THE EFFECTS OF 1-MCP ON *SUCROSE TRANSPORTER* (*SUT*) GENE EXPRESSION IN CABERNET SAUVIGNON BERRY

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ผลของ 1-MCP ต่อการแสดงออกของยีนซูโครสทรานสปอร์ตเตอร์ในผลองุ่นพันธุ์ คาบาเนซูวิกยง

นางสาวธีรา เกื้อปัญญากูล

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Suranaree University of Technology has approved this thesis submitted in partial fulfillment of the requirements for a Master's Degree.

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ฮอร์โมนเอธิลีนไม่มีผลเกี่ยวข้องกับการสุกในพืชจำพวก non-climacteric ซึ่งต่างจากพวกที่เป็น climacteric การสุกของพืชที่เป็น climacteric เกี่ยวข้องโดยตรงกับการผลิตและการใช้เอธิลีน พืชจำพวกองุ่น (*Vitis vinifera*)จัดอยู่ในกลุ่ม non-climacteric ซึ่งการสุก และการเข้าสี (veraison) ไม่ได้รับอิทธิพลโดยตรงจากฮอร์โมนเอธิลีน ในการทดลองนี้ ได้ศึกษาถึงผลของฮอร์โมนเอธิลีนต่อการสุกในช่วงการเข้าสีขององุ่น โดยนำผลองุ่นพันธุ์คาบาเนซูวิกยงมาบ่มด้วยสาร 1-MCP (1-methylcyclopropene) ซึ่งเป็นสารยับยั้งการทำงานของ ethylene receptor การบ่มได้ทำทิ้งไว้เป็นเวลา 24 ชั่วโมงแล้วจึงเก็บตัวอย่างดังกล่าวมาสกัด RNA หลังจากที่ได้สกัด RNA จากผลองุ่นทั้งจากกลุ่มทดลอง และกลุ่มควบคุมแล้ว ได้นำไปทดสอบการแสดงออกของยีนอย่างกว้างโดยใช้เทคนิค microarray พบว่ายีน *sucrose transporter* (*SUT*)ในองุ่นกลุ่มทดลองมีการแสดงออกลดลง จากนั้นได้ศึกษาระดับการแสดงออกของยีนนี้อย่างละเอียดอีกครั้งด้วยเทคนิค semi-quantitative RT-PCR ผลที่ได้จากการทำ semi-quantitative RT-PCR แสดงให้เห็นว่า องุ่นที่ถูกบ่มด้วยสาร 1-MCP ซึ่งไม่สามารถนำเอธิลีนไปใช้ได้ มีการแสดงออกของยีน *SUT* ลดลงในองุ่นที่ถูกบ่มเมื่ออายุ 8 สัปดาห์ นอกจากนี้ยังพบว่าขนาดของผลองุ่น ณ วันเก็บเกี่ยวในกลุ่มทดลองมีขนาดเล็กกว่าองุ่นในกลุ่มควบคุมอีกด้วย

สาขาเทคโนโลยีชีวภาพ	ลายมือชื่อนักศึกษา.....................................
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TIRA KUAPUNYAKOON : THE EFFECTS OF 1-MCP ON *SUCROSE TRANSPORTER* (*SUT*) GENE EXPRESSION IN CABERNET SAUVIGNON BERRY. THESIS ADVISOR : ASST. PROF. CHOKCHAI WANAPU, Ph.D. 114 PP. ISBN 974-533-371-9

CABERNET SAUVIGNON/ 1-MCP/GENE EXPRESSION/ SUCROSE TRANSPORTER/ MICROARRAY/ RT-PCR

Ethylene does not involve with the ripeness of the non-climacteric fruit which is different from the climacteric fruit. The ripeness of climacteric one involves directly to the ethylene production and utilization. Grape (*Vitis vinifera*) is considered to be non-climacteric fruit which its ripening or veraison was not influenced directly by ethylene.

This experiment studied the effects of ethylene on grape berry ripening by incubated Cabernet sauvignon berries with 1-MCP (1-methylcyclopropene) which is the blocking substance of ethylene receptor. The incubation was set up within 24 hours before the berries were picked up. After that total RNA was extracted from both the sampled berries and control berries. The microarray technique was used to obtain a first global screening.

It was found that *sucrose transporter* (*SUT*) gene expression was reduced. Then, the expression level of this gene was definable measured by semi-quantitative RT-PCR. The results from RT-PCR in 1-MCP-treated groups which could not use ethylene showed the lower expression of *sucrose transporter* gene, especially in the group incubated in week 8. Besides, it was found that the size of berries from 1-MCP-treated group at harvest was smaller than control group.

School of Biotechnology

Academic Year 2004

Student's Signature…………………………....

Advisor's Signature…………………………..….

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Co-advisor's Signature…………………...…...

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Tira Kuapunyakoon

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LIST OF ABBREVIATIONS

ACC = 1-aminocyclopropane-1-carboxilic acid
ACS = ACC Synthase
ACO = ACC Oxidase
CAM = Calmodulin
CDPK = Membrane-bound Ca^{2+} dependent protein kinase
CTR1 = Constitutive triple response 1 (protein kinase)
DEPC = Diethylpyrrocarbonate
E8 = Fruit ripening protein named E8
EILs = Ethylene insensitive 3-like
EINs = Ethylene insensitive
ERF1 = Ethylene responsive element binding factor 1
EREBPs = Ethylene responsive elements binding proteins
ERS = Ethylene response sensor
ETRs = Ethylene receptor
FW = Formula weight
HCN = Cyanide
HXK = Hexokinase
HXT = Hexose transporter
JA = Jasmonic acid
LeETRs = Ethylene receptors in Tomato (*Lycopersicon esculentum*)
MACC = Malonyl-1-aminocyclopropane-1-carboxilic acid
MAPK = Mitogen-activated protein kinase
MAPKK = Mitogen-activated protein kinase kinase
MAPKKK = Mitogen-activated protein kinase kinase kinase
MTA = 5’methylthioadenosine

LIST OF ABBREVIATIONS (Continued)

nor = *non-ripening* gene

NR = Never-ripe protein

PGRs = Plant growth regulatory substances

PP = Protein phosphatase

PVPP = Polyvinylpolypyrrolidone

rin = *ripening-inhibitor* gene

SAM = S-adenosylmethionine or S-AdoMet

SNFl = Sucrose non-fermenting 1

SUT = Sucrose transporter

SUT = *Sucrose transporter* gene

Vvht1 = *Vitis vinifera* hexose transporter gene

UFGT = UDP flavonoid glycosyl transferase

CHAPTER I

INTRODUCTION

Plants have evolved numerous mechanisms for seed dispersal in order to sustain their generations and offspring. Fruits are representative of a good example of genetic expansion. They have tried to live their heredity by producing numerous amounts of seed. For examples, tomato, melon and jack fruit, or even if more complex fruits such as strawberry and pineapple, they have a lot of seeds for their lively mechanisms. Fruits can be divided into dehiscent (dry) fruit and non-dehiscent (fleshy) fruit (Giovannoni, 2001). Examples of dehiscent fruit are legumes and the siliques of many of the Brassicaceae, including *Arabidopsis thaliana*.

The ripe characteristic is the correlation between biochemical and physiological events that happen at the terminal stage of fruit development such as an increased respiration, chlorophyll degradation, production of essential oils, cell wall loosing and degradation, and an increase in ethylene production (Rhodes, 1980 and Abeles et al, 1992). These events generally include modification of texture, heightened levels of flavor and aromatic volatiles, increased susceptibility to post harvest pathogens, alterations in pigment biosynthesis and accumulation, conversation of starch to sugars and the transferring of sugar and mineral into fruit tissues (Giovannoni, 2001). In addition to these phenomena, there are variations on ripening of different fruits. Some of these reflect the diversity of specific species or cultivars. For example, the color of ripe apples can be red, yellow, or green and different pigments are responsible for these colors (Abeles et al, 1992).

1.1 Climacteric and non-climacteric fruit

The terms climacteric and non-climacteric are used to describe fruit which ripen when treated with ethylene, and those that do not. The distinguished terms of climacteric and non-climacteric, is on the basis of respiration and ethylene biosynthesis rates (Giovannoni, 2001 and Abeles et al, 1992). In the climacteric fruits, ethylene is necessary for the coordination and completion of ripening. Their respiration and ethylene production will increase during the ripening stage. It is assumed that the rising level of ethylene in ripening time is to ensure a maximum rate of ripening, senescence and abscission. Similarly, the roles of increased respiration is to provide the energy used in catabolic processes (Abeles et al, 1992). Fruits can be more ripened after they are picked off from their trees. They can emit ethylene gas to make the adjacent fruits to be ripened. The examples of climacteric fruit are tomato, avocado, banana, peaches, plums, apple and mango (Giovannoni, 2001). Their ripening is thought to be ethylene dependent mechanism. The examples of climacteric and non-climacteric fruits are summarized in table 1.

According to Giovannoni (2001), these non-climacteric fruits, including grape do not require ethylene circulation for their ripening. Their ripening is considered to be ethylene independent, which means, after they are harvested, they will not continue on their ripening metabolism. The pattern of ethylene production and respiration during ripening and after harvest is not received any considerable interest to study, due to some of these fruits, such as pineapple and strawberry, are composed of non-ovarian tissue. And cucumber are harvested and consumed as immature fruit, while others, such as citrus, are harvested after ripening is complete. Some plants such as bell peppers, are horticultural selections in which normal ripening is inhibited (Abeles et al, 1992). The researches involve to ethylene are more on the area of climacteric than non-climacteric. Therefore, the roles of ethylene in these plants are more elucidated on the area of climacteric than non-climacteric.

Table 1 List of fruit characterized as being climacteric or non-climacteric when harvested at commercial maturity (rewrite from Abeles et al, 1992).

climacteric	Non-climacteric
Apple	Bell pepper
Avocado	Cherry
Banana	Citrus
Cantaloupe	Grape
Cherimoya	Chinese jujube
Feijoa	Pineapple
Fig	Snap bean
Jujube	Strawberry
Mango	Watermelon
Olive	
Passion fruit	
Paw paw	
Persimmon	
Peach	
Pear	
Plum	
Tomato	

In recent years, scientists have paid more attention on the study of molecular basis of development and ripening of fleshy fruits involves to ethylene production. That was the beginning of the studying of the molecular regulation of ethylene responsive genes in climacteric fruit. Tomato was a good candidate which was very popular for ethylene study in climacteric fruit. Penarrubia et al. (1992) found that, the inhibition of *E8* gene expression, an ethylene-responsive gene which is transcriptional activated at the onset of ripening, resulted in overproduction of ethylene hormone during the ripening of detached tomato fruit. One year later, Montgomery et al. (1993) succeeded in identification of ethylene-responsive region in the promoter of a tomato ripening gene (*E4* gene). Additionally, in the last five years, Lui et al. (1999) characterized the ethylene biosynthesis associated with ripening in banana fruit. Most of ethylene studies have been done for climacteric fruit, due to the obvious manner of ethylene change during their ripening. On the other hand, ethylene regulation in non-climacteric fruit is still undercover and unclear.

