>	No homology	3.137	0.02200	<b>4920.57</b>	<b>16367.55</b>
<i>UCOESTup1315</i>	No homology	3.133	0.03690	<b>20.76</b>	<b>44.63</b>
<i>UCOESTup1317</i>	No homology	3.127	0.00646	<b>106.19</b>	<b>275.60</b>
<i>UCOESTup1318</i>	No homology	3.123	0.03110	<b>267.07</b>	<b>826.41</b>
<i>UCOESTup1323</i>	No homology	3.108	0.01690	<b>36.61</b>	<b>96.23</b>
<i>UCOESTup1327</i>	No homology	3.104	0.00980	<b>267.07</b>	<b>826.41</b>
<i>UCOESTup1328</i>	No homology	3.096	0.00399	<b>79.22</b>	<b>191.62</b>
<i>UCOESTup1336</i>	No homology	3.085	0.00593	<b>13.23</b>	<b>24.36</b>
<i>UCOESTup1341</i>	No homology	3.080	0.01250	<b>116.97</b>	<b>335.26</b>
<i>UCOESTup1347</i>	No homology	3.064	0.02180	<b>45.52</b>	<b>100.97</b>
<i>UCOESTup1348</i>	No homology	3.063	0.00091	<b>504.58</b>	<b>1512.79</b>
<i>UCOESTup1350</i>	No homology	3.059	0.00980	<b>78.54</b>	<b>241.96</b>

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<i>UCOESTup1353</i>	No homology	3.056	0.02810	<b>51.76</b>	<b>107.00</b>
<i>UCOESTup1352</i>	No homology	3.056	0.00108	<b>1419.62</b>	<b>4315.81</b>
<i>UCOESTup1359</i>	No homology	3.052	0.02380	<b>24.05</b>	<b>53.03</b>
<i>UCOESTup1360</i>	No homology	3.043	0.00282	<b>549.41</b>	<b>1500.14</b>
<i>UCOESTup1361</i>	No homology	3.043	0.00809	<b>172.82</b>	<b>496.37</b>
<i>UCOESTup1366</i>	No homology	3.034	0.00826	<b>81.93</b>	<b>193.10</b>
<i>UCOESTup1365</i>	No homology	3.034	0.00529	<b>112.73</b>	<b>256.18</b>
<i>UCOESTup1370</i>	No homology	3.029	0.00933	<b>34.24</b>	<b>77.73</b>
<i>UCOESTup1371</i>	No homology	3.029	0.01200	<b>63.38</b>	<b>114.24</b>
<i>UCOESTup1372</i>	No homology	3.026	0.00280	<b>1421.02</b>	<b>3671.36</b>
<i>UCOESTup1373</i>	No homology	3.023	0.02250	<b>15.40</b>	<b>26.32</b>
<i>UCOESTup1376</i>	No homology	3.021	0.00432	<b>323.05</b>	<b>944.89</b>
<i>UCOESTup1382</i>	No homology	3.013	0.04290	<b>145.51</b>	<b>327.08</b>
<i>UCOESTup1384</i>	No homology	3.007	0.01190	<b>39.17</b>	<b>94.23</b>
<i>UCOESTup1385</i>	No homology	3.006	0.00732	<b>228.92</b>	<b>606.53</b>
<i>UCOESTup1390</i>	No homology	2.998	0.00792	<b>86.51</b>	<b>211.06</b>
<i>UCOESTup1392</i>	No homology	2.996	0.00087	<b>1478.41</b>	<b>4023.87</b>
<i>UCOESTup1394</i>	No homology	2.995	0.00270	<b>132.37</b>	<b>368.02</b>
<i>UCOESTup1403</i>	No homology	2.983	0.03960	<b>34.92</b>	<b>105.55</b>
<i>UCOESTup1406</i>	No homology	2.975	0.00136	<b>1228.66</b>	<b>3505.36</b>
<i>UCOESTup1407</i>	No homology	2.975	0.00440	<b>1145.58</b>	<b>3729.79</b>
<i>UCOESTup1408</i>	No homology	2.974	0.01220	<b>332.93</b>	<b>974.37</b>
<i>UCOESTup1409</i>	No homology	2.973	0.00073	<b>828.55</b>	<b>2352.17</b>
<i>UCOESTup1410</i>	No homology	2.973	0.00812	<b>43.22</b>	<b>104.39</b>
<i>UCOESTup1411</i>	No homology	2.972	0.00318	<b>219.92</b>	<b>665.89</b>
<i>UCOESTup1412</i>	No homology	2.970	0.00334	<b>150.20</b>	<b>431.62</b>
<i>UCOESTup1413</i>	No homology	2.970	0.00659	<b>931.66</b>	<b>2469.00</b>
<i>UCOESTup1415</i>	No homology	2.969	0.00272	<b>348.67</b>	<b>924.51</b>
<i>UCOESTup1417</i>	No homology	2.968	0.00076	<b>722.42</b>	<b>2111.01</b>
<i>UCOESTup1419</i>	No homology	2.950	0.01270	<b>357.49</b>	<b>1028.10</b>
<i>UCOESTup1420</i>	No homology	2.950	0.02690	<b>34.57</b>	<b>67.35</b>
<i>UCOESTup1424</i>	No homology	2.947	0.04180	<b>18.82</b>	<b>33.00</b>
<i>UCOESTup1423</i>	No homology	2.947	0.00686	<b>1438.78</b>	<b>4219.76</b>
<i>UCOESTup1422</i>	No homology	2.947	0.00686	<b>590.26</b>	<b>1779.18</b>
<i>UCOESTup1427</i>	No homology	2.94	0.00081	<b>2628.44</b>	<b>7258.60</b>
<i>UCOESTup1429</i>	No homology	2.938	0.00628	<b>1351.61</b>	<b>4474.49</b>
<i>UCOESTup1437</i>	No homology	2.917	0.00370	<b>111.37</b>	<b>287.37</b>
<i>UCOESTup1440</i>	No homology	2.916	0.00833	<b>17.45</b>	<b>29.22</b>
<i>UCOESTup1442</i>	No homology	2.914	0.02570	<b>18.59</b>	<b>27.67</b>
<i>UCOESTup1444</i>	No homology	2.905	0.00785	<b>52.23</b>	<b>131.04</b>
<i>UCOESTup1445</i>	No homology	2.904	0.00454	<b>996.62</b>	<b>2888.85</b>
<i>UCOESTup1447</i>	No homology	2.903	0.00122	<b>693.46</b>	<b>1970.84</b>
<i>UCOESTup1448</i>	No homology	2.903	0.00752	<b>870.01</b>	<b>2506.18</b>
<i>UCOESTup1450</i>	No homology	2.897	0.00501	<b>139.22</b>	<b>311.32</b>
<i>UCOESTup1452</i>	No homology	2.895	0.00135	<b>274.63</b>	<b>782.69</b>

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<i>UCOESTup1454</i>	No homology	2.894	0.00442	<b>37.92</b>	<b>85.02</b>
<i>UCOESTup1467</i>	No homology	2.874	0.00118	<b>275.97</b>	<b>774.92</b>
<i>UCOESTup1471</i>	No homology	2.868	0.01020	<b>1378.77</b>	<b>4347.86</b>
<i>UCOESTup1472</i>	No homology	2.865	0.01040	<b>24.62</b>	<b>48.86</b>
<i>UCOESTup1473</i>	No homology	2.864	0.01690	<b>166.34</b>	<b>429.75</b>
<i>UCOESTup1475</i>	No homology	2.862	0.00452	<b>41.07</b>	<b>98.93</b>
<i>UCOESTup1476</i>	No homology	2.860	0.00079	<b>3143.63</b>	<b>9143.28</b>
<i>UCOESTup1479</i>	No homology	2.858	0.00082	<b>1287.31</b>	<b>3824.01</b>
<i>UCOESTup1484</i>	No homology	2.851	0.01740	<b>188.93</b>	<b>405.56</b>
<i>UCOESTup1485</i>	No homology	2.851	0.02580	<b>22.74</b>	<b>40.00</b>
<i>UCOESTup1486</i>	No homology	2.847	0.00228	<b>435.14</b>	<b>1147.58</b>
<i>UCOESTup1487</i>	No homology	2.846	0.00365	<b>18.26</b>	<b>97.07</b>
<i>UCOESTup1489</i>	No homology	2.845	0.02170	<b>220.24</b>	<b>673.19</b>
<i>UCOESTup1490</i>	No homology	2.844	0.03350	<b>758.59</b>	<b>2257.02</b>
<i>UCOESTup1494</i>	No homology	2.837	0.00096	<b>1933.34</b>	<b>4959.51</b>
<i>UCOESTup1496</i>	No homology	2.836	0.00216	<b>1300.86</b>	<b>4182.99</b>
<i>UCOESTup1500</i>	No homology	2.830	0.03430	<b>46.38</b>	<b>116.00</b>
<i>UCOESTup1501</i>	No homology	2.828	0.00097	<b>7086.90</b>	<b>20892.26</b>
<i>UCOESTup1505</i>	No homology	2.819	0.00218	<b>340.26</b>	<b>920.99</b>
<i>UCOESTup1506</i>	No homology	2.818	0.02660	<b>15.20</b>	<b>24.46</b>
<i>UCOESTup1510</i>	No homology	2.814	0.04330	<b>22.06</b>	<b>39.00</b>
<i>UCOESTup1511</i>	No homology	2.812	0.03280	<b>37.74</b>	<b>80.87</b>
<i>UCOESTup1513</i>	No homology	2.810	0.02170	<b>123.04</b>	<b>257.68</b>
<i>UCOESTup1514</i>	No homology	2.809	0.03120	<b>452.92</b>	<b>1381.76</b>
<i>UCOESTup1516</i>	No homology	2.806	0.00167	<b>421.33</b>	<b>1148.95</b>
<i>UCOESTup1517</i>	No homology	2.805	0.00494	<b>15.70</b>	<b>27.36</b>
<i>UCOESTup1518</i>	No homology	2.802	0.00467	<b>34.05</b>	<b>71.91</b>
<i>UCOESTup1521</i>	No homology	2.799	0.00747	<b>594.33</b>	<b>1671.53</b>
<i>UCOESTup1522</i>	No homology	2.798	0.00143	<b>4425.73</b>	<b>12402.55</b>
<i>UCOESTup1525</i>	No homology	2.791	0.00454	<b>149.46</b>	<b>413.74</b>
<i>UCOESTup1528</i>	No homology	2.785	0.00119	<b>682.46</b>	<b>1921.53</b>
<i>UCOESTup1529</i>	No homology	2.785	0.00193	<b>1703.10</b>	<b>4826.51</b>
<i>UCOESTup1536</i>	No homology	2.781	0.00190	<b>15.64</b>	<b>26.02</b>
<i>UCOESTup1537</i>	No homology	2.780	0.01260	<b>66.24</b>	<b>151.01</b>
<i>UCOESTup1538</i>	No homology	2.779	0.00564	<b>139.01</b>	<b>361.14</b>
<i>UCOESTup1539</i>	No homology	2.777	0.00130	<b>4071.96</b>	<b>11072.67</b>
<i>UCOESTup1540</i>	No homology	2.776	0.00924	<b>65.68</b>	<b>151.45</b>
<i>UCOESTup1541</i>	No homology	2.773	0.00240	<b>1030.38</b>	<b>2811.60</b>
<i>UCOESTup1545</i>	No homology	2.769	0.00787	<b>1582.90</b>	<b>4334.98</b>
<i>UCOESTup1547</i>	No homology	2.768	0.03010	<b>89.38</b>	<b>229.49</b>
<i>UCOESTup1548</i>	No homology	2.767	0.02080	<b>1535.35</b>	<b>4485.50</b>
<i>UCOESTup1550</i>	No homology	2.765	0.00969	<b>214.52</b>	<b>606.61</b>
<i>UCOESTup1551</i>	No homology	2.764	0.01200	<b>125.57</b>	<b>320.64</b>
<i>UCOESTup1552</i>	No homology	2.764	0.03580	<b>21.55</b>	<b>42.45</b>
<i>UCOESTup1554</i>	No homology	2.763	0.01970	<b>141.36</b>	<b>364.73</b>

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<i>UCOESTup1555</i>	No homology	2.763	0.04960	<b>227.41</b>	<b>672.57</b>
<i>UCOESTup1557</i>	No homology	2.761	0.02370	<b>11.50</b>	<b>20.29</b>
<i>UCOESTup1558</i>	No homology	2.760	0.00163	<b>1332.70</b>	<b>3626.46</b>
<i>UCOESTup1561</i>	No homology	2.755	0.04360	<b>1310.60</b>	<b>3697.84</b>
<i>UCOESTup1564</i>	No homology	2.75	0.03060	<b>152.00</b>	<b>412.35</b>
<i>UCOESTup1567</i>	No homology	2.748	0.02900	<b>67.04</b>	<b>110.54</b>
<i>UCOESTup1572</i>	No homology	2.746	0.01040	<b>226.07</b>	<b>504.72</b>
<i>UCOESTup1575</i>	No homology	2.745	0.02740	<b>21.99</b>	<b>46.07</b>
<i>UCOESTup1577</i>	No homology	2.743	0.02630	<b>21.04</b>	<b>40.51</b>
<i>UCOESTup1578</i>	No homology	2.742	0.04260	<b>48.89</b>	<b>104.76</b>
<i>UCOESTup1580</i>	No homology	2.739	0.00269	<b>21.47</b>	<b>45.93</b>
<i>UCOESTup1586</i>	No homology	2.731	0.04080	<b>278.95</b>	<b>800.72</b>
<i>UCOESTup1590</i>	No homology	2.727	0.03080	<b>125.88</b>	<b>351.79</b>
<i>UCOESTup1595</i>	No homology	2.718	0.00355	<b>212.99</b>	<b>568.44</b>
<i>UCOESTup1596</i>	No homology	2.717	0.01130	<b>39.94</b>	<b>97.57</b>
<i>UCOESTup1598</i>	No homology	2.714	0.02610	<b>13.09</b>	<b>21.03</b>
<i>UCOESTup1601</i>	No homology	2.710	0.00567	<b>2170.36</b>	<b>5903.39</b>
<i>UCOESTup1602</i>	No homology	2.709	0.01390	<b>17.10</b>	<b>29.98</b>
<i>UCOESTup1617</i>	No homology	2.697	0.02540	<b>325.00</b>	<b>901.31</b>
<i>UCOESTup1622</i>	No homology	2.688	0.00712	<b>130.86</b>	<b>283.65</b>
<i>UCOESTup1627</i>	No homology	2.682	0.00133	<b>169.82</b>	<b>433.42</b>
<i>UCOESTup1629</i>	No homology	2.681	0.01070	<b>24.03</b>	<b>45.39</b>
<i>UCOESTup1630</i>	No homology	2.677	0.01010	<b>2802.45</b>	<b>6968.29</b>
<i>UCOESTup1637</i>	No homology	2.671	0.04480	<b>21.06</b>	<b>41.57</b>
<i>UCOESTup1639</i>	No homology	2.669	0.00271	<b>693.68</b>	<b>2018.21</b>
<i>UCOESTup1640</i>	No homology	2.669	0.03110	<b>749.82</b>	<b>2009.89</b>
<i>UCOESTup1638</i>	No homology	2.669	0.00130	<b>1143.58</b>	<b>2812.49</b>
<i>UCOESTup1642</i>	No homology	2.666	0.00350	<b>307.18</b>	<b>796.59</b>
<i>UCOESTup1644</i>	No homology	2.663	0.00458	<b>20.29</b>	<b>37.60</b>
<i>UCOESTup1645</i>	No homology	2.66	0.03700	<b>99.22</b>	<b>239.67</b>
<i>UCOESTup1646</i>	No homology	2.658	0.04950	<b>126.86</b>	<b>380.98</b>
<i>UCOESTup1648</i>	No homology	2.655	0.01460	<b>162.82</b>	<b>364.56</b>
<i>UCOESTup1656</i>	No homology	2.640	0.00699	<b>610.71</b>	<b>1630.37</b>
<i>UCOESTup1657</i>	No homology	2.639	0.00191	<b>3362.78</b>	<b>8517.05</b>
<i>UCOESTup1661</i>	No homology	2.633	0.02920	<b>29.93</b>	<b>64.79</b>
<i>UCOESTup1664</i>	No homology	2.631	0.03010	<b>70.14</b>	<b>175.19</b>
<i>UCOESTup1668</i>	No homology	2.625	0.00784	<b>29.33</b>	<b>73.33</b>
<i>UCOESTup1672</i>	No homology	2.620	0.00628	<b>286.16</b>	<b>742.48</b>
<i>UCOESTup1677</i>	No homology	2.615	0.03880	<b>269.73</b>	<b>731.85</b>
<i>UCOESTup1680</i>	No homology	2.609	0.00415	<b>142.24</b>	<b>360.29</b>
<i>UCOESTup1681</i>	No homology	2.608	0.03500	<b>14.25</b>	<b>23.16</b>
<i>UCOESTup1684</i>	No homology	2.605	0.00176	<b>203.81</b>	<b>522.89</b>
<i>UCOESTup1689</i>	No homology	2.601	0.00594	<b>2176.06</b>	<b>5809.40</b>
<i>UCOESTup1692</i>	No homology	2.594	0.02540	<b>18.53</b>	<b>31.48</b>
<i>UCOESTup1694</i>	No homology	2.592	0.01730	<b>91.26</b>	<b>224.22</b>

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<i>UCOESTup1693</i>	No homology	2.592	0.00777	<b>274.68</b>	<b>708.72</b>
<i>UCOESTup1696</i>	No homology	2.589	0.01890	<b>36.22</b>	<b>61.29</b>
<i>UCOESTup1697</i>	No homology	2.585	0.00116	<b>1490.64</b>	<b>3765.17</b>
<i>UCOESTup1702</i>	No homology	2.583	0.00706	<b>99.59</b>	<b>251.48</b>
<i>UCOESTup1705</i>	No homology	2.582	0.01150	<b>280.34</b>	<b>666.35</b>
<i>UCOESTup1703</i>	No homology	2.582	0.00112	<b>166.25</b>	<b>409.36</b>
<i>UCOESTup1708</i>	No homology	2.577	0.02200	<b>2731.84</b>	<b>762.72</b>
<i>UCOESTup1709</i>	No homology	2.576	0.01880	<b>59.53</b>	<b>110.29</b>
<i>UCOESTup1711</i>	No homology	2.574	0.00183	<b>568.87</b>	<b>1456.97</b>
<i>UCOESTup1712</i>	No homology	2.574	0.01960	<b>71.67</b>	<b>162.39</b>
<i>UCOESTup1716</i>	No homology	2.570	0.03150	<b>31.20</b>	<b>62.97</b>
<i>UCOESTup1718</i>	No homology	2.569	0.02590	<b>1038.73</b>	<b>2370.64</b>
<i>UCOESTup1720</i>	No homology	2.566	0.00282	<b>1618.32</b>	<b>4114.39</b>
<i>UCOESTup1733</i>	No homology	2.551	0.00732	<b>490.28</b>	<b>1354.65</b>
<i>UCOESTup1734</i>	No homology	2.550	0.02190	<b>658.05</b>	<b>1719.68</b>
<i>UCOESTup1735</i>	No homology	2.549	0.02520	<b>325.49</b>	<b>899.34</b>
<i>UCOESTup1736</i>	No homology	2.549	0.04330	<b>232.74</b>	<b>626.53</b>
<i>UCOESTup1738</i>	No homology	2.547	0.01700	<b>54.51</b>	<b>113.99</b>
<i>UCOESTup1743</i>	No homology	2.545	0.04180	<b>33.40</b>	<b>37.84</b>
<i>UCOESTup1746</i>	No homology	2.541	0.03270	<b>9.78</b>	<b>16.26</b>
<i>UCOESTup1748</i>	No homology	2.540	0.03340	<b>114.33</b>	<b>263.53</b>
<i>UCOESTup1750</i>	No homology	2.539	0.03100	<b>147.55</b>	<b>337.32</b>
<i>UCOESTup1756</i>	No homology	2.537	0.01070	<b>13.61</b>	<b>23.41</b>
<i>UCOESTup1759</i>	No homology	2.535	0.01150	<b>95.72</b>	<b>210.85</b>
<i>UCOESTup1764</i>	No homology	2.530	0.02530	<b>252.40</b>	<b>644.33</b>
<i>UCOESTup1765</i>	No homology	2.530	0.03030	<b>70.08</b>	<b>186.01</b>
<i>UCOESTup1767</i>	No homology	2.529	0.00272	<b>607.04</b>	<b>1637.71</b>
<i>UCOESTup1768</i>	No homology	2.528	0.03900	<b>102.76</b>	<b>277.57</b>
<i>UCOESTup1770</i>	No homology	2.527	0.02490	<b>255.81</b>	<b>681.58</b>
<i>UCOESTup1773</i>	No homology	2.524	0.02180	<b>175.18</b>	<b>451.67</b>
<i>UCOESTup1777</i>	No homology	2.521	0.01190	<b>78.71</b>	<b>176.53</b>
<i>UCOESTup1778</i>	No homology	2.521	0.01730	<b>685.16</b>	<b>1811.19</b>
<i>UCOESTup1786</i>	No homology	2.508	0.01120	<b>1324.16</b>	<b>3342.12</b>
<i>UCOESTup1787</i>	No homology	2.507	0.03800	<b>65.43</b>	<b>156.78</b>
<i>UCOESTup1790</i>	No homology	2.505	0.00162	<b>604.68</b>	<b>1667.24</b>
<i>UCOESTup1791</i>	No homology	2.504	0.00244	<b>829.80</b>	<b>2009.49</b>
<i>UCOESTup1792</i>	No homology	2.504	0.03710	<b>32.47</b>	<b>69.53</b>
<i>UCOESTup1793</i>	No homology	2.503	0.00264	<b>1222.35</b>	<b>2857.10</b>
<i>UCOESTup1794</i>	No homology	2.503	0.00628	<b>708.49</b>	<b>1655.97</b>
<i>UCOESTup1795</i>	No homology	2.503	0.02580	<b>176.44</b>	<b>427.31</b>
<i>UCOESTup1796</i>	No homology	2.502	0.00378	<b>1799.88</b>	<b>4473.78</b>
<i>UCOESTup1799</i>	No homology	2.499	0.02670	<b>268.60</b>	<b>664.58</b>
<i>UCOESTup1800</i>	No homology	2.498	0.00116	<b>1759.44</b>	<b>4676.03</b>
<i>UCOESTup1803</i>	No homology	2.497	0.00303	<b>249.06</b>	<b>663.13</b>
<i>UCOESTup1805</i>	No homology	2.493	0.01890	<b>347.04</b>	<b>866.84</b>

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<i>UCOESTup1812</i>	No homology	2.484	0.04370	<b>17.14</b>	<b>26.59</b>
<i>UCOESTup1824</i>	No homology	2.469	0.00670	<b>156.18</b>	<b>380.24</b>
<i>UCOESTup1830</i>	No homology	2.464	0.02840	<b>16.58</b>	<b>27.44</b>
<i>UCOESTup1834</i>	No homology	2.461	0.00343	<b>18.29</b>	<b>29.18</b>
<i>UCOESTup1836</i>	No homology	2.461	0.01810	<b>55.93</b>	<b>117.29</b>
<i>UCOESTup1838</i>	No homology	2.459	0.00691	<b>369.28</b>	<b>866.79</b>
<i>UCOESTup1839</i>	No homology	2.459	0.04650	<b>24.46</b>	<b>39.50</b>
<i>UCOESTup1842</i>	No homology	2.456	0.02140	<b>18.57</b>	<b>27.80</b>
<i>UCOESTup1843</i>	No homology	2.455	0.00510	<b>254.32</b>	<b>582.41</b>
<i>UCOESTup1846</i>	No homology	2.454	0.02390	<b>471.56</b>	<b>2646.84</b>
<i>UCOESTup1845</i>	No homology	2.454	0.01310	<b>448.38</b>	<b>875.87</b>
<i>UCOESTup1847</i>	No homology	2.452	0.00145	<b>685.25</b>	<b>1666.56</b>
<i>UCOESTup1851</i>	No homology	2.450	0.03380	<b>80.00</b>	<b>166.90</b>
<i>UCOESTup1852</i>	No homology	2.449	0.00185	<b>1397.50</b>	<b>3328.61</b>
<i>UCOESTup1857</i>	No homology	2.448	0.02710	<b>149.22</b>	<b>343.06</b>
<i>UCOESTup1858</i>	No homology	2.446	0.00111	<b>532.93</b>	<b>1201.37</b>
<i>UCOESTup1863</i>	No homology	2.443	0.03440	<b>69.70</b>	<b>143.15</b>
<i>UCOESTup1864</i>	No homology	2.442	0.00250	<b>2950.03</b>	<b>7274.46</b>
<i>UCOESTup1871</i>	No homology	2.439	0.00200	<b>2081.25</b>	<b>4607.51</b>
<i>UCOESTup1876</i>	No homology	2.435	0.02730	<b>16.65</b>	<b>25.46</b>
<i>UCOESTup1880</i>	No homology	2.432	0.00191	<b>966.63</b>	<b>2039.33</b>
<i>UCOESTup1882</i>	No homology	2.430	0.03580	<b>71.04</b>	<b>140.13</b>
<i>UCOESTup1884</i>	No homology	2.428	0.00167	<b>21.97</b>	<b>35.01</b>
<i>UCOESTup1887</i>	No homology	2.426	0.00785	<b>37.67</b>	<b>75.14</b>
<i>UCOESTup1888</i>	No homology	2.426	0.03900	<b>2922.82</b>	<b>7522.94</b>
<i>UCOESTup1886</i>	No homology	2.426	0.00396	<b>16.65</b>	<b>25.46</b>
<i>UCOESTup1889</i>	No homology	2.425	0.01860	<b>33.86</b>	<b>67.25</b>
<i>UCOESTup1890</i>	No homology	2.425	0.03060	<b>81.71</b>	<b>148.15</b>
<i>UCOESTup1891</i>	No homology	2.422	0.04530	<b>104.26</b>	<b>179.78</b>
<i>UCOESTup1892</i>	No homology	2.420	0.04070	<b>49.13</b>	<b>92.82</b>
<i>UCOESTup1902</i>	No homology	2.409	0.00270	<b>158.68</b>	<b>335.62</b>
<i>UCOESTup1905</i>	No homology	2.409	0.03390	<b>17.46</b>	<b>26.16</b>
<i>UCOESTup1908</i>	No homology	2.406	0.03680	<b>26.71</b>	<b>50.76</b>
<i>UCOESTup1911</i>	No homology	2.402	0.01300	<b>25.15</b>	<b>44.45</b>
<i>UCOESTup1913</i>	No homology	2.401	0.00184	<b>1219.73</b>	<b>2767.29</b>
<i>UCOESTup1916</i>	No homology	2.398	0.03270	<b>39.75</b>	<b>68.49</b>
<i>UCOESTup1918</i>	No homology	2.396	0.00467	<b>129.02</b>	<b>264.75</b>
<i>UCOESTup1920</i>	No homology	2.395	0.01980	<b>35.72</b>	<b>58.90</b>
<i>UCOESTup1925</i>	No homology	2.388	0.00641	<b>60.19</b>	<b>113.11</b>
<i>UCOESTup1926</i>	No homology	2.387	0.00200	<b>533.77</b>	<b>1274.88</b>
<i>UCOESTup1927</i>	No homology	2.387	0.02660	<b>119.50</b>	<b>261.49</b>
<i>UCOESTup1930</i>	No homology	2.383	0.00719	<b>14.93</b>	<b>27.84</b>
<i>UCOESTup1932</i>	No homology	2.382	0.00607	<b>238.07</b>	<b>611.40</b>
<i>UCOESTup1933</i>	No homology	2.382	0.03950	<b>48.31</b>	<b>87.89</b>
<i>UCOESTup1935</i>	No homology	2.381	0.00542	<b>25.64</b>	<b>59.28</b>

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<i>UCOESTup1936</i>	No homology	2.381	0.01250	<b>50.19</b>	<b>102.09</b>
<i>UCOESTup1937</i>	No homology	2.380	0.00889	<b>121.87</b>	<b>283.06</b>
<i>UCOESTup1941</i>	No homology	2.379	0.01450	<b>805.37</b>	<b>1961.42</b>
<i>UCOESTup1946</i>	No homology	2.372	0.00821	<b>72.30</b>	<b>153.24</b>
<i>UCOESTup1945</i>	No homology	2.372	0.00194	<b>66.64</b>	<b>467.44</b>
<i>UCOESTup1950</i>	No homology	2.370	0.04100	<b>26.40</b>	<b>54.29</b>
<i>UCOESTup1949</i>	No homology	2.370	0.03040	<b>89.04</b>	<b>196.03</b>
<i>UCOESTup1951</i>	No homology	2.369	0.00167	<b>174.82</b>	<b>398.07</b>
<i>UCOESTup1956</i>	No homology	2.366	0.03720	<b>56.38</b>	<b>114.57</b>
<i>UCOESTup1957</i>	No homology	2.363	0.00522	<b>104.16</b>	<b>219.25</b>
<i>UCOESTup1959</i>	No homology	2.363	0.02700	<b>29.17</b>	<b>56.52</b>
<i>UCOESTup1960</i>	No homology	2.363	0.04970	<b>23.35</b>	<b>36.14</b>
<i>UCOESTup1958</i>	No homology	2.363	0.01940	<b>102.18</b>	<b>264.90</b>
<i>UCOESTup1961</i>	No homology	2.362	0.00859	<b>182.39</b>	<b>446.95</b>
<i>UCOESTup1969</i>	No homology	2.356	0.00190	<b>638.04</b>	<b>1441.82</b>
<i>UCOESTup1970</i>	No homology	2.356	0.00572	<b>692.89</b>	<b>1539.22</b>
<i>UCOESTup1972</i>	No homology	2.355	0.01010	<b>540.98</b>	<b>1166.71</b>
<i>UCOESTup1973</i>	No homology	2.354	0.03350	<b>17.53</b>	<b>26.71</b>
<i>UCOESTup1974</i>	No homology	2.354	0.03370	<b>24.08</b>	<b>35.72</b>
<i>UCOESTup1975</i>	No homology	2.351	0.00372	<b>400.28</b>	<b>966.12</b>
<i>UCOESTup1976</i>	No homology	2.351	0.00880	<b>1047.94</b>	<b>2813.95</b>
<i>UCOESTup1978</i>	No homology	2.351	0.03530	<b>164.74</b>	<b>333.78</b>
<i>UCOESTup1979</i>	No homology	2.348	0.01100	<b>203.58</b>	<b>508.40</b>
<i>UCOESTup1980</i>	No homology	2.346	0.00726	<b>155.24</b>	<b>354.14</b>
<i>UCOESTup1982</i>	No homology	2.345	0.03520	<b>251.78</b>	<b>596.43</b>
<i>UCOESTup1984</i>	No homology	2.343	0.00193	<b>1677.37</b>	<b>6990.01</b>
<i>UCOESTup1985</i>	No homology	2.342	0.00193	<b>746.41</b>	<b>1513.34</b>
<i>UCOESTup1987</i>	No homology	2.341	0.01550	<b>944.63</b>	<b>2244.91</b>
<i>UCOESTup1989</i>	No homology	2.337	0.00467	<b>768.80</b>	<b>1668.35</b>
<i>UCOESTup1994</i>	No homology	2.335	0.00574	<b>1108.64</b>	<b>2866.46</b>
<i>UCOESTup1995</i>	No homology	2.335	0.01110	<b>446.02</b>	<b>974.70</b>
<i>UCOESTup1997</i>	No homology	2.334	0.01020	<b>379.24</b>	<b>890.17</b>
<i>UCOESTup2003</i>	No homology	2.332	0.02140	<b>619.07</b>	<b>1498.08</b>
<i>UCOESTup2004</i>	No homology	2.331	0.00728	<b>140.30</b>	<b>230.83</b>
<i>UCOESTup2008</i>	No homology	2.330	0.01550	<b>16.89</b>	<b>33.02</b>
<i>UCOESTup2013</i>	No homology	2.326	0.00354	<b>587.26</b>	<b>1389.14</b>
<i>UCOESTup2018</i>	No homology	2.323	0.04670	<b>26.60</b>	<b>46.88</b>
<i>UCOESTup2020</i>	No homology	2.320	0.03940	<b>57.87</b>	<b>86.45</b>
<i>UCOESTup2024</i>	No homology	2.318	0.03120	<b>14.01</b>	<b>25.00</b>
<i>UCOESTup2025</i>	No homology	2.317	0.00339	<b>239.68</b>	<b>517.22</b>
<i>UCOESTup2026</i>	No homology	2.317	0.01810	<b>211.85</b>	<b>475.02</b>
<i>UCOESTup2024</i>	No homology	2.316	0.00185	<b>14.01</b>	<b>25.00</b>
<i>UCOESTup2030</i>	No homology	2.315	0.00765	<b>951.33</b>	<b>2220.91</b>
<i>UCOESTup2032</i>	No homology	2.314	0.00766	<b>1978.33</b>	<b>4602.34</b>
<i>UCOESTup2033</i>	No homology	2.312	0.01370	<b>133.14</b>	<b>177.95</b>

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<i>UCOESTup2036</i>	No homology	2.310	0.01170	<b>941.66</b>	<b>2161.90</b>
<i>UCOESTup2040</i>	No homology	2.306	0.01070	<b>814.43</b>	<b>1852.54</b>
<i>UCOESTup2041</i>	No homology	2.306	0.03080	<b>172.49</b>	<b>384.41</b>
<i>UCOESTup2044</i>	No homology	2.304	0.04340	<b>33.25</b>	<b>64.70</b>
<i>UCOESTup2046</i>	No homology	2.303	0.00250	<b>1003.33</b>	<b>2339.14</b>
<i>UCOESTup2049</i>	No homology	2.301	0.04220	<b>15.52</b>	<b>23.69</b>
<i>UCOESTup2053</i>	No homology	2.297	0.01530	<b>272.38</b>	<b>598.19</b>
<i>UCOESTup2055</i>	No homology	2.295	0.00388	<b>926.42</b>	<b>1995.24</b>
<i>UCOESTup2060</i>	No homology	2.291	0.01060	<b>2348.55</b>	<b>5250.01</b>
<i>UCOESTup2061</i>	No homology	2.29	0.00223	<b>113.62</b>	<b>243.06</b>
<i>UCOESTup2067</i>	No homology	2.288	0.03560	<b>24.66</b>	<b>46.13</b>
<i>UCOESTup2068</i>	No homology	2.287	0.00737	<b>32.27</b>	<b>56.27</b>
<i>UCOESTup2073</i>	No homology	2.285	0.01790	<b>33.27</b>	<b>56.46</b>
<i>UCOESTup2075</i>	No homology	2.283	0.00641	<b>28.52</b>	<b>50.99</b>
<i>UCOESTup2089</i>	No homology	2.276	0.04010	<b>15.16</b>	<b>27.62</b>
<i>UCOESTup2091</i>	No homology	2.274	0.01890	<b>22.09</b>	<b>34.78</b>
<i>UCOESTup2094</i>	No homology	2.273	0.04550	<b>16.82</b>	<b>25.02</b>
<i>UCOESTup2095</i>	No homology	2.271	0.00228	<b>733.71</b>	<b>1660.53</b>
<i>UCOESTup2097</i>	No homology	2.269	0.00575	<b>676.04</b>	<b>1545.38</b>
<i>UCOESTup2102</i>	No homology	2.266	0.01270	<b>268.27</b>	<b>603.17</b>
<i>UCOESTup2108</i>	No homology	2.263	0.04970	<b>106.86</b>	<b>223.39</b>
<i>UCOESTup2118</i>	No homology	2.259	0.00255	<b>269.20</b>	<b>593.36</b>
<i>UCOESTup2121</i>	No homology	2.259	0.00875	<b>187.67</b>	<b>384.28</b>
<i>UCOESTup2122</i>	No homology	2.259	0.01390	<b>71.77</b>	<b>141.00</b>
<i>UCOESTup2123</i>	No homology	2.259	0.03550	<b>42.58</b>	<b>87.31</b>
<i>UCOESTup2125</i>	No homology	2.258	0.01350	<b>2870.01</b>	<b>6629.47</b>
<i>UCOESTup2126</i>	No homology	2.258	0.04890	<b>47.10</b>	<b>106.83</b>
<i>UCOESTup2128</i>	No homology	2.257	0.03640	<b>134.17</b>	<b>271.09</b>
<i>UCOESTup2129</i>	No homology	2.257	0.04650	<b>18.49</b>	<b>30.14</b>
<i>UCOESTup2135</i>	No homology	2.253	0.04290	<b>13.56</b>	<b>24.69</b>
<i>UCOESTup2137</i>	No homology	2.249	0.03410	<b>181.30</b>	<b>380.32</b>
<i>UCOESTup2141</i>	No homology	2.245	0.01640	<b>295.86</b>	<b>629.88</b>
<i>UCOESTup2145</i>	No homology	2.244	0.03550	<b>15.43</b>	<b>30.70</b>
<i>UCOESTup2142</i>	No homology	2.244	0.00202	<b>1791.87</b>	<b>4020.09</b>
<i>UCOESTup2146</i>	No homology	2.243	0.00186	<b>6835.40</b>	<b>13549.29</b>
<i>UCOESTup2150</i>	No homology	2.239	0.00193	<b>129.87</b>	<b>264.36</b>
<i>UCOESTup2152</i>	No homology	2.238	0.00270	<b>2758.42</b>	<b>6008.04</b>
<i>UCOESTup2156</i>	No homology	2.237	0.00397	<b>1071.17</b>	<b>2292.01</b>
<i>UCOESTup2157</i>	No homology	2.237	0.00916	<b>656.00</b>	<b>1464.48</b>
<i>UCOESTup2162</i>	No homology	2.235	0.02130	<b>484.57</b>	<b>1060.14</b>
<i>UCOESTup2160</i>	No homology	2.235	0.00196	<b>1303.17</b>	<b>2965.45</b>
<i>UCOESTup2168</i>	No homology	2.231	0.01040	<b>180.71</b>	<b>401.07</b>
<i>UCOESTup2171</i>	No homology	2.228	0.00258	<b>345.19</b>	<b>789.95</b>
<i>UCOESTup2178</i>	No homology	2.226	0.04760	<b>29.89</b>	<b>53.49</b>
<i>UCOESTup2179</i>	No homology	2.225	0.01930	<b>432.15</b>	<b>919.78</b>

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<i>UCOESTup2186</i>	No homology	2.219	0.00418	<b>4401.67</b>	<b>9262.91</b>
<i>UCOESTup2187</i>	No homology	2.219	0.00625	<b>1038.73</b>	<b>2370.64</b>
<i>UCOESTup2190</i>	No homology	2.216	0.00949	<b>281.20</b>	<b>501.95</b>
<i>UCOESTup2193</i>	No homology	2.215	0.01140	<b>40.02</b>	<b>76.93</b>
<i>UCOESTup2196</i>	No homology	2.212	0.00509	<b>338.88</b>	<b>734.55</b>
<i>UCOESTup2199</i>	No homology	2.211	0.01460	<b>61.99</b>	<b>136.52</b>
<i>UCOESTup2200</i>	No homology	2.211	0.01480	<b>93.40</b>	<b>185.45</b>
<i>UCOESTup2198</i>	No homology	2.211	0.01050	<b>4401.67</b>	<b>9262.91</b>
<i>UCOESTup2206</i>	No homology	2.204	0.04950	<b>28.15</b>	<b>44.92</b>
<i>UCOESTup2211</i>	No homology	2.202	0.01270	<b>86.66</b>	<b>168.93</b>
<i>UCOESTup2212</i>	No homology	2.201	0.02470	<b>381.47</b>	<b>819.98</b>
<i>UCOESTup2213</i>	No homology	2.200	0.00920	<b>140.47</b>	<b>286.15</b>
<i>UCOESTup2214</i>	No homology	2.199	0.02490	<b>265.28</b>	<b>555.89</b>
<i>UCOESTup2217</i>	No homology	2.198	0.01520	<b>138.76</b>	<b>279.63</b>
<i>UCOESTup2220</i>	No homology	2.193	0.00582	<b>102.35</b>	<b>222.68</b>
<i>UCOESTup2221</i>	No homology	2.193	0.03240	<b>54.67</b>	<b>99.05</b>
<i>UCOESTup2224</i>	No homology	2.192	0.03940	<b>46.77</b>	<b>78.11</b>
<i>UCOESTup2227</i>	No homology	2.190	0.01840	<b>256.23</b>	<b>554.11</b>
<i>UCOESTup2232</i>	No homology	2.186	0.00628	<b>3192.97</b>	<b>7696.50</b>
<i>UCOESTup2233</i>	No homology	2.186	0.00628	<b>568.47</b>	<b>1203.03</b>
<i>UCOESTup2235</i>	No homology	2.185	0.01050	<b>623.05</b>	<b>1252.07</b>
<i>UCOESTup2239</i>	No homology	2.183	0.00263	<b>3350.21</b>	<b>7504.87</b>
<i>UCOESTup2241</i>	No homology	2.183	0.01740	<b>39.90</b>	<b>73.51</b>
<i>UCOESTup2245</i>	No homology	2.18	0.00628	<b>440.30</b>	<b>942.96</b>
<i>UCOESTup2251</i>	No homology	2.177	0.00367	<b>889.88</b>	<b>1858.60</b>
<i>UCOESTup2252</i>	No homology	2.177	0.02530	<b>129.30</b>	<b>234.09</b>
<i>UCOESTup2255</i>	No homology	2.175	0.02420	<b>13.46</b>	<b>19.55</b>
<i>UCOESTup2256</i>	No homology	2.175	0.04680	<b>22.48</b>	<b>46.46</b>
<i>UCOESTup2258</i>	No homology	2.173	0.00278	<b>2244.92</b>	<b>5332.50</b>
<i>UCOESTup2259</i>	No homology	2.173	0.00291	<b>499.35</b>	<b>967.95</b>
<i>UCOESTup2260</i>	No homology	2.173	0.00724	<b>64.20</b>	<b>123.06</b>
<i>UCOESTup2261</i>	No homology	2.173	0.02200	<b>17.61</b>	<b>33.59</b>
<i>UCOESTup2262</i>	No homology	2.173	0.03010	<b>51.50</b>	<b>96.89</b>
<i>UCOESTup2263</i>	No homology	2.172	0.00449	<b>400.14</b>	<b>837.34</b>
<i>UCOESTup2264</i>	No homology	2.171	0.01080	<b>29.45</b>	<b>45.65</b>
<i>UCOESTup2265</i>	No homology	2.170	0.01490	<b>51.81</b>	<b>97.05</b>
<i>UCOESTup2268</i>	No homology	2.169	0.02760	<b>408.44</b>	<b>829.33</b>
<i>UCOESTup2275</i>	No homology	2.165	0.00298	<b>49.44</b>	<b>69.59</b>
<i>UCOESTup2280</i>	No homology	2.163	0.01580	<b>2344.57</b>	<b>5144.25</b>
<i>UCOESTup2279</i>	No homology	2.163	0.01520	<b>148.56</b>	<b>312.47</b>
<i>UCOESTup2289</i>	No homology	2.158	0.00620	<b>1537.67</b>	<b>3193.03</b>
<i>UCOESTup2291</i>	No homology	2.157	0.00522	<b>287.20</b>	<b>569.49</b>
<i>UCOESTup2294</i>	No homology	2.156	0.03240	<b>478.16</b>	<b>1020.29</b>
<i>UCOESTup2295</i>	No homology	2.156	0.03540	<b>2295.82</b>	<b>5321.24</b>
<i>UCOESTup2297</i>	No homology	2.155	0.03300	<b>20.69</b>	<b>32.63</b>

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<i>UCOESTup2301</i>	No homology	2.153	0.02930	<b>51.04</b>	<b>80.91</b>
<i>UCOESTup2303</i>	No homology	2.151	0.00845	<b>120.82</b>	<b>231.40</b>
<i>UCOESTup2307</i>	No homology	2.149	0.00925	<b>273.08</b>	<b>608.82</b>
<i>UCOESTup2311</i>	No homology	2.146	0.00196	<b>1072.95</b>	<b>2245.90</b>
<i>UCOESTup2314</i>	No homology	2.146	0.03870	<b>37.64</b>	<b>60.92</b>
<i>UCOESTup2319</i>	No homology	2.140	0.01340	<b>170.39</b>	<b>351.87</b>
<i>UCOESTup2322</i>	No homology	2.137	0.00587	<b>27.43</b>	<b>60.12</b>
<i>UCOESTup2323</i>	No homology	2.137	0.01680	<b>169.88</b>	<b>357.99</b>
<i>UCOESTup2325</i>	No homology	2.136	0.01100	<b>7203.57</b>	<b>15494.53</b>
<i>UCOESTup2326</i>	No homology	2.136	0.03570	<b>29.37</b>	<b>55.01</b>
<i>UCOESTup2324</i>	No homology	2.136	0.00288	<b>298.12</b>	<b>633.23</b>
<i>UCOESTup2329</i>	No homology	2.134	0.00393	<b>1103.61</b>	<b>2403.58</b>
<i>UCOESTup2330</i>	No homology	2.134	0.00489	<b>978.83</b>	<b>1926.62</b>
<i>UCOESTup2335</i>	No homology	2.132	0.00539	<b>260.24</b>	<b>547.56</b>
<i>UCOESTup2338</i>	No homology	2.131	0.04440	<b>85.65</b>	<b>152.96</b>
<i>UCOESTup2345</i>	No homology	2.126	0.00221	<b>759.52</b>	<b>1926.58</b>
<i>UCOESTup2348</i>	No homology	2.124	0.01550	<b>32.77</b>	<b>58.36</b>
<i>UCOESTup2353</i>	No homology	2.122	0.02890	<b>32.74</b>	<b>49.75</b>
<i>UCOESTup2354</i>	No homology	2.121	0.00360	<b>3458.82</b>	<b>7240.60</b>
<i>UCOESTup2355</i>	No homology	2.121	0.00904	<b>224.18</b>	<b>440.21</b>
<i>UCOESTup2358</i>	No homology	2.118	0.00384	<b>2279.71</b>	<b>5037.96</b>
<i>UCOESTup2366</i>	No homology	2.113	0.00732	<b>105.46</b>	<b>202.64</b>
<i>UCOESTup2369</i>	No homology	2.111	0.00934	<b>83.31</b>	<b>167.33</b>
<i>UCOESTup2374</i>	No homology	2.108	0.02140	<b>62.94</b>	<b>113.60</b>
<i>UCOESTup2376</i>	No homology	2.106	0.02980	<b>53.42</b>	<b>116.44</b>
<i>UCOESTup2379</i>	No homology	2.105	0.00929	<b>26.92</b>	<b>43.48</b>
<i>UCOESTup2380</i>	No homology	2.104	0.00936	<b>19.03</b>	<b>24.27</b>
<i>UCOESTup2382</i>	No homology	2.102	0.04360	<b>80.86</b>	<b>146.34</b>
<i>UCOESTup2384</i>	No homology	2.101	0.02750	<b>21.05</b>	<b>31.17</b>
<i>UCOESTup2387</i>	No homology	2.100	0.02020	<b>2345.75</b>	<b>4848.25</b>
<i>UCOESTup2392</i>	No homology	2.096	0.00816	<b>101.34</b>	<b>200.32</b>
<i>UCOESTup2394</i>	No homology	2.095	0.00523	<b>1326.43</b>	<b>2913.54</b>
<i>UCOESTup2395</i>	No homology	2.095	0.00809	<b>7793.02</b>	<b>16712.12</b>
<i>UCOESTup2400</i>	No homology	2.094	0.00987	<b>76.87</b>	<b>143.73</b>
<i>UCOESTup2402</i>	No homology	2.092	0.00264	<b>4448.58</b>	<b>9407.16</b>
<i>UCOESTup2406</i>	No homology	2.089	0.01060	<b>511.12</b>	<b>1126.46</b>
<i>UCOESTup2411</i>	No homology	2.086	0.03470	<b>17.67</b>	<b>31.05</b>
<i>UCOESTup2414</i>	No homology	2.084	0.03010	<b>30.53</b>	<b>48.26</b>
<i>UCOESTup2415</i>	No homology	2.083	0.01660	<b>50.02</b>	<b>89.50</b>
<i>UCOESTup2420</i>	No homology	2.080	0.00776	<b>198.41</b>	<b>439.43</b>
<i>UCOESTup2423</i>	No homology	2.079	0.02150	<b>217.65</b>	<b>393.29</b>
<i>UCOESTup2422</i>	No homology	2.079	0.02020	<b>84.72</b>	<b>164.40</b>
<i>UCOESTup2428</i>	No homology	2.074	0.00507	<b>6721.26</b>	<b>13584.66</b>
<i>UCOESTup2429</i>	No homology	2.074	0.04600	<b>154.28</b>	<b>313.28</b>
<i>UCOESTup2431</i>	No homology	2.072	0.00599	<b>191.80</b>	<b>417.95</b>

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<i>UCOESTup2433</i>	No homology	2.072	0.02170	<b>90.84</b>	<b>154.91</b>
<i>UCOESTup2434</i>	No homology	2.072	0.04400	<b>109.55</b>	<b>208.26</b>
<i>UCOESTup2441</i>	No homology	2.068	0.03430	<b>210.27</b>	<b>475.31</b>
<i>UCOESTup2442</i>	No homology	2.067	0.01400	<b>1653.22</b>	<b>3547.63</b>
<i>UCOESTup2444</i>	No homology	2.066	0.01170	<b>185.99</b>	<b>372.34</b>
<i>UCOESTup2446</i>	No homology	2.066	0.02110	<b>64.57</b>	<b>116.05</b>
<i>UCOESTup2449</i>	No homology	2.065	0.01490	<b>430.28</b>	<b>917.22</b>
<i>UCOESTup2453</i>	No homology	2.064	0.02560	<b>27.08</b>	<b>42.17</b>
<i>UCOESTup2457</i>	No homology	2.061	0.00940	<b>378.76</b>	<b>686.74</b>
<i>UCOESTup2459</i>	No homology	2.060	0.01090	<b>602.22</b>	<b>1205.69</b>
<i>UCOESTup2461</i>	No homology	2.060	0.04220	<b>21.72</b>	<b>33.88</b>
<i>UCOESTup2460</i>	No homology	2.060	0.01550	<b>1349.22</b>	<b>2669.74</b>
<i>UCOESTup2463</i>	No homology	2.059	0.00458	<b>870.64</b>	<b>1694.49</b>
<i>UCOESTup2468</i>	No homology	2.058	0.02120	<b>104.24</b>	<b>194.72</b>
<i>UCOESTup2472</i>	No homology	2.057	0.00845	<b>2421.97</b>	<b>4930.77</b>
<i>UCOESTup2476</i>	No homology	2.055	0.02480	<b>50.21</b>	<b>94.20</b>
<i>UCOESTup2481</i>	No homology	2.053	0.03960	<b>31.84</b>	<b>40.38</b>
<i>UCOESTup2482</i>	No homology	2.052	0.00698	<b>108.92</b>	<b>203.14</b>
<i>UCOESTup2481</i>	No homology	2.049	0.00380	<b>31.84</b>	<b>40.38</b>
<i>UCOESTup2494</i>	No homology	2.047	0.03640	<b>23.61</b>	<b>35.78</b>
<i>UCOESTup2498</i>	No homology	2.041	0.00604	<b>339.63</b>	<b>707.23</b>
<i>UCOESTup2500</i>	No homology	2.041	0.01460	<b>119.16</b>	<b>243.29</b>
<i>UCOESTup2501</i>	No homology	2.040	0.04340	<b>700.45</b>	<b>1462.55</b>
<i>UCOESTup2504</i>	No homology	2.039	0.02290	<b>122.50</b>	<b>276.91</b>
<i>UCOESTup2505</i>	No homology	2.038	0.00900	<b>189.34</b>	<b>390.68</b>
<i>UCOESTup2508</i>	No homology	2.037	0.04020	<b>21.17</b>	<b>31.29</b>
<i>UCOESTup2509</i>	No homology	2.035	0.00496	<b>1316.65</b>	<b>2164.94</b>
<i>UCOESTup2510</i>	No homology	2.035	0.01460	<b>278.13</b>	<b>580.61</b>
<i>UCOESTup2511</i>	No homology	2.034	0.01360	<b>182.39</b>	<b>358.86</b>
<i>UCOESTup2512</i>	No homology	2.033	0.03400	<b>109.58</b>	<b>218.52</b>
<i>UCOESTup2513</i>	No homology	2.031	0.00247	<b>6877.58</b>	<b>13547.74</b>
<i>UCOESTup2516</i>	No homology	2.030	0.02160	<b>263.16</b>	<b>537.42</b>
<i>UCOESTup2519</i>	No homology	2.030	0.04920	<b>31.26</b>	<b>126.79</b>
<i>UCOESTup2522</i>	No homology	2.027	0.01030	<b>352.83</b>	<b>717.14</b>
<i>UCOESTup2523</i>	No homology	2.027	0.01930	<b>31.23</b>	<b>41.02</b>
<i>UCOESTup2529</i>	No homology	2.021	0.01640	<b>1044.27</b>	<b>2090.55</b>
<i>UCOESTup2534</i>	No homology	2.018	0.01030	<b>175.59</b>	<b>342.41</b>
<i>UCOESTup2538</i>	No homology	2.017	0.04950	<b>15.44</b>	<b>20.71</b>
<i>UCOESTup2540</i>	No homology	2.016	0.02160	<b>80.68</b>	<b>124.93</b>
<i>UCOESTup2541</i>	No homology	2.015	0.00512	<b>2192.86</b>	<b>4334.37</b>
<i>UCOESTup2543</i>	No homology	2.014	0.00326	<b>1013.69</b>	<b>2003.74</b>
<i>UCOESTup2547</i>	No homology	2.013	0.03080	<b>75.71</b>	<b>146.50</b>
<i>UCOESTup2548</i>	No homology	2.012	0.00652	<b>2121.29</b>	<b>4252.09</b>
<i>UCOESTup2552</i>	No homology	2.009	0.00458	<b>364.23</b>	<b>744.28</b>
<i>UCOESTup2557</i>	No homology	2.006	0.00432	<b>14146.60</b>	<b>28806.14</b>

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<i>UCOESTup2558</i>	No homology	2.006	0.01090	<b>325.73</b>	<b>634.41</b>
<i>UCOESTup2563</i>	No homology	2.004	0.00292	<b>5.900.70</b>	<b>12016.60</b>
<i>UCOESTup2564</i>	No homology	2.004	0.00309	<b>226.84</b>	<b>429.02</b>
<i>UCOESTup2567</i>	No homology	2.002	0.00383	<b>4516.47</b>	<b>7921.56</b>
<i>UCOESTup2571</i>	No homology	2.000	0.00337	<b>926.77</b>	<b>1849.23</b>

**Table 11. Genes with no homology up regulated in fruit ripen receptacles analyzed by microarray experiment.**

Magnitudes of relative induction to fruit ripen receptacles, *p*-value ( $\leq 0.05$ ) and u.a.e (arbitrary units of expression) in green and red fruits are given. Mean value of u.a.e is 1771.57. Columns show the best annotated matches from the search results of tBlastX analysis, species, putative function and match e- value.

Gene	Array	p-value	QRT-PCR
UCOESTup1780	2.51	0.00155	12.0 ± 1.7
UCOESTup642	5.72	0.00275	14.0 ± 2.1
UCOESTup888	4.32	0.00643	3.7 ± 4.4
UCOESTup123	25.75	0.00033	19.0 ± 2.1
UCOESTup41	74.04	0.01270	206.4 ± 1.9
UCOESTup44	69.37	0.00005	168.0 ± 15.4
UCOESTup445	7.76	0.00029	20.0 ± 1.76
UCOESTup79	40.21	0.00017	50.0 ± 4.2
UCOESTup605	6.02	0.00089	18.0 ± 0.23
UCOESTup344	9.56	0.00036	32.0 ± 0.2
UCOESTup355	9.29	0.00044	16.8 ± 0.2
UCOESTup101	31.81	0.00011	82.9 ± 7.5
UCOESTup14	170.16	0.00007	675.0 ± 7.8
UCOESTup1864	2.44	0.00250	7.0 ± 0.9
UCOESTup1583	2.73	0.00262	3.26 ± 0.04
UCOESTup892	4.31	0.00621	13.25 ± 0.87
UCOESTup612	5.94	0.00020	22.1 ± 0.6
UCOESTup374	327.91	0.01630	458.5 ± 6.7
UCOESTup2138	2.24	0.00225	5.40 ± 0.03
UCOESTup2056	82.95	0.01160	91.0 ± 1.4
UCOESTup303	10.66	0.00016	17.8 ± 22.3
UCOESTup429	8.09	0.00034	13.0 ± 0.5
UCOESTup1474	58.63	0.00152	340.0 ± 4.6
UCOESTup324	10.01	0.00016	25.9 ± 2.4
UCOESTup53	58.17	0.00055	63.2 ± 5.6
UCOESTup67	46.06	0.00005	70.86 ± 0.89
UCOESTup505	7.061	0.00379	14.83 ± 0.77
UCOESTup857	4.44	0.00046	9.94 ± 0.13
UCOESTup1766	2.52	0.00117	3.24 ± 0.02
UCOESTup262	12.05	0.00029	14.61 ± 0.20
UCOESTup161	49.92	0.00010	146.55 ± 2.31
UCOESTup181	17.15	0.00034	187.4 ± 1.4
UCOESTup56	52.83	0.00016	85.8 ± 0.9
UCOESTup808	20.67	0.00090	61.1 ± 1.2
UCOESTup529	6.64	0.00336	18.2 ± 0.2
UCOESTup61	49.87	0.00011	293.5 ± 0.2
UCOESTup130	24.42	0.00007	54.4 ± 0.4
UCOESTup399	8.47	0.00743	14.7 ± 0.2
UCOESTup575	6.24	0.00060	13.5 ± 0.1
UCOESTup691	5.36	0.00027	22.7 ± 0.3
UCOESTup1395	2.99	0.00142	3.40 ± 0.02
UCOESTup325	10.00	0.00062	18.4 ± 2.4
UCOESTup410	8.33	0.0168	21.82 ± 1.21
UCOESTup77	40.86	0.00007	91.01 ± 1.55
UCOESTup271	11.74	0.00011	19.2 ± 0.3
UCOESTup1610	2.70	0.02320	2.9 ± 0.3
UCOESTup366	8.96	0.00020	18.2 ± 0.2

Table 12. Comparison of relative gene expression values obtained by QRT-PCR and microarrays analysis of different genes in fruit green receptacle *versus* red-ripen receptacle.

## CHAPTER 2: THE FRUIT RIPENING RELATED GENE *FaAAT2* ENCODES AN ACYL TRANSFERASE INVOLVED IN STRAWBERRY AROMA BIOGENESIS

### 1. ABSTRACT

Short-chain esters contribute to the blend of volatiles that define the strawberry aroma. The last step in their biosynthesis is catalyzed by alcohol acyl-transferase (AAT) that catalyzes the esterification of an acyl moiety from acyl-CoA with an alcohol. This study identified a novel strawberry alcohol acyltransferase (*FaAAT2*) gene whose expression pattern during fruit receptacle growth and ripening is in accordance with the production of esters throughout strawberry fruit ripening. The full-length *FaAAT2* cDNA was cloned and expressed in *Escherichia coli* and its activity was analyzed with a set of acyl-CoA and alcohol substrates. The semi-purified *FaAAT2* enzyme had activity with C1 to C8 straight chain alcohols and aromatic alcohols in the presence of acetyl-CoA. Cinnamyl alcohol was the most efficient acyl acceptor. When *FaAAT2* gene expression was transiently downregulated in the fruit receptacle by agroinfiltration, the volatile ester production was significantly reduced in strawberry fruit. The results suggest that the *FaAAT2* gene has a significant role in the production of esters that contribute to the final strawberry fruit flavour.

### 2. INTRODUCTION

Volatile esters play several roles in higher plants. They make flowers more attractive to pollinators and dispersing animals, act as protectants against pathogens by inducing several important plant defense pathways, and contribute to the aroma of ripe fruit (D'Auria *et al.*, 2007). These compounds are produced by all soft fruit species during ripening and play an important role determining the final sensory quality of fruit (Manríquez *et al.*, 2006). In fruits like apple (*Malus domestica*), pear (*Pyrus communis*) and banana (*Musa sapientum*), esters are the main components of their characteristic aroma while in strawberry they only contribute to the blend of volatiles that define the aroma (Beekwilder *et al.*, 2004). The strawberry aroma is determined by more than 300 compounds consisting of alcohols, aldehydes, esters, sulfur compounds and furanone derivatives (Zebetakis and Holden, 1997), but only about 20 of these compounds actually contribute to its aroma and flavour (Forney *et al.*, 2000). Some authors consider methyl butanoate, ethyl butanoate, methyl hexanoate, hexyl acetate, ethyl hexanoate in addition to 2,5-dimethyl-4-hydroxy-3(2H)-furanone (HDMF, furaneol) and its methyl ether as the most important constituents of the characteristic strawberry aroma (Larsen *et al.*, 1992; Jetli *et al.*, 2007). Analyses of volatiles from fruit of different *Fragaria* varieties identified some common esters (ethyl acetate, methyl butanoate, 2-methylbutyl acetate, octyl acetate, octyl butanoate, hexyl acetate, ethyl heptanoate, 2-hexenyl butanoate, benzyl acetate and hexyl 2-methylbutanoate) in both *F. chiloensis* fruits and several *F. x ananassa* cultivars (Drawert *et al.*, 1973; Hirvi and Honkanen, 1982). However, some esters found in *F. chiloensis* (hexyl propanoate, ethyl 4-decenoate, 2-phenylethyl propanoate and ethyl 2,4 decadienoate) have not been described previously in *F. x ananassa* (Pyysalo *et al.*, 1979; Zebetakis *et al.*, 1997; Azodanlou *et al.*, 2003; Berna *et al.*, 2007; González *et al.*, 2009).

The last step in the biosynthesis of volatile esters is catalyzed by alcohol acyltransferase (AAT), a key enzyme in aroma biochemistry (Fellman *et al.*, 2000). This enzyme catalyzes the

esterification of an acyl moiety from acyl-CoA onto an alcohol (Yamashita *et al.*, 1977; Aharoni *et al.*, 2000; Olías *et al.*, 2000; Beekwilder *et al.*, 2004). The formation of a broad range of esters in the different types of fruit results from the combination of different alcohols and acyl-CoAs (Schwab, 2003). The volatile compounds produced by a fruit are determined by substrate availability and not only by AAT specificity (Tressl *et al.*, 1973; Knee *et al.*, 1981; De Pooter *et al.*, 1983; Jayanty *et al.*, 2002; Schwab, 2003), although this enzyme participates in the rate limiting step in ester biosynthesis (Defilippi *et al.*, 2005).

Due to their role in ester biosynthesis, several AAT enzymes and their corresponding genes have been studied in some fruit species with high commercial interest such as banana (Beekwilder *et al.*, 2004), apple (Soulery *et al.*, 2005; Li *et al.*, 2006), melon (*Cucumis melo*) (Yahyaoui *et al.*, 2002; El-Sharkawy *et al.*, 2005), apricot (*Prunus armeniaca L.*) (González-Agüero *et al.*, 2009), grape (*Vitis vinifera L.*) (Wang *et al.*, 2005; Kalua *et al.*, 2009), papaya (*Vasconcellea pubescens*) (Balbontin *et al.*, 2010), peach (*Prunus persica*) (Zang *et al.*, 2010) and strawberry (Pérez *et al.*, 1993; Aharoni *et al.*, 2000; Olías *et al.*, 2002; González *et al.*, 2009). The expression of the AAT genes always increased in these fruits throughout ripening and after harvest correlating with the total content of esters, thus suggesting that this gene family could be responsible for the production of important esters related to ripe fruit aroma (Aharoni *et al.*, 2000; Yahyaoui *et al.*, 2002; González *et al.*, 2009). Moreover, alcohol levels in peach fruit decreased during postharvest ripening, apparently by their use as substrates for the formation of different esters (Zhang *et al.*, 2010).

The AAT proteins share several common motifs with the BAHD superfamily of acyltransferases (D'Auria *et al.*, 2006). Among them, the HXXXD motif located in the middle of the protein sequence is highly conserved in higher plants and yeasts and has been suggested to be involved in the catalytic mechanism (D'Auria, 2006). In fact, the replacement of the histidine residue in this motif causes the loss of protein function (Bayer *et al.*, 2004). Another highly conserved motif in AAT proteins is the DFGWG sequence. This motif is located near the carboxylic end of the protein and, apparently, has a structural function keeping the conformational integrity of the enzyme structure (El-Sharkawy *et al.*, 2005; D'Auria, 2006).

Several AAT genes have been isolated from *F. x ananassa* cv. "Elsanta" (SAAT) (Aharoni *et al.*, 2000), wild strawberry *F. vesca* (VAAT) (Beekwilder *et al.*, 2004) and *F. chiloensis* (*FcAAT1*) (González *et al.*, 2009). In all cases, these genes reached their maximum transcript levels in red-ripened fruits suggesting that their corresponding enzymes are involved in the biosynthesis of volatile esters in the strawberry fruit receptacle. The SAAT enzyme prefers medium chain aliphatic alcohols in combination with different acyl-CoAs as substrates. In contrast, with the tertiary monoterpene linalool as substrate, activity was insignificant. Although the phylogenetic analysis indicated that VAAT and SAAT are closely related, their enzymatic activities were quite different. In this way, VAAT is more active towards short chain alcohol substrates, which are not preferred by SAAT (Beekwilder *et al.*, 2004). These results correlate with the substrate preference observed for different AAT enzymes isolated from both wild and cultivated varieties (Olías *et al.*, 2002).

Furthermore, it has been shown that AAT proteins from different sources such as banana and melon (BanAAT and CmAAT1, respectively) have a similar preference towards alcohols and similar activity profiles (Beekwilder *et al.*, 2004; El-Sharkawy *et al.*, 2005). This enzymatic behaviour has been ascribed to a special form of convergent evolution, in which new enzymes with the same function appeared in different plants from a shared pool of related enzymes with

similar functions while related members (as VAAT and SAAT) show important differences in their specificity (Pichersky and Gang, 2000).

This study reports the identification and characterization of a new strawberry ripening-related AAT gene, *FaAAT2*. The semi-purified recombinant enzyme has been obtained and its enzymatic affinity for different alcohols and acyl-CoA substrates studied. This study also provides evidence for the possible role of *FaAAT2* in the biosynthesis of esters that contribute to the strawberry fruit flavour through transitory silencing of the *FaAAT2* expression in strawberry fruit receptacle.

### 3. RESULTS

#### 3.1. Isolation and sequence analysis of *FaAAT2* gene

The complete DNA sequence of the putative full-length *FaAAT2* cDNA (JN089766) was amplified by 3'- and 5'-RACE and contained 1656 bp with an open reading frame of 1176 bp encoding a polypeptide of 392 amino acid residues with a predicted molecular mass of 43.2 KD (Fig. 1). Although the length of *FaAAT2* cDNA was shorter than other plant AAT, it was similar to other AAT from different strawberry varieties as *F. x chiloensis* (*FcAAT1*: 1620 bp; ORF 1384; 450 Aa and 50.4 kDa) and *F. x camarosa* cv. Elsanta (*SAAT*: 1618 bp; 452 Aa and 50.7 kDa). The sequence also contained 62 and 417 bp of 5' and 3'-UTR, respectively. Both RACE experiment and bioinformatic analysis of *FaAAT2* cDNA were repeated several times with the same results confirming that the cDNA isolated was a full-length cDNA that contains the entire ORF corresponding to the *FaAAT2* protein. The sequence alignment of the putative *FaAAT2* protein and other plant acyltransferases showed that all share the characteristic HXXXDG (residues 174 to 179), DFGWG (residues 422 to 426) and LXXYYPLAGR (residues 80 to 89) motifs of the BAHD protein family (Fig. 2). In addition, the corresponding *AAT2* full-length cDNA from the wild variety *F. vesca* (*FvAAT2*) was isolated in order to compare the *FaAAT2* gene with its closest ortholog. The sequence comparison of the *FaAAT2* and the *FvAAT2* genes showed a sequence similarity of 99.6 % (Fig. 1).

The phylogenetic tree of selected members the acyl transferase family provides four main subgroups of protein sequences (Fig. 3). The *FaAAT2* protein was clustered into subgroup III close to other AATs related to the synthesis of esters in melon (*CmAAT1-3*), papaya (*VpAAT1*), and *Clarkia breweri* (*CbBEBT*). However, the highest similarity at the amino acid level was found between *FaAAT2* and *MdAAT2* (*Malus domestica*), *MpAAT1* (*Malus pumilla*) and *PcAAT1* (*Pyrus comunis*), with 62 %, 61 % and 62 % respectively.

AAT proteins recently discovered in different strawberry species such as *F. x ananassa* cv. Elsanta (*SAAT*), *F. vesca* (*VAAT*) and *F. chiloensis* (*FcAAT1*) belong to a different subgroup than *FaAAT2*. The comparison of the *FaAAT2* sequence with *SAAT*, *VAAT*, and *FcAAT1* sequences revealed identities at the amino acid level of 21 %, 22 % and 22 %, respectively. These results indicate that the *FaAAT2* protein is different from the other AAT proteins previously described in strawberry fruit.

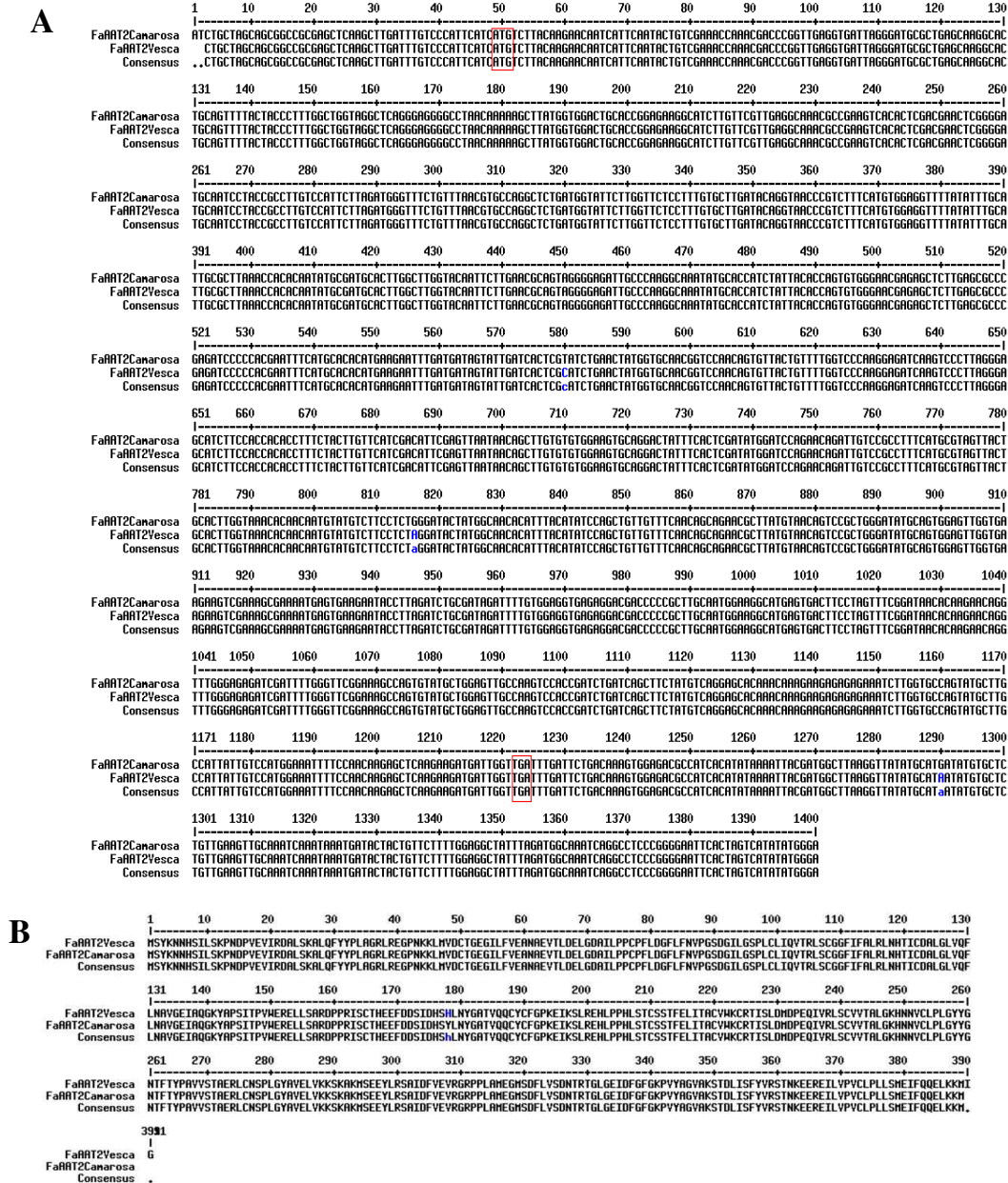
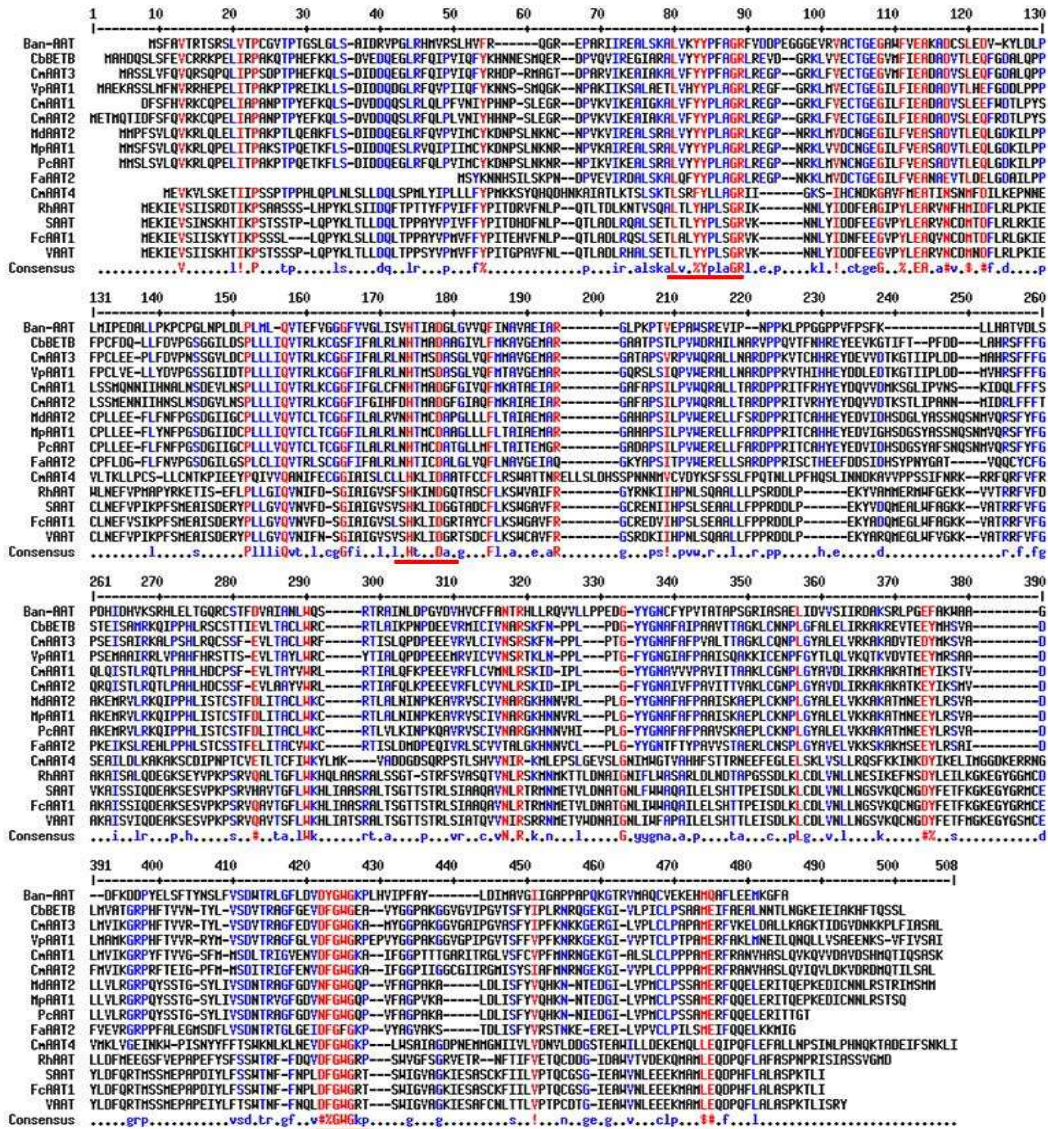
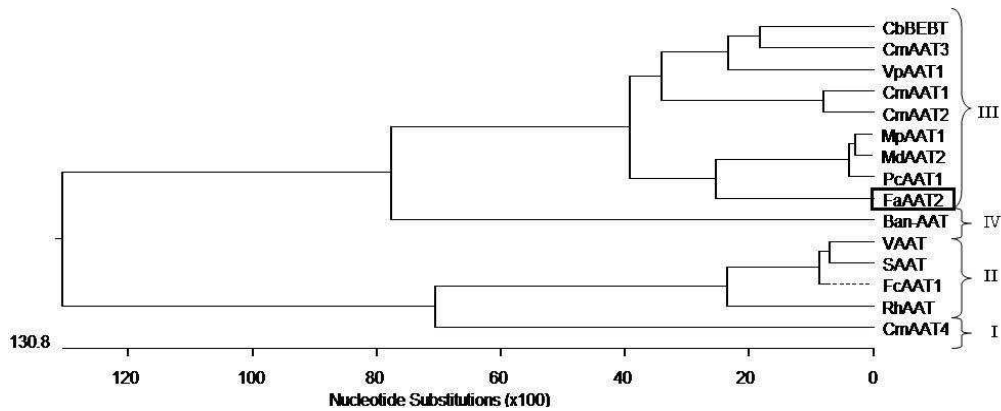


Fig. 1. Alignments of the cDNA nucleotide sequences (A) and protein sequences (B) of *FaAAT2* (*F. x ananassa* cv. *Camarosa*) and *FvAAT2* (*F. Vesca*). The residues that differ in both sequences are highlighted in blue. The start and end codon of translation is highlighted with a red box.



**Fig. 2.** Alignments of the deduced *FaAAT2* sequence with other family members of BADH acyl-transferases of known function from different floral and fruit species. The three conserved motifs which are characteristic of most AATs are underlined in red: LALYYPLSGR, HKLID (related to the catalytic activity and conserved within the BAHD acyl-transferase family) and DFGWG (highly conserved within the BAHD protein family and apparently required for conformation integrity of the protein structure). Sequences correspond to GenBank data library accession numbers: CmAAT1 (CAA94432); CmAAT2 (AAL77060); CmAAT3 (AAW51125); CmAAT4 (AAW51126); CbBEBT (AAN09796); VpAAT1 (FJ548610); SAAT (AAG13130); FcAAT1 (FJ548610); FvAAT (AAN07090); MdAAT2 (AAS79797); MpAAT1 (AAU14879); FaAAT2 (JN089766); Ban-AAT1 (CAC09063); PcAAT1 (AAS48090); RHAAT (AAW31948). Sequences were aligned using MultAling Program; "Multiple sequence alignment with hierarchical clustering"; F. CORPET, 1988, Nucl. Acids Res., 16 (22), 10881-10890.



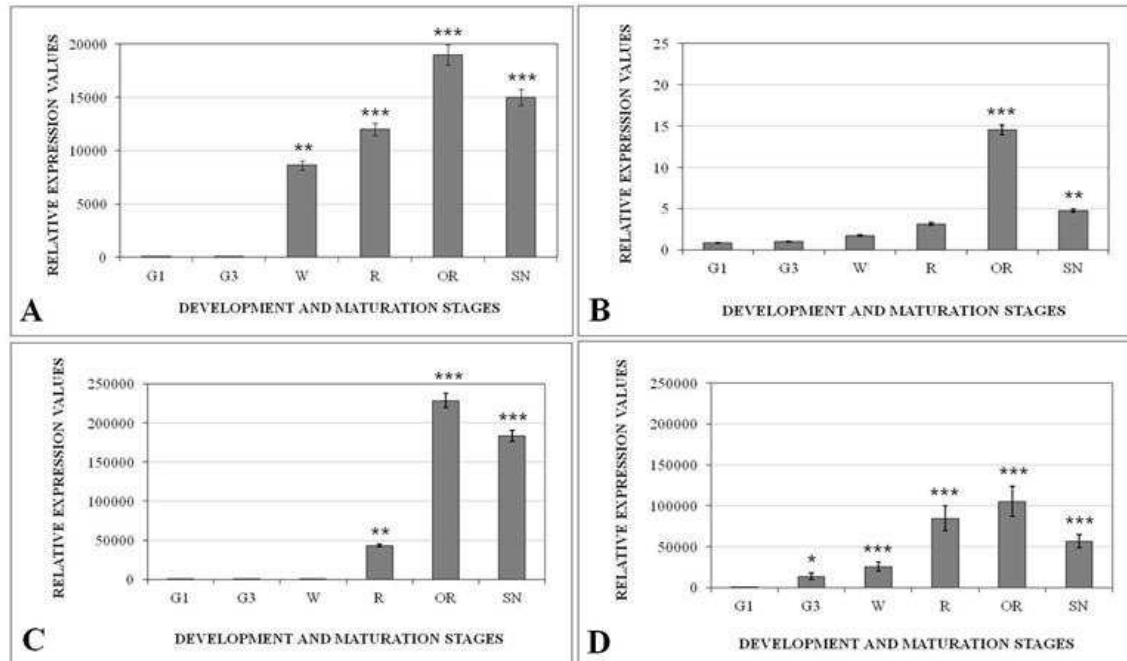


**Fig. 3. Phylogenetic analysis of *FaAAT2* protein.** In the phylogenetic tree, the length of each pair of branches represents the distance between sequence pairs, while the units at the bottom indicate the number of substitution events. The scale below the tree indicates the number of "Nucleotide Substitutions" for both DNA and protein sequences. Sequences are the same as those used in Figure 2. Sequences were aligned using MegAlign (Windows 32; MegAlign 5.00; DNASTAR).

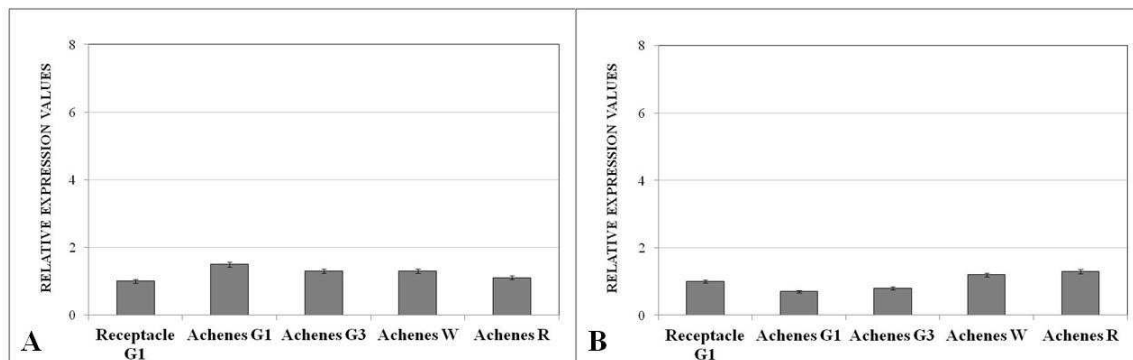
### 3.2. Gene expression studies

Transcript analysis in fruits of the cultivated *F. x ananassa* cv. Camarosa variety and wild *F. vesca* variety showed that *FaAAT2* gene expression was quite low in the early stages of fruit development followed by a significant increase during the ripening process, which starts at the white stage of receptacle ripening (Fig. 4A and 4B). The maximum level of *FaAAT2* transcripts was observed in overripe fruit receptacles, with a slight decrease in expression in the senescent stage. However, the relative expression level of *FaAAT2* in fruits of *F. vesca* was much lower than in the cultivated variety. A comparison of *SAAT* and *FaAAT2* transcript levels in fruits of the *F. x ananassa* cv. Camarosa (Fig. 4A and 4C) and the wild variety *F. vesca* (Fig. 4B and 4D) showed that *SAAT* and *FaAAT2* genes have similar expression patterns but the relative expression level of *SAAT* was significantly higher in *F. vesca* than that of *FaAAT2*.

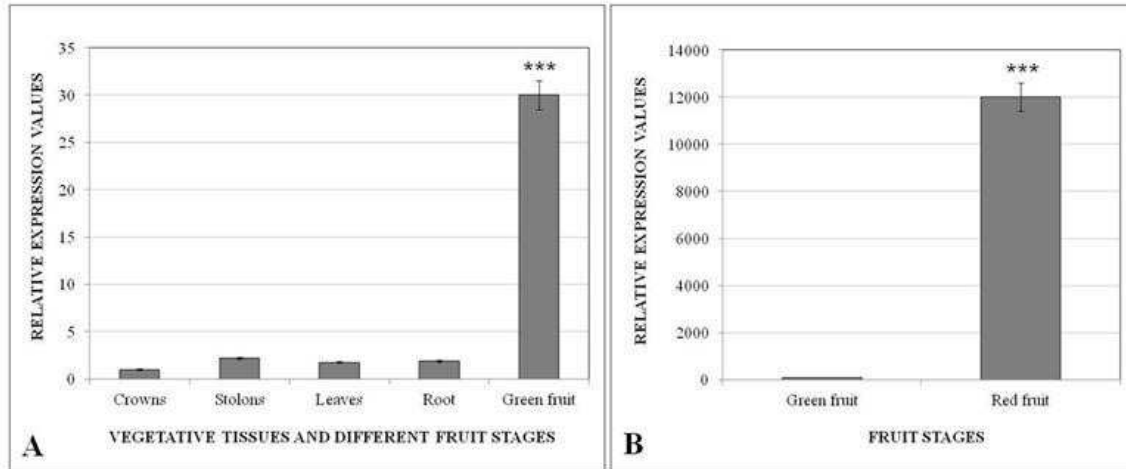
*FaAAT2* and *SAAT* were weakly expressed in achenes (Fig. 5A and 5B) in all fruit ripening stages. Besides, *FaAAT2* was barely expressed in vegetative tissues and roots (Fig. 6A) but the production of *FaAAT2* transcripts increased dramatically in the ripe fruit receptacle indicating that the expression of *FaAAT2* gene was quite specific of the fruit receptacle (Fig. 6B).



**Fig. 4. Developmental expression of the strawberry *FaAAT2* (A and B) and *SAAT* (C and D) genes in fruit receptacle of a *F. x ananassa* cv. Camarosa (A and C) and *F. vesca* (B and D) variety respectively.** Results were obtained by QRT-PCR using *FaAAT2* and *SAAT* specific primers. Quantification is based on Ct values as described in Materials and Methods. The increase in mRNA value was relative to the G1-Ct value of each experiment which was assigned an arbitrary value equal to unity. Mean values  $\pm$  SD of five independent experiments are shown. G1: small-sized green fruit; G3: full-sized green fruit (both stages of development); W: white stage; R: red stage; OR: overripe stage; SN: senescent stage. Statistical significance with respect to reference sample (G1 fruits) was determined by the Student's *t*-test. (\*\*) *p*-value < 0.01 and (\*\*\*) *p*-value < 0.001.

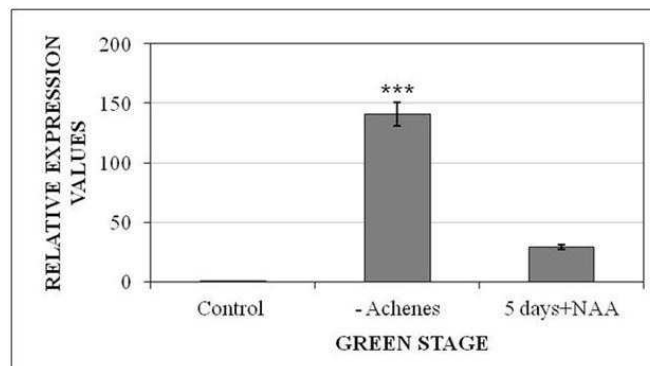


**Fig. 5 Developmental expression of the strawberry *FaAAT2* (A) and *SAAT* (B) genes in achenes of *F. x ananassa* cv. Camarosa variety.** Results were obtained by QRT-PCR using *FaAAT2* and *SAAT* specific primers. Quantification is based on Ct values as described in Materials and Methods. The increase in mRNA value was relative to the receptacle G1-Ct value of each experiment which was assigned an arbitrary value equal to unity. Mean values  $\pm$  SD of five independent experiments are shown. G1: small-sized green fruit; G3: full-sized green fruit (both stages of development); W: white stage; R: red stage.



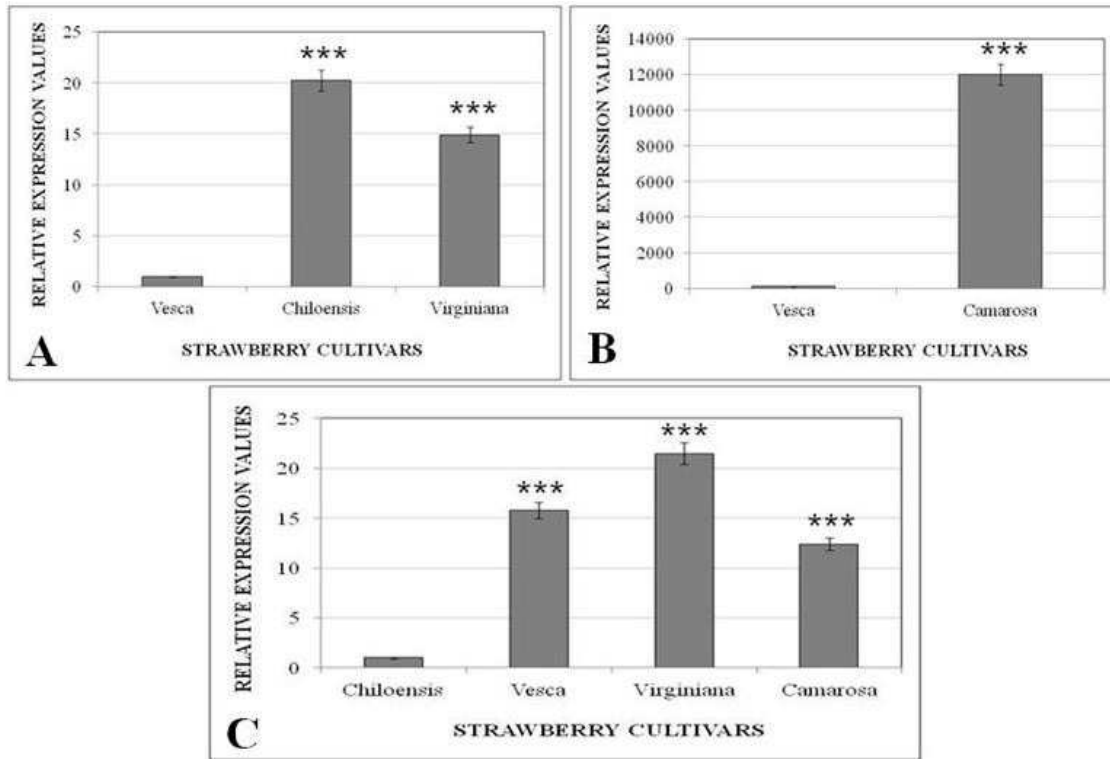
**Fig. 6. Analysis by QRT-PCR of the strawberry *FaAAT2* gene expression in different vegetative tissues (A) and strawberry receptacles of mature (red) and immature (green) fruits (B).** The results were obtained using *FaAAT2* specific primers. Quantification is based on Ct values as described in Materials and Methods. The increase in mRNA values was relative to crowns tissue, which had the lowest *FaAAT2* expression and was assigned an arbitrary value equal to unity. Statistical significance with respect to reference sample (crowns tissue) was determined by the Student's *t*-test. (\*\*\*) *p*-value < 0.001.

The comparative gene expression analysis in receptacle of control fruits and deached green fruits demonstrated a clear increase of *FaAAT2* gene expression in deached fruits that was reverted after the external application of auxin (NAA) on deached fruits (Fig. 7). This result showed that the *FaAAT2* expression is negatively regulated by auxins released from the achenes into the fruit receptacle.



**Fig. 7. Analysis of the effects of removing achenes from G2 developing fruits and their treatment with auxins on *FaAAT2* gene expression by QRT-PCR.** The auxin treatments were performed with a lanolin paste with 1 mM NAA in 1 % (w/v) DMSO applied on the fruit surface. The increase in mRNA values was relative to G2 fruit (control), which was assigned an arbitrary value equal to unity. Control: middle-sized green fruit receptacle (G2 fruit); - Achenes: G2 fruit receptacle without achenes for 5 days; 5 days + NAA: G2 fruit receptacle without achenes plus NAA for 5 days (added at day zero). Statistical significance with respect to control sample (G2 fruits) was determined by the Student's *t*-test. (\*\*\*) *p*-value < 0.001.

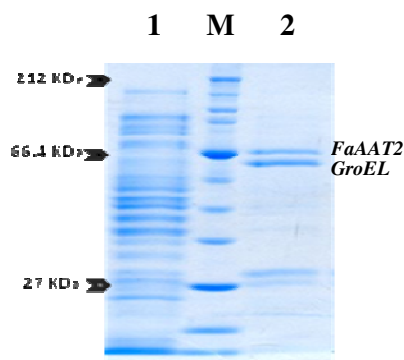
*FaAAT2* and *SAAT* expression was also analyzed in ripe fruits of different strawberry cultivars. *FaAAT2* was highly expressed in fruits of the cultivated variety *F. x ananassa* cv. Camarosa, showed intermediate expression levels in the cultivars *F. virginiana* and *F. chiloensis*, and showed the lowest level of expression in the wild variety *F. vesca* (Fig. 8A and 8B). *SAAT* transcript levels were higher in fruits of *F. virginiana* and *F. vesca* than in *F. x ananassa* cv. Camarosa and *F. chiloensis* (Fig. 8C).



**Fig. 8. Analysis by QRT-PCR of *FaAAT2* (A and B) and *SAAT* (C) gene expression in different strawberry cultivars.** The results were obtained using *FaAAT2* and *SAAT* specific primers for each gene. Quantification is based on Ct values as described in Materials and Methods. The increase in mRNA values was relative to the mRNA level found in the *F. vesca* variety, which was assigned an arbitrary value of unity. Statistical significance with respect to reference sample was determined by the Student's *t*-test. (\*\*\*) *p*-value < 0.001.

### 3.3. Enzymatic characterization of *FaAAT2* protein expressed in *Escherichia coli*

The coding region of the *FaAAT2* cDNA cloned in frame with GST-tag was used to express the recombinant *FaAAT2* enzyme in *E. coli*. Protein SDS-PAGE analysis showed a band that could not be detected in the control samples and presumably corresponded to the recombinant *FaAAT2*-GST protein (Fig. 9). The molecular mass of the *FaAAT2*-GST protein was 70 kD (43 kD plus 27 kD of the GST-tag) which is coincident with the estimated size deduced from the full length cDNA corresponding to the *FaAAT2* gene and, for this reason, the recombinant protein was not sequenced.



**Fig. 9. Purification of FaAAT2 protein from induced *E. coli* culture.** 1, Sample induced with *IPTG*; 2, Purified recombinant FaAAT2 protein; M, protein markers. An additional protein was co-purified by affinity chromatography and identified as the *E. coli* chaperon protein GroEL, which seems to bind to FaAAT2 during the purification process. The presence of *E. coli* GroEL may assist FaAAT2 to remain soluble throughout the purification procedure (Souleyre *et al.*, 2005).

Different alcohols were independently fed to *FaAAT2*-expressing *E. coli* to determine whether the recombinant FaAAT2 protein possessed enzymatic activity and to clarify its substrate preference (Table 1). When alcohols such as methanol, ethanol, propanol, butanol, pentanol, hexanol, heptanol, octanol, geraniol, eugenol, benzyl alcohol, 2-phenyl ethanol and cinnamyl alcohol were added, the formation of different types of ester could be detected. Esters such as nonyl acetate, decyl acetate, farnesyl acetate, neryl acetate, etc. were never detected. The results showed that the FaAAT2 protein can use endogenous *E. coli* acetyl-CoA when acyl-CoA substrate is not supplied exogenously. Moreover, methyl butanoate, ethyl hexanoate, and hexyl hexanoate were also detected (Table 1) indicating that the FaAAT2 protein can also use longer endogenous acyl-CoA molecules as substrates. The FaAAT2 protein was able to produce esters using endogenous *E. coli* acyl-CoAs and 15 different alcohols tested in this study.

To characterize the enzymatic activity of FaAAT2 recombinant protein, the FaAAT2-GST fusion protein was semi-purified from an induced crude *E. coli* extract using GST-tag resin and assessed the substrate specificity of the protein *in vitro* by supplying a range of alcohols and acyl-CoAs. The volatile esters produced were analysed by GC-MS. The kinetic properties of FaAAT2 were determined using combinations of 13 alcohols were tested at saturation concentration (20 mM) with four different acyl-CoAs as donors (acetyl-CoA, propionyl-CoA, butyryl-CoA and hexanoyl-CoA) at different concentrations (Table 2). The specificity constant for acetyl-CoA was highest when cinnamyl alcohol was used as co-substrate ( $K_{cat}/K_m$   $50.53 \text{ sec}^{-1}\mu\text{M}^{-1}$ ) whereas in the presence of hexanol and octanol it was  $42.95 \text{ sec}^{-1}\mu\text{M}^{-1}$  and  $18.92 \text{ sec}^{-1}\mu\text{M}^{-1}$ , respectively. Much lower specificity constants were observed for propionyl-CoA, butyryl-CoA and hexanoyl-CoA, independent of the alcohol used, except for eugenol. Thus, when hexanol was used as co-substrate, the specificity constant for acetyl-CoA was  $42.95 \text{ sec}^{-1}\mu\text{M}^{-1}$ , and  $5.85 \text{ sec}^{-1}\mu\text{M}^{-1}$ ,  $0.515 \text{ sec}^{-1}\mu\text{M}^{-1}$  and  $0.215 \text{ sec}^{-1}\mu\text{M}^{-1}$  for propionyl-CoA, butyryl-CoA and hexanoyl-CoA, respectively. This suggests that acetyl-CoA is the preferred acyl donor of FaAAT2 *in vivo* (Table 3).

To study the specificity of FaAAT2 for the alcohol substrates, different concentrations of alcohols were used in combination with acetyl-CoA at saturated concentration (0.1 mM) (Table

4). The specificity constant was highest for cinnamyl alcohol ( $727 \text{ sec}^{-1} \text{ mM}^{-1}$ ) followed by hexanol ( $314 \text{ sec}^{-1} \text{ mM}^{-1}$ ) and octanol ( $208 \text{ sec}^{-1} \text{ mM}^{-1}$ ).

Alcohol added	Carbon number	Esters expected	Esters produced in <i>E. coli</i> <sup>a</sup>	Esters produced by purified FaAAT2 <sup>b</sup>	Esters produced in the control assay <sup>c</sup>	Reported from strawberry*
Methanol	C1:0	Methyl acetate	+	+	-	+
		Methyl propanoate	+	+	-	+
		Methyl butanoate	+	+	-	+
		Methyl hexanoate	+	+	-	+
Ethanol	C2:0	Ethyl acetate	+	+	-	+
		Ethyl butanoate	+	+	-	+
		Ethyl hexanoate	+	+	-	+
		Ethyl heptanoate	+	n.d	-	+
Propanol	C3:0	Propyl acetate	+	+	-	+
		Propyl propanoate	-	-	-	-
		Propyl butanoate	-	-	-	-
		Propyl hexanoate	-	-	-	+
2-Propanol	C3:0	2-Propyl acetate	-	-	-	+
Butanol	C4:0	Butyl acetate	+	+	-	+
		Butyl propanoate	+	+	-	-
		Butyl butanoate	+	+	-	+
		Butyl hexanoate	+	+	-	+
		Butyl octanoate	+	n.d	-	+
2-Butanol	C4:0	2-Butyl acetate	-	-	-	+
3-Methylbutanol	C5:0	3-Methylbutyl acetate	-	-	-	+
Pentanol	C5:0	Pentyl acetate	+	+	-	+
		Pentyl propanoate	+	-	-	-
		Pentyl hexanoate	-	-	-	+
Hexanol	C6:0	Hexyl acetate	+	+	-	+
		Hexyl propanoate	+	+	-	+
		Hexyl butanoate	+	+	-	+
		Hexyl hexanoate	+	+	-	+
		Hexyl octanoate	+	n.d	-	+
Hex-3(Z)-enol	C6:1	Hexen-3(Z)-enyl acetate	+	-	-	+
Hex-2(E)-enol	C6:1	Hexen-2(E)-enyl acetate	-	-	-	+
Heptanol	C7:0	Heptyl acetate	+	+	-	-
		Heptyl butanoate	+	+	-	-
Octanol	C8:0	Octyl acetate	+	+	-	+
		Octyl propanoate	+	+	-	-
		Octyl butanoate	+	+	-	+
		Octyl hexanoate	+	+	-	+
Oct-1-en-3-ol	C8:1	Oct-1-en-3-yl acetate	-	-	-	-
Nonanol	C9:0	Nonyl acetate	-	-	-	-
Decanol	C10:0	Decyl acetate	-	-	-	+
Geraniol	C10:2	Geranyl acetate	+	+	-	-
Linalool	C10:2	Linalyl acetate	-	-	-	-
Farnesol	C15:3	Farnesyl acetate	-	-	-	-
Benzyl alcohol	C7:3	Benzyl acetate	+	+	-	+
Nerol	C10:2	Neryl acetate	-	-	-	-
Nerolidol	C15:3	Nerolidyl acetate	-	-	-	-
Eugenol	C10:4	Eugenyl acetate	+	+	-	-
Furfuryl alcohol	C5:2	Furfuryl acetate	+	-	-	-
2-Phenylethanol	C6:3	2-Phenylethyl acetate	+	+	-	+
		2-Phenylethyl propanoate	+	+	-	+
		2-Phenylethyl butanoate	+	+	-	-
Cinnamyl alcohol	C9:4	Cinnamyl acetate	+	+	-	-

**Table 1. Alcohol substrates used with acetyl-CoA in the FaAAT2 recombinant enzyme assay and esters produced by purified FaAAT2 protein.** The enzyme assays were performed with the recombinant FaAAT2 protein before (<sup>a</sup>) and after (<sup>b</sup>) of its purification. In all assays, the empty vector pGEX-T4 was employed as control (<sup>c</sup>). The esters indicated were produced by the activity of the FaAAT2 recombinant enzyme and not by the internal alcohol acyl transferase activity from *E. coli*. n.d: not determined. (\*) Zabetakis and Holden, 1997; Pysalo *et al.*, 1979.

Co-substrate S2 (Saturated concentration)	Co-substrate S1 Acetyl-CoA (Variable concentration)	Co-substrate S1 Propionyl-CoA (Variable concentration)	Co-substrate S1 Butyryl-CoA (Variable concentration)	Co-substrate S1 Hexanoyl-CoA (Variable concentration)
Methanol	1.05	0.11	0.53	0.17
Ethanol	0.16	0.14	0.03	0.27
Propanol	3.41	n.d	n.d	n.d
Butanol	7.51	0.02	0.04	0.18
Pentanol	10.49	n.d	n.d	n.d
Hexanol	42.95	5.85	0.515	0.215
Heptanol	9.98	2.22	n.d	n.d
Octanol	18.92	6.14	0.05	0.06
Geraniol	33.41	3.25	5.07	5.50
Benzyl alcohol	0.25	1.85	0.09	0.39
Eugenol	12.1	33.41	0.10	n.d
2-Phenylethanol	0.43	0.37	0.23	0.13
Cinnamyl alcohol	50.53	5.00	1.58	0.68

**Table 2. Kinetic parameters [ $K_{cat}/K_m$  ( $\text{sec}^{-1}\mu\text{M}^{-1}$ )] of the purified recombinant *FaAAT2* enzyme for different types of alcohols in combination with different Acyl-CoA molecules. Alcohols were used at saturated concentration (20 mM) while the acyl-CoAs were used at variable concentration (0.01 mM, 0.1 mM, 0.25 mM, 1 mM and 2.5 mM). n.d: ester not detected.**

Co-substrate S2 (20 mM)	Co-substrate S1 (Variable concentration)	Km ( $\mu\text{M}$ )	Vmax ( $\text{nmol}\cdot\text{sec}^{-1}$ $\text{mg}^{-1}\text{prot}$ )	Kcat (Vmax / conc. enzyme)
Methanol	Acetyl-CoA	$4.0 \pm 1.4$	$0.08 \pm 0.01$	4.2
Ethanol	Acetyl-CoA	$8.0 \pm 0.7$	$0.02 \pm 0.01$	1.2
Propanol	Acetyl-CoA	$28.0 \pm 0.8$	$0.2 \pm 0.0$	57.3
Butanol	Acetyl-CoA	$29.0 \pm 0.2$	$0.4 \pm 0.1$	217
Pentanol	Acetyl-CoA	$26.0 \pm 0.4$	$0.5 \pm 0.0$	272
Hexanol	Acetyl-CoA	$5.4 \pm 0.3$	$0.4 \pm 0.1$	231
Heptanol	Acetyl-CoA	$38.0 \pm 0.1$	$0.7 \pm 0.1$	375
Octanol	Acetyl-CoA	$36.0 \pm 0.9$	$1.3 \pm 0.7$	681
Geraniol	Acetyl-CoA	$49.0 \pm 0.7$	$0.8 \pm 0.2$	391
Benzyl alcohol	Acetyl-CoA	$26.0 \pm 1.4$	$0.1 \pm 0.01$	6.5
Eugenol	Acetyl-CoA	$31.0 \pm 0.2$	$0.7 \pm 0.1$	376
2-Phenyl ethanol	Acetyl-CoA	$53.0 \pm 0.9$	$0.04 \pm 0.02$	23
Cinnamyl alcohol	Acetyl-CoA	$77.0 \pm 0.1$	$7.8 \pm 0.9$	3890

**Table 3.** Kinetic parameters [ $K_{\text{cat}}/K_{\text{m}}$  ( $\text{sec}^{-1}\mu\text{M}^{-1}$ )] of the purified recombinant *FaAAT2* protein using different alcohol substrates at saturated concentration (20 mM) and Acetyl-CoA at variable concentration (0.01 mM, 0.1 mM, 0.25 mM, 1 mM and 2.5 mM). n.d: ester not detected.



Co-substrate S2 (0.1mM)	Co-substrate S1 (Variable concentration)	Km (mM)	Vmax (nmol.sec <sup>-1</sup> mg <sup>-1</sup> prot)	Kcat (Vmax / conc. enzyme)	K <sub>cat</sub> /K <sub>m</sub> (sec <sup>-1</sup> mM <sup>-1</sup> )
Acetyl-CoA	Methanol	4.05 ± 0.07	0.03 ± 0.01	18.5	4.5
Acetyl-CoA	Ethanol	4.35 ± 0.05	0.01 ± 0.00	7.5	1.7
Acetyl-CoA	Propanol	2.40 ± 0.27	0.03 ± 0.01	17.5	7.2
Acetyl-CoA	Butanol	2.34 ± 0.31	0.04 ± 0.02	21.5	9.1
Acetyl-CoA	Pentanol	5.78 ± 0.87	0.81 ± 0.24	407	71.0
Acetyl-CoA	Hexanol	1.53 ± 0.02	0.96 ± 0.45	483	314
Acetyl-CoA	Heptanol	2.71 ± 0.08	0.34 ± 0.12	170	62
Acetyl-CoA	Octanol	2.23 ± 0.02	0.93 ± 0.05	466	208
Acetyl-CoA	Benzyl alcohol	4.57 ± 0.89	0.04 ± 0.01	23.5	5.14
Acetyl-CoA	2-Phenyl ethanol	4.32 ± 0.76	0.09 ± 0.01	49.6	11.4
Acetyl-CoA	Eugenol	3.78 ± 0.45	1.09 ± 0.04	548.5	150
Acetyl-CoA	Geraniol	2.04 ± 0.32	0.74 ± 0.01	370.5	180
Acetyl-CoA	Cinnamyl alcohol	2.03 ± 0.78	2.81 ± 0.54	1480	727

**Table 4.** Kinetic parameters of the purified recombinant FaAAT2 enzyme with different types of alcohols at variable concentration (1 mM, 5 mM, 10 mM, 20 mM, 60 mM) in combination with Acetyl-CoA (0.1 mM).

### 3.4. Determination of alcohols and volatile esters from strawberry fruit

The analysis of esters emitted during strawberry fruit ripening showed that the highest concentration of esters was always detected in the red fruit stage in *F. x ananassa* cv. Camarosa and *F. vesca* (Table 5). The most abundant esters were acetates, followed by butanoates, and hexanoates. Butyl acetate, ethyl acetate, ethyl butanoate and ethyl hexanoate are the esters which contribute to the strawberry fruit aroma (Jetti *et al.*, 2007). The major esters detected in *F. vesca* were octyl acetate, hexyl acetate and butyl butanoate. In contrast, the most abundant esters detected in *F. x ananassa* cv. Camarosa were methyl butanoate, methyl acetate, methyl hexanoate and hexyl acetate. Some of the esters present in *F. vesca* (e.g. ethyl acetate, pentyl acetate, heptyl acetate and myrtenyl acetate) did not appear in *F. x ananassa* and other esters present in the commercial variety (e.g. methyl acetate, methyl propionate, and butyl acetate) were not detected in the wild variety. The concentration of many alcohols increased or remained constant during strawberry fruit ripening, correlating with increased levels of their respective esters. Thus, ethanol and octanol appeared in the red fruit stage of *F. vesca* whereas the hexanol concentration increased during ripening. The same holds for butanol, hexanol and octanol in *F. x ananassa* cv. Camarosa. On the other hand, the level of alcohols such as heptanol and nonanol decreased during fruit development in *F. vesca*. These alkanols could not be detected in red fruits of *F. x ananassa* cv. Camarosa.

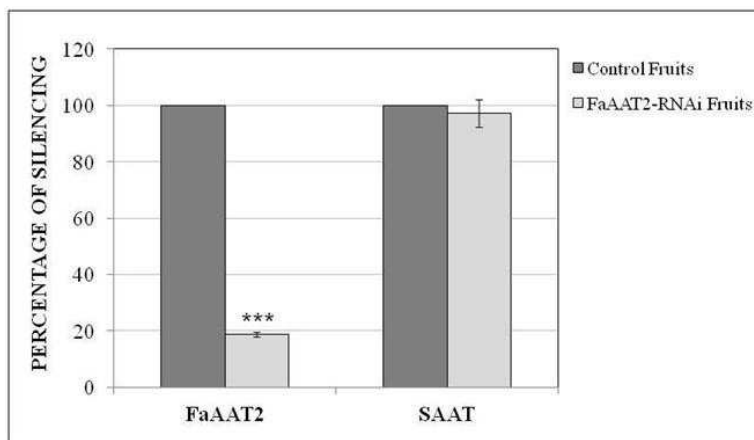
Chapter 2: The fruit ripening related gene *FaAAT2* encodes an acyl transferase involved in strawberry aroma biogenesis

	<i>Fragaria vesca</i>			<i>Fragaria x ananassa</i> cv. Camarosa				
	G	W	R	G1	G2	G3	W	R
Ethyl acetate			3.2 ± 0.3			15.9 ± 4.6	18.5 ± 3.7	
Ethanol			5.8 ± 1.2	9.1 ± 2.0	6.7 ± 1.3	6.8 ± 1.9		
Methyl acetate								16 ± 5
Methyl propanoate								0.7 ± 0.1
Methyl butanoate			4.7 ± 0.3					78.3 ± 4.1
Methyl 3-methylbutanoate								3.5 ± 0.3
Ethyl butanoate			60 ± 7					2.1 ± 0.5
Butanol								0.3 ± 0.1
2-Butanol				0.5 ± 0.1				
1-Methylethyl butanoate								9.9 ± 1.7
Butyl butanoate			30.1 ± 9.2					1.2 ± 0.2
Butyl acetate								2.2 ± 0.9
2-methylbutyl acetate				2.3 ± 1.2				1.4 ± 0.9
3-methylbutyl acetate								1.7 ± 0.7
3-methylbutyl butanoate								0.3 ± 0.0
Propyl butanoate			0.7 ± 0.3					
Methyl 4-methyl pentanoate								0.2 ± 0.0
Pent-1-en-3-ol	6.3 ± 1.3	1.7 ± 0.8		3.4 ± 0.3	3.8 ± 2.5	3.1 ± 2.0	1.8 ± 0.1	0.3 ± 0.0
Pent-2(Z)-enol	3.4 ± 1.2	1.6 ± 0.5			2.1 ± 0.8	1.5 ± 0.6	0.9 ± 0.0	0.4 ± 0.0
Methyl hexanoate			18.0 ± 5.1					14.0 ± 3.1
Ethyl hexanoate			61.0 ± 8.5					1.9 ± 0.9
3-methylbut-2-enyl acetate			3.0 ± 0.4					
3-methylbut-3-enyl acetate	1.8 ± 0.7							
Pentanol	8.3 ± 1.3	2.8 ± 0.9	3.4 ± 0.1	2.3 ± 0.0	2.0 ± 1.0	3.7 ± 0.7	8.0 ± 0.3	7.6 ± 0.3
2-Pentanol								
Pentyl acetate			1.7 ± 0.3	3.3 ± 1.1				
2-Heptyl acetate			13 ± 2					
Hexyl acetate			97 ± 10					4.2 ± 1.7
Hex-2(E)-enyl acetate			45.0 ± 4.6					1.4 ± 0.0
Hex-3(Z)-enyl acetate			23 ± 7	3.4 ± 1.0		0.2 ± 0.0	0.5 ± 0.1	0.3 ± 0.0
Heptanol	2.9 ± 0.9							
3-Ethyl-4-methyl pentanol	3.3 ± 0.1							
Heptyl butanoate			0.9 ± 0.1					
Heptyl acetate			0.4 ± 0.0					
Hexanol	4.0 ± 0.8	4.5 ± 0.5	13 ± 2	1.7 ± 0.4	1.4 ± 0.2	1.5 ± 0.0	0.8 ± 0.0	1.1 ± 0.0
Hex-3(Z)-enol	8.9 ± 1.8	6.8 ± 1.7	2.8 ± 0.6	1.3 ± 0.0	10.1 ± 2.0	9.7 ± 0.3	2.0 ± 0.6	0.6 ± 0.0
Hex-2(E)-enol			14 ± 2	1.5 ± 0.2	1.4 ± 0.0	1 ± 0.1	0.9 ± 0.0	
Hex-3(Z)-enylbutanoate			0.3 ± 0.1					
Butyl hexanoate			4.5 ± 1.0					0.1 ± 0.0
Hexyl butanoate			1.5 ± 0.5					0.3 ± 0.6
3-methyl butyl butanoate								0.2 ± 0.1
Ethyl octanoate			4.4 ± 0.2					
Hex-2(E)-enyl acetate								3.7 ± 0.7
Non-2-enol				2.3 ± 0.2			0.1 ± 0.0	2.7 ± 0.1
Octyl acetate			273 ± 15					0.2 ± 0.0
Hex-2(E)-enyl butanoate			4.1 ± 0.7					
Nonanol	2.2 ± 0.8	1.1 ± 0.1	0.5 ± 0.1					
2-Nonanol			96 ± 16					
Linalool	5.4 ± 1.2	1.1 ± 0.8	1.3 ± 0.3	9.0 ± 0.3	7.1 ± 0.6	2.2 ± 0.1	0.4 ± 0.1	7.5 ± 1.2
Methyl decanoate			1.3 ± 0.7					
Octanol			72 ± 7				0.1 ± 0.0	1.3 ± 0.7
Oct-1-en-3-ol	4.11 ± 0.2	9.27 ± 2.1		1.2 ± 0.3	1.8 ± 0.7	2.6 ± 0.4	3.2 ± 1.1	3.2 ± 0.6
Octyl butanoate			18 ± 4					0.3 ± 0.0
Phenyl ethanol	3.9 ± 0.6			0.2 ± 0.0	0.1 ± 0.0			
Benzyl acetate								0.3 ± 0.0
Benzyl decanoate			5.4 ± 1.2					0.7 ± 0.1
Benzyl alcohol	5.2 ± 0.3	1.6 ± 0.5		3.9 ± 1.0	1.5 ± 0.8	1.1 ± 0.0	0.4 ± 0.0	
Myrtenol	2.2 ± 0.4	2.1 ± 0.6	5.9 ± 1.9	1.5 ± 0.7	0.3 ± 0.1	0.2 ± 0.0		
Myrtenyl acetate			28 ± 6					

**Table 5. GC-MS analysis of alcohols and volatile esters present in red ripe strawberry fruit from both *F. x ananassa* cv. Camarosa and *F. vesca* varieties.** The values are shown in pmol.L<sup>-1</sup>. G, G1, G2 and G3: green strawberry fruits in different development stages; W: white strawberry fruits; R: red strawberry fruits.

### 3.5. Silencing of the *FaAAT2* gene by agroinfiltration

The expression of the *FaAAT2* gene in strawberry fruit underwent a transitory down-regulation by RNAi. The analysed transgenic fruits showed an important reduction of *FaAAT2* gene expression level while the expression *SAAT* gene remained constant (Fig. 10). Moreover, the production of volatile esters such as ethyl acetate, methyl acetate, methyl butanoate, methyl 2-methylbutanoate, methyl 2-methylbutanoate, methyl hexanoate, ethyl hexanoate, butyl acetate, and hexyl acetate was reduced in *FaAAT2* silenced fruits (Table 6).



**Fig. 10.** Analysis by QRT-PCR of *FaAAT2* and *SAAT* gene expression in transgenic strawberry fruits agroinfiltrated with the pFRN-*FaAAT2* construct and control fruits only agroinfiltrated with the empty pFRN vector. The silencing level is expressed as a percentage. Statistical significance was determined by the Student's *t*-test. (\*\*\*) *p*-value <0.001.

	<i>FaAAT2</i> (ppm)	CONTROL (ppm)
Ethyl acetate	0.50 ± 0.03*	1.04 ± 0.27
Methyl acetate	0.60 ± 0.36**	3.26 ± 1.01
Methyl butanoate	0.54 ± 0.30*	1.35 ± 0.09
Methyl-2/3-methyl butanoate <sup>(1)</sup>	0.87 ± 0.58*	3.01 ± 1.15
Ethyl butanoate	0.05 ± 4.47*	0.89 ± 0.54
Methyl hexanoate	2.65 ± 1.06	4.57 ± 1.81
Ethyl hexanoate	0.78 ± 0.45*	3.33 ± 1.75
Butyl acetate	0.02 ± 0.00	0.11 ± 0.07
Hexyl acetate	0.13 ± 0.33	0.70 ± 0.17
Ethanol	4.25 ± 1.22**	47.53 ± 5.85
Hexanol	0.66 ± 0.08	2.61 ± 0.77

**Table 6.** GC-MS quantification of alcohols and volatile esters in strawberry red fruit cv. Elsanta with the *FaAAT2* gene expression silenced by agroinfiltration. Three biological replicates were used for this analysis. <sup>(1)</sup> Methyl-2/3-methyl butanoate stands for the co-elution of methyl 2-methyl butanoate and methyl 3-methyl butanoate. It was calculated with the internal standard method assuming a response factor of one. The values are shown in ppm. (\*) *p*-value < 0.05 and (\*\*) *p*-value < 0.01.

## 4. DISCUSSION

Since volatile esters play a fundamental role in developing the characteristic strawberry aroma during ripening, this study was focused on the novel strawberry alcohol acyl-CoA transferase 2 (*FaAAT2*), a gene which encodes an important enzyme involved in fruit aroma biogenesis (Pérez *et al.*, 1993; Pérez *et al.*, 1996; Aharoni *et al.*, 2000; Olias *et al.*, 2002; Beekwilder *et al.*, 2004; González *et al.*, 2009).

*FaAAT2* shares the characteristic motifs of the BAHD class III acyltransferases involved in the production of volatile ester in flowers and ripening fruits. The HXXXDG motif, corresponding to residues 174 to 179 (Fig. 2), is shared by several other families of enzymes that use coenzyme-A thioesters and seems to be involved in catalysis (St-Pierre & De Luca, 2000; D'Auria, 2006). However, although in *FaAAT2* the histidine and aspartic acid residues are conserved, the glycine residue is substituted by alanine. This replacement occurs in other plant AAT such as CbBEBt from *Clarkia breweri* (D'Auria *et al.*, 2002), VpAAT1 from *Vasconcellea pubescens* (Balbontin *et al.*, 2010) and CmAAT3 from *Cucumis melo* (El-Sharkawy *et al.*, 2005); while the glycine residue is substituted by methionine in BEAT from *Clarkia breweri*. The second conserved motif of *FaAAT2* protein is the DFGWG motif, corresponding to residues 422 to 426 (Fig. 2), which is located near the carboxyl terminus and seems to play a role in the maintenance of the enzyme structure (El-Sharkawy *et al.*, 2005; D'Auria, 2006). This motif shows the substitution of a tryptophan residue by phenylalanine. In addition, the *FaAAT2* protein has a third consensus sequence, LXXYYPLAGR (residues 80 to 89), previously described in other AAT proteins such as SAAT and BEAT (Aharoni *et al.*, 2000), and VpAAT1 (Balbontin *et al.*, 2010). Although less conserved than the previous ones, this motif is located at the N terminus and it is common among AAT involved in the synthesis of volatile compounds in fruits and flowers (Balbontin *et al.*, 2010). Nevertheless, its function could also be related with the use of acetyl-CoA as co-substrate during the enzymatic reaction (Aharoni *et al.*, 2000).

Moreover, the majority of BAHD class III members accept a diverse range of alcohol substrates and utilize acetyl-CoA as the major acyl donor, a behaviour that matches with the strawberry *FaAAT2* protein. Like BanAAT1 from banana, the *FaAAT2* protein has preference for the formation of cinnamyl and geranyl acetate (Beekwilder *et al.*, 2004). However, it can also produce benzyl acetate as can CmAAT3 from *Cucumis melo*, CbBEBt and CbBEAT (both from *Clarkia*), all of which are included into subgroup III in the phylogenetic analysis (Dudareva *et al.*, 1998; D'Auria *et al.*, 2002). Contrarily to what one may expect, other AAT proteins isolated from strawberry fruit, such as SAAT, VAAT and FcAAT1 (Aharoni *et al.*, 2000; Beekwilder *et al.*, 2004; González *et al.*, 2009) were included in the subgroup II which is phylogenetically more distant, although SAAT and VAAT share with *FaAAT2* the ability to produce geranyl acetate and other esters present in strawberry fruit, such as hexyl acetate and octyl acetate (Aharoni *et al.*, 2000; Beekwilder *et al.*, 2004).

SAAT and *FaAAT2* transcript levels increase dramatically during the late stages of fruit ripening in the receptacles (Fig. 4A and 4B) and their expression is negatively regulated by auxins (Fig. 7, Aharoni *et al.*, 2000). This gene expression pattern was coincident with those reported previously for other strawberry ripening related genes, many of them related with the organoleptic properties of the strawberry fruit (Medina-Escobar *et al.*, 1997b; Moyano *et al.*, 1998; Blanco-Portales *et al.*, 2004; Raab *et al.*, 2006). However, a comparative study of *FaAAT2* and SAAT gene expression in different strawberry cultivars throughout fruit ripening also showed significant quantitative differences (Fig. 4B and 4D). Cultivar dependent AAT

activity was also demonstrated in four different varieties of strawberry (Pérez *et al.*, 1996). In these varieties, AAT activity clearly increased in the later fruit maturation stages, being much higher in the "Chandler" and "Oso Grande" varieties than in variety "I-101" (Pérez *et al.*, 1996). The low AAT specific activity in the "I-101" variety could be correlated with the poor flavour of its fruits (López-Aranda *et al.*, 1995), suggesting that AAT activity influences the aroma level of strawberry fruits.

Among the substrates found in strawberry fruit, the FaAAT2 protein has preference for C6-C10 alcohols, being most active with hexanol followed by octanol and heptanol (Table 1 and 4). The specificity and activity are lower with short chain alcohols. This preference of FaAAT2 for substrates is quite similar to the preference of the partially purified AAT from variety "Chandler", which preferably uses hexanol and shows lower activity with short chain alcohols (the activity with ethanol was 25 % compared to hexanol) (Pérez *et al.*, 1993). Moreover, both enzymes show higher activity when using linear alcohols than using branched chain ones with the same number of carbons, like the yeast AAT (Yoshioka and Hasimoto, 1981). In contrast, the SAAT protein (*F. x ananassa* cv. Elsanta) also accepts longer chain alcohols as substrates and is active with heptanol and octanol but less with nonanol and decanol with respect to hexanol (Aharoni *et al.*, 2000). FaAAT2, like the SAAT protein did not have significant activity towards unsaturated C6 derivatives. The same behaviour was observed with the C3 isomer 2-propanol, the C4 isomer 2-butanol and the acyclic monoterpene alcohol linalool.

Recently, other plant AAT proteins have been characterized. The VAAT (*F. vesca*) protein shows a preference for small aliphatic alcohols (C4-C6) (Beekwilder *et al.*, 2004), in contrast to SAAT and FaAAT2. However, while VAAT and SAAT had only a modest activity with cinnamyl alcohol as substrate, this compound is the best substrate for BanAAT (Beekwilder *et al.*, 2004) and FaAAT2. These results suggest that SAAT, VAAT and FaAAT2 can clearly produce esters, such as hexyl acetate and octyl acetate, present in both wild and cultivated strawberry varieties, and therefore may well be implicated in determining the aroma of strawberry fruits. Geraniol is the preferred alcohol substrate for RhAAT from hybrid rose (*Rosa x hybrida*) being the presence of geranyl acetate in the rose flowers associated with RhAAT activity (Shalit *et al.*, 2003). Although SAAT (Beekwilder *et al.*, 2004) and FaAAT2 showed high substrate specificity for geraniol (Tables 1 and 4), the strawberry fruit is devoid of geranyl acetate (Table 5). Other studies performed with partially purified AAT from different commercial strawberry varieties showed an activity pattern similar to FaAAT2, a higher affinity for the straight-chain alcohols (C2 to C7) and a lower activity with butanol (Olias *et al.*, 2002). Moreover, Olias *et al.* (2002) proved that hexanol was the preferred alcohol for American cultivars ("Camarosa" and "Sweet Charlie") which is consistent with our results for the FaAAT2 protein (Table 4). However, it is now obvious that strawberry has more than one AAT enzyme, therefore the results of Olias *et al.* (2002) could be due to a mixture of AAT enzymes rather than to one specific AAT. Thus, these coincidences must be carefully considered.

The preference of FaAAT2 for shorter acyl-CoA molecules as substrate in combination with aliphatic C6-C8 alcohols (Tables 2 and 3) is similar to the partially purified AAT activity from the "Chandler" cultivar, which uses acetyl-CoA as preferred substrate (Pérez *et al.*, 1993), while the SAAT activity prefers long acyl-CoAs combined with aliphatic C4-C9 alcohols as substrates (Aharoni *et al.*, 2000). Similarly, the AAT activity characterized from the "Oso Grande" cultivar shows increasing preference for acyl-CoA molecules with increasing numbers of carbons, reaching its highest activity with hexanoyl-CoA (Olias *et al.*, 2002).

The specificity constant ( $K_{cat} / K_m$ ) of *FaAAT2* for acetyl-CoA was higher with cinnamyl alcohol and hexanol as cosubstrate than with octanol (Table 2), despite both hexanol and octanol are involved in the formation of volatiles in strawberry fruit. Thus, the *FaAAT2* enzyme seems to be more efficient for the production of cinnamyl acetate and hexyl acetate than for octyl acetate. Comparison of the kinetic parameters of *FaAAT2* with those of other proteins reported from strawberry (Aharoni *et al.*, 2000; Perez *et al.*, 1996; Olías *et al.*, 2002) clearly shows that *FaAAT2* differs from AAT proteins reported in other varieties of strawberry until now.

In general, the wide range of acyl-CoAs and alcohol substrates available in strawberry is related to the great variety of esters found in this fruit (Zabetakis and Holden, 1997). However this cannot fully explain the difference in composition of esters between the developing stages and the different cultivars of strawberry (Aharoni *et al.*, 2000). In this sense, the availability of substrates depending on the activity of several catabolic pathways, such as lipid breakdown, could be determinants of the esters composition in the strawberry fruit (Ueda and Ogata, 1976).

Despite the fact that the maximum of AAT activity and gene expression usually appear in the maturation stages (Aharoni *et al.*, 2000; Gonzalez *et al.*, 2009), the AAT activity has also been detected in white fruits in the cultivar “Chandler” (Pérez *et al.*, 1996). Indeed, some esters, like hex-3-enyl acetate which are present in green and white stages fruits of the cultivar “Camarosa” have been detected in early developmental stages (Table 5). Nevertheless, the main increase of fruit esters occurs in the red stage where especially acetates such as hexyl acetate and octyl acetate have been detected. Although both acetates appear in commercial and wild varieties, the amount of hexyl acetate synthesized in *F. x ananassa* cv. Camarosa is greater than octyl acetate probably due to the specificity of the *FaAAT2* enzyme for hexanol and acetyl-CoA substrates and the high expression of *FaAAT2* in this variety (Fig. 8). By contrast, the amount of octyl acetate is greater than hexyl acetate in *F. vesca*, suggesting the involvement of other AAT such as SAAT in the synthesis of esters. In general, these data seem to indicate that the amount of esters present in the fruit depends on the availability of substrates and specificity of the AAT enzyme(s). On the other hand and, according to the expression patterns, the absence of esters in immature stages of the strawberry fruit could be associated with the absence of precursors and low activity of alcohol acyl transferases activity (Yamashita *et al.*, 1977).

Volatile ester production was significantly reduced in strawberry fruit after transient down regulation of *FaAAT2* gene expression (Table 6). This reduction of volatile esters is probably caused only by the decrease of the alcohol acyl transferase activity due to silencing of the *FaAAT2* gene as the SAAT gene expression remained constant (Fig. 10). This suggests that *FaAAT2* is involved in the formation of esters such as ethyl acetate, methyl acetate, methyl butanoate, methyl-2/3-methyl butanoate, ethyl butanoate, and ethyl hexanoate, implicated in the aroma of strawberry fruit. On the other hand, the levels of ethanol and hexanol also decreased drastically in transiently silenced fruits (Table 6). Enhanced metabolism and/or decreased production of the alcohols could be a consequence of the silencing process. However, the underlying mechanism remained elusive.

In conclusion, this study suggests that *FaAAT2* is involved in the synthesis of strawberry fruit volatiles. This theory is supported by its maximum gene expression during ripe stages and the increase in its activity throughout the ripening process in parallel with the production of esters. Factors such as the substrate availability, participation of other AAT proteins and mechanisms

of gene regulation are other fundamentals that determine the characteristic aroma of strawberry fruit.

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## CHAPTER 3: *FaMYB10* PLAYS A MAJOR ROLE IN THE REGULATION OF THE FLAVONOID/PHENYLPROPANOID METABOLISM DURING THE RIPENING OF *FRAGARIA X ANANASSA* FRUITS

### 1. ABSTRACT

We provide strong evidence to indicate that the *Fragaria x ananassa FaMYB10* transcription factor (TF) plays a major and key role in the regulation of the expression of the genes of the flavonoid/phenylpropanoid (F/P) metabolism during the ripening of the fruit. *FaMYB10* gene expression is mainly confined to the fruit receptacles at the ripening stage and is repressed by auxins and activated by abscisic acid (ABA) in parallel to the ripening process. Anthocyanin production did not occur when we silenced *FaMYB10* after infiltrating fruits with live *Agrobacterium* cells harboring *FaMYB10*-RNAi constructs. The expression of *FaMYB10* was increased in fruit receptacle in the absence of auxins. However, a lack of *FaMYB10* expression occurred after adding the synthetic auxin NAA to the fruits, and also when ABA biosynthesis was inhibited. An earlier and greater accumulation of anthocyanins was observed in water stressed fruits that was accompanied by both, an increase in the ABA content and in the expression of *FaMYB10*. High-throughput transcriptomic analyses performed in fruits with both up and down-regulated *FaMYB10* expression clearly indicated that this TF regulates the expression of most of the genes involved in F/P metabolism related to the ripening. So, this gene could induce both the Early-regulated Biosynthesis Genes (*EBGs*) and the Late-regulated Biosynthesis Genes (*LBGs*) involved in both flavonols and anthocyanins production in fruit ripened receptacles.

### 2. INTRODUCTION

The accumulation of anthocyanin pigments in fruits is an important indicator of ripeness and fruit quality. Pigments influence the attraction of pollinators and predators helping seed dispersal, and playing an important role in plant protection against biotic and abiotic stresses (Feild *et al.*, 2001; Winkel-Shirley, 2001; Regan *et al.*, 2001; Schaefer *et al.*, 2004; Tanaka *et al.*, 2008). In strawberries, the red coloration of fruit receptacles is mainly due to the accumulation of the anthocyanin pelargonidin 3-*O*-glucoside (Perkins-Veazie, 1995; Lin-Wang *et al.*, 2010; Kawanobu *et al.*, 2011) and this plays a major role in consumer preference and marketability (Chiu *et al.*, 2010; Yang *et al.*, 2010; Carvalho *et al.*, 2010; Hichri *et al.*, 2011).

The flavonoid/phenylpropanoid pathway in plants (F/P metabolism) is responsible for the biosynthesis of anthocyanins. These pathways are organized in different metabolic branches that account for the synthesis of many different compounds such as hydroxycinnamic acid, isoflavones, flavonols, phlobaphenes and pro-anthocyanidins. They are responsible for the major red, purple, violet and blue pigments found in many flowers and fruits (Petroni and Tonelli, 2011).

Many highly conserved transcription factors (TFs) are known to regulate the expression of the genes involved in the F/P metabolism. They are mainly R2R3-MYB TFs interacting or

not with specific basic helix-loop-helix (bHLH) proteins and/or with a set of proteins containing conserved WD40 repeats to form the so-called ternary MBW complexes (Petroni and Tonelli, 2011; Hichri *et al.*, 2011). To date, there are documented cases of isolated or group of genes or branches of the F/P metabolism that are directly or indirectly regulated by these TFs (Petroni and Tonelli, 2011; Hichri *et al.*, 2011). In monocot maize, the genes responsible for the biosynthesis of anthocyanins are activated as a single unit by a whole MBW complex. In *Arabidopsis* plants however, there is a co-activator independent R2R3-MYB TF lacking both bHLH and WD40 that regulates the expression of the Early-regulated Biosynthesis group of Genes (*EBGs*), and a whole MBW-TF complex that regulates the expression of the Late-regulated Biosynthesis group of Genes (*LBGs*) (Petroni and Tonelli, 2011). In some *Rosacea* species such as apple and grape, anthocyanin biosynthesis is regulated mainly by MYB–bHLH complexes lacking WD40 (Takos *et al.*, 2006; Ban *et al.*, 2007; Espley *et al.*, 2007). In grapes (*Vitis vinifera*), anthocyanin biosynthesis is controlled by a single locus containing four MYB genes. Two of them, named *VvMYBA1* and *VvMYBA2* respectively, are involved in the regulation of the skin color (Kobayashi *et al.*, 2004; Cutanda-Perez *et al.*, 2009). Mutations in the promoter region of *VvmybA1* or in the coding region of *VvMYBA2* lead to a loss of anthocyanin biosynthesis in the skin, thus rendering white grapes (Kobayashi *et al.*, 2004). Although it was mentioned that *VvMYBA1* and *VvMYBA2* were exclusively regulating the expression of the *UFGT* gene (Boss *et al.*, 1996), a recent study indicates that *VvMYBA1* also regulates the expression of the anthocyanin vacuolar transporters *GST* and *MATE*, and also genes involved in anthocyanin methylation (Cutanda-Perez *et al.*, 2009). In apple (*Malus x domestica*), there are three different alleles of one same MYB gene (*MYB10*, *MYB1* and *MYBA*) controlling the red pigmentation of the fruit (Ban *et al.*, 2007; Takos *et al.*, 2006, Chagne *et al.*, 2007; Lin-Wang *et al.*, 2010). While *MYB1* and *MYBA* are involved in the anthocyanin biosynthesis in the skin, the *MYB10* gene is implicated both in the skin and the flesh (Ban *et al.*, 2007; Takos *et al.*, 2006). Recently, it has also been shown that the expression profile of putative orthologs of *MYB10* found in 20 different *Rosaceous* fruits, including strawberry, correlated with the anthocyanin production throughout the fruit ripening process, and that this required the presence of specific bHLH proteins (Lin-Wang *et al.*, 2010; Petroni and Tonelli, 2011, Espley *et al.*, 2007; Palapol *et al.*, 2009; Niu *et al.*, 2010). In tomato and pepper, some R2R3-MYB genes such as *LeMYB12*, *LeANT1*, *LeAN2* and *CaA*, also regulate the biosynthesis of anthocyanins and flavonols (reviewed by Petroni and Tonelli, 2011). In general, it has been reported that these TFs activate the expression of *LBGs* genes during fruit development (Borovsky *et al.*, 2004).

Most of the above studies represent cases showing that one of several of these MYB TFs regulate either a particular branch or group of genes implicated in the F/P metabolism, or is determinant in the expression of any or some of these genes in a specific tissue. The cases describing TFs playing a general or a broader regulatory role in the F/P metabolism are scarce. Exceptions are the maize gene and the *VvMYB5a/5b* genes that play a general regulatory role in *Vitis vinifera*, since they can apparently control at the same time the expression of all branches of the F/P metabolism, including those implicated in anthocyanin biosynthesis (Deluc *et al.*, 2006).

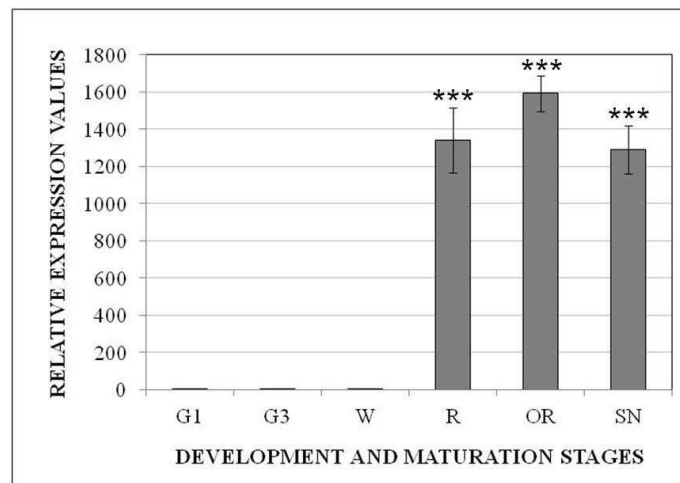
Here, we present novel data indicating that the *Fragaria FaMYB10* gene could play a role similar to that of *VvMYB5a/5b*, the latter being candidate for a TF that in strawberries plays a major and general role in the global control of the F/P metabolism throughout the ripening of the fruit. High-throughput transcriptomic and metabolomic analyses performed in fruits, where the expression of *FaMYB10* was either enhanced or transiently down-

regulated, clearly indicate that this TF regulates the expression of all the genes involved in the F/P metabolism related to flavonols and anthocyanins production. We also show that the expression of this *FaMYB10* gene takes place mainly in the receptacle, is repressed by auxins and induced by abscisic acid (ABA), which can explain the molecular bases of the recently described role of this latter hormone in the strawberry ripening process (Chai *et al.*, 2011; Jia *et al.*, 2011).

### 3. RESULTS

#### 3.1. *FaMYB10* is a receptacle-specific gene with its highest level of expression taking place in ripened and senescent fruit

We analyzed by means of semi-quantitative real-time PCR (qRT-PCR) the level of expression of *FaMYB10* in both receptacles and achenes throughout different stages of fruit development and ripening. In receptacles, *FaMYB10* was expressed at very low levels during the early G1 (green 1), G3 (green 3) and W (white) stages of fruit development (Fig. 1). A substantial and dramatic increase in its transcript levels took place however, during the R (red), OR (over-ripe) and SN (senescent) stages with a peak or maximum expression observed in the OR stage.

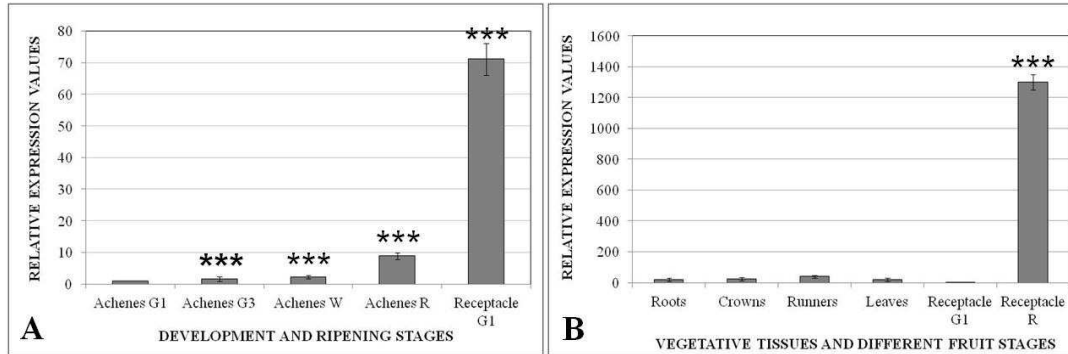


**Fig. 1. Developmental expression of the strawberry *FaMYB10* gene in fruit receptacles of *Fragaria x ananassa* cv. Camarosa.** Results were obtained by QRT-PCR using specific primers for *FaMYB10* gene. Quantification is based on Ct values as described in Materials and Methods. The increase in the mRNA value was relative to the G1-Ct value of each experiment which was assigned an arbitrary value equal to unity. Mean values  $\pm$  SD of five independent experiments are shown. G1: small-sized green fruit; G3: full-sized green fruit (both stages of development); W: white stage; R: red stage; OR: overripe stage; SN: senescent stage. Statistical significance with respect to the reference sample (G1 fruits) was determined by the Student's *t*-test. (\*\*\*) *p*-value < 0.001.

In achenes, *FaMYB10* was expressed at very low levels throughout all developmental and ripening stages studied when compared with the expression level obtained in the fruit receptacle at the G1-stage (Fig. 2A). The same happened when we studied the expression of

this gene in all vegetative tissues analyzed such as leaves, crowns, roots and runners (Fig. 2B).

All these data taken together allow us to define *FaMYB10* as a receptacle specific gene predominantly expressed during the ripening and senescence stages of fruit development.

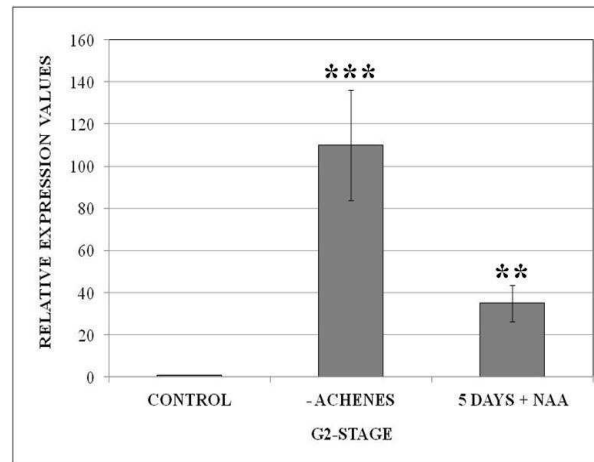


**Fig. 2. Analysis by QRT-PCR of the strawberry *FaMYB10* expression in achenes of *F. x ananassa* cv. Camarosa (A) and different vegetative tissues against immature G1 fruits and ripe R fruits (B).** The results were obtained using specific primers for *FaMYB10* gene. Quantification is based on Ct values as described in Materials and Methods. The increase in the mRNA values was relative to achenes G1-Ct value (A) and R-stage receptacle (B), which had the lowest *FaMYB10* expression in both experiments and was assigned an arbitrary value equal to unity. Mean values  $\pm$  SD of five independent experiments are shown. G1: small-sized green fruit; G3: full-sized green fruit (both stages of development); W: white stage; R: red stage. Statistical significance with respect to reference sample (Achenes G1 and roots) was determined by the Student's *t*-test. (\*\*\*) *p*-value < 0.001.

### 3.2. The expression of *FaMYB10* gene in fruit receptacles is repressed by auxins and activated by abscisic acid (ABA)

It has been proposed that a defined ABA / auxin content ratio present in receptacles could be a signal that triggers the fruit ripening process (Perkins-Veazie, 1995). Auxins are mainly produced by achenes and released afterwards to the receptacles, promoting receptacle growth and development and preventing at the same time a premature ripening. In addition, some recent reports have suggested that the phytohormone ABA may also be involved in the production of anthocyanins during the ripening of strawberry fruits (Chai *et al.*, (2011), Jia *et al.*, (2011)). Therefore, we studied how these two hormones affect *FaMYB10* expression.

To analyze the *in vivo* effects of auxins, we followed two complementary experiments. In the first one, we mechanically removed the achenes from several G2 fruits, and compared the *FaMYB10* transcript levels by real-time PCR after 5 days with that of untreated control fruits. A clear and substantial increase in the amount of *FaMYB10* transcripts was observed in the de-achened fruits in comparison with control fruits. The second experiment was done by determining that the increase in the *FaMYB10* expression in the de-achened fruits was abolished by the external application of auxins (NAA) (Fig. 3).

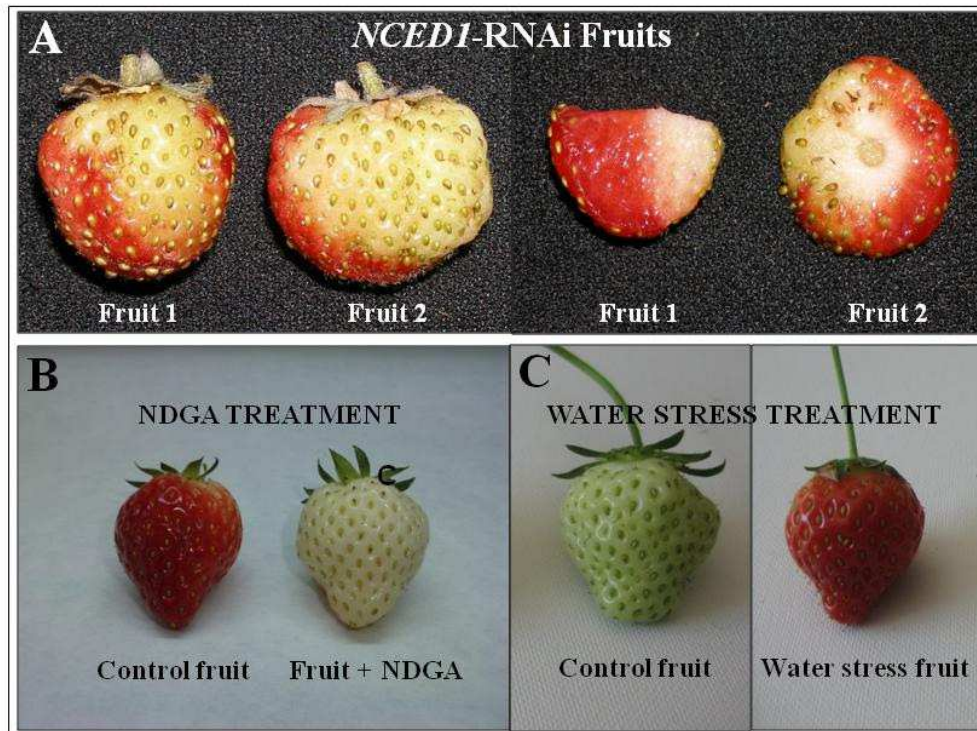


**Fig. 3. Analysis by QRT-PCR of the effects of removing achenes from G2 developing fruits and their treatment with auxins on *FaMYB10* gene expression.** The auxin treatment was performed with a lanolin paste with 1mM NAA in 1 % (w/v) DMSO applied on the fruit surface. The increase in the mRNA value was relative to control (G2 fruit), which was assigned an arbitrary value equal to unity. Mean values  $\pm$  SD of three independent experiments are shown. Control: middle-sized green fruit receptacle (G2 fruit); - achenes: G2 fruit receptacle without achenes for 5 days; 5 days + NAA: G2 fruit receptacle without achenes plus NAA for 5 days (added at day zero). Statistical significance with respect to control sample (G2 fruits) was determined by the Student's *t*-test. (\*\*) *p*-value < 0.01 and (\*\*\*) *p*-value < 0.001.

To assess the role played by ABA in the regulation of the *FaMYB10* expression, we modulated the ABA content (down and up) through three experimental approaches: 1) by transiently inhibiting the expression of the *FaNCED* gene coding 9 cis-epoxy-carotenoid dioxygenase, the key enzyme responsible for the biosynthesis of ABA. This was accomplished through *in vivo* agroinfiltration with live *Agrobacterium* cells harboring *FaNCED1*-RNAi constructs; 2) by adding nordihydroguaiaretic acid (NDGA), a known inhibitor of this 9 cis-epoxy-carotenoid dioxygenase activity; and 3) by starving plant of water, as water stress is known to increase the content of ABA in the plants.

A lack of red coloration was observed in fruits that were either agroinfiltrated with *FaNCED1*-RNAi constructs or treated with the inhibitor NDGA (Fig 4A and B). In contrast, an early appearance and also a substantial increase in fruit red coloration was noticed in fruits subjected to water stress (Fig. 4C). It is worth mentioning that the agroinfiltration was done only in half of the receptacles with *Agrobacterium* harboring the *FaNCED1*-RNAi construct, while the other half was agroinfiltrated with bacteria harboring the same vector but lacking the RNAi sequences that were then used as control. We observed no noticeable changes in the half lacking the RNAi construct in relation to untreated fruits.

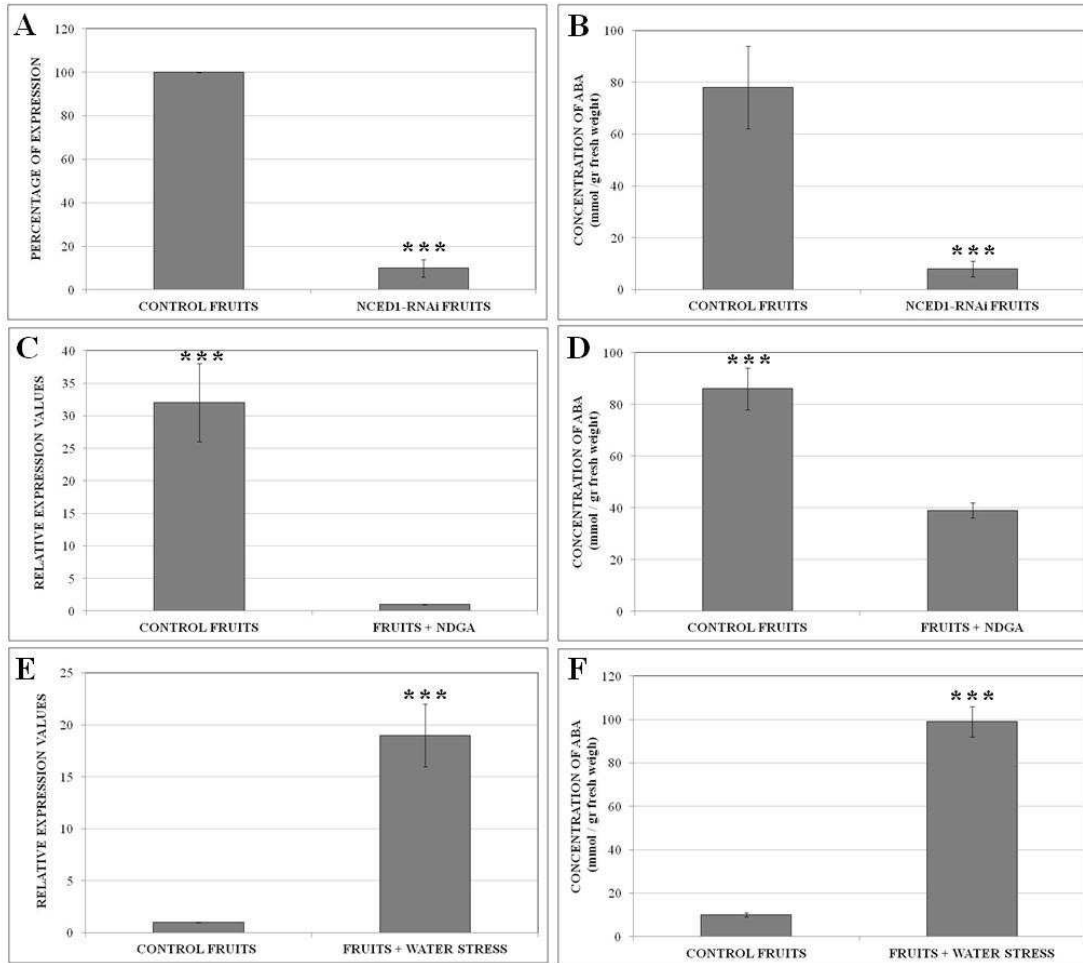




**Fig. 4.** (A) Strawberry G-W fruits agroinfiltrated with the *NCEDI*-RNAi construct; (B) G-W fruits treated with NDGA. Control fruit: G-W fruit injected with H<sub>2</sub>O; Fruit + NDGA: G-W fruits injected with NDGA (100  $\mu$ M), both samples were harvested 8 days after the beginning of the treatment; (C) Strawberry G-W fruits under water stress. Control fruit: fruits with the pedicels immersed on MS medium with sucrose; Water stress fruit: fruits with the pedicels kept air pedicels. Both samples were harvested 4 days after the beginning of the treatment. The cultivar used in all experiments was *Fragaria x ananassa* cv. Elsanta.

Substantial changes in the ABA content (either increases or decreases) in the receptacles occurred under the three different experimental procedures described above (Fig. 5B, D and F). In all of these cases, expression of *FaMYB10* transcripts always correlated with that of the ABA content (Fig. 5A, C and E). These results strongly suggest that ABA present in the receptacles can positively regulate the expression of *FaMYB10* and that this TF plays an important role in the regulation of genes involved in the anthocyanin biosynthesis in this fruit.

Taken together, these results indicate that *FaMYB10* gene expression is clearly regulated by both the ABA and the auxin content of the fruit receptacle, fulfilling a putative molecular explanation to the findings described by Perkins-Veazie (1995).



**Fig. 5.** Analysis by QRT-PCR of *FaMYB10* gene expression (A, C and E) and quantification of ABA concentration (B, D and F). (A and B) Control fruit: strawberry fruits infiltrated with empty pFRN vector; NCED1-RNAi fruits: transgenic strawberry fruits agroinfiltrated with the *FaNCED1*-pFRN construct. (C and D) Control fruits: G-W fruits injected with H<sub>2</sub>O; Fruits + NDGA: G-W fruits injected with NDGA 100  $\mu$ M. (E and F) Control fruit: fruits with the pedicels immersed on MS medium with sucrose; fruits + water stress: fruits with the pedicels kept air pedicels. Statistical significance with respect to reference sample was determined by the Student's *t*-test in all experiments. (\*\*\*) *p*-value < 0.001

### 3.3. The expression of the *FaMYB10* gene correlated with the anthocyanin content in the different tissues of the strawberry receptacle

Anthocyanin accumulation in fruit receptacles is not uniform. These pigments are mainly accumulated in the external parenchyma, followed in amount by the internal parenchyma and with the lowest concentration of pigment accumulated in the pith (Fig. 6). When we

dissected the different parts of the receptacles and analyzed both the anthocyanin content and the level of *FaMYB10* expression, a clear and close relationship was observed (Fig. 7).

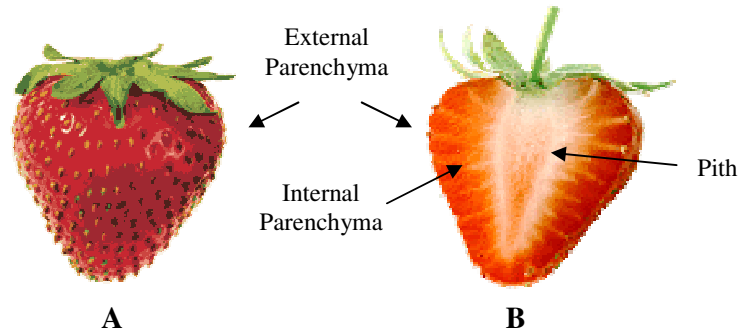


Fig. 6. (A) Whole strawberry fruit. (B) Different tissues of fruit receptacle analyzed: external parenchyma, internal parenchyma and pith.

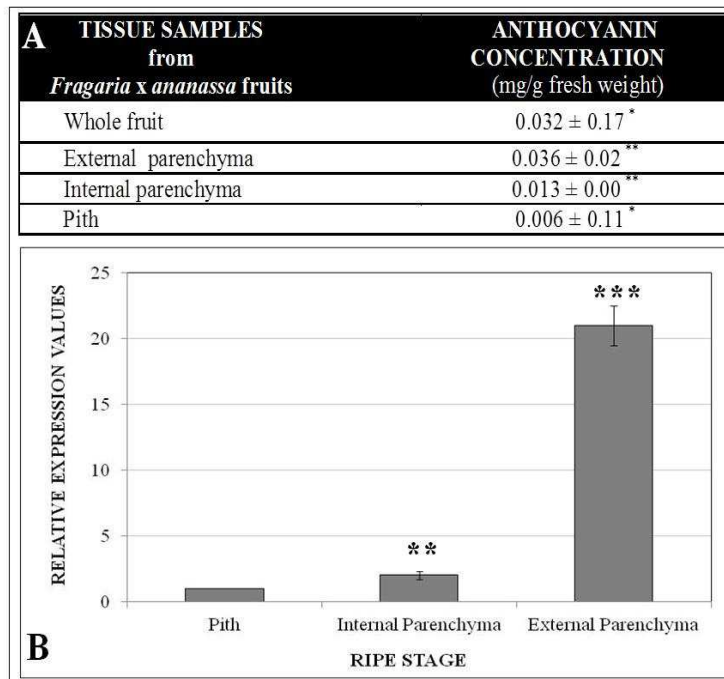
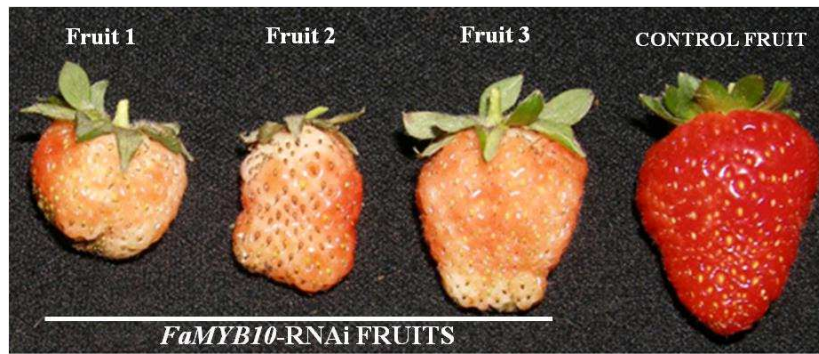


Fig. 7. (A) Quantification of anthocyanins in different R-stage *Fragaria x ananassa* fruit tissues. Values were calculated by absorbance measurements at 515 nm of processed extracts from strawberry red fruits. (\*)  $p$ -value < 0.05 and (\*\*)  $p$ -value < 0.01. (B) Analysis by QRT-PCR of *FaMYB10* gene expression in Pith, internal and external Parenchyma tissues from R-stage *Fragaria x ananassa* fruits. The increase in mRNA value was relative to the Pith-Ct, which had the lowest *FaMYB10* expression and was assigned an arbitrary value equal to unity. Mean values ± SD of three independent experiments are shown. Statistical significance with respect to reference sample (Pith tissue) was determined by the Student's  $t$ -test (\*\*)  $p$ -value < 0.01 and (\*\*\*)  $p$ -value < 0.001.

### 3.4. Transcriptomic analyses show that *FaMYB10* is a global regulator of the flavonoid/phenylpropanoid pathway

To identify the putative target genes regulated by *FaMYB10*, a high-throughput transcriptomic analysis was performed using a 35K custom oligo-based microarray platform of the *Fragaria* genus (named FraGenomics35K). The transcriptome of fruit receptacles transiently silenced by *FaMYB10*-RNAi approaches (20 fruits presenting 97% or more of *FaMYB10* silencing) was compared to that of control fruit receptacles agroinfiltrated with the empty pFRN vector. The reduction in *FaMYB10* expression was also accompanied, in all the cases, by a clear decrease in the anthocyanin content of the receptacles (Fig. 8). These results corroborate previous data (Lin-Wang *et al.*, 2010) and support the involvement of the *FaMYB10* gene in the anthocyanin production in strawberry fruits throughout the ripening process.



**Fig. 8.** Strawberry transgenic fruits (*Fragaria x ananassa* cv Elsanta) agroinfiltrated with the *FaMYB10*-pFRN construct. Control fruit: G-W fruit agroinfiltrated with the empty pFRN vector; *FaMYB10*-RNAi fruits: G-W fruits agroinfiltrated with the *FaMYB10*-pFRN construct.

Comparative microarray analysis yielded a set of genes whose expression was down-regulated in *FaMYB10* agroinfiltrated fruit receptacles compared with control receptacles (Table 1). We focussed on the most clearly down-regulated gene by choosing a 2.0-fold cut off and a  $p$ -value  $\leq 0.05$ . From the group of selected genes, 15 of them belong to the F/P pathway, including homologs of early and late biosynthetic genes such as phenylalanine ammonia lyase (*PAL*) (*UCOESTup755*), cinnamate-4-hydroxylase (*C4H*) (*UCOESTup677*), flavanone 3-hydroxylase (*F3H*) (*UCOESTup1565*), 4-coumarate-CoA ligase (*4CL*) (*UCOESTup2205*), chalcone synthase (*CHS*) (*UCOESTup1441*), chalcone isomerase (*CHI*) (*UCOESTup2572*; *UCOESTup2573*), dihydroflavonol reductase (*DFR*) (*UCOESTup838*), flavonol synthase (*FLS*) (*UCOESTup1098*), UDP-glucose:flavonoid-3-O-glucosyltransferase (*UFGT*) (*UCOESTup694*; *UCOESTup14*), cinnamoyl-CoA reductase (*CCR*) (*UCOESTup583*), cinnamyl alcohol dehydrogenase (*CAD*) (*UCOESTup60*), a putative eugenol synthase (*PCBER*) (*UCOESTup499*) and UDP-glucose:cinnamate glucosyltransferase (*FaGT2*) (*UCOESTup15*). Moreover, the enzyme synthesizing some precursors of the F/P pathway, shikimate dehydrogenase (*UCOESTup1134*), was also down-regulated in silenced *FaMYB10*-RNAi transgenic fruits (Table 1).