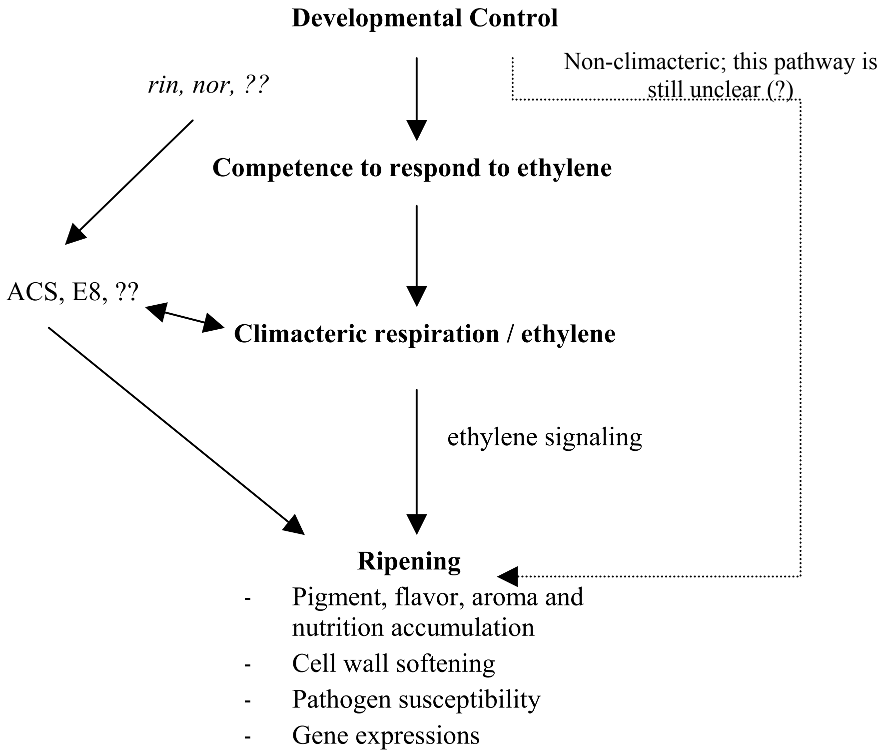


Figure 1 Ripening development in climacteric (solid line) and non-climacteric (dashed line) fruit (derived from Giovannoni, 2001)

Even if in climacteric fruits, there are many suspected points that can not be explained (as indicated as ‘?’ in Figure 1). But, all of the knowledge from many climacteric plants were pooled together to determine the synthesis pathway of ethylene (Figure 2).

1.2 Grape ripening

There are three stages of the grape ripening, stage I, after flowering grape will enter a short period of cell division, followed by vacuolar swelling caused by the storage of organic acids and by cell enlargement. The acidity of the berries reaches a maximum at the end of this stage. Stage II, approximately seven to ten weeks after flowering, is a lag phase characterized by slow growth. Stage III, starts with fast softening, rapid accumulation of sugars and amino acids, decrease of acidity, and expansion of the flesh cells (Fillon et al, 1999). Grape ripening (veraison, the entry to stage III of grape ripening) is characterized by a drop in acidity, an increase in soluble solids and in some cultivars, an increase in an anthocyanin levels. Ethylene production is high in one week after anthesis, decrease during growth and increase again when the fruit is mature (Arshad and Frankenberger, 2002). In some works suggested, ethylene was still low in concentration during the ripening. As in many fruits, the level of abscisic acid increases, while auxin and cytokinin level decrease. Auxin was though to play the major role in ripening. However, ethylene in the form of ethephon treatment has been found to increase or decrease ripening. Application of ethephon to immature grapes delayed growth and ripening. On the other hand, if ethephon was applied at the end of the growth phase and before veraison, the ripening will increase. Grape development and ripening seems to be the result of temporal events not under the direct control of ethylene (Arshad and Frankenberger, 2002).

1.3 Ethylene and its properties, production and signaling pathway

Plant growth and development are regulated by the naturally occurring plant growth regulatory substances (PGRs). They can be classified into five classes: auxins, gibberellins, cytokinins, ethylene and abscisic acid (Arshad and Frankenberger, 2002).

Ethylene is an unsaturated two-carbon gas that has received considerable study as a regulation of plant growth. It is a volatile compound produced by the plant itself. Because the volatiles compound move and diffuse rapidly, so they can act as the regulators and coordinators in the growth and development of plants.

1.3.1 Roles of ethylene

Ethylene (C_2H_4) is a plant hormone involves to the regulation of many physiological response. It was first defined as a ‘ripening hormone’ (Arshad and Frankenberger, 2002). Noichinda (2000) found that 0.1 ppm of internal ethylene concentration resulted in rapid appearance of the yellow color of lime pell. And higher concentration of 0.45 ppm caused of abscission between fruit and fruit stem, 0.65 ppm will increase the aroma of limes. Later, it was found that ethylene has more roles in plant physiology as following (Abeles et al, 1992 and Arshad and Frankenberger, 2002).

1) Effects on cellular physiology in organisms other than higher plants; such as animals, bacteria, fungi, algae, non-vascular plant, ferns.

2) Effects on cellular physiology in higher plants; ethylene regulates the photosynthesis, respiration, transpiration, translocation, pigmentation (chlorophyll levels and terpene biosynthesis), phenolic compounds (isocoumarin, anthocyanin and lipid synthesis), hormone synthesis and levels (auxin transport and degradation, gibberellic acid, cytokinin and abscisic acid).

3) Regulation of dormancy and growth; such as pollen, seed germination, bud break, apical dominance, sprouting of geophytes, cell division, cell wall synthesis, cell elongation, swelling, coiling and curvatures and leaf expansion.

4) Tissue culture and embryogenesis; ethylene can promote the growth of callus in some plants such as peach and sunflower and prevent the differentiation of tobacco.

5) Epinasty; ethylene also controls the planar form of a leave.

6) Hook opening; the hook is assumed to be an adaptation which facilitates the penetration of soil by germinating seedlings. The decreased level of ethylene production inside the hook results in hook opening.

7) Developmental effects such as root initiation**;** peg development, root hair initiation, root nodule formation, storage organ formation (tuber and bulb), xylem formation, flowering (floral promotion, floral inhibition and sexual development).

8) Response to gravity; ethylene alters the form of root and stem growth. Roots go from diagravitropic (horizontal plan) to negatively gravitropic, stems go from negatively gravitropic to diagravitropic. Normally, roots are positively gravitropic and stems are negatively gravitropic.

9) Thigmomoephogenesis; this term is the concept of mechanical disturbance of stems by wind and roots by soil. The primary response of stems and roots to increase ethylene production is an inhibition of elongation coupled with lateral swelling.

10) Exudation; resin and latex formation and gummosis enhancement. Ethylene is thought to increase the gum and resin productions in some plants.

11) Hypertrophy; the potential of producing of masses of expanded and separated cells in plant cortical tissue. The hypertrophy is due to the ethylene production.

12) Aging and senescence of leaves and floral

1.3.2 Physical and chemical properties of ethylene

Ethylene is a two carbon symmetrical compound with one double bond. Its molecular weight is 28.05. It freezes at -181°C, melts at -169.5°C and boils at -103.7°C. It has a relative density to air of 0.978. It is flammable and colorless, and has a sweet, ether-like odor. Its diffusion coefficient in air is approximately 10,000 times of that in water. Its solubility in water is approximately 140 ppm at 25°C and 760 mm Hg pressure. It is 14 times more soluble in lipids than in water and the water/gas partition coefficient for ethylene is 0.081 (Arshad and Frankenberger, 2002). The solubility of gases in lipids is positively correlated with their effectiveness as anesthetics. Ethylene is an anesthetic. It is important to recall that ethylene acts in the liquid phase but is normally measured as a component of the gas phase. Its specific volume of 861.5 ml/g at 21°C is the same as nitrogen, more than that of air (830.2 ml/g), and greater than that of oxygen (755.4 ml/g) or carbon dioxide (547 ml/g). Ethylene has nearly full biological activity at 1 μl/l. This corresponds to 6.5 x 10^{-9} M at 25°C. Solutes in the cytoplasm decrease the solubility of ethylene in the aqueous phase of the cell (Abeles et al, 1992).

1.3.3 Ethylene production and signaling pathway

The formation of S-adenosylmethionine (S-AdoMet) is catalyzed by S-adenosylmethionine synthase (SAM synthase) from the methionine by using one molecule of ATP per one molecule of synthesized S-AdoMet. The S-AdoMet is the methyl group donor for many cellular molecules (methylated acceptors), including nucleic acids, proteins, and lipids. In addition, the S-AdoMet is a precursor of the polyamine synthesis pathway (Spermidine/Spermine biosynthesis pathway). 1-aminocyclopropane-1-carboxilic acid (ACC) is the immediate precursor of ethylene production. The rate-limiting step of ethylene synthesis is the conversion of S-AdoMet to ACC by ACC synthase under most conditions. 5'methylthioadenosine (MTA) is the by-product generated along with ACC production by ACC synthase. Recycling of MTA back to methionine conserves the methylthio group and is able to maintain a constant concentration of cellular methionine even when ethylene is rapidly synthesized. Malonylation of ACC to malonyl-ACC (MACC) deprives the ACC pool and reduces the ethylene production. ACC oxidase catalyses the final step of ethylene synthesis using ACC as a substrate, then carbon dioxide and cyanide (HCN) are released (Wang et al., 2002).