### **3.5. *FaMYB10* regulates the expression of other genes coding transcriptional factors that could be implicated in the ripening process**

It is important to mention that in addition to the flavonoid/phenylpropanoid and the *FaMYB10* (*UCOESTup51*) genes, some other TFs or co-activators were clearly down-regulated in the transgenic *FaMYB10*-silenced fruits such as MYB EOII (*UCOESTup67*), MADS box (*UCOESTup525*), bHLH (*UCOESTup1652*), NAC (*UCOESTup766*), NPR1 (*UCOESTup56*), DOF (*UCOESTup76*), RING-H2 finger protein (*UCOESTup1936*) and Cys2/His2 zinc-finger (*UCOESTup680*) (Table 1). These results strongly indicate that all these transcription factors would act downstream of *FaMYB10*, and also that they could be directly or indirectly controlled by this gene. Interestingly, microarray analysis showed that the expression levels of the vast majority of genes putatively regulated by *FaMYB10* were also induced during the ripening of the fruit receptacles (Table 1 and 2).

### **3.6. *FaMYB10* also regulates the expression of other genes apparently not involved in the flavonoid/phenylpropanoid metabolism**

In addition to the flavonoid/phenylpropanoid pathway structural genes, a down-regulation of the expression of some genes putatively involved in flavonoid modification and transport, such as those showing a strong similarity to MATE (*UCOESTup257*; *UCOESTup450*) or GSTs (*UCOESTup2*; *UCOESTup813*) transporters was observed (Table 1). A set of different genes was also down-regulated in silenced *FaMYB10-RNAi* transgenic fruits such as those potentially coding an AAA-type ATPase (*UCOEST218489*), a HXXXD-type acyl-transferase (*UCOESTup327*), a cyclo-DOPA 5-O-glucosyltransferase (*UCOESTup415*), a f-box protein (*UCOEST441*), a proline-rich receptor-like protein kinase (*UCOESTup1103*), a LRR receptor serine/threonine protein kinase (*UCOESTup302*), a pathogenesis-related thaumatin (*UCOESTup712*), a Fra a2 allergen (*UCOESTup787*), a pentatricopeptide repeat-containing protein (*UCOESTup222*), an enolase (*UCOESTup517*), a serine/threonine-protein kinase (*UCOESTup967*), a beta-glucosidase (*UCOESTup151*), a hexokinase-1 (*UCOESTup1055*), two putative abscisic acid receptors (*UCOESTup1025*; *UCOESTup888*), a short chain dehydrogenase/reductase (*UCOESTup508*), a 2-oxoglutarate-dependent dioxygenase (*UCOESTup114*) and a DVL1 protein (*UCOESTup608*) (Table 2). As in the case of the flavonoid/phenylpropanoid structural genes or genes coding transcriptional factors, their expression was additionally up-regulated in ripened-fruits (Table 2).

In addition, the transcriptome analysis revealed that a down regulation took place in transgenic *FaMYB10-RNAi* receptacles for both, genes coding proteins with still unknown functions or those not showing any hits in blast searches. The expression of all these unknown genes was also up-regulated in ripened-receptacles.

### **3.7. Metabolite profiling of *FaMYB10* silenced receptacles confirm that this transcription factor is a general regulator of the flavonoid/phenylpropanoid metabolism in ripened strawberry fruits**

To determine if the transcriptomic changes observed in *FaMYB10* silenced fruits were accompanied by metabolite variations, the major soluble phenolic compounds were quantified by LC-MS in both control and transgenic *FaMYB10*-RNAi fruits (Fig. 9). As expected, substantially lower levels of anthocyanins (pelargonidin-3-glucoside, pelargonidin-3-glucoside-malonate, and cyanidin-3-glucoside) and flavonols (kaempferol-glucoside, kaempferol-glucuronide, and quercetin-glucuronide) but higher concentrations of phenylpropanoids (cinnamoyl glucose, caffeoyl glucose, and feruloyl glucose) were detected in transiently silenced fruits compared with untreated fruit. In contrast to this observation, the level of the phenylpropanoid 4-coumaroyl glucose decreased and the concentration of the flavonoid naringenin-glucoside increased in *FaMYB10*-RNAi fruits. The amount of catechin and epicatechin-catechin-dimers remained unchanged while higher and lower levels of epiafzelechin-glucoside and epiafzelechin-catechin-dimers were detected in transgenic fruit, respectively. The concentrations of some metabolites, not directly involved in the phenolics pathway (ascorbic acid and 4-hydroxy-2,5-dimethyl-3(2H)-furanol glucoside) were also affected by the silencing of *FaMYB10*.

GENES	Putative function	<i>FaMYB10</i> silenced fruits <i>Down regulated</i>		Fruit ripen receptacles <i>Up regulated</i>		Species	e-value	Best Match BlastX
		Fold	p-value	Fold	p-value			
<b>Flavonoids</b>								
<i>UCOESTup1134</i>	Shikimate dehydrogenase	3.455	0.00696	3.545	0.00186	<i>Populus trichocarpa</i>	0.0	XM_002319546.1
<i>UCOESTup755</i>	Phenylalanine ammonia lyase ( <i>PAL</i> )	19.942	0.00099	4.987	0.00032	<i>Rubus idaeus</i>	0.0	AF237955.1
<i>UCOESTup677</i>	Cinnamate-4-hydroxylase ( <i>C4H</i> )	3.778	0.00202	5.436	0.00025	<i>Rubus occidentalis</i>	0.0	FJ554629.1
<i>UCOESTup1565</i>	Flavanone 3-hydroxylase ( <i>F3H</i> )	3.081	0.00143	2.749	0.00113	<i>Fragaria x ananassa</i>	0.0	AB201760.1
<i>UCOESTup2205</i>	4-Coumarate-CoA ligase ( <i>ACL</i> )	3.050	0.01690	2.204	0.01940	<i>Medicago truncatula</i>	0.0	XM_003612611.1
<i>UCOESTup1441</i>	Chalcone synthase ( <i>CHS</i> )	3.951	0.00099	2.914	0.00507	<i>Fragaria x ananassa</i>	0.0	AY997297.1
<i>UCOESTup2572</i>	Chalcone isomerase ( <i>CHI</i> )	3.109	0.00132	3.725	0.01590	<i>Fragaria x ananassa</i>	5.00E-154	AB201755.1
<i>UCOESTup2573</i>	Chalcone isomerase ( <i>CHI</i> )	2.394	0.00275	6.132	0.04550	<i>Prunus persica</i>	8e-116	HM543569.1
<i>UCOESTup838</i>	Dihydroflavonol reductase ( <i>DFR</i> )	3.093	0.00210	4.517	0.00120	<i>Vitis vinifera</i>	1.00E-146	XM_003633468.1
<i>UCOESTup1098</i>	Flavonol synthase ( <i>FLS</i> )	3.284	0.00367	3.724	0.00300	<i>Medicago truncatula</i>	4.00E-126	XM_003609420.1
<i>UCOESTup694</i>	UDP-glucose 3'-O-Flavonoid glucosyltransferase	2.167	0.00527	5.345	0.00029	<i>Hieracium pilosella</i>	2e -138	EU561020.1
<i>UCOESTup12</i>	UDP-glucose:flavonoid-3-O-glucosyltransferase ( <i>UFGT</i> )	7.888	0.00127	202.079	0.00011	<i>Fragaria x ananassa</i>	0.0	AY575056.1
<b>Phenylpropanoids</b>								
<i>UCOESTup583</i>	Cinnamoyl-CoA reductase ( <i>CCR</i> )	3.861	0.01080	6.188	0.00026	<i>Populus trichocarpa</i>	1.00E-158	XM_002314016.1
<i>UCOESTup60</i>	Cinnamyl alcohol dehydrogenase ( <i>CAD</i> )	4.391	0.00109	50.572	0.00058	<i>Fragaria x ananassa</i>	0.0	U63534.1
<i>UCOESTup499</i>	Eugenol synthase ( <i>PCBER3</i> )	2.659	0.01270	7.142	0.00036	<i>Pyrus communis</i>	1.00E-170	AF071477.1
<i>UCOESTup14</i>	UDP-glucose:cinnamate glucosyltransferase ( <i>FaGT2</i> )	4.756	0.00106	170.167	0.00007	<i>Fragaria x ananassa</i>	0.0	AY663784.1
<b>Transporters</b>								
<i>UCOESTup257</i>	MATE efflux family protein	5.508	0.00289	12.176	0.00038	<i>Arabidopsis thaliana</i>	0.0	NM_103646.3
<i>UCOESTup450</i>	MATE efflux family protein	5.114	0.00214	7.702	0.00264	<i>Arabidopsis thaliana</i>	1.00E-134	NM_104614.4
<i>UCOESTup2</i>	Glutathione -S-transferase	4.112	0.00095	529.169	0.00007	<i>Malus x domestica</i>	3.00E-115	JN573600.1
<i>UCOESTup813</i>	Glutathione-S-transferase	2.538	0.00260	4.630	0.00036	<i>Rheum australe</i>	2.00E-114	EU931209.1
<b>Transcription factors</b>								
<i>UCOESTup51</i>	R2R3 MYB transcription factor ( <i>MYB10</i> )	6.525	0.00111	62.013	0.00028	<i>Fragaria x ananassa</i>	2e-134	EU155162.1
<i>UCOESTup67</i>	Myb EOII	3.588	0.00170	46.063	0.00005	<i>P. sativum</i>	5e-82	Y11105.1
<i>UCOESTup525</i>	Agamous-like MADS-box protein	4.172	0.03730	6.711	0.00460	<i>Glycine max</i>	6.00E-56	XM_003534204.1
<i>UCOESTup1652</i>	Transcription factor bHLH66	4.290	0.00344	2.652	0.00114	<i>Medicago truncatula</i>	5.00E-32	XM_003590628.1
<i>UCOESTup766</i>	NAC domain protein	8.737	0.04560	4.906	0.00277	<i>Populus trichocarpa</i>	3e -66	XM_002314042.1
<i>UCOESTup56</i>	NPR1	4.280	0.00142	52.835	0.00016	<i>Populus trichocarpa</i>	0.0	XM_002308869.1
<i>UCOESTup76</i>	Dof zinc finger protein	3.176	0.00728	41.029	0.00011	<i>Glycine max</i>	1,00E-45	XM_003537068.1
<i>UCOESTup1936</i>	RING-H2 finger protein	6.631	0.00103	2.381	0.01250	<i>Vitis vinifera</i>	3e-44	XM_003634245.1
<i>UCOESTup680</i>	Cys2/His2 zinc-finger transcription factor	2.144	0.03040	5.426	0.00071	<i>Silene latifolia</i>	3e -51	DQ017764.1

**Table 1. Main genes down regulated in transgenic *FaMYB10*-RNAi fruits analyzed by microarray experiment.**

Magnitudes of relative induction to fruits transformed with *FaMYB10*-pFRN construct, to fruit ripen receptacles and *p*-value ( $\leq 0.05$ ) are given. Columns show the best annotated matches from the search results of tBlastX analysis, species, putative function and match e- value.

GENE	Putative function	<i>FaMYB10</i> silenced fruits Down regulated		Fruit ripen receptacles Up regulated		Species	e-value	Best Match BlastX
		Fold	p-value	Fold	p-value			
<i>UCOESTup202</i>	AAA-ATPase-like protein	7.934	0.00880	15.455	0.00063	<i>Solanum tuberosum</i>	0.0	DQ191627.1
<i>UCOESTup327</i>	HXXXD-type acyl-transferase	7.231	0.00099	9.988	0.00240	<i>Arabidopsis thaliana</i>	2e -44	NM_102288.6
<i>UCOESTup415</i>	Cyclo-DOPA 5-O-glucosyltransferase	6.375	0.00113	8.282	0.00028	<i>Mirabilis jalapa</i>	2.00E-148	AB182643.1
<i>UCOESTup1103</i>	Proline-rich receptor-like protein kinase	5.312	0.00775	3.615	0.00053	<i>Glycine max</i>	0.0	XM_003547220.1
<i>UCOESTup302</i>	LRR receptor serine/threonine protein kinase	3.276	0.00242	10.655	0.00013	<i>Ricinus communis</i>	1e -60	XM_002515360.1
<i>UCOESTup441</i>	F-Box family protein	4.974	0.00216	7.797	0.00252	<i>Populus trichocarpa</i>	3.00E-40	XM_002307964.1
<i>UCOESTup712</i>	Pathogenesis-related thaumatin	4.234	0.00175	5.176	0.02270	<i>Arabidopsis thaliana</i>	9e -93	NM_120027.3
<i>UCOESTup787</i>	Fra a2 allergen	4.025	0.00517	4.807	0.00195	<i>Fragaria x ananassa</i>	1.00E-102	GQ148818.1
<i>UCOESTup222</i>	Pentatricopeptide repeat-containing protein	3.748	0.00130	13.928	0.00040	<i>Arabidopsis thaliana</i>	0.0	NM_120914.2
<i>UCOESTup517</i>	Enolase	3.346	0.00115	6.783	0.00045	<i>Vitis vinifera</i>	0.0	XM_002274298.1
<i>UCOESTup967</i>	Serine/threonine-protein kinase	3.234	0.00274	4.032	0.00190	<i>Arabidopsis thaliana</i>	2.00E-122	NM_112761.3
<i>UCOESTup151</i>	Beta-Glucosidase	3.145	0.00143	20.93	0.00018	<i>Lotus japonicus</i>	1.00E-143	EU710846.1
<i>UCOESTup1055</i>	Hexokinase 1	3.054	0.00128	3.768	0.00057	<i>Eriobotrya japonica</i>	0.0	JF414121.1
<i>UCOESTup1025</i>	Abscisic acid receptor PYL2	3.041	0.00283	3.862	0.00049	<i>Medicago truncatula</i>	2.00E-34	XM_003588977.1
<i>UCOESTup888</i>	Abscisic acid receptor PYR1	3.001	0.00410	4.326	0.00643	<i>Fragaria x ananassa</i>	1.00E-61	JF268669.1
<i>UCOESTup508</i>	Short chain dehydrogenase/reductase	3.011	0.00172	6.945	0.00034	<i>Nandina domestica</i>	3.00E-98	FJ789568.1
<i>UCOESTup114</i>	2-Oxoglutarate-dependent dioxygenase	2.939	0.00160	27.853	0.00013	<i>Populus trichocarpa</i>	2.00E-151	XM_002313047.1
<i>UCOESTup608</i>	DVL1	2.151	0.00233	5.960	0.00067	<i>Arabidopsis thaliana</i>	1.00E-13	BK001754.1
<i>UCOESTup1021</i>	Uncharacterized protein	12.125	0.01120	3.870	0.00201	<i>Glycine max</i>	2.00E-07	XM_003555855.1
<i>UCOESTup605</i>	Uncharacterized protein	7.315	0.00287	6.024	0.00089	<i>Zea mays</i>	8.00E-13	NM_001152047.1
<i>UCOESTup1106</i>	Uncharacterized protein	3.558	0.00173	3.609	0.00109	<i>Arabidopsis thaliana</i>	0.0	NM_119498.3
<i>UCOESTup812</i>	Uncharacterized protein	3.128	0.00380	4.644	0.01590	<i>Arabidopsis lyrata</i>	1.00E-04	XM_002882032.1
<i>UCOESTup110</i>	Uncharacterized protein	3.099	0.00522	28.77	0.00076	<i>Vitis vinifera</i>	0.0	FQ380191.1
<i>UCOESTup220</i>	Uncharacterized protein	2.555	0.00427	14.257	0.00034	<i>Ricinus communis</i>	2.00E-22	XM_002527212.1
<i>UCOESTup321</i>	Uncharacterized protein	2.492	0.00217	10.105	0.00020	<i>Vitis vinifera</i>	0.0	XM_002277408.1
<i>UCOESTup1046</i>	Uncharacterized protein	2.392	0.00833	3.800	0.00631	<i>Medicago truncatula</i>	2.00E-08	XM_003610592.1
<i>UCOESTup742</i>	Uncharacterized protein	2.166	0.00295	5.040	0.00437	<i>Vitis vinifera</i>	5e -56	XM_002273433.1
<i>UCOESTup1541</i>	Uncharacterized protein	2.037	0.00941	2.773	0.00240	<i>Glycine max</i>	4.00E-75	XM_003551188.1
<i>UCOESTup476</i>	Uncharacterized protein	3.689	0.01380	7.463	0.00043	<i>Populus trichocarpa</i>	7e -77	XM_002317162.1
<i>UCOESTup1508</i>	Uncharacterized protein	3.542	0.00369	2.816	0.04160	<i>Vitis vinifera</i>	7.00E-47	AM453978.1
<i>UCOESTup848</i>	Uncharacterized protein	5.033	0.00095	4.485	0.00466	<i>Gossypium hirsutum</i>	1.00E-21	EU373080.1
<i>UCOESTup637</i>	Uncharacterized protein	4.017	0.03310	5.790	0.0261	<i>Malus x domestica</i>	2e -14	FN823234.1
<i>UCOESTup50</i>	No homology	88.069	0.00113	63.614	0.00022			
<i>UCOESTup80</i>	No homology	17.143	0.00117	39.913	0.00009			
<i>UCOESTup379</i>	No homology	15.271	0.00168	8.754	0.00044			
<i>UCOESTup22</i>	No homology	5.932	0.00142	119.016	0.00013			
<i>UCOESTup753</i>	No homology	5.357	0.00107	5.013	0.00198			
<i>UCOESTup470</i>	No homology	5.117	0.04850	7.534	0.00065			
<i>UCOESTup1031</i>	No homology	5.076	0.02480	3.851	0.02080			

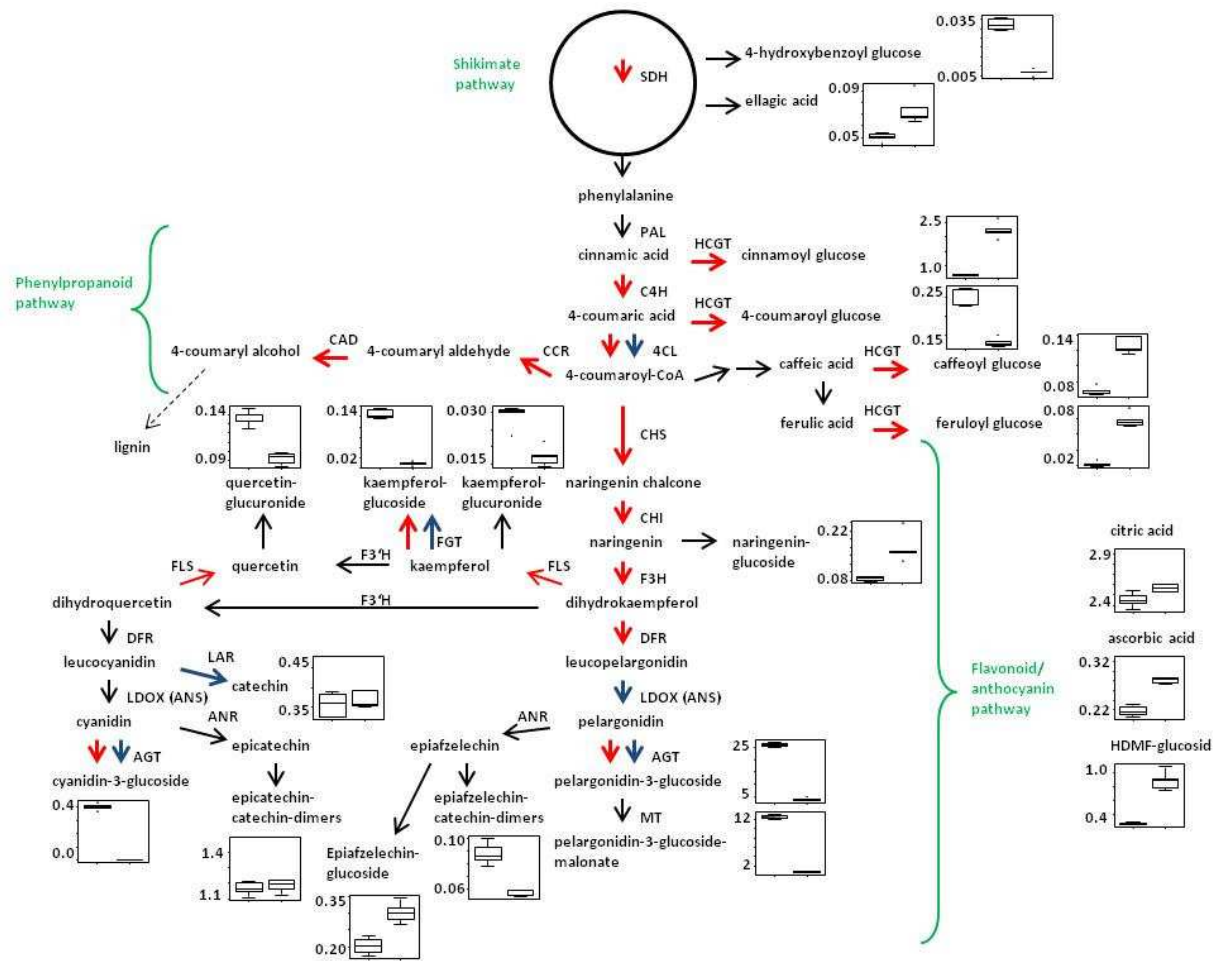
(Table continues on following page)



<i>UCOESTup1247</i>	No homology	5.054	0.00101	3.288	0.00711
<i>UCOESTup614</i>	No homology	4.619	0.00352	5.925	0.00059
<i>UCOESTup265</i>	No homology	4.475	0.00184	11.993	0.00572
<i>UCOESTup122</i>	No homology	4.217	0.00101	25.925	0.00007
<i>UCOESTup986</i>	No homology	4.200	0.00522	3.970	0.00413
<i>UCOESTup360</i>	No homology	4.104	0.00271	9.176	0.00207
<i>UCOESTup66</i>	No homology	3.484	0.00195	47.247	0.00046
<i>UCOESTup1</i>	No homology	3.448	0.00122	2303.220	0.00006
<i>UCOESTup1033</i>	No homology	3.318	0.01340	3.843	0.00867
<i>UCOESTup1019</i>	No homology	3.246	0.02010	3.871	0.00111
<i>UCOESTup215</i>	No homology	3.104	0.03330	14.479	0.02140
<i>UCOESTup1262</i>	No homology	3.016	0.00192	3.246	0.00063
<i>UCOESTup95</i>	No homology	2.919	0.00201	33.654	0.00054
<i>UCOESTup245</i>	No homology	2.769	0.01880	12.895	0.04350
<i>UCOESTup1181</i>	No homology	2.767	0.00593	3.452	0.00485
<i>UCOESTup137</i>	No homology	2.697	0.00253	23.078	0.00012
<i>UCOESTup1720</i>	No homology	2.610	0.00217	2.566	0.00282
<i>UCOESTup63</i>	No homology	2.53	0.02050	49.042	0.00010
<i>UCOESTup509</i>	No homology	2.508	0.00775	6.923	0.00033
<i>UCOESTup428</i>	No homology	2.443	0.00669	8.180	0.00315
<i>UCOESTup610</i>	No homology	4.959	0.00105	5.955	0.00102
<i>UCOESTup610</i>	No homology	4.959	0.00105	5.955	0.00102

**Table 2. Main genes down regulated in transgenic *FaMYB10*-RNAi fruits analyzed by microarray experiment.**

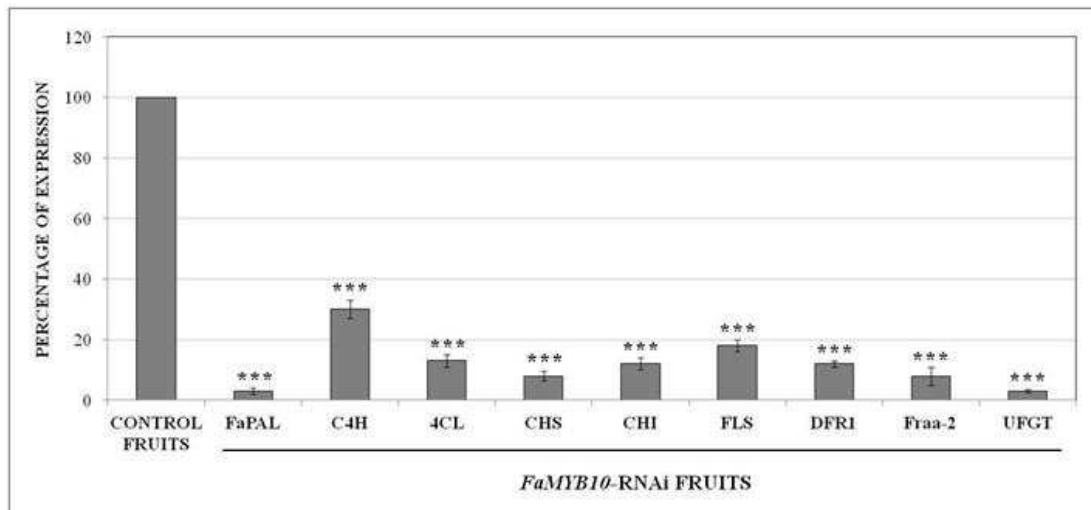
Magnitudes of relative induction to fruits transformed with *FaMYB10*-pFRN construct, to fruit ripen receptacles and *p*-value ( $\leq 0.05$ ) are given. Columns show the best annotated matches from the search results of tBlastX analysis, species, putative function and match e- value.



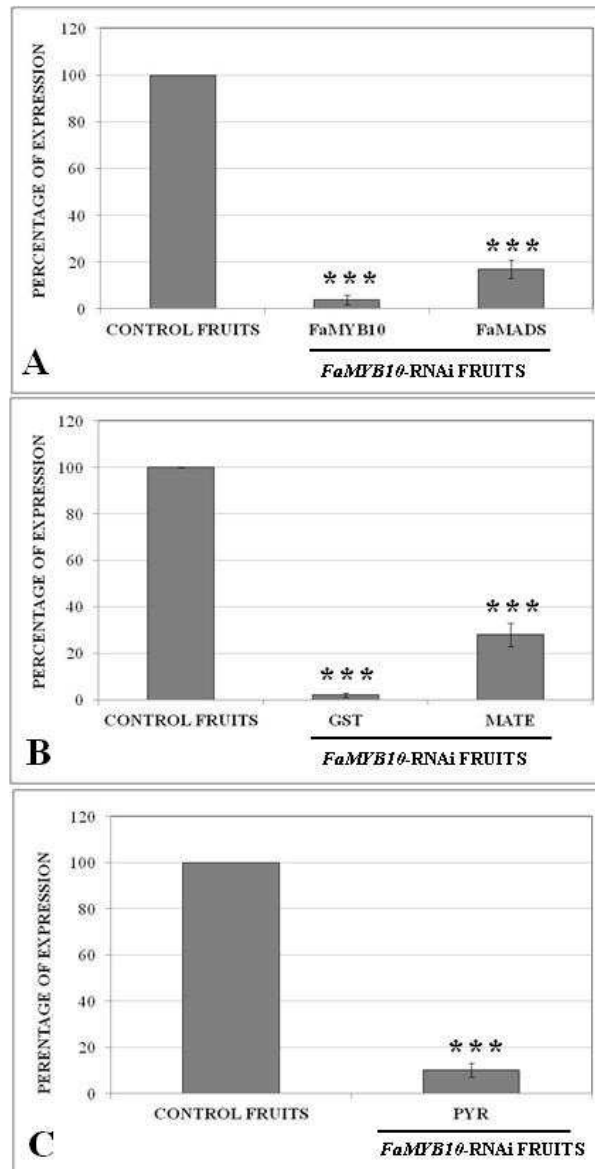
**Fig. 9. Part of the phenylpropanoid, flavonoid and anthocyanin pathway.** Enzymes whose genes are down- and up-regulated due to the silencing of *FaMYB10* are shown in red and blue, respectively. Boxplots show the levels of metabolites in control fruit (left) in comparison to their levels in *FaMYB10* silenced fruit (right). *4CL*: 4-coumaroyl-CoA ligase, *AGT*: anthocyanidin glucosyltransferase, *ANR*: anthocyanidin reductase, *ANS*: anthocyanidin synthase, *C4H*: cinnamic acid 4-hydroxylase, *CAD*: 4-coumaryl alcohol dehydrogenase, *CCR*: 4-coumaroyl-CoA reductase, *CHI*: chalcone isomerase, *CHS*: chalcone synthase, *DFR*: dihydroflavonol reductase, *F3H*: flavanone 3-hydroxylase, *F3'H*: flavonoid 3'-hydroxylase, *FGT*: flavonoid glucosyltransferase, *HCGT*: (hydroxy)cinnamic acid glucosyltransferase, *LAR*: leucoanthocyanidin reductase, *LDOX*: leucoanthocyanidin dioxygenase, *MT*: malonyl transferase, *PAL*: phenylalanine ammonia lyase and *SDH*: shikimate dehydrogenase.

### 3.8. Validation by means of QRT-PCR analysis of the microarray data

The DNA microarray technique involves the possibility of co-hybridisation between very similar nucleotide sequences, so it was necessary to further validate our microarray analyses by real-time PCR (Fig. 10). The results confirmed that *FaMYB10*-RNAi silenced plants had reduced levels of gene coding for enzymes involved in the P/F pathway (Fig. 10), transporters (Fig. 11A), transcription factors (Fig. 11B) and PYR abscisic acid receptor (Fig. 11C).



**Fig. 10.** Analysis by QRT-PCR of different genes corresponding to flavonoid/phenylpropanoid biosynthetic pathway in transgenic strawberry fruits with the *FaMYB10* expression silenced. The silencing level of each gene is expressed as a percentage. Enzyme names are abbreviated as follows: Phe ammonia-lyase (*FaPAL*), cinnamic acid 4-hydroxylase (*C4H*), 4-coumaroyl:CoA-ligase (*4CL*), chalcone synthase (*CHS*), chalcone isomerase (*CHI*), flavonol synthase (*FLS*), dihydroflavonol 4-reductase (*DFR1*), *Fraa-2* and UDPG flavonoid glucosyl transferase (*UFGT*). Statistical significance with respect to reference sample was determined by the Student's *t*-test. (\*\*\*) *p*-value < 0.001.



**Fig. 11.** Analysis by QRT-PCR of different genes in transgenic strawberry fruits with the *FaMYB10* expression silenced. The silencing level is expressed as a percentage. (A) Analysis of transcription factors, (B) analysis of transporters and (C) analysis of *PYR* abscisic acid receptor. Statistical significance with respect to reference sample was determined by the Student's *t*-test. (\*\*\*) *p*-value < 0.001.

## 4. DISCUSSION

### 4.1. Expression of *FaMYB10* is fruit specific and related to the expression of genes involved in the F/P metabolism

Our results show that *FaMYB10* expression was confined mainly to the fruit receptacles, with it not being or being scarcely expressed in all other vegetative tissues analyzed such as leaves, stems and runners. The expression was also very low in the early developmental stage of the fruit, it experienced a substantial increase at the onset of the ripening stage, and coincided with the development of the red color in the fruit when the F/P metabolism was fully active. All these data taken together allow us to define this gene as a true and specific receptacle gene, which is related to ripening.

In agreement with this, the *FaMYB10* expression coincided with that of many other genes related to ripening, and with the biosynthesis of many compounds involved in the organoleptic properties of the fruit (Aharoni *et al.*, 2002; Medina-Escobar *et al.*, 1997a and b; Moyano *et al.*, 1998; Blanco-Portales *et al.*, 2002; Benitez-Burraco *et al.*, 2003; Raab *et al.*, 2006; Griesser *et al.*, 2008). Since *FaMYB10* is a known transcription factor with confirmed regulatory features, we first became interested in evaluating whether this gene was regulated by auxins and abscisic acid, hormones that are clearly involved in the ripening of this fruit, and also in those genes whose expression could be directly or indirectly regulated by this gene. These two tasks were performed by RT-PCR and a high-throughput microarray analysis.

### 4.2. *FaMYB10* gene expression is regulated by the hormones auxin and abscisic acid, the key hormones controlling the ripening of the fruit

Although orthologous of the *MYB10* gene have been isolated from at least 20 rosaceous species (Lin-Wang *et al.* 2010), little is known about the hormonal regulation of the *FaMYB10* gene. In strawberry, it is generally assumed that decay in the auxin production taking place during fruit development is at least partly responsible for the triggering of the ripening process (Perkins-Veazie, 1995). These auxins, synthesized by the achenes and released to the receptacles in the early phase of development of the fruit, are thought to be responsible for changes in both the cell number and size of the fruit. Once the receptacle size reaches its culmination (in the white stage), auxin production declines and this is taken as a signal that triggers the ripening process in which the white fruit becomes red due mainly to the activation of the F/P pathway and fully in charge of the characteristic aroma and scents. In accordance with this, the expression of many strawberry ripening-related genes is being repressed by auxins (Medina-Escobar *et al.*, 1997a and b; Moyano *et al.*, 1998; Blanco-Portales *et al.*, 2002; Benitez-Burraco *et al.*, 2003; Raab *et al.*, 2006; Griesser *et al.*, 2008).

In this paper, we have found that *FaMYB10* expression is also down-regulated by auxins. The onset of *FaMYB10* expression took place in the normal development of the fruit just after the white stage, when auxin production is known to decay. To test whether auxins can regulate *FaMYB10*, two different experiments were performed. Firstly, we were able to see both an early appearance of *FaMYB10* transcripts and of the production of the red color when we removed the achenes from the fruit at early stages of development. This achene

removal is known to suppress the source of endogenous auxins. Secondly and in agreement with this, we observed a dramatic reduction in the levels of *FaMYB10* transcript when the synthetic auxin NAA was applied to the surface of the same de-achened fruits. All these results suggest that *FaMYB10* expression is indeed directly or indirectly regulated by auxins.

Also, it has been suggested that the plant hormone abscisic acid (ABA) is involved in the ripening of both climacteric and non-climacteric fruits (Rodrigo *et al.*, 2006; Zhang *et al.*, 2009). Actually, it is considered that the ABA/auxin content ratio is the true signal that initiates strawberry fruit ripening (Perkins-Veazie, 1995; Jiang and Joyce, 2003). Indeed, some studies have indicated that ABA promotes the strawberry ripening related production of anthocyanins (Chai *et al.*, 2011; Jia *et al.*, 2011). However, although it is known that the level of ABA content gradually increases during the ripening, little is known about how this hormone regulates the strawberry ripening genes. In this work, we clearly show that when we modulated the level of ABA in the receptacles, a concomitant and parallel change in the expression of the *FaMYB10* took place. So, when the ABA content decreases as a consequence of either the transient silencing of *FaNCE1* by infiltration with RNAi-harboring *Agrobacterium* cells or the inhibition of the main enzyme in the ABA biosynthetic pathway by the inhibitor NDGA, a decrease in the *FaMYB10* expression was observed (Fig. 5). Higher levels of the same transcript were observed however, when ABA content increased as a result of subjecting the fruits to water stress. In fact, in both climacteric and non-climacteric fruits, water deficiency accelerates ripening and induces changes in metabolites and gene expression and this is accompanied by a rise in the ABA content (Castellarin *et al.*, 2007; Gong *et al.*, 2010). In grape, drought stress induces an increase in the ABA content and, consequently, an increase in the biosynthesis of flavonoids and the activation of drought inducible genes (Yamaguchi-Shinozaki and Shinozaki, 2005). We measured the ABA content and were able to prove that all these changes in the level of *FaMYB10* transcripts were accompanied by a lower or higher production of both the ABA content and of that of anthocyanins, respectively. This provides molecular evidence that could explain the recent results obtained by Chai *et al.*, (2011) and Jia *et al.*, (2011), who observed a decrease in the anthocyanin content in strawberry ripened fruits when ABA production is blocked in receptacles. This does not exclude the possibility of ABA regulating the expression of other metabolic ripening-related pathways as well. Again, these results strongly support the fact that ABA could be regulating directly or indirectly *FaMYB10* gene expression.

Thus, a clear parallelism is observed between the disappearance of auxin, the appearance of ABA, and the repression or induction of *FaMYB10*

### **4.3. High-throughput transcriptomic analysis with control and silenced *FaMYB10* plants indicates that this gene plays a key role in the ripening process**

The transcriptomic analysis presented herein revealed that many of the genes involved in the F/P metabolism, from phenylalanine ammonia lyase (*PAL*) to *UFGT*, can be directly or indirectly up-regulated by *FaMYB10*. Interestingly, all of these genes are also up-regulated in the red ripened stage of the receptacles during normal development. This supports the possibility that the *FaMYB10* gene is fulfilling a key central role by regulating most, if not all, of the biosynthetic genes related to the F/P pathway that are related to ripening. One exception, however, is the expression of anthocyanidin synthase (*ANS*) genes that remain

unchanged in *FaMYB10* silenced receptacles, suggesting the existence of a different regulatory mechanism controlling the expression of this particular gene.

In *Vitis vinifera*, a broad regulatory role was demonstrated for VvMYB5b, a R2R3 transcription factor that regulates all branches of the biosynthesis of flavonoids, including anthocyanins and the phenylpropanoids pathways (Deluc *et al.*, 2008). However, VvMYB5b does not regulate *UFGT* gene expression and this role is played by both VvMYBBA1 and VvMYBBA2 (Walker *et al.*, 2007). In strawberry, however, *FaMYB10* alone could play the same physiological role as that of VvMYB5b, VvMYBA1 and VvMYBA2 all together, since it seems to regulate by itself the biosynthesis of flavonoids and the expression of *UFGT*. As with *FaMYB10*, the over-expression of GMYB10 in *Gerbera hybrida*, an anthocyanin regulator MYB TF, increased the expression of *PAL*, *C4H*, *CHI*, *F3H*, and *GST* genes in petals (Laitinen *et al.*, 2008). However, both VvMYB5b and GMYB10 additionally regulate the expression of the *ANS* gene, whereas *FaMYB10* does not. Similar to *FaMYB10*, over-expression of VvMYB5a in stamens of grapevine induced all of the structural genes of the flavonoid/phenylpropanoid pathway, except *ANS*, and this activation correlated with a strong accumulation of anthocyanins in epidermal cells (Deluc *et al.*, 2006).

In strawberry, the R2R3 *FaMYB1* TF is weakly induced in ripened fruits (Aharoni *et al.*, 2001). This opens up the possibility that this TF could be regulating any of the F/P genes. However, it has been shown that the ectopic over-expression of the *Fragaria FaMYB1* in tobacco flowers did not affect the expression of *PAL*, *C4H*, *4CL*, *CHS*, *F3H*, *DFR*, *UDP-rhamnosyl transferase* and the *CAD* genes (Aharoni *et al.*, 2001). In these same transgenic *FaMYB1* tobacco plants, the expression of the anthocyanin synthase (*ANS*) gene was clearly down-regulated. On the contrary, our transcriptomic analyses show that all of these genes except *ANS* could be regulated by *FaMYB10* in ripening fruits.

In agreement with our proposal, reduced levels of anthocyanins and flavonols were detected in *FaMYB10*-RNAi fruits in comparison with control fruits. The concentrations of the proanthocyanins catechin and its dimer, however, were not altered (Fig. 8). On the other hand, the impact of *FaMYB10* down-regulation on the amounts of epiafzelchin derivatives was mixed. The higher levels of phenylpropanoyl glucosides in *FaMYB10*-RNAi receptacles point to a redirection of the pathway towards early intermediates of the phenolic pathway similar to that observed in *FaCHS*-RNAi fruit (Hoffmann *et al.*, 2006). In addition, two metabolites not directly related to the anthocyanin pathway namely ascorbic acid and HDMF-glucoside, accumulated upon down-regulation of *FaMYB10*. These compounds are linked with carbohydrate metabolism and indicate alterations in this pathway consistent with the reduced transcript levels of hexokinase-1 and sucrose phosphate synthase gene 1 (Raab *et al.*, 2006).

*FaMYB10* also activates the expression of the *GST* and *MATE* transporters, whose induction was also observed in ripened receptacles. In *Vitis vinifera*, these genes have been associated with the sequestration of flavonoids and anthocyanin into the vacuoles (Gómez *et al.*, 2011). However, the expression of glutathion-S-transferase (*GST*) was not regulated by *FaMYB1* (Aharoni *et al.*, 2001).

#### 4.4. *FaMYB10* regulates many other transcription factors implicated in ripening

Throughout the fruit ripening process, at least 144 genes putatively coding TF were induced in the red-ripened receptacle (data not shown). The expression of 11 of them was down-regulated in *FaMYB10*-RNAi transgenic fruits, suggesting that these transcriptional factors could be under the control of *FaMYB10*. Among them, we found putative homologous genes of EOBII MYB, NAC and DOFTFs. The *EOBII* (Emission Of Benzenoids II) gene of *Petunia hybrida* encodes a R2R3 MYB TF that regulates the expression of structural phenylpropanoid genes involved in the production of the volatile phenylpropanoid phenylethyl alcohol, benzylbenzoate, eugenol and isoeugenol, components of the floral scent (Spitzer-Rimon *et al.*, 2010). On the other hand, a regulatory relationship between the NACTFs and deposition of lignins in the cell wall of vascular cells has been proposed (Zhong *et al.*, 2010). This lignin biosynthesis is controlled by lignin-specific MYB TF that activates the expression of genes coding enzymes of the phenylpropanoid pathway (Zhong *et al.*, 2010). In this sense, it is worth noting that the presence of lignin in xylem cells of the fibrovascular strands of the receptacle was detected in all stages of development and ripening (Aharoni *et al.*, 2002). These studies have also demonstrated that the cinnamyl alcohol dehydrogenase protein was immunolocalized in immature xylem cells undergoing active lignification (Aharoni *et al.*, 2002). Recently, in *Arabidopsis thaliana*, the involvement of a DOF TF (*AtDOF4;2*) in the regulation of the phenylpropanoid metabolism and in the auxin transport has been proposed (Skyrycz *et al.*, 2007). Concurrently to the down regulation of these genes, we have also observed that the expression of genes belonging to the phenylpropanoid pathway and potentially producing these volatiles or lignins, such as cinnamyl-CoA reductase, cinnamyl alcohol dehydrogenase and a putative eugenol synthase, were also down-regulated in transgenic *FaMYB10* silenced fruits. The involvement of EOBII in the regulation of biosynthetic genes responsible for the production of phenylpropanoid volatiles is also supported by the high expression of this transcription factor in petals, where these volatiles are strongly produced and emitted (Spitzer-Rimon *et al.*, 2010). Thus, our results open the possibility that *FaMYB10* could also be regulating the biosynthesis of lignins and/or phenylpropanoid volatiles by activation of the *FaEOBII* and *FaDOF* expression.

Moreover, the *FaMYB10* gene appears to be involved in other ripening-related processes. So, we found that *FaMYB10* induces a gene encoding a homolog of the non-expressor of pathogenesis related (*NPR1*) genes. These genes are the master regulators of the salicylic acid-mediated systemic acquired resistance by acting as co-activators through their interaction with TGA TFs (Zhang *et al.*, 1999; Zhou *et al.*, 2000). The expression of the homologous *FvNPR1* strawberry gene was also highly up-regulated in ripened receptacles. This protein forms an oligomer in its inactive state and is excluded from the nucleus. After activation by redox changes, the monomeric form emerges and accumulates in the nucleus where it interacts with TGA TFs thus activating gene expression (Mou *et al.*, 2003). To date, a link between *NPR1*-like genes and the ripening of the fruit has not been established although the strong induction of this gene in ripened fruit receptacles suggests novel roles for this co-activator related to this process. It is noteworthy that some studies have related the oxidative stress (a process activating *NPR1* proteins), to some auxin-independent expression programs involved in strawberry ripening (Aharoni *et al.*, 2002). Also, the *NPR1* protein would act downstream of the *FaMYB10* transcription factor.



The expression of a gene homologous to DEVIL/ROTUNDIFOLIA (*DVL/ROT*) was also repressed in *FaMYB10* silenced fruits. In plants, these genes are involved in signalling processes related to development and differentiation (Valdivia *et al.*, 2012).

ABA plays an important role in the induction of the anthocyanin biosynthesis throughout strawberry fruit ripening. Two of the genes whose expression is down-regulated in transgenic *FaMYB10-RNAi* fruits code putative ABA receptors (*UCOESTup1025* and *UCOESTup888*) (Chai *et al.*, 2011). As with *FaMYB10*, the silencing in strawberry fruit receptacles of the homologous ABA receptor *FaPYRI*, leads to a strong reduction in the anthocyanin content (Chai *et al.*, 2011). The *UCOESTup888* sequence isolated from *Fragaria* is homologous to *FaPYRI*, and both putative ABA receptors were induced in ripened receptacles. All these data taken together indicate that *FaMYB10* could induce both ABA receptors during the ripening process, thus enhancing the response to ABA.

As in other studies performed with R2R3 TFs, *FaMYB10* is regulating a set of genes that either have an unknown function or lack any homology with sequences deposited in the public databases (this work, Toghe *et al.*, 2005; Laitinen *et al.*, 2008; Terrier *et al.*, 2009; Cutanda-Perez *et al.*, 2009). Obviously, the biological significance of this regulatory role for R2R3 MYB genes has not yet been addressed. We cannot discard the fact that these genes are regulated by ABA receptors or other transcription factors and regulatory proteins that act downstream of *FaMYB10*.

In short, we present novel functional data indicating that *FaMYB10* regulates the homologous *EBG* and *LBG* genes of the F/P pathway that are related to the biosynthesis of anthocyanins in the strawberry fruit receptacle. In addition it simultaneously represses those genes involved in the proanthocyanidins (PAs) biosynthesis. *FaMYB10* expression is strongly regulated by ABA and auxins, and shows an expression almost restricted to the receptacle. The high-throughput transcriptomic analyses performed in transgenic strawberry fruits also show that *FaMYB10* regulates the expression of many important TF implicated in their ripening. All these data strongly indicate that, in strawberry, *FaMYB10* is a TF playing a major and general role in the ripening process, acting very likely in a prominent part of the signalling transduction cascade.

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## CONCLUSIONS

1. - We have selected two genes (*FaAAT2* and *FaMYB10*) potentially involved in the fruit ripening process from an oligo microarray of strawberry fruit.
2. - The strawberry *FaAAT2* gene shows significant homology of sequence with other genes of higher plants involved in the biogenesis of the fruit flavor.
3. - The *FaAAT2* gene is conserved in both *Fragaria x ananassa* and *Fragaria vesca* varieties.
4. - The *FaAAT2* expression significantly increased in receptacle during strawberry fruit ripening and it is negatively regulated by auxin.
5. - The *FaAAT2* gene is a new gene, different to *SAAT* gene previously described, whose protein has the highest enzymatic activity in presence of straight chain alcohols and aromatic alcohols with acetyl-CoA, being the cinnamyl alcohol its favorite substrate.
6. - *FaAAT2* protein has substrate preference for C6-C10 alcohols, being more active with hexanol and heptanol followed by octanol.
7. - The volatiles production associated with the aroma of ripened strawberry fruit was reduced after the transient silencing of *FaAAT2* expression, indicating a clear correlation between the concentration of volatile esters, the expression level of this gene and the final aroma of the fruit strawberry.
8. - The *FaMYB10* transcription factor has a relevant role in overall control of the flavonoid / phenylpropanoid metabolism along the ripening strawberry process.
9. - *FaMYB10* gene expression is induced along the strawberry receptacle ripening, being barely detected in achenes and vegetative tissues. Moreover, the *FaMYB10* expression is negatively regulated by auxin and it is induced by abscisic acid.
10. - Transient silencing of *FaMYB10* expression reduced the levels of genes encode for enzymes involved in the phenylpropanoids/flavonoids pathway. Thus, this TF regulated the Early-regulated Biosynthesis Genes (*EBGs*), the Late-regulated Biosynthesis Genes (*LBGs*) and genes of the general pathway involved in both flavonols and anthocyanins production in fruit ripened receptacles.
11. - The transcriptomic analyses performed in transgenic strawberry fruits also showed that *FaMYB10* regulates the expression of other genes apparently not involved in the flavonoid/phenylpropanoid metabolism and of many TFs implicated in the ripening strawberry process.

## CONCLUSIONES

- 1.- A partir de un microarray de oligos de fruto de fresa, se han seleccionado dos genes (*FaAAT2* y *FaMYB10*) potencialmente implicados en el proceso de maduración del fruto.
- 2.- El gen *FaAAT2* de fresa presenta homología significativa de secuencia con otros genes de plantas superiores implicados en la biogénesis del aroma del fruto.
- 3.- El gen *FaAAT2* está conservado en las variedades *Fragaria x ananassa* y *Fragaria vesca*.
- 4.- La expresión del gen *FaAAT2* aumenta significativamente en receptáculo de fruto de fresa durante su maduración y está negativamente regulada por auxinas.
- 5.- El gen *FaAAT2* es un gen nuevo, diferente al gen *SAAT* previamente descrito en fresa, cuya proteína presenta su mayor actividad enzimática en presencia de alcoholes de cadena lineal y alcoholes aromáticos con acetil-CoA, siendo su sustrato favorito el cinnamil alcohol.
- 6.- La proteína *FaAAT2* tiene preferencia por los alcoholes C6-C10, siendo más activa con hexanol seguida de octanol y heptanol.
- 7.- La producción de volátiles relacionados con el aroma del fruto de fresa maduro se redujo tras el silenciamiento transitorio de la expresión del gen *FaAAT2* lo que indica una clara correlación entre la concentración de ésteres volátiles, el nivel de expresión de este gen y el aroma final del fruto de fresa.
- 8.- El factor de transcripción *FaMYB10* posee un papel importante en el control global del metabolismo de flavonoides/fenilpropanoides a lo largo del proceso de maduración del fruto de fresa.
- 9.- La expresión del gen *FaMYB10* se induce claramente durante el proceso de maduración del receptáculo de fruto de fresa, siendo apenas detectada en aquenios y en tejidos vegetativos. Además, dicha expresión se encuentra negativamente regulada por auxinas y es inducida por ácido abscísico.
- 10.- El silenciamiento transitorio de la expresión del gen *FaMYB10* reduce los niveles de los genes que codifican a enzimas implicadas en la vía de flavonoides/fenilpropanoides. Por lo tanto, este TF regula los *Early-regulated Biosynthesis Genes* (EBGs), los *Late-regulated Biosynthesis Genes* (LBGs) y genes de la ruta general implicados en la producción de flavonoles y antocianinas en receptáculo de fruto maduro.
- 11.- Los análisis transcriptómicos realizados en frutos transgénicos de fresa también mostraron que el gen *FaMYB10* regula la expresión de otros genes aparentemente no implicados en el metabolismo de flavonoides/fenilpropanoide y de algunos TF implicados en el proceso de maduración de la fresa.



**SUPPLEMENTARY MATERIAL*****DOWN REGULATED GENES***

<b>GENES</b>	<b>Putative function</b>	<b>Fold</b>	<b>p-value</b>	<b>Species</b>	<b>e-value</b>	<b>Best Match BlastX</b>
<i>UCOESTdown1</i>	Carotenoid cleavage dioxygenase	181.471	0.00029	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003622507.1</a>
<i>UCOESTdown2</i>	No homology	136.616	0.000404			
<i>UCOESTdown3</i>	GDSL esterase/lipase	117.511	0.000443	<i>Medicago truncatula</i>	4.00E-165	<a href="#">XM_003626447.1</a>
<i>UCOESTdown4</i>	Cytochrome P450	105.537	0.000352	<i>Populus trichocarpa</i>	5.00E-84	<a href="#">XM_002323046.1</a>
<i>UCOESTdown5</i>	Cytochrome P450	88.985	0.000762	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003606175.1</a>
<i>UCOESTdown6</i>	UDP-Glycosyltransferase	88.666	0.000554	<i>Arabidopsis thaliana</i>	3.00E-122	<a href="#">NM_124778.3</a>
<i>UCOESTdown7</i>	Uncharacterized protein	79.121	0.000123	<i>Vitis vinifera</i>	6.00E-95	<a href="#">XM_002275087.2</a>
<i>UCOESTdown8</i>	Flavin-containing monooxygenase	75.679	0.000146	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_125522.3</a>
<i>UCOESTdown9</i>	No homology	73.024	0.00156			
<i>UCOESTdown10</i>	GDSL esterase/lipase	68.153	0.000716	<i>Medicago truncatula</i>	2.00E-135	<a href="#">XM_003593694.1</a>
<i>UCOESTdown11</i>	GDSL esterase/lipase	67.936	0.0016	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002868350.1</a>
<i>UCOESTdown12</i>	GDSL esterase/lipase	67.411	0.00628	<i>Medicago truncatula</i>	2.00E-165	<a href="#">XM_003601494.1</a>
<i>UCOESTdown13</i>	GDSL esterase/lipase	64.065	0.00103	<i>Medicago truncatula</i>	2.00E-127	<a href="#">XM_003629222.1</a>
<i>UCOESTdown14</i>	Beta 1-3 glucanase	62.245	0.000173	<i>Vitis riparia</i>	1.00E-100	<a href="#">EU676805.1</a>
<i>UCOESTdown15</i>	Ethylene-responsive transcription factor ERF039	60.601	0.00101	<i>Arabidopsis thaliana</i>	4.00E-45	<a href="#">NM_117777.2</a>
<i>UCOESTdown16</i>	TRANSPARENT TESTA 12	60.285	0.000177	<i>Glycine max</i>	0.0	<a href="#">XM_003533555.1</a>
<i>UCOESTdown17</i>	bHLH transcription factor 36	59.912	0.0000757	<i>Medicago truncatula</i>	5.00E-37	<a href="#">XM_003607421.1</a>
<i>UCOESTdown18</i>	Laccase 1b	57.658	0.00216	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002322926.1</a>
<i>UCOESTdown19</i>	ABC transporter G family member 8	57.503	0.000132	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_124664.2</a>
<i>UCOESTdown20</i>	Omega-hydroxypalmitate O-feruloyl transferase	56.922	0.00031	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003634174.1</a>
<i>UCOESTdown21</i>	Amino acid transporter family protein	53.997	0.00021	<i>Arabidopsis lyrata</i>	3.00E-131	<a href="#">XM_002870913.1</a>
<i>UCOESTdown22</i>	No homology	52.976	0.000263			
<i>UCOESTdown23</i>	MYB transcription factor (MYB22)	52.636	0.000539	<i>Malus x domestica</i>	3.00E-82	<a href="#">DQ074470.1</a>
<i>UCOESTdown24</i>	Nitrate excretion transporter 1	51.406	0.000149	<i>Vitis vinifera</i>	3.00E-140	<a href="#">XM_002281870.1</a>
<i>UCOESTdown25</i>	No homology	49.671	0.00114			

(Table continues on following page)

<i>UCOESTdown26</i>	Uncharacterized protein	48.940	0.000224	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002265839.2</a>
<i>UCOESTdown27</i>	(-)-Germacrene D synthase	48.834	0.000108	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003634648.1</a>
<i>UCOESTdown28</i>	No homology	48.404	0.0000893			
<i>UCOESTdown29</i>	Uncharacterized protein	45.746	0.00013	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002285193.1</a>
<i>UCOESTdown30</i>	Thaumatococin-like protein	44.957	0.000133	<i>Prunus persica</i>	2.00E-68	<a href="#">AF362988.1</a>
<i>UCOESTdown31</i>	LysM type receptor kinase	44.018	0.00083	<i>Lotus japonicus</i>	6.00E-48	<a href="#">AB506702.1</a>
<i>UCOESTdown32</i>	Terpene synthase 1	41.434	0.00189	<i>Populus trichocarpa</i>	2.00E-88	<a href="#">JF449450.1</a>
<i>UCOESTdown33</i>	Disease resistance protein	41.001	0.000347	<i>Medicago truncatula</i>	1.00E-36	<a href="#">XM_003605911.1</a>
<i>UCOESTdown34</i>	MYB transcription factor 39 (MYB39)	40.227	0.00092	<i>Glycine max</i>	4.00E-86	<a href="#">XM_003523768.1</a>
<i>UCOESTdown35</i>	MYB transcription factor 25 (MYN25)	39.510	0.000347	<i>Malus x domestica</i>	9.00E-77	<a href="#">HM122620.1</a>
<i>UCOESTdown36</i>	Uncharacterized protein	39.107	0.000405	<i>Vitis vinifera</i>	2.00E-57	<a href="#">XM_002283847.2</a>
<i>UCOESTdown37</i>	Cyclopropane fatty acid synthase	38.407	0.000311	<i>Gossypium hirsutum</i>	0.0	<a href="#">AY574038.1</a>
<i>UCOESTdown38</i>	Xyloglucan endotransglucosylase/hydrolase 9	37.739	0.000129	<i>Malus x domestica</i>	5.00E-180	<a href="#">EU494968.1</a>
<i>UCOESTdown39</i>	Alcohol acyl transferase	37.071	0.0000972	<i>Pyrus communis</i>	5.00E-144	<a href="#">AY534530.1</a>
<i>UCOESTdown40</i>	No homology	34.829	0.000175			
<i>UCOESTdown41</i>	Aluminum-activated malate transporter	34.779	0.0000733	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002278958.1</a>
<i>UCOESTdown42</i>	LRR receptor-like serine/threonine- protein kinase	34.438	0.00251	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003608935.1</a>
<i>UCOESTdown43</i>	Uncharacterized protein	34.418	0.00013	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002277746.1</a>
<i>UCOESTdown44</i>	Laccase 90a	34.008	0.000368	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002312150.1</a>
<i>UCOESTdown45</i>	E)-Beta-caryophyllene synthase	33.509	0.041	<i>Vitis vinifera</i>	1.00E-174	<a href="#">JF808010.1</a>
<i>UCOESTdown46</i>	GDSL esterase/lipase	33.499	0.000266	<i>Vitis vinifera</i>	1.00E-128	<a href="#">XM_002277228.1</a>
<i>UCOESTdown47</i>	Protein LURP-one-related 4	32.998	0.000115	<i>Vitis vinifera</i>	2.00E-59	<a href="#">XM_002269401.1</a>
<i>UCOESTdown48</i>	No homology	32.998	0.000115			
<i>UCOESTdown49</i>	No homology	32.861	0.00307			
<i>UCOESTdown50</i>	No homology	32.772	0.000353			
<i>UCOESTdown51</i>	bHLH transcription factor	32.749	0.000335	<i>Medicago truncatula</i>	2.00E-100	<a href="#">XM_003595029.1</a>
<i>UCOESTdown52</i>	Flavin-containing monooxygenase FMO GS-OX 9	32.700	0.000211	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002281455.2</a>
<i>UCOESTdown53</i>	Squamosa promoter binding like- protein	32.547	0.000209	<i>Glycine max</i>	3.00E-70	<a href="#">XM_003521039.1</a>
<i>UCOESTdown54</i>	GDSL esterase/lipase	32.452	0.00058	<i>Arabidopsis thaliana</i>	4.00E-131	<a href="#">NM_100809.4</a>
<i>UCOESTdown55</i>	MYB transcription factor 1 (MYBPA1)	32.072	0.000223	<i>Vitis vinifera</i>	1.00E-93	<a href="#">AM259485.1</a>

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<i>UCOESTdown56</i>	No homology	32.054	0.000492			
<i>UCOESTdown57</i>	Indole-3-glycerol phosphate lyase	31.320	0.000582	<i>Vitis vinifera</i>	5.00E-115	<a href="#">XM_002281563.2</a>
<i>UCOESTdown58</i>	Integral membrane protein	30.039	0.000184	<i>Medicago truncatula</i>	8.00E-32	<a href="#">XM_003615428.1</a>
<i>UCOESTdown59</i>	Glycosyltransferase	30.034	0.000138	<i>Arabidopsis thaliana</i>	9.00E-120	<a href="#">NM_126388.2</a>
<i>UCOESTdown60</i>	Anthocyanidin 3-O-glucosyltransferase	30.008	0.000781	<i>Medicago truncatula</i>	4.00E-69	<a href="#">XM_003593627.1</a>
<i>UCOESTdown61</i>	No homology	29.787	0.000441			
<i>UCOESTdown62</i>	ABC transporter G family member 10	29.660	0.000723	<i>Glycine max</i>	0.0	<a href="#">XM_003539566.1</a>
<i>UCOESTdown63</i>	bHLH transcription factor 25	29.453	0.00574	<i>Vitis vinifera</i>	2.00E-74	<a href="#">XM_002270412.2</a>
<i>UCOESTdown64</i>	No homology	29.407	0.00116			
<i>UCOESTdown65</i>	Uncharacterized protein	29.372	0.000116	<i>Medicago truncatula</i>	3.00E-21	<a href="#">XM_003627383.1</a>
<i>UCOESTdown66</i>	Hydroxycinnamoyl CoA shikimate/quinate hydroxycinnamoyltransferase 3	29.195	0.000149	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002321689.1</a>
<i>UCOESTdown67</i>	Serine carboxypeptidase 18	29.132	0.00315	<i>Vitis vinifera</i>	3.00E-93	<a href="#">XM_002265806.1</a>
<i>UCOESTdown68</i>	Laccase 90a	28.980	0.000152	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002312150.1</a>
<i>UCOESTdown69</i>	Uncharacterized protein	28.233	0.00372	<i>Medicago truncatula</i>	1.00E-59	<a href="#">XM_003629963.1</a>
<i>UCOESTdown70</i>	Aspartic proteinase nepenthesin-1	27.924	0.0162	<i>Vitis vinifera</i>	2.00E-150	<a href="#">XM_002264590.2</a>
<i>UCOESTdown71</i>	Xyloglucan glycosyltransferase	27.836	0.000118	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003604103.1</a>
<i>UCOESTdown72</i>	No homology	27.325	0.00168			
<i>UCOESTdown73</i>	Leucine-rich repeat receptor-like protein kinase	27.305	0.000112	<i>Medicago truncatula</i>	2.00E-44	<a href="#">XM_003596183.1</a>
<i>UCOESTdown74</i>	2-Hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase	26.451	0.00069	<i>Medicago truncatula</i>	3.00E-123	<a href="#">XM_003607755.1</a>
<i>UCOESTdown75</i>	Protein LURP-one-related 4	26.248	0.0024	<i>Vitis vinifera</i>	1.00E-48	<a href="#">XM_002269433.1</a>
<i>UCOESTdown76</i>	Epoxide hydrolase	26.170	0.0157	<i>Medicago truncatula</i>	1.00E-133	<a href="#">XM_003622307.1</a>
<i>UCOESTdown77</i>	Xyloglucan endotransglucosylase/hydrolase 3	26.158	0.000883	<i>Malus x domestica</i>	0.0	<a href="#">EU494962.1</a>
<i>UCOESTdown78</i>	UDP Flavonoid 3-O-glucosyltransferase	25.849	0.000442	<i>Medicago truncatula</i>	1.00E-145	<a href="#">XM_003610115.1</a>
<i>UCOESTdown79</i>	Squamosa promoter binding like-protein	25.802	0.000572	<i>Betula pendula</i>	2.00E-38	<a href="#">AJ558184.1</a>
<i>UCOESTdown80</i>	No homology	25.030	0.00175			
<i>UCOESTdown81</i>	Uncharacterized protein	24.837	0.00206	<i>Glycine max</i>	7.00E-100	<a href="#">XM_003552403.1</a>
<i>UCOESTdown82</i>	No homology	24.224	0.000379			
<i>UCOESTdown83</i>	Uncharacterized protein	24.054	0.000176	<i>Vitis vinifera</i>	6.00E-43	<a href="#">XM_002279975.2</a>

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<i>UCOESTdown84</i>	No homology	23.595	0.0000808			
<i>UCOESTdown85</i>	Alcohol acyl transferase	23.525	0.00505	<i>Malus x domestica</i>	0.0	<a href="#">AY512893.1</a>
<i>UCOESTdown86</i>	Leucine-rich repeat receptor kinase	23.520	0.000162	<i>Arabidopsis thaliana</i>	5.00E-107	<a href="#">FJ708663.1</a>
<i>UCOESTdown87</i>	MYB transcription factor 15 (MYB15)	23.266	0.00269	<i>Rosa rugosa</i>	6.00E-123	<a href="#">FR828548.1</a>
<i>UCOESTdown88</i>	Zinc finger CCCH-containing protein	22.945	0.000116	<i>Medicago truncatula</i>	3.00E-110	<a href="#">XM_003605795.1</a>
<i>UCOESTdown89</i>	MYB transcription factor 86 (MYB86)	22.897	0.000408	<i>Vitis vinifera</i>	1.00E-87	<a href="#">XM_002272968.1</a>
<i>UCOESTdown90</i>	Uncharacterized protein	22.771	0.000334	<i>Vitis vinifera</i>	3.00E-59	<a href="#">XM_002264822.1</a>
<i>UCOESTdown91</i>	Uncharacterized protein	22.297	0.000994	<i>Vitis vinifera</i>	1.00E-15	<a href="#">XM_002271145.1</a>
<i>UCOESTdown92</i>	Uncharacterized protein	22.122	0.00281	<i>Vitis vinifera</i>	2.00E-168	<a href="#">XM_002277006.1</a>
<i>UCOESTdown93</i>	Phospholipid:diacylglycerol acyltransferase 2	21.988	0.000883	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002270965.1</a>
<i>UCOESTdown94</i>	LRR receptor-like serine/threonine-protein kinase ERECTA	21.972	0.000169	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002280019.2</a>
<i>UCOESTdown95</i>	GDSL esterase/lipase	21.860	0.00221	<i>Glycine max</i>	0.0	<a href="#">NM_001253160.1</a>
<i>UCOESTdown96</i>	NAD(P)H-quinone oxidoreductase subunit M	21.653	0.00194	<i>Vitis vinifera</i>	5.00E-91	<a href="#">XM_002285848.1</a>
<i>UCOESTdown97</i>	ABC transporter G family member 5	21.586	0.00145	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002274586.1</a>
<i>UCOESTdown98</i>	Fasciclin-like arabinogalactan protein 1	21.293	0.000442	<i>Glycine max</i>	1.00E-152	<a href="#">XM_003532130.1</a>
<i>UCOESTdown99</i>	Phytoene dehydrogenase	21.231	0.00203	<i>Glycine max</i>	0.0	<a href="#">XM_003524705.1</a>
<i>UCOESTdown100</i>	Phytochrome E	21.223	0.003	<i>Vitis riparia</i>	0.0	<a href="#">EU436656.1</a>
<i>UCOESTdown101</i>	Actin-related protein 2/3 complex	21.061	0.00155	<i>Vitis vinifera</i>	8.00E-103	<a href="#">XM_002282005.2</a>
<i>UCOESTdown102</i>	No homology	20.997	0.00457			
<i>UCOESTdown103</i>	Uncharacterized protein	20.818	0.00377	<i>Vitis vinifera</i>	3.00E-70	<a href="#">XM_002284170.2</a>
<i>UCOESTdown104</i>	Lipid transfer protein III	20.757	0.00148	<i>Prunus amygdalus</i>	6.00E-35	<a href="#">X96716.1</a>
<i>UCOESTdown105</i>	Uncharacterized protein	20.650	0.000137	<i>Vitis vinifera</i>	9.00E-43	<a href="#">XM_002271622.2</a>
<i>UCOESTdown106</i>	BAHD acyltransferase DCR	20.483	0.0128	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002278765.2</a>
<i>UCOESTdown107</i>	Rho GDP-dissociation inhibitor	20.474	0.000805	<i>Medicago truncatula</i>	9.00E-67	<a href="#">XM_003630452.1</a>
<i>UCOESTdown108</i>	No homology	20.433	0.00421			
<i>UCOESTdown109</i>	Uncharacterized protein	20.290	0.000231	<i>Vitis vinifera</i>	9.00E-136	<a href="#">XM_002271989.1</a>
<i>UCOESTdown110</i>	No homology	20.274	0.000362			
<i>UCOESTdown111</i>	Uncharacterized protein	20.158	0.00103	<i>Glycine max</i>	0.0	<a href="#">XM_003547871.1</a>
<i>UCOESTdown112</i>	Nudix hydrolase 8	20.066	0.000369	<i>Glycine max</i>	3.00E-165	<a href="#">NM_001254102.1</a>
<i>UCOESTdown113</i>	WRKY transcription factor 23-1	19.850	0.000846	<i>Dimocarpus longan</i>		<a href="#">JF708959.1</a>
<i>UCOESTdown114</i>	COBRA-like protein 4	19.755	0.00053	<i>Glycine max</i>	1.00E-97	<a href="#">NM_001255848.1</a>
<i>UCOESTdown115</i>	Uncharacterized protein	19.720	0.00106	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002278472.2</a>

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<i>UCOESTdown116</i>	MYB transcription factor 3R-1	19.551	0.000758	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002281492.2</a>
<i>UCOESTdown117</i>	UDP-Glucose: flavonol 3-O-glucosyltransferase	19.543	0.00178	<i>Rosa hybrid</i>	0.0	<a href="#">AB201051.1</a>
<i>UCOESTdown118</i>	No homology	19.428	0.000773			
<i>UCOESTdown119</i>	Wound-induced protein 1	19.272	0.00211	<i>Vitis vinifera</i>	2.00E-51	<a href="#">XM_003632541.1</a>
<i>UCOESTdown120</i>	Receptor-like protein kinase 2	19.111	0.00124	<i>Glycine max</i>	5.00E-164	<a href="#">NM_001250085.1</a>
<i>UCOESTdown121</i>	Patatin group A-3	19.061	0.000146	<i>Glycine max</i>	2.00E-159	<a href="#">XM_003527665.1</a>
<i>UCOESTdown122</i>	Dihydrodipicolinate reductase 3	18.898	0.0019	<i>Vitis vinifera</i>	1.00E-156	<a href="#">XM_002274666.1</a>
<i>UCOESTdown123</i>	O-Fucosyltransferase	18.858	0.00102	<i>Vitis vinifera</i>	1.00E-172	<a href="#">XM_002265839.2</a>
<i>UCOESTdown124</i>	Disease resistance response protein 206	18.672	0.000188	<i>Vitis vinifera</i>	3.00E-97	<a href="#">XM_002276441.1</a>
<i>UCOESTdown125</i>	Protein kinase	18.532	0.00133	<i>Arabidopsis thaliana</i>	1.00E-68	<a href="#">NM_115635.3</a>
<i>UCOESTdown126</i>	Polygalacturonase	18.518	0.000494	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002266564.2</a>
<i>UCOESTdown127</i>	Flavonol synthase (FLS)	18.364	0.00723	<i>Fragaria x ananassa</i>	0.0	<a href="#">DQ087252.1</a>
<i>UCOESTdown128</i>	Rubredoxin	18.343	0.00116	<i>Arabidopsis thaliana</i>	5.00E-37	<a href="#">NM_124480.2</a>
<i>UCOESTdown129</i>	Lipid-transfer protein DIR1	18.326	0.00565	<i>Vitis vinifera</i>	3.00E-33	<a href="#">XM_002263131.2</a>
<i>UCOESTdown130</i>	Allene oxide cyclase (AOC)	18.318	0.0185	<i>Camellia sinensis</i>	1.00E-87	<a href="#">HQ889679.1</a>
<i>UCOESTdown131</i>	Laccase-17	18.312	0.00231	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003632156.1</a>
<i>UCOESTdown132</i>	No homology	18.291	0.000393			
<i>UCOESTdown133</i>	No homology	18.252	0.0147			
<i>UCOESTdown134</i>	Protein SRG1	18.233	0.00108	<i>Vitis vinifera</i>	2.00E-127	<a href="#">XM_002271112.1</a>
<i>UCOESTdown135</i>	Uncharacterized protein	18.206	0.00747	<i>Arabidopsis thaliana</i>	1.00E-81	<a href="#">NM_121167.2</a>
<i>UCOESTdown136</i>	No homology	18.170	0.0199			
<i>UCOESTdown137</i>	Rop-interacting receptor-like cytoplasmic kinase 1	18.158	0.00489	<i>Medicago truncatula</i>	0.0	<a href="#">FM886833.1</a>
<i>UCOESTdown138</i>	COBRA-like protein 4	18.007	0.000743	<i>Glycine max</i>	5.00E-114	<a href="#">NM_001255146.1</a>
<i>UCOESTdown139</i>	Basic 7S globulin	17.958	0.00792	<i>Medicago truncatula</i>	6.00E-101	<a href="#">XM_003626266.1</a>
<i>UCOESTdown140</i>	Proline-rich cell wall protein 1	17.734	0.00169	<i>Vitis vinifera</i>	3.00E-55	<a href="#">XM_002285396.2</a>
<i>UCOESTdown141</i>	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin	17.699	0.000948	<i>Arabidopsis thaliana</i>	8.00E-47	<a href="#">NM_180369.3</a>
<i>UCOESTdown142</i>	Receptor-like protein kinase	17.600	0.00299	<i>Arabidopsis thaliana</i>	0.0	<a href="#">AK221060.1</a>
<i>UCOESTdown143</i>	Subtilisin serine proteinase	17.416	0.00451	<i>Arabidopsis thaliana</i>	0.0	<a href="#">AY096357.1</a>
<i>UCOESTdown144</i>	Uncharacterized protein	17.238	0.00483	<i>Glycine max</i>	3.00E-98	<a href="#">XM_003520163.1</a>
<i>UCOESTdown145</i>	No homology	17.161	0.00126			
<i>UCOESTdown146</i>	No homology	17.140	0.000183			
<i>UCOESTdown147</i>	No homology	17.083	0.00119			

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<i>UCOESTdown148</i>	No homology	17.030	0.00504			
<i>UCOESTdown149</i>	No homology	16.999	0.00565			
<i>UCOESTdown150</i>	Beta-D-galactosidase	16.946	0.000761	<i>Pyrus pyrifolia</i>	0.0	<a href="#">AB190369.1</a>
<i>UCOESTdown151</i>	Basic blue protein	16.902	0.000291	<i>Vitis vinifera</i>	9.00E-51	<a href="#">XM_002285700.2</a>
<i>UCOESTdown152</i>	Peroxidase 20	16.811	0.0076	<i>Glycine max</i>	4.00E-90	<a href="#">XM_003516593.1</a>
<i>UCOESTdown153</i>	Cellulose synthase 4	16.642	0.0064	<i>Betula luminifera</i>	0.0	<a href="#">FJ410446.1</a>
<i>UCOESTdown154</i>	LysM GPI-anchored protein 1	16.499	0.00108	<i>Vitis vinifera</i>	3.00E-12	<a href="#">XM_002276088.1</a>
<i>UCOESTdown155</i>	Cyclin A1	16.418	0.000363	<i>Solanum lycopersicum</i>	0.0	<a href="#">NM_001246833.1</a>
<i>UCOESTdown156</i>	bHLH transcription factor 11	16.307	0.000777	<i>Malus x domestica</i>	3.00E-124	<a href="#">HM122452.1</a>
<i>UCOESTdown157</i>	Uncharacterized protein	16.298	0.000224	<i>Vitis vinifera</i>	2.00E-17	<a href="#">XM_002268912.1</a>
<i>UCOESTdown158</i>	Pentatricopeptide repeat-containing protein	16.287	0.00259	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002281906.2</a>
<i>UCOESTdown159</i>	Pathogenesis-related protein PR-1	16.211	0.00555	<i>Glycine max</i>	3.00E-98	<a href="#">XR_137403.1</a>
<i>UCOESTdown160</i>	GDSL esterase/lipase	16.192	0.00013	<i>Medicago truncatula</i>	6.00E-160	<a href="#">XM_003597997.1</a>
<i>UCOESTdown161</i>	Uncharacterized protein	15.998	0.00409	<i>Glycine max</i>	4.00E-125	<a href="#">XM_003550063.1</a>
<i>UCOESTdown162</i>	No homology	15.954	0.00553			
<i>UCOESTdown163</i>	Uncharacterized protein	15.887	0.00191	<i>Glycine max</i>	3.00E-37	<a href="#">NM_001250525.1</a>
<i>UCOESTdown164</i>	Respiratory burst oxidase protein	15.822	0.000114	<i>Glycine max</i>	0.0	<a href="#">XM_003546477.1</a>
<i>UCOESTdown165</i>	S-RNase	15.772	0.00678	<i>Medicago truncatula</i>	1.00E-16	<a href="#">XM_003599193.1</a>
<i>UCOESTdown166</i>	Cytochrome P450 A	15.712	0.000209	<i>Capsicum annuum</i>	0.0	<a href="#">HM581974.1</a>
<i>UCOESTdown167</i>	Cytochrome P450	15.512	0.00225	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002273775.2</a>
<i>UCOESTdown168</i>	Uncharacterized protein	15.452	0.00142	<i>Vitis vinifera</i>	8.00E-174	<a href="#">XM_003631190.1</a>
<i>UCOESTdown169</i>	Interactor of constitutive active ROPs 3	15.425	0.0011	<i>Vitis vinifera</i>	2.00E-180	<a href="#">XM_002281991.2</a>
<i>UCOESTdown170</i>	Glucan endo-1,3-beta-glucosidase 13	15.324	0.00045	<i>Glycine max</i>	0.0	<a href="#">XM_003530467.1</a>
<i>UCOESTdown171</i>	No homology	15.258	0.00162			
<i>UCOESTdown172</i>	F-box protein	15.229	0.00033	<i>Vitis vinifera</i>	9.00E-107	<a href="#">XM_002267190.2</a>
<i>UCOESTdown173</i>	No homology	15.193	0.000173			
<i>UCOESTdown174</i>	Uncharacterized protein	15.181	0.00483	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002265015.2</a>
<i>UCOESTdown175</i>	(E,E)-Alpha-farnesene synthase 1	15.142	0.0021	<i>Malus x domestica</i>	0.0	<a href="#">AY182241.2</a>
<i>UCOESTdown176</i>	Uncharacterized protein	15.134	0.000513	<i>Vitis vinifera</i>	3.00E-103	<a href="#">XM_002278746.1</a>
<i>UCOESTdown177</i>	No homology	15.033	0.00203			
<i>UCOESTdown178</i>	Acid phosphatase 1	14.975	0.00366	<i>Glycine max</i>	3.00E-92	<a href="#">XM_003521259.1</a>
<i>UCOESTdown179</i>	ABC transporter G	14.901	0.000285	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002276005.1</a>
<i>UCOESTdown180</i>	Uncharacterized protein	14.882	0.00048	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002275030.1</a>

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<i>UCOESTdown181</i>	Leucine-rich repeat receptor kinase	14.870	0.00104	<i>Arabidopsis thaliana</i>	0.0	<a href="#">FJ708701.1</a>
<i>UCOESTdown182</i>	No homology	14.849	0.000133			
<i>UCOESTdown183</i>	No homology	14.837	0.000508			
<i>UCOESTdown184</i>	Anion exchanger family protein	14.499	0.000121	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002311328.1</a>
<i>UCOESTdown185</i>	G2/mitotic-specific cyclin S13-6	14.342	0.0164	<i>Vitis vinifera</i>	5.00E-162	<a href="#">XM_002283116.1</a>
<i>UCOESTdown186</i>	Kinesin-4	14.340	0.00472	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003600366.1</a>
<i>UCOESTdown187</i>	Caffeoyl-CoA O-methyltransferase	14.311	0.00251	<i>Vitis vinifera</i>	4.00E-180	<a href="#">XM_002272027.2</a>
<i>UCOESTdown188</i>	No homology	14.304	0.000559			
<i>UCOESTdown189</i>	Flavonol sulfotransferase	14.245	0.000535	<i>Medicago truncatula</i>	2.00E-60	<a href="#">XM_003628690.1</a>
<i>UCOESTdown190</i>	Cyclic nucleotide-gated ion channel 2	14.245	0.00342	<i>Glycine max</i>	0.0	<a href="#">XM_003552501.1</a>
<i>UCOESTdown191</i>	Rubredoxin	14.223	0.000347	<i>Vitis vinifera</i>	8.00E-75	<a href="#">XM_002276370.1</a>
<i>UCOESTdown192</i>	Aspartic proteinase nepenthesin-1	14.199	0.000192	<i>Glycine max</i>	6.00E-139	<a href="#">XM_003526841.1</a>
<i>UCOESTdown193</i>	Glycogenin glucosyltransferase	14.193	0.000122	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003589149.1</a>
<i>UCOESTdown194</i>	Beta-fructofuranosidase	14.105	0.000549	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002282141.2</a>
<i>UCOESTdown195</i>	Uncharacterized protein	14.105	0.0052	<i>Glycine max</i>	7.00E-23	<a href="#">XM_003552105.1</a>
<i>UCOESTdown196</i>	Major pollen allergen Bet v 1-L	14.055	0.00152	<i>Medicago truncatula</i>	6.00E-30	<a href="#">XM_003600129.1</a>
<i>UCOESTdown197</i>	WRKY transcription factor 4	14.022	0.000181	<i>Vitis vinifera</i>	8.00E-59	<a href="#">GU270834.1</a>
<i>UCOESTdown198</i>	bHLH transcription factor	14.016	0.0176	<i>Arabidopsis lyrata</i>	1.00E-28	<a href="#">XM_002865784.1</a>
<i>UCOESTdown199</i>	Nitrite transporter	13.924	0.000309	<i>Cucumis sativus</i>	0.0	<a href="#">Z69370.2</a>
<i>UCOESTdown200</i>	Laccase-14	13.886	0.00545	<i>Vitis vinifera</i>	2.00E-168	<a href="#">XM_002263949.2</a>
<i>UCOESTdown201</i>	Uncharacterized protein	13.883	0.00258	<i>Glycine max</i>	0.0	<a href="#">XM_003540880.1</a>
<i>UCOESTdown202</i>	Protein ODORANT1	13.875	0.00319	<i>Glycine max</i>	2.00E-110	<a href="#">XM_003549830.1</a>
<i>UCOESTdown203</i>	Glycosyltransferase	13.849	0.00207	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002264040.2</a>
<i>UCOESTdown204</i>	Glycine cleavage system H protein	13.749	0.00192	<i>Medicago truncatula</i>	1.00E-95	<a href="#">XP_003611464.1</a>
<i>UCOESTdown205</i>	No homology	13.748	0.000209			
<i>UCOESTdown206</i>	Jasmonate-induced protein	13.723	0.00323	<i>Zea mays</i>	4.00E-26	<a href="#">NM_001156693.1</a>
<i>UCOESTdown207</i>	Serine carboxypeptidase 25	13.644	0.00113	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_111077.3</a>
<i>UCOESTdown208</i>	Vinorine synthase	13.601	0.00249	<i>Medicago truncatula</i>	4.00E-147	<a href="#">XM_003601793.1</a>
<i>UCOESTdown209</i>	Cytochrome P450	13.567	0.00527	<i>Glycine max</i>	3.00E-158	<a href="#">XM_003529146.1</a>
<i>UCOESTdown210</i>	Phytochrome E	13.482	0.00173	<i>Glycine max</i>	0.0	<a href="#">XM_003534982.1</a>
<i>UCOESTdown211</i>	Ethylene-responsive transcription factor ERF027	13.414	0.00505	<i>Arabidopsis thaliana</i>	2.00E-34	<a href="#">NM_101133.2</a>
<i>UCOESTdown212</i>	bHLH transcription factor 61	13.413	0.000163	<i>Vitis vinifera</i>	4.00E-55	<a href="#">XM_002278835.2</a>
<i>UCOESTdown213</i>	Uncharacterized protein	13.399	0.000179	<i>Vitis vinifera</i>	1.00E-34	<a href="#">XM_002274907.2</a>
<i>UCOESTdown214</i>	No homology	13.364	0.000822			

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<i>UCOESTdown215</i>	No homology	13.331	0.000364			
<i>UCOESTdown216</i>	Uncharacterized protein	13.33	0.000267	<i>Vitis vinifera</i>	8.00E-46	<a href="#">XM_002284772.1</a>
<i>UCOESTdown217</i>	Methyl jasmonate esterase	13.317	0.000986	<i>Medicago truncatula</i>	2.00E-20	<a href="#">XM_003626701.1</a>
<i>UCOESTdown218</i>	Sulfotransferase 16	13.274	0.00203	<i>Vitis vinifera</i>	2.00E-66	<a href="#">XM_002268631.2</a>
<i>UCOESTdown219</i>	Serine/threonine-protein kinase-like protein CCR1	13.262	0.000335	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002276007.1</a>
<i>UCOESTdown220</i>	Serine carboxypeptidase 18	13.181	0.00013	<i>Vitis vinifera</i>	5.00E-151	<a href="#">XM_003633151.1</a>
<i>UCOESTdown221</i>	Exopolyphosphatase	13.156	0.000178	<i>Vitis vinifera</i>	3.00E-173	<a href="#">XP_002278296.1</a>
<i>UCOESTdown222</i>	Calcium-binding protein CML45	13.144	0.000837	<i>Glycine max</i>	2.00E-30	<a href="#">XM_003552486.1</a>
<i>UCOESTdown223</i>	MYB transcription factor R2R3	13.128	0.000594	<i>Populus tremuloides</i>	2.00E-71	<a href="#">FJ573152.1</a>
<i>UCOESTdown224</i>	Isocitrate lyase	13.075	0.00109	<i>Cucumis sativus</i>	0.0	<a href="#">P49296.1</a>
<i>UCOESTdown225</i>	Beta-1,3-glucanase 4	13.039	0.0151	<i>Arabidopsis thaliana</i>	5.00E-56	<a href="#">NM_122040.3</a>
<i>UCOESTdown226</i>	MYB transcription factor 9 (MYB9)	13.030	0.00032	<i>Malus x domestica</i>	7.00E-87	<a href="#">DQ267900.1</a>
<i>UCOESTdown227</i>	No homology	13.029	0.00186			
<i>UCOESTdown228</i>	Uncharacterized protein	13.024	0.00257	<i>Glycine max</i>	1.00E-14	<a href="#">XM_003522943.1</a>
<i>UCOESTdown229</i>	Uncharacterized protein	12.938	0.00029	<i>Vitis vinifera</i>	2.00E-47	<a href="#">XM_002268128.2</a>
<i>UCOESTdown230</i>	Thiazole biosynthetic enzyme	12.894	0.00413	<i>Citrus sinensis</i>	0.0	<a href="#">O23787.1</a>
<i>UCOESTdown231</i>	No homology	12.882	0.0107			
<i>UCOESTdown232</i>	BTB/POZ domain-containing protein	12.869	0.000336	<i>Vitis vinifera</i>	5.00E-43	<a href="#">XM_003633385.1</a>
<i>UCOESTdown233</i>	Uncharacterized protein	12.855	0.00461	<i>Vitis vinifera</i>	3.00E-74	<a href="#">XM_002264822.1</a>
<i>UCOESTdown234</i>	Copalyl diphosphate synthase	12.838	0.00583	<i>Populus trichocarpa</i>	0.0	<a href="#">XP_002302110.1</a>
<i>UCOESTdown235</i>	Uncharacterized protein	12.831	0.00194	<i>Vitis vinifera</i>	3.00E-59	<a href="#">XM_002278357.1</a>
<i>UCOESTdown236</i>	Beta-ketoacyl-CoA synthase	12.827	0.0132	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002308606.1</a>
<i>UCOESTdown237</i>	Receptor protein kinase ZmPK1	12.793	0.000297	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003632660.1</a>
<i>UCOESTdown238</i>	Uncharacterized protein	12.759	0.00124	<i>Vitis vinifera</i>	2.00E-40	<a href="#">XM_002275404.2</a>
<i>UCOESTdown239</i>	Sieve element occlusion b (SEOb)	12.730	0.00294	<i>Malus x domestica</i>	4.00E-129	<a href="#">HM162888.1</a>
<i>UCOESTdown240</i>	DNA-directed RNA polymerase II subunit RPB7	12.717	0.009	<i>Vitis vinifera</i>	1.00E-52	<a href="#">XM_002284185.2</a>
<i>UCOESTdown241</i>	GDSL esterase/lipase	12.655	0.00272	<i>Arabidopsis thaliana</i>	3.00E-172	<a href="#">NM_106106.2</a>
<i>UCOESTdown242</i>	Uncharacterized protein	12.638	0.00428	<i>Vitis vinifera</i>	1.00E-122	<a href="#">XM_002284694.2</a>
<i>UCOESTdown243</i>	Peptide/nitrate transporter	12.606	0.012	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002265314.2</a>
<i>UCOESTdown244</i>	Basic blue protein	12.574	0.0017	<i>Vitis vinifera</i>	3.00E-25	<a href="#">XM_002275927.1</a>
<i>UCOESTdown245</i>	Mitogen-activated protein kinase kinase kinase 2	12.571	0.000964	<i>Glycine max</i>	1.00E-99	<a href="#">NM_001254074.1</a>
<i>UCOESTdown246</i>	Uncharacterized protein	12.514	0.00171	<i>Glycine max</i>	1.00E-14	<a href="#">XM_003517309.1</a>

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<i>UCOESTdown247</i>	Uncharacterized protein	12.496	0.000122	<i>Vitis vinifera</i>	1.00E-166	<a href="#">XM_002280379.2</a>
<i>UCOESTdown248</i>	No homology	12.449	0.00191			
<i>UCOESTdown249</i>	Mechanosensitive channel of small conductance 10	12.401	0.000166	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_180479.1</a>
<i>UCOESTdown250</i>	Glycogenin-1	12.381	0.000848	<i>Glycine max</i>	0.0	<a href="#">XM_003554516.1</a>
<i>UCOESTdown251</i>	Uncharacterized protein	12.378	0.0245	<i>Vitis vinifera</i>	8.00E-84	<a href="#">XM_002285813.2</a>
<i>UCOESTdown252</i>	Magnesium chelatase H subunit	12.376	0.000405	<i>Fragaria x ananassa</i>	0.0	<a href="#">JF682517.1</a>
<i>UCOESTdown253</i>	Serine/threonine-protein kinase STN8	12.375	0.000355	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002273102.2</a>
<i>UCOESTdown254</i>	NSP-interacting kinase 1 (NIK1)	12.334	0.00145	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_121605.2</a>
<i>UCOESTdown255</i>	Leucine-rich repeat receptor-like protein kinase	12.278	0.000116	<i>Arabidopsis thaliana</i>	0.0	<a href="#">FJ708750.1</a>
<i>UCOESTdown256</i>	Cytochrome P450	12.273	0.000736	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002314081.1</a>
<i>UCOESTdown257</i>	Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase	12.258	0.00359	<i>Vitis vinifera</i>	3.00E-66	<a href="#">XM_002275495.2</a>
<i>UCOESTdown258</i>	Uncharacterized protein	12.186	0.000326	<i>Vitis vinifera</i>	6.00E-33	<a href="#">XP_002284090.1</a>
<i>UCOESTdown259</i>	Phosphate transporter 1 pho1	12.146	0.00379	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002315536.1</a>
<i>UCOESTdown260</i>	Peptidyl-prolyl cis-trans isomerase	11.999	0.00815	<i>Medicago truncatula</i>	5.00E-126	<a href="#">XM_003609031.1</a>
<i>UCOESTdown261</i>	Uncharacterized protein	11.990	0.00568	<i>Glycine max</i>	1.00E-55	<a href="#">XM_003521273.1</a>
<i>UCOESTdown262</i>	WD-repeat protein	11.989	0.00162	<i>Gossypium hirsutum</i>	0.0	<a href="#">AF530910.1</a>
<i>UCOESTdown263</i>	Uncharacterized protein	11.965	0.000176	<i>Glycine max</i>	3.00E-24	<a href="#">XM_003538587.1</a>
<i>UCOESTdown264</i>	Uncharacterized protein	11.912	0.000573	<i>Arabidopsis thaliana</i>	5.00E-43	<a href="#">NM_114928.4</a>
<i>UCOESTdown265</i>	Flavin-containing monooxygenase FMO	11.890	0.00336	<i>Vitis vinifera</i>	0.0	<a href="#">XP_002281467.1</a>
<i>UCOESTdown266</i>	Glucan endo-1,3-beta-glucosidase 13	11.863	0.000739	<i>Glycine max</i>	2.00E-53	<a href="#">XM_003539235.1</a>
<i>UCOESTdown267</i>	Flavonol sulfotransferase	11.817	0.00549	<i>Vitis vinifera</i>	3.00E-66	<a href="#">XM_002267173.1</a>
<i>UCOESTdown268</i>	Beta-glucosidase D2	11.642	0.000493	<i>Medicago truncatula</i>	1.00E-132	<a href="#">XM_003597461.1</a>
<i>UCOESTdown269</i>	3-ketoacyl-CoA reductase	11.628	0.00175	<i>Medicago truncatula</i>	1.00E-132	<a href="#">XP_003629590.1</a>
<i>UCOESTdown270</i>	Blue copper protein	11.571	0.00327	<i>Arabidopsis thaliana</i>	6.00E-46	<a href="#">AY072426.1</a>
<i>UCOESTdown271</i>	Protein SRG1	11.490	0.000352	<i>Glycine max</i>	2.00E-63	<a href="#">XM_003552138.1</a>
<i>UCOESTdown272</i>	Vacuolar processing enzyme 1 (VPE1)	11.489	0.0104	<i>Solanum tuberosum</i>	8.00E-72	<a href="#">EU605871.1</a>
<i>UCOESTdown273</i>	Anthocyanidin reductase (ANR)	11.452	0.00029	<i>Fragaria x ananassa</i>	0.0	<a href="#">DQ664192.1</a>
<i>UCOESTdown274</i>	GDSL esterase/lipase	11.428	0.000364	<i>Glycine max</i>	6.00E-116	<a href="#">XM_003544974.1</a>
<i>UCOESTdown275</i>	Uncharacterized protein	11.380	0.0013	<i>Glycine max</i>	3.00E-49	<a href="#">XM_003526370.1</a>
<i>UCOESTdown276</i>	Peroxidase 11	11.361	0.00113	<i>Vitis vinifera</i>	2.00E-165	<a href="#">XM_002270624.1</a>
<i>UCOESTdown277</i>	Glucan endo-1,3-beta-glucosidase	11.352	0.000942	<i>Vitis vinifera</i>	7.00E-98	<a href="#">XM_002279561.2</a>

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<i>UCOESTdown278</i>	No homology	11.331	0.000335			
<i>UCOESTdown279</i>	2-Succinylbenzoate--CoA ligase	11.302	0.00389	<i>Vitis vinifera</i>	0.0	<a href="#">XP_002263998.1</a>
<i>UCOESTdown280</i>	Carotenoid cleavage dioxygenase 8	11.289	0.0112	<i>Glycine max</i>	0.0	<a href="#">XM_003522665.1</a>
<i>UCOESTdown281</i>	No homology	11.253	0.00109			
<i>UCOESTdown282</i>	Phospholipase A1-Igama1	11.222	0.000621	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003632945.1</a>
<i>UCOESTdown283</i>	No homology	11.178	0.000871			
<i>UCOESTdown284</i>	No homology	11.128	0.000122			
<i>UCOESTdown285</i>	Uncharacterized protein	11.128	0.000131	<i>Vitis vinifera</i>	5.00E-30	<a href="#">XM_003631408.1</a>
<i>UCOESTdown286</i>	Desiccation-related protein PCC13-62	11.118	0.000651	<i>Vitis vinifera</i>	1.00E-52	<a href="#">XM_002267015.1</a>
<i>UCOESTdown287</i>	Uncharacterized protein	11.087	0.000251	<i>Glycine max</i>	1.00E-53	<a href="#">XM_003548972.1</a>
<i>UCOESTdown288</i>	MYB transcription factor 9 (MYB9)	11.075	0.000281	<i>Rosa rugosa</i>	2.00E-75	<a href="#">FR828542.1</a>
<i>UCOESTdown289</i>	Nitrate excretion transporter 2	11.044	0.000644	<i>Glycine max</i>	1.00E-168	<a href="#">XM_003543430.1</a>
<i>UCOESTdown290</i>	Thromboxane-A synthase	11.016	0.000867	<i>Glycine max</i>	0.0	<a href="#">XM_003527703.1</a>
<i>UCOESTdown291</i>	Lysine histidine transporter 1	11.010	0.00322	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002265685.1</a>
<i>UCOESTdown292</i>	Subtilisin	11.005	0.000151	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003592338.1</a>
<i>UCOESTdown293</i>	No homology	10.986	0.00647			
<i>UCOESTdown294</i>	No homology	10.956	0.00338			
<i>UCOESTdown295</i>	Nitrate excretion transporter 1	10.873	0.00731	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002281889.2</a>
<i>UCOESTdown296</i>	Thaumatococin-like protein	10.845	0.000348	<i>Prunus avium</i>	9.00E-102	<a href="#">U32440.1</a>
<i>UCOESTdown297</i>	GRF domain class transcription factor	10.790	0.00116	<i>Malus x domestica</i>	0.0	<a href="#">HM122562.1</a>
<i>UCOESTdown298</i>	No homology	10.751	0.000958			
<i>UCOESTdown299</i>	MYC2	10.743	0.00142	<i>Hevea brasiliensis</i>	1.00E-100	<a href="#">HM061097.1</a>
<i>UCOESTdown300</i>	Uncharacterized protein	10.734	0.000177	<i>Vitis vinifera</i>	6.00E-180	<a href="#">XM_002262625.2</a>
<i>UCOESTdown301</i>	Long chain acyl-CoA synthetase 1	10.732	0.000181	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_130292.3</a>
<i>UCOESTdown302</i>	Syntaxin-112	10.723	0.00119	<i>Vitis vinifera</i>	3.00E-108	<a href="#">XM_002284031.1</a>
<i>UCOESTdown303</i>	No homology	10.684	0.0257			
<i>UCOESTdown304</i>	Uncharacterized protein	10.659	0.000695	<i>Vitis vinifera</i>	1.00E-105	<a href="#">XM_002268943.1</a>
<i>UCOESTdown305</i>	Uncharacterized protein	10.646	0.000178	<i>Vitis vinifera</i>	1.00E-122	<a href="#">XM_002280011.2</a>
<i>UCOESTdown306</i>	AP2 domain class transcription factor	10.642	0.00213	<i>Malus x domestica</i>	1.00E-42	<a href="#">GU732478.1</a>
<i>UCOESTdown307</i>	O-Fucosyltransferase	10.622	0.000225	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002284363.1</a>
<i>UCOESTdown308</i>	Ethylene-responsive transcription factor SHINE	10.602	0.0153	<i>Medicago truncatula</i>	6.00E-54	<a href="#">XM_003603360.1</a>
<i>UCOESTdown309</i>	65-kDa Microtubule-associated protein 8	10.600	0.00403	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002271743.2</a>
<i>UCOESTdown310</i>	No homology	10.575	0.000699			

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<i>UCOESTdown311</i>	Polyphenol oxidase	10.551	0.00545	<i>Populus trichocarpa</i>	6.00E-180	<a href="#">JN001936.1</a>
<i>UCOESTdown312</i>	Protochlorophyllide reductase	10.546	0.00123	<i>Glycine max</i>	0.0	<a href="#">XM_003540404.1</a>
<i>UCOESTdown313</i>	Protein TRANSPARENT TESTA	10.545	0.000352	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003613051.1</a>
<i>UCOESTdown314</i>	Disease resistance protein	10.509	0.000297	<i>Vitis vinifera</i>	7.00E-57	<a href="#">XM_002263252.1</a>
<i>UCOESTdown315</i>	Apolipoprotein D	10.505	0.00469	<i>Medicago truncatula</i>	9.00E-146	<a href="#">XM_003617436.1</a>
<i>UCOESTdown316</i>	Subtilisin protease (SBT1.1A)	10.501	0.00904	<i>Nicotiana tabacum</i>	0.0	<a href="#">EF373046.1</a>
<i>UCOESTdown317</i>	Nodulin	10.491	0.00116	<i>Medicago truncatula</i>	2.00E-77	<a href="#">XM_003592077.1</a>
<i>UCOESTdown318</i>	Glycerol-phosphate acyltransferase	10.447	0.00599	<i>Medicago truncatula</i>	2.00E-166	<a href="#">XM_003589809.1</a>
<i>UCOESTdown319</i>	DOF transcription factor 11	10.434	0.000466	<i>Malus x domestica</i>	1.00E-118	<a href="#">HM122542.1</a>
<i>UCOESTdown320</i>	UDP-Rhamnose:rhamnosyltransferase 4 (GT4)	10.362	0.00674	<i>Fragaria x ananassa</i>	4.00E-86	<a href="#">AY663787.1</a>
<i>UCOESTdown321</i>	Laccase/diphenol oxidase	10.355	0.000388	<i>Castanea dentata</i>	0.0	<a href="#">GQ465371.1</a>
<i>UCOESTdown322</i>	Xylogalacturonan beta-1,3- xylosyltransferase	10.324	0.000655	<i>Medicago truncatula</i>	8.00E-72	<a href="#">XM_003616469.1</a>
<i>UCOESTdown323</i>	Beta-galactosidase	10.317	0.000402	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003597169.1</a>
<i>UCOESTdown324</i>	No homology	10.315	0.000386			
<i>UCOESTdown325</i>	Uncharacterized protein	10.313	0.00042	<i>Vitis vinifera</i>	9.00E-77	<a href="#">XM_002268943.1</a>
<i>UCOESTdown326</i>	No homology	10.289	0.00124			
<i>UCOESTdown327</i>	Uncharacterized protein	10.257	0.00696	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002266275.1</a>
<i>UCOESTdown328</i>	COBRA-like protein 4	10.251	0.00353	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_121567.4</a>
<i>UCOESTdown329</i>	Uncharacterized protein	10.245	0.00461	<i>Glycine max</i>	0.0	<a href="#">XM_003552225.1</a>
<i>UCOESTdown330</i>	Phosphate transporter PHO1 homolog 3	10.221	0.000407	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002264984.2</a>
<i>UCOESTdown331</i>	Uncharacterized protein	10.220	0.00667	<i>Vitis vinifera</i>	2.00E-156	<a href="#">XM_002285573.2</a>
<i>UCOESTdown332</i>	Uncharacterized protein	10.218	0.00198	<i>Vitis vinifera</i>	7.00E-143	<a href="#">XM_002263548.1</a>
<i>UCOESTdown333</i>	Glucan endo-1,3-beta-glucosidase 3	10.196	0.00399	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002274792.2</a>
<i>UCOESTdown334</i>	Kinesin-4	10.185	0.00609	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003612949.1</a>
<i>UCOESTdown335</i>	UDP-Rhamnose:rhamnosyltransferase 1	10.183	0.0168	<i>Vitis vinifera</i>	6.00E-171	<a href="#">XM_002275814.1</a>
<i>UCOESTdown336</i>	Protein ABIL5	10.169	0.00532	<i>Glycine max</i>	6.00E-66	<a href="#">XM_003528881.1</a>
<i>UCOESTdown337</i>	Uncharacterized protein	10.167	0.000149	<i>Populus trichocarpa</i>	8.00E-58	<a href="#">XM_002324936.1</a>
<i>UCOESTdown338</i>	No homology	10.163	0.000449			
<i>UCOESTdown339</i>	Pentatricopeptide repeat-containing protein	10.139	0.000656	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002269495.1</a>
<i>UCOESTdown340</i>	Histone-lysine N-methyltransferase	10.133	0.00887	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003624458.1</a>

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<i>UCOESTdown341</i>	S-Acyltransferase	10.128	0.000958	<i>Glycine max</i>	8.00E-178	<a href="#">XM_003535249.1</a>
<i>UCOESTdown342</i>	Sieve element occlusion b (SEOb)	10.110	0.0028	<i>Malus x domestica</i>	3.00E-108	<a href="#">HM162888.1</a>
<i>UCOESTdown343</i>	No homology	10.097	0.00622			
<i>UCOESTdown344</i>	No homology	10.072	0.000417			
<i>UCOESTdown345</i>	Uncharacterized protein	10.057	0.0163	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002269998.1</a>
<i>UCOESTdown346</i>	No homology	10.049	0.000883			
<i>UCOESTdown347</i>	No homology	10.025	0.000758			
<i>UCOESTdown348</i>	Uncharacterized protein	10.020	0.0016	<i>Glycine max</i>	1.00E-151	<a href="#">XM_003517267.1</a>
<i>UCOESTdown349</i>	Uncharacterized protein	10.020	0.0016	<i>Glycine max</i>	1.00E-151	<a href="#">XM_003517267.1</a>
<i>UCOESTdown350</i>	Uncharacterized protein	10.010	0.00013	<i>Glycine max</i>	3.00E-10	<a href="#">NM_001250408.1</a>
<i>UCOESTdown351</i>	Uncharacterized protein	9.987	0.00406	<i>Glycine max</i>	5.00E-45	<a href="#">XM_003524790.1</a>
<i>UCOESTdown352</i>	Quinone oxidoreductase	9.980	0.000747	<i>Glycine max</i>	2.00E-152	<a href="#">XM_003551972.1</a>
<i>UCOESTdown353</i>	Uncharacterized protein	9.962	0.0033	<i>Glycine max</i>	7.00E-41	<a href="#">XM_003532084.1</a>
<i>UCOESTdown354</i>	GDSL esterase/lipase	9.960	0.000647	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_001198299.1</a>
<i>UCOESTdown355</i>	No homology	9.945	0.00787			
<i>UCOESTdown356</i>	ABC transporter family	9.934	0.000325	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002306263.1</a>
<i>UCOESTdown357</i>	Thromboxane-A synthase	9.906	0.000157	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002279050.2</a>
<i>UCOESTdown358</i>	Cytochrome P450 monooxygenase	9.868	0.00178	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003592328.1</a>
<i>UCOESTdown359</i>	Defensin-like protein 6	9.862	0.00614	<i>Vitis vinifera</i>	3.00E-12	<a href="#">XM_002272877.2</a>
<i>UCOESTdown360</i>	Uncharacterized protein	9.852	0.000366	<i>Vitis vinifera</i>	7.00E-40	<a href="#">XM_002274044.1</a>
<i>UCOESTdown361</i>	Expansin-A23	9.844	0.00028	<i>Vitis vinifera</i>	3.00E-101	<a href="#">XM_002276604.1</a>
<i>UCOESTdown362</i>	Secondary cell wall-related glycosyltransferase	9.815	0.00217	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003602535.1</a>
<i>UCOESTdown363</i>	Sieve element occlusion e (SEOE)	9.798	0.000775	<i>Glycine max</i>	2.00E-33	<a href="#">NM_001254039.1</a>
<i>UCOESTdown364</i>	Peroxidase 66	9.758	0.00189	<i>Vitis vinifera</i>	1.00E-165	<a href="#">XM_002264415.1</a>
<i>UCOESTdown365</i>	bHLH transcription factor 14	9.751	0.00639	<i>Arabidopsis thaliana</i>	2.00E-75	<a href="#">NM_116313.2</a>
<i>UCOESTdown366</i>	4-Coumarate:CoA ligase 1	9.729	0.00549	<i>Rubus idaeus</i>	0.0	<a href="#">AF239687.1</a>
<i>UCOESTdown367</i>	Ras-related protein RABA3	9.729	0.0106	<i>Glycine max</i>	4.00E-108	<a href="#">XM_003528729.1</a>
<i>UCOESTdown368</i>	F-box protein	9.715	0.00242	<i>Populus trichocarpa</i>	8.00E-25	<a href="#">XM_002305619.1</a>
<i>UCOESTdown369</i>	Zinc finger protein CONSTANS-LIKE 16	9.644	0.000703	<i>Glycine max</i>	5.00E-88	<a href="#">XM_003535679.1</a>
<i>UCOESTdown370</i>	Nudix hydrolase 1	9.618	0.000173	<i>Vitis vinifera</i>	1.00E-38	<a href="#">XM_002278360.2</a>
<i>UCOESTdown371</i>	Exopolyphosphatase	9.603	0.000871	<i>Lupinus albus</i>	7.00E-60	<a href="#">AM886536.2</a>
<i>UCOESTdown372</i>	No homology	9.577	0.00192			
<i>UCOESTdown373</i>	Epoxide hydrolase	9.568	0.00116	<i>B. distachyon</i>	2.00E-99	<a href="#">XM_003564891.1</a>

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<i>UCOESTdown374</i>	Epidermis-specific secreted glycoprotein EP1	9.512	0.00148	<i>Glycine max</i>	1.00E-162	<a href="#">XM_003543164.1</a>
<i>UCOESTdown375</i>	No homology	9.509	0.000994			
<i>UCOESTdown376</i>	Polygalacturonase	9.505	0.00631	<i>Medicago truncatula</i>	1.00E-36	<a href="#">XM_003613933.1</a>
<i>UCOESTdown377</i>	Uncharacterized protein	9.490	0.00202	<i>Vitis vinifera</i>	3.00E-72	<a href="#">XM_002273882.1</a>
<i>UCOESTdown378</i>	Uncharacterized protein	9.448	0.000177	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002273882.1</a>
<i>UCOESTdown379</i>	FERONIA receptor kinase	9.416	0.0031	<i>Glycine max</i>	0.0	<a href="#">NM_001251502.1</a>
<i>UCOESTdown380</i>	Endoglucanase 24	9.412	0.00193	<i>Glycine max</i>	0.0	<a href="#">XM_003523462.1</a>
<i>UCOESTdown381</i>	Hydroxysteroid 11-beta-dehydrogenase	9.399	0.000782	<i>Glycine max</i>	1.00E-167	<a href="#">NM_001254330.1</a>
<i>UCOESTdown382</i>	Beta-1,4-xylosyltransferase IRX10L	9.396	0.000222	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003631316.1</a>
<i>UCOESTdown383</i>	NAC transcription factor 12	9.384	0.000902	<i>Malus x domestica</i>	1.00E-158	<a href="#">HM122654.1</a>
<i>UCOESTdown384</i>	RNA polymerase sigma factor rpoD	9.362	0.000757	<i>Vitis vinifera</i>	2.00E-135	<a href="#">XM_002272408.1</a>
<i>UCOESTdown385</i>	Protein LOL1	9.346	0.0094	<i>Glycine max</i>	1.00E-66	<a href="#">XM_003549934.1</a>
<i>UCOESTdown386</i>	Malate dehydrogenase	9.328	0.00614	<i>C.vulgaris</i>	0.0	<a href="#">M33148.1</a>
<i>UCOESTdown387</i>	GDSL esterase/lipase	9.292	0.000304	<i>Vitis vinifera</i>	4.00E-119	<a href="#">XM_002262660.1</a>
<i>UCOESTdown388</i>	No homology	9.281	0.000811			
<i>UCOESTdown389</i>	No homology	9.277	0.000799			
<i>UCOESTdown390</i>	Uncharacterized protein	9.264	0.0193	<i>Vitis vinifera</i>	4.00E-15	<a href="#">XM_002263716.1</a>
<i>UCOESTdown391</i>	Acyl:Coa ligase acetate-coa synthetase 8	9.260	0.000647	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002305201.1</a>
<i>UCOESTdown392</i>	Pectate lyase	9.217	0.0011	<i>Salix gilgiana</i>	0.0	<a href="#">AB048260.1</a>
<i>UCOESTdown393</i>	Cinnamyl alcohol dehydrogenase (CAD)	9.186	0.00271	<i>Triticum aestivum</i>	1.00E-101	<a href="#">GU563724.1</a>
<i>UCOESTdown394</i>	DnaJ domain family	9.182	0.0195	<i>Medicago truncatula</i>	1.00E-50	<a href="#">XM_003603153.1</a>
<i>UCOESTdown395</i>	Fructose-1,6-bisphosphatase I	9.180	0.000354	<i>Fragaria x ananassa</i>	0.0	<a href="#">EU185333.1</a>
<i>UCOESTdown396</i>	Serine/threonine-protein kinase Nek2	9.173	0.000486	<i>Glycine max</i>	0.0	<a href="#">XM_003520789.1</a>
<i>UCOESTdown397</i>	Xyloglucan glycosyltransferase 5	9.144	0.00324	<i>Glycine max</i>	0.0	<a href="#">XM_003522622.1</a>
<i>UCOESTdown398</i>	xyloglucan endotransglucosylase/hydrolase protein	9.132	0.00871	<i>Vitis vinifera</i>	4.00E-79	<a href="#">XM_003632406.1</a>
<i>UCOESTdown399</i>	ZF-HD homeobox protein	9.115	0.000378	<i>Vitis vinifera</i>	9.00E-80	<a href="#">XM_002283497.2</a>
<i>UCOESTdown400</i>	Uncharacterized protein	9.110	0.00455	<i>Medicago truncatula</i>	3.00E-39	<a href="#">XM_003618395.1</a>
<i>UCOESTdown401</i>	Ethylene-responsive transcription factor ERF110	9.098	0.000355	<i>Medicago truncatula</i>	3.00E-38	<a href="#">XM_003602466.1</a>
<i>UCOESTdown402</i>	Peptide transporter	9.086	0.00155	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003605118.1</a>
<i>UCOESTdown403</i>	Cell surface receptor daf-1	9.074	0.000966	<i>Vitis vinifera</i>	0.0	<a href="#">XP_002275567.1</a>

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<i>UCOESTdown404</i>	Uncharacterized protein	9.066	0.000401	<i>Vitis vinifera</i>	1.00E-167	<a href="#">XM_002279382.2</a>
<i>UCOESTdown405</i>	Syntaxin-related protein KNOLLE	9.020	0.000989	<i>Vitis vinifera</i>	2.00E-140	<a href="#">XM_002283062.1</a>
<i>UCOESTdown406</i>	Phospholipase A1-Igamm2	9.016	0.000347	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_128607.3</a>
<i>UCOESTdown407</i>	E3 ubiquitin-protein ligase ORTHRUS 2	9.014	0.00358	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_104576.5</a>
<i>UCOESTdown408</i>	SPL transcription factor 4	8.982	0.00922	<i>Malus x domestica</i>	7.00E-55	<a href="#">HM122687.1</a>
<i>UCOESTdown409</i>	No homology	8.975	0.0103			
<i>UCOESTdown410</i>	Uncharacterized protein	8.966	0.0017	<i>Vitis vinifera</i>	2.00E-55	<a href="#">XM_002265803.2</a>
<i>UCOESTdown411</i>	Cytochrome P450	8.925	0.00416	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002312869.1</a>
<i>UCOESTdown412</i>	No homology	8.914	0.00511			
<i>UCOESTdown413</i>	Alpha-1,4 glucan phosphorylase L-2	8.902	0.00376	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002274539.2</a>
<i>UCOESTdown414</i>	No homology	8.890	0.000334			
<i>UCOESTdown415</i>	Cyclic nucleotide-gated ion channel 1	8.888	0.0112	<i>Glycine max</i>	1.00E-61	<a href="#">XM_003523331.1</a>
<i>UCOESTdown416</i>	No homology	8.887	0.00842			
<i>UCOESTdown417</i>	Root phototropism protein 3	8.853	0.000672	<i>Vitis vinifera</i>	9.00E-176	<a href="#">XM_002280977.2</a>
<i>UCOESTdown418</i>	No homology	8.837	0.0221			
<i>UCOESTdown419</i>	E3 ubiquitin-protein ligase MARCH3	8.834	0.00568	<i>Medicago truncatula</i>	1.00E-17	<a href="#">XM_003613721.1</a>
<i>UCOESTdown420</i>	Cysteine-rich repeat secretory protein 3	8.811	0.00295	<i>Glycine max</i>	2.00E-39	<a href="#">XM_003535328.1</a>
<i>UCOESTdown421</i>	Alpha-galactosidase 1 (AGAL1)	8.809	0.00299	<i>Arabidopsis thaliana</i>	3.00E-78	<a href="#">NM_120922.4</a>
<i>UCOESTdown422</i>	Sulfate/bicarbonate/oxalate exchanger and transporter sat-1	8.796	0.000369	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002302240.1</a>
<i>UCOESTdown423</i>	Uncharacterized protein	8.790	0.000959	<i>Glycine max</i>	4.00E-52	<a href="#">XM_003522842.1</a>
<i>UCOESTdown424</i>	WRKY transcription factor	8.770	0.000759	<i>Medicago truncatula</i>	2.00E-55	<a href="#">XM_003602147.1</a>
<i>UCOESTdown425</i>	Patellin-4	8.723	0.0013	<i>Glycine max</i>	4.00E-178	<a href="#">NM_001255320.1</a>
<i>UCOESTdown426</i>	Polygalacturonase	8.716	0.0231	<i>Arabidopsis thaliana</i>	4.00E-17	<a href="#">AY113876.1</a>
<i>UCOESTdown427</i>	bHLH transcription factor 9	8.712	0.00263	<i>Malus x domestica</i>	7.00E-91	<a href="#">HM122461.1</a>
<i>UCOESTdown428</i>	Uncharacterized protein	8.704	0.000525	<i>Vitis vinifera</i>	7.00E-127	<a href="#">XM_002284420.1</a>
<i>UCOESTdown429</i>	Cytochrome P450	8.699	0.000674	<i>Vitis vinifera</i>	7.00E-72	<a href="#">XM_003634189.1</a>
<i>UCOESTdown430</i>	RING finger family protein	8.693	0.0146	<i>Medicago truncatula</i>	1.00E-33	<a href="#">XM_003617494.1</a>
<i>UCOESTdown431</i>	Fructose-bisphosphate aldolase	8.693	0.00259	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003607017.1</a>
<i>UCOESTdown432</i>	PHYTOCHROME KINASE SUBSTRATE 4	8.687	0.00962	<i>Vitis vinifera</i>	2.00E-51	<a href="#">XP_002266745.1</a>
<i>UCOESTdown433</i>	Uncharacterized protein	8.629	0.00136	<i>Glycine max</i>	2.00E-64	<a href="#">XM_003526010.1</a>
<i>UCOESTdown434</i>	LRR receptor-like serine/threonine-protein kinase GSO1	8.614	0.000432	<i>Vitis vinifera</i>	4.00E-177	<a href="#">XM_002270006.2</a>

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<i>UCOESTdown435</i>	Peptide transporter PTR3-A	8.613	0.0188	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002271180.2</a>
<i>UCOESTdown436</i>	Uncharacterized protein	8.613	0.00989	<i>Arabidopsis thaliana</i>	1.00E-52	<a href="#">NM_113280.2</a>
<i>UCOESTdown437</i>	2-Aminoethanethiol dioxxygenase	8.608	0.00182	<i>Glycine max</i>	4.00E-98	<a href="#">XM_003553991.1</a>
<i>UCOESTdown438</i>	Uncharacterized protein	8.592	0.000715	<i>Glycine max</i>	8.00E-36	<a href="#">XM_003520637.1</a>
<i>UCOESTdown439</i>	Bidirectional sugar transporter SWEET10	8.585	0.000797	<i>Vitis vinifera</i>	1.00E-97	<a href="#">XM_002284208.1</a>
<i>UCOESTdown440</i>	Triacylglycerol lipase 2 Ribulose-1,5 biphosphate	8.564	0.00963	<i>Vitis vinifera</i>	2.00E-176	<a href="#">XM_002275971.2</a>
<i>UCOESTdown441</i>	carboxylase/oxygenase large subunit N-methyltransferase	8.527	0.000465	<i>Glycine max</i>	1.00E-99	<a href="#">XM_003556720.1</a>
<i>UCOESTdown442</i>	No homology	8.515	0.000355			
<i>UCOESTdown443</i>	Aldehyde dehydrogenase	8.514	0.000441	<i>Glycine max</i>	0.0	<a href="#">XM_003532023.1</a>
<i>UCOESTdown444</i>	Uncharacterized protein	8.513	0.00222	<i>Glycine max</i>	5.00E-90	<a href="#">XM_003535277.1</a>
<i>UCOESTdown445</i>	MTERF protein	8.511	0.000363	<i>Medicago truncatula</i>	1.00E-128	<a href="#">XM_003595545.1</a>
<i>UCOESTdown446</i>	WRKY transcription factor 53	8.494	0.000326	<i>Vitis vinifera</i>	2.00E-62	<a href="#">XM_002267757.2</a>
<i>UCOESTdown447</i>	AP2 domain class transcription factor	8.491	0.00103	<i>Malus x domestica</i>	8.00E-44	<a href="#">GU732455.1</a>
<i>UCOESTdown448</i>	Glycosyltransferase	8.490	0.000573	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002264075.2</a>
<i>UCOESTdown449</i>	No homology	8.489	0.00215			
<i>UCOESTdown450</i>	No homology	8.480	0.0019			
<i>UCOESTdown451</i>	Tyrosine-sulfated glycopeptide receptor 1	8.471	0.00659	<i>Arabidopsis thaliana</i>	7.00E-132	<a href="#">NM_105889.5</a>
<i>UCOESTdown452</i>	No homology	8.445	0.000739			
<i>UCOESTdown453</i>	Omega-3 desaturase	8.442	0.00141	<i>Malus x domestica</i>	0.0	<a href="#">AY551558.1</a>
<i>UCOESTdown454</i>	Pentatricopeptide repeat-containing protein	8.421	0.0231	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002276912.1</a>
<i>UCOESTdown455</i>	No homology	8.389	0.0211			
<i>UCOESTdown456</i>	Polyphenol oxidase	8.387	0.00124	<i>Populus trichocarpa</i>	2.00E-175	<a href="#">JN001936.1</a>
<i>UCOESTdown457</i>	No homology	8.383	0.0146			
<i>UCOESTdown458</i>	MYB transcription factor 18 (MYB18)	8.376	0.00617	<i>Rosa rugosa</i>	7.00E-164	<a href="#">FR828551.1</a>
<i>UCOESTdown459</i>	RuBisCO small subunit	8.371	0.000224	<i>Pyrus pyrifolia</i>	1.00E-96	<a href="#">D00572.1</a>
<i>UCOESTdown460</i>	Uncharacterized protein	8.369	0.000278	<i>Glycine max</i>	1.00E-84	<a href="#">XR_136331.1</a>
<i>UCOESTdown461</i>	Uncharacterized protein	8.369	0.000278	<i>Glycine max</i>	1.00E-84	<a href="#">XR_136331.1</a>
<i>UCOESTdown462</i>	Uncharacterized protein	8.365	0.0478	<i>Glycine max</i>	1.00E-14	<a href="#">XM_003529299.1</a>
<i>UCOESTdown463</i>	Aspartic proteinase nepenthesin-1	8.357	0.000782	<i>Glycine max</i>	6.00E-85	<a href="#">XM_003545898.1</a>
<i>UCOESTdown464</i>	Beta-glucosidase 13	8.340	0.000294	<i>Vitis vinifera</i>	1.00E-90	<a href="#">XM_002276808.2</a>

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<i>UCOESTdown465</i>	Pectate lyase	8.326	0.000523	<i>Arabidopsis thaliana</i>	3.00E-173	<a href="#">AY058064.1</a>
<i>UCOESTdown466</i>	6-Phosphofructo-2-kinase/fructose-2,6-biphosphatase	8.325	0.000348	<i>Medicago truncatula</i>	1.00E-63	<a href="#">XM_003611023.1</a>
<i>UCOESTdown467</i>	TCP domain class transcription factor (TCP5)	8.299	0.00381	<i>Malus x domestica</i>	2.00E-122	<a href="#">HM122697.1</a>
<i>UCOESTdown468</i>	No homology	8.299	0.00314			
<i>UCOESTdown469</i>	No homology	8.294	0.00669			
<i>UCOESTdown470</i>	Kinase family protein	8.291	0.00116	<i>Arabidopsis thaliana</i>	3.00E-29	<a href="#">NM_125238.4</a>
<i>UCOESTdown471</i>	bHLH transcription factor 93	8.286	0.00268	<i>Vitis vinifera</i>	4.00E-93	<a href="#">XM_002264371.1</a>
<i>UCOESTdown472</i>	Protein MOTHER of FT and TF 1 (E12A11)	8.268	0.00793	<i>Arabidopsis thaliana</i>	1.00E-91	<a href="#">NM_101672.3</a>
<i>UCOESTdown473</i>	Protein MOTHER of FT and TF 1	8.268	0.00793	<i>Vitis vinifera</i>	5.00E-102	<a href="#">XM_003634150.1</a>
<i>UCOESTdown474</i>	Uncharacterized protein	8.249	0.00547	<i>Glycine max</i>	2.00E-41	<a href="#">XM_003545603.1</a>
<i>UCOESTdown475</i>	Uncharacterized protein	8.244	0.000457	<i>Vitis vinifera</i>	8.00E-37	<a href="#">XM_002281805.2</a>
<i>UCOESTdown476</i>	No homology	8.157	0.00161			
<i>UCOESTdown477</i>	Fatty acyl-CoA reductase 3	8.150	0.00281	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002263091.1</a>
<i>UCOESTdown478</i>	Cc-nbs-lrr resistance protein	8.129	0.00165	<i>Medicago truncatula</i>	4.00E-25	<a href="#">XM_003590048.1</a>
<i>UCOESTdown479</i>	Uncharacterized protein	8.129	0.000277	<i>Glycine max</i>	6.00E-39	<a href="#">XM_003546360.1</a>
<i>UCOESTdown480</i>	No homology	8.118	0.0184			
<i>UCOESTdown481</i>	Starch-branching enzyme I (SbeI)	8.115	0.000774	<i>Nelumbo nucifera</i>	0.0	<a href="#">FJ592190.1</a>
<i>UCOESTdown482</i>	Cytochrome BC1 synthesis (BCS1)	8.099	0.000353	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_114953.2</a>
<i>UCOESTdown483</i>	No homology	8.096	0.000174			
<i>UCOESTdown484</i>	Uncharacterized protein	8.090	0.000781	<i>Vitis vinifera</i>	7.00E-149	<a href="#">XM_002277155.1</a>
<i>UCOESTdown485</i>	Superman-like protein FRASUP1	8.085	0.0221	<i>Fragaria virginiana</i>	2.00E-125	<a href="#">GU830919.1</a>
<i>UCOESTdown486</i>	HD domain class transcription factor 1	8.076	0.000655	<i>Malus x domestica</i>	7.00E-82	<a href="#">HM122567.1</a>
<i>UCOESTdown487</i>	Uncharacterized protein	8.059	0.0179	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002282134.1</a>
<i>UCOESTdown488</i>	Uncharacterized protein	8.056	0.000915	<i>Medicago truncatula</i>	3.00E-52	<a href="#">XM_003609926.1</a>
<i>UCOESTdown489</i>	No homology	8.051	0.00647			
<i>UCOESTdown490</i>	AP2 domain-containing transcription factor	8.028	0.000168	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002302351.1</a>
<i>UCOESTdown491</i>	No homology	8.015	0.000652			
<i>UCOESTdown492</i>	UDP-Glucose:glucosyltransferase	8.015	0.000652	<i>Lycium barbarum</i>	0.0	<a href="#">AB360632.1</a>
<i>UCOESTdown493</i>	No homology	7.995	0.00176			
<i>UCOESTdown494</i>	Disease resistance protein	7.984	0.00333	<i>Arabidopsis thaliana</i>	2.00E-67	<a href="#">NM_179678.2</a>
<i>UCOESTdown495</i>	Protein CHUP1	7.939	0.000513	<i>Vitis vinifera</i>	7.00E-85	<a href="#">XM_002264356.1</a>

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<i>UCOESTdown496</i>	Senescence-associated protein DIN1	7.914	0.0238	<i>Medicago truncatula</i>	2.00E-62	<a href="#">XM_003612222.1</a>
<i>UCOESTdown497</i>	AP2 domain class transcription factor	7.910	0.00382	<i>Malus x domestica</i>	3.00E-73	<a href="#">GU732437.1</a>
<i>UCOESTdown498</i>	Sugar transport protein 13	7.900	0.000756	<i>Glycine max</i>	0.0	<a href="#">XM_003517533.1</a>
<i>UCOESTdown499</i>	FERONIA receptor kinase	7.862	0.00267	<i>Arabidopsis thaliana</i>	0.0	<a href="#">EF681137.1</a>
<i>UCOESTdown500</i>	(RS)-Norcochlorine 6-O-methyltransferase	7.855	0.00263	<i>Vitis vinifera</i>	6.00E-127	<a href="#">XM_002277440.2</a>
<i>UCOESTdown501</i>	Glucan endo-1,3-beta-glucosidase	7.852	0.000602	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003601566.1</a>
<i>UCOESTdown502</i>	Uncharacterized protein	7.804	0.00199	<i>Vitis vinifera</i>	2.00E-63	<a href="#">XM_002284801.1</a>
<i>UCOESTdown503</i>	Zinc finger family protein	7.796	0.00135	<i>Arabidopsis lyrata</i>	1.00E-45	<a href="#">XM_002888817.1</a>
<i>UCOESTdown504</i>	No homology	7.793	0.00255			
<i>UCOESTdown505</i>	Stearoyl acyl carrier protein desaturase	7.790	0.0276	<i>Lupinus luteus</i>	0.0	<a href="#">AF139377.1</a>
<i>UCOESTdown506</i>	D-Inositol-3-phosphate glycosyltransferase	7.786	0.000283	<i>Glycine max</i>	0.0	<a href="#">XM_003541994.1</a>
<i>UCOESTdown507</i>	Pentatricopeptide repeat protein	7.783	0.00559	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002280883.2</a>
<i>UCOESTdown508</i>	No homology	7.779	0.000286			
<i>UCOESTdown509</i>	Protein FD	7.767	0.00358	<i>Vitis vinifera</i>	3.00E-16	<a href="#">XM_003635211.1</a>
<i>UCOESTdown510</i>	Sodium transporter HKT1	7.741	0.00203	<i>Vitis vinifera</i>	1.00E-129	<a href="#">XM_002270950.2</a>
<i>UCOESTdown511</i>	F-box protein	7.734	0.00707	<i>Populus trichocarpa</i>	6.00E-35	<a href="#">XM_002298382.1</a>
<i>UCOESTdown512</i>	Alpha expansin A3	7.725	0.000208	<i>Rosa hybrid</i>	6.00E-144	<a href="#">AB370118.1</a>
<i>UCOESTdown513</i>	No homology	7.721	0.0453			
<i>UCOESTdown514</i>	Uncharacterized protein	7.716	0.000442	<i>Arabidopsis thaliana</i>	2.00E-73	<a href="#">AF325103.1</a>
<i>UCOESTdown515</i>	Chorismate mutase	7.705	0.00359	<i>Fagus sylvatica</i>	2.00E-100	<a href="#">DQ166527.1</a>
<i>UCOESTdown516</i>	Regulator of ribonuclease protein 3	7.693	0.00246	<i>Vitis vinifera</i>	1.00E-59	<a href="#">XM_002265932.1</a>
<i>UCOESTdown517</i>	No homology	7.686	0.000735			
<i>UCOESTdown518</i>	Nitrite transporter	7.686	0.000522	<i>Glycine max</i>	0.0	<a href="#">XM_003516780.1</a>
<i>UCOESTdown519</i>	No homology	7.664	0.0024			
<i>UCOESTdown520</i>	GDSL esterase/lipase	7.661	0.011	<i>Vitis vinifera</i>	2.00E-61	<a href="#">XM_002278183.2</a>
<i>UCOESTdown521</i>	Uncharacterized protein	7.656	0.00331	<i>Glycine max</i>	0.0	<a href="#">XM_003525523.1</a>
<i>UCOESTdown522</i>	NBS resistance protein	7.653	0.00393	<i>Hordeum vulgare</i>	5.00E-59	<a href="#">AJ507093.1</a>
<i>UCOESTdown523</i>	No homology	7.631	0.00218			
<i>UCOESTdown524</i>	Methyl-CpG-binding domain 7	7.630	0.019	<i>Arabidopsis lyrata</i>	2.00E-14	<a href="#">XM_002866305.1</a>
<i>UCOESTdown525</i>	Chaperone protein ClpB1	7.629	0.0348	<i>Glycine max</i>	0.0	<a href="#">XM_003550595.1</a>
<i>UCOESTdown526</i>	Uncharacterized protein	7.625	0.00264	<i>Vitis vinifera</i>	2.00E-15	<a href="#">XM_002272616.1</a>
<i>UCOESTdown527</i>	NAC transcription factor	7.622	0.00173	<i>Populus trichocarpa</i>	4.00E-37	<a href="#">XM_002327730.1</a>
<i>UCOESTdown528</i>	Subtilisin protease SDD1	7.592	0.0153	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002267185.2</a>

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<i>UCOESTdown529</i>	Uncharacterized protein	7.583	0.00404	<i>Glycine max</i>	8.00E-87	<a href="#">XM_003534897.1</a>
<i>UCOESTdown530</i>	Polyphenol oxidase	7.578	0.0123	<i>Prunus salicina</i>	0.0	<a href="#">JF681036.1</a>
<i>UCOESTdown531</i>	Ornithine decarboxylase	7.562	0.0103	<i>Theobroma cacao</i>	1.00E-136	<a href="#">EF122792.1</a>
<i>UCOESTdown532</i>	bHLH transcription factor 135	7.530	0.0164	<i>Vitis vinifera</i>	7.00E-14	<a href="#">XM_002268255.1</a>
<i>UCOESTdown533</i>	Pathogenesis-related thaumatin	7.528	0.0268	<i>Arabidopsis thaliana</i>		<a href="#">NM_001036732.1</a>
<i>UCOESTdown534</i>	No homology	7.523	0.0188			
<i>UCOESTdown535</i>	WRKY transcription factor 58	7.520	0.000692	<i>Glycine max</i>	4.00E-36	<a href="#">NM_001250709.1</a>
<i>UCOESTdown536</i>	Disease resistance protein	7.506	0.000436	<i>Vitis vinifera</i>	2.00E-12	<a href="#">XM_002265413.2</a>
<i>UCOESTdown537</i>	Heme-binding protein 2	7.491	0.00171	<i>Vitis vinifera</i>	3.00E-101	<a href="#">XM_002266483.2</a>
<i>UCOESTdown538</i>	Heat stress transcription factor A-3	7.484	0.00182	<i>Vitis vinifera</i>	1.00E-145	<a href="#">XM_002277302.2</a>
<i>UCOESTdown539</i>	Cytochrome P450	7.475	0.00024	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002264012.2</a>
<i>UCOESTdown540</i>	Ribulose-1,5 biphosphate carboxylase/oxygenase large subunit N-methyltransferase	7.462	0.00223	<i>Nicotiana tabacum</i>	7.00E-102	<a href="#">U35620.1</a>
<i>UCOESTdown541</i>	Retinol dehydrogenase 14	7.457	0.000655	<i>Glycine max</i>	3.00E-120	<a href="#">XM_003523046.1</a>
<i>UCOESTdown542</i>	Neutral amino acid transport protein	7.446	0.00301	<i>Medicago truncatula</i>	2.00E-146	<a href="#">XM_003629658.1</a>
<i>UCOESTdown543</i>	Invertase inhibitor	7.446	0.0023	<i>Vitis vinifera</i>	8.00E-18	<a href="#">XM_002282275.2</a>
<i>UCOESTdown544</i>	Laccase-9	7.444	0.0477	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002270856.2</a>
<i>UCOESTdown545</i>	Uncharacterized protein	7.433	0.00343	<i>Vitis vinifera</i>	1.00E-176	<a href="#">XM_002273117.1</a>
<i>UCOESTdown546</i>	C2H2-type zinc finger protein	7.431	0.00155	<i>Arabidopsis thaliana</i>	4.00E-95	<a href="#">BT001215.1</a>
<i>UCOESTdown547</i>	Receptor-like protein kinase	7.415	0.0106	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003592876.1</a>
<i>UCOESTdown548</i>	1,4-Alpha-glucan-branching enzyme	7.414	0.00671	<i>Glycine max</i>	0.0	<a href="#">XM_003523032.1</a>
<i>UCOESTdown549</i>	Serine/threonine-protein kinase PBS1	7.407	0.00385	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002266186.1</a>
<i>UCOESTdown550</i>	Filament- plant protein	7.405	0.00552	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003634358.1</a>
<i>UCOESTdown551</i>	Uncharacterized protein	7.403	0.000574	<i>Arabidopsis thaliana</i>	7.00E-31	<a href="#">NM_103885.3</a>
<i>UCOESTdown552</i>	Blue copper protein	7.385	0.00405	<i>Vitis vinifera</i>	1.00E-50	<a href="#">XM_002281250.1</a>
<i>UCOESTdown553</i>	Uncharacterized protein	7.385	0.0367	<i>Vitis vinifera</i>	4.00E-162	<a href="#">XM_003632112.1</a>
<i>UCOESTdown554</i>	No homology	7.335	0.00359			
<i>UCOESTdown555</i>	Protease Do-like 14	7.334	0.00447	<i>Vitis vinifera</i>	2.00E-152	<a href="#">XM_002279642.2</a>
<i>UCOESTdown556</i>	Uncharacterized protein	7.312	0.0127	<i>Glycine max</i>	0.0	<a href="#">XM_003532710.1</a>
<i>UCOESTdown557</i>	Violaxanthin de-epoxidase	7.301	0.00207	<i>Citrus sinensis</i>	0.0	<a href="#">HM036682.1</a>
<i>UCOESTdown558</i>	Uncharacterized protein	7.300	0.00239	<i>Vitis vinifera</i>	2.00E-117	<a href="#">XM_002282894.1</a>
<i>UCOESTdown559</i>	Chaperone protein dnaJ 11	7.295	0.000409	<i>Vitis vinifera</i>	2.00E-37	<a href="#">XM_002277554.2</a>
<i>UCOESTdown560</i>	MYB transcription factor 4 (MYB4)	7.291	0.00276	<i>Glycine max</i>	4.00E-54	<a href="#">NM_001254089.1</a>
<i>UCOESTdown561</i>	Uncharacterized protein	7.289	0.011	<i>Vitis vinifera</i>	2.00E-169	<a href="#">XM_002282694.2</a>

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<i>UCOESTdown562</i>	Agmatine coumaroyltransferase	7.286	0.022	<i>Glycine max</i>	4.00E-105	<a href="#">XM_003554846.1</a>
<i>UCOESTdown563</i>	NHL repeat-containing protein 2	7.278	0.000599	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002277528.1</a>
<i>UCOESTdown564</i>	Galacturonosyltransferase 2	7.271	0.0011	<i>Vitis vinifera</i>	2.00E-159	<a href="#">XM_002269146.1</a>
<i>UCOESTdown565</i>	Uncharacterized protein	7.269	0.00791	<i>Vitis vinifera</i>	4.00E-92	<a href="#">XM_002285077.1</a>
<i>UCOESTdown566</i>	AP2/ERF domain-containing transcription factor	7.268	0.00265	<i>Populus trichocarpa</i>	3.00E-44	<a href="#">XM_002326970.1</a>
<i>UCOESTdown567</i>	No homology	7.256	0.00037			
<i>UCOESTdown568</i>	No homology	7.256	0.00307			
<i>UCOESTdown569</i>	Type I inositol-1,4,5-trisphosphate 5-phosphatase	7.235	0.00923	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003630016.1</a>
<i>UCOESTdown570</i>	UDP-Glucuronosyl/UDP-glucosyl transferase	7.235	0.00251	<i>Arabidopsis lyrata</i>	3.00E-139	<a href="#">XM_002884096.1</a>
<i>UCOESTdown571</i>	Uncharacterized protein	7.231	0.000517	<i>Glycine max</i>	5.00E-128	<a href="#">NM_001254552.1</a>
<i>UCOESTdown572</i>	Defensin-like protein	7.210	0.00783	<i>Pyrus pyrifolia</i>	8.00E-05	<a href="#">AB052687.1</a>
<i>UCOESTdown573</i>	Leucoanthocyanidin dioxygenase	7.186	0.00285	<i>Medicago truncatula</i>	8.00E-178	<a href="#">XM_003604626.1</a>
<i>UCOESTdown574</i>	Leucine-rich repeat receptor-kinase	7.176	0.00021	<i>Arabidopsis thaliana</i>	0.0	<a href="#">FJ708809.1</a>
<i>UCOESTdown575</i>	No homology	7.145	0.00105			
<i>UCOESTdown576</i>	Ankyrin repeat-containing protein	7.144	0.000296	<i>Vitis vinifera</i>	4.00E-78	<a href="#">XM_002263717.2</a>
<i>UCOESTdown577</i>	Lipid-transfer protein DIR1	7.133	0.00169	<i>Vitis vinifera</i>	1.00E-34	<a href="#">XM_002268706.2</a>
<i>UCOESTdown578</i>	LRR receptor-like serine/threonine-protein kinase	7.113	0.000437	<i>Vitis vinifera</i>	2.00E-135	<a href="#">XM_002274372.1</a>
<i>UCOESTdown579</i>	No homology	7.106	0.00131			
<i>UCOESTdown580</i>	Anthranilate N-benzoyltransferase protein	7.102	0.0333	<i>Medicago truncatula</i>	3.00E-179	<a href="#">XM_003617318.1</a>
<i>UCOESTdown581</i>	D6-type cyclin	7.089	0.00442	<i>Populus trichocarpa</i>	6.00E-108	<a href="#">AM746128.1</a>
<i>UCOESTdown582</i>	No homology	7.072	0.0044			
<i>UCOESTdown583</i>	GATA domain class transcription factor (GATA1)	7.067	0.00345	<i>Malus x domestica</i>	2.00E-112	<a href="#">HM122551.1</a>
<i>UCOESTdown584</i>	(+)-Neomenthol dehydrogenase	7.063	0.00294	<i>Vitis vinifera</i>	9.00E-136	<a href="#">XM_002274934.2</a>
<i>UCOESTdown585</i>	L-Ascorbate oxidase	7.040	0.000291	<i>Glycine max</i>	0.0	<a href="#">XM_003523159.1</a>
<i>UCOESTdown586</i>	Uncharacterized protein	7.035	0.00072	<i>Glycine max</i>	8.00E-75	<a href="#">XM_003553120.1</a>
<i>UCOESTdown587</i>	E3 ubiquitin-protein ligase PUB23	7.029	0.00209	<i>Vitis vinifera</i>	1.00E-171	<a href="#">XM_002267402.2</a>
<i>UCOESTdown588</i>	No homology	7.029	0.00227			
<i>UCOESTdown589</i>	Xyloglucan endotransglucosylase/hydrolase	7.025	0.00283	<i>Rosa hybrid</i>	2.00E-161	<a href="#">AB428381.1</a>

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<i>UCOESTdown590</i>	No homology	7.020	0.00046			
<i>UCOESTdown591</i>	No homology	7.019	0.00791			
<i>UCOESTdown592</i>	SPL transcription factor 1	7.010	0.000781	<i>Malus x domestica</i>	2.00E-145	<a href="#">HM122684.1</a>
<i>UCOESTdown593</i>	No homology	7.001	0.006			
<i>UCOESTdown594</i>	WRKY transcription factor 12	6.980	0.000206	<i>Malus x domestica</i>	3.00E-87	<a href="#">HM122715.1</a>
<i>UCOESTdown595</i>	High mobility group family (HMGB913)	6.971	0.00256	<i>Populus trichocarpa</i>	4.00E-135	<a href="#">XM_002303600.1</a>
<i>UCOESTdown596</i>	Glutaredoxin family protein	6.962	0.000789	<i>Arabidopsis lyrata</i>	1.00E-53	<a href="#">XM_002887835.1</a>
<i>UCOESTdown597</i>	Transcription activator GLK1	6.951	0.000408	<i>Vitis vinifera</i>	3.00E-92	<a href="#">XM_002275194.2</a>
<i>UCOESTdown598</i>	Serine carboxypeptidase	6.951	0.00166	<i>Medicago truncatula</i>	2.00E-102	<a href="#">XM_003604883.1</a>
<i>UCOESTdown599</i>	Uncharacterized protein	6.939	0.00538	<i>Vitis vinifera</i>	1.00E-30	<a href="#">XM_002270265.1</a>
<i>UCOESTdown600</i>	Tir-nbs-lrr resistance protein	6.937	0.00674	<i>Populus trichocarpa</i>	8.00E-27	<a href="#">XM_002325465.1</a>
<i>UCOESTdown601</i>	Aluminum-activated malate transporter 2	6.921	0.000572	<i>Vitis vinifera</i>	3.00E-125	<a href="#">XM_002279286.1</a>
<i>UCOESTdown602</i>	F-box protein	6.919	0.00588	<i>Vitis vinifera</i>	2.00E-59	<a href="#">XM_002282116.2</a>
<i>UCOESTdown603</i>	Tubby-like F-box protein 5	6.919	0.00588	<i>Vitis vinifera</i>	2.00E-59	<a href="#">XM_002282116.2</a>
<i>UCOESTdown604</i>	No homology	6.917	0.0136			
<i>UCOESTdown605</i>	Beta- glucosidase	6.895	0.00247	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002278327.1</a>
<i>UCOESTdown606</i>	Uncharacterized protein	6.882	0.000918	<i>Vitis vinifera</i>	3.00E-27	<a href="#">XM_003632582.1</a>
<i>UCOESTdown607</i>	No homology	6.867	0.00338			
<i>UCOESTdown608</i>	No homology	6.867	0.00111			
<i>UCOESTdown609</i>	Cyclin-U1-1	6.854	0.0306	<i>Medicago truncatula</i>	3.00E-87	<a href="#">XM_003596982.1</a>
<i>UCOESTdown610</i>	Ferric reduction oxidase 7	6.825	0.00457	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002266687.2</a>
<i>UCOESTdown611</i>	Protein WAX2	6.820	0.0108	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002263751.2</a>
<i>UCOESTdown612</i>	Aspartic proteinase nepenthesin-1	6.806	0.00161	<i>Glycine max</i>	3.00E-103	<a href="#">XM_003532851.1</a>
<i>UCOESTdown613</i>	Ras-related protein RABC2a	6.795	0.0111	<i>Vitis vinifera</i>	3.00E-94	<a href="#">XM_002265726.2</a>
<i>UCOESTdown614</i>	Beta-glucosidase D7	6.787	0.00313	<i>Medicago truncatula</i>	3.00E-80	<a href="#">XM_003615676.1</a>
<i>UCOESTdown615</i>	Leucine-rich repeat receptor-like protein kinase	6.783	0.000655	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_112345.6</a>
<i>UCOESTdown616</i>	Wall-associated receptor kinase 1	6.772	0.0292	<i>Vitis vinifera</i>	2.00E-23	<a href="#">XM_002266749.2</a>
<i>UCOESTdown617</i>	Cyclic nucleotide-gated ion channel 1	6.749	0.00365	<i>Glycine max</i>	4.00E-39	<a href="#">XM_003526651.1</a>
<i>UCOESTdown618</i>	No homology	6.734	0.000821			
<i>UCOESTdown619</i>	No homology	6.733	0.000178			
<i>UCOESTdown620</i>	Uncharacterized protein	6.717	0.00118	<i>Vitis vinifera</i>	1.00E-95	<a href="#">XM_003631274.1</a>
<i>UCOESTdown621</i>	No homology	6.709	0.00731			

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<i>UCOESTdown622</i>	NAC domain-containing protein 100	6.695	0.00196	<i>Vitis vinifera</i>	2.00E-123	<a href="#">XM_002280776.1</a>
<i>UCOESTdown623</i>	125 kDa kinesin-related protein	6.685	0.0188	<i>Glycine max</i>	0.0	<a href="#">XM_003541346.1</a>
<i>UCOESTdown624</i>	Ascorbate peroxidase	6.685	0.00179	<i>Jatropha curcas</i>	2.00E-131	<a href="#">GQ337076.1</a>
<i>UCOESTdown625</i>	Phosphatase 2C 38	6.678	0.00128	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002276595.2</a>
<i>UCOESTdown626</i>	GDSL esterase/lipase	6.671	0.0108	<i>Vitis vinifera</i>	1.00E-145	<a href="#">XM_002271815.1</a>
<i>UCOESTdown627</i>	No homology	6.661	0.000348			
<i>UCOESTdown628</i>	Leucine-rich repeat receptor-like protein kinase	6.649	0.00849	<i>Arabidopsis thaliana</i>	0.0	<a href="#">FJ708680.1</a>
<i>UCOESTdown629</i>	GDSL esterase/lipase	6.634	0.0021	<i>Arabidopsis lyrata</i>	7.00E-69	<a href="#">XM_002871001.1</a>
<i>UCOESTdown630</i>	Uncharacterized protein	6.632	0.000241	<i>Arabidopsis thaliana</i>	2.00E-40	<a href="#">NM_202842.2</a>
<i>UCOESTdown631</i>	Myb transcription factor	6.619	0.0046	<i>Rubus idaeus</i>	2.00E-124	<a href="#">FJ527833.1</a>
<i>UCOESTdown632</i>	Uncharacterized protein	6.608	0.0154	<i>Vitis vinifera</i>	2.00E-47	<a href="#">XM_002283303.2</a>
<i>UCOESTdown633</i>	Uncharacterized protein	6.604	0.000574	<i>Glycine max</i>	2.00E-92	<a href="#">XM_003556067.1</a>
<i>UCOESTdown634</i>	Cc-nbs-1rr resistance protein	6.593	0.004	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002332516.1</a>
<i>UCOESTdown635</i>	Sulfite oxidase	6.59	0.00781	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_111057.3</a>
<i>UCOESTdown636</i>	Squamosa promoter binding like-protein	6.578	0.000366	<i>Vitis vinifera</i>	8.00E-36	<a href="#">XM_002274466.2</a>
<i>UCOESTdown637</i>	Kinesin heavy chain DNA binding protein	6.575	0.00664	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003629305.1</a>
<i>UCOESTdown638</i>	No homology	6.572	0.0104			
<i>UCOESTdown639</i>	Carotenoid 9,10(9',10')-cleavage dioxygenase 1	6.571	0.0152	<i>Vitis vinifera</i>	8.00E-131	<a href="#">XM_002281274.2</a>
<i>UCOESTdown640</i>	Pentatricopeptide repeat-containing protein	6.563	0.0128	<i>Vitis vinifera</i>	6.00E-98	<a href="#">XM_003633049.1</a>
<i>UCOESTdown641</i>	Ferredoxin I (fdn-1)	6.558	0.0136	<i>Nicotiana tabacum</i>	5.00E-44	<a href="#">AY864890.1</a>
<i>UCOESTdown642</i>	Fatty acyl-CoA reductase	6.555	0.00321	<i>Vitis vinifera</i>	2.00E-144	<a href="#">XM_002263148.1</a>
<i>UCOESTdown643</i>	Transmembrane protein	6.543	0.00355	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003616949.1</a>
<i>UCOESTdown644</i>	Calcium-binding protein PBP1	6.543	0.00031	<i>Vitis vinifera</i>	2.00E-53	<a href="#">XM_002281842.2</a>
<i>UCOESTdown645</i>	No homology	6.539	0.000232			
<i>UCOESTdown646</i>	DNA-damage-repair/toleration protein DRT100	6.527	0.00413	<i>Medicago truncatula</i>	2.00E-163	<a href="#">XM_003599058.1</a>
<i>UCOESTdown647</i>	Gibberellin 3-oxidase (GA3ox)	6.519	0.000409	<i>Fragaria x ananassa</i>	0.0	<a href="#">DQ195505.1</a>
<i>UCOESTdown648</i>	Cytochrome P450	6.507	0.000906	<i>Camellia japonica</i>	2.00E-138	<a href="#">DQ086118.1</a>
<i>UCOESTdown649</i>	Uncharacterized protein	6.504	0.00844	<i>Glycine max</i>	1.00E-105	<a href="#">XM_003552776.1</a>
<i>UCOESTdown650</i>	ocs element-binding factor 1	6.488	0.0237	<i>Vitis vinifera</i>	2.00E-52	<a href="#">XM_002278702.1</a>

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<i>UCOESTdown651</i>	No homology	6.488	0.0107			
<i>UCOESTdown652</i>	Cytochrome P450	6.473	0.0306	<i>Glycine max</i>	0.0	<a href="#">XM_003532120.1</a>
<i>UCOESTdown653</i>	Serine threonine kinase-containing protein	6.467	0.0011	<i>Arabidopsis thaliana</i>	7.00E-48	<a href="#">NM_124148.3</a>
<i>UCOESTdown654</i>	Uncharacterized protein	6.445	0.000567	<i>Arabidopsis thaliana</i>	1.00E-93	<a href="#">NM_001202614.1</a>
<i>UCOESTdown655</i>	LRR receptor-like serine/threonine-protein kinase	6.437	0.00731	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002283560.2</a>
<i>UCOESTdown656</i>	Uncharacterized protein	6.432	0.000324	<i>Glycine max</i>	7.00E-144	<a href="#">XM_003546956.1</a>
<i>UCOESTdown657</i>	Flavone synthase II	6.431	0.0035	<i>Camellia sinensis</i>	2.00E-150	<a href="#">FJ169499.1</a>
<i>UCOESTdown658</i>	Protein TRANSPARENT TESTA 12	6.416	0.0379	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002273991.2</a>
<i>UCOESTdown659</i>	K+ channel protein (KPe1)	6.403	0.000214	<i>Populus euphratica</i>	0.0	<a href="#">EU382998.1</a>
<i>UCOESTdown660</i>	1-Deoxy-D-xylulose 5-phosphate synthase	6.386	0.00183	<i>Populus trichocarpa</i>	0.0	<a href="#">EU693019.1</a>
<i>UCOESTdown661</i>	Uncharacterized protein	6.386	0.0191	<i>Vitis vinifera</i>	1.00E-95	<a href="#">XM_002263155.1</a>
<i>UCOESTdown662</i>	Protease inhibitor/seed storage/lipid transfer protein family protein	6.383	0.00575	<i>Arabidopsis lyrata</i>	6.00E-35	<a href="#">XM_002879666.1</a>
<i>UCOESTdown663</i>	Malate dehydrogenase	6.381	0.00134	<i>Solanum lycopersicum</i>	1.00E-169	<a href="#">NM_001247223.1</a>
<i>UCOESTdown664</i>	No homology	6.380	0.000403			
<i>UCOESTdown665</i>	Rho GTPase activating protein with PAK-box/P21-Rho-binding domain	6.375	0.00643	<i>Arabidopsis thaliana</i>	2.00E-134	<a href="#">NM_116544.3</a>
<i>UCOESTdown666</i>	Uncharacterized protein	6.375	0.00412	<i>Glycine max</i>	0.0	<a href="#">XM_003532859.1</a>
<i>UCOESTdown667</i>	No homology	6.371	0.00488			
<i>UCOESTdown668</i>	Beta-galactosidase	6.356	0.000437	<i>Prunus persica</i>	0.0	<a href="#">AY874412.1</a>
<i>UCOESTdown669</i>	Peroxisomal small heat shock protein	6.356	0.00102	<i>Glycine max</i>	8.00E-55	<a href="#">NM_001251515.1</a>
<i>UCOESTdown670</i>	No homology	6.351	0.00337			
<i>UCOESTdown671</i>	Uncharacterized protein	6.338	0.0111	<i>Glycine max</i>	6.00E-149	<a href="#">XM_003550375.1</a>
<i>UCOESTdown672</i>	Cell division cycle-associated 7	6.322	0.0082	<i>Medicago truncatula</i>	1.00E-72	<a href="#">XM_003619812.1</a>
<i>UCOESTdown673</i>	No homology	6.315	0.00208			
<i>UCOESTdown674</i>	Endochitinase and N-acetylglucosamine-binding hemagglutinin	6.312	0.000297	<i>Parkia platycephala</i>	4.00E-130	<a href="#">AM749839.1</a>
<i>UCOESTdown675</i>	G2/mitotic-specific cyclin-1	6.300	0.000209	<i>Vitis vinifera</i>	1.00E-144	<a href="#">XM_002278103.1</a>
<i>UCOESTdown676</i>	Homeobox-leucine zipper protein ATHB-40	6.297	0.036	<i>Arabidopsis lyrata</i>	2.00E-56	<a href="#">XM_002866948.1</a>

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<i>UCOESTdown677</i>	S-locus-like receptor protein kinase	6.297	0.00446	<i>Prunus persica</i>	0.0	<a href="#">AY645718.1</a>
<i>UCOESTdown678</i>	Uncharacterized protein	6.287	0.00864	<i>Vitis vinifera</i>	5.00E-180	<a href="#">XM_002264687.2</a>
<i>UCOESTdown679</i>	MYB transcription factor LBM3	6.285	0.000213	<i>Nicotiana tabacum</i>	1.00E-75	<a href="#">U72762.1</a>
<i>UCOESTdown680</i>	Galactinol synthase (GolS1)	6.284	0.00736	<i>Coffea arabica</i>	0.0	<a href="#">GQ497218.1</a>
<i>UCOESTdown681</i>	Proton-dependent oligopeptide transport family protein	6.264	0.00115	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002875692.1</a>
<i>UCOESTdown682</i>	Disease resistance protein	6.253	0.0192	<i>Vitis vinifera</i>	4.00E-176	<a href="#">XM_003634234.1</a>
<i>UCOESTdown683</i>	Uncharacterized protein	6.237	0.000393	<i>Vitis vinifera</i>	6.00E-74	<a href="#">XM_002264822.1</a>
<i>UCOESTdown684</i>	No homology	6.231	0.00539			
<i>UCOESTdown685</i>	MYB transcription factor 167 (MYB167)	6.226	0.00339	<i>Populus trichocarpa</i>	1.00E-81	<a href="#">FJ807472.1</a>
<i>UCOESTdown686</i>	Nudix hydrolase 12	6.215	0.00662	<i>Vitis vinifera</i>	8.00E-67	<a href="#">XM_002277331.2</a>
<i>UCOESTdown687</i>	BZIP domain class transcription factor (BZIP8)	6.208	0.00026	<i>Malus x domestica</i>	5.00E-50	<a href="#">HM122481.1</a>
<i>UCOESTdown688</i>	Laccase-9	6.206	0.000131	<i>Vitis vinifera</i>	6.00E-142	<a href="#">XM_002263910.2</a>
<i>UCOESTdown689</i>	Leucine-rich repeat receptor-like protein kinase	6.179	0.0027	<i>Arabidopsis thaliana</i>	2.00E-38	<a href="#">FJ708657.1</a>
<i>UCOESTdown690</i>	Rhomboid family protein	6.161	0.00138	<i>Arabidopsis thaliana</i>	1.00E-90	<a href="#">AB195671.1</a>
<i>UCOESTdown691</i>	G-type lectin S-receptor serine/threonine-protein kinase RKS1	6.159	0.0154	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002270658.2</a>
<i>UCOESTdown692</i>	Uncharacterized protein	6.157	0.0138	<i>Vitis vinifera</i>	1.00E-42	<a href="#">XM_002283303.2</a>
<i>UCOESTdown693</i>	No homology	6.156	0.0169			
<i>UCOESTdown694</i>	ABC transporter family	6.156	0.015	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002322728.1</a>
<i>UCOESTdown695</i>	E3 ubiquitin-protein ligase SINAT3	6.154	0.0179	<i>Vitis vinifera</i>	2.00E-80	<a href="#">XM_002277676.2</a>
<i>UCOESTdown696</i>	E3 ubiquitin-protein ligase COP1	6.151	0.000372	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002270294.2</a>
<i>UCOESTdown697</i>	Protein NDR1	6.141	0.000797	<i>Arabidopsis thaliana</i>	8.00E-46	<a href="#">AF021346.1</a>
<i>UCOESTdown698</i>	No homology	6.136	0.00044			
<i>UCOESTdown699</i>	L-type lectin-domain containing receptor kinase S.4	6.121	0.00045	<i>Glycine max</i>	0.0	<a href="#">XM_003552142.1</a>
<i>UCOESTdown700</i>	No homology	6.120	0.0134			
<i>UCOESTdown701</i>	Uncharacterized protein	6.110	0.002	<i>Glycine max</i>	4.00E-143	<a href="#">XM_003523414.1</a>
<i>UCOESTdown702</i>	Extracellular calcium sensing receptor (CAS)	6.103	0.00315	<i>Castanopsis chinensis</i>	4.00E-175	<a href="#">JN630474.1</a>
<i>UCOESTdown703</i>	Serine carboxypeptidase 18	6.096	0.00857	<i>Vitis vinifera</i>	2.00E-151	<a href="#">XM_003631658.1</a>
<i>UCOESTdown704</i>	Non-specific lipid-transfer protein	6.069	0.000711	<i>Vitis vinifera</i>	1.00E-39	<a href="#">XM_003632265.1</a>

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<i>UCOESTdown705</i>	No homology	6.067	0.00167			
<i>UCOESTdown706</i>	No homology	6.065	0.0442			
<i>UCOESTdown707</i>	ABC transporter B family member 26	6.064	0.011	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002272819.1</a>
<i>UCOESTdown708</i>	Rop guanine nucleotide exchange factor 1	6.053	0.000783	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002282276.1</a>
<i>UCOESTdown709</i>	No homology	6.050	0.000533			
<i>UCOESTdown710</i>	Sodium/hydrogen exchanger 4	6.043	0.00297	<i>Vitis vinifera</i>		<a href="#">XM_002276777.1</a>
<i>UCOESTdown711</i>	Uncharacterized protein	6.042	0.00111	<i>Glycine max</i>	3.00E-51	<a href="#">NM_001251725.1</a>
<i>UCOESTdown712</i>	Cyclin-SDS (SDS)	6.034	0.0173	<i>Arabidopsis thaliana</i>	7.00E-91	<a href="#">NM_101344.2</a>
<i>UCOESTdown713</i>	LEAFY protein	6.029	0.0231	<i>Chaenomeles sinensis</i>	1.00E-132	<a href="#">AB162038.1</a>
<i>UCOESTdown714</i>	No homology	6.027	0.0436			
<i>UCOESTdown715</i>	Serine hydroxymethyltransferase 2	6.023	0.00154	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002310880.1</a>
<i>UCOESTdown716</i>	Uncharacterized protein	6.008	0.000903	<i>Glycine max</i>	2.00E-50	<a href="#">XM_003554818.1</a>
<i>UCOESTdown717</i>	Uncharacterized protein	5.994	0.0163	<i>Vitis vinifera</i>	3.00E-125	<a href="#">XM_002284094.2</a>
<i>UCOESTdown718</i>	Ankyrin repeat-containing protein	5.992	0.035	<i>Vitis vinifera</i>	1.00E-99	<a href="#">XM_002263717.2</a>
<i>UCOESTdown719</i>	Uncharacterized protein	5.992	0.0018	<i>Vitis vinifera</i>	7.00E-75	<a href="#">XM_002283742.2</a>
<i>UCOESTdown720</i>	Phosphoesterase	5.988	0.000554	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002880796.1</a>
<i>UCOESTdown721</i>	Uncharacterized protein	5.983	0.000781	<i>Vitis vinifera</i>	2.00E-45	<a href="#">XM_002284772.1</a>
<i>UCOESTdown722</i>	MYB transcription factor 32 (MYB32)	5.979	0.00921	<i>Malus x domestica</i>	2.00E-83	<a href="#">HM122624.1</a>
<i>UCOESTdown723</i>	F-box protein	5.969	0.000368	<i>Glycine max</i>	7.00E-126	<a href="#">XM_003528836.1</a>
<i>UCOESTdown724</i>	No homology	5.964	0.0127			
<i>UCOESTdown725</i>	Uncharacterized protein	5.962	0.00128	<i>Vitis vinifera</i>	5.00E-145	<a href="#">XM_002282136.2</a>
<i>UCOESTdown726</i>	4-Coumarate-CoA ligase	5.961	0.0173	<i>Arabidopsis thaliana</i>	0.0	<a href="#">AY250838.1</a>
<i>UCOESTdown727</i>	F-box protein	5.961	0.00192	<i>Vitis vinifera</i>	2.00E-113	<a href="#">XM_002277759.1</a>
<i>UCOESTdown728</i>	Benzoyl coenzyme A: benzyl alcohol benzoyl transferase	5.958	0.00815	<i>Petunia x hybrida</i>	0.0	<a href="#">AY563157.1</a>
<i>UCOESTdown729</i>	Zinc finger family protein	5.947	0.00026	<i>Malus x domestica</i>	1.00E-124	<a href="#">AB116545.1</a>
<i>UCOESTdown730</i>	Thaumatococcus-like protein	5.943	0.00954	<i>Glycine max</i>	4.00E-141	<a href="#">NM_001253327.1</a>
<i>UCOESTdown731</i>	HLIP/One helix protein (Lil2)	5.942	0.00636	<i>Populus trichocarpa</i>	3.00E-38	<a href="#">XM_002309038.1</a>
<i>UCOESTdown732</i>	Sodium symporter family protein	5.936	0.000601	<i>Arabidopsis lyrata</i>	1.00E-161	<a href="#">XM_002889153.1</a>
<i>UCOESTdown733</i>	Peroxidase (PO3)	5.935	0.00356	<i>Populus trichocarpa</i>	1.00E-162	<a href="#">FJ807475.1</a>
<i>UCOESTdown734</i>	Uncharacterized protein	5.934	0.015	<i>Vitis vinifera</i>	2.00E-150	<a href="#">XM_002277853.1</a>
<i>UCOESTdown735</i>	RING finger and CHY zinc finger domain-containing protein 1	5.929	0.00329	<i>Vitis vinifera</i>	1.00E-170	<a href="#">XM_002268157.2</a>