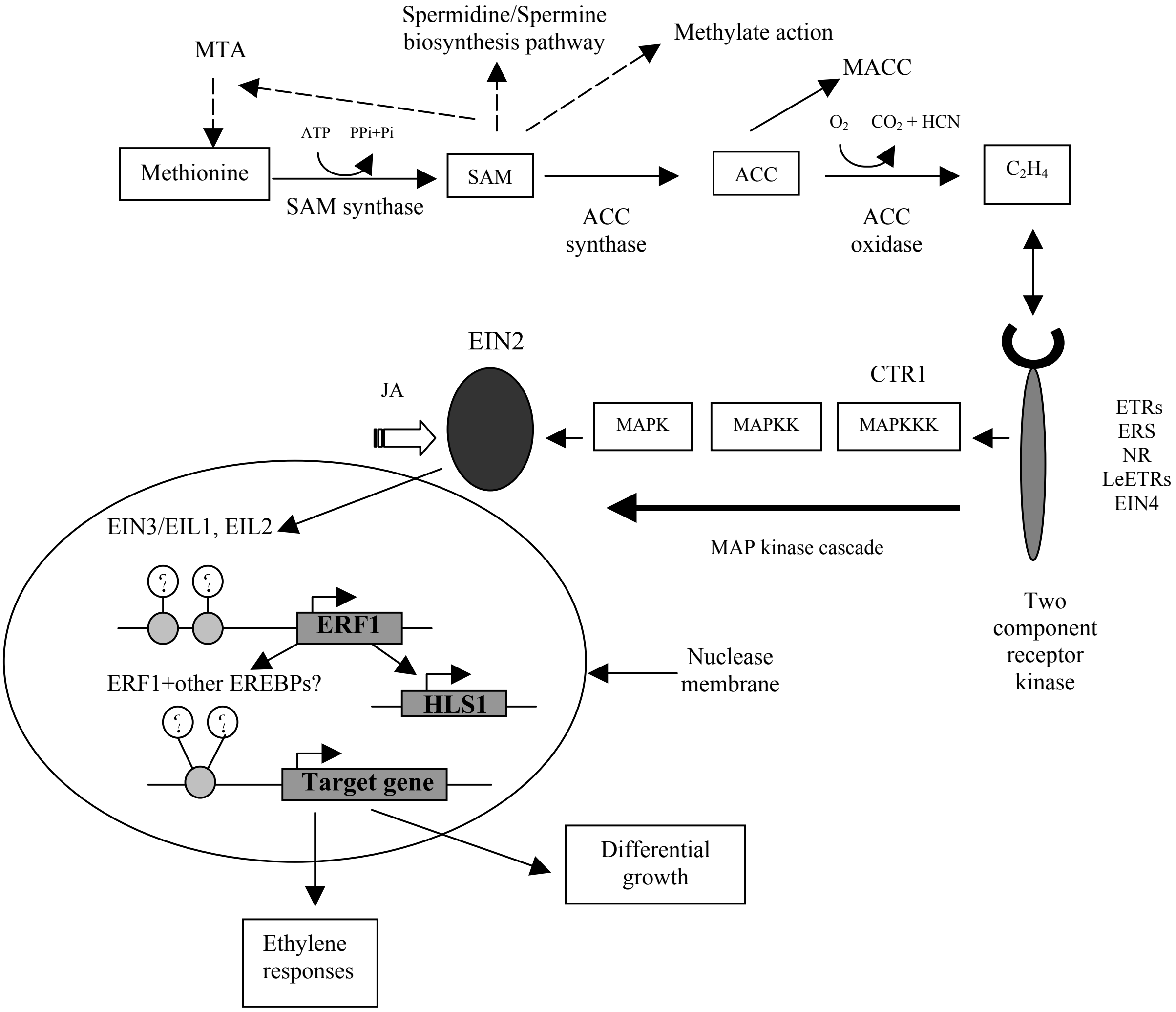


Figure 2 Ethylene biosynthesis and signaling pathway in plants (derived from Giovannoni, 2001; Wang et al., 2002).

There are five ethylene receptors in Arabidopsis plant, ETR1, ETR2, EIN4, ERS1, and ERS2. ETR1 and ERS1 contain three transmembrane domains and a conserved histidine kinase domain, and have been shown to function as homodimers.

ETR2, EIN4, and ERS2 have four membrane-spanning regions and a degenerate histidine kinase domain. Only ETR1, ETR2, and EIN4 have receiver domains at their C termini. From Figure 2, ethylene binding occurs at the N-terminal transmembrane domain of the receptors, and a copper co-factor is required for the binding. In the absence of an ethylene signal, ethylene receptors activate a Raf (a serine/threonine kinase, originally isolated as a viral gene contributing to cellular transformation)-like kinase named CTR1. Then CTR1 will negatively regulate the downstream ethylene response pathway, possibly through a MAPK cascade. Binding of ethylene inactivates the receptors, resulting in deactivation of CTR1, which allows EIN2 to function as a positive regulator of the ethylene pathway. EIN2 contains the N-terminal hydrophobic domain and the novel hydrophilic C terminus. EIN2 positively signals downstream to the EIN3 family of transcription factors located in the nucleus. EIN3 binds to the promoter of *ERF1* gene and activates its transcription in an ethylene-dependent manner. Transcription factors ERF1 and other EREBPs can interact with the GCC box in the promoter of target genes and activate downstream ethylene responses (Wang et al., 2002).

Ethylene causes color changes in some crops and softening or flavor changes in others (Kumar and Walia, 2003). In past, grape was considered not require ethylene for their maturation and ripening development (Giovannoni, 2001). However, El-kereamy and his colleague (2003) showed that ethylene is also important for the grape to develop and ripe. They suggested that exogenous ethylene stimulates the long term expression of genes related to anthocyanin biosynthesis in grape berry (cv. Cabernet sauvignon). Besides, Chervin (in press) confirmed by studying the requirement of ethylene hormone for grape ripening in berry of

Cabernet sauvignon. Even though, the function of ethylene in non-climacteric fruit ripening is still unclear, but according to those studies, ethylene is also important to drive the completion of grape ripeness. In addition, blocking of ethylene hormone effect during veraison stage caused the smaller size of Cabernet sauvignon berry.

1.4 Ethylene receptor inhibitor; 1-Methylcyclopropane (1-MCP)

1-MCP (1-methylcyclopropene) depicted in Figure 4 permanently blocks ethylene binding to its receptor (Figure 3). 1-MCP performs competitive kinetics with ethylene before the compound is bound. After these permanent blocking compounds have bound, competition has not been demonstrated because the receptor has been inactivated for too long (Sisler and Serek, 1999). The fruit may still produce some ethylene but there is no response to any ethylene. In a normal plant response, ethylene attaches to a receptor molecule and a response occurs (Figure 2). Ethylene attaching to the receptor is like a “key” fitting in a “lock,” with ethylene as the “key” and the receptor as the “lock.” When ethylene attaches to the receptor, it is like the lock turns and a door opens. A cascade of events then takes place such as the fruit begins to soften, leaves turn yellow, or flowers drop off. 1-MCP also can act as a “key” that goes into the “lock,” but it is unable to turn the “lock” and “open the door.” When the 1-MCP “key” is in the “lock,” it is not possible for the ethylene “key” to go in the lock. The 1-MCP stops the “lock” from turning so the door can not open. It is in this way, that 1-MCP act as an ethylene inhibitor in plants. 1-MCP can be a very valuable tool when incorporated into a good post harvest program (Blankenship, 2001).

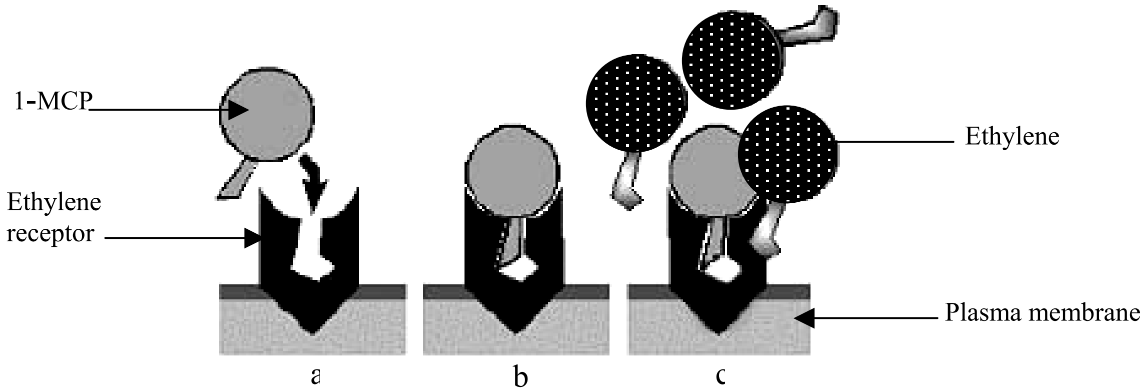


Figure 3 Function of 1-methylcyclopropene (Blankenship, 2001). a= molecules of 1-MCP also bind to the ethylene receptors; b= 1-MCP blocks the receptors without any sent message because the receptors are not unlocked; c= the 1-MCP is not released, so molecules of ethylene are unable to bind the receptor (derived from Blankenship, 2001).

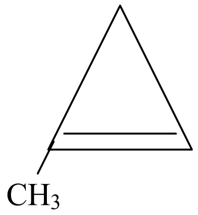


Figure 4 Structure of 1-methylcyclopropene (Sisler and Serek, 1999)

1.5 Sugar transportation in ripening fruit berry

The ripening of grape is characterized by massive sugar imported into the berries. But the events triggering this process and the pathways of transportation are still poorly knew (Fillion et al., 1999). During grape berry ripening, sucrose is transported from leaves to berries, and then is accumulated in the berry vacuoles as glucose and fructose. This accumulation normally begins eight weeks post-flowering and continues until the fruit is ripe at sixteen weeks (Davies and Robinson, 1996). Ethylene is one of the promoting molecules that induce the accumulation of sugar in the grape berry cell (Fillion et. al., 1999). Sugars control the expression of many plant genes and many metabolic and developmental processes (Koch, 1996). There are three different sugar-sensing systems in plants; HXK sensing system, hexose transport associated sensor and sucrose specific pathway which may involve a signaling Sucrose Transporter (Smeekens and Rook, 1997).

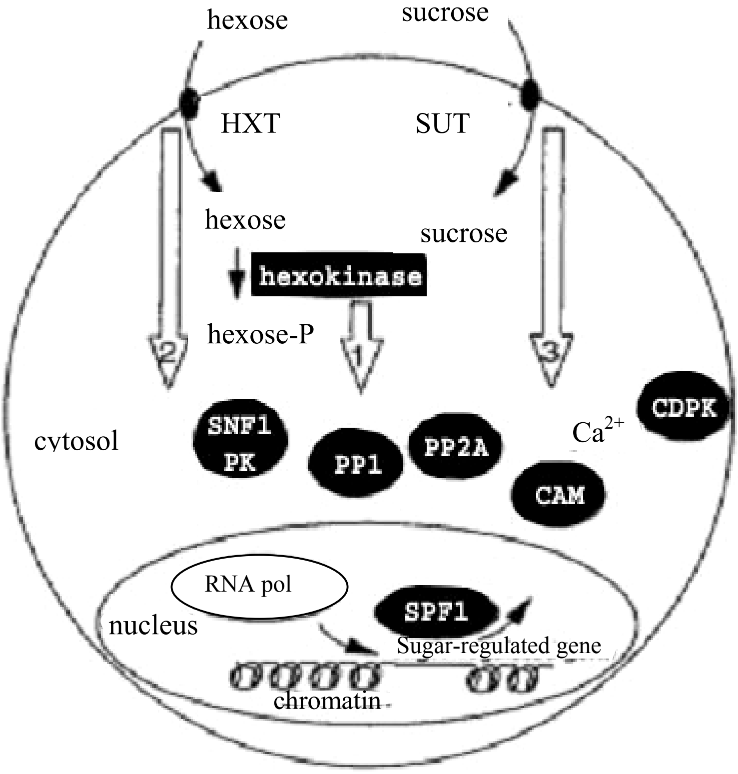


Figure 5 Sugar sensing mechanism discovered in plants (Smeekens and Rook, 1997).

HXK and metabolite transporters (hexose, HXT, and Sucrose, SUT) are proposed to function as sugar sensors that initiate signal transduction processes as indicated by the open arrows numbered 1, 2, and 3 (Figure 5). Sucrose non-fermenting 1 (SNFl) homologs, protein phosphatases (PPl and PP2A), Ca^{2+} concentration, calmodulin (CAM), and a membrane-bound Ca^{2+} dependent protein kinase (CDPK) have been implicated in signal transduction. SPF l is a DNA-binding protein (a transcription factor) that binds to *cis*- elements in the promoters of several sugar-regulated genes. SPF1 mRNA levels are down-regulated by sugars, suggesting that it acts as a negative regulator (Smeekens and Rook, 1997).

If the *SUT* gene expression in grape berry is suppressed when treated with 1-MCP, it means ethylene should involve to the expression of *SUT* gene. The reducing amount of *SUT* transcripts effects on the amount of encoded SUT protein, which has the function involves to the transportation of sucrose into the cell. Finally, the berry cell will lack of sugar for being the transcriptional promoting factors to drive the metabolism of berry development. This may causes the smaller size of grape berry at harvesting date in the grape berries treated by 1-MCP.

1.6 Ethylene level and size of Cabernet sauvignon berry

Internal ethylene concentration (Figure 6), ACC concentration, ACO activity and colored berry (Figure 7) were measured (Chervin, inpress).

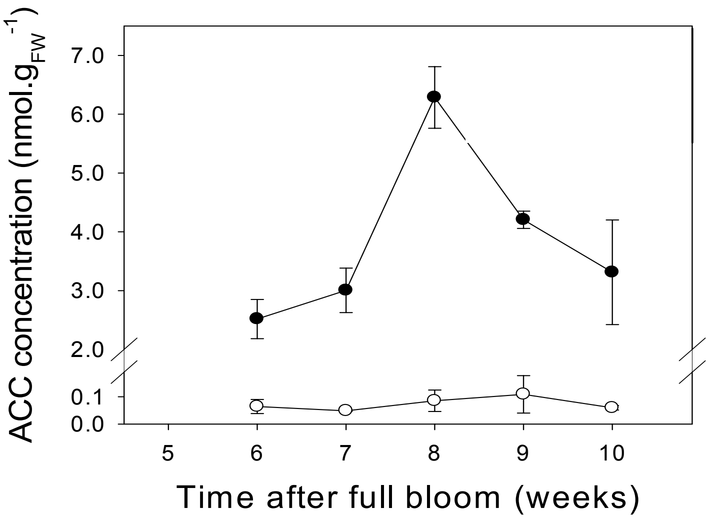


Figure 6 ACC concentration measurement from week 5 to 10 postflowering,

● = Total ACC and ○ = Free ACC (Chervin, inpress)

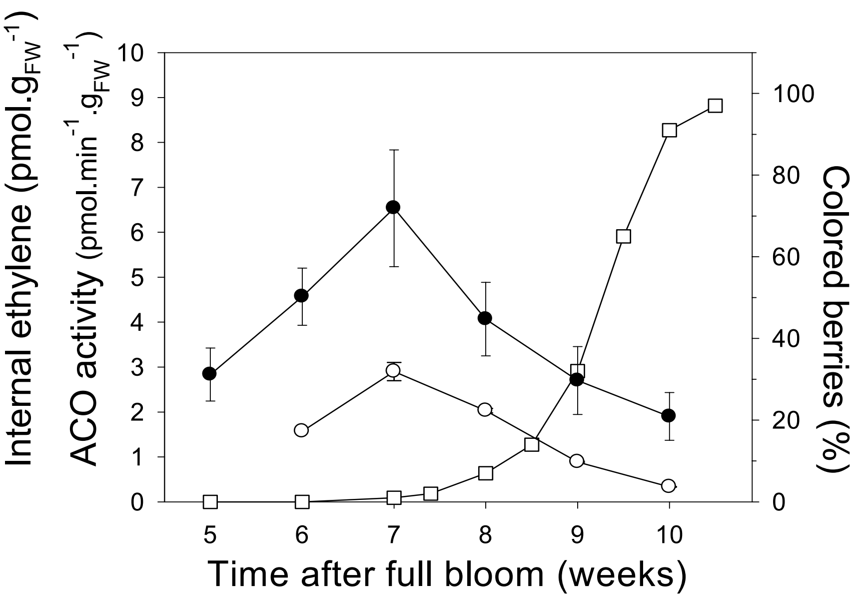


Figure 7 ACO Activity, Internal ethylene and percentage of colored berries from week 5 to 10 postplowering, ● = Internal ethylene, ○ = ACO activity and □ = % of colored berry (Chervin, inpress)

In 2002, the berries of *V. vinifera* L. cv Cabernet sauvignon that grown in local vineyard in Toulouse, France were treated randomly with 1-MCP by Dr. Chevin and his coworkers. Those berries were covered with plastic bag, then 1-MCP was sprayed into the plastic bags. They were left for 24 hours before they were picked up and freezed at -80°C for following molecular analysis. Those samples were incubated and collected at week fifth to tenth postflowering. The control groups were also covered by plastic bag without 1-MCP for 24 hour before they were collected, to get rid of an effect of the bag. Then, whole berry samples were cleaned rapidly and frozen immediately in liquid nitrogen. These samples were stored at –70°C for further analysis.

Some clusters in the same times of those 1-MCP incubations in each week were left on their tree without any plastic bags and incubations in order to allow normal growth, and then their size at week fifteenth (harvesting date) was measured.

According to the data in Figure 6 and 7, grape berries from week 7 and 8 were selected for further analyze in molecular studies. During these weeks, the level of internal ethylene, ACO activity and ACC concentration were highest significantly. So, the collected berries from these two weeks were used to observe the level of gene expression by microarray and semi-quantitative RT-PCR technique.

Physiological stages of grape ripening begins in stage I, the berry will show a short period of cell division, follows by vacuolar swelling resulting from the storage of organic acids and cell enlargement. Stage II; approximately 7-10 weeks post flowering, has slow growth and enter to lag phase (Fillon et al., 1999). Even if there was no difference in the phenotypic changes, but according to the results above, it showed much biochemical changes in the berry. In stage II that seemed nothing interesting happened, was actually very important. The intermediates and substrates and the ripening related-gene transcripts that were involve to the production of enzymes and hormone for ripe procedure were much produced and accumulated in the berry cell, waiting for the signal transduction to enter the stage III of ripening. In stage III, grape berry will start with fast growing, then cell wall would be softening by the effects of polygalacturonase and pectin methylesterase enzyme (Giovannoni, 2001). The berry would transport and accumulate more sugars and amino acids. The organic acid level in the berry would be dropped, so that the acid/sugar balance will be declined rapidly (Fillon et al., 1999).

Some clusters in the same times of those 24 hours 1-MCP incubation in each week were left on their tree without any plastic bags and no more incubation, in order to let them to grow up normally, and then the berry size at harvest was measured. According to Figure 8, the size of berries that were treated by 1-MCP once at week 6, 7 and 8 (then let them grew up naturally) were smaller than the berries that had never been treated by 1-MCP (control group). On the other hand, grape berries from week 5 were not affected by the incubation as same as the grape berries from since week 8, that did not show any difference in the berry size.

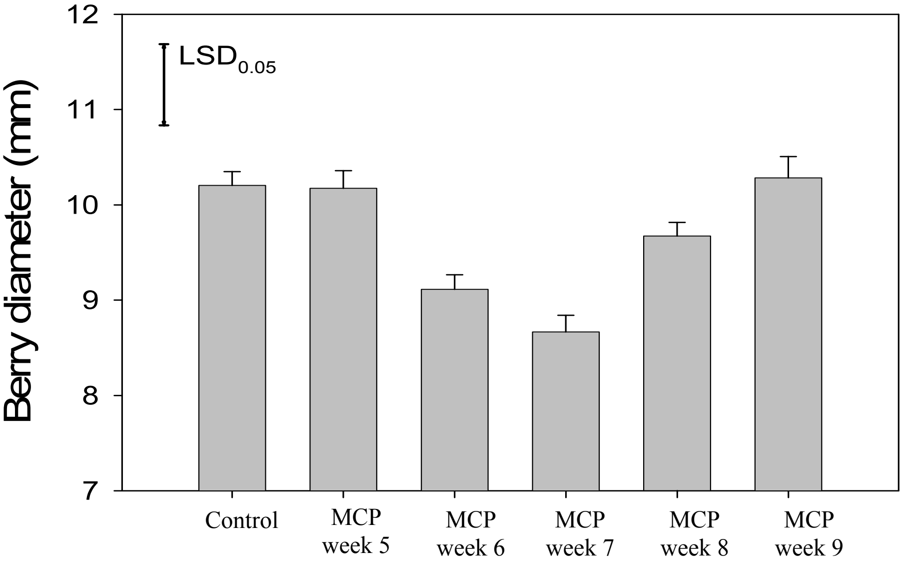


Figure 8 Size of grape berry treated by 1-MCP at each age (Chervin, inpress)

Research Objective

To determine the expression of *SUT* gene in grape (*Vitis vinifera* L. cv. Cabernet sauvignon), which depends upon ethylene by using the inhibitor of ethylene receptor (1-MCP) during veraison stages. In order to obtain the major objective, two main methodologies were involved as following;

1.2.1 Primary screening by oligoarray technique to check the global expression.

1.2.2 Measure the level of *SUT* gene expression by RT-PCR.

CHAPTER II

MATERIALS AND METHODS

2.1 Materials

2.1.1 *V. vinifera* L. cv Cabernet sauvignon grape berries of year 2002

2.1.2 Spin column for RNA extraction

2.1.3 Cotton wool

2.1.4 Glass slide that carries the array of 3,360 spots which are homologue to 3,360 genes of plants (included positive and negative control spots)

2.1.5 Genepix 3 and Sigmacan Software for transformation of the hybridization intensity to numeric data

2.1.6 Primer 3 software for primer design

2.2 Apparatuses

2.2.1 Grinding machine or mortar and pestle

2.2.2 Balance ; Sartorius universal, P.M .P. LABORATOIRE

2.2.3 Swinging rotor centrifuge; Eppendrof 5810 R and a small scale centrifuge; Eppendrof 5415 R

2.2.4 Laminar hood; Holten HBB 2448 LaminAir

2.2.5 Autoclave; Hirayama, HA 300D

2.2.6 Gel electrophoresis with UV photo taking apparatus; UVP

2.2.7 Refrigerator (4^{o}C, -20^{o}C and $–70^{o}$C)

2.2.8 Vacuum dryer pump; Glaswerk, Werthem, GL 32

2.2.9 Speed-vac (concentrator); Jouan, RCT 60

2.2.10 Incubator; Memmert, BE 500

2.2.11 Thermocycler; Stratagene, Robo Cycler, GRADIENT 40

2.2.12 PCR machine; Applied Biosystems, GeneAmp, PCR System 9700

2.2.13 Water bath; National Labnet Company, SWB 5050

2.2.14 UV-VIS Spectrophotometer; Eppendrof, BioPhotometer

2.2.15 Scanner for microarray; Axon Genepix 4000B

2.3 Chemicals and molecular analysis kit

2.3.1 Chemical for storage of berry samples

Liquid nitrogen

2.3.2 Chemical for RNA extraction

Extraction buffer

300 mM Tris-HCl (pH8.3)

5M $NaClO_4$

5mM Polyethyleneglycol (4000 FW)

1% (w/v) SDS

8.5% (w/v) Insoluble polyvinylpolypyrolidone (PVPP)