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<i>UCOESTdown736</i>	UDP-Glucose: glucosyltransferase	5.924	0.0256	<i>Rosa hybrid</i>	0.0	<a href="#">AB292797.1</a>
<i>UCOESTdown737</i>	Uncharacterized protein	5.923	0.00167	<i>Glycine max</i>	6.00E-105	<a href="#">XM_003540807.1</a>
<i>UCOESTdown738</i>	Actin-related protein 2	5.920	0.000402	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002272449.2</a>
<i>UCOESTdown739</i>	WRKY transcription factor	5.915	0.00987	<i>Medicago truncatula</i>	4.00E-37	<a href="#">XM_003630070.1</a>
<i>UCOESTdown740</i>	No homology	5.911	0.014			
<i>UCOESTdown741</i>	Beta-glucosidase 13	5.902	0.000431	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002270386.2</a>
<i>UCOESTdown742</i>	Protein IQ-DOMAIN 31	5.891	0.000213	<i>Glycine max</i>	2.00E-163	<a href="#">XM_003524839.1</a>
<i>UCOESTdown743</i>	Kinesin protein KIF3A	5.886	0.0017	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003620357.1</a>
<i>UCOESTdown744</i>	No homology	5.886	0.013			
<i>UCOESTdown745</i>	Ankyrin repeat-containing protein	5.885	0.000273	<i>Vitis vinifera</i>	4.00E-80	<a href="#">XM_002263717.2</a>
<i>UCOESTdown746</i>	No homology	5.884	0.002			
<i>UCOESTdown747</i>	Beta-1,4-xylosyltransferase IRX9H	5.876	0.000494	<i>Glycine max</i>	9.00E-160	<a href="#">NM_001255189.1</a>
<i>UCOESTdown748</i>	Peptide/nitrate transporter	5.873	0.000226	<i>Glycine max</i>	0.0	<a href="#">XM_003552094.1</a>
<i>UCOESTdown749</i>	ZF-HD homeobox protein	5.871	0.00132	<i>Vitis vinifera</i>	5.00E-65	<a href="#">XM_002281335.2</a>
<i>UCOESTdown750</i>	Uncharacterized protein	5.865	0.000285	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002273957.2</a>
<i>UCOESTdown751</i>	Wall-associated receptor kinase	5.863	0.00247	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003607133.1</a>
<i>UCOESTdown752</i>	Uncharacterized protein	5.857	0.00155	<i>Glycine max</i>	2.00E-38	<a href="#">NM_001251347.1</a>
<i>UCOESTdown753</i>	Phosphoribulokinase	5.849	0.00375	<i>Glycine max</i>	0.0	<a href="#">XM_003534257.1</a>
<i>UCOESTdown754</i>	Myosin family protein with Dil domain	5.846	0.0239	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_104334.1</a>
<i>UCOESTdown755</i>	Glutamate receptor 2.8	5.832	0.000569	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003631793.1</a>
<i>UCOESTdown756</i>	No homology	5.823	0.00489			
<i>UCOESTdown757</i>	Triose phosphate/phosphate translocator	5.818	0.00101	<i>Vitis vinifera</i>	1.00E-174	<a href="#">XM_002267904.2</a>
<i>UCOESTdown758</i>	NAC transcription factor 2	5.817	0.00289	<i>Arabidopsis thaliana</i>	5.00E-16	<a href="#">NM_112419.3</a>
<i>UCOESTdown759</i>	Chromatin remodeling complex subunit (CHR905)	5.811	0.0151	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002325607.1</a>
<i>UCOESTdown760</i>	Aspartic proteinase nepenthesin-1	5.811	0.0229	<i>Glycine max</i>	0.0	<a href="#">XM_003519987.1</a>
<i>UCOESTdown761</i>	Uncharacterized protein	5.807	0.00155	<i>Glycine max</i>	9.00E-90	<a href="#">XM_003529787.1</a>
<i>UCOESTdown762</i>	Lysine/histidine transporter 3	5.804	0.00119	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002315918.1</a>
<i>UCOESTdown763</i>	Receptor kinase (DIPM2)	5.776	0.0131	<i>Malus x domestica</i>	0.0	<a href="#">DQ184949.1</a>
<i>UCOESTdown764</i>	Ubiquitin carboxyl-terminal hydrolase	5.77	0.00627	<i>Medicago truncatula</i>	2.00E-108	<a href="#">XM_003609807.1</a>
<i>UCOESTdown765</i>	Y3-J8 Leucine-rich repeat family protein	5.768	0.00029	<i>Citrus trifoliata</i>	9.00E-115	<a href="#">HM596719.1</a>
<i>UCOESTdown766</i>	No homology	5.768	0.00477			
<i>UCOESTdown767</i>	NAC transcription factor 72	5.765	0.0143	<i>Populus trichocarpa</i>	1.00E-96	<a href="#">XM_002313644.1</a>

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<i>UCOESTdown768</i>	33 kDa Ribonucleoprotein	5.751	0.00174	<i>Glycine max</i>	7.00E-66	<a href="#">XM_003521451.1</a>
<i>UCOESTdown769</i>	Cc-nbs-lrr resistance protein	5.749	0.00242	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002310708.1</a>
<i>UCOESTdown770</i>	Dynein light chain LC6, flagellar outer arm	5.735	0.00891	<i>Glycine max</i>	3.00E-33	<a href="#">XM_003539979.1</a>
<i>UCOESTdown771</i>	Trihelix transcription factor GT-2	5.727	0.000206	<i>Vitis vinifera</i>	2.00E-157	<a href="#">XM_002266159.1</a>
<i>UCOESTdown772</i>	Aminomethyltransferase	5.716	0.00155	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002272665.1</a>
<i>UCOESTdown773</i>	Cysteine proteinase	5.715	0.0031	<i>Medicago truncatula</i>	3.00E-178	<a href="#">XM_003603823.1</a>
<i>UCOESTdown774</i>	Anthocyanidin reductase (ANR)	5.706	0.0152	<i>Fragaria x ananassa</i>	0.0	<a href="#">DQ664193.1</a>
<i>UCOESTdown775</i>	Uncharacterized protein	5.706	0.0103	<i>Vitis vinifera</i>	4.00E-09	<a href="#">XM_002284231.1</a>
<i>UCOESTdown776</i>	Laccase-4	5.704	0.00209	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002280380.1</a>
<i>UCOESTdown777</i>	Receptor kinase (DIPM3)	5.704	0.00392	<i>Malus x domestica</i>	0.0	<a href="#">DQ184950.1</a>
<i>UCOESTdown778</i>	Polygalacturonase	5.693	0.0047	<i>Elaeis guineensis</i>	3.00E-98	<a href="#">AY291339.1</a>
<i>UCOESTdown779</i>	Uncharacterized protein	5.690	0.00122	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002278854.1</a>
<i>UCOESTdown780</i>	TIC 62	5.678	0.00193	<i>Vitis vinifera</i>	2.00E-95	<a href="#">XM_003631578.1</a>
<i>UCOESTdown781</i>	Uncharacterized protein	5.677	0.0204	<i>Glycine max</i>	5.00E-62	<a href="#">XM_003545477.1</a>
<i>UCOESTdown782</i>	bHLH transcription factor 2	5.673	0.00381	<i>Malus x domestica</i>	9.00E-72	<a href="#">HM122456.1</a>
<i>UCOESTdown783</i>	HVA22 protein f	5.666	0.000329	<i>Glycine max</i>	3.00E-59	<a href="#">XM_003532057.1</a>
<i>UCOESTdown784</i>	Zinc finger protein CONSTANS-LIKE 16	5.656	0.0106	<i>Vitis vinifera</i>	7.00E-111	<a href="#">XM_002282542.2</a>
<i>UCOESTdown785</i>	Serine/threonine-protein kinase Nek2	5.655	0.00042	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003632280.1</a>
<i>UCOESTdown786</i>	TMV resistance protein N	5.655	0.00415	<i>Vitis vinifera</i>	2.00E-73	<a href="#">XM_002263110.1</a>
<i>UCOESTdown787</i>	No homology	5.653	0.000912			
<i>UCOESTdown788</i>	NADP-dependent alkenal double bond reductase P1	5.652	0.000348	<i>Glycine max</i>	2.00E-122	<a href="#">NM_001252964.1</a>
<i>UCOESTdown789</i>	Uncharacterized protein	5.651	0.000685	<i>Glycine max</i>	1.00E-14	<a href="#">NM_001249736.1</a>
<i>UCOESTdown790</i>	Cysteine-rich repeat secretory protein 15	5.642	0.00206	<i>Vitis vinifera</i>	8.00E-103	<a href="#">XM_002274353.2</a>
<i>UCOESTdown791</i>	subtilisin protease SDD1	5.631	0.000255	<i>Glycine max</i>	0.0	<a href="#">XM_003524134.1</a>
<i>UCOESTdown792</i>	Epidermis-specific secreted glycoprotein EP1	5.629	0.00263	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002283114.2</a>
<i>UCOESTdown793</i>	Peroxidase 47	5.618	0.00509	<i>Glycine max</i>	5.00E-148	<a href="#">XM_003534005.1</a>
<i>UCOESTdown794</i>	Disease resistance protein	5.615	0.00351	<i>Medicago truncatula</i>	3.00E-10	<a href="#">XM_003605911.1</a>
<i>UCOESTdown795</i>	Sieve element occlusion d (SEOD)	5.613	0.00329	<i>Glycine max</i>	0.0	<a href="#">NM_001254532.1</a>
<i>UCOESTdown796</i>	Pistil extensin	5.609	0.00165	<i>Vitis vinifera</i>	1.00E-51	<a href="#">XM_002274257.2</a>
<i>UCOESTdown797</i>	Triose phosphate translocator	5.600	0.000557	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002278793.1</a>

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<i>UCOESTdown798</i>	DOF transcription factor 5	5.590	0.00304	<i>Vitis vinifera</i>	9.00E-69	<a href="#">XM_002266482.2</a>
<i>UCOESTdown799</i>	Disease resistance protein	5.590	0.000767	<i>Vitis vinifera</i>	4.00E-132	<a href="#">XM_003634923.1</a>
<i>UCOESTdown800</i>	LEAFY (LFY) protein	5.588	0.00386	<i>Pyrus pyrifolia</i>	2.00E-77	<a href="#">AB162035.1</a>
<i>UCOESTdown801</i>	Pentatricopeptide repeat-containing protein	5.582	0.00103	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002267263.2</a>
<i>UCOESTdown802</i>	Glycerol-3-phosphate dehydrogenase	5.582	0.0151	<i>Vitis vinifera</i>	2.00E-46	<a href="#">EU088415.1</a>
<i>UCOESTdown803</i>	Ankyrin repeat-containing protein	5.575	0.016	<i>Vitis vinifera</i>	1.00E-51	<a href="#">XM_002275347.1</a>
<i>UCOESTdown804</i>	Do-like 9	5.561	0.00307	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_123384.2</a>
<i>UCOESTdown805</i>	Uncharacterized protein	5.559	0.000534	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002274405.2</a>
<i>UCOESTdown806</i>	28 kDa Ribonucleoprotein	5.556	0.00747	<i>Glycine max</i>	1.00E-66	<a href="#">XM_003528718.1</a>
<i>UCOESTdown807</i>	NAC transcription factor 145	5.551	0.00792	<i>Arabidopsis thaliana</i>	1.00E-104	<a href="#">NM_112654.1</a>
<i>UCOESTdown808</i>	Reticulon protein B9	5.55	0.000576	<i>Arabidopsis thaliana</i>	1.00E-63	<a href="#">NM_112710.1</a>
<i>UCOESTdown809</i>	TIC 62	5.549	0.000378	<i>Vitis vinifera</i>	9.00E-46	<a href="#">XM_002284626.2</a>
<i>UCOESTdown810</i>	FKBP-type peptidyl-prolyl cis-trans isomerase 4	5.542	0.000904	<i>Arabidopsis thaliana</i>	2.00E-82	<a href="#">NM_120132.3</a>
<i>UCOESTdown811</i>	C2H2-type zinc finger protein	5.526	0.00691	<i>Medicago truncatula</i>	6.00E-46	<a href="#">CR932963.2</a>
<i>UCOESTdown812</i>	Uncharacterized protein	5.524	0.000692	<i>Vitis vinifera</i>	3.00E-24	<a href="#">XM_002272606.1</a>
<i>UCOESTdown813</i>	FKBP-type peptidyl-prolyl cis-trans isomerase 1	5.521	0.000914	<i>Vitis vinifera</i>	1.00E-103	<a href="#">XM_002264399.2</a>
<i>UCOESTdown814</i>	Lectin-receptor protein kinase 3	5.521	0.000576	<i>Nicotiana tabacum</i>	0.0	<a href="#">AB265223.1</a>
<i>UCOESTdown815</i>	Mitogen-activated protein kinase kinase (MKK1)	5.511	0.00845	<i>Capsicum annuum</i>	2.00E-146	<a href="#">GQ249256.1</a>
<i>UCOESTdown816</i>	GDSL esterase/lipase	5.506	0.0164	<i>Medicago truncatula</i>	4.00E-94	<a href="#">XM_003589480.1</a>
<i>UCOESTdown817</i>	Lipid phosphate phosphatase 3	5.506	0.00054	<i>Glycine max</i>	5.00E-134	<a href="#">NM_001255244.1</a>
<i>UCOESTdown818</i>	Uncharacterized protein	5.496	0.000609	<i>Vitis vinifera</i>	1.00E-180	<a href="#">XM_002273844.1</a>
<i>UCOESTdown819</i>	Uncharacterized protein	5.496	0.000309	<i>Vitis vinifera</i>	3.00E-100	<a href="#">XM_002275472.2</a>
<i>UCOESTdown820</i>	Uncharacterized protein	5.491	0.0128	<i>Glycine max</i>	3.00E-81	<a href="#">XM_003540179.1</a>
<i>UCOESTdown821</i>	MYB transcription factor	5.489	0.00695	<i>Arabidopsis thaliana</i>	1.00E-91	<a href="#">NM_112141.2</a>
<i>UCOESTdown822</i>	Pterin-4-alpha-carbinolamine dehydratase 1	5.483	0.000974	<i>Glycine max</i>	2.00E-48	<a href="#">XM_003518577.1</a>
<i>UCOESTdown823</i>	No homology	5.469	0.0163			
<i>UCOESTdown824</i>	Uncharacterized protein	5.464	0.000481	<i>Glycine max</i>	3.00E-58	<a href="#">XM_003551209.1</a>
<i>UCOESTdown825</i>	No homology	5.463	0.0184			
<i>UCOESTdown826</i>	GPI-anchored protein	5.460	0.000653	<i>Medicago truncatula</i>	8.00E-44	<a href="#">XM_003610619.1</a>
<i>UCOESTdown827</i>	Uncharacterized protein	5.458	0.00393	<i>Vitis vinifera</i>	1.00E-60	<a href="#">XM_003631526.1</a>

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<i>UCOESTdown828</i>	Leucine-rich repeat receptor-like protein kinase	5.457	0.00686	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003620710.1</a>
<i>UCOESTdown829</i>	No homology	5.445	0.0229			
<i>UCOESTdown830</i>	Inactive receptor kinase	5.445	0.00717	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_128230.2</a>
<i>UCOESTdown831</i>	Receptor-like protein kinase	5.434	0.0143	<i>Vitis vinifera</i>	4.00E-56	<a href="#">XM_002268052.1</a>
<i>UCOESTdown832</i>	Homeobox-leucine zipper protein HDG2	5.431	0.0346	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_001197982.1</a>
<i>UCOESTdown833</i>	Uncharacterized protein	5.43	0.000871	<i>Brachypodium distachyon</i>	4.00E-21	<a href="#">XM_003578222.1</a>
<i>UCOESTdown834</i>	Polygalacturonase	5.411	0.000493	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002278894.2</a>
<i>UCOESTdown835</i>	No homology	5.405	0.0461			
<i>UCOESTdown836</i>	Uncharacterized protein	5.399	0.00273	<i>Glycine max</i>	3.00E-151	<a href="#">XM_003541195.1</a>
<i>UCOESTdown837</i>	Uncharacterized protein	5.397	0.000973	<i>Glycine max</i>	2.00E-54	<a href="#">XM_003550032.1</a>
<i>UCOESTdown838</i>	11S globulin precursor isoform 1A Mrna	5.396	0.00328	<i>Ficus pumila</i>	2.00E-133	<a href="#">EF091694.1</a>
<i>UCOESTdown839</i>	No homology	5.386	0.0186			
<i>UCOESTdown840</i>	Uncharacterized protein	5.386	0.00631	<i>Glycine max</i>	2.00E-04	<a href="#">XM_003521880.1</a>
<i>UCOESTdown841</i>	Leucine-rich repeat receptor-like protein kinase	5.381	0.0266	<i>Arabidopsis thaliana</i>	0.0	<a href="#">FJ708794.1</a>
<i>UCOESTdown842</i>	Glucan endo-1,3-beta-glucosidase	5.380	0.00439	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003607797.1</a>
<i>UCOESTdown843</i>	No homology	5.364	0.00383			
<i>UCOESTdown844</i>	Lysosomal Pro-X carboxypeptidase	5.361	0.003	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002281582.2</a>
<i>UCOESTdown845</i>	Uncharacterized protein	5.360	0.000623	<i>Glycine max</i>	4.00E-42	<a href="#">NM_001248309.1</a>
<i>UCOESTdown846</i>	PGR5 protein 1A	5.355	0.000366	<i>Glycine max</i>	5.00E-140	<a href="#">XM_003549825.1</a>
<i>UCOESTdown847</i>	Receptor kinase (DIPM4)	5.349	0.000734	<i>Malus x domestica</i>	0.0	<a href="#">DQ184951.1</a>
<i>UCOESTdown848</i>	Cc-nbs-lrr resistance protein	5.342	0.00793	<i>Populus trichocarpa</i>	9.00E-57	<a href="#">XM_002332062.1</a>
<i>UCOESTdown849</i>	No homology	5.341	0.00657			
<i>UCOESTdown850</i>	Uncharacterized protein	5.330	0.00854	<i>Arabidopsis thaliana</i>	3.00E-20	<a href="#">NM_115134.2</a>
<i>UCOESTdown851</i>	No homology	5.326	0.00189			
<i>UCOESTdown852</i>	Uncharacterized protein	5.323	0.000293	<i>Vitis vinifera</i>	1.00E-43	<a href="#">XM_002273330.1</a>
<i>UCOESTdown853</i>	Uncharacterized protein	5.323	0.000293	<i>Vitis vinifera</i>	1.00E-43	<a href="#">XM_002273330.1</a>
<i>UCOESTdown854</i>	Uncharacterized protein	5.319	0.00135	<i>Arabidopsis thaliana</i>	1.00E-72	<a href="#">NM_105088.3</a>
<i>UCOESTdown855</i>	No homology	5.313	0.0419			
<i>UCOESTdown856</i>	Peptidyl-prolyl cis-trans isomerase CYP38	5.310	0.00347	<i>Glycine max</i>	0.0	<a href="#">XM_003541460.1</a>

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<i>UCOESTdown857</i>	Uncharacterized protein	5.309	0.00126	<i>Vitis vinifera</i>	2.00E-74	<a href="#">XM_002271145.1</a>
<i>UCOESTdown858</i>	Squalene epoxidase 1	5.305	0.000811	<i>Nigella sativa</i>	0.0	<a href="#">FJ232947.1</a>
<i>UCOESTdown859</i>	D-xylose-proton symporter-like 2	5.303	0.000441	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002277040.2</a>
<i>UCOESTdown860</i>	Bark storage protein A	5.300	0.0152	<i>Vitis vinifera</i>	5.00E-173	<a href="#">XM_002283949.2</a>
<i>UCOESTdown861</i>	Uncharacterized protein	5.292	0.00692	<i>Vitis vinifera</i>	2.00E-68	<a href="#">XM_003634256.1</a>
<i>UCOESTdown862</i>	No homology	5.291	0.00329			
<i>UCOESTdown863</i>	Receptor-like protein kinase	5.284	0.025	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003622166.1</a>
<i>UCOESTdown864</i>	Ca <sup>2+</sup> antiporter/cation exchanger	5.282	0.00799	<i>Populus trichocarpa</i>	4.00E-144	<a href="#">XM_002313345.1</a>
<i>UCOESTdown865</i>	No homology	5.273	0.0177			
<i>UCOESTdown866</i>	Glutathione peroxidase	5.272	0.00355	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003611054.1</a>
<i>UCOESTdown867</i>	Respiratory burst oxidase protein	5.271	0.0186	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003626207.1</a>
<i>UCOESTdown868</i>	3-Dehydroquinone dehydratase / shikimate dehydrogenase isoform 1	5.268	0.00104	<i>Nicotiana tabacum</i>	0.0	<a href="#">AY578144.1</a>
<i>UCOESTdown869</i>	Allantoin permease	5.264	0.00571	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002264904.1</a>
<i>UCOESTdown870</i>	No homology	5.262	0.000872			
<i>UCOESTdown871</i>	Ferric-chelate reductase 1	5.259	0.00491	<i>Glycine max</i>	4.00E-135	<a href="#">XR_137357.1</a>
<i>UCOESTdown872</i>	Uncharacterized protein	5.249	0.00376	<i>Glycine max</i>	0.0	<a href="#">XM_003523680.1</a>
<i>UCOESTdown873</i>	NBS resistance protein	5.243	0.00159	<i>Populus trichocarpa</i>	4.00E-90	<a href="#">XM_002318332.1</a>
<i>UCOESTdown874</i>	Beta-galactosidase 3	5.242	0.000413	<i>Prunus persica</i>	0.0	<a href="#">GU462128.1</a>
<i>UCOESTdown875</i>	Uncharacterized protein	5.238	0.00126	<i>Arabidopsis thaliana</i>	5.00E-35	<a href="#">NM_115382.4</a>
<i>UCOESTdown876</i>	Momilactone A synthase	5.237	0.00236	<i>Vitis vinifera</i>	2.00E-95	<a href="#">XM_002267005.2</a>
<i>UCOESTdown877</i>	Structural maintenance chromosomes 4	5.232	0.00143	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003633808.1</a>
<i>UCOESTdown878</i>	Pentatricopeptide repeat-containing protein	5.226	0.00797	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002276396.2</a>
<i>UCOESTdown879</i>	Uncharacterized protein	5.226	0.000261	<i>Arabidopsis thaliana</i>	2.00E-11	<a href="#">NM_113122.4</a>
<i>UCOESTdown880</i>	Amino-acid acetyltransferase	5.224	0.00121	<i>Glycine max</i>	3.00E-08	<a href="#">XM_003517304.1</a>
<i>UCOESTdown881</i>	Glyceraldehyde-3-phosphate dehydrogenase B subunit	5.221	0.0412	<i>Glycine max</i>	0.0	<a href="#">NM_001250206.1</a>
<i>UCOESTdown882</i>	No homology	5.213	0.0331			
<i>UCOESTdown883</i>	No homology	5.205	0.0244			
<i>UCOESTdown884</i>	Serine/threonine-protein kinase Nek5	5.201	0.000574	<i>Glycine max</i>	0.0	<a href="#">XM_003543370.1</a>
<i>UCOESTdown885</i>	Cellulose synthase	5.200	0.000859	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002266237.2</a>
<i>UCOESTdown886</i>	Uncharacterized protein	5.178	0.000442	<i>Glycine max</i>	6.00E-36	<a href="#">XM_003527304.1</a>
<i>UCOESTdown887</i>	No homology	5.176	0.00251			
<i>UCOESTdown888</i>	Exocyst complex component 6	5.175	0.000443	<i>Vitis vinifera</i>	7.00E-47	<a href="#">XM_002271110.1</a>

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<i>UCOESTdown889</i>	Laccase 110c	5.174	0.0155	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002309033.1</a>
<i>UCOESTdown890</i>	ABC transporter family	5.156	0.00308	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002315061.1</a>
<i>UCOESTdown891</i>	Glycosyltransferase family GT8 protein (GATL1.1)	5.149	0.000364	<i>Populus deltoides</i>	0.0	<a href="#">GQ464114.1</a>
<i>UCOESTdown892</i>	IQ domain-containing protein	5.145	0.000781	<i>Medicago truncatula</i>	2.00E-135	<a href="#">XM_003603115.1</a>
<i>UCOESTdown893</i>	Solute carrier family 22 member 3	5.142	0.00217	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002265209.2</a>
<i>UCOESTdown894</i>	Cc-nbs-lrr resistance protein	5.135	0.00287	<i>Populus trichocarpa</i>	2.00E-75	<a href="#">XM_002318867.1</a>
<i>UCOESTdown895</i>	No homology	5.133	0.000362			
<i>UCOESTdown896</i>	Uncharacterized protein	5.130	0.00257	<i>Vitis vinifera</i>	2.00E-53	<a href="#">XM_003634809.1</a>
<i>UCOESTdown897</i>	Polygalacturonase	5.119	0.0499	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003631225.1</a>
<i>UCOESTdown898</i>	Beta-glucosidase 44	5.117	0.00137	<i>Glycine max</i>	6.00E-133	<a href="#">XM_003534098.1</a>
<i>UCOESTdown899</i>	Nudix hydrolase 2	5.114	0.015	<i>Vitis vinifera</i>	2.00E-23	<a href="#">XM_002268248.2</a>
<i>UCOESTdown900</i>	a-Type carbonic anhydrase	5.114	0.00124	<i>Lotus japonicus</i>	9.00E-73	<a href="#">AM503635.1</a>
<i>UCOESTdown901</i>	No homology	5.110	0.00123			
<i>UCOESTdown902</i>	Uncharacterized protein	5.108	0.00106	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002270531.2</a>
<i>UCOESTdown903</i>	Cyclin-dependent kinase C-2	5.107	0.00036	<i>Glycine max</i>	4.00E-149	<a href="#">XP_003519496.1</a>
<i>UCOESTdown904</i>	Uncharacterized protein	5.107	0.000734	<i>Glycine max</i>	6.00E-16	<a href="#">XM_003532960.1</a>
<i>UCOESTdown905</i>	ABC transporter B family member 11	5.105	0.00441	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002273951.1</a>
<i>UCOESTdown906</i>	Uncharacterized protein	5.097	0.00377	<i>Brachypodium distachyon</i>	2.00E-21	<a href="#">XM_003563523.1</a>
<i>UCOESTdown907</i>	Uncharacterized protein	5.095	0.0198	<i>Vitis vinifera</i>	2.00E-123	<a href="#">XM_002282656.2</a>
<i>UCOESTdown908</i>	Myo-inositol oxygenase	5.089	0.000289	<i>Eucalyptus grandis</i>	3.00E-167	<a href="#">EU737109.1</a>
<i>UCOESTdown909</i>	No homology	5.084	0.000273			
<i>UCOESTdown910</i>	GDSL esterase/lipase	5.079	0.00471	<i>Arabidopsis lyrata</i>	1.00E-139	<a href="#">XM_002877855.1</a>
<i>UCOESTdown911</i>	Leucine-rich repeat receptor-like protein kinase	5.079	0.00048	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_103082.2</a>
<i>UCOESTdown912</i>	No homology	5.077	0.00424			
<i>UCOESTdown913</i>	Receptor-like protein kinase	5.077	0.000783	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003637030.1</a>
<i>UCOESTdown914</i>	Uncharacterized protein	5.076	0.038	<i>Vitis vinifera</i>	5.00E-123	<a href="#">XM_003632352.1</a>
<i>UCOESTdown915</i>	Uncharacterized protein	5.072	0.00377	<i>Vitis vinifera</i>	2.00E-14	<a href="#">XM_002270063.2</a>
<i>UCOESTdown916</i>	S-adenosyl-L-methionine-dependent methyltransferase	5.063	0.00869	<i>Vitis vinifera</i>	7.00E-174	<a href="#">XM_002282543.1</a>
<i>UCOESTdown917</i>	Protein CUP-SHAPED COTYLEDON 3	5.056	0.00024	<i>Vitis vinifera</i>	2.00E-106	<a href="#">XM_002273186.2</a>
<i>UCOESTdown918</i>	Werner syndrome ATP helicase	5.055	0.00623	<i>Glycine max</i>	0.0	<a href="#">XM_003553114.1</a>

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<i>UCOESTdown919</i>	Uncharacterized protein	5.054	0.00618	<i>Vitis vinifera</i>	4.00E-20	<a href="#">XM_002274883.2</a>
<i>UCOESTdown920</i>	Proline-rich cell wall protein gene	5.048	0.000872	<i>Medicago sativa</i>	4.00E-18	<a href="#">AF028841.1</a>
<i>UCOESTdown921</i>	Lipase	5.047	0.00155	<i>Medicago truncatula</i>	7.00E-72	<a href="#">XM_003593699.1</a>
<i>UCOESTdown922</i>	NAC transcription factor 6	5.046	0.0104	<i>Nicotiana tabacum</i>	1.00E-04	<a href="#">EU753263.1</a>
<i>UCOESTdown923</i>	Uncharacterized protein	5.041	0.00114	<i>Glycine max</i>	2.00E-94	<a href="#">XM_003548265.1</a>
<i>UCOESTdown924</i>	Glutamate-gated kainate-type ion channel receptor subunit GluR5	5.038	0.00222	<i>Populus trichocarpa</i>	5.00E-115	<a href="#">XM_002324457.1</a>
<i>UCOESTdown925</i>	Uncharacterized protein	5.037	0.000468	<i>Glycine max</i>	0.0	<a href="#">XM_003517554.1</a>
<i>UCOESTdown926</i>	Cucumisin	5.036	0.0131	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002280336.2</a>
<i>UCOESTdown927</i>	Pectate lyase	5.027	0.00271	<i>Vitis vinifera</i>	4.00E-83	<a href="#">GU270835.1</a>
<i>UCOESTdown928</i>	Protein IQ-DOMAIN 14	5.016	0.0146	<i>Vitis vinifera</i>	4.00E-50	<a href="#">XM_002265085.1</a>
<i>UCOESTdown929</i>	Uncharacterized protein	5.012	0.00994	<i>Glycine max</i>	8.00E-117	<a href="#">XM_003521304.1</a>
<i>UCOESTdown930</i>	Glycerol-3-phosphate dehydrogenase	5.008	0.000294	<i>Medicago truncatula</i>	3.00E-117	<a href="#">XM_003625057.1</a>
<i>UCOESTdown931</i>	LRR receptor-like serine/threonine-protein kinase	4.991	0.000299	<i>Glycine max</i>	6.00E-155	<a href="#">NM_001251230.1</a>
<i>UCOESTdown932</i>	Geranylgeranyl reductase	4.987	0.00203	<i>Prunus persica</i>	0.0	<a href="#">AY230212.1</a>
<i>UCOESTdown933</i>	No homology	4.983	0.00312			
<i>UCOESTdown934</i>	Uncharacterized protein	4.982	0.000774	<i>Vitis vinifera</i>	1.00E-68	<a href="#">XM_002277173.2</a>
<i>UCOESTdown935</i>	Ethylene responsive transcription factor 12 (ERF12)	4.964	0.00343	<i>Prunus salicina</i>	6.00E-37	<a href="#">FJ026003.1</a>
<i>UCOESTdown936</i>	B3 domain-containing transcription factor FUS3	4.954	0.00649	<i>Arabidopsis thaliana</i>	2.00E-07	<a href="#">NM_113591.3</a>
<i>UCOESTdown937</i>	Leucine-rich repeat receptor-kinase	4.954	0.00276	<i>Arabidopsis thaliana</i>	3.00E-165	<a href="#">NM_126031.4</a>
<i>UCOESTdown938</i>	Homeodomain-leucine zipper protein HAT14	4.948	0.00142	<i>Arabidopsis thaliana</i>	3.00E-81	<a href="#">AJ431182.2</a>
<i>UCOESTdown939</i>	Caffeic acid 3-O-methyltransferase	4.945	0.00031	<i>Medicago truncatula</i>	6.00E-133	<a href="#">XM_003626569.1</a>
<i>UCOESTdown940</i>	Pre-mRNA-splicing factor SLU7-A	4.935	0.00247	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_105239.5</a>
<i>UCOESTdown941</i>	Receptor-like protein kinase 3	4.932	0.0057	<i>Glycine max</i>	0.0	<a href="#">NM_001248151.1</a>
<i>UCOESTdown942</i>	Pectin methylesterase 1	4.929	0.00311	<i>Prunus persica</i>	0.0	<a href="#">AB231903.1</a>
<i>UCOESTdown943</i>	11S legumin protein (11S-2)	4.929	0.00029	<i>Carya illinoensis</i>	5.00E-143	<a href="#">EU113052.1</a>
<i>UCOESTdown944</i>	Uncharacterized protein	4.929	0.00534	<i>Vitis vinifera</i>	4.00E-73	<a href="#">XM_002277862.1</a>
<i>UCOESTdown945</i>	Blue copper protein	4.927	0.000597	<i>Medicago truncatula</i>	4.00E-63	<a href="#">XM_003604216.1</a>
<i>UCOESTdown946</i>	AP2 domain class transcription factor	4.921	0.000257	<i>Malus x domestica</i>	8.00E-51	<a href="#">GU732441.1</a>
<i>UCOESTdown947</i>	No homology	4.921	0.0097			
<i>UCOESTdown948</i>	No homology	4.913	0.000761			

(Table continues on following page)

<i>UCOESTdown949</i>	Flagellin-sensing 2- protein gene	4.912	0.0028	<i>Lotus japonicus</i>	0.0	<a href="#">JN099749.1</a>
<i>UCOESTdown950</i>	LRR receptor-like serine/threonine-protein kinase FLS2	4.912	0.0028	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002272283.2</a>
<i>UCOESTdown951</i>	Uncharacterized protein	4.910	0.00774	<i>Glycine max</i>	5.00E-106	<a href="#">XM_003537341.1</a>
<i>UCOESTdown952</i>	Leucine-rich repeat receptor-like protein kinase	4.908	0.00637	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002894516.1</a>
<i>UCOESTdown953</i>	Leucine-rich repeat/extensin	4.907	0.000652	<i>Nicotiana plumbaginifolia</i>	1.00E-158	<a href="#">AB273717.1</a>
<i>UCOESTdown954</i>	Disease resistance protein	4.901	0.0016	<i>Medicago truncatula</i>	3.00E-81	<a href="#">XM_003613710.1</a>
<i>UCOESTdown955</i>	Ferric reduction oxidase 7	4.900	0.0225	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_124352.3</a>
<i>UCOESTdown956</i>	Uncharacterized protein	4.899	0.000433	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002279219.2</a>
<i>UCOESTdown957</i>	GDSL esterase/lipase	4.878	0.00459	<i>Arabidopsis thaliana</i>	2.00E-164	<a href="#">NM_116343.3</a>
<i>UCOESTdown958</i>	Esterase	4.869	0.00111	<i>Medicago truncatula</i>	4.00E-66	<a href="#">XM_003611782.1</a>
<i>UCOESTdown959</i>	MYB transcription factor	4.868	0.0215	<i>Arabidopsis lyrata</i>	4.00E-36	<a href="#">XM_002869977.1</a>
<i>UCOESTdown960</i>	Uncharacterized protein	4.866	0.0455	<i>Glycine max</i>	1.00E-78	<a href="#">XM_003555435.1</a>
<i>UCOESTdown961</i>	NBS resistance protein	4.865	0.00864	<i>Medicago truncatula</i>	1.00E-49	<a href="#">XM_003588950.1</a>
<i>UCOESTdown962</i>	Uncharacterized protein	4.863	0.000854	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003634347.1</a>
<i>UCOESTdown963</i>	kinesin-4	4.860	0.000586	<i>Vitis vinifera</i>	8.00E-34	<a href="#">XM_002269201.2</a>
<i>UCOESTdown964</i>	Phosphate transporter 1pho1	4.851	0.0112	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002314998.1</a>
<i>UCOESTdown965</i>	Laccase 1	4.843	0.000346	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_101674.3</a>
<i>UCOESTdown966</i>	Hyoscyamine 6-dioxygenase	4.835	0.0407	<i>Glycine max</i>	6.00E-85	<a href="#">XM_003536889.1</a>
<i>UCOESTdown967</i>	UDP-Glycosyltransferase	4.831	0.000782	<i>Arabidopsis thaliana</i>	5.00E-149	<a href="#">NM_180266.2</a>
<i>UCOESTdown968</i>	Beta-1,3-galactosyltransferase 12	4.828	0.00564	<i>Arabidopsis thaliana</i>	7.00E-142	<a href="#">NM_128168.4</a>
<i>UCOESTdown969</i>	Uncharacterized protein	4.827	0.00192	<i>Vitis vinifera</i>	2.00E-27	<a href="#">XM_002276633.1</a>
<i>UCOESTdown970</i>	Uncharacterized protein	4.826	0.000735	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002266893.2</a>
<i>UCOESTdown971</i>	Uncharacterized protein	4.825	0.00756	<i>Glycine max</i>	2.00E-87	<a href="#">XM_003549328.1</a>
<i>UCOESTdown972</i>	Cytochrome P450	4.824	0.00313	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002332645.1</a>
<i>UCOESTdown973</i>	GDSL esterase/lipase	4.824	0.000982	<i>Arabidopsis thaliana</i>	2.00E-95	<a href="#">AY072081.1</a>
<i>UCOESTdown974</i>	F-box protein	4.818	0.00302	<i>Glycine max</i>	1.00E-86	<a href="#">XM_003517179.1</a>
<i>UCOESTdown975</i>	Tubby-like F-box protein 5, transcript variant 1	4.818	0.00302	<i>Vitis vinifera</i>	1.00E-89	<a href="#">XM_002265768.2</a>
<i>UCOESTdown976</i>	S-locus lectin protein kinase family protein	4.816	0.0132	<i>Arabidopsis lyrata</i>	1.00E-62	<a href="#">XM_002872744.1</a>
<i>UCOESTdown977</i>	Peptide/nitrate transporter	4.815	0.000757	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002272140.2</a>
<i>UCOESTdown978</i>	Vacuolar iron transporter	4.813	0.00494	<i>Arabidopsis thaliana</i>	4.00E-30	<a href="#">NM_118925.2</a>

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<i>UCOESTdown979</i>	11-Beta-hydroxysteroid dehydrogenase	4.809	0.00281	<i>Arabidopsis thaliana</i>	6.00E-106	<a href="#">AK221698.1</a>
<i>UCOESTdown980</i>	Glycerol-3-phosphate dehydrogenase [NAD+]	4.808	0.00487	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002271381.1</a>
<i>UCOESTdown981</i>	Magnesium transporter MRS2-I	4.803	0.0352	<i>Glycine max</i>	3.00E-31	<a href="#">XM_003556340.1</a>
<i>UCOESTdown982</i>	Beta-1,3-galactosyltransferase 19	4.799	0.00986	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002268567.2</a>
<i>UCOESTdown983</i>	Uncharacterized protein	4.798	0.0159	<i>Glycine max</i>	1.00E-44	<a href="#">XM_003541249.1</a>
<i>UCOESTdown984</i>	1,4-Dihydroxy-2-naphthoyl-CoA synthase	4.797	0.000759	<i>Vitis vinifera</i>	6.00E-176	<a href="#">XM_002267464.1</a>
<i>UCOESTdown985</i>	Rhodanese- domain-containing protein	4.793	0.00427	<i>Arabidopsis thaliana</i>	4.00E-95	<a href="#">NM_129784.3</a>
<i>UCOESTdown986</i>	Uncharacterized protein	4.790	0.00637	<i>Medicago truncatula</i>	1.00E-10	<a href="#">XM_003637530.1</a>
<i>UCOESTdown987</i>	Uncharacterized protein	4.788	0.000534	<i>Glycine max</i>	4.00E-166	<a href="#">XM_003522745.1</a>
<i>UCOESTdown988</i>	Uncharacterized protein	4.788	0.00217	<i>Vitis vinifera</i>	1.00E-19	<a href="#">XM_002272606.1</a>
<i>UCOESTdown989</i>	Transmembrane protein 53	4.782	0.0435	<i>Vitis vinifera</i>	1.00E-151	<a href="#">XM_002276030.1</a>
<i>UCOESTdown990</i>	Protein CUP-SHAPED COTYLEDON 1	4.777	0.0284	<i>Glycine max</i>	2.00E-106	<a href="#">XM_003534121.1</a>
<i>UCOESTdown991</i>	Laccase-9	4.777	0.000208	<i>Vitis vinifera</i>	2.00E-162	<a href="#">XM_002263835.2</a>
<i>UCOESTdown992</i>	No homology	4.776	0.0013			
<i>UCOESTdown993</i>	Uncharacterized protein	4.776	0.00103	<i>Glycine max</i>	6.00E-153	<a href="#">XM_003536865.1</a>
<i>UCOESTdown994</i>	Cystathionine beta-synthase	4.775	0.0348	<i>Arabidopsis thaliana</i>	3.00E-65	<a href="#">NM_001123971.1</a>
<i>UCOESTdown995</i>	Protein IQ-DOMAIN 1	4.769	0.000309	<i>Vitis vinifera</i>	1.00E-61	<a href="#">XM_002272493.1</a>
<i>UCOESTdown996</i>	No homology	4.768	0.00149			
<i>UCOESTdown997</i>	Transcription factor GLABRA 3	4.765	0.00123	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002270203.2</a>
<i>UCOESTdown998</i>	Flavin-containing monooxygenase FMO GS-OX5	4.758	0.00176	<i>Medicago truncatula</i>	5.00E-164	<a href="#">XM_003611223.1</a>
<i>UCOESTdown999</i>	Isochorismatase hydrolase	4.758	0.00124	<i>Mangifera indica</i>	6.00E-87	<a href="#">EU513270.1</a>
<i>UCOESTdown1000</i>	DNA (cytosine-5)-methyltransferase DRM2	4.75	0.00977	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002264190.1</a>
<i>UCOESTdown1001</i>	Protein kinase	4.749	0.00048	<i>Glycine max</i>	0.0	<a href="#">XP_003520542.1</a>
<i>UCOESTdown1002</i>	Thymidine kinase	4.749	0.000284	<i>Medicago truncatula</i>	1.00E-109	<a href="#">XP_003601580.1</a>
<i>UCOESTdown1003</i>	Uncharacterized protein	4.749	0.022	<i>Medicago truncatula</i>	3.00E-19	<a href="#">XM_003619601.1</a>
<i>UCOESTdown1004</i>	DNA topoisomerase II	4.746	0.00411	<i>Nicotiana tabacum</i>	0.0	<a href="#">AY169238.2</a>
<i>UCOESTdown1005</i>	No homology	4.746	0.000479			
<i>UCOESTdown1006</i>	Thaumatococin-like protein	4.743	0.00342	<i>Pyrus pyrifolia</i>	2.00E-129	<a href="#">AB006009.1</a>
<i>UCOESTdown1007</i>	Acid alpha galactosidase 1	4.739	0.00726	<i>Cucumis sativus</i>	8.00E-131	<a href="#">DQ320569.1</a>
<i>UCOESTdown1008</i>	GDSL esterase/lipase	4.739	0.00365	<i>Arabidopsis thaliana</i>	8.00E-139	<a href="#">NM_123128.2</a>

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<i>UCOESTdown1009</i>	Uncharacterized protein	4.736	0.0229	<i>Vitis vinifera</i>	8.00E-19	<a href="#">XM_002274050.1</a>
<i>UCOESTdown1010</i>	Uncharacterized protein	4.735	0.0264	<i>Glycine max</i>	1.00E-32	<a href="#">XM_003533607.1</a>
<i>UCOESTdown1011</i>	Uncharacterized protein	4.729	0.00185	<i>Glycine max</i>	3.00E-42	<a href="#">XM_003551147.1</a>
<i>UCOESTdown1012</i>	Uncharacterized protein	4.728	0.000959	<i>Vitis vinifera</i>	6.00E-52	<a href="#">XM_002270477.1</a>
<i>UCOESTdown1013</i>	Ankyrin repeat-containing protein	4.727	0.0104	<i>Vitis vinifera</i>	2.00E-29	<a href="#">XM_002267840.2</a>
<i>UCOESTdown1014</i>	Squamosa promoter binding like-protein	4.725	0.0056	<i>Betula platyphylla</i>	8.00E-47	<a href="#">AY921636.1</a>
<i>UCOESTdown1015</i>	No homology	4.715	0.00464			
<i>UCOESTdown1016</i>	11S globulin precursor isoform 1B	4.711	0.000758	<i>Ficus pumila</i>	9.00E-151	<a href="#">EF091695.1</a>
<i>UCOESTdown1017</i>	Monocopper oxidase	4.701	0.000302	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_001203775.1</a>
<i>UCOESTdown1018</i>	Leucine-rich repeat receptor-like protein kinase	4.701	0.000298	<i>Arabidopsis thaliana</i>	0.0	<a href="#">FJ708634.1</a>
<i>UCOESTdown1019</i>	F-box protein	4.697	0.0131	<i>Vitis vinifera</i>	6.00E-103	<a href="#">XM_002273002.1</a>
<i>UCOESTdown1020</i>	No homology	4.685	0.00487			
<i>UCOESTdown1021</i>	No homology	4.685	0.000656			
<i>UCOESTdown1022</i>	Uncharacterized protein	4.685	0.00122	<i>Glycine max</i>	2.00E-21	<a href="#">XM_003554387.1</a>
<i>UCOESTdown1023</i>	No homology	4.684	0.0253			
<i>UCOESTdown1024</i>	Wall-associated receptor kinase 2	4.681	0.00318	<i>Arabidopsis lyrata</i>	3.00E-22	<a href="#">XM_002890389.1</a>
<i>UCOESTdown1025</i>	BRI1 kinase inhibitor 1	4.678	0.000549	<i>Vitis vinifera</i>	1.00E-83	<a href="#">XM_002284610.1</a>
<i>UCOESTdown1026</i>	WRKY transcription factor	4.674	0.00459	<i>Medicago truncatula</i>	2.00E-45	<a href="#">XM_003588783.1</a>
<i>UCOESTdown1027</i>	Heparan-alpha-glucosaminide N-acetyltransferase	4.669	0.000803	<i>Glycine max</i>	0.0	<a href="#">XM_003532288.1</a>
<i>UCOESTdown1028</i>	Expansin-B3	4.665	0.00038	<i>Vitis vinifera</i>	4.00E-123	<a href="#">XM_002267091.2</a>
<i>UCOESTdown1029</i>	No homology	4.665	0.00643			
<i>UCOESTdown1030</i>	Galacturonosyltransferase	4.660	0.00213	<i>Vitis vinifera</i>	6.00E-26	<a href="#">XM_002269146.1</a>
<i>UCOESTdown1031</i>	Desiccation-related protein PCC13-62	4.659	0.0462	<i>Vitis vinifera</i>	1.00E-60	<a href="#">XM_002267015.1</a>
<i>UCOESTdown1032</i>	Uncharacterized protein	4.656	0.00217	<i>Glycine max</i>	2.00E-09	<a href="#">XM_003554078.1</a>
<i>UCOESTdown1033</i>	Cytochrome P450	4.655	0.0435	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002299521.1</a>
<i>UCOESTdown1034</i>	No homology	4.650	0.0225			
<i>UCOESTdown1035</i>	Protein SHORT-ROOT	4.641	0.0266	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002267032.2</a>
<i>UCOESTdown1036</i>	Glucan endo-1,3-beta-glucosidase	4.637	0.00721	<i>Glycine max</i>	1.00E-44	<a href="#">NM_001253095.1</a>
<i>UCOESTdown1037</i>	Squamosa promoter binding like-protein	4.636	0.0174	<i>Vitis vinifera</i>	1.00E-134	<a href="#">XM_002265167.2</a>
<i>UCOESTdown1038</i>	Uncharacterized protein	4.634	0.00583	<i>Glycine max</i>	1.00E-33	<a href="#">NM_001250500.1</a>
<i>UCOESTdown1039</i>	Cyclin-A3-4 (CYCA3;4)	4.624	0.0053	<i>Arabidopsis thaliana</i>	5.00E-133	<a href="#">NM_103617.4</a>

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<i>UCOESTdown1040</i>	Uncharacterized protein	4.608	0.042	<i>Glycine max</i>	1.00E-101	<a href="#">XM_003545931.1</a>
<i>UCOESTdown1041</i>	Uncharacterized protein	4.605	0.000322	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_115434.2</a>
<i>UCOESTdown1042</i>	No homology	4.604	0.0011			
<i>UCOESTdown1043</i>	Uncharacterized protein	4.604	0.00255	<i>Glycine max</i>	5.00E-40	<a href="#">XM_003516685.1</a>
<i>UCOESTdown1044</i>	LRR receptor-like serine/threonine-protein kinase ALE2	4.602	0.00493	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002275850.2</a>
<i>UCOESTdown1045</i>	No homology	4.601	0.000676			
<i>UCOESTdown1046</i>	Uncharacterized protein	4.599	0.0235	<i>Vitis vinifera</i>	5.00E-46	<a href="#">XM_002271319.2</a>
<i>UCOESTdown1047</i>	Chorismate mutase 2 (CM2)	4.592	0.000152	<i>Arabidopsis thaliana</i>	4.00E-72	<a href="#">AY065238.1</a>
<i>UCOESTdown1048</i>	Uncharacterized protein	4.582	0.00207	<i>Glycine max</i>	1.00E-57	<a href="#">XM_003516256.1</a>
<i>UCOESTdown1049</i>	No homology	4.581	0.00512			
<i>UCOESTdown1050</i>	Uncharacterized protein	4.578	0.000364	<i>Glycine max</i>	8.00E-22	<a href="#">XM_003527412.1</a>
<i>UCOESTdown1051</i>	Uncharacterized protein	4.578	0.000364	<i>Glycine max</i>	8.00E-23	<a href="#">XM_003543311.1</a>
<i>UCOESTdown1052</i>	Vacuolar protein sorting-associated protein 24 homolog 1	4.576	0.00459	<i>Glycine max</i>	1.00E-81	<a href="#">NM_001253033.1</a>
<i>UCOESTdown1053</i>	GDSL esterase/lipase	4.574	0.0381	<i>Medicago truncatula</i>	2.00E-93	<a href="#">XM_003629222.1</a>
<i>UCOESTdown1054</i>	Flavonoid 3' hydroxylase	4.568	0.00032	<i>Artemisia annua</i>	8.00E-121	<a href="#">DQ363131.1</a>
<i>UCOESTdown1055</i>	Cysteine-rich receptor protein kinase 3	4.558	0.00235	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_105721.1</a>
<i>UCOESTdown1056</i>	Uncharacterized protein	4.558	0.00138	<i>Glycine max</i>	6.00E-83	<a href="#">XM_003539009.1</a>
<i>UCOESTdown1057</i>	No homology	4.555	0.00215			
<i>UCOESTdown1058</i>	Uncharacterized protein	4.555	0.00257	<i>Vitis vinifera</i>	5.00E-66	<a href="#">XM_003635171.1</a>
<i>UCOESTdown1059</i>	No homology	4.553	0.0178			
<i>UCOESTdown1060</i>	Uncharacterized protein	4.553	0.000462	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002280073.1</a>
<i>UCOESTdown1061</i>	Uncharacterized protein	4.552	0.00766	<i>Vitis vinifera</i>	2.00E-57	<a href="#">XM_002275164.1</a>
<i>UCOESTdown1062</i>	No homology	4.547	0.0481			
<i>UCOESTdown1063</i>	No homology	4.540	0.00831			
<i>UCOESTdown1064</i>	Structural maintenance chromosomes	4.538	0.0362	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003629031.1</a>
<i>UCOESTdown1065</i>	Nudix hydrolase 1	4.537	0.0364	<i>Arabidopsis thaliana</i>	5.00E-54	<a href="#">NM_105549.3</a>
<i>UCOESTdown1066</i>	No homology	4.535	0.00126			
<i>UCOESTdown1067</i>	Uncharacterized protein	4.532	0.0312	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002282142.2</a>
<i>UCOESTdown1068</i>	Cryptochrome DASH	4.530	0.00326	<i>Medicago truncatula</i>	1.00E-36	<a href="#">XM_003603475.1</a>
<i>UCOESTdown1069</i>	Aspartic proteinase nepenthesin-1	4.527	0.00037	<i>Glycine max</i>	0.0	<a href="#">XM_003530159.1</a>
<i>UCOESTdown1070</i>	No homology	4.527	0.00142			
<i>UCOESTdown1071</i>	Basic 7S globulin	4.526	0.00552	<i>Vitis vinifera</i>	2.00E-91	<a href="#">XM_002280472.1</a>
<i>UCOESTdown1072</i>	Glucose-6-phosphate 1-dehydrogenase	4.519	0.00127	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002276951.2</a>

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<i>UCOESTdown1073</i>	WEE1 kinase	4.518	0.0151	<i>Glycine max</i>	0.0	<a href="#">CAL64061.1</a>
<i>UCOESTdown1074</i>	Indole-3-acetate O-methyltransferase 1	4.516	0.000323	<i>Glycine max</i>	0.0	<a href="#">XM_003551710.1</a>
<i>UCOESTdown1075</i>	No homology	4.515	0.00299			
<i>UCOESTdown1076</i>	Cell division control protein 45 (CDC45)	4.514	0.00503	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_113414.2</a>
<i>UCOESTdown1077</i>	Uncharacterized protein	4.510	0.00179	<i>Medicago truncatula</i>	1.00E-29	<a href="#">XM_003626536.1</a>
<i>UCOESTdown1078</i>	Squalene monooxygenase	4.501	0.000388	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002265096.1</a>
<i>UCOESTdown1079</i>	Peptide transporter family	4.498	0.00234	<i>Medicago truncatula</i>	1.00E-174	<a href="#">XM_003618322.1</a>
<i>UCOESTdown1080</i>	Uncharacterized protein	4.497	0.0351	<i>Glycine max</i>	3.00E-54	
<i>UCOESTdown1081</i>	Leucine-rich repeat receptor-like protein kinase	4.496	0.00134	<i>Arabidopsis thaliana</i>	7.00E-132	<a href="#">NM_104492.3</a>
<i>UCOESTdown1082</i>	bHLH transcription factor 41	4.491	0.0159	<i>Vitis vinifera</i>	3.00E-82	<a href="#">XM_002279450.1</a>
<i>UCOESTdown1083</i>	Purine permease 3	4.49	0.000781	<i>Vitis vinifera</i>	5.00E-133	<a href="#">XM_002285682.2</a>
<i>UCOESTdown1084</i>	AP2-like ethylene-responsive transcription factor ANT	4.481	0.0007	<i>Medicago truncatula</i>	2.00E-157	<a href="#">XM_003627218.1</a>
<i>UCOESTdown1085</i>	Beta-1,3-glucanase	4.480	0.000838	<i>Arabidopsis thaliana</i>	0.0	<a href="#">AK118068.1</a>
<i>UCOESTdown1086</i>	No homology	4.480	0.0299			
<i>UCOESTdown1087</i>	Sulfite exporter TauE/SafE	4.479	0.00341	<i>Arabidopsis thaliana</i>	1.00E-137	<a href="#">NM_179737.1</a>
<i>UCOESTdown1088</i>	22.7 kDa class IV heat shock protein	4.475	0.000494	<i>Medicago truncatula</i>	9.00E-21	<a href="#">XM_003617009.1</a>
<i>UCOESTdown1089</i>	Uncharacterized protein	4.475	0.0107	<i>Vitis vinifera</i>	4.00E-113	<a href="#">XM_002279928.1</a>
<i>UCOESTdown1090</i>	Uncharacterized protein	4.471	0.000576	<i>Vitis vinifera</i>	7.00E-163	<a href="#">XM_002278412.1</a>
<i>UCOESTdown1091</i>	Protein Argonaute 16	4.468	0.00167	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002271411.2</a>
<i>UCOESTdown1092</i>	Uncharacterized protein	4.462	0.00671	<i>Glycine max</i>	5.00E-62	<a href="#">XM_003544298.1</a>
<i>UCOESTdown1093</i>	Fasciclin-like arabinogalactan protein 1	4.461	0.00126	<i>Gossypium hirsutum</i>	3.00E-56	<a href="#">EF470298.1</a>
<i>UCOESTdown1094</i>	Uncharacterized protein	4.457	0.0103	<i>Vitis vinifera</i>	3.00E-159	<a href="#">XM_002267396.2</a>
<i>UCOESTdown1095</i>	E2F transcription factor	4.456	0.00103	<i>Medicago truncatula</i>	5.00E-110	<a href="#">XM_003608884.1</a>
<i>UCOESTdown1096</i>	No homology	4.456	0.000458			
<i>UCOESTdown1097</i>	F-box/LRR-repeat protein	4.456	0.0109	<i>Medicago truncatula</i>	6.00E-18	<a href="#">XM_003603344.1</a>
<i>UCOESTdown1098</i>	No homology	4.454	0.00288			
<i>UCOESTdown1099</i>	Uncharacterized protein	4.453	0.0157	<i>Arabidopsis thaliana</i>	5.00E-35	<a href="#">NM_180787.1</a>
<i>UCOESTdown1100</i>	No homology	4.452	0.00545			
<i>UCOESTdown1101</i>	Uncharacterized protein	4.452	0.0218	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002277970.1</a>
<i>UCOESTdown1102</i>	Alpha-L-fucosidase 2	4.449	0.00637	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002270163.2</a>
<i>UCOESTdown1103</i>	Lecithine cholesterol acyltransferase	4.448	0.00314	<i>Medicago truncatula</i>	0.0	<a href="#">AF533771.1</a>
<i>UCOESTdown1104</i>	Transcription factor DP	4.439	0.00155	<i>Populus trichocarpa</i>	2.00E-63	<a href="#">XM_002326161.1</a>

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<i>UCOESTdown1105</i>	kinesin protein KIF18B	4.436	0.0122	<i>Glycine max</i>	0.0	<a href="#">XM_003525591.1</a>
<i>UCOESTdown1106</i>	Dynein light chain	4.435	0.0113	<i>Vitis vinifera</i>	4.00E-33	<a href="#">XM_002282255.1</a>
<i>UCOESTdown1107</i>	No homology	4.435	0.00355			
<i>UCOESTdown1108</i>	Uncharacterized protein	4.434	0.00683	<i>Vitis vinifera</i>	5.00E-107	<a href="#">XM_002270969.2</a>
<i>UCOESTdown1109</i>	O-Fucosyltransferase	4.430	0.00228	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_113929.4</a>
<i>UCOESTdown1110</i>	Omega-3 desaturase (pxh-15)	4.430	0.0011	<i>Pelargonium x hortorum</i>	0.0	<a href="#">AF020204.1</a>
<i>UCOESTdown1111</i>	Uncharacterized protein	4.429	0.0104	<i>Vitis vinifera</i>	4.00E-98	<a href="#">XM_002265480.2</a>
<i>UCOESTdown1112</i>	AP2 domain class transcription factor 48	4.427	0.00367	<i>Malus x domestica</i>	5.00E-66	<a href="#">GU732472.1</a>
<i>UCOESTdown1113</i>	BTB/POZ domain-containing protein	4.420	0.00214	<i>Glycine max</i>	0.0	<a href="#">XM_003529634.1</a>
<i>UCOESTdown1114</i>	No homology	4.402	0.0141			
<i>UCOESTdown1115</i>	MYB transcription factor 2 (MYB2)	4.397	0.0206	<i>Rosa hybrid</i>	0.0	<a href="#">FR828553.1</a>
<i>UCOESTdown1116</i>	RING-finger and BRCT domain-containing protein	4.391	0.0065	<i>Arabidopsis thaliana</i>	4.00E-91	<a href="#">NM_105388.2</a>
<i>UCOESTdown1117</i>	Uncharacterized protein	4.389	0.0282	<i>Vitis vinifera</i>	5.00E-76	<a href="#">XM_002263882.2</a>
<i>UCOESTdown1118</i>	Uncharacterized protein	4.388	0.000412	<i>Vitis vinifera</i>	9.00E-97	<a href="#">XM_002268304.2</a>
<i>UCOESTdown1119</i>	S27 Early-responsive to dehydration 4	4.387	0.00134	<i>Brassica rapa</i>	9.00E-50	<a href="#">EU186363.1</a>
<i>UCOESTdown1120</i>	No homology	4.379	0.000858			
<i>UCOESTdown1121</i>	Calcium-dependent protein kinase 29	4.379	0.0145	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NP_974150.2</a>
<i>UCOESTdown1122</i>	Disease resistance protein	4.376	0.000913	<i>Vitis vinifera</i>	2.00E-59	<a href="#">XM_002268171.2</a>
<i>UCOESTdown1123</i>	Uncharacterized protein	4.367	0.0179	<i>Vitis vinifera</i>	2.00E-77	<a href="#">XM_002271696.1</a>
<i>UCOESTdown1124</i>	No homology	4.366	0.00247			
<i>UCOESTdown1125</i>	Tubulin beta-1 (Tub1)	4.365	0.00188	<i>Gossypium hirsutum</i>	0.0	<a href="#">AF484959.1</a>
<i>UCOESTdown1126</i>	Uncharacterized protein	4.360	0.0267	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003635040.1</a>
<i>UCOESTdown1127</i>	No homology	4.356	0.00384			
<i>UCOESTdown1128</i>	No homology	4.356	0.00885			
<i>UCOESTdown1129</i>	C2H2L domain class transcription factor	4.355	0.00255	<i>Malus x domestica</i>	2.00E-59	<a href="#">HM122502.1</a>
<i>UCOESTdown1130</i>	No homology	4.354	0.000525			
<i>UCOESTdown1131</i>	Ethylene responsive transcription factor 1a (ERF1a)	4.353	0.017	<i>Prunus salicina</i>	5.00E-75	<a href="#">FJ026009.1</a>
<i>UCOESTdown1132</i>	Leucine-rich repeat receptor-like protein kinase	4.353	0.00994	<i>Arabidopsis thaliana</i>	2.00E-120	<a href="#">FJ708678.1</a>
<i>UCOESTdown1133</i>	Cytochrome P450 monooxygenase	4.345	0.00457	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003590394.1</a>

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<i>UCOESTdown1134</i>	Sulfotransferase	4.345	0.00639	<i>Mangifera indica</i>	2.00E-107	<a href="#">HQ586002.1</a>
<i>UCOESTdown1135</i>	Uncharacterized protein	4.343	0.000639	<i>Vitis vinifera</i>	1.00E-106	<a href="#">XM_002279757.1</a>
<i>UCOESTdown1136</i>	Uncharacterized protein	4.341	0.000816	<i>Glycine max</i>	1.00E-122	<a href="#">XR_136813.1</a>
<i>UCOESTdown1137</i>	Cytochrome P450	4.339	0.00799	<i>Populus trichocarpa</i>	2.00E-90	<a href="#">XM_002315972.1</a>
<i>UCOESTdown1138</i>	Anthocyanidin 3-O-glucosyltransferase	4.339	0.00236	<i>Medicago truncatula</i>	1.00E-57	<a href="#">XM_003596619.1</a>
<i>UCOESTdown1139</i>	No homology	4.33	0.0307			
<i>UCOESTdown1140</i>	Heat shock protein (Gmhspl7.5-E)	4.328	0.00635	<i>Soybean (Glycine max)</i>	6.00E-61	<a href="#">M11395.1</a>
<i>UCOESTdown1141</i>	Uncharacterized protein	4.327	0.000477	<i>Vitis vinifera</i>	4.00E-97	<a href="#">XM_002274610.2</a>
<i>UCOESTdown1142</i>	bHLH transcription factor 151	4.326	0.000845	<i>Medicago truncatula</i>	1.00E-75	<a href="#">XM_003600879.1</a>
<i>UCOESTdown1143</i>	Uncharacterized protein	4.325	0.0237	<i>Arabidopsis thaliana</i>	5.00E-106	<a href="#">BT000295.1</a>
<i>UCOESTdown1144</i>	No homology	4.316	0.00564			
<i>UCOESTdown1145</i>	No homology	4.316	0.00305			
<i>UCOESTdown1146</i>	Trehalose-6-phosphate synthase (TPS1)	4.311	0.00609	<i>Solanum lycopersicum</i>	0.0	<a href="#">NM_001246967.1</a>
<i>UCOESTdown1147</i>	Thioesterase	4.311	0.000573	<i>Arabidopsis lyrata</i>	1.00E-27	<a href="#">XM_002878324.1</a>
<i>UCOESTdown1148</i>	Uncharacterized protein	4.308	0.0166	<i>Vitis vinifera</i>	5.00E-91	<a href="#">XM_002272534.1</a>
<i>UCOESTdown1149</i>	L-Ascorbate oxidase	4.307	0.000524	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002270795.1</a>
<i>UCOESTdown1150</i>	LRR receptor-like serine/threonine-protein kinase RBK1	4.299	0.0166	<i>Vitis vinifera</i>	4.00E-172	<a href="#">XP_003635501.1</a>
<i>UCOESTdown1151</i>	Chloroplast small heat shock protein 1	4.298	0.000852	<i>Potentilla discolor</i>	1.00E-108	<a href="#">HM629425.1</a>
<i>UCOESTdown1152</i>	U-box domain-containing protein 20	4.297	0.00386	<i>Glycine max</i>	2.00E-143	<a href="#">XM_003533268.1</a>
<i>UCOESTdown1153</i>	Cytochrome P450	4.295	0.00536	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002275079.1</a>
<i>UCOESTdown1154</i>	DNAJ heat shock N-terminal domain-containing protein	4.292	0.04	<i>Arabidopsis thaliana</i>	5.00E-179	<a href="#">XM_002880256.1</a>
<i>UCOESTdown1155</i>	3-Hydroxyisobutyrate dehydrogenase	4.286	0.000819	<i>Arabidopsis thaliana</i>	8.00E-131	<a href="#">NM_118211.4</a>
<i>UCOESTdown1156</i>	Potassium channel AKT2/3	4.282	0.00214	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002268888.1</a>
<i>UCOESTdown1157</i>	Uncharacterized protein	4.282	0.000981	<i>Vitis vinifera</i>	5.00E-18	<a href="#">XM_002281014.1</a>
<i>UCOESTdown1158</i>	Uncharacterized protein	4.274	0.000362	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002266335.1</a>
<i>UCOESTdown1159</i>	Uncharacterized protein	4.274	0.0122	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002268992.2</a>
<i>UCOESTdown1160</i>	Uncharacterized protein	4.274	0.0122	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002268992.2</a>
<i>UCOESTdown1161</i>	Hydrolase, alpha/beta fold family protein	4.273	0.00156	<i>Arabidopsis thaliana</i>	1.00E-98	<a href="#">NM_119816.4</a>
<i>UCOESTdown1162</i>	Uncharacterized protein	4.273	0.00742	<i>Vitis vinifera</i>	1.00E-29	<a href="#">XM_003632062.1</a>
<i>UCOESTdown1163</i>	Cellulose synthase 7	4.270	0.000841	<i>Populus tremuloides</i>	0.0	<a href="#">AY162180.1</a>

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<i>UCOESTdown1164</i>	Outward rectifying potassium channel	4.270	0.00123	<i>Medicago truncatula</i>	9.00E-114	<a href="#">XM_003617756.1</a>
<i>UCOESTdown1165</i>	No homology	4.266	0.0135			
<i>UCOESTdown1166</i>	No homology	4.262	0.000829			
<i>UCOESTdown1167</i>	Uncharacterized protein	4.256	0.0281	<i>Vitis vinifera</i>	6.00E-176	<a href="#">XM_002268814.1</a>
<i>UCOESTdown1168</i>	Protein WAX2	4.254	0.00432	<i>Glycine max</i>	0.0	<a href="#">XR_136391.1</a>
<i>UCOESTdown1169</i>	Receptor-like protein kinase	4.254	0.022	<i>Vitis vinifera</i>	2.00E-61	<a href="#">XM_002268052.1</a>
<i>UCOESTdown1170</i>	Uncharacterized protein	4.254	0.0047	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002283355.1</a>
<i>UCOESTdown1171</i>	Rop guanine nucleotide exchange factor 1-	4.252	0.00717	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002277035.2</a>
<i>UCOESTdown1172</i>	Uncharacterized protein	4.252	0.00383	<i>Vitis vinifera</i>	5.00E-17	<a href="#">XM_002268842.2</a>
<i>UCOESTdown1173</i>	Equilibrative nucleoside transporter	4.251	0.0424	<i>Populus trichocarpa</i>	3.00E-168	<a href="#">XM_002304952.1</a>
<i>UCOESTdown1174</i>	Receptor protein kinase	4.245	0.00365	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002282089.1</a>
<i>UCOESTdown1175</i>	No homology	4.228	0.00611			
<i>UCOESTdown1176</i>	Uncharacterized protein	4.227	0.00219	<i>Glycine max</i>	2.00E-07	<a href="#">XM_003541028.1</a>
<i>UCOESTdown1177</i>	GDSL esterase/lipase	4.218	0.000422	<i>Arabidopsis thaliana</i>	7.00E-137	<a href="#">NM_122186.1</a>
<i>UCOESTdown1178</i>	Ankyrin repeat-containing protein	4.215	0.000567	<i>Vitis vinifera</i>	4.00E-165	<a href="#">XM_002277431.2</a>
<i>UCOESTdown1179</i>	Phytosulfokines 3	4.215	0.00249	<i>Vitis vinifera</i>	9.00E-12	<a href="#">XM_002276236.1</a>
<i>UCOESTdown1180</i>	F-box/FBD/LRR-repeat protein	4.213	0.00583	<i>Medicago truncatula</i>	3.00E-31	<a href="#">XM_003599569.1</a>
<i>UCOESTdown1181</i>	Uncharacterized protein	4.210	0.00186	<i>Glycine max</i>	2.00E-32	<a href="#">XM_003531166.1</a>
<i>UCOESTdown1182</i>	Aspartic proteinase nepenthesin-1	4.206	0.0447	<i>Brachypodium distachyon</i>	2.00E-18	<a href="#">XM_003578161.1</a>
<i>UCOESTdown1183</i>	Uncharacterized protein	4.202	0.0071	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002285840.2</a>
<i>UCOESTdown1184</i>	Uncharacterized protein	4.201	0.00253	<i>Arabidopsis thaliana</i>	8.00E-46	<a href="#">NM_119908.3</a>
<i>UCOESTdown1185</i>	mScS family protein	4.199	0.000586	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003592629.1</a>
<i>UCOESTdown1186</i>	Microtubule-associated protein SPIRAL2	4.196	0.00971	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002266022.1</a>
<i>UCOESTdown1187</i>	No homology	4.195	0.0283			
<i>UCOESTdown1188</i>	Uncharacterized protein	4.195	0.0126	<i>Populus trichocarpa</i>	5.00E-34	<a href="#">EF144983.1</a>
<i>UCOESTdown1189</i>	Brefeldin A-inhibited guanine	4.193	0.00351	<i>Glycine max</i>	XM_003550538.1	<a href="#">0.0</a>
<i>UCOESTdown1190</i>	Glucosylmannan 4-beta-mannosyltransferase 9	4.191	0.000645	<i>Glycine max</i>	0.0	<a href="#">XM_003554366.1</a>
<i>UCOESTdown1191</i>	Callose synthase (GSL04)	4.190	0.000845	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_001202964.1</a>
<i>UCOESTdown1192</i>	No homology	4.188	0.00287			
<i>UCOESTdown1193</i>	Cyclin A3-1 (CYCA3;1)	4.187	0.0113	<i>Arabidopsis thaliana</i>	6.00E-101	<a href="#">NM_123674.1</a>
<i>UCOESTdown1194</i>	Uncharacterized protein	4.186	0.0117	<i>Vitis vinifera</i>	9.00E-32	<a href="#">XM_002265737.1</a>

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<i>UCOESTdown1195</i>	Patatin	4.180	0.00463	<i>Vigna unguiculata</i>	1.00E-120	<a href="#">AF193067.1</a>
<i>UCOESTdown1196</i>	Sugar transporter ERD6	4.179	0.000533	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003609515.1</a>
<i>UCOESTdown1197</i>	No homology	4.177	0.00107			
<i>UCOESTdown1198</i>	Uncharacterized protein	4.170	0.00598	<i>Glycine max</i>	4.00E-154	<a href="#">XM_003524301.1</a>
<i>UCOESTdown1199</i>	No homology	4.169	0.00793			
<i>UCOESTdown1200</i>	Glucmannan 4-beta-mannosyltransferase 2	4.168	0.000353	<i>Glycine max</i>	0.0	<a href="#">XM_003538098.1</a>
<i>UCOESTdown1201</i>	HVA22 protein a	4.168	0.00321	<i>Medicago truncatula</i>	2.00E-21	<a href="#">XM_003609003.1</a>
<i>UCOESTdown1202</i>	DNA topoisomerase II	4.165	0.00589	<i>Malus x domestica</i>	3.00E-83	<a href="#">AM167520.1</a>
<i>UCOESTdown1203</i>	Ubiquitin carboxyl-terminal hydrolase	4.165	0.0483	<i>Medicago truncatula</i>	6.00E-39	<a href="#">XM_003589896.1</a>
<i>UCOESTdown1204</i>	Uncharacterized protein	4.165	0.00322	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003604047.1</a>
<i>UCOESTdown1205</i>	Polyol/monosaccharide transporter (PMT2)	4.164	0.00256	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002280942.1</a>
<i>UCOESTdown1206</i>	Polyubiquitin 2	4.159	0.0301	<i>Isotricha prostoma</i>	1.00E-32	<a href="#">AJ965264.1</a>
<i>UCOESTdown1207</i>	Wall-associated receptor kinase	4.156	0.0066	<i>Vitis vinifera</i>	1.00E-64	<a href="#">XM_003634352.1</a>
<i>UCOESTdown1208</i>	MADS transcription factor 20	4.152	0.00348	<i>Malus x domestica</i>	2.00E-47	<a href="#">HM122604.1</a>
<i>UCOESTdown1209</i>	Receptor kinase (DIPM1)	4.152	0.0121	<i>Malus x domestica</i>	0.0	<a href="#">DQ184948.1</a>
<i>UCOESTdown1210</i>	Zinc finger CCCH domain-containing protein 18	4.146	0.0473	<i>Arabidopsis thaliana</i>	6.00E-118	<a href="#">NM_126543.6</a>
<i>UCOESTdown1211</i>	Transmembrane protein 53	4.146	0.00193	<i>Vitis vinifera</i>	4.00E-133	<a href="#">XM_002276030.1</a>
<i>UCOESTdown1212</i>	Uncharacterized protein	4.145	0.00283	<i>Glycine max</i>	2.00E-105	<a href="#">XM_003543320.1</a>
<i>UCOESTdown1213</i>	Galactosyltransferase	4.144	0.0108	<i>Arabidopsis thaliana</i>	6.00E-89	<a href="#">NM_125131.1</a>
<i>UCOESTdown1214</i>	Peroxidase 29	4.143	0.00955	<i>Vitis vinifera</i>	3.00E-55	<a href="#">XM_002272943.1</a>
<i>UCOESTdown1215</i>	Glucan endo-1,3-beta-glucosidase	4.141	0.000573	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003616234.1</a>
<i>UCOESTdown1216</i>	Protein Argonaute 7	4.140	0.0233	<i>Glycine max</i>	0.0	<a href="#">XM_003516242.1</a>
<i>UCOESTdown1217</i>	No homology	4.133	0.0067			
<i>UCOESTdown1218</i>	No homology	4.131	0.00639			
<i>UCOESTdown1219</i>	Uncharacterized protein	4.131	0.000574	<i>Glycine max</i>	8.00E-49	<a href="#">XM_003551147.1</a>
<i>UCOESTdown1220</i>	Uncharacterized protein	4.124	0.00179	<i>Vitis vinifera</i>	1.00E-145	<a href="#">XM_002264343.2</a>
<i>UCOESTdown1221</i>	RAN2 small Ras-GTP-binding nuclear	4.119	0.000626	<i>Arabidopsis thaliana</i>	2.00E-82	<a href="#">BT000424.1</a>
<i>UCOESTdown1222</i>	NBS resistance protein	4.111	0.0175	<i>Populus trichocarpa</i>	2.00E-118	<a href="#">XM_002310710.1</a>
<i>UCOESTdown1223</i>	No homology	4.109	0.0428			
<i>UCOESTdown1224</i>	31 kDa Ribonucleoprotein	4.107	0.0014	<i>Medicago truncatula</i>	8.00E-68	<a href="#">XM_003612827.1</a>
<i>UCOESTdown1225</i>	Uncharacterized protein	4.106	0.0106	<i>Glycine max</i>	1.00E-45	<a href="#">XP_003540889.1</a>
<i>UCOESTdown1226</i>	No homology	4.105	0.000923			

(Table continues on following page)



<i>UCOESTdown1227</i>	Elongation of fatty acids protein A	4.105	0.00461	<i>Vitis vinifera</i>	2.00E-86	<a href="#">XM_002283475.1</a>
<i>UCOESTdown1228</i>	Mechanosensitive ion channel domain-containing protein	4.105	0.000965	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002873503.1</a>
<i>UCOESTdown1229</i>	Carboxymethylenebutenolidase	4.103	0.00256	<i>Medicago truncatula</i>	1.00E-117	<a href="#">XM_003597946.1</a>
<i>UCOESTdown1230</i>	Uncharacterized protein	4.102	0.00797	<i>Vitis vinifera</i>	6.00E-18	<a href="#">XM_002277250.1</a>
<i>UCOESTdown1231</i>	GDSL esterase/lipase	4.100	0.000765	<i>Medicago truncatula</i>	4.00E-49	<a href="#">XM_003618248.1</a>
<i>UCOESTdown1232</i>	Uncharacterized protein	4.099	0.011	<i>Glycine max</i>	5.00E-136	<a href="#">XM_003539820.1</a>
<i>UCOESTdown1233</i>	No homology	4.098	0.00353			
<i>UCOESTdown1234</i>	No homology	4.092	0.0274			
<i>UCOESTdown1235</i>	Lipase	4.092	0.00211	<i>Vitis vinifera</i>	3.00E-67	<a href="#">XM_002285755.1</a>
<i>UCOESTdown1236</i>	Uncharacterized protein	4.091	0.0136	<i>Vitis vinifera</i>	1.00E-119	<a href="#">XM_002274412.2</a>
<i>UCOESTdown1237</i>	Histone H2A 2	4.090	0.0138	<i>Arabidopsis thaliana</i>	1.00E-30	<a href="#">NM_001203923.1</a>
<i>UCOESTdown1238</i>	Uncharacterized protein	4.088	0.0253	<i>Vitis vinifera</i>	7.00E-86	<a href="#">XM_002274630.1</a>
<i>UCOESTdown1239</i>	No homology	4.085	0.019			
<i>UCOESTdown1240</i>	LRR receptor-like serine/threonine-protein kinase	4.085	0.0101	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003632870.1</a>
<i>UCOESTdown1241</i>	Protein SRG1	4.084	0.0139	<i>Glycine max</i>	1.00E-120	<a href="#">XM_003552137.1</a>
<i>UCOESTdown1242</i>	Uncharacterized protein	4.083	0.00213	<i>Vitis vinifera</i>	1.00E-34	<a href="#">XM_002275913.1</a>
<i>UCOESTdown1243</i>	WRKY transcription factor 9	4.079	0.00986	<i>Malus x domestica</i>	7.00E-141	<a href="#">HM122727.1</a>
<i>UCOESTdown1244</i>	Endo-1,3-beta-glucanase	4.075	0.00126	<i>Pyrus pyrifolia</i>	0.0	<a href="#">FJ589788.1</a>
<i>UCOESTdown1245</i>	Disease resistance protein	4.074	0.0165	<i>Vitis vinifera</i>	2.00E-93	<a href="#">XM_002263543.2</a>
<i>UCOESTdown1246</i>	Cytochrome P450	4.071	0.000703	<i>Populus trichocarpa</i>		<a href="#">XM_002315974.1</a>
<i>UCOESTdown1247</i>	Protein TRANSPARENT TESTA	4.071	0.00111	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003628901.1</a>
<i>UCOESTdown1248</i>	Receptor-like kinase RHG1	4.070	0.000438	<i>Glycine max</i>	0.0	<a href="#">NM_001248836.1</a>
<i>UCOESTdown1249</i>	Uncharacterized protein	4.070	0.00445	<i>Vitis vinifera</i>	1.00E-142	<a href="#">XM_002267567.1</a>
<i>UCOESTdown1250</i>	Uncharacterized protein	4.058	0.00981	<i>Medicago truncatula</i>	1.00E-77	<a href="#">XM_003612302.1</a>
<i>UCOESTdown1251</i>	Uncharacterized protein	4.058	0.00981	<i>Medicago truncatula</i>	1.00E-77	<a href="#">XM_003612302.1</a>
<i>UCOESTdown1252</i>	Uncharacterized protein	4.057	0.000525	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002264939.2</a>
<i>UCOESTdown1253</i>	NAC transcription factor 61	4.056	0.0141	<i>Populus trichocarpa</i>	6.00E-102	<a href="#">XM_002302636.1</a>
<i>UCOESTdown1254</i>	Peroxidase 72	4.056	0.0249	<i>Vitis vinifera</i>	1.00E-169	<a href="#">XM_002275273.2</a>
<i>UCOESTdown1255</i>	Fasciclin-like arabinogalactan protein	4.055	0.00188	<i>Gossypium hirsutum</i>	8.00E-161	<a href="#">EF672639.1</a>
<i>UCOESTdown1256</i>	Cullin-1	4.054	0.00429	<i>Glycine max</i>	2.00E-111	<a href="#">XM_003546328.1</a>
<i>UCOESTdown1257</i>	Sec14 cytosolic factor	4.048	0.000441	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003603918.1</a>
<i>UCOESTdown1258</i>	No homology	4.048	0.00834			
<i>UCOESTdown1259</i>	Ribulose biphosphate carboxylase	4.042	0.000873	<i>Medicago truncatula</i>	2.00E-76	<a href="#">XM_003610047.1</a>