1% (v/v) ß-mercaptoethanol

Purification solution

Phenol:Chloroform:Isoamyl alcohol (25:24:1)

Chloroform:Isoamyl alcohol (24 :1)

Absolute Ethanol (molecular analysis grade)

3 M Sodium acetate

2.3.3 Chemical for DNase digestion

Per 30 µg of total RNA using;

1 µl of RNasin (RNase inhibitor) (Promega, USA)

20 µl of 10X RQ_1 DNase buffer (Promega, USA)

8µl of RQ_1 RNase-free DNase (Promega, USA)

The final volume were adjusted to 200 µl by RNase-free H_2O

2.3.4 Chemical for gel electrophoresis

Agarose gel

1X TAE buffer (40 mM Tris-acetate and 1 mM EDTA (pH 8.0))

2.3.5 Chemical for gel staining

5 µg/ml Ethidiumbromide in water

2.3.6 Molecular analysis kits

cDNA Synthesis System Kit, High Pure RNA Tissue Kit, Mega-Script T7 Kit (Roche, France)

Fluorescently labeled UTP (Amersham Pharmacia Biotech, UK)

RQ1 RNase-free DNase Kit (Promega, USA)

Reverse Transcription System Kit (Promega, USA)

2.3.7 Reagents for making RNase-free glass and plastic ware and RNase-free water (respectively)

0.1 N NaOH and 0.2% SDS

0.1 % Diethylpyrocarbon (DEPC) in water

2.3.8 Solutions for PCR amplification (Promega, USA)

25 mM $MgCl_2$

10 x Mg free buffer

10 mM dNTP

50 µM primers

0.5 µl of Taq polymerase

Ultra-pure water

2.3.9 Solution for microarray

Hybridization buffer

50 mM Sodium phosphate pH 8.0

50% Formamide

20X SSC stock solution (3.0 M NaCl and 0.3 M Sodium citrate)

6X SSC

50X Denhardt's stock solution (1% w/v Ficoll400, 1% w/v PVPP, 1% w/v bovine serum albumin (Sigma, Fraction 5))

5X Denhardt's solution

0.5% SDS

Washing solution

2X SSC

0.1% SDS

1X SSC

0.5X SSC

0.2X SSC

2.4 Methods

2.4.1 Cabernet sauvignon berries

The berry for molecular analysis was provided from Dr. Chervin. These berries were from local vineyard in Toulouse, France grown in 2002. The method of berry treatment was in the introduction.

2.4.2 RNA extraction

Frozen grape berry from week 7 and 8 which showed the highest ethylene peak was ground into powder by grinding machine which was pre-cooled with liquid N_2, before 4 g of each sample was introduced into 16 ml extraction buffer. The samples were allowed to be thawed before reaching the extraction buffer. The mixture then was shaken vigorously for few minutes, and after it was transferred into the spin column tubes containing cotton wool. The liquid part was collected through cotton wool filtration by centrifugation at 160 x g at 4°C for 15 min. Then 2.5 Volume of absolute ethanol (pre-cooled at –20°C) was added into the collected liquid, and incubated at –20°C for at least 20 min. After incubation it was centrifuged at 2,000 x g at 4°C for 15 min, liquid part was discarded. The collected pellet was washed with 500 µl of 70% ethanol (pre-cool at –20°C), then ethanol was removed without disturbing the pellet. The pellet was resuspended with 500 µl DEPC-treated water. The next steps were proceeded by adding 500 µl phenol:chloroform:isoamyl alcohol (25 :24 :1), then shaking for few minutes prior to centrifugation at 4,500 x g for 2 min. The upper phase liquid was transferred to a new clean 1.5 ml tubes, and another 500 µl of phenol-chloroform:isoamyl alcohol (25 :24 :1) was added. It was centrifuged at 4,500 x g for 2 min. The step of phenol:chloroform:isoamyl alcohol purification was repeated 3 times. Then, the upper phase liquid was transferred into a new clean 1.5 ml tube, then 500 µl of chloroform:isoamyl alcohol (24 :1) was added. The mixture was shaken before centrifuged at 4,500 x g for 4 min. The upper phase was collected without disturbing the solid part on the interphase. Then 0.1 Volume of 3M sodium acetate and 2.5 Volume absolute ethanol (pre-cooled at –20^{o}C) were added and incubated overnight at –20^{o}C. After that, the precipitated pellet was packed by centrifugation at 7,700 x g for 15 min at 4^{o}C. Then, the pellet was vacuum dried for 15 min. Dry pellet was resuspended again in 300 µl of DEPC-treated water. The quality of extracted RNA was checked by agarose gel electrophoresis using ethidiumbromide staining, and its amount was measured by spectrophotometer at A_{260}. The absorbance at A_{280} was also measured in order to calculate the purity of RNA sample ($A_{260/280}$).

2.4.3 DNase digestion

Thirty microgram of total RNA was introduced into 1 µl of RNasin (RNase inhibitor), 20 µl of 10X RQ_1 DNase buffer, 8µl of RQ_1 DNase (1 U/µl, promega), and the final volume was adjusted to 200 µl by water. All solutions was kept on ice during preparing and mixing. Then, the mixture was incubated at 37^{o}C for 30 min. In order to stop the reaction of the DNase, 200 µl of phenol:chloroform:isoamyl alcohol (25:24:1) was added into the mixture and shaken gently for a few minutes. It was centrifuged at 6,000 x g for 10 min. Upper phase was transferred into a new clean 1.5 ml tube, then 2.5 Volume absolute ethanol and 0.1 Volume sodium acetate were added. The mixture was precipitated at -70^{o}C for at least 2 hours (to 2.5 hours). After incubation, it was centrifuged at 4,000 x g for 10 min in order to collect the pellet.

Supernatant was discarded, before the pellet was washed by 70% ethanol. It was centrifuged again at 4,000 x g for 5 min. The pellet was dried prior to dissolve with 10 µl of filtrated ultra pure water.

In order to check the purity of RNA after DNase treatment, the agarose gel electrophoresis with ethydiumbromide staining and the PCR amplification using specific primers were done. These primers were designed from the intron part of anthocyanin production related gene named UDP flavonoid glycosyl transferase *(UFGT*) from *V. vinifera* (El-Kereamy et al., 2003). The sequences of these primers which were 5’CTG CAGGGC CTA ACT CAC TC 3’ (forward) and 5’TAG GTA GCA CTT GGC CCA TC 3’ (reverse) were obtained by Primer 3, a primer designing software.

2.4.4 Microarray

The total RNA from 1-MCP-treated berries from week 7 and 8 were pooled together and the total RNA from control berries from week 7 and 8 were done the same way. Only 2 samples were conducted for global hybridization screening by microarray. MCP-treated group was stained with Cy5 which emitted the red light, while control group was colored by Cy3 which gave green fluorescence.

The glass slide for the microarray was designed from the up-to-date genes which were already known. Fifty base pair long oligonucleotides were synthesized and attached onto the glass slide by covalently binding with their 5’amino modified end. The glass slide contained 3,360 spot complementary to those 3,360 genes. The spots of *Desmin* were the negative control while the *Luciferase* were the positive one (Table D). This glass slide was produced by the sub-institute of INRA, Montpellier, France. There were 2 halves in the glass slide. The top half of the slide was arrayed by 3,360 spots, and the bottom half was done in the same way to make the replication of those 3,360 spots. In each half comprised of 16 blocks (Figure 14), and each block has 14 x 15 spots (Figure 13).

Antisense RNA amplification and simultaneous Cy3 and Cy5 (Cyanine dye) labeling were performed using a modified protocol of *in vitro* transcription (Baugh et al., 2001; Puskas et al., 2002 and Relogio et al., 2002). The Cy3 has fluorescent characteristics similar to tetramethylrhodamine. The color of the solution is pink but the emitted spectrum is green which could be absorbed at A_{532}. On the other hand, the Cy5 which is the greenish blue solution of fluorescein gives red spectrum of A_{635}. Twenty microgram of total RNA was reversetranscribed with dT+T7 primer using a cDNA Synthesis System Kit (Roche). After purification by High Pure RNA Tissue Kit (Roche) and quantification of the double stranded cDNA, T7 linear amplification from Mega Script T7 Kit (Roche) with fluorescent labeled UTP (Amersham Pharmacia Biotech) was performed onto 200 ng cDNA. Labeled cRNA was created by T7 RNA polymerase. Hybridization was performed with 10 μg of labeled purified and fragmented cRNA during 16-20 hours at $42^{o}C$ in 240 μl hybridization buffer. Arrays were washed by immersion into 2X SSC, 0.1% SDS for 5 min (1 slides in 50 ml), 1X SSC for 5 min, 0.5X SSC for 5 min, 0.2X SSC for 5 min and got rid of the water on the slide by brief centrifugation. Hybridized microarrays were scanned simultaneously for Cy3 and Cy5 emission with an Axon Genepix 4000B scanner.

2.4.5 Semi-quantitative RT-PCR

The sequences of the primers using in semi-quantitative RT-PCR amplification were 5’TGC CTT GAT ATC CAC ACG AA 3’ (forward) and 5’GGA CCC TGG ATT TAT CAG CA 3’ (reverse). They were also obtained by Primer 3 software. These primers was designed from the mRNA of *sucrose transporter* gene, (AF021809_1 (AF021809) putative sucrose transporter [*Vitis vinifera*] mRNA) from GeneBank.

The expression of *SUT* gene was further analyzed by semi-quantitative RT-PCR. The level of band intensity showed the relative amount of the cDNA template that was synthesized by the reverse transcriptase (Promega). First, total RNAs were changed into cDNAs by the Reverse Transcription System Kit (Promega), then the cDNA templates were used continuously in normal PCR amplification to measure the relative amount of PCR products. All protocols and solutions of RT-PCR amplification would follow upon the protocol of Reverse Transcription System Kit (Promega). The *β-tubulin* gene was used as the internal standard to normalize the amplified signal.

The intensity of band was changed into the numeric data. First, the bands were framed by the Imaging software. Each frame had equal size, so the inner area was also equal. Then, it was set into a monochrome style before analyzed by Sigmascan Software (El-Kereamy et al., 2003). Sigmascan changed the intensity signal of each framed band into the digital data. Then, these data were saved in the Excel format. Finally, the graph was illustrated by Excel program. The data for plotting the graph was normalized by subtraction of the *β-tubulin* intensity value out of the *SUT* value.

CHAPTER III

RESULTS AND DISCUSSIONS

3.1 RNA extraction

The modification was done to obtain the sufficient purified total RNA. The extraction buffer comprised of 300 mM Tris-HCl (pH8.3), 5M $NaClO_4$, 5mM polyethyleneglycol (4000FW), 1% (w/v) SDS and 8.5% (w/v) insoluble PVPP. The chemicals were put all together and aggregated at 4^oC overnight, in order to saturate the insoluble PVPP, before it was use, 1% (v/v) ß-mercaptoethanol was added subsequently in the extraction buffer. This method was very effective in particular for grape berry cell both green and mature berry, because there were polyethyleneglycol and insoluble PVPP acted as the solid matrix to capture and protect the released total RNA through the extraction steps, until the total RNA was eluted in the steps of purification. Moreover, the ß-mercaptoethanol played a good co-operative role as a reducing agent that destroyed the sulfide bonds of the ribonuclease so that the total RNA was prevented.

Figure 9 and 10 showed the bands of total RNA extracted from control and 1-MCP treated groups. Figure 9 were the RNA samples from week 7. There were 1-MCP treated groups (***M***) and controls (***C***) which were divided into 3 replications (A, B and C). Within those 3 replications there were 2 sub-replications each indicated by I and II. Figure 10 were the RNA samples from week 8, and all description for each lane was same as week 7.

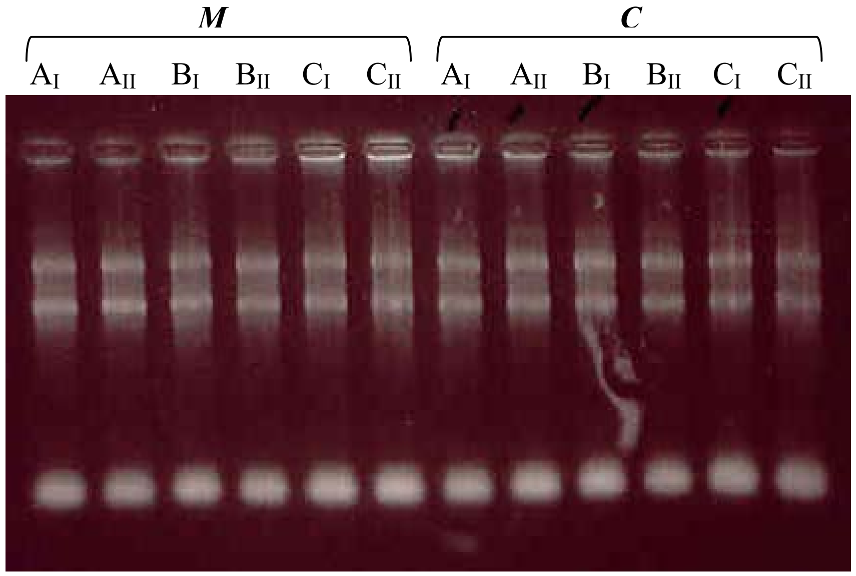


Figure 9 Total RNA extracted from grape berry in week 7, ***C***= control, ***M***= 1-MCP- treated, A= replication 1, B= replication 2, C= replication 3, I=sub-replication 1, II=sub-replication 2

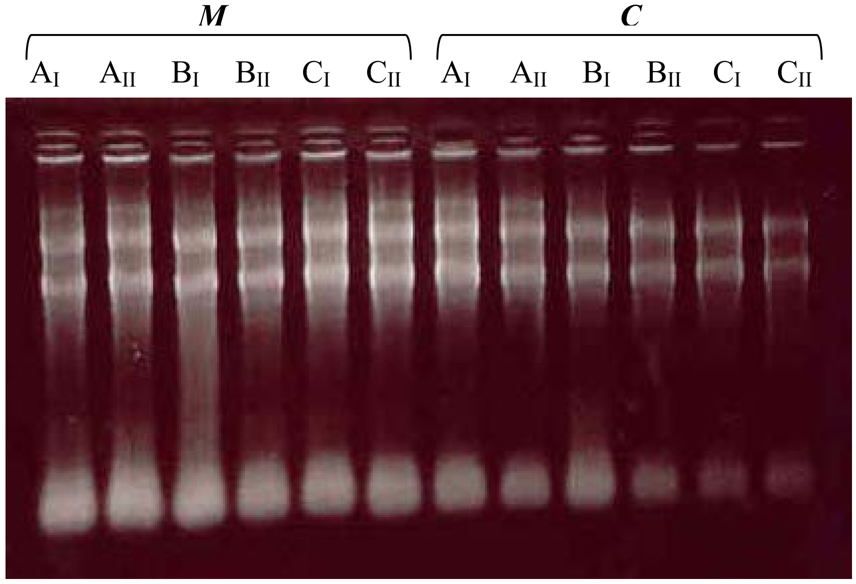


Figure 10 Total RNA extracted from grape berry in week 8, ***C***= control, ***M***= 1-MCP- treated, A= replication 1, B= replication 2, C= replication 3, I=sub-replication 1, II=sub-replication 2

It is generally known that grape is a high polyphenolic compounds and polysaccharides plant. These organic compounds in the grape cell will disturb the nucleic acid extraction as well as in the purification steps by binding to the nucleic acid permanently. So, general methods for the total RNA extraction from this plant are not efficient for isolating high quality of RNA from berry tissues. The method of RNA extraction applied for grape should be modified by the addition of insoluble polyvinylpolypyrrolidone or PVPP (Sigma) and the reducing agent β-mercaptoethanol. The solid matrix will compete to those polyphenolic compounds to bind to the released and partially purified RNA (Geuna et al, 1998), then subtracted from the extraction buffer which contain most of the contaminants.

First, the attempt to use RNA Extraction Kit (Quigen) failed. Even if the application of the kit was designed for all kinds of plant, but it was still insufficient for RNA extraction from high polyphenolic compound plant such as grape. According to the reason above, using the kit for RNA extraction failed due to no solid matrix or PVPP composed in the kit. So, there was nothing to protect the RNA from the naturally contaminated organic compounds.

3.2 DNase digestion

DNase digestion was important for the purification of total RNA. The next steps of microarray and semiquantitative RT-PCR needed high purity of sample RNA, because they involved nucleic acid hybridization. If there was DNA contamination in the total RNA samples, it will result in wrong interpretation data analysis of microarray and the unidentified bands in semiquantitative RT-PCR.

Shorter incubation time with higher amount of DNase gave better quality of RNA than longer time with the lower amount (experimental data was not shown). Even if, DNase should not digest RNA, but leaving the RNA samples at 37^{o}C for a long time gave the opportunity to the contaminated RNase to work and digest the total RNA. Therefore, less risk was to allow the RNA to stay as short as possible in that 37^{o}C incubator, in order to shorten the time for contaminated RNase to work.

According to Figure 11, there were no DNA bands showed in the gel. It could say that total RNA were clean and purify enough for further hybridization by microarray technique and semiquantitative RT-PCR. However, in order to confirm the absence of DNA in the RNA samples, the primers designed especially for PCR amplification of grape DNA was used. These primers were designed from the intron part of anthocyanin production related gene (*UFGT*) from grape (El-Kereamy et al., 2003).

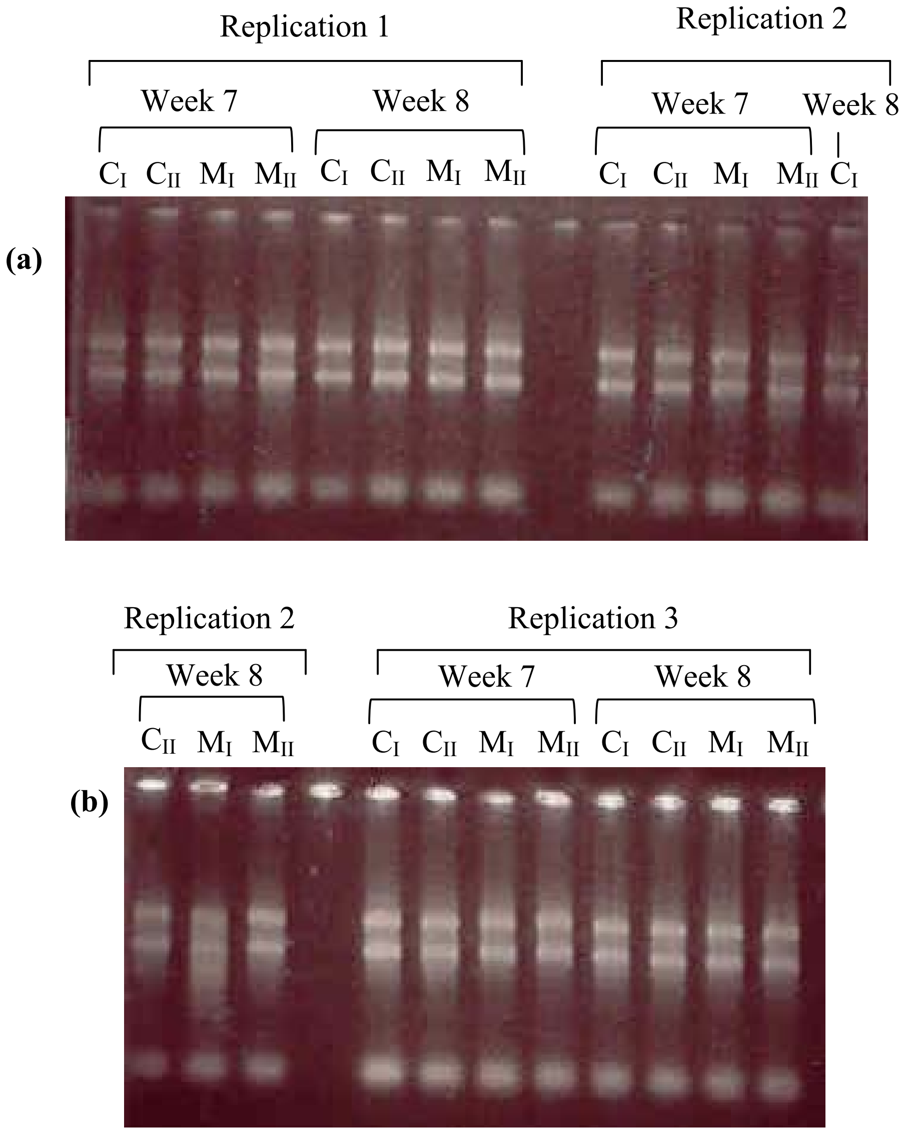


Figure 11 a, b Total RNA from week 7 and 8 after treated with RQ1 RNase-free DNase, C= control, M= 1-MCP- treated, I= replication 1, II= replication 2

Figure 12 showed the absence of contaminated DNA in the chosen RNA samples. Perhaps, there was some amount of DNA left in the samples, but it was so much few to promote any PCR amplification or to interfere to the further hybridization techniques. However, these selected RNA samples were pure enough for further analyzed by microarray and semiquantitative RT-PCR.