(Table continues on following page)

<i>UCOESTdown1260</i>	HIT zinc finger protein	4.041	0.00208	<i>Arabidopsis thaliana</i>	4.00E-43	<a href="#">NM_104524.3</a>
<i>UCOESTdown1261</i>	Peroxisomal membrane protein PMP22	4.041	0.011	<i>Vitis vinifera</i>	9.00E-107	<a href="#">XM_002285314.2</a>
<i>UCOESTdown1262</i>	No homology	4.038	0.000913			
<i>UCOESTdown1263</i>	High mobility group family	4.035	0.00411	<i>Populus trichocarpa</i>	2.00E-20	<a href="#">XP_002310906.1</a>
<i>UCOESTdown1264</i>	No homology	4.035	0.00675			
<i>UCOESTdown1265</i>	Uncharacterized protein	4.032	0.000519	<i>Glycine max</i>	6.00E-08	<a href="#">XM_003539771.1</a>
<i>UCOESTdown1266</i>	GDSL esterase/lipase	4.029	0.000789	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_121449.2</a>
<i>UCOESTdown1267</i>	Uncharacterized protein	4.029	0.00511	<i>Glycine max</i>	7.00E-18	<a href="#">NM_001249790.1</a>
<i>UCOESTdown1268</i>	No homology	4.028	0.0104			
<i>UCOESTdown1269</i>	kinesin-1	4.027	0.00168	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002265264.1</a>
<i>UCOESTdown1270</i>	No homology	4.024	0.0336			
<i>UCOESTdown1271</i>	Tyrosine aminotransferase	4.020	0.00191	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002276515.1</a>
<i>UCOESTdown1272</i>	Uncharacterized protein	4.018	0.00444	<i>Vitis vinifera</i>	3.00E-41	<a href="#">XM_002278891.2</a>
<i>UCOESTdown1273</i>	Uncharacterized protein	4.015	0.00176	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002265250.1</a>
<i>UCOESTdown1274</i>	No homology	4.014	0.00281			
<i>UCOESTdown1275</i>	High affinity inorganic phosphate transporter	4.013	0.00878	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002307780.1</a>
<i>UCOESTdown1276</i>	Uncharacterized protein	4.008	0.00409	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002276719.2</a>
<i>UCOESTdown1277</i>	S-Acyltransferase	4.006	0.00492	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002274043.2</a>
<i>UCOESTdown1278</i>	No homology	4.001	0.0239			
<i>UCOESTdown1279</i>	No homology	4.001	0.0381			
<i>UCOESTdown1280</i>	No homology	4.000	0.00511			
<i>UCOESTdown1281</i>	MORC family CW-type zinc finger protein 3	3.996	0.00102	<i>Vitis vinifera</i>	7.00E-167	<a href="#">XM_002278649.2</a>
<i>UCOESTdown1282</i>	Uncharacterized protein	3.996	0.00215	<i>Glycine max</i>	9.00E-113	<a href="#">XM_003526606.1</a>
<i>UCOESTdown1283</i>	Uncharacterized protein	3.996	0.00215	<i>Glycine max</i>	9.00E-113	<a href="#">XM_003526606.1</a>
<i>UCOESTdown1284</i>	Lectin- receptor kinase 7	3.993	0.0011	<i>Medicago truncatula</i>	0.0	<a href="#">AY358028.1</a>
<i>UCOESTdown1285</i>	Uncharacterized protein	3.991	0.00675	<i>Arabidopsis lyrata</i>	8.00E-92	<a href="#">XM_002880366.1</a>
<i>UCOESTdown1286</i>	Pectinesterase	3.988	0.0018	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003626150.1</a>
<i>UCOESTdown1287</i>	No homology	3.988	0.000553			
<i>UCOESTdown1288</i>	No homology	3.987	0.0345			
<i>UCOESTdown1289</i>	Nephrocystin-3	3.985	0.000573	<i>Glycine max</i>	0.0	<a href="#">XM_003548364.1</a>
<i>UCOESTdown1290</i>	No homology	3.984	0.0191			
<i>UCOESTdown1291</i>	Thaumatococcus-like protein	3.981	0.000656	<i>Medicago truncatula</i>	2.00E-132	<a href="#">XM_003631053.1</a>
<i>UCOESTdown1292</i>	Isochorismatase	3.978	0.0253	<i>Medicago truncatula</i>	2.00E-64	<a href="#">XM_003589676.1</a>

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<i>UCOESTdown1293</i>	GDSL esterase/lipase	3.971	0.0496	<i>Arabidopsis thaliana</i>	2.00E-110	<a href="#">NM_118813.2</a>
<i>UCOESTdown1294</i>	SPX and EXS domain-containing protein	3.970	0.0397	<i>Medicago truncatula</i>	2.00E-101	<a href="#">XM_003623825.1</a>
<i>UCOESTdown1295</i>	Glucan endo-1,3-beta-glucosidase 11	3.968	0.0103	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002265743.2</a>
<i>UCOESTdown1296</i>	No homology	3.963	0.00326			
<i>UCOESTdown1297</i>	Protein TIFY 10A	3.961	0.0016	<i>Vitis vinifera</i>	4.00E-23	<a href="#">XM_002272327.2</a>
<i>UCOESTdown1298</i>	Callose synthase	3.958	0.00051	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003599771.1</a>
<i>UCOESTdown1299</i>	No homology	3.956	0.0241			
<i>UCOESTdown1300</i>	No homology	3.955	0.00564			
<i>UCOESTdown1301</i>	No homology	3.953	0.000994			
<i>UCOESTdown1302</i>	Ankyrin repeat-containing protein	3.949	0.0399	<i>Vitis vinifera</i>	2.00E-161	<a href="#">XM_003534832.1</a>
<i>UCOESTdown1303</i>	No homology	3.949	0.0062			
<i>UCOESTdown1304</i>	Sugar transport protein 14	3.949	0.000586	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_106370.5</a>
<i>UCOESTdown1305</i>	Squalene synthase	3.946	0.00374	<i>Glycine max</i>	0.0	<a href="#">NM_001249436.1</a>
<i>UCOESTdown1306</i>	F-box/LRR-repeat protein	3.941	0.00875	<i>Vitis vinifera</i>	2.00E-81	<a href="#">XM_002283859.2</a>
<i>UCOESTdown1307</i>	Peroxidase 43	3.938	0.0158	<i>Vitis vinifera</i>	7.00E-129	<a href="#">XM_002270914.2</a>
<i>UCOESTdown1308</i>	Uncharacterized protein	3.935	0.00565	<i>Vitis vinifera</i>	2.00E-27	<a href="#">XM_002281293.2</a>
<i>UCOESTdown1309</i>	No homology	3.930	0.00709			
<i>UCOESTdown1310</i>	NAC transcription factor 37	3.929	0.0239	<i>Populus trichocarpa</i>	2.00E-114	<a href="#">XM_002318252.1</a>
<i>UCOESTdown1311</i>	No homology	3.922	0.00163			
<i>UCOESTdown1312</i>	Bloom syndrome protein- protein	3.921	0.0485	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003591153.1</a>
<i>UCOESTdown1313</i>	No homology	3.921	0.00182			
<i>UCOESTdown1314</i>	Oxysterol-binding family protein	3.921	0.00257	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002867718.1</a>
<i>UCOESTdown1315</i>	Uncharacterized protein	3.921	0.0327	<i>Vitis vinifera</i>	3.00E-89	<a href="#">XM_002275963.1</a>
<i>UCOESTdown1316</i>	Disease resistance protein	3.919	0.00257	<i>Vitis vinifera</i>	3.00E-61	<a href="#">XM_002269008.2</a>
<i>UCOESTdown1317</i>	Trehalose-phosphate phosphatase	3.917	0.000624	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002264435.2</a>
<i>UCOESTdown1318</i>	Uncharacterized protein	3.915	0.0177	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002285083.1</a>
<i>UCOESTdown1319</i>	Cyclin-dependent kinase inhibitor 1	3.907	0.00765	<i>Vitis vinifera</i>	2.00E-28	<a href="#">XP_002282199.2</a>
<i>UCOESTdown1320</i>	No homology	3.906	0.00337			
<i>UCOESTdown1321</i>	Uncharacterized protein	3.905	0.00116	<i>Vitis vinifera</i>	1.00E-24	<a href="#">XM_002277741.1</a>
<i>UCOESTdown1322</i>	B3 domain-containing transcription factor LEC2	3.901	0.000646	<i>Arabidopsis thaliana</i>	3.00E-24	<a href="#">NM_102595.2</a>
<i>UCOESTdown1323</i>	Brassinosteroid-responsive RING-H2 (BRH1)	3.899	0.0446	<i>Arabidopsis thaliana</i>	8.00E-56	<a href="#">NM_116011.2</a>
<i>UCOESTdown1324</i>	L-Ascorbate oxidase	3.899	0.00473	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002272844.2</a>

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<i>UCOESTdown1325</i>	No homology	3.898	0.0168			
<i>UCOESTdown1326</i>	CMT-type DNA-methyltransferase	3.897	0.035	<i>Elaeis guineensis</i>	9.00E-35	<a href="#">EU117217.1</a>
<i>UCOESTdown1327</i>	Phosphoglycerate/bisphosphoglycerate mutase	3.895	0.0387	<i>Arabidopsis thaliana</i>	1.00E-180	<a href="#">NM_001161258.1</a>
<i>UCOESTdown1328</i>	Uncharacterized protein	3.893	0.0396	<i>Arabidopsis thaliana</i>	8.00E-148	<a href="#">NM_117337.2</a>
<i>UCOESTdown1329</i>	Protein tas	3.891	0.00359	<i>Vitis vinifera</i>	2.00E-178	<a href="#">XM_002281299.2</a>
<i>UCOESTdown1330</i>	No homology	3.891	0.000746			
<i>UCOESTdown1331</i>	Uncharacterized protein	3.890	0.000504	<i>Vitis vinifera</i>	1.00E-124	<a href="#">XM_002280501.2</a>
<i>UCOESTdown1332</i>	Uncharacterized protein	3.883	0.00208	<i>Populus trichocarpa</i>	1.00E-91	<a href="#">XM_002324814.1</a>
<i>UCOESTdown1333</i>	Uncharacterized protein	3.881	0.00525	<i>Vitis vinifera</i>	1.00E-48	<a href="#">XM_002264822.1</a>
<i>UCOESTdown1334</i>	ABC transporter G family member 32	3.879	0.00178	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002284849.1</a>
<i>UCOESTdown1335</i>	No homology	3.876	0.0094			
<i>UCOESTdown1336</i>	Interactor of constitutive active ROPs 4	3.873	0.00461	<i>Vitis vinifera</i>	2.00E-108	<a href="#">XM_002271791.2</a>
<i>UCOESTdown1337</i>	Uncharacterized protein	3.871	0.0011	<i>Glycine max</i>	5.00E-40	<a href="#">XM_003516685.1</a>
<i>UCOESTdown1338</i>	bHLH transcription factor 30	3.870	0.00809	<i>Glycine max</i>	4.00E-70	<a href="#">XM_003529320.1</a>
<i>UCOESTdown1339</i>	Glucose-6-phosphate 1-epimerase	3.869	0.000671	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002280184.1</a>
<i>UCOESTdown1340</i>	Receptor-like protein kinase	3.867	0.000815	<i>Arabidopsis thaliana</i>	0.0	<a href="#">AF370596.1</a>
<i>UCOESTdown1341</i>	F-box protein	3.867	0.00111	<i>Medicago truncatula</i>	1.00E-15	<a href="#">XM_003594039.1</a>
<i>UCOESTdown1342</i>	EPIDERMAL PATTERNING FACTOR	3.865	0.0187	<i>Medicago truncatula</i>	1.00E-24	<a href="#">XM_003609297.1</a>
<i>UCOESTdown1343</i>	Uncharacterized protein	3.864	0.000783	<i>Vitis vinifera</i>	9.00E-46	<a href="#">XM_002282841.1</a>
<i>UCOESTdown1344</i>	Uncharacterized protein	3.863	0.00461	<i>Vitis vinifera</i>	7.00E-33	<a href="#">XM_002263403.1</a>
<i>UCOESTdown1345</i>	Ankyrin repeat-containing protein	3.857	0.0114	<i>Vitis vinifera</i>	8.00E-75	<a href="#">XM_002269596.2</a>
<i>UCOESTdown1346</i>	Cytochrome P450	3.854	0.00117	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002321885.1</a>
<i>UCOESTdown1347</i>	No homology	3.853	0.00469			
<i>UCOESTdown1348</i>	Flavonoid 3' hydroxylase (F3'H)	3.853	0.00331	<i>Vitis vinifera</i>	0.0	<a href="#">DQ786632.2</a>
<i>UCOESTdown1349</i>	LRR receptor-like serine/threonine-protein kinase	3.853	0.000781	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002264144.2</a>
<i>UCOESTdown1350</i>	ABC transporter G family member 32	3.849	0.0066	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_128248.1</a>
<i>UCOESTdown1351</i>	Inactive hydroxysteroid dehydrogenase	3.847	0.0199	<i>Vitis vinifera</i>	8.00E-125	<a href="#">XM_002281938.2</a>
<i>UCOESTdown1352</i>	Uncharacterized protein	3.846	0.0196	<i>Vitis vinifera</i>	4.00E-136	<a href="#">XM_002270344.2</a>
<i>UCOESTdown1353</i>	LRR receptor-like serine/threonine-protein kinase	3.845	0.0109	<i>Vitis vinifera</i>	3.00E-38	<a href="#">XM_002264144.2</a>
<i>UCOESTdown1354</i>	Uncharacterized protein	3.844	0.0488	<i>Vitis vinifera</i>	1.00E-40	<a href="#">XM_002272606.1</a>
<i>UCOESTdown1355</i>	No homology	3.843	0.0369			

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<i>UCOESTdown1356</i>	K(+) efflux antiporter 3	3.843	0.00373	<i>Glycine max</i>	0.0	<a href="#">XM_003529223.1</a>
<i>UCOESTdown1357</i>	Beta-glucosidase	3.836	0.0477	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_114567.4</a>
<i>UCOESTdown1358</i>	Uncharacterized protein	3.836	0.00465	<i>Vitis vinifera</i>		<a href="#">XM_003631526.1</a>
<i>UCOESTdown1359</i>	Uncharacterized protein	3.834	0.00178	<i>Vitis vinifera</i>	1.00E-21	<a href="#">XM_002277741.1</a>
<i>UCOESTdown1360</i>	Universal stress protein (USP) family protein	3.830	0.00742	<i>Arabidopsis thaliana</i>	7.00E-29	<a href="#">NM_180386.2</a>
<i>UCOESTdown1361</i>	GDSL esterase/lipase	3.829	0.00128	<i>Vitis vinifera</i>	7.00E-137	<a href="#">XM_002267159.2</a>
<i>UCOESTdown1362</i>	Uncharacterized protein	3.828	0.00124	<i>Vitis vinifera</i>	4.00E-135	<a href="#">XM_002280940.1</a>
<i>UCOESTdown1363</i>	Luminal-binding protein 5	3.827	0.000408	<i>Vitis vinifera</i>	0.0	<a href="#">XR_078022.1</a>
<i>UCOESTdown1364</i>	Uncharacterized protein	3.826	0.0152	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002265234.2</a>
<i>UCOESTdown1365</i>	No homology	3.824	0.00505			
<i>UCOESTdown1366</i>	Lipid-binding START domain-containing protein	3.820	0.0185	<i>Arabidopsis thaliana</i>	7.00E-76	<a href="#">NM_124358.2</a>
<i>UCOESTdown1367</i>	No homology	3.818	0.0287			
<i>UCOESTdown1369</i>	Uncharacterized protein	3.817	0.00525	<i>Zea mays</i>	2.00E-137	<a href="#">NM_001149721.1</a>
<i>UCOESTdown1370</i>	BURP domain-containing protein 3	3.815	0.000638	<i>Vitis vinifera</i>	1.00E-50	<a href="#">XM_002284344.2</a>
<i>UCOESTdown1371</i>	HD domain class transcription factor 8	3.813	0.0171	<i>Malus x domestica</i>	1.00E-49	<a href="#">HM122587.1</a>
<i>UCOESTdown1372</i>	No homology	3.813	0.0331			
<i>UCOESTdown1373</i>	Formin- protein AHF1	3.812	0.000476	<i>Arabidopsis thaliana</i>	0.0	<a href="#">AF174427.1</a>
<i>UCOESTdown1374</i>	Uncharacterized protein	3.810	0.0109	<i>Arabidopsis thaliana</i>	3.00E-25	<a href="#">NM_001085004.2</a>
<i>UCOESTdown1375</i>	Rhomboid-related intramembrane serine protease	3.806	0.0213	<i>Arabidopsis thaliana</i>	3.00E-84	<a href="#">NM_123212.2</a>
<i>UCOESTdown1376</i>	Uncharacterized protein	3.806	0.00049	<i>Glycine max</i>	3.00E-46	<a href="#">XM_003555827.1</a>
<i>UCOESTdown1377</i>	Uncharacterized protein	3.805	0.00576	<i>Glycine max</i>	2.00E-176	<a href="#">XM_003524261.1</a>
<i>UCOESTdown1378</i>	Cyclic nucleotide-regulated ion channel protein	3.795	0.000913	<i>Arabidopsis thaliana</i>	2.00E-48	<a href="#">BT000991.1</a>
<i>UCOESTdown1379</i>	Replication factor C subunit	3.787	0.0247	<i>Medicago truncatula</i>	5.00E-115	<a href="#">XM_003604021.1</a>
<i>UCOESTdown1380</i>	Uncharacterized protein	3.778	0.00107	<i>Glycine max</i>	7.00E-70	<a href="#">XM_003531240.1</a>
<i>UCOESTdown1381</i>	No homology	3.775	0.000479			
<i>UCOESTdown1382</i>	Quinone oxidoreductase (QR)	3.773	0.0107	<i>Fragaria x ananassa</i>	9.00E-08	<a href="#">AY158836.1</a>
<i>UCOESTdown1383</i>	Myb transcription factor	3.772	0.017	<i>Medicago truncatula</i>	4.00E-79	<a href="#">XM_003612810.1</a>
<i>UCOESTdown1384</i>	Leucine-rich repeat receptor-like protein kinase	3.769	0.000774	<i>Glycine max</i>	0.0	<a href="#">NM_001252801.1</a>
<i>UCOESTdown1385</i>	GDSL esterase/lipase	3.766	0.0315	<i>Arabidopsis thaliana</i>	2.00E-173	<a href="#">NM_113550.3</a>

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<i>UCOESTdown1386</i>	RING-H2 finger protein ATL18	3.765	0.0249	<i>Arabidopsis thaliana</i>	1.00E-12	<a href="#">NM_119975.1</a>
<i>UCOESTdown1387</i>	Cytochrome P450	3.760	0.0477	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002331297.1</a>
<i>UCOESTdown1388</i>	Leucine-rich repeat receptor-like protein kinase	3.760	0.00377	<i>Arabidopsis thaliana</i>	2.00E-83	<a href="#">NM_127894.1</a>
<i>UCOESTdown1389</i>	GDSL-lipase protein	3.759	0.0179	<i>Capsicum annuum</i>	3.00E-118	<a href="#">AY775336.1</a>
<i>UCOESTdown1390</i>	Subtilisin protease	3.755	0.00606	<i>Glycine max</i>	0.0	<a href="#">XM_003524192.1</a>
<i>UCOESTdown1391</i>	Xyloglucan galactosyltransferase KATAMARI1	3.753	0.000524	<i>Glycine max</i>	6.00E-162	<a href="#">XM_003537471.1</a>
<i>UCOESTdown1392</i>	FKBP-type peptidyl-prolyl cis-trans isomerase 5	3.753	0.0026	<i>Glycine max</i>	7.00E-35	<a href="#">NM_001253264.1</a>
<i>UCOESTdown1393</i>	Pathogenesis-related protein 1a (PR1a)	3.753	0.00708	<i>Prunus persica</i>	5.00E-77	<a href="#">JF694923.1</a>
<i>UCOESTdown1394</i>	No homology	3.752	0.0127			
<i>UCOESTdown1395</i>	Receptor-like protein kinase	3.749	0.003	<i>Vitis vinifera</i>	0.0	<a href="#">XP_002272617.2</a>
<i>UCOESTdown1396</i>	No homology	3.747	0.00126			
<i>UCOESTdown1397</i>	No homology	3.745	0.00198			
<i>UCOESTdown1398</i>	IST1 protein	3.741	0.0122	<i>Medicago truncatula</i>	1.00E-134	<a href="#">XM_003629156.1</a>
<i>UCOESTdown1399</i>	Uncharacterized protein	3.737	0.0282	<i>Vitis vinifera</i>	9.00E-60	<a href="#">XM_002270098.1</a>
<i>UCOESTdown1400</i>	bHLH transcription factor 2	3.736	0.0147	<i>Malus x domestica</i>	9.00E-86	<a href="#">HM122456.1</a>
<i>UCOESTdown1401</i>	Sedoheptulose-1,7-bisphosphatase (SBPase)	3.735	0.0232	<i>Cucumis sativus</i>	0.0	<a href="#">FJ911553.1</a>
<i>UCOESTdown1402</i>	Cytochrome b reductase	3.734	0.0132	<i>Medicago truncatula</i>	2.00E-66	<a href="#">XM_003638312.1</a>
<i>UCOESTdown1403</i>	No homology	3.734	0.0182			
<i>UCOESTdown1404</i>	Ascorbate oxidase	3.734	0.000849	<i>Nicotiana tabacum</i>	4.00E-124	<a href="#">D43624.1</a>
<i>UCOESTdown1405</i>	No homology	3.731	0.00779			
<i>UCOESTdown1406</i>	Methyl jasmonate esterase	3.730	0.0298	<i>Solanum tuberosum</i>	6.00E-66	<a href="#">AY684102.1</a>
<i>UCOESTdown1407</i>	Uncharacterized protein	3.725	0.0196	<i>Populus trichocarpa</i>	5.00E-31	<a href="#">XM_002319890.1</a>
<i>UCOESTdown1408</i>	Dihydrolipoyllysine-residue acetyltransferase component of acetoin cleaving system	3.724	0.00126	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002283565.1</a>
<i>UCOESTdown1409</i>	Protein IQ-DOMAIN 14	3.720	0.049	<i>Vitis vinifera</i>	4.00E-33	<a href="#">XM_003635408.1</a>
<i>UCOESTdown1410</i>	No homology	3.719	0.00181			
<i>UCOESTdown1411</i>	No homology	3.718	0.0016			
<i>UCOESTdown1412</i>	Uncharacterized protein	3.718	0.0333	<i>Arabidopsis thaliana</i>	3.00E-74	<a href="#">AY072348.1</a>
<i>UCOESTdown1413</i>	Pentatricopeptide repeat-containing protein	3.711	0.000497	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002266786.1</a>

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<i>UCOESTdown1414</i>	Germin- protein subfamily 1 member 1	3.709	0.00505	<i>Glycine max</i>	1.00E-73	<a href="#">NM_001254530.1</a>
<i>UCOESTdown1415</i>	Uncharacterized protein	3.709	0.00113	<i>Glycine max</i>	2.00E-41	<a href="#">NM_001251226.1</a>
<i>UCOESTdown1416</i>	Pectinesterase 66	3.708	0.00052	<i>Glycine max</i>	3.00E-72	<a href="#">XM_003545068.1</a>
<i>UCOESTdown1417</i>	N-acetyltransferase ESCO2	3.705	0.00108	<i>Vitis vinifera</i>	3.00E-101	<a href="#">XM_002263493.1</a>
<i>UCOESTdown1418</i>	Uncharacterized protein	3.696	0.000781	<i>Vitis vinifera</i>	4.00E-178	<a href="#">XM_002278383.1</a>
<i>UCOESTdown1419</i>	Uncharacterized protein	3.692	0.0183	<i>Vitis vinifera</i>	5.00E-126	<a href="#">XM_002268194.1</a>
<i>UCOESTdown1420</i>	Uncharacterized protein	3.692	0.0103	<i>Vitis vinifera</i>	4.00E-52	<a href="#">XM_002276002.1</a>
<i>UCOESTdown1421</i>	Aquaporin, MIP family, TIP subfamily	3.690	0.000523	<i>Populus trichocarpa</i>	5.00E-113	<a href="#">XM_002331879.1</a>
<i>UCOESTdown1422</i>	NAC transcription factor 18	3.687	0.0083	<i>Malus x domestica</i>	9.00E-98	<a href="#">HM122659.1</a>
<i>UCOESTdown1423</i>	No homology	3.684	0.0295			
<i>UCOESTdown1424</i>	Calcium-dependent protein kinase	3.682	0.00129	<i>Malus x domestica</i>	0.0	<a href="#">AAR28084.1</a>
<i>UCOESTdown1425</i>	Uncharacterized protein	3.681	0.0203	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002276467.2</a>
<i>UCOESTdown1426</i>	Glutaredoxin family protein	3.677	0.00079	<i>Arabidopsis lyrata</i>	8.00E-75	<a href="#">XM_002874593.1</a>
<i>UCOESTdown1427</i>	Protein MKS1	3.676	0.00646	<i>Glycine max</i>	4.00E-20	<a href="#">XM_003526807.1</a>
<i>UCOESTdown1428</i>	No homology	3.676	0.00261			
<i>UCOESTdown1429</i>	Uncharacterized protein	3.676	0.0363	<i>Vitis vinifera</i>	3.00E-75	<a href="#">XM_002263223.1</a>
<i>UCOESTdown1430</i>	Inactive receptor kinase	3.672	0.00307	<i>Glycine max</i>	0.0	<a href="#">XM_003519247.1</a>
<i>UCOESTdown1431</i>	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 1	3.668	0.00415	<i>Vitis vinifera</i>	0.0	<a href="#">XP_002282227.2</a>
<i>UCOESTdown1432</i>	70 kDa Peptidyl-prolyl isomerase	3.666	0.0019	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003589002.1</a>
<i>UCOESTdown1433</i>	Uncharacterized protein	3.665	0.0014	<i>Populus trichocarpa</i>	1.00E-64	<a href="#">XM_002324214.1</a>
<i>UCOESTdown1434</i>	18.2 kDa Class I heat shock protein	3.663	0.00233	<i>Medicago truncatula</i>	1.00E-50	<a href="#">XM_003618742.1</a>
<i>UCOESTdown1435</i>	No homology	3.660	0.0321			
<i>UCOESTdown1436</i>	No homology	3.659	0.000839			
<i>UCOESTdown1437</i>	Pathogenesis-related protein (PR1)	3.659	0.0112	<i>Vitis vinifera</i>	3.00E-49	<a href="#">XM_002273752.2</a>
<i>UCOESTdown1438</i>	No homology	3.657	0.00522			
<i>UCOESTdown1439</i>	Uncharacterized protein	3.657	0.00185	<i>Plantago major</i>	9.00E-52	<a href="#">AJ843979.1</a>
<i>UCOESTdown1440</i>	No homology	3.653	0.00179			
<i>UCOESTdown1441</i>	Uncharacterized protein	3.653	0.0035	<i>Vitis vinifera</i>	2.00E-51	<a href="#">XM_002276447.1</a>
<i>UCOESTdown1442</i>	Acylamino-acid-releasing enzyme	3.652	0.0484	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003613852.1</a>
<i>UCOESTdown1443</i>	Rab9 effector protein with kelch motifs	3.651	0.000778	<i>Glycine max</i>	0.0	<a href="#">XR_136856.1</a>
<i>UCOESTdown1444</i>	No homology	3.65	0.00107			
<i>UCOESTdown1445</i>	No homology	3.648	0.000988			
<i>UCOESTdown1446</i>	CONSTANS-like zinc finger protein	3.645	0.0366	<i>Medicago truncatula</i>	1.00E-27	<a href="#">XM_003622218.1</a>

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<i>UCOESTdown1447</i>	No homology	3.645	0.0235			
<i>UCOESTdown1448</i>	FKBP-type peptidyl-prolyl cis-trans	3.643	0.0106	<i>Vitis vinifera</i>	1.00E-83	<a href="#">XM_002273024.2</a>
<i>UCOESTdown1449</i>	Non-symbiotic hemoglobin class 1 (GLB1)	3.643	0.000959	<i>Malus x domestica</i>	8.00E-89	<a href="#">AY224132.1</a>
<i>UCOESTdown1450</i>	Wall-associated receptor kinase	3.643	0.018	<i>Medicago truncatula</i>	6.00E-128	<a href="#">XM_003638018.1</a>
<i>UCOESTdown1451</i>	E3 ubiquitin-protein ligase PRT1	3.641	0.00134	<i>Glycine max</i>	1.00E-38	<a href="#">XM_003530823.1</a>
<i>UCOESTdown1452</i>	Uncharacterized protein	3.641	0.0035	<i>Glycine max</i>	2.00E-128	<a href="#">XM_003525471.1</a>
<i>UCOESTdown1453</i>	Peptide chain release factor 2	3.640	0.00199	<i>Glycine max</i>	1.00E-121	<a href="#">XM_003535847.1</a>
<i>UCOESTdown1454</i>	Uncharacterized protein	3.637	0.00164	<i>Populus trichocarpa</i>	7.00E-57	<a href="#">XM_002298576.1</a>
<i>UCOESTdown1455</i>	Peroxidase 1	3.636	0.0259	<i>Litchi chinensis</i>	1.00E-111	<a href="#">FJ157351.1</a>
<i>UCOESTdown1456</i>	Chalcone isomerase	3.636	0.00156	<i>Arabidopsis thaliana</i>	1.00E-75	<a href="#">NM_104230.1</a>
<i>UCOESTdown1457</i>	Peptide/nitrate transporter	3.633	0.000643	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002276035.1</a>
<i>UCOESTdown1458</i>	Cyclin-dependent kinase inhibitor 7	3.629	0.00342	<i>Populus trichocarpa</i>	4.00E-28	
<i>UCOESTdown1459</i>	No homology	3.628	0.015			
<i>UCOESTdown1460</i>	Uncharacterized protein	3.628	0.000561	<i>Vitis vinifera</i>	2.00E-51	<a href="#">XM_002276447.1</a>
<i>UCOESTdown1461</i>	Receptor-like protein kinase	3.625	0.00105	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002282309.2</a>
<i>UCOESTdown1462</i>	Sulfate/bicarbonate/oxalate exchanger and transporter sat-1	3.624	0.00648	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002303243.1</a>
<i>UCOESTdown1463</i>	No homology	3.621	0.0153			
<i>UCOESTdown1464</i>	Uncharacterized protein	3.621	0.00903	<i>Arabidopsis thaliana</i>	2.00E-64	<a href="#">NM_126155.2</a>
<i>UCOESTdown1465</i>	Uncharacterized protein	3.621	0.049	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002281576.1</a>
<i>UCOESTdown1466</i>	ABC transporter G family member 11	3.619	0.0169	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002270611.1</a>
<i>UCOESTdown1467</i>	Uncharacterized protein	3.616	0.000449	<i>Glycine max</i>	5.00E-55	<a href="#">XM_003532604.1</a>
<i>UCOESTdown1468</i>	Tubby-like F-box protein 5, transcript variant 1	3.615	0.0392	<i>Vitis vinifera</i>	2.00E-157	<a href="#">XM_002272011.2</a>
<i>UCOESTdown1469</i>	Ankyrin repeat-containing protein	3.613	0.0214	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002270261.1</a>
<i>UCOESTdown1470</i>	No homology	3.613	0.0451			
<i>UCOESTdown1471</i>	No homology	3.612	0.00141			
<i>UCOESTdown1472</i>	Fasciclin-like arabinogalactan protein 14	3.610	0.00383	<i>Gossypium hirsutum</i>	0.0	<a href="#">EF672640.1</a>
<i>UCOESTdown1473</i>	Ascorbate oxidase	3.609	0.000829	<i>Nicotiana tabacum</i>	2.00E-78	<a href="#">D43624.1</a>
<i>UCOESTdown1474</i>	No homology	3.608	0.0143			
<i>UCOESTdown1475</i>	Phosphatidylinositol-4-phosphate 5-kinase	3.608	0.00548	<i>Arabidopsis thaliana</i>	0.0	<a href="#">XP_002882563.1</a>
<i>UCOESTdown1476</i>	Uncharacterized protein	3.606	0.00116	<i>Vitis vinifera</i>	4.00E-61	<a href="#">XM_002266904.2</a>

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<i>UCOESTdown1477</i>	Brevis radix- 2	3.604	0.00117	<i>Vitis vinifera</i>	2.00E-163	<a href="#">XM_002276132.1</a>
<i>UCOESTdown1478</i>	No homology	3.600	0.0022			
<i>UCOESTdown1479</i>	Uncharacterized protein	3.599	0.000704	<i>Glycine max</i>	2.00E-29	<a href="#">XM_003522335.1</a>
<i>UCOESTdown1480</i>	Uncharacterized protein	3.598	0.014	<i>Glycine max</i>	1.00E-179	<a href="#">XM_003553529.1</a>
<i>UCOESTdown1481</i>	No homology	3.597	0.000669			
<i>UCOESTdown1482</i>	Uncharacterized protein	3.595	0.0161	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002275334.1</a>
<i>UCOESTdown1483</i>	Remorin family protein	3.589	0.00479	<i>Arabidopsis thaliana</i>	4.00E-67	<a href="#">NM_126277.1</a>
<i>UCOESTdown1484</i>	LysM domain-containing GPI-anchored protein 1	3.588	0.000759	<i>Arabidopsis thaliana</i>	1.00E-160	<a href="#">NM_102036.3</a>
<i>UCOESTdown1485</i>	Wall-associated receptor kinase 22	3.587	0.00404	<i>Arabidopsis thaliana</i>	5.00E-128	<a href="#">NM_179577.1</a>
<i>UCOESTdown1486</i>	Uncharacterized protein	3.5800	0.00409	<i>Arabidopsis thaliana</i>	2.00E-31	<a href="#">NM_120601.4</a>
<i>UCOESTdown1487</i>	Uncharacterized protein	3.580	0.00045	<i>Arabidopsis thaliana</i>	5.00E-18	<a href="#">AF370212.1</a>
<i>UCOESTdown1488</i>	F-box protein	3.579	0.0386	<i>Medicago truncatula</i>	2.00E-18	<a href="#">XM_003608803.1</a>
<i>UCOESTdown1489</i>	Disease resistance protein	3.578	0.000611	<i>Vitis vinifera</i>	1.00E-45	<a href="#">XM_002276554.1</a>
<i>UCOESTdown1490</i>	No homology	3.570	0.0426			
<i>UCOESTdown1491</i>	GDSL esterase/lipase	3.570	0.025	<i>Arabidopsis lyrata</i>	3.00E-157	<a href="#">XM_002875859.1</a>
<i>UCOESTdown1492</i>	Peptidyl-prolyl cis-trans isomerase	3.569	0.0169	<i>Medicago truncatula</i>	2.00E-109	<a href="#">XM_003621003.1</a>
<i>UCOESTdown1493</i>	No homology	3.566	0.0102			
<i>UCOESTdown1494</i>	Vacuolar iron transporter 1	3.566	0.0168	<i>Vitis vinifera</i>	4.00E-95	<a href="#">XM_002273020.1</a>
<i>UCOESTdown1495</i>	Uncharacterized protein	3.566	0.00198	<i>Glycine max</i>	1.00E-146	<a href="#">XM_003546127.1</a>
<i>UCOESTdown1496</i>	No homology	3.562	0.00892			
<i>UCOESTdown1497</i>	No homology	3.561	0.00199			
<i>UCOESTdown1498</i>	No homology	3.560	0.00787			
<i>UCOESTdown1499</i>	Beta-glucosidase	3.558	0.00297	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003598965.1</a>
<i>UCOESTdown1500</i>	DNA methyltransferase (DMT903)	3.558	0.000788	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002299098.1</a>
<i>UCOESTdown1501</i>	Uncharacterized protein	3.554	0.00354	<i>Vitis vinifera</i>	5.00E-176	<a href="#">XM_002281359.2</a>
<i>UCOESTdown1502</i>	MAC/Perforin domain-containing protein (NSL1)	3.548	0.000636	<i>Arabidopsis thaliana</i>	7.00E-179	<a href="#">NM_102605.2</a>
<i>UCOESTdown1503</i>	Uncharacterized protein	3.546	0.0146	<i>Glycine max</i>	3.00E-19	<a href="#">XM_003517665.1</a>
<i>UCOESTdown1504</i>	Transcription factor X1	3.544	0.00178	<i>Medicago truncatula</i>	5.00E-38	<a href="#">XM_003616363.1</a>
<i>UCOESTdown1505</i>	Ribose-5-phosphate isomerase A	3.544	0.0455	<i>Medicago truncatula</i>	2.00E-109	<a href="#">XM_003594568.1</a>
<i>UCOESTdown1506</i>	AP2-like ethylene-responsive transcription factor	3.543	0.0333	<i>Vitis vinifera</i>	3.00E-123	<a href="#">XM_002272123.1</a>
<i>UCOESTdown1507</i>	No homology	3.543	0.000513			
<i>UCOESTdown1508</i>	Uncharacterized protein	3.539	0.000522	<i>Glycine max</i>	1.00E-153	<a href="#">XM_003528749.1</a>

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<i>UCOESTdown1509</i>	Uncharacterized protein	3.538	0.00126	<i>Vitis vinifera</i>	2.00E-120	<a href="#">XM_002277216.1</a>
<i>UCOESTdown1510</i>	Cytochrome P450	3.534	0.000942	<i>Pyrus communis</i>	0.0	<a href="#">AF386512.1</a>
<i>UCOESTdown1511</i>	Uncharacterized protein	3.534	0.00092	<i>Glycine max</i>	1.00E-63	<a href="#">XM_003529147.1</a>
<i>UCOESTdown1512</i>	Monodehydroascorbate reductase	3.532	0.0134	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002282964.1</a>
<i>UCOESTdown1513</i>	Multiple C2 and transmembrane domain-containing protein 2	3.530	0.0407	<i>Glycine max</i>	0.0	<a href="#">XM_003534441.1</a>
<i>UCOESTdown1514</i>	Uncharacterized protein	3.530	0.00489	<i>Vitis vinifera</i>	3.00E-38	<a href="#">XM_002263111.2</a>
<i>UCOESTdown1515</i>	Allergenic isoflavone reductase-like protein Bet v 6.0102	3.529	0.00516	<i>Betula pendula</i>	1.00E-167	<a href="#">AF282850.1</a>
<i>UCOESTdown1516</i>	No homology	3.528	0.0161			
<i>UCOESTdown1517</i>	No homology	3.527	0.00367			
<i>UCOESTdown1518</i>	Uncharacterized protein	3.526	0.00572	<i>Glycine max</i>	7.00E-13	<a href="#">XM_003548032.1</a>
<i>UCOESTdown1519</i>	Uncharacterized protein	3.526	0.000724	<i>Glycine max</i>	1.00E-51	<a href="#">XM_003516424.1</a>
<i>UCOESTdown1520</i>	Uncharacterized protein	3.526	0.000724	<i>Glycine max</i>	1.00E-51	<a href="#">XM_003516424.1</a>
<i>UCOESTdown1521</i>	NAC transcription factor	3.519	0.0191	<i>Medicago truncatula</i>	3.00E-145	<a href="#">XM_003630639.1</a>
<i>UCOESTdown1522</i>	Zinc finger CCCH domain-containing protein 54	3.512	0.0015	<i>Arabidopsis thaliana</i>	2.00E-62	<a href="#">NM_120832.2</a>
<i>UCOESTdown1523</i>	U-box domain-containing protein 30	3.511	0.00112	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002267109.2</a>
<i>UCOESTdown1524</i>	Zinc finger CCCH domain-containing protein	3.510	0.000528	<i>Medicago truncatula</i>	2.00E-77	<a href="#">XM_003610908.1</a>
<i>UCOESTdown1525</i>	Cellulose synthase 3	3.497	0.000673	<i>Betula luminifera</i>	0.0	<a href="#">FJ410445.1</a>
<i>UCOESTdown1526</i>	Ankyrin repeat-containing protein	3.496	0.00659	<i>Vitis vinifera</i>	4.00E-154	<a href="#">XM_002274030.2</a>
<i>UCOESTdown1527</i>	CYCLOIDEA-like protein (CYC) g	3.494	0.0186	<i>Linaria vulgaris</i>	1.00E-25	<a href="#">AF512603.1</a>
<i>UCOESTdown1528</i>	Uncharacterized protein	3.493	0.000905	<i>Arabidopsis thaliana</i>	1.00E-76	<a href="#">NM_122469.2</a>
<i>UCOESTdown1529</i>	Uncharacterized protein	3.492	0.00187	<i>Vitis vinifera</i>	7.00E-94	<a href="#">XM_002280773.2</a>
<i>UCOESTdown1530</i>	Glycerol-3-phosphate dehydrogenase 1 [NAD(P)+]	3.490	0.0033	<i>Glycine max</i>	6.00E-55	<a href="#">XM_003518088.1</a>
<i>UCOESTdown1531</i>	Homeobox-leucine zipper protein HAT4	3.486	0.0325	<i>Vitis vinifera</i>	1.00E-95	<a href="#">XM_002263157.2</a>
<i>UCOESTdown1532</i>	kinase G11A	3.483	0.000666	<i>Glycine max</i>	0.0	<a href="#">XP_003521068.1</a>
<i>UCOESTdown1533</i>	DNA polymerase III polC-type	3.479	0.0365	<i>Medicago truncatula</i>	4.00E-117	<a href="#">XM_003630007.1</a>
<i>UCOESTdown1534</i>	Uncharacterized protein	3.479	0.0125	<i>Vitis vinifera</i>	3.00E-167	<a href="#">XM_002279750.2</a>
<i>UCOESTdown1535</i>	Uncharacterized protein	3.476	0.00278	<i>Glycine max</i>	3.00E-107	<a href="#">XM_003533311.1</a>
<i>UCOESTdown1536</i>	Kinesin-3	3.472	0.00228	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003607657.1</a>
<i>UCOESTdown1537</i>	No homology	3.470	0.0018			

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<i>UCOESTdown1538</i>	Receptor-like protein kinase	3.466	0.000734	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003607938.1</a>
<i>UCOESTdown1539</i>	BZIP domain class transcription factor (BZIP17)	3.464	0.0383	<i>Malus x domestica</i>	0.0	<a href="#">HM122469.1</a>
<i>UCOESTdown1540</i>	Nudix hydrolase 2	3.459	0.0171	<i>Glycine max</i>	1.00E-26	<a href="#">XM_003534902.1</a>
<i>UCOESTdown1541</i>	No homology	3.455	0.0135			
<i>UCOESTdown1542</i>	Cytochrome P450	3.449	0.0108	<i>Populus trichocarpa</i>	2.00E-53	<a href="#">XM_002309980.1</a>
<i>UCOESTdown1543</i>	MYB transcription factor 17 (MYB17)	3.448	0.00656	<i>Rosa rugosa</i>	7.00E-135	<a href="#">FR828550.1</a>
<i>UCOESTdown1544</i>	Sugar transporter ERD6-like 7	3.448	0.0323	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002270891.2</a>
<i>UCOESTdown1545</i>	Uncharacterized protein	3.446	0.0418	<i>Vitis vinifera</i>	9.00E-23	<a href="#">XM_002280862.2</a>
<i>UCOESTdown1546</i>	Uncharacterized protein	3.445	0.00147	<i>Glycine max</i>	7.00E-23	<a href="#">NM_001251620.1</a>
<i>UCOESTdown1547</i>	Cytochrome P450	3.443	0.000783	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002322570.1</a>
<i>UCOESTdown1548</i>	No homology	3.443	0.00408			
<i>UCOESTdown1549</i>	No homology	3.442	0.0436			
<i>UCOESTdown1550</i>	Uncharacterized protein	3.442	0.00552	<i>Glycine max</i>	3.00E-106	<a href="#">NM_001254119.1</a>
<i>UCOESTdown1551</i>	Uncharacterized protein	3.439	0.0161	<i>Arabidopsis thaliana</i>	7.00E-26	<a href="#">NM_121931.3</a>
<i>UCOESTdown1552</i>	No homology	3.437	0.0076			
<i>UCOESTdown1553</i>	Uncharacterized protein	3.43	0.00149	<i>Glycine max</i>	2.00E-46	<a href="#">XM_003519677.1</a>
<i>UCOESTdown1554</i>	No homology	3.428	0.00571			
<i>UCOESTdown1555</i>	Uncharacterized protein	3.428	0.000743	<i>Arabidopsis thaliana</i>	1.00E-27	<a href="#">NM_130228.1</a>
<i>UCOESTdown1556</i>	Uncharacterized protein	3.428	0.00497	<i>Glycine max</i>	1.00E-16	<a href="#">XR_137670.1</a>
<i>UCOESTdown1557</i>	Calcium-binding EF hand family protein	3.426	0.00278	<i>Arabidopsis lyrata</i>	2.00E-61	<a href="#">XM_002880056.1</a>
<i>UCOESTdown1558</i>	Lipase	3.425	0.043	<i>Medicago truncatula</i>	5.00E-162	<a href="#">XM_003608551.1</a>
<i>UCOESTdown1559</i>	Uncharacterized protein	3.425	0.0109	<i>Vitis vinifera</i>	7.00E-57	<a href="#">XM_002265204.2</a>
<i>UCOESTdown1560</i>	Uncharacterized protein	3.424	0.00996	<i>Vitis vinifera</i>	2.00E-09	<a href="#">XM_002283138.2</a>
<i>UCOESTdown1561</i>	Potassium transporter 8	3.423	0.000656	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002274920.2</a>
<i>UCOESTdown1562</i>	No homology	3.420	0.00173			
<i>UCOESTdown1563</i>	Cc-nbs-lrr resistance protein	3.420	0.0257	<i>Populus trichocarpa</i>	2.00E-55	<a href="#">XM_002321779.1</a>
<i>UCOESTdown1564</i>	Uncharacterized protein	3.419	0.000594	<i>Glycine max</i>	2.00E-105	<a href="#">XM_003547061.1</a>
<i>UCOESTdown1565</i>	No homology	3.418	0.00228			
<i>UCOESTdown1566</i>	Uncharacterized protein	3.413	0.034	<i>Arabidopsis thaliana</i>	7.00E-24	<a href="#">NM_001084341.2</a>
<i>UCOESTdown1567</i>	Uncharacterized protein	3.408	0.00133	<i>Glycine max</i>	5.00E-67	<a href="#">XM_003552911.1</a>
<i>UCOESTdown1568</i>	WUSCHEL-related homeobox 4	3.401	0.00461	<i>Glycine max</i>	2.00E-77	<a href="#">NM_001254491.1</a>
<i>UCOESTdown1569</i>	GDSL esterase/lipase	3.399	0.00117	<i>Arabidopsis thaliana</i>	3.00E-85	<a href="#">NM_129374.3</a>
<i>UCOESTdown1570</i>	Cytochrome P450	3.397	0.000206	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002333707.1</a>

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<i>UCOESTdown1571</i>	UDP-Glycosyltransferase	3.397	0.002	<i>Vitis vinifera</i>	9.00E-151	<a href="#">XM_002268347.2</a>
<i>UCOESTdown1572</i>	Uncharacterized protein	3.395	0.00215	<i>Vitis vinifera</i>	4.00E-138	<a href="#">XM_002276491.2</a>
<i>UCOESTdown1573</i>	No homology	3.387	0.00215			
<i>UCOESTdown1574</i>	No homology	3.386	0.000673			
<i>UCOESTdown1575</i>	Lactoylglutathione lyase	3.385	0.0428	<i>Arabidopsis lyrata</i>	5.00E-68	<a href="#">XM_002892366.1</a>
<i>UCOESTdown1576</i>	No homology	3.381	0.000989			
<i>UCOESTdown1577</i>	Allene oxide cyclase	3.381	0.000589	<i>Vitis vinifera</i>	1.00E-101	<a href="#">XM_003633705.1</a>
<i>UCOESTdown1578</i>	Uncharacterized protein	3.379	0.00471	<i>Vitis vinifera</i>	2.00E-51	<a href="#">XM_002273641.1</a>
<i>UCOESTdown1579</i>	Expansin-A20-	3.376	0.0154	<i>Vitis vinifera</i>	3.00E-115	<a href="#">XM_002283109.1</a>
<i>UCOESTdown1580</i>	GRAS family transcription factor (GRAS35)	3.376	0.00309	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002299182.1</a>
<i>UCOESTdown1581</i>	Trehalose-phosphate phosphatase	3.375	0.00242	<i>Glycine max</i>	2.00E-179	<a href="#">XM_003538581.1</a>
<i>UCOESTdown1582</i>	No homology	3.372	0.0348			
<i>UCOESTdown1583</i>	Leucine-rich repeat receptor-like protein kinase	3.367	0.000582	<i>Ipomoea batatas</i>	0.0	<a href="#">AB125890.2</a>
<i>UCOESTdown1584</i>	No homology	3.366	0.00833			
<i>UCOESTdown1585</i>	E3 ubiquitin-protein ligase HERC1	3.363	0.0013	<i>Glycine max</i>	0.0	<a href="#">XM_003551450.1</a>
<i>UCOESTdown1586</i>	No homology	3.362	0.0143			
<i>UCOESTdown1587</i>	bHLH transcription factor 25	3.360	0.0335	<i>Medicago truncatula</i>	3.00E-55	<a href="#">XM_003611451.1</a>
<i>UCOESTdown1588</i>	Uncharacterized protein	3.359	0.00114	<i>Arabidopsis thaliana</i>	4.00E-68	<a href="#">NM_129134.3</a>
<i>UCOESTdown1589</i>	Myb transcription factor	3.353	0.00719	<i>Medicago truncatula</i>	1.00E-54	<a href="#">XM_003612608.1</a>
<i>UCOESTdown1590</i>	vinorine synthase	3.350	0.0267	<i>Vitis vinifera</i>	7.00E-93	<a href="#">XM_002267044.1</a>
<i>UCOESTdown1591</i>	DNA repair protein XRCC2-like protein	3.349	0.00242	<i>Arabidopsis thaliana</i>	1.00E-56	<a href="#">NM_001037064.1</a>
<i>UCOESTdown1592</i>	No homology	3.348	0.0485			
<i>UCOESTdown1593</i>	No homology	3.348	0.0407			
<i>UCOESTdown1594</i>	Serine/threonine-protein kinase	3.347	0.0393	<i>Medicago truncatula</i>	2.00E-59	<a href="#">XM_003624326.1</a>
<i>UCOESTdown1595</i>	No homology	3.346	0.0139			
<i>UCOESTdown1596</i>	L-type lectin-domain containing receptor kinase S.7	3.346	0.0455	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002268789.1</a>
<i>UCOESTdown1597</i>	Uncharacterized protein	3.346	0.00483	<i>Vitis vinifera</i>	2.00E-43	<a href="#">XM_002273717.2</a>
<i>UCOESTdown1598</i>	No homology	3.344	0.0239			
<i>UCOESTdown1599</i>	MADS transcription factor 1	3.342	0.00849	<i>Aristolochia fimbriata</i>	9.00E-97	<a href="#">FN386479.1</a>
<i>UCOESTdown1600</i>	No homology	3.342	0.00188			

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<i>UCOESTdown1601</i>	No homology	3.340	0.00647			
<i>UCOESTdown1602</i>	Uncharacterized protein	3.340	0.00197	<i>Vitis vinifera</i>	2.00E-59	<a href="#">XM_002279998.2</a>
<i>UCOESTdown1603</i>	Uncharacterized protein	3.339	0.046	<i>Glycine max</i>	4.00E-44	<a href="#">XM_003550785.1</a>
<i>UCOESTdown1604</i>	U-box domain-containing protein 50	3.336	0.00388	<i>Glycine max</i>	0.0	<a href="#">XM_003533372.1</a>
<i>UCOESTdown1605</i>	No homology	3.336	0.0463			
<i>UCOESTdown1606</i>	Pentatricopeptide repeat protein	3.335	0.00179	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002284360.1</a>
<i>UCOESTdown1607</i>	Cyclic nucleotide-gated ion channel 1	3.334	0.0066	<i>Vitis vinifera</i>	4.00E-23	<a href="#">XM_002268956.1</a>
<i>UCOESTdown1608</i>	bHLH transcription factor 30	3.329	0.00354	<i>Glycine max</i>	1.00E-67	<a href="#">NM_001254190.1</a>
<i>UCOESTdown1609</i>	Pentatricopeptide repeat-containing protein	3.325	0.0272	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003635118.1</a>
<i>UCOESTdown1610</i>	Uncharacterized protein	3.318	0.00502	<i>Vitis vinifera</i>	3.00E-137	<a href="#">XM_002279547.2</a>
<i>UCOESTdown1611</i>	Uncharacterized protein	3.316	0.00373	<i>Vitis vinifera</i>	5.00E-98	<a href="#">XM_002279466.1</a>
<i>UCOESTdown1612</i>	Uncharacterized protein	3.315	0.00222	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002273500.1</a>
<i>UCOESTdown1613</i>	ABC transporter	3.312	0.0018	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003630052.1</a>
<i>UCOESTdown1614</i>	Phosphoenolpyruvate/phosphate translocator 2	3.311	0.00564	<i>Glycine max</i>	4.00E-152	<a href="#">NM_001255280.1</a>
<i>UCOESTdown1615</i>	Uncharacterized protein	3.310	0.00908	<i>Arabidopsis thaliana</i>	1.00E-34	<a href="#">NM_126191.2</a>
<i>UCOESTdown1616</i>	Uncharacterized protein	3.310	0.00295	<i>Vitis vinifera</i>	7.00E-27	<a href="#">XM_002283501.2</a>
<i>UCOESTdown1617</i>	30S ribosomal protein S5	3.309	0.00625	<i>Glycine max</i>	3.00E-96	<a href="#">XM_003529287.1</a>
<i>UCOESTdown1618</i>	Diacylglycerol kinase	3.305	0.000523	<i>Arabidopsis lyrata</i>	1.00E-165	<a href="#">XP_002880215.1</a>
<i>UCOESTdown1619</i>	NAD(P)H-dependent oxidoreductase 1	3.304	0.00278	<i>Vitis vinifera</i>	4.00E-147	<a href="#">XM_002285162.1</a>
<i>UCOESTdown1620</i>	Ubiquitin carboxyl-terminal hydrolase	3.304	0.000829	<i>Medicago truncatula</i>	1.00E-107	<a href="#">XM_003612856.1</a>
<i>UCOESTdown1621</i>	MLO13 protein (MLO13)	3.300	0.00203	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002282180.2</a>
<i>UCOESTdown1622</i>	No homology	3.300	0.0135			
<i>UCOESTdown1623</i>	No homology	3.298	0.0021			
<i>UCOESTdown1624</i>	No homology	3.291	0.0375			
<i>UCOESTdown1625</i>	Menaquinone biosynthesis methyltransferase ubiE (MTR_5g033700) mRNA, complete cds	3.288	0.026	<i>Medicago truncatula</i>	4.00E-113	<a href="#">XM_003613133.1</a>
<i>UCOESTdown1626</i>	Uncharacterized protein	3.287	0.0135	<i>Glycine max</i>	4.00E-82	<a href="#">XM_003551479.1</a>
<i>UCOESTdown1627</i>	Peptide transporter PTR1	3.286	0.0486	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003613510.1</a>
<i>UCOESTdown1628</i>	kinesin-4	3.283	0.0123	<i>Glycine max</i>	0.0	<a href="#">XM_003521531.1</a>
<i>UCOESTdown1629</i>	Uncharacterized protein	3.283	0.0059	<i>Vitis vinifera</i>	1.00E-112	<a href="#">XM_002266953.2</a>
<i>UCOESTdown1630</i>	Uncharacterized protein	3.282	0.000733	<i>Vitis vinifera</i>	4.00E-159	<a href="#">XM_002268792.2</a>

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<i>UCOESTdown1631</i>	Uncharacterized protein	3.279	0.0146	<i>Vitis vinifera</i>	2.00E-83	<a href="#">XM_002285633.2</a>
<i>UCOESTdown1632</i>	Pectinesterase 8	3.276	0.0325	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002267806.1</a>
<i>UCOESTdown1633</i>	No homology	3.274	0.00735			
<i>UCOESTdown1634</i>	G-type lectin S-receptor	3.274	0.00359	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002280681.2</a>
<i>UCOESTdown1635</i>	MYB transcription factor 16 (MYB16)	3.272	0.048	<i>Rosa rugosa</i>	7.00E-169	<a href="#">FR828549.1</a>
<i>UCOESTdown1636</i>	Pentatricopeptide repeat-containing protein	3.270	0.0134	<i>Glycine max</i>	0.0	<a href="#">XM_003535646.1</a>
<i>UCOESTdown1637</i>	Uncharacterized protein	3.270	0.00954	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002274871.2</a>
<i>UCOESTdown1638</i>	Zinc finger protein	3.266	0.00424	<i>Vitis vinifera</i>	9.00E-49	<a href="#">XM_002272509.1</a>
<i>UCOESTdown1639</i>	No homology	3.265	0.0472			
<i>UCOESTdown1640</i>	Leucine-rich repeat receptor-like protein kinase	3.265	0.00234	<i>Glycine max</i>	0.0	<a href="#">XM_003522462.1</a>
<i>UCOESTdown1641</i>	Uncharacterized protein	3.264	0.00376	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002276895.1</a>
<i>UCOESTdown1642</i>	No homology	3.261	0.0181			
<i>UCOESTdown1643</i>	No homology	3.261	0.0143			
<i>UCOESTdown1644</i>	No homology	3.261	0.00322			
<i>UCOESTdown1645</i>	No homology	3.258	0.0346			
<i>UCOESTdown1646</i>	Uncharacterized protein	3.254	0.00158	<i>Vitis vinifera</i>	1.00E-48	<a href="#">XM_002282482.1</a>
<i>UCOESTdown1647</i>	Reticulon protein B17	3.253	0.0379	<i>Vitis vinifera</i>	8.00E-103	<a href="#">XM_002275120.2</a>
<i>UCOESTdown1648</i>	Cyclin-T1-4	3.251	0.00596	<i>Vitis vinifera</i>	1.00E-51	<a href="#">XM_002281072.2</a>
<i>UCOESTdown1649</i>	No homology	3.248	0.00246			
<i>UCOESTdown1650</i>	Benzoyl coenzyme A: benzyl alcohol benzoyl transferase	3.245	0.0146	<i>Nicotiana tabacum</i>	3.00E-152	<a href="#">AF500202.1</a>
<i>UCOESTdown1651</i>	Glycolate oxidase (GOX)	3.242	0.00114	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002278068.2</a>
<i>UCOESTdown1652</i>	Uncharacterized protein	3.240	0.00351	<i>Glycine max</i>	5.00E-129	<a href="#">XM_003528541.1</a>
<i>UCOESTdown1653</i>	No homology	3.238	0.00323			
<i>UCOESTdown1654</i>	Uncharacterized protein	3.237	0.00575	<i>Glycine max</i>	1.00E-20	<a href="#">XM_003547123.1</a>
<i>UCOESTdown1655</i>	No homology	3.234	0.0366			
<i>UCOESTdown1656</i>	DNA mismatch repair protein MLH3 (MLH3)	3.233	0.00393	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_119717.6</a>
<i>UCOESTdown1657</i>	Ankyrin repeat-containing protein	3.233	0.000818	<i>Vitis vinifera</i>	4.00E-52	<a href="#">XM_002269596.2</a>
<i>UCOESTdown1658</i>	No homology	3.231	0.00242			
<i>UCOESTdown1659</i>	F-box protein	3.230	0.00198	<i>Vitis vinifera</i>	7.00E-83	<a href="#">XM_002280345.2</a>
<i>UCOESTdown1660</i>	Aspartic proteinase nepenthesin-1	3.229	0.00479	<i>Glycine max</i>	5.00E-121	<a href="#">XM_003520825.1</a>
<i>UCOESTdown1661</i>	Lipase	3.228	0.0261	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003611321.1</a>

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<i>UCOESTdown1662</i>	Phosphatase 2C 63	3.228	0.000573	<i>Glycine max</i>	2.00E-167	<a href="#">XM_003538750.1</a>
<i>UCOESTdown1663</i>	Sodium-coupled neutral amino acid	3.225	0.00101	<i>Glycine max</i>	3.00E-142	<a href="#">XM_003519363.1</a>
<i>UCOESTdown1664</i>	Purine permease 4	3.225	0.00185	<i>Vitis vinifera</i>	1.00E-85	<a href="#">XM_002263417.1</a>
<i>UCOESTdown1665</i>	Metalloendoproteinase 1	3.222	0.00792	<i>Vitis vinifera</i>	3.00E-142	<a href="#">XM_002267262.2</a>
<i>UCOESTdown1666</i>	No homology	3.222	0.00899			
<i>UCOESTdown1667</i>	No homology	3.222	0.0044			
<i>UCOESTdown1668</i>	Serine/threonine-protein phosphatase 7 long form homolog	3.221	0.000974	<i>Vitis vinifera</i>	1.00E-15	<a href="#">XM_003633179.1</a>
<i>UCOESTdown1669</i>	Uncharacterized protein	3.221	0.00139	<i>Vitis vinifera</i>		<a href="#">XM_002282361.2</a>
<i>UCOESTdown1670</i>	No homology	3.220	0.00108			
<i>UCOESTdown1671</i>	Uncharacterized protein	3.219	0.00164	<i>Glycine max</i>	0.0	<a href="#">XR_136298.1</a>
<i>UCOESTdown1672</i>	Uncharacterized protein	3.218	0.00205	<i>Arabidopsis thaliana</i>	2.00E-94	<a href="#">NM_103591.3</a>
<i>UCOESTdown1673</i>	WRKY transcription factor 18	3.215	0.00309	<i>Cucumis sativus</i>	8.00E-73	<a href="#">GU984018.1</a>
<i>UCOESTdown1674</i>	No homology	3.215	0.00199			
<i>UCOESTdown1675</i>	Acyl-CoA-binding domain-containing protein	3.210	0.0259	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003609558.1</a>
<i>UCOESTdown1676</i>	Multidrug and toxin extrusion protein 2	3.209	0.012	<i>Vitis vinifera</i>	8.00E-85	<a href="#">XM_002274772.1</a>
<i>UCOESTdown1677</i>	GDSL esterase/lipase	3.208	0.0439	<i>Medicago truncatula</i>	4.00E-57	<a href="#">XM_003617029.1</a>
<i>UCOESTdown1678</i>	No homology	3.207	0.00748			
<i>UCOESTdown1679</i>	Uncharacterized protein	3.207	0.00178	<i>Glycine max</i>	0.0	<a href="#">XM_003522715.1</a>
<i>UCOESTdown1680</i>	No homology	3.205	0.00702			
<i>UCOESTdown1681</i>	Uncharacterized protein	3.204	0.00305	<i>Glycine max</i>	3.00E-56	<a href="#">XM_003521264.1</a>
<i>UCOESTdown1682</i>	Sugar transporter ERD6-like 7	3.203	0.00122	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_130369.3</a>
<i>UCOESTdown1683</i>	Proton-dependent oligopeptide transport family protein	3.203	0.0343	<i>Arabidopsis lyrata</i>	4.00E-29	<a href="#">XM_002881517.1</a>
<i>UCOESTdown1684</i>	Squalene monooxygenase	3.202	0.022	<i>Glycine max</i>	2.00E-46	<a href="#">XM_002271492.2</a>
<i>UCOESTdown1685</i>	Cytochrome P450	3.201	0.00183	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002519431.1</a>
<i>UCOESTdown1686</i>	Leucine-rich repeat receptor-like protein kinase	3.201	0.00198	<i>Arabidopsis thaliana</i>	0.0	<a href="#">FJ708646.1</a>
<i>UCOESTdown1687</i>	No homology	3.198	0.00151			
<i>UCOESTdown1688</i>	Subtilisin protease	3.197	0.0189	<i>Vitis vinifera</i>	3.00E-153	<a href="#">XM_002282797.1</a>
<i>UCOESTdown1689</i>	Uncharacterized protein	3.197	0.0262	<i>Glycine max</i>	7.00E-26	<a href="#">XR_136470.1</a>
<i>UCOESTdown1690</i>	Phosphoglycerate kinase	3.195	0.00873	<i>Glycine max</i>	0.0	<a href="#">XP_003543912.1</a>
<i>UCOESTdown1691</i>	Purple acid phosphatase (PAP1)	3.193	0.00493	<i>Medicago truncatula</i>	0.0	<a href="#">AY804257.1</a>
<i>UCOESTdown1692</i>	Homeobox-leucine zipper protein	3.191	0.0485	<i>Glycine max</i>	1.00E-64	<a href="#">XM_003530102.1</a>

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<i>UCOESTdown1693</i>	Nephrocystin-3	3.189	0.00318	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002272261.1</a>
<i>UCOESTdown1694</i>	Receptor-like protein kinase	3.186	0.0103	<i>Medicago truncatula</i>	2.00E-33	<a href="#">XP_003592622.1</a>
<i>UCOESTdown1695</i>	Uncharacterized protein	3.186	0.0381	<i>Vitis vinifera</i>	2.00E-70	<a href="#">XM_002268717.2</a>
<i>UCOESTdown1696</i>	No homology	3.184	0.00143			
<i>UCOESTdown1697</i>	No homology	3.184	0.0138			
<i>UCOESTdown1698</i>	Diacylglycerol kinase	3.183	0.00463	<i>Solanum lycopersicum</i>	0.0	<a href="#">AAG23129.1</a>
<i>UCOESTdown1699</i>	No homology	3.181	0.0269			
<i>UCOESTdown1700</i>	1-Cys peroxiredoxin (Per1)	3.178	0.00142	<i>Fagopyrum esculentum</i>	1.00E-111	<a href="#">AF191099.1</a>
<i>UCOESTdown1701</i>	Ribosomal protein L11 methyltransferase	3.176	0.00462	<i>Vitis vinifera</i>	6.00E-115	<a href="#">XM_002282577.2</a>
<i>UCOESTdown1702</i>	CTD small phosphatase	3.170	0.00719	<i>Vitis vinifera</i>	2.00E-91	<a href="#">XM_002264960.2</a>
<i>UCOESTdown1703</i>	FtsZ protein	3.169	0.0014	<i>Medicago truncatula</i>	5.00E-171	<a href="#">XM_003617618.1</a>
<i>UCOESTdown1704</i>	No homology	3.168	0.00092			
<i>UCOESTdown1705</i>	No homology	3.167	0.0144			
<i>UCOESTdown1706</i>	Uncharacterized protein	3.167	0.00341	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002284155.1</a>
<i>UCOESTdown1707</i>	Condensin complex components subunit	3.166	0.00321	<i>Populus trichocarpa</i>	3.00E-49	<a href="#">XM_002304369.1</a>
<i>UCOESTdown1708</i>	No homology	3.166	0.000673			
<i>UCOESTdown1709</i>	Receptor-like protein kinase	3.166	0.00632	<i>Glycine max</i>	0.0	<a href="#">NM_001251105.1</a>
<i>UCOESTdown1710</i>	No homology	3.165	0.000892			
<i>UCOESTdown1711</i>	No homology	3.165	0.0419			
<i>UCOESTdown1712</i>	LRR receptor-like serine/threonine-protein kinase	3.165	0.0313	<i>Glycine max</i>	4.00E-32	<a href="#">XM_003531768.1</a>
<i>UCOESTdown1713</i>	Resistance response protein 206	3.163	0.00265	<i>Vitis vinifera</i>	3.00E-60	<a href="#">XM_002266416.2</a>
<i>UCOESTdown1714</i>	11S globulin precursor isoform 3B	3.159	0.000872	<i>Ficus pumila</i>	2.00E-141	<a href="#">EF091698.1</a>
<i>UCOESTdown1715</i>	Uncharacterized protein	3.158	0.000756	<i>Glycine max</i>	6.00E-38	<a href="#">XM_003534864.1</a>
<i>UCOESTdown1716</i>	Uncharacterized protein	3.157	0.00316	<i>Vitis vinifera</i>	1.00E-117	<a href="#">XM_002267468.2</a>
<i>UCOESTdown1717</i>	Aquaporin, MIP family, TIP subfamily	3.156	0.00784	<i>Populus trichocarpa</i>	2.00E-121	<a href="#">XM_002309512.1</a>
<i>UCOESTdown1718</i>	Seed biotinylated protein 68 kDa isoform mRNA, complete cds	3.155	0.00308	<i>Glycine max</i>	4.00E-41	<a href="#">GQ168590.1</a>
<i>UCOESTdown1719</i>	Uncharacterized protein	3.155	0.0227	<i>Vitis vinifera</i>	3.00E-130	<a href="#">XM_002281397.2</a>
<i>UCOESTdown1720</i>	Uncharacterized protein	3.155	0.0227	<i>Vitis vinifera</i>	3.00E-130	<a href="#">XM_002281397.2</a>
<i>UCOESTdown1721</i>	Uncharacterized protein	3.154	0.000782	<i>Glycine max</i>	0.0	<a href="#">XM_003543523.1</a>

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<i>UCOESTdown1722</i>	Uncharacterized protein	3.154	0.000821	<i>Vitis vinifera</i>	2.00E-100	<a href="#">XM_002277277.2</a>
<i>UCOESTdown1723</i>	No homology	3.152	0.0197			
<i>UCOESTdown1724</i>	No homology	3.152	0.00157			
<i>UCOESTdown1725</i>	Uncharacterized protein	3.152	0.00417	<i>Vitis vinifera</i>	4.00E-21	<a href="#">XM_002276392.1</a>
<i>UCOESTdown1726</i>	NAC transcription factor 145	3.151	0.0268	<i>Populus trichocarpa</i>	3.00E-13	<a href="#">XM_002323167.1</a>
<i>UCOESTdown1727</i>	Tir-nbs-lrr resistance protein	3.151	0.00359	<i>Populus trichocarpa</i>	4.00E-102	<a href="#">XM_002333364.1</a>
<i>UCOESTdown1728</i>	No homology	3.150	0.00209			
<i>UCOESTdown1729</i>	Universal stress protein A	3.150	0.0121	<i>Vitis vinifera</i>	1.00E-47	<a href="#">XM_002275827.1</a>
<i>UCOESTdown1730</i>	C3HL domain class transcription factor	3.148	0.0455	<i>Malus x domestica</i>	8.00E-112	<a href="#">HM122517.1</a>
<i>UCOESTdown1731</i>	31 kDa Ribonucleoprotein	3.148	0.00339	<i>Vitis vinifera</i>	1.00E-98	<a href="#">XM_002270197.2</a>
<i>UCOESTdown1732</i>	Serine carboxypeptidase 50	3.146	0.00106	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002280635.1</a>
<i>UCOESTdown1733</i>	No homology	3.145	0.0493			
<i>UCOESTdown1734</i>	No homology	3.144	0.00392			
<i>UCOESTdown1735</i>	MLO protein 13	3.141	0.00574	<i>Vitis vinifera</i>	1.00E-93	<a href="#">XM_002266891.2</a>
<i>UCOESTdown1736</i>	Wall-associated receptor kinase	3.141	0.00355	<i>Medicago truncatula</i>	8.00E-113	<a href="#">XM_003607133.1</a>
<i>UCOESTdown1737</i>	Myrosinase-binding protein	3.139	0.0131	<i>Medicago truncatula</i>	2.00E-22	<a href="#">XM_003615649.1</a>
<i>UCOESTdown1738</i>	Uncharacterized protein	3.139	0.0158	<i>Vitis vinifera</i>	6.00E-104	<a href="#">XM_003631923.1</a>
<i>UCOESTdown1739</i>	No homology	3.135	0.00514			
<i>UCOESTdown1740</i>	Uncharacterized protein	3.131	0.0401	<i>Vitis vinifera</i>	4.00E-29	<a href="#">XM_002272606.1</a>
<i>UCOESTdown1741</i>	BZIP transcription factor bZIP39	3.128	0.00126	<i>Medicago truncatula</i>	3.00E-52	<a href="#">XM_003625733.1</a>
<i>UCOESTdown1742</i>	Lactosylceramide 4-alpha-galactosyltransferase	3.127	0.00618	<i>Medicago truncatula</i>	1.00E-128	<a href="#">XM_003593501.1</a>
<i>UCOESTdown1743</i>	Sex determination protein tasselseed-2	3.123	0.0239	<i>Glycine max</i>	1.00E-136	<a href="#">XM_003521480.1</a>
<i>UCOESTdown1744</i>	Serine carboxypeptidase 45	3.119	0.0138	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002268136.1</a>
<i>UCOESTdown1745</i>	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	3.119	0.00217	<i>Glycine max</i>	0.0	<a href="#">XM_003549502.1</a>
<i>UCOESTdown1746</i>	LOB domain-containing protein 27	3.112	0.023	<i>Vitis vinifera</i>	1.00E-64	<a href="#">XM_003634222.1</a>
<i>UCOESTdown1747</i>	Mitogen-activated protein kinase kinase kinase 2	3.110	0.006	<i>Vitis vinifera</i>	7.00E-130	<a href="#">XP_003634728.1</a>
<i>UCOESTdown1748</i>	No homology	3.109	0.00148			
<i>UCOESTdown1749</i>	DNA replication licensing factor MCM6	3.108	0.0157	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003625530.1</a>
<i>UCOESTdown1750</i>	Myrcene synthase	3.108	0.0168	<i>Vitis vinifera</i>	7.00E-144	<a href="#">XM_002266983.2</a>
<i>UCOESTdown1751</i>	MYB transcription factor	3.105	0.00174	<i>Arabidopsis thaliana</i>	2.00E-53	<a href="#">AY519620.1</a>
<i>UCOESTdown1752</i>	Uncharacterized protein	3.105	0.00916	<i>Glycine max</i>	8.00E-67	<a href="#">XP_003517842.1</a>

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<i>UCOESTdown1753</i>	ABC transporter G family member 9	3.104	0.0159	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002281913.1</a>
<i>UCOESTdown1754</i>	No homology	3.103	0.00104			
<i>UCOESTdown1755</i>	Cytochrome P450	3.101	0.046	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002320035.1</a>
<i>UCOESTdown1756</i>	Uncharacterized protein	3.098	0.00354	<i>Vitis vinifera</i>	8.00E-70	<a href="#">XM_002267881.1</a>
<i>UCOESTdown1757</i>	Uncharacterized protein	3.098	0.00232	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003634318.1</a>
<i>UCOESTdown1758</i>	No homology	3.096	0.00376			
<i>UCOESTdown1759</i>	No homology	3.096	0.0182			
<i>UCOESTdown1760</i>	No homology	3.096	0.000744			
<i>UCOESTdown1761</i>	Calcium-binding protein CML31	3.096	0.00175	<i>Glycine max</i>	5.00E-44	<a href="#">XM_003525652.1</a>
<i>UCOESTdown1762</i>	Uncharacterized protein	3.096	0.00246	<i>Glycine max</i>	3.00E-102	<a href="#">XM_003519142.1</a>
<i>UCOESTdown1763</i>	Uncharacterized protein	3.095	0.0432	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003634318.1</a>
<i>UCOESTdown1764</i>	Uncharacterized protein	3.093	0.0279	<i>Vitis vinifera</i>	2.00E-18	<a href="#">XM_002284091.2</a>
<i>UCOESTdown1765</i>	No homology	3.092	0.000812			
<i>UCOESTdown1766</i>	Serine/threonine-protein kinase	3.091	0.0105	<i>Arabidopsis thaliana</i>	1.00E-112	<a href="#">NP_171661.1</a>
<i>UCOESTdown1767</i>	Uncharacterized protein	3.091	0.00704	<i>Glycine max</i>	4.00E-122	<a href="#">XM_003540761.1</a>
<i>UCOESTdown1768</i>	Cytochrome P450	3.090	0.0317	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002313726.1</a>
<i>UCOESTdown1769</i>	Self-incompatibility S1 family protein	3.089	0.00219	<i>Arabidopsis thaliana</i>	8.00E-17	<a href="#">NM_121244.1</a>
<i>UCOESTdown1770</i>	Epimerase family protein slr1223	3.088	0.0266	<i>Glycine max</i>	7.00E-162	<a href="#">XM_003540912.1</a>
<i>UCOESTdown1771</i>	Uncharacterized protein	3.088	0.0033	<i>Vitis vinifera</i>	7.00E-49	<a href="#">XM_002282516.2</a>
<i>UCOESTdown1772</i>	Calcineurin-like metallo-phosphoesterase	3.086	0.00177	<i>Arabidopsis thaliana</i>	6.00E-164	<a href="#">NM_100574.4</a>
<i>UCOESTdown1773</i>	No homology	3.085	0.0455			
<i>UCOESTdown1774</i>	Transcription factor SPEECHLESS	3.083	0.0306	<i>Arabidopsis thaliana</i>	7.00E-57	<a href="#">NM_124700.2</a>
<i>UCOESTdown1775</i>	Lacase/diphenol oxidase	3.083	0.00905	<i>Castanea mollissima</i>	0.0	<a href="#">FJ231469.1</a>
<i>UCOESTdown1776</i>	Membrane-associated kinase regulator 6	3.083	0.00216	<i>Glycine max</i>	8.00E-44	<a href="#">NM_001254065.1</a>
<i>UCOESTdown1777</i>	No homology	3.079	0.00569			
<i>UCOESTdown1778</i>	Uncharacterized protein	3.074	0.00224	<i>Glycine max</i>	2.00E-91	<a href="#">XM_003556652.1</a>
<i>UCOESTdown1779</i>	21 kDa protein	3.073	0.00631	<i>Vitis vinifera</i>	2.00E-69	<a href="#">XM_002263992.2</a>
<i>UCOESTdown1780</i>	No homology	3.072	0.00432			
<i>UCOESTdown1781</i>	E3 ubiquitin-protein ligase	3.071	0.00649	<i>Vitis vinifera</i>	6.00E-48	<a href="#">XM_002271615.1</a>
<i>UCOESTdown1782</i>	LysM type receptor kinase	3.065	0.0455	<i>Sesbania rostrata</i>	0.0	<a href="#">EF408056.2</a>
<i>UCOESTdown1783</i>	Double-stranded RNA-binding protein 5	3.064	0.000914	<i>Vitis vinifera</i>	1.00E-99	<a href="#">XM_002275016.2</a>
<i>UCOESTdown1784</i>	6-Phosphofructokinase 3	3.063	0.0015	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002283238.1</a>

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<i>UCOESTdown1785</i>	Galactinol--sucrose galactosyltransferase 6	3.063	0.00373	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002285382.2</a>
<i>UCOESTdown1786</i>	Uncharacterized protein	3.063	0.00723	<i>Glycine max</i>	6.00E-85	<a href="#">XM_003525708.1</a>
<i>UCOESTdown1787</i>	Glutamyl-tRNA reductase	3.060	0.00156	<i>Cucumis sativus</i>	0.0	<a href="#">D50407.1</a>
<i>UCOESTdown1788</i>	Glutathione S-transferase	3.056	0.00779	<i>Nicotiana tabacum</i>	2.00E-34	<a href="#">D10524.1</a>
<i>UCOESTdown1789</i>	Leucine-rich repeat receptor-like protein kinase	3.055	0.00448	<i>Arabidopsis thaliana</i>	0.0	<a href="#">FJ708723.1</a>
<i>UCOESTdown1790</i>	Calcium-binding protein CML31	3.054	0.0009	<i>Glycine max</i>	4.00E-63	<a href="#">XM_003553870.1</a>
<i>UCOESTdown1791</i>	GDSL esterase/lipase	3.052	0.00453	<i>Medicago truncatula</i>	6.00E-113	<a href="#">XM_003528683.1</a>
<i>UCOESTdown1792</i>	F-box protein	3.051	0.0313	<i>Vitis vinifera</i>	3.00E-50	<a href="#">XM_002279318.2</a>
<i>UCOESTdown1793</i>	70 kDa Heat shock protein (hsp70)	3.051	0.0153	<i>Capparis spinosa</i>	5.00E-46	<a href="#">EU574936.1</a>
<i>UCOESTdown1794</i>	Adenosine 3'-phospho 5'-phosphosulfate transporter	3.050	0.00267	<i>Medicago truncatula</i>	1.00E-178	<a href="#">XM_003623801.1</a>
<i>UCOESTdown1795</i>	MYB transcription factor 86 (MYB86)	3.049	0.00655	<i>Arabidopsis thaliana</i>	2.00E-75	<a href="#">NM_180548.3</a>
<i>UCOESTdown1796</i>	Uncharacterized protein	3.047	0.00583	<i>Vitis vinifera</i>	1.00E-94	<a href="#">XP_002271355.2</a>
<i>UCOESTdown1797</i>	No homology	3.046	0.0476			
<i>UCOESTdown1798</i>	No homology	3.044	0.0436			
<i>UCOESTdown1799</i>	ZIP transcription factor bZIP132	3.038	0.00695	<i>Glycine max</i>	1.00E-85	<a href="#">NM_001251070.1</a>
<i>UCOESTdown1800</i>	Aquaporin PIP1-3	3.038	0.00594	<i>Vitis vinifera</i>	7.00E-115	<a href="#">XM_002276569.2</a>
<i>UCOESTdown1801</i>	kinesin-4	3.035	0.00895	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002278567.2</a>
<i>UCOESTdown1802</i>	bHLH transcription factor	3.034	0.0133	<i>Arabidopsis thaliana</i>	1.00E-52	<a href="#">NM_100451.3</a>
<i>UCOESTdown1803</i>	No homology	3.031	0.00125			
<i>UCOESTdown1804</i>	Glutamate carboxypeptidase 2	3.025	0.013	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002267239.2</a>
<i>UCOESTdown1805</i>	Cleavage stimulation factor 64	3.025	0.0154	<i>Arabidopsis thaliana</i>	9.00E-51	<a href="#">AF515695.1</a>
<i>UCOESTdown1806</i>	Oleosin 16 kDa	3.024	0.00231	<i>Vitis vinifera</i>	4.00E-53	<a href="#">XM_002273206.1</a>
<i>UCOESTdown1807</i>	Uncharacterized protein	3.017	0.00581	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002275160.2</a>
<i>UCOESTdown1808</i>	No homology	3.014	0.019			
<i>UCOESTdown1809</i>	Serine/threonine-protein kinase	3.013	0.000948	<i>Cucumis melo</i>	0.0	<a href="#">ADN33721.1</a>
<i>UCOESTdown1810</i>	No homology	3.010	0.0172			
<i>UCOESTdown1811</i>	WUSCHEL-related homeobox 3	3.009	0.00705	<i>Vitis vinifera</i>	1.00E-36	<a href="#">XM_002281671.1</a>
<i>UCOESTdown1812</i>	Microtubule-associated protein 70-5	3.006	0.00408	<i>Vitis vinifera</i>	9.00E-161	<a href="#">XM_002267902.2</a>
<i>UCOESTdown1813</i>	Glutamate dehydrogenase	3.005	0.00076	<i>Actinidia chinensis</i>	0.0	<a href="#">EF063568.1</a>
<i>UCOESTdown1814</i>	Hydroxyproline-rich glycoprotein family protein	3.000	0.00121	<i>Arabidopsis thaliana</i>	4.00E-38	<a href="#">NM_001125376.1</a>
<i>UCOESTdown1815</i>	Histidine phosphotransfer protein	2.999	0.0285	<i>Glycine max</i>	4.00E-52	<a href="#">XM_003556446.1</a>