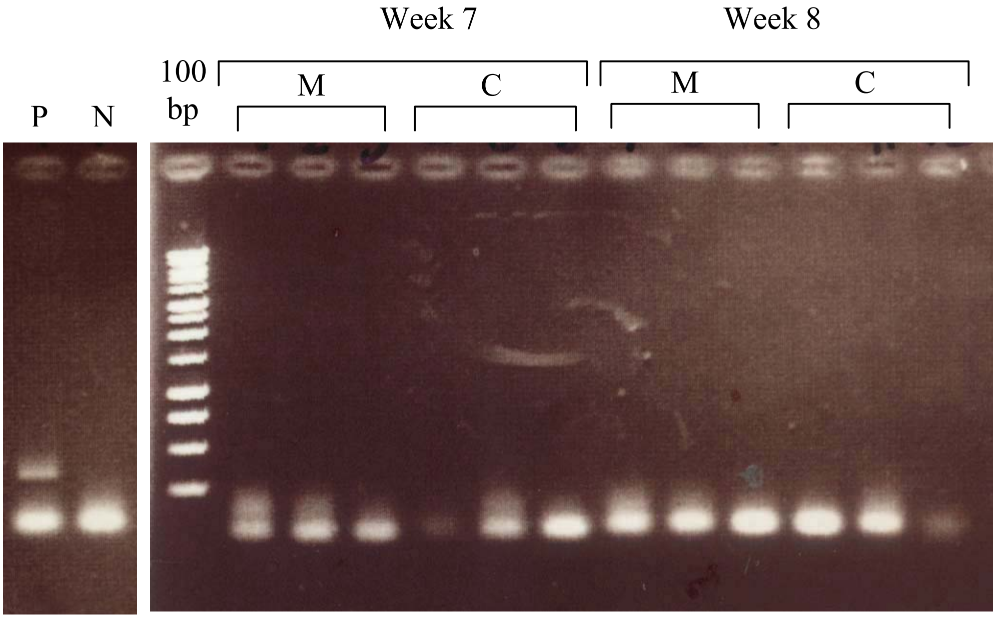


Figure 12 PCR amplification of intronUFGT primer, M= 1-MCP treated, C= control, N= negative control and P= positive control

3.3 Microarray

Microarray technique was selected to observe the global hybridization of genes in Cabernet sauvignon both 1-MCP trated group and control.

Figure 14 showed part of the photo of oligoarray taken from an Axon Genepix 4000B scanner. The red spot is the emitted spectra of Cy5, the green spot is belonged to Cy3 and the yellow is the combination of the equal amount of Cy3 and Cy5. The spots showed red spectra were referred to the induction of the gene expression effected by 1-MCP. The green spectra were referred to the inhibition of the gene expression effected by 1-MCP and the yellow spectra did not show any effects from 1-MCP.

Each spot showed in the Figure 15 was a synthesized oligonucleotide fragment that complemented to a known gene. The 3,360 spots were used to be the templates for making the oligonucleotides. These oligonucleotides were attached onto the glass slide by the commercial microarray-robot. The top half of the slide was arrayed by 3,360 spots, while the bottom half was the replication of those 3,360 spots. In each half comprised of 16 blocks of spots, and each block has 14 x 15 spots (Figure 13).

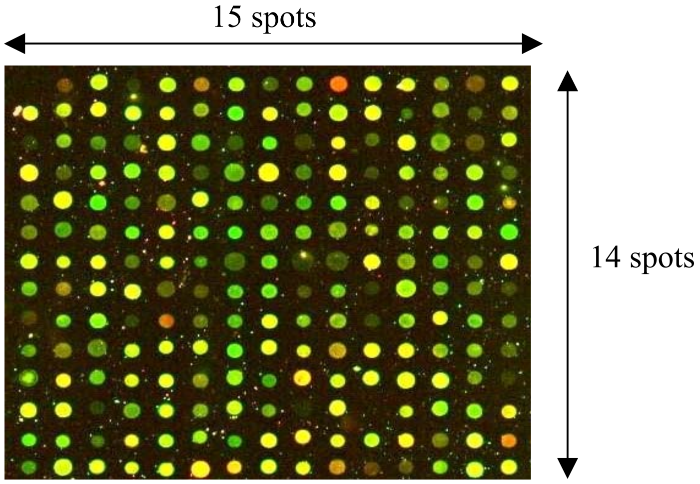


Figure 13 A block of the oligoarray obtained from an Axon Genepix 4000B scanner

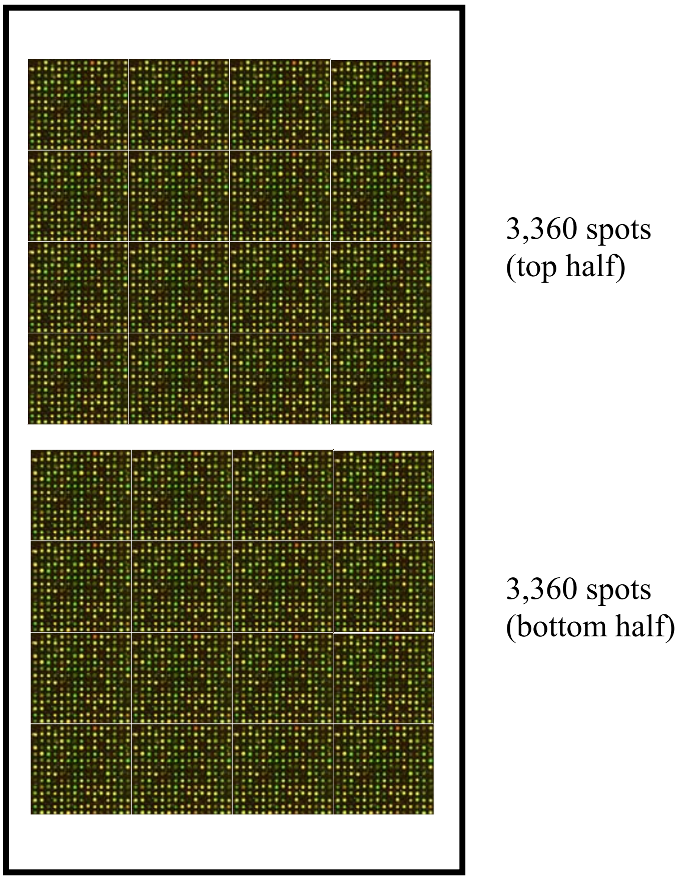


Figure 14 The spot position in the slide of oligoarray

The non-numeric data was changed into the numeric one by the Genepix 3 software. The hybridization intensity of each spot was transformed into the digital data which could save in the format of Excel file. These data would be analyzed in Microsoft Excel program to see which gene was suppressed or induced by 1-MCP treatment.

The normalized values of the transformed hybridization intensity in Table A were analyzed from the raw data. After excluding 15% of the highest and 15% of the lowest values to lower the data variation, the calculated mean ratio of the 70% remaining values were used to normalize the intensity ratios to 1 (Girke et al., 2000). The intensity value of the spot was subtracted by the intensity value of the background for both Cy3 and Cy5. Then the value of Cy5 was normalized to be equal with the range of Cy3. Then, the average Cy5/Cy3 (red/green emitted light) ratio was calculated. This ratio showed the inhibition and the induction of the genes on the glass slide. The values that were less than 1 indicated the suppressed gene expression by 1-MCP. On the other hand, the more than 1 values showed the inducible gene expression by 1-MCP.

Table A (Appendix A) showed the average analyzed values of 3,360 spots of two replications. Each spot from the picture would be transferred into the digital values according to its position in the block, row and column. From

Table B (Appendix A) indicated the concluded microarray results of all *V. vinifera* genes in Table A. *Sucrose Transporter* (*SUT,* the squared value), the gene of interest was suppressed by 1-MCP. Its average Cy5/Cy3 ratio was less than 1.00 (it was 0.843). However, there were many candidates that were inhibited by 1-MCP, such as calmodulin (0.429), polyphenol oxidase (0.398), vacolar invertase 1 GIN1

(0.496), putative serinr/threonine kinase GDBrPK (0.557), chalcone synthase (0.584) and beta 1-3 glucanase (0.288), but according to the previous microarray values conducted by our cooperative group in INRA, Monpellier, France (data was not shown) the good candidate gene that involved to the reduction size of grape berry was *Sucrose Transporter*.

Table C (Appendix A) was also made to see whether or not some ethylene related genes were affected by this 1-MCP treatment. *AP2/EREBP-like transcription* (AC012187), *putative ethylene receptor* (*V. vinifera*) and *ethylene responsive element binding protein* (*Fagus* sp.) were inhibited while *DNA binding protein EREBP-4* (common tobacco), *ethylene responsive element binding protein* (*Fagus* sp.), *ethylene responsive element binding factor* (*Fagus* sp.*), ethylene responsive element binding factor* (*Nicotiana* sp.) and *ACC synthase* (*Prunus armeniaca*) were a little bit enhanced. Three fifth of *ethylene responsive element binding proteins and factor* and *ACC synthase* from Table C were induced, perhaps, due to the feed back control of the hormonal circulation system in order to maintain the level of ethylene in the cells.

Anyway, another sugar transporter such as *hexose transporter* was also inhibited, so that *hexokinase* was induced. This was another feed back control system of the cell lacking of sugars.

Table D (Appendix A) showed the microarray values of positive (*Luciferase; luc*) and negative control (*Desmin; des*) of microarray and internal standard genes (*β-tubulin*) of RT-PCR. These values were varied, but some of them showed a good result for being a control.

3.4 Semi-quantitative RT-PCR

The results from microarray revealed the global hybridization of grape gene expression. The primers for the amplification of *sucrose transporter* gene, (AF021809_1 (AF021809) putative sucrose transporter [*Vitis vinifera*] mRNA) were designed from the sequence from GeneBank.

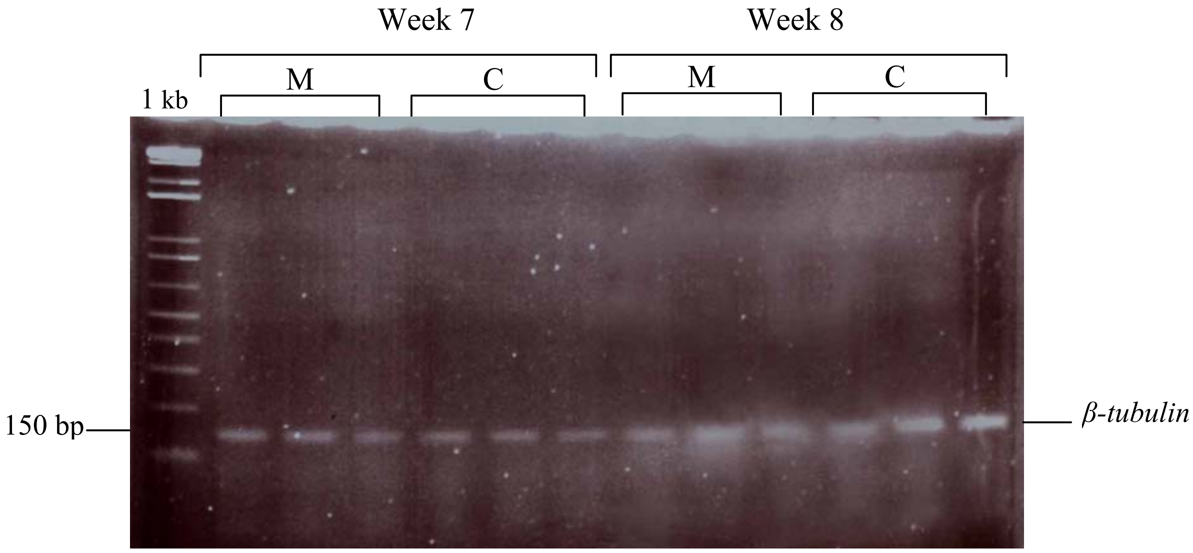


Figure 15 The expression level of *β-tubulin*

The internal standard was *β-tubulin* gene. This gene was not affected by 1-MCP treatment (Table A, Appendix A). The result was confirmed by the constant level of PCR amplification from the same cDNA template that reverse transcribed from the studying RNA sample (week 7 and 8 of 2002). β-tubulin is the dynamic component of microtubules. It formed the dimmer with α-tubulin to produce protofilament. Microtubules are dynamic structures, the assembled tubule is in equilibrium with a pool of tubulin subunits. There is continuous flux of tubulin into and out of the assembled form (Lewin, 1997). So, the expression of *β-tubulin* gene was constant and not depending on the 1-MCP treatment.