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<i>UCOESTdown1816</i>	No homology	2.998	0.0147			
<i>UCOESTdown1817</i>	No homology	2.998	0.0294			
<i>UCOESTdown1818</i>	No homology	2.997	0.0048			
<i>UCOESTdown1819</i>	Adenosine 3'-phospho 5'-phosphosulfate transporter 2	2.993	0.0309	<i>Vitis vinifera</i>	2.00E-179	<a href="#">XM_002273054.2</a>
<i>UCOESTdown1820</i>	Uncharacterized protein	2.993	0.000912	<i>Glycine max</i>	0.0	<a href="#">XM_003535923.1</a>
<i>UCOESTdown1821</i>	Protease Do-like 8	2.991	0.0077	<i>Vitis vinifera</i>	3.00E-82	<a href="#">XM_002278063.2</a>
<i>UCOESTdown1822</i>	Cysteine/histidine-rich C1 domain-containing protein	2.991	0.0404	<i>Arabidopsis thaliana</i>	4.00E-77	<a href="#">NP_200802.1</a>
<i>UCOESTdown1823</i>	50S ribosomal protein L9	2.990	0.00259	<i>Arabidopsis thaliana</i>	2.00E-73	<a href="#">NM_114358.3</a>
<i>UCOESTdown1824</i>	Leucine-rich repeat receptor kinase	2.988	0.00718	<i>Arabidopsis thaliana</i>	0.0	<a href="#">FJ708810.1</a>
<i>UCOESTdown1825</i>	Pentatricopeptide repeat-containing protein	2.987	0.0108	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002269158.1</a>
<i>UCOESTdown1826</i>	C2 and GRAM domain-containing protein	2.987	0.00185	<i>Glycine max</i>	0.0	<a href="#">XP_003546208.1</a>
<i>UCOESTdown1827</i>	Endoglucanase 11	2.986	0.00129	<i>Glycine max</i>	0.0	<a href="#">XM_003519406.1</a>
<i>UCOESTdown1828</i>	No homology	2.983	0.0063			
<i>UCOESTdown1829</i>	bHLH transcription factor 93	2.979	0.00853	<i>Vitis vinifera</i>	1.00E-104	<a href="#">XM_002285559.1</a>
<i>UCOESTdown1830</i>	Uncharacterized protein	2.979	0.0181	<i>Vitis vinifera</i>	4.00E-49	<a href="#">XM_002282516.2</a>
<i>UCOESTdown1831</i>	MADS transcription factor 19	2.978	0.0025	<i>Malus x domestica</i>	3.00E-114	<a href="#">HM122602.1</a>
<i>UCOESTdown1832</i>	Uncharacterized protein	2.978	0.00381	<i>Glycine max</i>	1.00E-54	<a href="#">XM_003535705.1</a>
<i>UCOESTdown1833</i>	FKBP-type peptidyl-prolyl cis-trans isomerase 6	2.973	0.00841	<i>Vitis vinifera</i>	6.00E-104	<a href="#">XM_002274921.1</a>
<i>UCOESTdown1834</i>	F-box protein	2.971	0.0195	<i>Populus trichocarpa</i>	3.00E-174	<a href="#">XM_002308468.1</a>
<i>UCOESTdown1835</i>	No homology	2.970	0.000653			
<i>UCOESTdown1836</i>	Protein SRG1	2.969	0.00079	<i>Vitis vinifera</i>	1.00E-164	<a href="#">XM_002268252.1</a>
<i>UCOESTdown1837</i>	No homology	2.969	0.0069			
<i>UCOESTdown1838</i>	Uncharacterized protein	2.969	0.0111	<i>Glycine max</i>	1.00E-05	<a href="#">XM_003538587.1</a>
<i>UCOESTdown1839</i>	Subtilisin protease SDD1	2.968	0.0031	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002275435.1</a>
<i>UCOESTdown1840</i>	F-box/LRR-repeat protein	2.968	0.0143	<i>Arabidopsis thaliana</i>	3.00E-13	<a href="#">NM_123527.1</a>
<i>UCOESTdown1841</i>	Uncharacterized protein	2.968	0.00126	<i>Vitis vinifera</i>	6.00E-113	<a href="#">XM_002269129.2</a>
<i>UCOESTdown1842</i>	WRKY transcription factor 17	2.967	0.0121	<i>Malus x domestica</i>	3.00E-103	<a href="#">HM122720.1</a>
<i>UCOESTdown1843</i>	Expansin	2.964	0.00912	<i>Rosa hybrid</i>	9.00E-67	<a href="#">AB370117.1</a>
<i>UCOESTdown1844</i>	No homology	2.964	0.0182			
<i>UCOESTdown1845</i>	Uncharacterized protein	2.964	0.0134	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002278195.1</a>

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<i>UCOESTdown1846</i>	Cc-nbs-lrr resistance protein	2.962	0.0232	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002332915.1</a>
<i>UCOESTdown1847</i>	No homology	2.961	0.0119			
<i>UCOESTdown1848</i>	No homology	2.961	0.00129			
<i>UCOESTdown1849</i>	Long-chain-alcohol oxidase FAO1	2.961	0.0434	<i>Glycine max</i>	0.0	<a href="#">XM_003535383.1</a>
<i>UCOESTdown1850</i>	Oleosin 15.8 kDa	2.960	0.0191	<i>Theobroma cacao</i>	4.00E-23	<a href="#">AF466103.1</a>
<i>UCOESTdown1851</i>	MYB transcription factor 16 (MYB16)	2.956	0.00374	<i>Malus x domestica</i>	3.00E-120	<a href="#">HM122617.1</a>
<i>UCOESTdown1852</i>	Disease resistance protein	2.956	0.0153	<i>Vitis vinifera</i>	0.0	<a href="#">XR_139763.1</a>
<i>UCOESTdown1853</i>	No homology	2.954	0.0278			
<i>UCOESTdown1854</i>	No homology	2.952	0.0271			
<i>UCOESTdown1855</i>	Formin protein 11	2.95	0.0066	<i>Glycine max</i>	0.0	<a href="#">XM_003555563.1</a>
<i>UCOESTdown1856</i>	Epoxide hydrolase 3	2.950	0.038	<i>Vitis vinifera</i>	1.00E-106	<a href="#">XR_077789.1</a>
<i>UCOESTdown1857</i>	dCTP pyrophosphatase 1	2.947	0.00196	<i>Vitis vinifera</i>	2.00E-44	<a href="#">XM_002266445.2</a>
<i>UCOESTdown1858</i>	Calcium-transporting ATPase 12	2.947	0.0096	<i>Vitis vinifera</i>	1.00E-167	<a href="#">XM_002270863.2</a>
<i>UCOESTdown1859</i>	ZF-HD homeobox protein	2.942	0.0426	<i>Vitis vinifera</i>	9.00E-66	<a href="#">XM_002285673.1</a>
<i>UCOESTdown1860</i>	Outward-rectifying potassium channel KCO1	2.942	0.0013	<i>Eucalyptus camaldulensis</i>	7.00E-136	<a href="#">AF175507.1</a>
<i>UCOESTdown1861</i>	Wall-associated receptor kinase 2	2.941	0.00319	<i>Vitis vinifera</i>	0.0	<a href="#">XP_002277331.2</a>
<i>UCOESTdown1862</i>	Snakin-2	2.934	0.00174	<i>Vitis vinifera</i>	1.00E-29	<a href="#">XM_003634205.1</a>
<i>UCOESTdown1863</i>	No homology	2.927	0.0214			
<i>UCOESTdown1864</i>	Uncharacterized protein	2.925	0.00149	<i>Vitis vinifera</i>	1.00E-16	<a href="#">XM_003635159.1</a>
<i>UCOESTdown1865</i>	WD repeat-containing protein 44	2.922	0.00429	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002275461.1</a>
<i>UCOESTdown1866</i>	Protease inhibitor/seed storage/lipid transfer protein family protein	2.916	0.00505	<i>Arabidopsis lyrata</i>	5.00E-36	<a href="#">XM_002883327.1</a>
<i>UCOESTdown1867</i>	Receptor-like protein kinase THESEUS 1	2.913	0.00574	<i>Vitis vinifera</i>	1.00E-116	<a href="#">XM_002285107.2</a>
<i>UCOESTdown1868</i>	No homology	2.912	0.0321			
<i>UCOESTdown1869</i>	No homology	2.912	0.0241			
<i>UCOESTdown1870</i>	Uncharacterized protein	2.912	0.000923	<i>Glycine max</i>	6.00E-61	<a href="#">XM_003536347.1</a>
<i>UCOESTdown1871</i>	F-box protein	2.911	0.0067	<i>Medicago truncatula</i>	6.00E-15	<a href="#">XM_003604989.1</a>
<i>UCOESTdown1872</i>	Uncharacterized protein	2.910	0.0123	<i>Glycine max</i>	6.00E-34	<a href="#">NM_001251724.1</a>
<i>UCOESTdown1873</i>	RNA-binding protein	2.909	0.0158	<i>Medicago truncatula</i>	3.00E-60	<a href="#">XM_003615083.1</a>
<i>UCOESTdown1874</i>	Aspartic proteinase nepenthesin-2	2.905	0.00321	<i>Glycine max</i>	2.00E-165	<a href="#">XM_003520664.1</a>
<i>UCOESTdown1875</i>	No homology	2.905	0.0386			
<i>UCOESTdown1876</i>	Uncharacterized protein	2.901	0.00205	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002270768.2</a>
<i>UCOESTdown1877</i>	No homology	2.900	0.00478			

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<i>UCOESTdown1878</i>	Uncharacterized protein	2.899	0.0023	<i>Glycine max</i>	2.00E-100	<a href="#">XM_003518596.1</a>
<i>UCOESTdown1879</i>	5'-AMP-activated protein kinase	2.890	0.00409	<i>Arabidopsis thaliana</i>	6.00E-76	<a href="#">NM_120421.2</a>
<i>UCOESTdown1880</i>	Uncharacterized protein	2.889	0.0344	<i>Sorghum bicolor</i>	2.00E-18	<a href="#">XM_002448855.1</a>
<i>UCOESTdown1881</i>	Cytochrome P450	2.888	0.00808	<i>Nicotiana tabacum</i>	0.0	<a href="#">AF092916.1</a>
<i>UCOESTdown1882</i>	Leucine-rich repeat receptor-like protein kinase	2.888	0.023	<i>Arabidopsis thaliana</i>	0.0	<a href="#">FJ708712.1</a>
<i>UCOESTdown1883</i>	Cullin 1 protein C (CUL1-C)	2.887	0.00107	<i>Petunia integrifolia</i>	6.00E-63	<a href="#">DQ250016.1</a>
<i>UCOESTdown1884</i>	Uncharacterized protein	2.887	0.00912	<i>Glycine max</i>	1.00E-09	<a href="#">XM_003552591.1</a>
<i>UCOESTdown1885</i>	No homology	2.885	0.0273			
<i>UCOESTdown1886</i>	Cinnamoyl-CoA reductase 1 (CCR1)	2.885	0.000177	<i>Betula platyphylla</i>	8.00E-107	<a href="#">JF732912.1</a>
<i>UCOESTdown1887</i>	No homology	2.884	0.0229			
<i>UCOESTdown1888</i>	No homology	2.880	0.0187			
<i>UCOESTdown1889</i>	Wall-associated receptor kinase 2	2.880	0.00462	<i>Vitis vinifera</i>	6.00E-178	<a href="#">XM_002277295.2</a>
<i>UCOESTdown1890</i>	Microtubule-associated protein MAP65-1a	2.877	0.00192	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003617595.1</a>
<i>UCOESTdown1891</i>	LysM type receptor kinase	2.877	0.0307	<i>Lotus japonicus</i>	2.00E-171	<a href="#">AB503692.1</a>
<i>UCOESTdown1892</i>	Calpain-type cysteine protease (DEK1)	2.876	0.0205	<i>Arabidopsis thaliana</i>	1.00E-93	<a href="#">NM_104411.3</a>
<i>UCOESTdown1893</i>	Uncharacterized protein	2.876	0.00409	<i>Vitis vinifera</i>	2.00E-161	<a href="#">XM_002265116.2</a>
<i>UCOESTdown1894</i>	Ubiquitin-like protein SMT3	2.875	0.00103	<i>Zea mays</i>	1.00E-49	<a href="#">EU954748.1</a>
<i>UCOESTdown1895</i>	Myristoyl-acyl carrier protein thioesterase	2.873	0.00441	<i>Medicago truncatula</i>	4.00E-138	<a href="#">XM_003602741.1</a>
<i>UCOESTdown1896</i>	N-acetyltransferase	2.871	0.0494	<i>Medicago truncatula</i>	3.00E-80	<a href="#">XM_003626329.1</a>
<i>UCOESTdown1897</i>	Uncharacterized protein	2.869	0.0109	<i>Vitis vinifera</i>	0.0	<a href="#">XP_002284392.2</a>
<i>UCOESTdown1898</i>	Exonuclease 1	2.866	0.0115	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002269381.2</a>
<i>UCOESTdown1899</i>	Uncharacterized protein	2.866	0.00221	<i>Glycine max</i>	1.00E-37	<a href="#">XM_003530515.1</a>
<i>UCOESTdown1900</i>	Uncharacterized protein	2.865	0.00145	<i>Glycine max</i>	9.00E-145	<a href="#">XM_003544755.1</a>
<i>UCOESTdown1901</i>	Uncharacterized protein	2.864	0.00474	<i>Glycine max</i>	0.0	<a href="#">XM_003550994.1</a>
<i>UCOESTdown1902</i>	No homology	2.863	0.0156			
<i>UCOESTdown1903</i>	No homology	2.862	0.00113			
<i>UCOESTdown1904</i>	No homology	2.859	0.00477			
<i>UCOESTdown1905</i>	No homology	2.859	0.0242			
<i>UCOESTdown1906</i>	DNA replication complex GINS protein SLD5	2.857	0.0117	<i>Glycine max</i>	1.00E-80	<a href="#">XM_003531576.1</a>
<i>UCOESTdown1907</i>	Uncharacterized protein	2.856	0.02	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002271134.1</a>
<i>UCOESTdown1908</i>	Lysine histidine transporter 1	2.855	0.00222	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_180778.3</a>

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<i>UCOESTdown1909</i>	No homology	2.854	0.0452			
<i>UCOESTdown1910</i>	Calcium-transporting ATPase	2.854	0.00205	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002264549.2</a>
<i>UCOESTdown1911</i>	Uncharacterized protein	2.854	0.00131	<i>Populus trichocarpa</i>	5.00E-150	<a href="#">AC210380.1</a>
<i>UCOESTdown1912</i>	No homology	2.851	0.0127			
<i>UCOESTdown1913</i>	Uncharacterized protein	2.851	0.00815	<i>Vitis vinifera</i>	7.00E-133	<a href="#">XM_002268416.1</a>
<i>UCOESTdown1914</i>	No homology	2.850	0.00829			
<i>UCOESTdown1915</i>	Uncharacterized protein	2.848	0.019	<i>Medicago truncatula</i>	8.00E-09	<a href="#">XM_003624882.1</a>
<i>UCOESTdown1916</i>	Xyloglucan glycosyltransferase 12	2.845	0.0092	<i>Glycine max</i>	0.0	<a href="#">XM_003544452.1</a>
<i>UCOESTdown1917</i>	FtsH protease (ftsH6)	2.842	0.000985	<i>Solanum lycopersicum</i>	0.0	<a href="#">NM_001247262.1</a>
<i>UCOESTdown1918</i>	No homology	2.840	0.00532			
<i>UCOESTdown1919</i>	Leucine-rich repeat receptor-like protein kinase	2.840	0.0499	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_111248.4</a>
<i>UCOESTdown1920</i>	Uncharacterized protein	2.839	0.00174	<i>Vitis vinifera</i>	4.00E-17	<a href="#">XM_002281014.1</a>
<i>UCOESTdown1921</i>	Chloroplastic group IIA intron splicing facilitator CRS1	2.836	0.00539	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002275475.1</a>
<i>UCOESTdown1922</i>	Dynein light chain	2.834	0.0428	<i>Medicago truncatula</i>	6.00E-49	<a href="#">XM_003609239.1</a>
<i>UCOESTdown1923</i>	Clavamate synthase	2.833	0.0366	<i>Glycine max</i>	4.00E-174	<a href="#">XM_003516813.1</a>
<i>UCOESTdown1924</i>	Uncharacterized protein	2.833	0.0144	<i>Vitis vinifera</i>	3.00E-103	<a href="#">XM_003634894.1</a>
<i>UCOESTdown1925</i>	LRR receptor-like serine/threonine-protein kinase	2.832	0.0019	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002278356.1</a>
<i>UCOESTdown1926</i>	Disease resistance protein PI-PLC X-box domain-containing	2.830	0.0234	<i>Arabidopsis thaliana</i>	7.00E-60	<a href="#">NM_104598.2</a>
<i>UCOESTdown1927</i>	protein DDB_G0293730- (LOC100258966), mRNA	2.829	0.000783	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002277109.2</a>
<i>UCOESTdown1928</i>	Neutral ceramidase	2.829	0.00185	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003601253.1</a>
<i>UCOESTdown1929</i>	Zinc finger CCCH domain-containing protein	2.827	0.0472	<i>Medicago truncatula</i>	5.00E-78	<a href="#">XM_003600565.1</a>
<i>UCOESTdown1930</i>	DnaJ-like zinc-finger protein	2.826	0.0298	<i>Medicago truncatula</i>	3.00E-56	<a href="#">XM_003592750.1</a>
<i>UCOESTdown1931</i>	No homology	2.823	0.0274			
<i>UCOESTdown1932</i>	Uncharacterized protein	2.822	0.00155	<i>Vitis vinifera</i>	4.00E-66	<a href="#">XM_002276593.1</a>
<i>UCOESTdown1933</i>	Uncharacterized protein	2.820	0.000854	<i>Glycine max</i>	3.00E-18	<a href="#">XM_003550085.1</a>
<i>UCOESTdown1934</i>	Uncharacterized protein	2.818	0.0181	<i>Vitis vinifera</i>	2.00E-148	<a href="#">XM_002273077.2</a>
<i>UCOESTdown1935</i>	Cysteine-rich receptor- protein kinase 29	2.817	0.00133	<i>Glycine max</i>	0.0	<a href="#">XM_003535620.1</a>

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<i>UCOESTdown1936</i>	Disease resistance RPP8	2.815	0.0291	<i>Medicago truncatula</i>	4.00E-148	<a href="#">XM_003595076.1</a>
<i>UCOESTdown1937</i>	Myosin heavy chain-related protein	2.814	0.00278	<i>Arabidopsis thaliana</i>	8.00E-70	<a href="#">NM_105009.2</a>
<i>UCOESTdown1938</i>	Uncharacterized protein	2.813	0.000863	<i>Glycine max</i>	6.00E-66	<a href="#">XM_003538413.1</a>
<i>UCOESTdown1939</i>	Peroxidase 73	2.812	0.00755	<i>Vitis vinifera</i>	9.00E-156	<a href="#">XM_002284242.2</a>
<i>UCOESTdown1940</i>	Ferrochelatase	2.812	0.000813	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003630368.1</a>
<i>UCOESTdown1941</i>	2-Oxoglutarate/Fe(II)-dependent dioxxygenase	2.812	0.00137	<i>Vitis vinifera</i>	1.00E-117	<a href="#">XM_002265780.1</a>
<i>UCOESTdown1942</i>	Uncharacterized protein	2.812	0.00122	<i>Fragaria x ananassa</i>	3.00E-80	<a href="#">AY695666.1</a>
<i>UCOESTdown1943</i>	AP2-like ethylene-responsive transcription factor AIL5	2.811	0.00294	<i>Arabidopsis thaliana</i>	1.00E-108	<a href="#">NM_125122.3</a>
<i>UCOESTdown1944</i>	Ring finger and CHY zinc finger domain-containing protein 1	2.810	0.0279	<i>Arabidopsis thaliana</i>	1.00E-78	<a href="#">NM_116162.5</a>
<i>UCOESTdown1945</i>	Uncharacterized protein	2.809	0.0195	<i>Glycine max</i>	2.00E-83	<a href="#">XM_003539944.1</a>
<i>UCOESTdown1946</i>	Quinohaemoprotein ethanol dehydrogenase type-1	2.807	0.0441	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003621104.1</a>
<i>UCOESTdown1947</i>	Reticuline oxidase	2.806	0.0162	<i>Vitis vinifera</i>	4.00E-46	<a href="#">XM_002277274.1</a>
<i>UCOESTdown1948</i>	18.6 kDa Heat-shock protein	2.802	0.0209	<i>Helianthus annuus</i>	2.00E-25	<a href="#">U46544.1</a>
<i>UCOESTdown1949</i>	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex	2.800	0.00143	<i>Vitis vinifera</i>	6.00E-08	<a href="#">XM_002270562.2</a>
<i>UCOESTdown1950</i>	Mitogen-activated protein kinase 1	2.797	0.00579	<i>Medicago sativa</i>	5.00E-134	<a href="#">CAE00640.1</a>
<i>UCOESTdown1951</i>	No homology	2.796	0.00432			
<i>UCOESTdown1952</i>	Lectin receptor kinase	2.795	0.00504	<i>Nicotiana benthamiana</i>	0.0	<a href="#">AB247455.1</a>
<i>UCOESTdown1953</i>	F-box protein	2.795	0.0324	<i>Vitis vinifera</i>	2.00E-146	<a href="#">XM_003632707.1</a>
<i>UCOESTdown1954</i>	Dehydroascorbate reductase	2.793	0.00289	<i>Fragaria x ananassa</i>	9.00E-108	<a href="#">HM045477.1</a>
<i>UCOESTdown1955</i>	Uncharacterized protein	2.791	0.00867	<i>Arabidopsis thaliana</i>	2.00E-108	<a href="#">NM_127678.3</a>
<i>UCOESTdown1956</i>	Uncharacterized protein	2.791	0.00867	<i>Arabidopsis thaliana</i>	2.00E-108	<a href="#">NM_127678.3</a>
<i>UCOESTdown1957</i>	Uncharacterized protein	2.791	0.00116	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002276592.1</a>
<i>UCOESTdown1958</i>	AP2-like ethylene-responsive transcription factor	2.787	0.00641	<i>Medicago truncatula</i>	3.00E-176	<a href="#">XM_003625090.1</a>
<i>UCOESTdown1959</i>	Uncharacterized protein	2.786	0.0187	<i>Arabidopsis thaliana</i>	4.00E-13	<a href="#">AK227511.1</a>
<i>UCOESTdown1960</i>	Homeobox-leucine zipper protein REVOLUTA (REV)	2.785	0.0137	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_125462.3</a>
<i>UCOESTdown1961</i>	Disease resistance protein	2.783	0.00217	<i>Glycine max</i>	5.00E-79	<a href="#">XM_003551013.1</a>

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<i>UCOESTdown1962</i>	65-kDa Microtubule-associated protein 3	2.782	0.0126	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002267548.1</a>
<i>UCOESTdown1963</i>	Leucine-rich repeat receptor-like protein kinase	2.782	0.0146	<i>Arabidopsis thaliana</i>	0.0	<a href="#">FJ708814.1</a>
<i>UCOESTdown1964</i>	Uncharacterized protein	2.782	0.0497	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002284228.2</a>
<i>UCOESTdown1965</i>	Uncharacterized protein	2.781	0.013	<i>Populus trichocarpa</i>	9.00E-52	<a href="#">XM_002324814.1</a>
<i>UCOESTdown1966</i>	Phytochrome kinase substrate	2.777	0.00729	<i>Medicago truncatula</i>	4.00E-22	<a href="#">XP_003628361.1</a>
<i>UCOESTdown1967</i>	Cinnamyl alcohol dehydrogenase 1 (CAD1)	2.775	0.0131	<i>Gossypium hirsutum</i>	9.00E-173	<a href="#">EU281304.1</a>
<i>UCOESTdown1968</i>	LRR receptor-like serine/threonine-protein kinase	2.775	0.0215	<i>Vitis vinifera</i>	5.00E-70	<a href="#">XM_002265948.2</a>
<i>UCOESTdown1969</i>	No homology	2.773	0.015			
<i>UCOESTdown1970</i>	Pectin acetyltransferase	2.771	0.000758	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003626041.1</a>
<i>UCOESTdown1971</i>	Bile acid Na <sup>+</sup> symporter family protein	2.771	0.00199	<i>Medicago truncatula</i>	2.00E-156	<a href="#">XM_003609154.1</a>
<i>UCOESTdown1972</i>	Uncharacterized protein	2.768	0.00459	<i>Vitis vinifera</i>	6.00E-74	<a href="#">XM_002281403.2</a>
<i>UCOESTdown1973</i>	SCL domain class transcription factor	2.765	0.0016	<i>Malus x domestica</i>	3.00E-49	<a href="#">HM122683.1</a>
<i>UCOESTdown1974</i>	Uncharacterized protein	2.765	0.00322	<i>Glycine max</i>	3.00E-27	<a href="#">NM_001251503.1</a>
<i>UCOESTdown1975</i>	Serine carboxypeptidase 18	2.762	0.00255	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003633151.1</a>
<i>UCOESTdown1976</i>	Chemocyanin	2.762	0.0259	<i>Vitis vinifera</i>	2.00E-07	<a href="#">XM_002266886.2</a>
<i>UCOESTdown1977</i>	Cytochrome P450	2.760	0.000866	<i>Glycine max</i>	4.00E-161	<a href="#">XM_003551577.1</a>
<i>UCOESTdown1978</i>	F-box protein	2.760	0.0491	<i>Medicago truncatula</i>	3.00E-41	<a href="#">XM_003612196.1</a>
<i>UCOESTdown1979</i>	No homology	2.757	0.0457			
<i>UCOESTdown1980</i>	No homology	2.756	0.0182			
<i>UCOESTdown1981</i>	LRR receptor-like serine/threonine-protein kinase	2.752	0.00122	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002279755.2</a>
<i>UCOESTdown1982</i>	Uncharacterized protein	2.750	0.00172	<i>Vitis vinifera</i>	6.00E-38	<a href="#">XM_003632581.1</a>
<i>UCOESTdown1983</i>	Endoglucanase 10	2.749	0.00133	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_106219.2</a>
<i>UCOESTdown1984</i>	No homology	2.746	0.0168			
<i>UCOESTdown1985</i>	Mitogen-activated protein kinase 2	2.746	0.00119	<i>Glycine max</i>	0.0	<a href="#">XP_003532933.1</a>
<i>UCOESTdown1986</i>	NSP-interacting kinase 2 (NIK2)	2.746	0.00156	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_113453.2</a>
<i>UCOESTdown1987</i>	Uncharacterized protein	2.746	0.0356	<i>Medicago truncatula</i>	1.00E-119	<a href="#">XM_003610741.1</a>
<i>UCOESTdown1988</i>	Neutral invertase (NIN1)	2.743	0.00265	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002280426.2</a>
<i>UCOESTdown1989</i>	Cysteine-rich receptor- protein kinase	2.743	0.0161	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003625108.1</a>
<i>UCOESTdown1990</i>	Uncharacterized protein	2.743	0.0188	<i>Glycine max</i>	1.00E-51	<a href="#">NM_001249473.1</a>
<i>UCOESTdown1991</i>	Uncharacterized protein	2.742	0.00374	<i>Vitis vinifera</i>	5.00E-92	<a href="#">XM_002275292.2</a>

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<i>UCOESTdown1992</i>	Mavicyanin	2.741	0.0472	<i>Glycine max</i>	2.00E-51	<a href="#">XM_003517534.1</a>
<i>UCOESTdown1993</i>	Leucine-rich repeat receptor-like protein kinase	2.741	0.0105	<i>Arabidopsis thaliana</i>	0.0	<a href="#">FJ708703.1</a>
<i>UCOESTdown1994</i>	L-Ascorbate oxidase	2.741	0.00379	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002281399.2</a>
<i>UCOESTdown1995</i>	Ethylene-responsive transcription factor CRF2	2.740	0.0362	<i>Arabidopsis thaliana</i>	2.00E-40	<a href="#">NM_202870.1</a>
<i>UCOESTdown1996</i>	Haloalkane dehalogenase	2.740	0.0051	<i>Vitis vinifera</i>	4.00E-158	<a href="#">XM_002263670.2</a>
<i>UCOESTdown1997</i>	WRKY transcription factor 22	2.739	0.00192	<i>Cucumis sativus</i>	2.00E-49	<a href="#">GU984021.1</a>
<i>UCOESTdown1998</i>	Tropinone reductase	2.739	0.0347	<i>Vitis vinifera</i>	2.00E-111	<a href="#">XM_002282719.2</a>
<i>UCOESTdown1999</i>	Protein TRANSPARENT TESTA	2.737	0.024	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003592538.1</a>
<i>UCOESTdown2000</i>	Nuclear transcription factor Y subunit B-3	2.736	0.0294	<i>Medicago truncatula</i>	2.00E-65	<a href="#">XM_003617764.1</a>
<i>UCOESTdown2001</i>	Nodulation protein H	2.736	0.0107	<i>Glycine max</i>	7.00E-150	<a href="#">XM_003529338.1</a>
<i>UCOESTdown2002</i>	ABC transporter G family member 11	2.736	0.0167	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003635390.1</a>
<i>UCOESTdown2003</i>	Cytochrome P450	2.732	0.00198	<i>Populus trichocarpa</i>	2.00E-167	<a href="#">XM_002320036.1</a>
<i>UCOESTdown2004</i>	Uncharacterized protein	2.732	0.0147	<i>Vitis vinifera</i>	6.00E-118	<a href="#">XM_002264822.1</a>
<i>UCOESTdown2005</i>	No homology	2.731	0.0437			
<i>UCOESTdown2006</i>	Glutathione transferase GSTU22	2.731	0.00528	<i>Populus trichocarpa</i>	5.00E-107	<a href="#">GQ377231.1</a>
<i>UCOESTdown2007</i>	Uncharacterized protein	2.730	0.00102	<i>Glycine max</i>	6.00E-57	<a href="#">XM_003537185.1</a>
<i>UCOESTdown2008</i>	Uncharacterized protein	2.730	0.00496	<i>Glycine max</i>	3.00E-88	<a href="#">XM_003556157.1</a>
<i>UCOESTdown2009</i>	Disease resistance protein	2.727	0.0208	<i>Vitis pseudoreticulata</i>	7.00E-74	<a href="#">JF500756.1</a>
<i>UCOESTdown2010</i>	Uncharacterized protein	2.726	0.00149	<i>Vitis vinifera</i>	1.00E-69	<a href="#">XM_002265197.2</a>
<i>UCOESTdown2011</i>	No homology	2.725	0.0181			
<i>UCOESTdown2012</i>	Uncharacterized protein	2.724	0.00242	<i>Glycine max</i>	0.0	<a href="#">XM_003535830.1</a>
<i>UCOESTdown2013</i>	ARM-repeat/tetratricopeptide repeat protein	2.722	0.00275	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_121058.2</a>
<i>UCOESTdown2014</i>	DNA replication licensing factor MCM3	2.721	0.00484	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002276029.1</a>
<i>UCOESTdown2015</i>	Uncharacterized protein	2.719	0.0371	<i>Glycine max</i>	6.00E-111	<a href="#">XM_003528267.1</a>
<i>UCOESTdown2016</i>	Uncharacterized protein	2.719	0.00312	<i>Vitis vinifera</i>	7.00E-121	<a href="#">XM_002271895.2</a>
<i>UCOESTdown2017</i>	7S vicilin (pec2a1a)	2.713	0.0105	<i>Carya illinoensis</i>	2.00E-26	<a href="#">EF689893.1</a>
<i>UCOESTdown2018</i>	LEAFY cotyledon1	2.711	0.0276	<i>Theobroma cacao</i>	1.00E-70	<a href="#">AM494833.1</a>
<i>UCOESTdown2019</i>	No homology	2.710	0.0479			
<i>UCOESTdown2020</i>	Uncharacterized protein	2.709	0.00529	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002262827.1</a>

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<i>UCOESTdown2021</i>	Uncharacterized protein	2.709	0.00463	<i>Vitis vinifera</i>	9.00E-169	<a href="#">XM_002274955.1</a>
<i>UCOESTdown2022</i>	Pentatricopeptide repeat-containing protein	2.708	0.0392	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002275545.2</a>
<i>UCOESTdown2023</i>	No homology	2.708	0.0261			
<i>UCOESTdown2024</i>	Cysteine-rich receptor- protein kinase	2.708	0.0015	<i>Medicago truncatula</i>	2.00E-88	<a href="#">XM_003600549.1</a>
<i>UCOESTdown2025</i>	Uncharacterized protein	2.708	0.0473	<i>Glycine max</i>	4.00E-82	<a href="#">NM_001250551.1</a>
<i>UCOESTdown2026</i>	No homology	2.705	0.00853			
<i>UCOESTdown2027</i>	Leucine-rich repeat receptor-like protein kinase	2.704	0.0241	<i>Medicago truncatula</i>	2.00E-51	<a href="#">XM_003623597.1</a>
<i>UCOESTdown2028</i>	No homology	2.701	0.00622			
<i>UCOESTdown2029</i>	No homology	2.70	0.00724			
<i>UCOESTdown2030</i>	No homology	2.697	0.017			
<i>UCOESTdown2031</i>	Carbohydrate esterase	2.697	0.00372	<i>Vitis vinifera</i>	9.00E-92	<a href="#">XM_002282992.1</a>
<i>UCOESTdown2032</i>	Disease resistance protein	2.695	0.0409	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002262717.1</a>
<i>UCOESTdown2033</i>	No homology	2.693	0.0333			
<i>UCOESTdown2034</i>	Cytochrome P450	2.692	0.000289	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003592229.1</a>
<i>UCOESTdown2035</i>	MATE efflux family protein ALF5	2.692	0.00209	<i>Vitis vinifera</i>	9.00E-28	<a href="#">XM_002282515.1</a>
<i>UCOESTdown2036</i>	ABC1 family protein	2.692	0.00192	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002885565.1</a>
<i>UCOESTdown2037</i>	No homology	2.690	0.0253			
<i>UCOESTdown2038</i>	Uncharacterized protein	2.6900	0.00133	<i>Arabidopsis thaliana</i>	4.00E-57	<a href="#">NM_130351.3</a>
<i>UCOESTdown2039</i>	Gamma-interferon-inducible lysosomal thiol reductase	2.687	0.0217	<i>Medicago truncatula</i>	2.00E-83	<a href="#">XM_003604522.1</a>
<i>UCOESTdown2040</i>	C2H2L domain class transcription factor (C2H2L2)	2.685	0.00211	<i>Malus x domestica</i>	5.00E-117	<a href="#">HM122493.1</a>
<i>UCOESTdown2041</i>	Histone deacetylase	2.685	0.00429	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002267480.1</a>
<i>UCOESTdown2042</i>	No homology	2.684	0.0135			
<i>UCOESTdown2043</i>	Elongation of fatty acids protein	2.681	0.0148	<i>Medicago truncatula</i>	6.00E-64	<a href="#">XM_003626265.1</a>
<i>UCOESTdown2044</i>	Cyclin-A3-2	2.679	0.0115	<i>Arabidopsis thaliana</i>	1.00E-109	<a href="#">NM_103614.4</a>
<i>UCOESTdown2045</i>	Uncharacterized protein	2.678	0.0122	<i>Arabidopsis thaliana</i>	5.00E-77	<a href="#">NM_126137.3</a>
<i>UCOESTdown2046</i>	WRKY transcription factor 1	2.677	0.00779	<i>Malus x domestica</i>	2.00E-69	<a href="#">HM122712.1</a>
<i>UCOESTdown2047</i>	No homology	2.677	0.000954			
<i>UCOESTdown2048</i>	Cationic amino acid transporter	2.673	0.0169	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002318229.1</a>
<i>UCOESTdown2049</i>	No homology	2.672	0.0164			
<i>UCOESTdown2050</i>	Leucine-rich repeat receptor-like protein kinase	2.672	0.0381	<i>Arabidopsis thaliana</i>	2.00E-71	<a href="#">NM_001198318.1</a>

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<i>UCOESTdown2051</i>	F-box protein	2.672	0.0054	<i>Medicago truncatula</i>	8.00E-59	<a href="#">XM_003629163.1</a>
<i>UCOESTdown2052</i>	S-Acyltransferase	2.669	0.00194	<i>Vitis vinifera</i>	2.00E-48	<a href="#">XM_002271416.2</a>
<i>UCOESTdown2053</i>	Receptor-like protein kinase	2.669	0.035	<i>Glycine max</i>	1.00E-21	<a href="#">XP_003543976.1</a>
<i>UCOESTdown2054</i>	Inactive leucine-rich repeat receptor kinase	2.667	0.00137	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002267617.1</a>
<i>UCOESTdown2055</i>	No homology	2.666	0.0096			
<i>UCOESTdown2056</i>	Uncharacterized protein	2.664	0.00486	<i>Glycine max</i>	0.0	<a href="#">XM_003518742.1</a>
<i>UCOESTdown2057</i>	No homology	2.663	0.00414			
<i>UCOESTdown2058</i>	Receptor-like protein 12	2.663	0.00322	<i>Vitis vinifera</i>	5.00E-121	<a href="#">XM_003633294.1</a>
<i>UCOESTdown2059</i>	DNA pol lambda (Poll)	2.662	0.00767	<i>Arabidopsis thaliana</i>	0.0	<a href="#">HQ009888.1</a>
<i>UCOESTdown2060</i>	Acyl-CoA thioesterase	2.662	0.0167	<i>Medicago truncatula</i>	2.00E-80	<a href="#">XM_003624200.1</a>
<i>UCOESTdown2061</i>	Uncharacterized protein	2.662	0.00181	<i>Vitis vinifera</i>	5.00E-156	<a href="#">XM_002270260.2</a>
<i>UCOESTdown2062</i>	50S ribosomal protein L35	2.661	0.00103	<i>Vitis vinifera</i>	2.00E-37	<a href="#">XM_002267777.2</a>
<i>UCOESTdown2063</i>	Uncharacterized protein	2.661	0.00155	<i>Glycine max</i>	1.00E-114	<a href="#">XM_003552854.1</a>
<i>UCOESTdown2064</i>	Disease resistance response protein 206	2.660	0.00177	<i>Vitis vinifera</i>	8.00E-72	<a href="#">XM_002283367.1</a>
<i>UCOESTdown2065</i>	RNA-dependent RNA polymerase	2.658	0.0102	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_127549.2</a>
<i>UCOESTdown2066</i>	No homology	2.658	0.0185			
<i>UCOESTdown2067</i>	Uncharacterized protein	2.658	0.000981	<i>Populus trichocarpa</i>	2.00E-35	<a href="#">XM_002306514.1</a>
<i>UCOESTdown2068</i>	No homology	2.657	0.00556			
<i>UCOESTdown2069</i>	No homology	2.656	0.0284			
<i>UCOESTdown2070</i>	Alcohol dehydrogenase	2.656	0.0027	<i>M.domestica</i>	0.0	<a href="#">Z48234.1</a>
<i>UCOESTdown2071</i>	No homology	2.655	0.00362			
<i>UCOESTdown2072</i>	Peroxidase 52	2.654	0.0194	<i>Glycine max</i>	5.00E-150	<a href="#">XM_003539952.1</a>
<i>UCOESTdown2073</i>	Glyoxal oxidase	2.654	0.0212	<i>Vitis vinifera</i>	1.00E-128	<a href="#">GQ468524.1</a>
<i>UCOESTdown2074</i>	No homology	2.654	0.0214			
<i>UCOESTdown2075</i>	F-box protein	2.654	0.00392	<i>Glycine max</i>	2.00E-113	<a href="#">XM_003528329.1</a>
<i>UCOESTdown2076</i>	Uncharacterized protein	2.654	0.0011	<i>Glycine max</i>	2.00E-110	<a href="#">XM_003531127.1</a>
<i>UCOESTdown2077</i>	Uncharacterized protein	2.654	0.0243	<i>Glycine max</i>	2.00E-150	<a href="#">XM_003554800.1</a>
<i>UCOESTdown2078</i>	No homology	2.652	0.0246			
<i>UCOESTdown2079</i>	U-box domain-containing protein 30	2.649	0.00497	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002285384.2</a>
<i>UCOESTdown2080</i>	3-Hydroxy-3-methylglutaryl coenzyme A reductase	2.648	0.000759	<i>Malus x domestica</i>	0.0	<a href="#">AF315713.1</a>
<i>UCOESTdown2081</i>	Methyl esterase 13	2.647	0.000989	<i>Arabidopsis thaliana</i>	7.00E-121	<a href="#">NM_102400.2</a>
<i>UCOESTdown2082</i>	No homology	2.646	0.00583			
<i>UCOESTdown2083</i>	Uncharacterized protein	2.646	0.0102	<i>Populus trichocarpa</i>	5.00E-93	<a href="#">XM_002315291.1</a>

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<i>UCOESTdown2084</i>	Serine carboxypeptidase 2	2.644	0.0202	<i>Vitis vinifera</i>	1.00E-62	<a href="#">XM_002283377.2</a>
<i>UCOESTdown2085</i>	BEL1-like homeodomain protein 4	2.641	0.00113	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002269634.1</a>
<i>UCOESTdown2086</i>	Beta-amylase 7	2.641	0.0011	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002273807.1</a>
<i>UCOESTdown2087</i>	Calcium-dependent protein kinase 34	2.641	0.00509	<i>Vitis vinifera</i>	0.0	<a href="#">XP_002275946.1</a>
<i>UCOESTdown2088</i>	Uncharacterized protein	2.641	0.00516	<i>Vitis vinifera</i>	1.00E-131	<a href="#">XM_002273733.1</a>
<i>UCOESTdown2089</i>	Branched-chain-amino-acid aminotransferase	2.638	0.00223	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002284879.2</a>
<i>UCOESTdown2090</i>	Uncharacterized protein	2.637	0.00165			
<i>UCOESTdown2091</i>	Aspartate carbamoyltransferase 2	2.636	0.00846	<i>Vitis vinifera</i>	6.00E-179	<a href="#">XM_002277379.2</a>
<i>UCOESTdown2092</i>	Sphingoid base hydroxylase 2	2.633	0.00461	<i>Vitis vinifera</i>	8.00E-112	<a href="#">XM_002265460.2</a>
<i>UCOESTdown2093</i>	Xylosyltransferase 1	2.632	0.0255	<i>Glycine max</i>	3.00E-111	<a href="#">XM_003530131.1</a>
<i>UCOESTdown2094</i>	Transcription factor TGA6	2.631	0.0471	<i>Glycine max</i>	1.00E-50	<a href="#">XM_003541651.1</a>
<i>UCOESTdown2095</i>	NBS resistance protein	2.631	0.012	<i>Medicago truncatula</i>	3.00E-22	<a href="#">XM_003636485.1</a>
<i>UCOESTdown2096</i>	Uncharacterized protein	2.631	0.00962	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002276668.1</a>
<i>UCOESTdown2097</i>	No homology	2.629	0.0154			
<i>UCOESTdown2098</i>	LRR receptor-like serine/threonine-protein kinase	2.629	0.0125	<i>Arabidopsis thaliana</i>	2.00E-172	<a href="#">AF024650.1</a>
<i>UCOESTdown2099</i>	Glycerol-phosphate acyltransferase	2.628	0.00163	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003627521.1</a>
<i>UCOESTdown2100</i>	Uncharacterized protein	2.628	0.0198	<i>Vitis vinifera</i>	3.00E-109	<a href="#">XM_002278991.1</a>
<i>UCOESTdown2101</i>	RNA methyltransferase	2.626	0.00641	<i>Medicago truncatula</i>	1.00E-112	<a href="#">XM_003628836.1</a>
<i>UCOESTdown2102</i>	No homology	2.626	0.00612			
<i>UCOESTdown2103</i>	bHLH transcription factor 123	2.625	0.0225	<i>Medicago truncatula</i>	2.00E-96	<a href="#">XM_003596496.1</a>
<i>UCOESTdown2104</i>	No homology	2.625	0.0144			
<i>UCOESTdown2105</i>	kinesin KIF4	2.624	0.00262	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002278343.2</a>
<i>UCOESTdown2106</i>	Protein RUPTURED POLLEN GRAIN	2.624	0.00164	<i>Medicago truncatula</i>	2.00E-61	<a href="#">XM_003635892.1</a>
<i>UCOESTdown2107</i>	Uncharacterized protein	2.624	0.000961	<i>Glycine max</i>	4.00E-97	<a href="#">XM_003534943.1</a>
<i>UCOESTdown2108</i>	No homology	2.623	0.0138			
<i>UCOESTdown2109</i>	Protein E6	2.622	0.0056	<i>Vitis vinifera</i>	5.00E-18	<a href="#">XM_002275144.2</a>
<i>UCOESTdown2110</i>	No homology	2.622	0.0407			
<i>UCOESTdown2111</i>	No homology	2.622	0.0349			
<i>UCOESTdown2112</i>	Uncharacterized protein	2.622	0.00172	<i>Populus trichocarpa</i>	4.00E-93	<a href="#">XM_002323313.1</a>
<i>UCOESTdown2113</i>	No homology	2.62	0.00954			
<i>UCOESTdown2114</i>	Hydroxypyruvate reductase	2.617	0.00361	<i>Bruguiera gymnorrhiza</i>	0.0	<a href="#">AB060810.1</a>

(Table continues on following page)

<i>UCOESTdown2115</i>	No homology	2.614	0.0133			
<i>UCOESTdown2116</i>	Early-responsive to dehydration-related protein	2.612	0.00126	<i>Populus euphratica</i>	0.0	<a href="#">HQ914442.1</a>
<i>UCOESTdown2117</i>	Xyloglucan endotransglucosylase/hydrolase 2	2.611	0.00561	<i>Rosa x borboniana</i>	0.0	<a href="#">DQ320658.2</a>
<i>UCOESTdown2118</i>	No homology	2.611	0.00458			
<i>UCOESTdown2119</i>	No homology	2.611	0.003			
<i>UCOESTdown2120</i>	No homology	2.611	0.00205			
<i>UCOESTdown2121</i>	Uncharacterized protein	2.611	0.00234	<i>Glycine max</i>	3.00E-64	<a href="#">XM_003522375.1</a>
<i>UCOESTdown2122</i>	Asparagine synthetase 1	2.610	0.0138	<i>Vitis vinifera</i>	0.0	<a href="#">JF796049.1</a>
<i>UCOESTdown2123</i>	F-box protein	2.609	0.0019	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002284045.2</a>
<i>UCOESTdown2124</i>	Protein NDR1	2.609	0.00146	<i>Vitis vinifera</i>	4.00E-59	<a href="#">XM_003633880.1</a>
<i>UCOESTdown2125</i>	Uncharacterized protein	2.608	0.0111	<i>Vitis vinifera</i>	7.00E-69	<a href="#">XM_002279807.1</a>
<i>UCOESTdown2126</i>	Uncharacterized protein	2.606	0.0044	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_100798.3</a>
<i>UCOESTdown2127</i>	No homology	2.605	0.00637			
<i>UCOESTdown2128</i>	Phosphatase 2A regulatory B subunit	2.605	0.00134	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_122462.1</a>
<i>UCOESTdown2129</i>	Uncharacterized protein	2.603	0.0143	<i>Vitis vinifera</i>	2.00E-167	<a href="#">XM_002270524.2</a>
<i>UCOESTdown2130</i>	Transcription factor PIF1	2.602	0.0279	<i>Medicago truncatula</i>	6.00E-50	<a href="#">XM_003625427.1</a>
<i>UCOESTdown2131</i>	Cysteine-rich receptor- protein kinase 25	2.602	0.0344	<i>Vitis vinifera</i>	4.00E-157	<a href="#">XM_003631474.1</a>
<i>UCOESTdown2132</i>	MYB transcription factor 8 (MYB8)	2.601	0.0112	<i>Rosa rugosa</i>	5.00E-133	<a href="#">FR828541.1</a>
<i>UCOESTdown2133</i>	Uncharacterized protein	2.601	0.00207	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002268563.2</a>
<i>UCOESTdown2134</i>	Uncharacterized protein	2.601	0.0254	<i>Glycine max</i>	2.00E-145	<a href="#">XM_003531087.1</a>
<i>UCOESTdown2135</i>	No homology	2.600	0.0456			
<i>UCOESTdown2136</i>	Centrin-2	2.598	0.0107	<i>Medicago truncatula</i>	1.00E-50	<a href="#">XM_003596484.1</a>
<i>UCOESTdown2137</i>	Outward rectifying potassium channel (ork)	2.597	0.0403	<i>Populus euphratica</i>	0.0	<a href="#">EU382997.1</a>
<i>UCOESTdown2138</i>	No homology	2.596	0.00112			
<i>UCOESTdown2139</i>	Pathogenesis-related protein 5	2.596	0.00389	<i>Glycine max</i>	1.00E-138	<a href="#">XM_003543740.1</a>
<i>UCOESTdown2140</i>	NAC transcription factor 10	2.595	0.00145	<i>Malus x domestica</i>	1.00E-81	<a href="#">HM122652.1</a>
<i>UCOESTdown2141</i>	Protein NDR1	2.594	0.0268	<i>Vitis vinifera</i>	7.00E-58	<a href="#">XM_002273816.2</a>
<i>UCOESTdown2142</i>	Uncharacterized protein	2.592	0.0208	<i>Vitis vinifera</i>	6.00E-87	<a href="#">XM_002283016.1</a>
<i>UCOESTdown2143</i>	Long chain fatty alcohol oxidase FAO2	2.591	0.0312	<i>Lotus japonicus</i>	0.0	<a href="#">AM900800.1</a>
<i>UCOESTdown2144</i>	S-Acyltransferase	2.5900	0.00596	<i>Arabidopsis thaliana</i>	4.00E-44	<a href="#">NM_104335.4</a>
<i>UCOESTdown2145</i>	Tropinone reductase	2.588	0.00637	<i>Glycine max</i>	5.00E-99	<a href="#">XM_003539497.1</a>

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<i>UCOESTdown2146</i>	Calmodulin protein	2.588	0.00816	<i>Elaeis guineensis</i>	1.00E-47	<a href="#">EF213076.1</a>
<i>UCOESTdown2147</i>	TMV resistance protein N	2.588	0.0191	<i>Medicago truncatula</i>	6.00E-41	<a href="#">XM_003624010.1</a>
<i>UCOESTdown2148</i>	Pentatricopeptide repeat-containing protein	2.585	0.0172	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002264920.1</a>
<i>UCOESTdown2149</i>	Cinnamyl alcohol dehydrogenase 9	2.585	0.0256	<i>Vitis vinifera</i>	5.00E-75	<a href="#">XM_002279796.2</a>
<i>UCOESTdown2150</i>	G-type lectin S-receptor-like serine/threonine-protein kinase RLK1	2.585	0.0315	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002283150.1</a>
<i>UCOESTdown2151</i>	FtsH protease	2.584	0.00117	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003597646.1</a>
<i>UCOESTdown2152</i>	LRR receptor-like serine/threonine-protein kinase RKF3	2.582	0.00272	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003632314.1</a>
<i>UCOESTdown2153</i>	MADS transcription factor 24	2.581	0.0486	<i>Vitis vinifera</i>	1.00E-66	<a href="#">XM_002276103.1</a>
<i>UCOESTdown2154</i>	Endonuclease/exonuclease/phosphatase family protein	2.580	0.00155	<i>Arabidopsis lyrata</i>	3.00E-145	<a href="#">XM_002882096.1</a>
<i>UCOESTdown2155</i>	Armadillo repeat-containing protein 6	2.577	0.0385	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002281804.1</a>
<i>UCOESTdown2156</i>	Uncharacterized protein	2.576	0.0426	<i>Vitis vinifera</i>	9.00E-112	<a href="#">XM_002275210.1</a>
<i>UCOESTdown2157</i>	Adenylyl-sulfate kinase	2.575	0.0121	<i>Glycine max</i>	5.00E-125	<a href="#">XP_003524691.1</a>
<i>UCOESTdown2158</i>	Dynammin-related protein 1C	2.574	0.00365	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002284883.1</a>
<i>UCOESTdown2159</i>	Peptide/nitrate transporter	2.574	0.0453	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003634558.1</a>
<i>UCOESTdown2160</i>	No homology	2.573	0.00246			
<i>UCOESTdown2161</i>	Calmodulin binding protein	2.573	0.0446	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003629681.1</a>
<i>UCOESTdown2162</i>	Uncharacterized protein	2.573	0.00468	<i>Vitis vinifera</i>	2.00E-71	<a href="#">XM_002265263.2</a>
<i>UCOESTdown2163</i>	Ca+2-binding EF hand protein (PM13)	2.572	0.000942	<i>Glycine max</i>	7.00E-120	<a href="#">NM_001250414.1</a>
<i>UCOESTdown2164</i>	Glucan endo-1,3-beta-glucosidase 7	2.571	0.0116	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_119613.7</a>
<i>UCOESTdown2165</i>	Ribonuclease H protein	2.570	0.003	<i>Glycine max</i>	1.00E-13	<a href="#">XM_003543046.1</a>
<i>UCOESTdown2166</i>	Mitogen-activated protein kinase kinase	2.570	0.0453	<i>Medicago truncatula</i>	1.00E-112	<a href="#">XP_003601120.1</a>
<i>UCOESTdown2167</i>	No homology	2.569	0.00463			
<i>UCOESTdown2168</i>	Uncharacterized protein	2.567	0.00138	<i>Populus trichocarpa</i>	1.00E-35	<a href="#">XM_002323998.1</a>
<i>UCOESTdown2169</i>	ZF-HD homeobox protein	2.566	0.00329	<i>Vitis vinifera</i>	7.00E-58	<a href="#">XM_002273766.1</a>
<i>UCOESTdown2170</i>	Sarcosine oxidase	2.566	0.0165	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002324345.1</a>
<i>UCOESTdown2171</i>	Uncharacterized protein	2.566	0.00301	<i>Vitis vinifera</i>	1.00E-102	<a href="#">XM_002273198.2</a>
<i>UCOESTdown2172</i>	No homology	2.565	0.00249			
<i>UCOESTdown2173</i>	No homology	2.565	0.0221			
<i>UCOESTdown2174</i>	DOF transcription factor 2	2.562	0.00678	<i>Malus x domestica</i>	1.00E-180	<a href="#">HM122543.1</a>
<i>UCOESTdown2175</i>	Uncharacterized protein	2.562	0.000984	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002270701.2</a>

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<i>UCOESTdown2176</i>	RING-H2 finger protein ATL1E	2.561	0.00936	<i>Medicago truncatula</i>	2.00E-56	<a href="#">XM_003611301.1</a>
<i>UCOESTdown2177</i>	Tyrosyl-tRNA synthetase	2.558	0.00641	<i>Glycine max</i>	7.00E-12	<a href="#">NM_001255168.1</a>
<i>UCOESTdown2178</i>	Uncharacterized protein	2.558	0.00801	<i>Vitis vinifera</i>	8.00E-40	<a href="#">XM_002283129.1</a>
<i>UCOESTdown2179</i>	D-3-Phosphoglycerate dehydrogenase	2.557	0.00221	<i>Vitis vinifera</i>	3.00E-152	<a href="#">XM_002282056.1</a>
<i>UCOESTdown2180</i>	Receptor-like protein kinase	2.557	0.00333	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002278659.1</a>
<i>UCOESTdown2181</i>	F-box protein	2.556	0.0392	<i>Medicago truncatula</i>	2.00E-06	<a href="#">XM_003604215.1</a>
<i>UCOESTdown2182</i>	Xyloglucan galactosyltransferase KATAMARI1	2.554	0.0396	<i>Glycine max</i>	5.00E-164	<a href="#">XM_003556564.1</a>
<i>UCOESTdown2183</i>	Uncharacterized protein	2.554	0.0158	<i>Populus trichocarpa</i>	2.00E-24	<a href="#">XM_002308565.1</a>
<i>UCOESTdown2184</i>	9-cis-epoxycarotenoid dioxygenase 3 (NCED)	2.553	0.00988	<i>Fragaria x ananassa</i>	0.0	<a href="#">HQ008771.1</a>
<i>UCOESTdown2185</i>	No homology	2.551	0.00181			
<i>UCOESTdown2186</i>	No homology	2.550	0.00258			
<i>UCOESTdown2187</i>	Uncharacterized protein	2.549	0.0317	<i>Vitis vinifera</i>	7.00E-83	<a href="#">XM_002268292.1</a>
<i>UCOESTdown2188</i>	G-type lectin S-receptor-like serine/threonine-protein kinase RKS1	2.545	0.0239	<i>Vitis vinifera</i>	1.00E-50	<a href="#">XM_002269261.2</a>
<i>UCOESTdown2189</i>	Uncharacterized protein	2.545	0.0162	<i>Vitis vinifera</i>	2.00E-38	<a href="#">XM_003635556.1</a>
<i>UCOESTdown2190</i>	No homology	2.542	0.0116			
<i>UCOESTdown2191</i>	No homology	2.542	0.00849			
<i>UCOESTdown2192</i>	Phosphoglycolate phosphatase	2.541	0.00858	<i>Medicago truncatula</i>	7.00E-102	<a href="#">XM_003590679.1</a>
<i>UCOESTdown2193</i>	Oxysterol-binding protein-related protein 1D	2.539	0.00143	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002282053.1</a>
<i>UCOESTdown2194</i>	Long-chain-alcohol oxidase FAO1	2.538	0.00129	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002285298.1</a>
<i>UCOESTdown2195</i>	Uncharacterized protein	2.538	0.00139	<i>Vigna mungo</i>	3.00E-12	<a href="#">AB038598.1</a>
<i>UCOESTdown2196</i>	Uncharacterized protein	2.538	0.00193	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002272051.1</a>
<i>UCOESTdown2197</i>	Fructokinase-2	2.537	0.0187	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003614066.1</a>
<i>UCOESTdown2198</i>	No homology	2.536	0.0016			
<i>UCOESTdown2199</i>	Two-pore channel 1 (ATTPC1)	2.536	0.00139	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002874814.1</a>
<i>UCOESTdown2200</i>	No homology	2.535	0.00246			
<i>UCOESTdown2201</i>	MYB transcription factor	2.534	0.0183	<i>Arabidopsis thaliana</i>	2.00E-73	<a href="#">AY519576.1</a>
<i>UCOESTdown2202</i>	MLO10 protein (MLO10)	2.532	0.00329	<i>Vitis vinifera</i>	6.00E-177	<a href="#">XM_002275324.1</a>
<i>UCOESTdown2203</i>	Pentatricopeptide repeat-containing protein	2.528	0.033	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002278683.1</a>
<i>UCOESTdown2204</i>	No homology	2.528	0.0378			
<i>UCOESTdown2205</i>	Proline-rich receptor-kinase PERK9	2.527	0.00521	<i>Vitis vinifera</i>	0.0	<a href="#">XP_002277905.1</a>

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<i>UCOESTdown2206</i>	No homology	2.523	0.0312			
<i>UCOESTdown2207</i>	NBS resistance protein	2.523	0.0274	<i>Populus trichocarpa</i>	2.00E-22	<a href="#">XM_002332963.1</a>
<i>UCOESTdown2208</i>	3-Dehydroquinase synthase	2.522	0.00104	<i>Vitis vinifera</i>	7.00E-175	<a href="#">XM_002282954.2</a>
<i>UCOESTdown2209</i>	Uncharacterized protein	2.521	0.0123	<i>Glycine max</i>	0.0	<a href="#">XM_003519538.1</a>
<i>UCOESTdown2210</i>	Cytochrome P450	2.519	0.0119	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002301387.1</a>
<i>UCOESTdown2211</i>	Uncharacterized protein	2.519	0.00195	<i>Glycine max</i>	0.0	<a href="#">XM_003538360.1</a>
<i>UCOESTdown2212</i>	Dynamin protein ARC5	2.518	0.0354	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002266693.2</a>
<i>UCOESTdown2213</i>	Uncharacterized protein	2.518	0.00692	<i>Vitis vinifera</i>	3.00E-73	<a href="#">XM_002278869.1</a>
<i>UCOESTdown2214</i>	50S ribosomal protein L27	2.517	0.0315	<i>Arabidopsis thaliana</i>	4.00E-74	<a href="#">NM_123460.4</a>
<i>UCOESTdown2215</i>	U-box domain-containing protein 7	2.517	0.00268	<i>Medicago truncatula</i>	2.00E-128	<a href="#">XM_003593719.1</a>
<i>UCOESTdown2216</i>	No homology	2.515	0.045			
<i>UCOESTdown2217</i>	ABC transporter family protein	2.515	0.0013	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002309995.1</a>
<i>UCOESTdown2218</i>	Uncharacterized protein	2.515	0.0028	<i>Medicago truncatula</i>	3.00E-67	<a href="#">XM_003609708.1</a>
<i>UCOESTdown2219</i>	Cysteine-rich receptor- protein kinase	2.514	0.0469	<i>Medicago truncatula</i>	7.00E-160	<a href="#">XM_003607666.1</a>
<i>UCOESTdown2220</i>	COL domain class transcription factor (COL10)	2.513	0.0215	<i>Malus x domestica</i>	3.00E-42	<a href="#">HM122526.1</a>
<i>UCOESTdown2221</i>	No homology	2.512	0.00433			
<i>UCOESTdown2222</i>	RING zinc finger protein	2.511	0.0275	<i>Medicago truncatula</i>	2.00E-63	<a href="#">XM_003602872.1</a>
<i>UCOESTdown2223</i>	Shikimate kinase	2.510	0.0155	<i>Populus trichocarpa</i>	4.00E-130	<a href="#">XM_002303402.1</a>
<i>UCOESTdown2224</i>	Cytochrome P450	2.509	0.029	<i>Vitis vinifera</i>	1.00E-82	<a href="#">XM_002279945.1</a>
<i>UCOESTdown2225</i>	Uncharacterized protein	2.509	0.00278	<i>Arabidopsis thaliana</i>	3.00E-74	<a href="#">NM_120744.2</a>
<i>UCOESTdown2226</i>	No homology	2.508	0.0115			
<i>UCOESTdown2227</i>	Uncharacterized protein	2.508	0.00143	<i>Medicago truncatula</i>	4.00E-48	<a href="#">XM_003608531.1</a>
<i>UCOESTdown2228</i>	Villin-1 (VLN1)	2.506	0.00138	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_001202706.1</a>
<i>UCOESTdown2229</i>	Ankyrin repeat-containing protein 13B	2.506	0.0321	<i>Glycine max</i>	0.0	<a href="#">XM_003550438.1</a>
<i>UCOESTdown2230</i>	Hydroquinone glucosyltransferase	2.505	0.0135	<i>Vitis vinifera</i>	5.00E-158	<a href="#">XM_002280887.2</a>
<i>UCOESTdown2231</i>	No homology	2.502	0.0115			
<i>UCOESTdown2232</i>	No homology	2.502	0.00981			
<i>UCOESTdown2233</i>	Uncharacterized protein	2.502	0.0258	<i>Populus trichocarpa</i>	1.00E-37	<a href="#">XM_002336255.1</a>
<i>UCOESTdown2234</i>	Uncharacterized protein	2.501	0.00234	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002311648.1</a>
<i>UCOESTdown2235</i>	Uncharacterized protein	2.500	0.0179	<i>Glycine max</i>	4.00E-73	<a href="#">XM_003526801.1</a>
<i>UCOESTdown2236</i>	No homology	2.498	0.00489			
<i>UCOESTdown2237</i>	O-Glucosyltransferase	2.498	0.0159	<i>Glycine max</i>	0.0	<a href="#">XM_003529904.1</a>
<i>UCOESTdown2238</i>	F-box/LRR-repeat protein	2.498	0.0111	<i>Glycine max</i>	2.00E-64	<a href="#">XM_003536424.1</a>
<i>UCOESTdown2239</i>	No homology	2.497	0.00946			

(Table continues on following page)

<i>UCOESTdown2240</i>	Pectin acetyltransferase	2.496	0.00583	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003609863.1</a>
<i>UCOESTdown2241</i>	aarF domain-containing protein kinase	2.496	0.0025	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003591892.1</a>
<i>UCOESTdown2242</i>	No homology	2.495	0.0126			
<i>UCOESTdown2243</i>	Anthocyanidin 3-O-glucosyltransferase	2.493	0.00236	<i>Medicago truncatula</i>	2.00E-127	<a href="#">XM_003615257.1</a>
<i>UCOESTdown2244</i>	Tir-nbs-lrr resistance protein	2.492	0.00184	<i>Populus trichocarpa</i>	9.00E-92	<a href="#">XM_002329173.1</a>
<i>UCOESTdown2245</i>	Uncharacterized protein	2.492	0.0161	<i>Arabidopsis thaliana</i>	9.00E-36	<a href="#">NM_118649.2</a>
<i>UCOESTdown2246</i>	Uncharacterized protein	2.492	0.00275	<i>Populus trichocarpa</i>	2.00E-41	<a href="#">XM_002316357.1</a>
<i>UCOESTdown2247</i>	Glycosyltransferase	2.491	0.0257	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002283982.2</a>
<i>UCOESTdown2248</i>	Rossmann-fold NAD(P)-binding domain-containing protein	2.489	0.0389	<i>Arabidopsis thaliana</i>	3.00E-93	<a href="#">NM_119302.4</a>
<i>UCOESTdown2249</i>	Chloride channel protein CLC-b	2.489	0.00722	<i>Glycine max</i>	0.0	<a href="#">XM_003553877.1</a>
<i>UCOESTdown2250</i>	Universal stress protein 1	2.487	0.0062	<i>Gossypium arboreum</i>	6.00E-68	<a href="#">EU309470.1</a>
<i>UCOESTdown2251</i>	40S ribosomal protein s12	2.485	0.0083	<i>Fragaria x ananassa</i>	2.00E-89	<a href="#">U19940.1</a>
<i>UCOESTdown2252</i>	No homology	2.484	0.00527			
<i>UCOESTdown2253</i>	Uncharacterized protein	2.483	0.00357	<i>Glycine max</i>	1.00E-20	<a href="#">XM_003516262.1</a>
<i>UCOESTdown2254</i>	Uncharacterized protein	2.483	0.00512	<i>Populus trichocarpa</i>	2.00E-88	<a href="#">XM_002331531.1</a>
<i>UCOESTdown2255</i>	Fasciclin-like arabinogalactan protein 4	2.482	0.0094	<i>Glycine max</i>	2.00E-137	<a href="#">XM_003546335.1</a>
<i>UCOESTdown2256</i>	Uncharacterized protein	2.481	0.0284	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002273091.2</a>
<i>UCOESTdown2257</i>	Uncharacterized protein	2.481	0.0284	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002273091.2</a>
<i>UCOESTdown2258</i>	Uncharacterized protein	2.480	0.0086	<i>Vitis vinifera</i>	4.00E-49	<a href="#">XM_002271009.2</a>
<i>UCOESTdown2259</i>	U-box domain-containing protein 43	2.479	0.0213	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002283933.2</a>
<i>UCOESTdown2260</i>	No homology	2.479	0.00209			
<i>UCOESTdown2261</i>	No homology	2.478	0.0105			
<i>UCOESTdown2262</i>	Histone H4	2.477	0.00174	<i>Paracentrotus lividus</i>	2.00E-50	<a href="#">Y16587.1</a>
<i>UCOESTdown2263</i>	abc transporter family protein	2.477	0.0493	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002877055.1</a>
<i>UCOESTdown2264</i>	Uncharacterized protein	2.477	0.0131	<i>Glycine max</i>	2.00E-79	<a href="#">XM_003531681.1</a>
<i>UCOESTdown2265</i>	Beta-glucosidase 1	2.476	0.00386	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002274626.2</a>
<i>UCOESTdown2266</i>	Cytochrome P450 monooxygenase	2.476	0.0177	<i>Glycine max</i>	2.00E-72	<a href="#">DQ394571.1</a>
<i>UCOESTdown2267</i>	Heat shock protein 101 (HSP101)	2.474	0.0125	<i>Funaria hygrometrica</i>	3.00E-35	<a href="#">DQ239566.1</a>
<i>UCOESTdown2268</i>	Xyloglucan endotransglycosylase 1	2.470	0.0133	<i>Litchi chinensis</i>	4.00E-114	<a href="#">DQ995515.1</a>
<i>UCOESTdown2269</i>	Pre-mRNA-Splicing factor ATP-dependent RNA helicase DHX16-like (LOC100244993), mRNA	2.470	0.00425	<i>Vitis vinifera</i>	2.00E-26	<a href="#">XM_002284379.1</a>
<i>UCOESTdown2270</i>	Pentatricopeptide repeat protein	2.470	0.00482	<i>Medicago truncatula</i>	1.00E-163	<a href="#">XM_003626560.1</a>

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<i>UCOESTdown2271</i>	No homology	2.470	0.0173			
<i>UCOESTdown2272</i>	Uncharacterized protein	2.470	0.00454	<i>Vitis vinifera</i>	1.00E-37	<a href="#">XM_002264686.2</a>
<i>UCOESTdown2273</i>	KDEL motif-containing protein 1	2.468	0.0481	<i>Glycine max</i>	0.0	<a href="#">XM_003517416.1</a>
<i>UCOESTdown2274</i>	Respiratory burst oxidase protein B	2.468	0.0125	<i>Glycine max</i>	0.0	<a href="#">XM_003554603.1</a>
<i>UCOESTdown2275</i>	Calmodulin-binding protein	2.464	0.00287	<i>Arabidopsis thaliana</i>	2.00E-164	<a href="#">NM_125083.2</a>
<i>UCOESTdown2276</i>	Synaptonemal complex protein 2	2.462	0.00274	<i>Vitis vinifera</i>	3.00E-145	<a href="#">XM_003634424.1</a>
<i>UCOESTdown2277</i>	Uncharacterized protein	2.462	0.00656	<i>Sorghum bicolor</i>	2.00E-90	<a href="#">XM_002436681.1</a>
<i>UCOESTdown2278</i>	No homology	2.461	0.0118			
<i>UCOESTdown2279</i>	Heat shock protein 22 (HSP22)	2.461	0.00166	<i>Metarhizium anisopliae</i>	2.00E-142	<a href="#">DQ393582.1</a>
<i>UCOESTdown2280</i>	Histone H4	2.460	0.00268	<i>Medicago truncatula</i>	1.00E-51	<a href="#">XM_003625433.1</a>
<i>UCOESTdown2281</i>	No homology	2.460	0.0182			
<i>UCOESTdown2282</i>	Reticuline oxidase	2.460	0.00796	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003594557.1</a>
<i>UCOESTdown2283</i>	Receptor-like protein kinase	2.460	0.0237	<i>Glycine max</i>	0.0	<a href="#">NM_001251607.1</a>
<i>UCOESTdown2284</i>	Uncharacterized protein	2.460	0.00257	<i>Vitis vinifera</i>	6.00E-77	<a href="#">XM_002276615.2</a>
<i>UCOESTdown2285</i>	Signal recognition particle receptor subunit beta	2.458	0.00272	<i>Arabidopsis thaliana</i>	2.00E-113	<a href="#">NM_203006.2</a>
<i>UCOESTdown2286</i>	Calcium-dependent protein kinase 20	2.458	0.00845	<i>Arabidopsis lyrata</i>	0.0	
<i>UCOESTdown2287</i>	S-locus F-Box protein c	2.457	0.00439	<i>Prunus dulcis</i>	8.00E-18	<a href="#">AB081587.1</a>
<i>UCOESTdown2288</i>	No homology	2.456	0.0196			
<i>UCOESTdown2289</i>	Class I cytosolic small heat shock protein	2.456	0.0123	<i>Potentilla discolor</i>	2.00E-84	<a href="#">HM629423.1</a>
<i>UCOESTdown2290</i>	S-locus F-Box protein c	2.455	0.0105	<i>Pyrus pyrifolia</i>	3.00E-20	<a href="#">AB545981.1</a>
<i>UCOESTdown2291</i>	Protein TIFY 6B	2.454	0.00151	<i>Vitis vinifera</i>	3.00E-57	<a href="#">XM_002282652.2</a>
<i>UCOESTdown2292</i>	No homology	2.452	0.0299			
<i>UCOESTdown2293</i>	High mobility group family	2.451	0.0308	<i>Populus trichocarpa</i>	4.00E-21	<a href="#">XM_002311480.1</a>
<i>UCOESTdown2294</i>	No homology	2.451	0.0113			
<i>UCOESTdown2295</i>	WPP domain-interacting tail-anchored protein 2	2.449	0.00453	<i>Glycine max</i>	0.0	<a href="#">XM_003520095.1</a>
<i>UCOESTdown2296</i>	Uncharacterized protein	2.449	0.00332	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002285512.2</a>
<i>UCOESTdown2297</i>	No homology	2.448	0.0118			
<i>UCOESTdown2298</i>	Sugar transporter ERD6-like 3	2.448	0.00251	<i>Vitis vinifera</i>	1.00E-15	<a href="#">XM_002263694.2</a>
<i>UCOESTdown2299</i>	Uncharacterized protein	2.448	0.00598	<i>Glycine max</i>	0.0	<a href="#">XM_003551644.1</a>
<i>UCOESTdown2300</i>	Histone H3	2.447	0.0229	<i>Nicotiana benthamiana</i>	2.00E-53	<a href="#">EF661029.1</a>

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<i>UCOESTdown2301</i>	Flavanone 3-dioxygenase	2.445	0.0441	<i>Glycine max</i>	0.0	<a href="#">XM_003523265.1</a>
<i>UCOESTdown2302</i>	Kinase G11A	2.445	0.00706	<i>Vitis vinifera</i>	0.0	<a href="#">XP_002265801.2</a>
<i>UCOESTdown2303</i>	No homology	2.444	0.00833			
<i>UCOESTdown2304</i>	Polyphenol oxidase	2.443	0.000352	<i>Ziziphus jujuba</i>	9.00E-28	<a href="#">HQ634289.1</a>
<i>UCOESTdown2305</i>	No homology	2.441	0.0356			
<i>UCOESTdown2306</i>	No homology	2.441	0.0227			
<i>UCOESTdown2307</i>	Methyltransferase PMT14	2.439	0.00216	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002282057.2</a>
<i>UCOESTdown2308</i>	Aquaporin TIP2 (TIP2;1)	2.439	0.00526	<i>Malus prunifolia</i>	7.00E-131	<a href="#">JF834204.1</a>
<i>UCOESTdown2309</i>	Nucleobase-ascorbate transporter 11	2.439	0.00197	<i>Glycine max</i>	0.0	<a href="#">XM_003534194.1</a>
<i>UCOESTdown2310</i>	Glucan endo-1,3-beta-glucosidase 2	2.438	0.00337	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002271955.2</a>
<i>UCOESTdown2311</i>	No homology	2.436	0.0106			
<i>UCOESTdown2312</i>	Protease Do-like protein	2.434	0.0055	<i>Medicago truncatula</i>	4.00E-16	<a href="#">XM_003593851.1</a>
<i>UCOESTdown2313</i>	Polyol/monosaccharide transporter (PMT4)	2.434	0.00167	<i>Vitis vinifera</i>	0.0	<a href="#">HQ323288.1</a>
<i>UCOESTdown2314</i>	Condensin-2 complex subunit D3	2.432	0.0342	<i>Glycine max</i>	0.0	<a href="#">XM_003533299.1</a>
<i>UCOESTdown2315</i>	Zeaxanthin epoxidase	2.432	0.00205	<i>Prunus armeniaca</i>	0.0	<a href="#">AF071888.1</a>
<i>UCOESTdown2316</i>	Receptor protein kinase TMK1	2.432	0.00205	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002274470.2</a>
<i>UCOESTdown2317</i>	Plastid-lipid-associated protein 4	2.432	0.00333	<i>Glycine max</i>	2.00E-105	<a href="#">XM_003547497.1</a>
<i>UCOESTdown2318</i>	Uncharacterized protein	2.431	0.00194	<i>Glycine max</i>	0.0	<a href="#">XM_003529484.1</a>
<i>UCOESTdown2319</i>	Glycine-rich protein 2b	2.430	0.00895	<i>Vitis vinifera</i>	2.00E-46	<a href="#">XM_002285801.2</a>
<i>UCOESTdown2320</i>	Bile acid:Na <sup>+</sup> symporter family protein	2.429	0.0025	<i>Populus trichocarpa</i>	2.00E-159	<a href="#">XM_002304411.1</a>
<i>UCOESTdown2321</i>	HSF domain class transcription factor (HSF2)	2.427	0.00147	<i>Malus x domestica</i>	3.00E-166	<a href="#">HM122590.1</a>
<i>UCOESTdown2322</i>	HSF domain class transcription factor (HSF2)	2.427	0.00147	<i>Malus x domestica</i>	3.00E-166	<a href="#">HM122590.1</a>
<i>UCOESTdown2323</i>	Pectinesterase/pectinesterase inhibitor 54	2.426	0.00984	<i>Glycine max</i>	4.00E-126	<a href="#">XM_003534930.1</a>
<i>UCOESTdown2324</i>	Uncharacterized protein	2.425	0.00268	<i>Glycine max</i>	1.00E-149	<a href="#">XM_003528702.1</a>
<i>UCOESTdown2325</i>	Lipase	2.423	0.00947	<i>Arabidopsis thaliana</i>	2.00E-171	<a href="#">AY050998.1</a>
<i>UCOESTdown2326</i>	Lysine histidine transporter	2.423	0.00429	<i>Vitis vinifera</i>	5.00E-10	<a href="#">XM_002284078.2</a>
<i>UCOESTdown2327</i>	Uncharacterized protein	2.422	0.00163	<i>Glycine max</i>	4.00E-40	<a href="#">XM_003523028.1</a>
<i>UCOESTdown2328</i>	Serine/threonine-protein kinase	2.421	0.0397	<i>Medicago truncatula</i>	2.00E-42	<a href="#">XP_003624374.1</a>
<i>UCOESTdown2329</i>	Uncharacterized protein	2.421	0.00131	<i>Populus trichocarpa</i>	3.00E-27	<a href="#">XM_002332239.1</a>
<i>UCOESTdown2330</i>	Calcium-dependent protein kinase	2.418	0.00257	<i>Medicago truncatula</i>	3.00E-136	<a href="#">XP_003590952.1</a>
<i>UCOESTdown2331</i>	Uncharacterized protein	2.418	0.0138	<i>Glycine max</i>	7.00E-134	<a href="#">XM_003535430.1</a>

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<i>UCOESTdown2332</i>	MYND finger family protein	2.417	0.00761	<i>Zea mays</i>	5.00E-27	<a href="#">NM_001157795.1</a>
<i>UCOESTdown2333</i>	Plastid-lipid-associated protein 8	2.417	0.00731	<i>Vitis vinifera</i>	6.00E-97	<a href="#">XM_002282843.2</a>
<i>UCOESTdown2334</i>	Replication protein A 70 kDa DNA-binding subunit	2.416	0.00485	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002283923.2</a>
<i>UCOESTdown2335</i>	Uncharacterized protein	2.416	0.0082	<i>Arabidopsis thaliana</i>	1.00E-95	<a href="#">NM_112917.4</a>
<i>UCOESTdown2336</i>	Uncharacterized protein	2.415	0.00244	<i>Arabidopsis thaliana</i>	6.00E-78	<a href="#">NM_126386.2</a>
<i>UCOESTdown2337</i>	Acylamino-acid-releasing enzyme	2.414	0.00453	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003613853.1</a>
<i>UCOESTdown2338</i>	Beta-galactosidase 3	2.413	0.0438	<i>Fragaria x ananassa</i>	1.00E-31	<a href="#">AJ278705.1</a>
<i>UCOESTdown2339</i>	Short-chain dehydrogenase Tic32	2.412	0.0457	<i>Pisum sativum</i>	2.00E-134	<a href="#">AY488758.1</a>
<i>UCOESTdown2340</i>	No homology	2.412	0.0276			
<i>UCOESTdown2341</i>	No homology	2.412	0.00747			
<i>UCOESTdown2342</i>	No homology	2.412	0.00183			
<i>UCOESTdown2343</i>	Sugar transporter ERD6-like 5	2.412	0.0144	<i>Vitis vinifera</i>	2.00E-118	<a href="#">XM_002263517.2</a>
<i>UCOESTdown2344</i>	Leucine-rich repeat receptor-like protein kinase	2.411	0.0224	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_001203695.1</a>
<i>UCOESTdown2345</i>	Uncharacterized protein	2.411	0.00576	<i>Medicago truncatula</i>	3.00E-18	<a href="#">XM_003593554.1</a>
<i>UCOESTdown2346</i>	Triacylglycerol lipase 2	2.410	0.0494	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002271716.1</a>
<i>UCOESTdown2347</i>	Cytochrome P450	2.408	0.00303	<i>Vitis vinifera</i>	1.00E-163	<a href="#">XM_002280933.1</a>
<i>UCOESTdown2348</i>	Adiponectin receptor protein 1	2.408	0.0031	<i>Glycine max</i>	7.00E-131	<a href="#">XM_003549480.1</a>
<i>UCOESTdown2349</i>	Ubiquitin carboxyl-terminal hydrolase 12	2.407	0.02	<i>Vitis vinifera</i>	1.00E-51	<a href="#">XM_002267519.2</a>
<i>UCOESTdown2350</i>	Uncharacterized protein	2.405	0.0451	<i>Vitis vinifera</i>	2.00E-44	<a href="#">XM_002270702.1</a>
<i>UCOESTdown2351</i>	Peptide transporter PTR1	2.404	0.00279	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003611405.1</a>
<i>UCOESTdown2352</i>	Cucumisin	2.403	0.0029	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002277527.1</a>
<i>UCOESTdown2353</i>	No homology	2.402	0.0186			
<i>UCOESTdown2354</i>	Serine/threonine-protein kinase CTRL1	2.402	0.00614	<i>Glycine max</i>	0.0	<a href="#">XM_003524952.1</a>
<i>UCOESTdown2355</i>	Uncharacterized protein	2.401	0.00918	<i>Populus trichocarpa</i>	1.00E-22	<a href="#">XM_002302797.1</a>
<i>UCOESTdown2356</i>	vinorine synthase	2.399	0.00271	<i>Vitis vinifera</i>	1.00E-57	<a href="#">XM_002267305.1</a>
<i>UCOESTdown2357</i>	Monocopper oxidase protein SKU5	2.397	0.00222	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002264989.2</a>
<i>UCOESTdown2358</i>	Protein BREAST CANCER SUSCEPTIBILITY 1	2.397	0.0015	<i>Glycine max</i>	7.00E-167	<a href="#">XM_003520560.1</a>
<i>UCOESTdown2359</i>	Phosphoethanolamine N-methyltransferase	2.397	0.00807	<i>Pyrus betulifolia</i>	0.0	<a href="#">JF968605.1</a>
<i>UCOESTdown2360</i>	Reticulon protein B21	2.393	0.00199	<i>Arabidopsis thaliana</i>	2.00E-61	<a href="#">NM_125185.3</a>
<i>UCOESTdown2361</i>	Protein Breast cancer susceptibility 1	2.393	0.0198	<i>Glycine max</i>	0.0	<a href="#">XM_003547149.1</a>

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<i>UCOESTdown2362</i>	Hydroxycinnamoyl CoA shikimate/quinate hydroxycinnamoyltransferase 3 (HCQ3)	2.393	0.00653	<i>Populus trichocarpa</i>	1.00E-62	<a href="#">XM_002332032.1</a>
<i>UCOESTdown2363</i>	Uncharacterized protein	2.393	0.0451	<i>Glycine max</i>	2.00E-09	<a href="#">NM_001254597.1</a>
<i>UCOESTdown2364</i>	Sugar transport protein 10	2.391	0.0136	<i>Glycine max</i>	0.0	<a href="#">XM_003533649.1</a>
<i>UCOESTdown2365</i>	Caffeic acid 3-O-methyltransferase	2.390	0.00293	<i>Vitis vinifera</i>	1.00E-175	<a href="#">XM_002264530.1</a>
<i>UCOESTdown2366</i>	Serine/threonine-protein kinase Aurora-3	2.390	0.0365	<i>Vitis vinifera</i>	1.00E-169	<a href="#">XP_002270462.1</a>
<i>UCOESTdown2367</i>	No homology	2.388	0.00594			
<i>UCOESTdown2368</i>	Uncharacterized protein	2.388	0.00338	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002279997.1</a>
<i>UCOESTdown2369</i>	Uncharacterized protein	2.387	0.0329	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002321093.1</a>
<i>UCOESTdown2370</i>	Zeaxanthin epoxidase	2.386	0.0333	<i>Vitis vinifera</i>	8.00E-61	<a href="#">XM_002273213.2</a>
<i>UCOESTdown2371</i>	Uncharacterized protein	2.386	0.0459	<i>Vitis vinifera</i>	6.00E-166	<a href="#">XM_002266361.1</a>
<i>UCOESTdown2372</i>	Uncharacterized protein	2.383	0.032	<i>Glycine max</i>	3.00E-34	<a href="#">XM_003534658.1</a>
<i>UCOESTdown2373</i>	Uncharacterized protein	2.381	0.0111	<i>Medicago truncatula</i>	6.00E-129	<a href="#">XM_003597463.1</a>
<i>UCOESTdown2374</i>	Pyruvate kinase (PK)	2.380	0.0162	<i>Eriobotrya japonica</i>	0.0	<a href="#">JF414125.2</a>
<i>UCOESTdown2375</i>	Uncharacterized protein	2.380	0.00158	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002332305.1</a>
<i>UCOESTdown2376</i>	Acyl-CoA-binding domain-containing protein 3	2.379	0.00937	<i>Glycine max</i>	1.00E-35	<a href="#">NM_001253351.1</a>
<i>UCOESTdown2377</i>	Uncharacterized protein	2.378	0.00815	<i>Glycine max</i>	1.00E-18	<a href="#">NM_001250949.1</a>
<i>UCOESTdown2378</i>	Uncharacterized protein	2.372	0.00872	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002312877.1</a>
<i>UCOESTdown2379</i>	Glucan endo-1,3-beta-glucosidase 13	2.368	0.00246	<i>Glycine max</i>	6.00E-65	<a href="#">NM_001255309.1</a>
<i>UCOESTdown2380</i>	LysM domain-containing GPI-anchored protein 1	2.368	0.043	<i>Glycine max</i>	2.00E-11	<a href="#">XM_003523398.1</a>
<i>UCOESTdown2381</i>	LysM -containing GPI-anchored 1	2.368	0.043	<i>Glycine max</i>	2.00E-11	<a href="#">XM_003523398.1</a>
<i>UCOESTdown2382</i>	Uncharacterized protein	2.368	0.00218	<i>Vitis vinifera</i>	3.00E-83	<a href="#">XM_002277454.1</a>
<i>UCOESTdown2383</i>	Aquaporin (PIP2;1)	2.367	0.0266	<i>Rosa hybrid</i>	5.00E-180	<a href="#">EU572717.1</a>
<i>UCOESTdown2384</i>	Phosphatase (AHG1)	2.366	0.0226	<i>Arabidopsis thaliana</i>	2.00E-31	<a href="#">NM_124555.2</a>
<i>UCOESTdown2385</i>	Uncharacterized protein	2.366	0.0467	<i>Populus trichocarpa</i>	1.00E-178	<a href="#">XM_002324404.1</a>
<i>UCOESTdown2386</i>	Uncharacterized protein	2.365	0.0234	<i>Glycine max</i>	1.00E-147	<a href="#">XM_003530162.1</a>
<i>UCOESTdown2387</i>	Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 5 (TPS5)	2.364	0.00142	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_117886.2</a>
<i>UCOESTdown2388</i>	Lipase	2.363	0.00239	<i>Arabidopsis thaliana</i>	3.00E-129	<a href="#">AY050984.1</a>
<i>UCOESTdown2389</i>	Telomerase reverse transcriptase	2.360	0.0185	<i>Populus trichocarpa</i>	0.0	<a href="#">EU909207.1</a>

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<i>UCOESTdown2390</i>	Tubulin beta-10 (Tub10)	2.360	0.00631	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002304456.1</a>
<i>UCOESTdown2391</i>	No homology	2.360	0.00618			
<i>UCOESTdown2392</i>	Polygalacturonase	2.359	0.00879	<i>Citrus sinensis</i>	0.0	<a href="#">EF185420.1</a>
<i>UCOESTdown2393</i>	F-box protein	2.358	0.00916	<i>Vitis vinifera</i>	6.00E-25	<a href="#">XM_002269205.1</a>
<i>UCOESTdown2394</i>	Anion transporter 3	2.357	0.0056	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002273784.2</a>
<i>UCOESTdown2395</i>	Enoyl-ACP reductase	2.355	0.00217	<i>Malus x domestica</i>	0.0	<a href="#">DQ266044.1</a>
<i>UCOESTdown2396</i>	Dehydrin 1	2.355	0.0199	<i>Helianthus niveus</i>	4.00E-05	<a href="#">AJ250147.1</a>
<i>UCOESTdown2397</i>	RING-H2 finger protein ATL70	2.353	0.0169	<i>Arabidopsis thaliana</i>	8.00E-25	<a href="#">NM_179923.1</a>
<i>UCOESTdown2398</i>	Ycf49 protein	2.353	0.0106	<i>Vitis vinifera</i>	3.00E-63	<a href="#">XM_003631382.1</a>
<i>UCOESTdown2399</i>	No homology	2.352	0.00404			
<i>UCOESTdown2400</i>	LRR receptor-like serine/threonine-protein kinase	2.352	0.00213	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003593361.1</a>
<i>UCOESTdown2401</i>	No homology	2.351	0.0105			
<i>UCOESTdown2402</i>	Nucleotide/sugar transporter family protein	2.350	0.0167	<i>Arabidopsis thaliana</i>	8.00E-179	<a href="#">NM_124977.3</a>
<i>UCOESTdown2403</i>	No homology	2.347	0.0118			
<i>UCOESTdown2404</i>	No homology	2.346	0.0137			
<i>UCOESTdown2405</i>	Uncharacterized protein	2.346	0.00845	<i>Populus trichocarpa</i>	2.00E-169	<a href="#">XM_002313129.1</a>
<i>UCOESTdown2406</i>	Pyruvate dehydrogenase E1 component subunit alpha	2.345	0.0484	<i>Glycine max</i>	0.0	<a href="#">XM_003548078.1</a>
<i>UCOESTdown2407</i>	No homology	2.344	0.022			
<i>UCOESTdown2408</i>	Glycosyltransferase	2.344	0.000651	<i>Solanum aculeatissimum</i>	2.00E-141	<a href="#">AB182387.1</a>
<i>UCOESTdown2409</i>	Uncharacterized protein	2.344	0.00343	<i>Vitis vinifera</i>	4.00E-59	<a href="#">XM_003631350.1</a>
<i>UCOESTdown2410</i>	Amine oxidase	2.343	0.00686	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002275836.2</a>
<i>UCOESTdown2411</i>	MADS transcription factor FBP24	2.342	0.0466	<i>Petunia x hybrida</i>	1.00E-50	<a href="#">AF335242.1</a>
<i>UCOESTdown2412</i>	No homology	2.342	0.0208			
<i>UCOESTdown2413</i>	Uncharacterized protein	2.341	0.00641	<i>Vitis vinifera</i>	5.00E-95	<a href="#">XP_002266425.1</a>
<i>UCOESTdown2414</i>	Cap guanine-N7 methyltransferase	2.340	0.0422	<i>Medicago truncatula</i>	1.00E-140	<a href="#">XM_003625968.1</a>
<i>UCOESTdown2415</i>	Kinase	2.340	0.00428	<i>Medicago truncatula</i>	3.00E-12	<a href="#">XM_003597025.1</a>
<i>UCOESTdown2416</i>	Myosin heavy chain kinase B	2.338	0.02	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002268891.1</a>
<i>UCOESTdown2417</i>	Uncharacterized protein	2.338	0.0213	<i>Vitis vinifera</i>	4.00E-108	<a href="#">XM_002274611.2</a>
<i>UCOESTdown2418</i>	Heme-binding protein 2	2.337	0.00842	<i>Zea mays</i>	3.00E-50	<a href="#">EU955166.1</a>
<i>UCOESTdown2419</i>	No homology	2.337	0.0257			
<i>UCOESTdown2420</i>	MidA protein	2.336	0.0135	<i>Medicago truncatula</i>	1.00E-46	<a href="#">XM_003594541.1</a>

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<i>UCOESTdown2421</i>	NBS resistance protein	2.336	0.0384	<i>Populus trichocarpa</i>	6.00E-60	<a href="#">XM_002316635.1</a>
<i>UCOESTdown2422</i>	GDSL esterase/lipase	2.333	0.00311	<i>Medicago truncatula</i>	6.00E-131	<a href="#">XM_003612691.1</a>
<i>UCOESTdown2423</i>	Receptor-like protein kinase	2.333	0.00829	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002284552.1</a>
<i>UCOESTdown2424</i>	AP2 domain class transcription factor	2.332	0.0419	<i>Malus x domestica</i>	5.00E-82	<a href="#">GU732463.1</a>
<i>UCOESTdown2425</i>	MYB transcription factor 134 (MYB134)	2.331	0.0074	<i>Populus tremuloides</i>	8.00E-73	<a href="#">FJ573151.1</a>
<i>UCOESTdown2426</i>	Calmodulin	2.331	0.00287	<i>M.domestica</i>	2.00E-78	<a href="#">X60738.1</a>
<i>UCOESTdown2427</i>	Uncharacterized protein	2.330	0.00345	<i>Vitis vinifera</i>	3.00E-146	<a href="#">XM_002265431.2</a>
<i>UCOESTdown2428</i>	MYB transcription factor 75 (MYB75)	2.328	0.00344	<i>Glycine max</i>	2.00E-78	<a href="#">NM_001248819.1</a>
<i>UCOESTdown2429</i>	Uncharacterized protein	2.328	0.0237	<i>Vitis vinifera</i>	3.00E-16	<a href="#">XM_002269568.2</a>
<i>UCOESTdown2430</i>	Shikimate kinase 1	2.325	0.000342	<i>Arabidopsis thaliana</i>	2.00E-76	<a href="#">NM_001125239.1</a>
<i>UCOESTdown2431</i>	Uncharacterized protein	2.323	0.0204	<i>Glycine max</i>	4.00E-95	<a href="#">XM_003516685.1</a>
<i>UCOESTdown2432</i>	SCL domain class transcription factor 23	2.322	0.00874	<i>Malus x domestica</i>	0.0	<a href="#">HM122677.1</a>
<i>UCOESTdown2433</i>	Ubiquitin-conjugating enzyme E2 37	2.322	0.00704	<i>Arabidopsis thaliana</i>	3.00E-65	<a href="#">NM_113362.1</a>
<i>UCOESTdown2434</i>	No homology	2.322	0.0146			
<i>UCOESTdown2435</i>	Beta-glucan elicitor receptor (Bger1)	2.322	0.0022	<i>Brassica napus</i>	3.00E-05	<a href="#">AY280868.2</a>
<i>UCOESTdown2436</i>	DNA replication licensing factor MCM9	2.321	0.0102	<i>Glycine max</i>	0.0	<a href="#">XM_003547040.1</a>
<i>UCOESTdown2437</i>	Cytochrome P450 monooxygenase	2.321	0.0256	<i>Medicago truncatula</i>	0.0	<a href="#">DQ335802.1</a>
<i>UCOESTdown2438</i>	No homology	2.320	0.00287			
<i>UCOESTdown2439</i>	Quinone-oxidoreductase	2.317	0.0239	<i>Glycine max</i>	4.00E-158	<a href="#">XM_003552055.1</a>
<i>UCOESTdown2440</i>	ABC transporter D family member	2.317	0.0155	<i>Medicago truncatula</i>	2.00E-23	<a href="#">XM_003595825.1</a>
<i>UCOESTdown2441</i>	No homology	2.316	0.0257			
<i>UCOESTdown2442</i>	Uncharacterized protein	2.316	0.0025	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002273088.1</a>
<i>UCOESTdown2443</i>	Uncharacterized protein	2.316	0.0492	<i>Glycine max</i>	6.00E-106	<a href="#">XM_003533404.1</a>
<i>UCOESTdown2444</i>	Synaptonemal complex protein 2	2.315	0.0121	<i>Vitis vinifera</i>	3.00E-104	<a href="#">XM_003634424.1</a>
<i>UCOESTdown2445</i>	Uncharacterized protein	2.315	0.0115	<i>Vitis vinifera</i>	6.00E-104	<a href="#">XM_002277776.2</a>
<i>UCOESTdown2446</i>	Replication licensing factor mcm4-B	2.314	0.0162	<i>Glycine max</i>	0.0	<a href="#">XM_003537806.1</a>
<i>UCOESTdown2447</i>	SNF1-related protein kinase regulatory subunit gamma-1	2.313	0.0172	<i>Glycine max</i>	1.00E-20	<a href="#">XP_003519058.1</a>
<i>UCOESTdown2448</i>	bHLH transcription factor 11	2.312	0.00217	<i>Malus x domestica</i>	0.0	<a href="#">DQ266451.1</a>
<i>UCOESTdown2449</i>	SPL transcription factor 2	2.312	0.00354	<i>Malus x domestica</i>	1.00E-103	<a href="#">HM122685.1</a>
<i>UCOESTdown2450</i>	Pentatricopeptide repeat-containing protein	2.312	0.00372	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002274188.2</a>

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<i>UCOESTdown2451</i>	High mobility group B protein 15	2.311	0.0239	<i>Glycine max</i>	5.00E-15	<a href="#">XM_003536743.1</a>
<i>UCOESTdown2452</i>	No homology	2.310	0.0304			
<i>UCOESTdown2453</i>	Uncharacterized protein	2.309	0.018	<i>Populus trichocarpa</i>	9.00E-12	<a href="#">XM_002297731.1</a>
<i>UCOESTdown2454</i>	HAP2	2.308	0.0476	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003611091.1</a>
<i>UCOESTdown2455</i>	Acyl-coenzyme A oxidase 4	2.308	0.005	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_115043.2</a>
<i>UCOESTdown2456</i>	Dehydroquinase dehydratase/ shikimate dehydrogenase 2	2.308	0.0253	<i>Populus trichocarpa</i>	2.00E-21	<a href="#">XM_002319546.1</a>
<i>UCOESTdown2457</i>	U-box domain-containing protein	2.307	0.00853	<i>Medicago truncatula</i>	1.00E-41	<a href="#">XM_003636353.1</a>
<i>UCOESTdown2458</i>	Adenosine deaminase	2.306	0.00203	<i>Vitis vinifera</i>	2.00E-174	<a href="#">XM_002265795.2</a>
<i>UCOESTdown2459</i>	No homology	2.305	0.0365			
<i>UCOESTdown2460</i>	Rac-like GTP binding protein	2.301	0.0462	<i>Medicago truncatula</i>	8.00E-16	<a href="#">XM_003635718.1</a>
<i>UCOESTdown2461</i>	No homology	2.300	0.0214			
<i>UCOESTdown2462</i>	Cinnamoyl CoA reductase 3 (CCRL3)	2.300	0.00334	<i>Populus trichocarpa</i>	2.00E-140	<a href="#">XM_002314017.1</a>
<i>UCOESTdown2463</i>	No homology	2.298	0.0413			
<i>UCOESTdown2464</i>	Uncharacterized protein	2.297	0.00828	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002269732.2</a>
<i>UCOESTdown2465</i>	Trigger factor type chaperone family protein	2.295	0.00326	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_124904.4</a>
<i>UCOESTdown2466</i>	Uncharacterized protein	2.295	0.00193	<i>Vitis vinifera</i>	2.00E-51	<a href="#">XM_002282174.2</a>
<i>UCOESTdown2467</i>	Cytochrome P450 monooxygenase	2.294	0.0279	<i>Medicago truncatula</i>	7.00E-23	<a href="#">XM_003636782.1</a>
<i>UCOESTdown2468</i>	bHLH transcription factor 145	2.292	0.0207	<i>Vitis vinifera</i>	2.00E-97	<a href="#">XM_002285669.2</a>
<i>UCOESTdown2469</i>	Amino acid permease	2.292	0.00351	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002334794.1</a>
<i>UCOESTdown2470</i>	Alpha-xylosidase	2.291	0.0212	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002282393.2</a>
<i>UCOESTdown2471</i>	Glycosyltransferase, CAZy family GT8	2.286	0.00686	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002301767.1</a>
<i>UCOESTdown2472</i>	Leucine-rich repeat receptor-like protein kinase	2.286	0.00399	<i>Arabidopsis thaliana</i>	0.0	<a href="#">FJ708744.1</a>
<i>UCOESTdown2473</i>	No homology	2.284	0.0159			
<i>UCOESTdown2474</i>	Pentatricopeptide repeat-containing protein	2.280	0.0102	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002264094.2</a>
<i>UCOESTdown2475</i>	ABC transporter family	2.280	0.00664	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002314859.1</a>
<i>UCOESTdown2476</i>	Leucine-rich repeat receptor-like protein kinase	2.279	0.0274	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_179207.2</a>
<i>UCOESTdown2477</i>	Progesterin and adipoq receptor protein 1	2.279	0.00711	<i>Vitis vinifera</i>	5.00E-09	<a href="#">XM_002274287.2</a>
<i>UCOESTdown2478</i>	F-box protein	2.279	0.0468	<i>Glycine max</i>	0.0	<a href="#">XM_003527019.1</a>
<i>UCOESTdown2479</i>	Protease Do-like 5	2.278	0.00474	<i>Vitis vinifera</i>	1.00E-87	<a href="#">XM_002271452.2</a>
<i>UCOESTdown2480</i>	Reticulon protein B13	2.278	0.00359	<i>Arabidopsis thaliana</i>	1.00E-40	<a href="#">NM_127928.2</a>

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<i>UCOESTdown2481</i>	Serine/threonine-protein kinase	2.277	0.015	<i>Vitis vinifera</i>	0.0	<a href="#">XP_002280602.1</a>
<i>UCOESTdown2482</i>	Uncharacterized protein	2.277	0.0055	<i>Populus trichocarpa</i>	2.00E-79	<a href="#">XM_002305709.1</a>
<i>UCOESTdown2483</i>	Squamosa promoter binding like-protein	2.276	0.0295	<i>Vitis vinifera</i>	4.00E-127	<a href="#">XM_002273498.2</a>
<i>UCOESTdown2484</i>	No homology	2.276	0.00227			
<i>UCOESTdown2485</i>	Uncharacterized protein	2.276	0.00283	<i>Vitis vinifera</i>	1.00E-46	<a href="#">XM_002279220.2</a>
<i>UCOESTdown2486</i>	Transmembrane emp24 domain-containing protein bai	2.275	0.00188	<i>Vitis vinifera</i>	4.00E-97	<a href="#">XM_002283848.2</a>
<i>UCOESTdown2487</i>	Formamidase	2.275	0.00234	<i>Lupinus albus</i>	0.0	<a href="#">FJ617192.1</a>
<i>UCOESTdown2488</i>	No homology	2.274	0.0265			
<i>UCOESTdown2489</i>	RING/FYVE/PHD zinc finger-containing protein	2.273	0.00366	<i>Arabidopsis thaliana</i>	4.00E-101	<a href="#">NM_202584.1</a>
<i>UCOESTdown2490</i>	Uncharacterized protein	2.273	0.0103	<i>Vitis vinifera</i>	2.00E-68	<a href="#">XM_002262874.2</a>
<i>UCOESTdown2491</i>	Glutamyl-tRNA(Gln) amidotransferase subunit A	2.271	0.0286	<i>Glycine max</i>	0.0	<a href="#">XM_003556455.1</a>
<i>UCOESTdown2492</i>	No homology	2.271	0.0179			
<i>UCOESTdown2493</i>	Oxidoreductase GLYR1	2.268	0.00273	<i>Vitis vinifera</i>	2.00E-157	<a href="#">XM_002280261.1</a>
<i>UCOESTdown2494</i>	SCL domain class transcription factor 11	2.266	0.00509	<i>Malus x domestica</i>	2.00E-46	<a href="#">HM122675.1</a>
<i>UCOESTdown2495</i>	Glutamine synthetase	2.264	0.0074	<i>Gossypium hirsutum</i>	0.0	<a href="#">EU223825.1</a>
<i>UCOESTdown2496</i>	D-xylose-proton symporter-like 3	2.263	0.00218	<i>Glycine max</i>	0.0	<a href="#">XM_003539546.1</a>
<i>UCOESTdown2497</i>	Ankyrin repeat-containing protein 1	2.262	0.00274	<i>Glycine max</i>	0.0	<a href="#">XM_003548493.1</a>
<i>UCOESTdown2498</i>	Receptor-like protein kinase	2.262	0.00622	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003596548.1</a>
<i>UCOESTdown2499</i>	Cell division cycle-associated 7	2.261	0.0184	<i>Vitis vinifera</i>	3.00E-67	<a href="#">XM_002267624.1</a>
<i>UCOESTdown2500</i>	No homology	2.26	0.00645			
<i>UCOESTdown2501</i>	AP-4 complex subunit mu-1	2.259	0.0256	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002281271.1</a>
<i>UCOESTdown2502</i>	Granule-bound starch synthase 2	2.259	0.00172	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002278434.2</a>
<i>UCOESTdown2503</i>	E3 ubiquitin-protein ligase RFWD3	2.257	0.0113	<i>Vitis vinifera</i>	2.00E-95	<a href="#">XM_002265997.1</a>
<i>UCOESTdown2504</i>	Fatty acid hydroperoxide lyase (HPL)	2.257	0.00467	<i>Psidium guajava</i>	0.0	<a href="#">AF239670.1</a>
<i>UCOESTdown2505</i>	Disease carrier protein	2.257	0.00289	<i>Vitis vinifera</i>	7.00E-152	<a href="#">XM_002278374.2</a>
<i>UCOESTdown2506</i>	Uncharacterized protein	2.257	0.00746	<i>Vitis vinifera</i>	1.00E-94	<a href="#">XM_002273007.1</a>
<i>UCOESTdown2507</i>	RING-H2 finger protein	2.256	0.00258	<i>Vitis vinifera</i>	3.00E-104	<a href="#">XM_002270917.2</a>
<i>UCOESTdown2508</i>	Acyl CoA synthetase	2.255	0.0158	<i>Arabidopsis thaliana</i>	1.00E-11	<a href="#">AY065424.1</a>
<i>UCOESTdown2509</i>	No homology	2.254	0.00396			
<i>UCOESTdown2510</i>	Uncharacterized protein	2.252	0.0147	<i>Vitis vinifera</i>	1.00E-43	<a href="#">XM_002283919.1</a>

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<i>UCOESTdown2511</i>	Uncharacterized protein	2.252	0.0159	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003631901.1</a>
<i>UCOESTdown2512</i>	Anoctamin-7	2.251	0.0194	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002276323.2</a>
<i>UCOESTdown2513</i>	Serine carboxypeptidase 42	2.250	0.00291	<i>Glycine max</i>	0.0	<a href="#">XM_003544692.1</a>
<i>UCOESTdown2514</i>	No homology	2.250	0.00215			
<i>UCOESTdown2515</i>	No homology	2.249	0.00468			
<i>UCOESTdown2516</i>	No homology	2.249	0.00994			
<i>UCOESTdown2517</i>	Uncharacterized protein	2.248	0.00368	<i>Arabidopsis thaliana</i>	2.00E-29	<a href="#">NM_106310.3</a>
<i>UCOESTdown2518</i>	Early nodulin-2	2.246	0.0279	<i>Glycine max</i>	1.00E-45	<a href="#">XR_136839.1</a>
<i>UCOESTdown2519</i>	Cc-nbs-lrr resistance protein	2.245	0.015	<i>Medicago truncatula</i>	5.00E-28	<a href="#">XM_003590048.1</a>
<i>UCOESTdown2520</i>	Uncharacterized protein	2.245	0.00954	<i>Vitis vinifera</i>	1.00E-95	<a href="#">XM_002270984.2</a>
<i>UCOESTdown2521</i>	Heavy-metal-associated domain--containing protein	2.244	0.02	<i>Arabidopsis thaliana</i>	7.00E-63	<a href="#">NM_105774.3</a>
<i>UCOESTdown2522</i>	Uncharacterized protein	2.244	0.00618	<i>Vitis vinifera</i>	3.00E-95	<a href="#">XM_003518015.1</a>
<i>UCOESTdown2523</i>	WRKY transcription factor 4	2.242	0.00757	<i>Malus x domestica</i>	1.00E-55	<a href="#">HM122723.1</a>
<i>UCOESTdown2524</i>	Uncharacterized protein	2.242	0.02	<i>Glycine max</i>	4.00E-39	<a href="#">XM_003528886.1</a>
<i>UCOESTdown2525</i>	UDP-glucuronate 4-epimerase 1	2.240	0.0349	<i>Glycine max</i>	0.0	<a href="#">XM_003549472.1</a>
<i>UCOESTdown2526</i>	Uncharacterized protein	2.240	0.0141	<i>Vitis vinifera</i>	4.00E-78	<a href="#">XM_002285481.1</a>
<i>UCOESTdown2527</i>	Uncharacterized protein	2.239	0.011	<i>Vitis vinifera</i>	8.00E-69	<a href="#">XM_002275667.1</a>
<i>UCOESTdown2528</i>	Thylakoid lumenal 17.9 kDa protein	2.238	0.00787	<i>Vitis vinifera</i>	6.00E-98	<a href="#">XM_002280185.2</a>
<i>UCOESTdown2529</i>	No homology	2.238	0.00227			
<i>UCOESTdown2530</i>	No homology	2.237	0.0198			
<i>UCOESTdown2531</i>	Glutathione S-transferase protein	2.236	0.0312	<i>Bruguiera gymnorhiza</i>	1.00E-85	<a href="#">JF791114.1</a>
<i>UCOESTdown2532</i>	Amino acid transport protein	2.235	0.00246	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002299081.1</a>
<i>UCOESTdown2533</i>	Serine/threonine-protein kinase	2.234	0.00206	<i>Vitis vinifera</i>	0.0	<a href="#">XP_002282732.2</a>
<i>UCOESTdown2534</i>	Transcription factor E2F	2.232	0.00469	<i>Medicago truncatula</i>	4.00E-140	<a href="#">XM_003606047.1</a>
<i>UCOESTdown2535</i>	Serine/threonine-protein kinase PBS1	2.231	0.0243	<i>Glycine max</i>	1.00E-162	<a href="#">XP_003553966.1</a>
<i>UCOESTdown2536</i>	No homology	2.229	0.0303			
<i>UCOESTdown2537</i>	Alpha-crystallin domain of heat shock protein	2.228	0.00253	<i>Arabidopsis thaliana</i>	4.00E-51	<a href="#">NM_104358.2</a>
<i>UCOESTdown2538</i>	Uncharacterized protein	2.228	0.00619	<i>Vitis vinifera</i>	4.00E-58	<a href="#">XM_002281945.1</a>
<i>UCOESTdown2539</i>	Uncharacterized protein	2.226	0.0271	<i>Glycine max</i>	4.00E-74	<a href="#">XM_003547290.1</a>
<i>UCOESTdown2540</i>	No homology	2.225	0.0179			
<i>UCOESTdown2541</i>	Uncharacterized protein	2.225	0.0306	<i>Glycine max</i>	3.00E-38	<a href="#">NM_001249980.1</a>
<i>UCOESTdown2542</i>	WRKY transcription factor 72-3	2.224	0.0311	<i>Dimocarpus longa</i>	6.00E-65	<a href="#">JF708966.1</a>

(Table continues on following page)

<i>UCOESTdown2543</i>	Uncharacterized protein	2.224	0.0247	<i>Vitis vinifera</i>	1.00E-20	<a href="#">XM_003633810.1</a>
<i>UCOESTdown2544</i>	Uncharacterized protein	2.224	0.00299	<i>Vitis vinifera</i>	4.00E-43	<a href="#">XM_002268108.1</a>
<i>UCOESTdown2545</i>	Uncharacterized protein	2.224	0.00237	<i>Vitis vinifera</i>	3.00E-167	<a href="#">XM_002280782.1</a>
<i>UCOESTdown2546</i>	AP2 domain class transcription factor	2.223	0.00588	<i>Malus x domestica</i>	4.00E-80	<a href="#">GU732446.1</a>
<i>UCOESTdown2547</i>	No homology	2.223	0.0386			
<i>UCOESTdown2548</i>	Uncharacterized protein	2.222	0.0205	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002272858.2</a>
<i>UCOESTdown2549</i>	Proline-rich receptor-like protein kinase PERK13	2.221	0.0326	<i>Glycine max</i>	0.0	<a href="#">XP_003552967.1</a>
<i>UCOESTdown2550</i>	Uncharacterized protein	2.219	0.02	<i>Medicago truncatula</i>	1.00E-43	<a href="#">XM_003629653.1</a>
<i>UCOESTdown2551</i>	Uncharacterized protein	2.219	0.02	<i>Medicago truncatula</i>	1.00E-43	<a href="#">XM_003629653.1</a>
<i>UCOESTdown2552</i>	50S ribosomal protein L4	2.217	0.0116	<i>Glycine max</i>	1.00E-103	<a href="#">XM_003528986.1</a>
<i>UCOESTdown2553</i>	Phosphatidylinositol-4-phosphate 5-kinase 1	2.217	0.038	<i>Vitis vinifera</i>	0.0	<a href="#">XP_002284379.1</a>
<i>UCOESTdown2554</i>	Aspartic proteinase nepenthesin-2	2.216	0.00548	<i>Vitis vinifera</i>	7.00E-160	<a href="#">XM_002285557.2</a>
<i>UCOESTdown2555</i>	No homology	2.216	0.00915			
<i>UCOESTdown2556</i>	Oleosin 2	2.216	0.0188	<i>Jatropha curcas</i>	2.00E-35	<a href="#">EU234463.2</a>
<i>UCOESTdown2557</i>	No homology	2.213	0.00205			
<i>UCOESTdown2558</i>	Serine/threonine protein kinase PBS1	2.211	0.0154	<i>Medicago truncatula</i>	0.0	<a href="#">XP_003595174.1</a>
<i>UCOESTdown2559</i>	Lectin-like protein kinase	2.210	0.0148	<i>Populus nigra</i>	0.0	<a href="#">AB030083.1</a>
<i>UCOESTdown2560</i>	Uncharacterized protein	2.209	0.0364	<i>Vitis vinifera</i>	2.00E-47	<a href="#">XM_002265080.1</a>
<i>UCOESTdown2561</i>	Uncharacterized protein	2.209	0.00675	<i>Glycine max</i>	0.0	<a href="#">XM_003547338.1</a>
<i>UCOESTdown2562</i>	Peroxiredoxin-2E	2.208	0.0102	<i>Glycine max</i>	9.00E-89	<a href="#">XM_003554367.1</a>
<i>UCOESTdown2563</i>	No homology	2.208	0.0457			
<i>UCOESTdown2564</i>	Uncharacterized protein	2.207	0.0108	<i>Vitis vinifera</i>	1.00E-65	<a href="#">XM_002267606.2</a>
<i>UCOESTdown2565</i>	Uncharacterized protein	2.207	0.00386	<i>Vitis vinifera</i>	5.00E-160	<a href="#">XM_002278549.1</a>
<i>UCOESTdown2566</i>	Uncharacterized protein	2.207	0.0108	<i>Vitis vinifera</i>	1.00E-65	<a href="#">XM_002267606.2</a>
<i>UCOESTdown2567</i>	No homology	2.206	0.038			
<i>UCOESTdown2568</i>	Aspartic proteinase nepenthesin-1	2.205	0.014	<i>Glycine max</i>	1.00E-28	<a href="#">XM_003529838.1</a>
<i>UCOESTdown2569</i>	No homology	2.205	0.0111			
<i>UCOESTdown2570</i>	No homology	2.204	0.0261			
<i>UCOESTdown2571</i>	Adenylyl-sulfate kinase 1	2.204	0.00584	<i>Arabidopsis thaliana</i>	6.00E-118	<a href="#">NP_179082.1</a>
<i>UCOESTdown2572</i>	Uncharacterized protein	2.204	0.00517	<i>Vitis vinifera</i>	7.00E-40	<a href="#">XM_002270166.2</a>
<i>UCOESTdown2573</i>	Ethylene response factor 4	2.203	0.0077	<i>Malus x domestica</i>	2.00E-79	<a href="#">JF412351.1</a>
<i>UCOESTdown2574</i>	Nucleoredoxin 3	2.203	0.00395	<i>Arabidopsis thaliana</i>	9.00E-153	<a href="#">NM_202922.1</a>
<i>UCOESTdown2575</i>	No homology	2.203	0.0106			

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<i>UCOESTdown2576</i>	No homology	2.202	0.0117			
<i>UCOESTdown2577</i>	Phospholipase A1-IIdelta	2.202	0.0194	<i>Vitis vinifera</i>	2.00E-68	<a href="#">XM_002281059.2</a>
<i>UCOESTdown2578</i>	Pentatricopeptide repeat-containing protein	2.200	0.00317	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002267318.1</a>
<i>UCOESTdown2579</i>	No homology	2.200	0.00544			
<i>UCOESTdown2580</i>	No homology	2.198	0.00803			
<i>UCOESTdown2581</i>	Mitogen-activated protein kinase kinase 6	2.198	0.00661	<i>Gossypium hirsutum</i>	0.0	<a href="#">ADR31547.1</a>
<i>UCOESTdown2582</i>	F-box protein	2.197	0.0448	<i>Populus trichocarpa</i>	2e-150	<a href="#">XM_002309246.1</a>
<i>UCOESTdown2583</i>	Inter-alpha-trypsin inhibitor heavy chain H3	2.194	0.0126	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002277605.1</a>
<i>UCOESTdown2584</i>	No homology	2.194	0.0274			
<i>UCOESTdown2585</i>	Uncharacterized protein	2.194	0.0116	<i>Glycine max</i>	7.00E-179	<a href="#">XR_137618.1</a>
<i>UCOESTdown2586</i>	Plastid-lipid-associated protein 10	2.193	0.0134	<i>Arabidopsis thaliana</i>	2.00E-106	<a href="#">NM_130259.2</a>
<i>UCOESTdown2587</i>	Uncharacterized protein	2.193	0.00409	<i>Vitis vinifera</i>	2.00E-92	<a href="#">XM_002268087.2</a>
<i>UCOESTdown2588</i>	No homology	2.192	0.00375			
<i>UCOESTdown2589</i>	Heat shock protein 17.8	2.192	0.00266	<i>Rosa chinensis</i>	1.00E-58	<a href="#">EF053229.1</a>
<i>UCOESTdown2590</i>	Transmembrane BAX inhibitor motif-containing protein 4	2.190	0.00763	<i>Zea mays</i>	2.00E-63	<a href="#">NM_001156335.1</a>
<i>UCOESTdown2591</i>	RNA-dependent RNA polymerase 5	2.188	0.0472	<i>Vitis vinifera</i>	2.00E-44	<a href="#">XM_002280455.1</a>
<i>UCOESTdown2592</i>	No homology	2.187	0.0148			
<i>UCOESTdown2593</i>	Phosphatase 2C	2.187	0.003	<i>Fragaria x ananassa</i>	0.0	<a href="#">JN616382.1</a>
<i>UCOESTdown2594</i>	HXXXD-type acyl-transferase	2.187	0.0162	<i>Arabidopsis thaliana</i>	2.00E-73	<a href="#">NM_113508.2</a>
<i>UCOESTdown2595</i>	Serine carboxypeptidase 18	2.186	0.0328	<i>Brachypodium distachyon</i>	4.00E-13	<a href="#">XM_003573710.1</a>
<i>UCOESTdown2596</i>	Granule bound starch synthase Ia precursor	2.185	0.0146	<i>Malus x domestica</i>	0.0	<a href="#">EU586115.1</a>
<i>UCOESTdown2597</i>	Bidirectional sugar transporter SWEET17	2.184	0.045	<i>Vitis vinifera</i>	1.00E-82	<a href="#">XM_002278946.1</a>
<i>UCOESTdown2598</i>	F-box/LRR-repeat protein	2.183	0.00222	<i>Vitis vinifera</i>	2e-71	<a href="#">XM_002264021.2</a>
<i>UCOESTdown2599</i>	Nodulation-related protein	2.181	0.00171	<i>Arabidopsis thaliana</i>	3.00E-140	<a href="#">NM_114922.4</a>
<i>UCOESTdown2600</i>	Nucleotide-sugar transporter family	2.181	0.00222	<i>Arabidopsis thaliana</i>		<a href="#">NM_122449.1</a>
<i>UCOESTdown2601</i>	Uncharacterized protein	2.181	0.00791	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002276172.1</a>
<i>UCOESTdown2602</i>	No homology	2.180	0.00908			
<i>UCOESTdown2603</i>	Vacuolar protein sorting protein	2.179	0.0167	<i>Vitis vinifera</i>	3.00E-86	<a href="#">XM_002277523.1</a>

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<i>UCOESTdown2604</i>	Beta-galactosidase 1	2.177	0.00247	<i>Fragaria x ananassa</i>	0.0	<a href="#">AJ278703.1</a>
<i>UCOESTdown2605</i>	Mitochondrial carrier protein	2.177	0.0285	<i>Fragaria x ananassa</i>	4.00E-19	<a href="#">AY642688.1</a>
<i>UCOESTdown2606</i>	Long-chain-alcohol O-fatty-acyltransferase	2.177	0.0059	<i>Vitis vinifera</i>	7.00E-115	<a href="#">XM_002276866.1</a>
<i>UCOESTdown2607</i>	Stress-induced receptor-like kinase precursor	2.177	0.0424	<i>Glycine max</i>	6.00E-40	<a href="#">NP_001238112.1</a>
<i>UCOESTdown2608</i>	Uncharacterized protein	2.175	0.0132	<i>Vitis vinifera</i>	1.00E-69	<a href="#">XM_002264822.1</a>
<i>UCOESTdown2609</i>	E3 ubiquitin-protein ligase SINAT2	2.174	0.00278	<i>Arabidopsis thaliana</i>	1.00E-169	<a href="#">NM_115666.1</a>
<i>UCOESTdown2610</i>	No homology	2.174	0.00977			
<i>UCOESTdown2611</i>	Mitogen-activated protein kinase homolog NTF3	2.174	0.00213	<i>Vitis vinifera</i>	0.0	<a href="#">XP_002281075.2</a>
<i>UCOESTdown2612</i>	Lipase	2.173	0.00687	<i>Vitis vinifera</i>	1.00E-161	<a href="#">XM_002271378.2</a>
<i>UCOESTdown2613</i>	Polygalacturonase	2.172	0.00219	<i>Arabidopsis thaliana</i>	0.0	<a href="#">AY128793.1</a>
<i>UCOESTdown2614</i>	Uncharacterized protein	2.172	0.0146	<i>Glycine max</i>	0.0	<a href="#">XM_003545932.1</a>
<i>UCOESTdown2615</i>	Protease Do-like 1	2.170	0.0044	<i>Vitis vinifera</i>	7.00E-112	<a href="#">XM_002267474.2</a>
<i>UCOESTdown2616</i>	F-box protein	2.170	0.0113	<i>Populus trichocarpa</i>	6e-22	<a href="#">XM_002320470.1</a>
<i>UCOESTdown2617</i>	Beta-D-galactosidase	2.169	0.00227	<i>Pyrus pyrifolia</i>	0.0	<a href="#">AB190364.1</a>
<i>UCOESTdown2618</i>	30S ribosomal protein 2	2.168	0.0101	<i>Glycine max</i>	3.00E-83	<a href="#">XM_003531379.1</a>
<i>UCOESTdown2619</i>	No homology	2.168	0.0482			
<i>UCOESTdown2620</i>	NAC domain-containing protein 100	2.167	0.00457	<i>Vitis vinifera</i>	3.00E-127	<a href="#">XM_002284789.1</a>
<i>UCOESTdown2621</i>	TLP domain class transcription factor 7	2.167	0.00359	<i>Malus x domestica</i>	0.0	<a href="#">HM122708.1</a>
<i>UCOESTdown2622</i>	TLP domain class transcription factor (TLP7)	2.167	0.00359	<i>Malus x domestica</i>	0.0	<a href="#">HM122708.1</a>
<i>UCOESTdown2623</i>	No homology	2.167	0.0405			
<i>UCOESTdown2624</i>	26.5 kDa Heat shock protein	2.167	0.0137	<i>Medicago truncatula</i>	3.00E-46	<a href="#">XM_003604342.1</a>
<i>UCOESTdown2625</i>	Uncharacterized protein	2.167	0.0335	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002274645.2</a>
<i>UCOESTdown2626</i>	Pentatricopeptide repeat-containing protein	2.166	0.0131	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002269948.2</a>
<i>UCOESTdown2627</i>	No homology	2.166	0.00222			
<i>UCOESTdown2628</i>	Inositol transporter 4	2.165	0.029	<i>Glycine max</i>	0.0	<a href="#">XM_003534687.1</a>
<i>UCOESTdown2629</i>	Uncharacterized protein	2.161	0.0205	<i>Arabidopsis thaliana</i>	1.00E-05	<a href="#">AK230056.1</a>
<i>UCOESTdown2630</i>	Uncharacterized protein	2.160	0.0171	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003632225.1</a>
<i>UCOESTdown2631</i>	DNA polymerase delta catalytic subunit	2.159	0.00792	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002264349.1</a>
<i>UCOESTdown2632</i>	MutS2 protein	2.159	0.0054	<i>Vitis vinifera</i>	2.00E-27	<a href="#">XM_002269836.2</a>

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<i>UCOESTdown2633</i>	Calcium-binding protein CML10	2.159	0.0196	<i>Vitis vinifera</i>	1.00E-56	<a href="#">XM_002279624.1</a>
<i>UCOESTdown2634</i>	Uncharacterized protein	2.157	0.00775	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002285693.2</a>
<i>UCOESTdown2635</i>	Peroxidase 17	2.156	0.00199	<i>Vitis vinifera</i>	2.00E-169	<a href="#">XM_002271047.1</a>
<i>UCOESTdown2636</i>	Chaperone BCS1-B	2.156	0.0245	<i>Glycine max</i>	0.0	<a href="#">XM_003554219.1</a>
<i>UCOESTdown2637</i>	No homology	2.156	0.0271			
<i>UCOESTdown2638</i>	NBS resistance protein	2.156	0.00411	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002326530.1</a>
<i>UCOESTdown2639</i>	Transmembrane protein 189	2.154	0.0266	<i>Vitis vinifera</i>	9.00E-125	<a href="#">XM_002280947.2</a>
<i>UCOESTdown2640</i>	No homology	2.154	0.0417			
<i>UCOESTdown2641</i>	No homology	2.154	0.019			
<i>UCOESTdown2642</i>	S-Acyltransferase	2.154	0.00318	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002268380.2</a>
<i>UCOESTdown2643</i>	No homology	2.152	0.0493			
<i>UCOESTdown2644</i>	No homology	2.152	0.00614			
<i>UCOESTdown2645</i>	Endoglucanase E1	2.150	0.0283	<i>Glycine max</i>	0.0	<a href="#">XM_003524201.1</a>
<i>UCOESTdown2646</i>	Alpha 1,4-glucan phosphorylase L	2.150	0.00813	<i>Vicia faba</i>	0.0	<a href="#">Z36880.1</a>
<i>UCOESTdown2647</i>	Methyltransferase PMT10	2.150	0.00338	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002285851.1</a>
<i>UCOESTdown2648</i>	Uncharacterized protein	2.147	0.0167	<i>Vitis vinifera</i>	1.00E-28	<a href="#">XM_003635550.1</a>
<i>UCOESTdown2649</i>	WD repeat-containing protein	2.146	0.0245	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003595642.1</a>
<i>UCOESTdown2650</i>	L-type lectin-domain containing receptor kinase IX.1	2.146	0.00807	<i>Vitis vinifera</i>	2.00E-149	<a href="#">XM_002262712.1</a>
<i>UCOESTdown2651</i>	Serine esterase domain-containing protein	2.145	0.00341	<i>Arabidopsis thaliana</i>	5.00E-130	<a href="#">NM_118709.3</a>
<i>UCOESTdown2652</i>	Galactoside 2-alpha-L-fucosyltransferase	2.144	0.0367	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002284752.1</a>
<i>UCOESTdown2653</i>	Sulfotransferase 2A (ST2A)	2.144	0.00763	<i>Arabidopsis thaliana</i>	2.00E-137	<a href="#">NM_120783.3</a>
<i>UCOESTdown2654</i>	Fructose-1,6-bisphosphatase	2.143	0.00458	<i>Fragaria x ananassa</i>	0.0	<a href="#">EU730788.1</a>
<i>UCOESTdown2655</i>	Uncharacterized protein	2.143	0.0193	<i>Glycine max</i>	6.00E-93	<a href="#">XM_003542531.1</a>
<i>UCOESTdown2656</i>	Uncharacterized protein	2.142	0.00719	<i>Glycine max</i>	5.00E-59	<a href="#">XM_003555571.1</a>
<i>UCOESTdown2657</i>	SNF1-related protein kinase regulatory subunit gamma-1	2.141	0.0485	<i>Vitis vinifera</i>	9.00E-160	<a href="#">XP_002277342.1</a>
<i>UCOESTdown2658</i>	NAC transcription factor 1	2.139	0.00674	<i>Malus x domestica</i>	3.00E-118	<a href="#">HM122673.1</a>
<i>UCOESTdown2659</i>	No homology	2.139	0.0285			
<i>UCOESTdown2660</i>	D-alanine--D-alanine ligase	2.139	0.00411	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003623472.1</a>
<i>UCOESTdown2661</i>	Fanconi anemia group D2 protein	2.138	0.0167	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002278218.2</a>
<i>UCOESTdown2662</i>	Serine/threonine-protein kinase PEPKR2	2.138	0.00351	<i>Glycine max</i>	0.0	<a href="#">XP_003523797.1</a>

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<i>UCOESTdown2663</i>	Uncharacterized protein	2.135	0.00416	<i>Vitis vinifera</i>	6.00E-90	<a href="#">XM_002267677.2</a>
<i>UCOESTdown2664</i>	Pentatricopeptide repeat-containing protein	2.134	0.0452	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002275748.1</a>
<i>UCOESTdown2665</i>	Cyclin-A2-4	2.133	0.00425	<i>Vitis vinifera</i>	1.00E-152	<a href="#">XM_002280556.2</a>
<i>UCOESTdown2666</i>	No homology	2.132	0.00474			
<i>UCOESTdown2667</i>	No homology	2.132	0.00615			
<i>UCOESTdown2668</i>	Phosphoglucomutase	2.131	0.0148	<i>phosphoglucomutase</i>	4.00E-35	<a href="#">XM_003556033.1</a>
<i>UCOESTdown2669</i>	Dehydrin 1	2.130	0.0342	<i>Prunus persica</i>	6.00E-10	<a href="#">AJ271620.1</a>
<i>UCOESTdown2670</i>	Xyloglucan endotransglucosylase/hydrolase	2.127	0.00576	<i>Rosa hybrid</i>	3.00E-171	<a href="#">AB428380.1</a>
<i>UCOESTdown2671</i>	G-type lectin S-receptor-serine/threonine-protein	2.127	0.00242	<i>Vitis vinifera</i>	3.00E-93	<a href="#">XM_002270186.2</a>
<i>UCOESTdown2672</i>	Glucose-1-phosphate adenylyltransferase	2.126	0.011	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002281187.2</a>
<i>UCOESTdown2673</i>	Uncharacterized protein	2.126	0.0205	<i>Vitis vinifera</i>	8.00E-81	<a href="#">XM_002280845.1</a>
<i>UCOESTdown2674</i>	Uncharacterized protein	2.125	0.0222	<i>Populus trichocarpa</i>	3.00E-56	<a href="#">XM_002315778.1</a>
<i>UCOESTdown2675</i>	Histone H3	2.124	0.00637	<i>Medicago truncatula</i>	6.00E-67	<a href="#">XM_003622933.1</a>
<i>UCOESTdown2676</i>	No homology	2.124	0.0281			
<i>UCOESTdown2677</i>	Dehydrin 2	2.124	0.00415	<i>Prunus persica</i>	2.00E-11	<a href="#">AY465376.1</a>
<i>UCOESTdown2678</i>	Structural maintenance of chromosomes protein 6	2.123	0.00411	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002278077.2</a>
<i>UCOESTdown2679</i>	Calcium-transporting ATPase 8	2.123	0.0209	<i>Glycine max</i>	2.00E-180	<a href="#">XM_002262793.2</a>
<i>UCOESTdown2680</i>	MADS transcription factor 1	2.122	0.00805	<i>Populus deltoides</i>	1.00E-43	<a href="#">EU121636.1</a>
<i>UCOESTdown2681</i>	No homology	2.121	0.00697			
<i>UCOESTdown2682</i>	Serine/threonine-protein kinase PBS1	2.119	0.0279	<i>Vitis vinifera</i>	0.0	<a href="#">XP_002281166.1</a>
<i>UCOESTdown2683</i>	Uncharacterized protein	2.119	0.00326	<i>Populus trichocarpa</i>	1.00E-87	<a href="#">XM_002311692.1</a>
<i>UCOESTdown2684</i>	Uncharacterized protein	2.118	0.0261	<i>Populus trichocarpa</i>	1.00E-117	<a href="#">XM_002328764.1</a>
<i>UCOESTdown2685</i>	Uncharacterized protein	2.117	0.00782	<i>Vitis vinifera</i>	1.00E-25	<a href="#">XM_002272568.1</a>
<i>UCOESTdown2686</i>	Uncharacterized protein	2.117	0.0153	<i>Populus trichocarpa</i>	8.00E-45	<a href="#">XM_002304833.1</a>
<i>UCOESTdown2687</i>	Uncharacterized protein	2.115	0.0061	<i>Medicago truncatula</i>	4.00E-58	<a href="#">XM_003596041.1</a>
<i>UCOESTdown2688</i>	No homology	2.113	0.045			
<i>UCOESTdown2689</i>	Phosphatidylinositol 4-kinase type 2-beta	2.113	0.0325	<i>Vitis vinifera</i>	0.0	<a href="#">XP_002278311.2</a>
<i>UCOESTdown2690</i>	Lysine histidine transporter 1	2.113	0.0424	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002268574.1</a>
<i>UCOESTdown2691</i>	Uncharacterized protein	2.113	0.00478	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002280286.1</a>

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<i>UCOESTdown2692</i>	Ribonuclease E	2.112	0.0204	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003615502.1</a>
<i>UCOESTdown2693</i>	Uncharacterized protein	2.112	0.0135	<i>Vitis vinifera</i>	3.00E-140	<a href="#">XM_002276362.1</a>
<i>UCOESTdown2694</i>	Sodium-coupled neutral amino acid transporter 6	2.111	0.00325	<i>Vitis vinifera</i>		<a href="#">XM_002278629.2</a>
<i>UCOESTdown2695</i>	MYB transcription factor 48 (MYB48)	2.110	0.03	<i>Vitis vinifera</i>	4.00E-85	<a href="#">XM_002273436.2</a>
<i>UCOESTdown2696</i>	No homology	2.110	0.0167			
<i>UCOESTdown2697</i>	ketose-bisphosphate aldolase class-II family protein	2.110	0.00282	<i>Arabidopsis lyrata</i>	0.0	<a href="#">XM_002892947.1</a>
<i>UCOESTdown2698</i>	Pseudouridine synthase A	2.109	0.0259	<i>Glycine max</i>	9.00E-18	<a href="#">XM_003519091.1</a>
<i>UCOESTdown2699</i>	S-Acyltransferase	2.109	0.0362	<i>Arabidopsis thaliana</i>	2.00E-83	<a href="#">NM_001203182.1</a>
<i>UCOESTdown2700</i>	No homology	2.106	0.00224			
<i>UCOESTdown2701</i>	No homology	2.106	0.00255			
<i>UCOESTdown2702</i>	Allene oxide synthase protein	2.106	0.00379	<i>Lonicera japonica</i>	0.0	<a href="#">DQ303120.1</a>
<i>UCOESTdown2703</i>	Uncharacterized protein	2.106	0.00257	<i>Glycine max</i>	0.0	<a href="#">XM_003531997.1</a>
<i>UCOESTdown2704</i>	WD repeat-containing protein DWA2	2.105	0.00676	<i>Glycine max</i>	0.0	<a href="#">XM_003523092.1</a>
<i>UCOESTdown2705</i>	Serine carboxypeptidase 20	2.105	0.0121	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002264418.2</a>
<i>UCOESTdown2706</i>	No homology	2.105	0.0223			
<i>UCOESTdown2707</i>	Glycerophosphodiester phosphodiesterase GDE1	2.105	0.00304	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002273432.2</a>
<i>UCOESTdown2708</i>	Uncharacterized protein	2.105	0.0495	<i>Sorghum bicolor</i>	1.00E-05	<a href="#">XM_002445522.1</a>
<i>UCOESTdown2709</i>	Phosphoglucomutase	2.102	0.0208	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002263777.1</a>
<i>UCOESTdown2710</i>	Purine permease 10	2.102	0.0122	<i>Vitis vinifera</i>	4.00E-134	<a href="#">XM_002274309.2</a>
<i>UCOESTdown2711</i>	Uncharacterized protein	2.100	0.0063	<i>Vitis vinifera</i>	3.00E-45	<a href="#">XM_002275774.1</a>
<i>UCOESTdown2712</i>	Methyl-CpG-binding domain 7	2.098	0.0234	<i>Arabidopsis lyrata</i>	2.00E-04	<a href="#">XM_002866305.1</a>
<i>UCOESTdown2713</i>	Filament- plant protein 4	2.098	0.00334	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002280270.2</a>
<i>UCOESTdown2714</i>	Disease resistance protein	2.097	0.0158	<i>Vitis vinifera</i>	2.00E-97	<a href="#">XM_003632417.1</a>
<i>UCOESTdown2715</i>	Uncharacterized protein	2.097	0.0197	<i>Vitis vinifera</i>	5.00E-155	<a href="#">XM_002280594.2</a>
<i>UCOESTdown2716</i>	Uncharacterized protein	2.097	0.0113	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002330253.1</a>
<i>UCOESTdown2717</i>	No homology	2.096	0.00819			
<i>UCOESTdown2718</i>	Uncharacterized protein	2.096	0.0135	<i>Glycine max</i>	5.00E-58	<a href="#">XM_003555571.1</a>
<i>UCOESTdown2719</i>	Uncharacterized protein	2.096	0.00849	<i>Vitis vinifera</i>	6.00E-50	<a href="#">XM_002275842.2</a>
<i>UCOESTdown2720</i>	Brassinosteroid-regulated protein BRU1	2.095	0.00457	<i>Vitis vinifera</i>	6.00E-137	<a href="#">XP_002262761.1</a>
<i>UCOESTdown2721</i>	Uncharacterized protein	2.094	0.0286	<i>Vitis vinifera</i>	3.00E-61	<a href="#">XM_002269434.2</a>
<i>UCOESTdown2722</i>	Serine/threonine-protein kinase	2.093	0.00387	<i>Vitis vinifera</i>	0.0	<a href="#">XP_002276606.1</a>

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<i>UCOESTdown2723</i>	Guanine nucleotide-binding protein alpha-1 subunit	2.091	0.00219	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002281826.2</a>
<i>UCOESTdown2724</i>	Aldehyde dehydrogenase family 3 member H1	2.091	0.0146	<i>Vitis vinifera</i>	7.00E-22	<a href="#">XM_002285830.1</a>
<i>UCOESTdown2725</i>	No homology	2.089	0.0493			
<i>UCOESTdown2726</i>	No homology	2.088	0.047			
<i>UCOESTdown2727</i>	Protein-tyrosine phosphatase-like member B	2.088	0.0059	<i>Medicago truncatula</i>	2.00E-51	<a href="#">XM_003606449.1</a>
<i>UCOESTdown2728</i>	DnaJ homolog subfamily C member 17	2.088	0.014	<i>Vitis vinifera</i>	6.00E-25	<a href="#">XM_002275821.1</a>
<i>UCOESTdown2729</i>	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit 3	2.087	0.0409	<i>Arabidopsis thaliana</i>	3.00E-111	<a href="#">NM_148160.2</a>
<i>UCOESTdown2730</i>	No homology	2.086	0.0326			
<i>UCOESTdown2731</i>	Heavy-metal-associated domain--containing protein	2.086	0.00305	<i>Arabidopsis thaliana</i>	4.00E-61	<a href="#">NM_001125938.1</a>
<i>UCOESTdown2732</i>	3-ketoacyl-CoA synthase	2.085	0.0129	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003592334.1</a>
<i>UCOESTdown2733</i>	Omega-6 fatty acid desaturase (FAD)	2.085	0.00227	<i>Hevea brasiliensis</i>	0.0	<a href="#">DQ023609.1</a>
<i>UCOESTdown2734</i>	Plasma membrane ATPase 1	2.085	0.031	<i>Glycine max</i>	0.0	<a href="#">XM_003543797.1</a>
<i>UCOESTdown2735</i>	Uncharacterized protein	2.085	0.00563	<i>Glycine max</i>	2.00E-121	<a href="#">XM_003530203.1</a>
<i>UCOESTdown2736</i>	No homology	2.084	0.0315			
<i>UCOESTdown2737</i>	Calcium-binding protein CML22	2.083	0.00243	<i>Vitis vinifera</i>	5.00E-86	<a href="#">XM_002266630.1</a>
<i>UCOESTdown2738</i>	Uncharacterized protein	2.083	0.00361	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002274645.2</a>
<i>UCOESTdown2739</i>	HD domain class transcription factor (HD20)	2.082	0.0193	<i>Malus x domestica</i>	2.00E-12	<a href="#">HM122578.1</a>
<i>UCOESTdown2740</i>	No homology	2.082	0.00418			
<i>UCOESTdown2741</i>	Uncharacterized protein	2.082	0.00446	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002268147.1</a>
<i>UCOESTdown2742</i>	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	2.081	0.0076	<i>Rosa canina</i>	2.00E-86	<a href="#">FN689381.1</a>
<i>UCOESTdown2743</i>	Uncharacterized protein	2.080	0.0195	<i>Glycine max</i>	1.00E-47	<a href="#">XM_003529427.1</a>
<i>UCOESTdown2744</i>	Uncharacterized protein	2.079	0.00721		1.00E-62	<a href="#">XM_003555571.1</a>
<i>UCOESTdown2745</i>	Uncharacterized protein	2.079	0.0293	<i>Glycine max</i>	5.00E-64	<a href="#">XM_003518476.1</a>
<i>UCOESTdown2746</i>	Uncharacterized protein	2.078	0.00631	<i>Vitis vinifera</i>	5.00E-29	<a href="#">XM_002274611.2</a>
<i>UCOESTdown2747</i>	DNA topoisomerase 6 subunit B	2.077	0.0353	<i>Medicago truncatula</i>	0.0	
<i>UCOESTdown2748</i>	Tubulin beta chain	2.077	0.00415	<i>Prunus salicina</i>	0.0	<a href="#">FJ157349.1</a>
<i>UCOESTdown2749</i>	WRKY transcription factor 54	2.076	0.0283	<i>Glycine max</i>	4.00E-68	<a href="#">NM_001250509.1</a>
<i>UCOESTdown2750</i>	Transmembrane protein 87B	2.076	0.00246	<i>Glycine max</i>	0.0	<a href="#">XM_003547739.1</a>

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<i>UCOESTdown2751</i>	l-2-Hydroxyglutarate dehydrogenase	2.076	0.00287	<i>Vitis vinifera</i>	1.00E-152	<a href="#">XM_002278807.1</a>
<i>UCOESTdown2752</i>	Serine/threonine-protein kinase aurora-1	2.076	0.00385	<i>Arabidopsis thaliana</i>	2.00E-19	<a href="#">NP_195009.1</a>
<i>UCOESTdown2753</i>	No homology	2.075	0.0126			
<i>UCOESTdown2754</i>	Sucrose proton symporter 2	2.075	0.0444	<i>Rosa hybrid</i>	0.0	<a href="#">HQ403679.1</a>
<i>UCOESTdown2755</i>	Phytol kinase 1	2.073	0.0179	<i>Arabidopsis thaliana</i>	1.00E-92	<a href="#">NP_196069.1</a>
<i>UCOESTdown2756</i>	Cation transport regulator 2	2.073	0.00351	<i>Vitis vinifera</i>	3.00E-116	<a href="#">XM_002283167.1</a>
<i>UCOESTdown2757</i>	Pentatricopeptide repeat-containing protein	2.072	0.0227	<i>Vitis vinifera</i>	1.00E-161	<a href="#">XM_002278354.1</a>
<i>UCOESTdown2758</i>	No homology	2.072	0.0248			
<i>UCOESTdown2759</i>	FKBP-type peptidyl-prolyl cis-trans isomerase 1	2.071	0.0162	<i>Vitis vinifera</i>	2.00E-99	<a href="#">XM_002264399.2</a>
<i>UCOESTdown2760</i>	Heavy-metal-associated domain--containing protein	2.071	0.0151	<i>Arabidopsis thaliana</i>	4.00E-62	<a href="#">NM_180520.2</a>
<i>UCOESTdown2761</i>	Uncharacterized protein	2.071	0.00502	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002282926.2</a>
<i>UCOESTdown2762</i>	No homology	2.070	0.00684			
<i>UCOESTdown2763</i>	Uncharacterized protein	2.069	0.00758	<i>Arabidopsis thaliana</i>	0.0	<a href="#">AK226263.1</a>
<i>UCOESTdown2764</i>	Uncharacterized protein	2.069	0.00618	<i>Vitis vinifera</i>	3.00E-166	<a href="#">XR_078112.2</a>
<i>UCOESTdown2765</i>	GDSL esterase/lipase	2.068	0.0396	<i>Medicago truncatula</i>	1.00E-71	<a href="#">XM_003624723.1</a>
<i>UCOESTdown2766</i>	Uncharacterized protein	2.068	0.00226	<i>Glycine max</i>	0.0	<a href="#">XM_003553037.1</a>
<i>UCOESTdown2767</i>	Uncharacterized protein	2.066	0.00303	<i>Glycine max</i>	4.00E-76	<a href="#">NM_001254211.1</a>
<i>UCOESTdown2768</i>	Uncharacterized protein	2.066	0.0257	<i>Vitis vinifera</i>	2.00E-63	<a href="#">XM_002279367.1</a>
<i>UCOESTdown2769</i>	Uncharacterized protein	2.065	0.00508	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002275905.2</a>
<i>UCOESTdown2770</i>	Lariat debranching enzyme	2.064	0.0305	<i>Glycine max</i>	0.0	<a href="#">XR_136495.1</a>
<i>UCOESTdown2771</i>	Protein CYP4	2.063	0.0457	<i>Glycine max</i>	0.0	<a href="#">XM_003523879.1</a>
<i>UCOESTdown2772</i>	No homology	2.063	0.0105			
<i>UCOESTdown2773</i>	4-Coumarate:CoA ligase 3	2.063	0.00231	<i>Rubus idaeus</i>	0.0	<a href="#">AF239685.1</a>
<i>UCOESTdown2774</i>	Serine/threonine protein kinase haspin	2.061	0.00655	<i>Medicago truncatula</i>	8.00E-150	<a href="#">XP_003626154.1</a>
<i>UCOESTdown2775</i>	Uncharacterized protein	2.061	0.025	<i>Vitis vinifera</i>	2.00E-46	<a href="#">XM_002283303.2</a>
<i>UCOESTdown2776</i>	Uncharacterized protein	2.058	0.00326	<i>Arabidopsis thaliana</i>	2.00E-72	<a href="#">NM_121138.2</a>
<i>UCOESTdown2777</i>	Protein IQ-DOMAIN 1	2.057	0.0158	<i>Vitis vinifera</i>	7.00E-76	<a href="#">XM_002274623.1</a>
<i>UCOESTdown2778</i>	PLANT CADMIUM RESISTANCE 2	2.057	0.00538	<i>Vitis vinifera</i>	9.00E-72	<a href="#">XM_002284783.1</a>
<i>UCOESTdown2779</i>	No homology	2.056	0.00338			
<i>UCOESTdown2780</i>	Uncharacterized protein	2.056	0.00372	<i>Glycine max</i>		<a href="#">XM_003545112.1</a>
<i>UCOESTdown2781</i>	Uncharacterized protein	2.054	0.00723	<i>Glycine max</i>	9.00E-38	<a href="#">NM_001253334.1</a>

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<i>UCOESTdown2782</i>	ATP-dependent zinc metalloprotease FtsH	2.053	0.00246	<i>Vitis vinifera</i>	1.00E-131	<a href="#">XM_002275929.2</a>
<i>UCOESTdown2783</i>	No homology	2.053	0.028			
<i>UCOESTdown2784</i>	Methyltransferase PMT25	2.053	0.00454	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_128981.3</a>
<i>UCOESTdown2785</i>	Uncharacterized protein	2.053	0.00361	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002272203.1</a>
<i>UCOESTdown2786</i>	Protein CbbY	2.052	0.0059	<i>Glycine max</i>	5.00E-119	<a href="#">XM_003531295.1</a>
<i>UCOESTdown2787</i>	Fasciclin-like arabinogalactan protein 17	2.051	0.0122	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002270285.2</a>
<i>UCOESTdown2788</i>	Inositol oxygenase 1 (MIOX1)	2.051	0.00316	<i>Arabidopsis thaliana</i>	1.00E-158	<a href="#">NM_101319.3</a>
<i>UCOESTdown2789</i>	Endo-1,3-beta-glucosidase 6	2.050	0.00602	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_125194.3</a>
<i>UCOESTdown2790</i>	ATP-dependent DNA helicase pcrA	2.050	0.0468	<i>Glycine max</i>	0.0	<a href="#">XM_003555445.1</a>
<i>UCOESTdown2791</i>	Uncharacterized protein	2.050	0.0296	<i>Vitis vinifera</i>	4.00E-14	<a href="#">XM_002276668.1</a>
<i>UCOESTdown2792</i>	No homology	2.048	0.00583			
<i>UCOESTdown2793</i>	Glucose and ribitol dehydrogenase	2.048	0.0407	<i>Medicago truncatula</i>	1.00E-66	<a href="#">XM_003591046.1</a>
<i>UCOESTdown2794</i>	Zinc finger family protein	2.047	0.00346	<i>Arabidopsis lyrata</i>	3.00E-65	<a href="#">XM_002884348.1</a>
<i>UCOESTdown2795</i>	LRR receptor-like serine/threonine-protein kinase	2.047	0.00347	<i>Vitis vinifera</i>	0.0	<a href="#">XP_002270928.1</a>
<i>UCOESTdown2796</i>	Uncharacterized protein	2.046	0.0071	<i>Vitis vinifera</i>	2.00E-45	<a href="#">XM_002265913.1</a>
<i>UCOESTdown2797</i>	No homology	2.045	0.00457			
<i>UCOESTdown2798</i>	Uncharacterized protein	2.045	0.0145	<i>Vitis vinifera</i>	3.00E-93	<a href="#">XM_002278854.1</a>
<i>UCOESTdown2799</i>	No homology	2.044	0.0361			
<i>UCOESTdown2800</i>	Uncharacterized protein	2.044	0.00305	<i>Arabidopsis thaliana</i>	0.0	<a href="#">AY056223.1</a>
<i>UCOESTdown2801</i>	Uncharacterized protein	2.043	0.0128	<i>Vitis vinifera</i>	6.00E-12	<a href="#">XM_003631772.1</a>
<i>UCOESTdown2802</i>	Uncharacterized protein	2.043	0.0365	<i>Vitis vinifera</i>	8.00E-35	<a href="#">XM_002270630.2</a>
<i>UCOESTdown2803</i>	Uncharacterized protein	2.042	0.039	<i>Vitis vinifera</i>	6.00E-117	<a href="#">XM_002280893.2</a>
<i>UCOESTdown2804</i>	No homology	2.040	0.0495			
<i>UCOESTdown2805</i>	Uncharacterized protein	2.040	0.00637	<i>Arabidopsis thaliana</i>	4.00E-14	<a href="#">NM_112286.4</a>
<i>UCOESTdown2806</i>	No homology	2.039	0.00759			
<i>UCOESTdown2807</i>	No homology	2.039	0.0182			
<i>UCOESTdown2808</i>	CBS domain-containing protein CBSX5	2.038	0.0335	<i>Glycine max</i>	1.00E-136	<a href="#">XM_003540407.1</a>
<i>UCOESTdown2809</i>	Patellin-6	2.038	0.00424	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_115026.1</a>
<i>UCOESTdown2810</i>	Protein CHUP1	2.035	0.0478	<i>Glycine max</i>	1.00E-89	<a href="#">XM_003550224.1</a>
<i>UCOESTdown2811</i>	Uncharacterized protein	2.035	0.0177	<i>Populus trichocarpa</i>	3.00E-64	<a href="#">XM_002330381.1</a>
<i>UCOESTdown2812</i>	Ubiquitin carboxyl-terminal hydrolase	2.034	0.019	<i>Vitis vinifera</i>	0.0	<a href="#">XM_003635004.1</a>

(Table continues on following page)

<i>UCOESTdown2813</i>	Neutral invertase	2.034	0.0408	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_119652.3</a>
<i>UCOESTdown2814</i>	Uncharacterized protein	2.034	0.00569	<i>Glycine max</i>	0.0	<a href="#">XM_003546400.1</a>
<i>UCOESTdown2815</i>	DNAJ heat shock protein	2.033	0.0116	<i>Arabidopsis thaliana</i>	4.00E-108	<a href="#">NM_104665.1</a>
<i>UCOESTdown2816</i>	Desiccation-related protein PCC13-62	2.033	0.00821	<i>Vitis vinifera</i>	2.00E-137	<a href="#">XM_002273623.2</a>
<i>UCOESTdown2817</i>	Cellulose synthase	2.032	0.0129	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002265919.2</a>
<i>UCOESTdown2818</i>	N-Hydroxythioamide S-beta-glucosyltransferase	2.031	0.00829	<i>Medicago truncatula</i>	3.00E-150	<a href="#">XM_003613303.1</a>
<i>UCOESTdown2819</i>	No homology	2.031	0.00848			
<i>UCOESTdown2820</i>	GDSL esterase/lipase	2.031	0.00999	<i>Arabidopsis thaliana</i>	2.00E-154	<a href="#">NM_105794.3</a>
<i>UCOESTdown2821</i>	Uncharacterized protein	2.031	0.0157	<i>Vitis vinifera</i>	5.00E-96	<a href="#">XM_002268065.2</a>
<i>UCOESTdown2822</i>	Uncharacterized protein	2.031	0.0107	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002284046.1</a>
<i>UCOESTdown2823</i>	Malate dehydrogenase	2.030	0.00517	<i>Medicago sativa</i>	0.0	<a href="#">AF020269.1</a>
<i>UCOESTdown2824</i>	DNA mismatch repair protein Msh6-2	2.029	0.0224	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003620465.1</a>
<i>UCOESTdown2825</i>	Esterase	2.029	0.0281	<i>Vitis vinifera</i>	2.00E-175	<a href="#">XM_002284659.2</a>
<i>UCOESTdown2826</i>	ProPhosphatase 2C 27	2.029	0.0085	<i>Glycine max</i>	4.00E-167	<a href="#">XM_003542620.1</a>
<i>UCOESTdown2827</i>	Uncharacterized protein	2.029	0.0175	<i>Vitis vinifera</i>	3.00E-38	<a href="#">XM_002283842.1</a>
<i>UCOESTdown2828</i>	WRKY transcription factor 13	2.027	0.00256	<i>Malus x domestica</i>	0.0	<a href="#">HM122716.1</a>
<i>UCOESTdown2829</i>	CCAAT-binding transcription factor family protein (NF-YA1)	2.026	0.0405	<i>Glycine max</i>	2.00E-63	<a href="#">NM_001248458.1</a>
<i>UCOESTdown2830</i>	Disease resistance protein	2.025	0.00904	<i>Vitis vinifera</i>	4.00E-27	<a href="#">XM_002264167.2</a>
<i>UCOESTdown2831</i>	No homology	2.024	0.0442			
<i>UCOESTdown2832</i>	Pentatricopeptide repeat-containing protein	2.023	0.0283	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003608483.1</a>
<i>UCOESTdown2833</i>	No homology	2.023	0.0245			
<i>UCOESTdown2834</i>	No homology	2.022	0.00501			
<i>UCOESTdown2835</i>	Serine carboxypeptidase 34	2.021	0.00912	<i>Glycine max</i>	0.0	<a href="#">XM_003540504.1</a>
<i>UCOESTdown2836</i>	kinesin protein KIF22	2.020	0.00351	<i>Vitis vinifera</i>	3.00E-170	<a href="#">XM_002271967.1</a>
<i>UCOESTdown2837</i>	No homology	2.020	0.0363			
<i>UCOESTdown2838</i>	Serine/threonine-protein kinase HT1	2.020	0.00343	<i>Vitis vinifera</i>	0.0	<a href="#">XP_002270753.1</a>
<i>UCOESTdown2839</i>	Protein RIK	2.019	0.00267	<i>Glycine max</i>	7.00E-50	<a href="#">XM_003530388.1</a>
<i>UCOESTdown2840</i>	No homology	2.017	0.0109			
<i>UCOESTdown2841</i>	Dehydration-responsive protein RD22	2.017	0.00571	<i>Prunus persica</i>	8.00E-149	<a href="#">AF319165.1</a>
<i>UCOESTdown2842</i>	Cadmium/zinc-transporting ATPase 3	2.017	0.0352	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002266529.2</a>
<i>UCOESTdown2843</i>	Uncharacterized protein	2.017	0.0284	<i>Medicago truncatula</i>	3.00E-34	<a href="#">XM_003595438.1</a>
<i>UCOESTdown2844</i>	Uncharacterized protein	2.017	0.00411	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002277970.1</a>

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<i>UCOESTdown2845</i>	Uncharacterized protein	2.017	0.0213	<i>Vitis vinifera</i>	5.00E-177	<a href="#">XM_002273838.2</a>
<i>UCOESTdown2846</i>	S-adenosyl-L-methionine synthetase	2.016	0.00612	<i>Malus xiaojinensis</i>	0.0	<a href="#">EU639408.1</a>
<i>UCOESTdown2847</i>	Uncharacterized protein	2.016	0.00709	<i>Medicago truncatula</i>	8.00E-10	<a href="#">XM_003605911.1</a>
<i>UCOESTdown2848</i>	Glycosyltransferase	2.015	0.00449	<i>Populus trichocarpa</i>	0.0	<a href="#">XM_002321035.1</a>
<i>UCOESTdown2849</i>	Uncharacterized protein	2.015	0.00812	<i>Glycine max</i>	3.00E-161	<a href="#">XM_003525303.1</a>
<i>UCOESTdown2850</i>	No homology	2.012	0.0421			
<i>UCOESTdown2851</i>	Aquaporin, MIP family, NIP subfamily	2.011	0.0144	<i>Populus trichocarpa</i>	2.00E-115	<a href="#">XM_002298954.1</a>
<i>UCOESTdown2852</i>	Uncharacterized protein	2.011	0.00731	<i>Glycine max</i>	5.00E-130	<a href="#">NM_001255749.1</a>
<i>UCOESTdown2853</i>	No homology	2.010	0.0399			
<i>UCOESTdown2854</i>	C2H2 zinc finger protein	2.009	0.00373	<i>Medicago truncatula</i>	2.00E-78	<a href="#">XM_003636665.1</a>
<i>UCOESTdown2855</i>	No homology	2.009	0.00601			
<i>UCOESTdown2856</i>	Uncharacterized protein	2.009	0.00609	<i>Vitis vinifera</i>	3.00E-95	<a href="#">XM_002279894.2</a>
<i>UCOESTdown2857</i>	Uncharacterized protein	2.009	0.0104	<i>Vitis vinifera</i>	6.00E-93	<a href="#">XM_003631235.1</a>
<i>UCOESTdown2858</i>	Cellulose synthase 5	2.008	0.0377	<i>Populus tomentosa</i>	0.0	<a href="#">HQ585873.1</a>
<i>UCOESTdown2859</i>	No homology	2.008	0.00284			
<i>UCOESTdown2860</i>	Nitrate transporter 1.2	2.008	0.0257	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002269657.2</a>
<i>UCOESTdown2861</i>	pre-mRNA-Splicing factor ATP-dependent RNA helicase	2.007	0.036	<i>Arabidopsis thaliana</i>	0.0	<a href="#">NM_001198198.1</a>
<i>UCOESTdown2862</i>	Uncharacterized protein	2.006	0.00844	<i>Glycine max</i>	4.00E-104	<a href="#">XM_003542645.1</a>
<i>UCOESTdown2863</i>	No homology	2.005	0.0378			
<i>UCOESTdown2864</i>	Uncharacterized protein	2.003	0.0283	<i>Arabidopsis thaliana</i>	4.00E-31	<a href="#">AK228760.1</a>
<i>UCOESTdown2865</i>	Tryptophan RNA-binding attenuator protein	2.002	0.0315	<i>Arabidopsis thaliana</i>	6.00E-21	<a href="#">NM_117845.3</a>
<i>UCOESTdown2866</i>	Isoamylase 1	2.002	0.00567	<i>Vitis vinifera</i>	0.0	<a href="#">XM_002265928.2</a>
<i>UCOESTdown2867</i>	Inactive leucine-rich repeat receptor kinase	2.002	0.0155	<i>Glycine max</i>	3.00E-144	<a href="#">NM_001254272.1</a>
<i>UCOESTdown2868</i>	Palmate-like pentafoliata 1 transcription factor	2.001	0.0329	<i>Populus trichocarpa</i>	2.00E-46	<a href="#">HM453338.1</a>
<i>UCOESTdown2869</i>	Arginine N-methyltransferase	2.001	0.0403	<i>Medicago truncatula</i>	0.0	<a href="#">XM_003608669.1</a>
<i>UCOESTdown2870</i>	Uncharacterized protein	2.001	0.0226	<i>Glycine max</i>	5.00E-98	<a href="#">XM_003544092.1</a>
<i>UCOESTdown2871</i>	Terminal flower 1 (TFL1)	2.000	0.0113	<i>Fragaria vesca</i>	9.00E-88	<a href="#">JN172097.1</a>