The number of cycle was an important factor for the amplification. The too few cycle might give an insufficiency for the amplification, and the too many cycle caused the saturation of the amplification. In both conditions would give the poor signal of bands. So, the optimum cycle number was estimated (Figure 16). In this study the middle values of 23-25 cycles were selected to use in the PCR amplification.

After the cDNA was synthesized by the Reverse Transcription System Kit using those DNA-free RNA samples as templates, the level of *SUT* gene expression was observed using the cDNAs as the templates in PCR reaction. In the PCR reaction, the cDNAs from week 7 and 8 were used as the templates and the primers of *SUT* and *β-tubulin* were used together for the amplification in a multiplex PCR reaction. The result was showed in Figure 17.

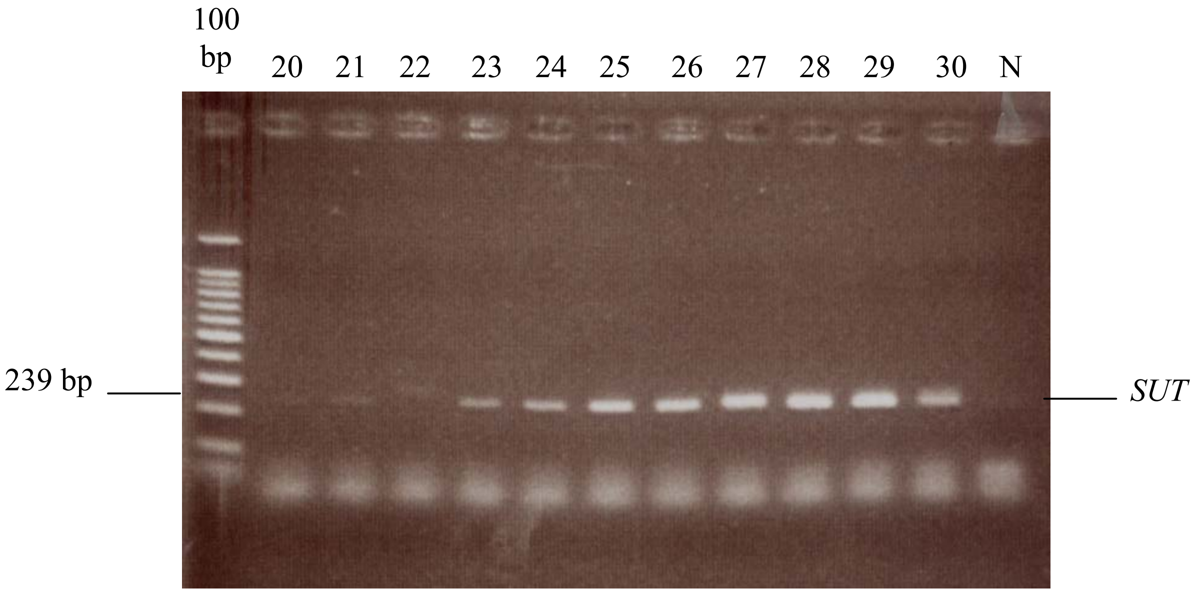


Figure 16 The PCR amplification in different number of cycle, the showed numbers were the cycle numbers and N=negative control

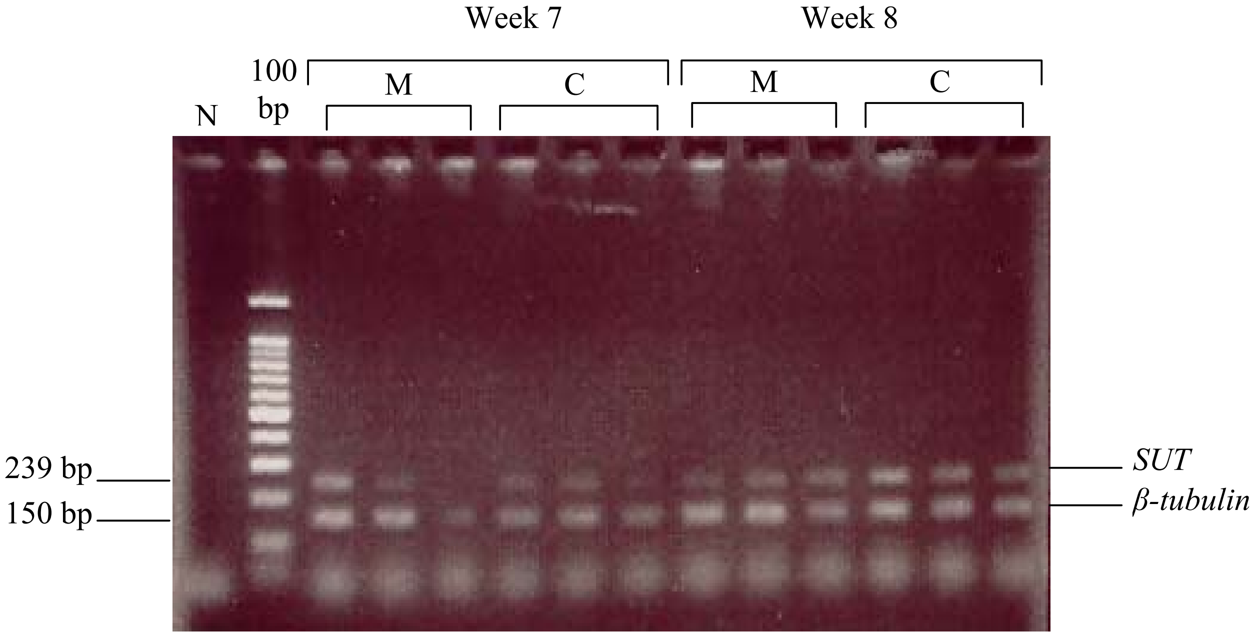


Figure 17 The expression level of *SUT* and *β-tubulin* gene, M= 1-MCP treated, C= control and N= negative control

The intensity of bands from Figure 17 was changed into the digital form. First, the bands were framed by the Imaging software (Figure 18). Each frame had equal size, so the inner area was also equal. Second, it was set to be monochrome style as showing in Figure 18 before analyzed by Sigmascan software (El-Kereamy et al., 2003). Sigmascan changed the intensity signal of each framed band into the digital data. Then, these data were saved in the Excel format. Finally, the graph was illustrated in Excel program (Figure 19). The data for plotting the graph was normalized by subtracted the intensity value of *β-tubulin* gene out of the intensity of *SUT* gene.

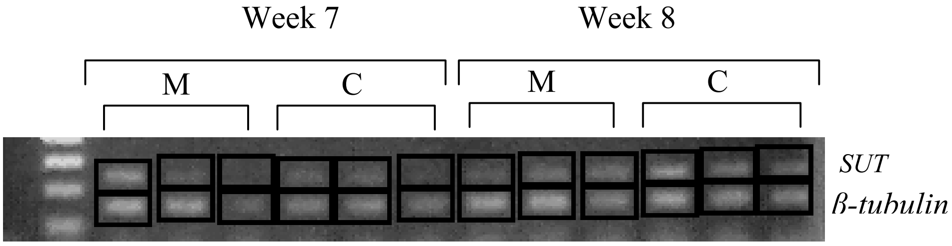


Figure 18 Framed monochrome picture of each bands from semi-quantitative RT-PCR amplification

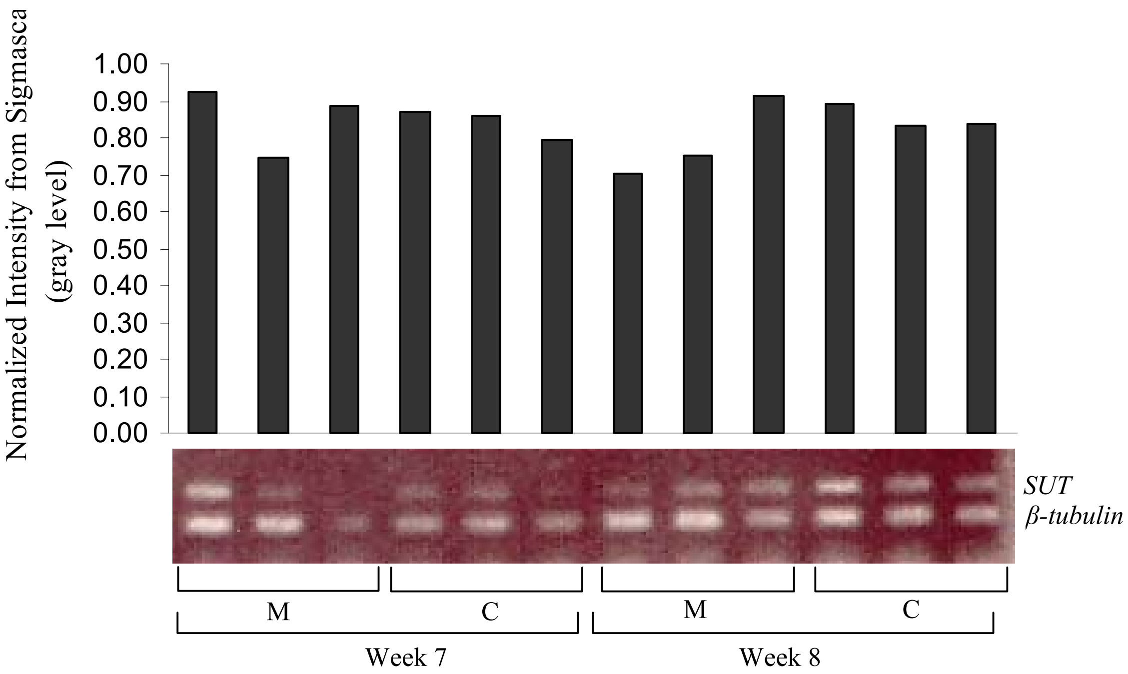


Figure 19 Analyzed data of band intensity from semi-quantitative RT-PCR amplification, M= 1-MCP-treated, C= control

The first three lanes in Figure 19 were the expression level of *SUT* gene in 1-MCP treated group of week 7 and the next three lanes were from control of the same week. While the last six lanes were from week 8, 1-MCP treated group and control respectively. The *SUT* gene expression was suppressed in berry treated by 1-MCP at week 8 (Figure 19).

According to result of Chevin in Figure 8, the size of grape berry at harvesting was smaller in week 6, 7 and 8. The smaller size of berry might be from the suppression of ripening and development-related gene during veraison.

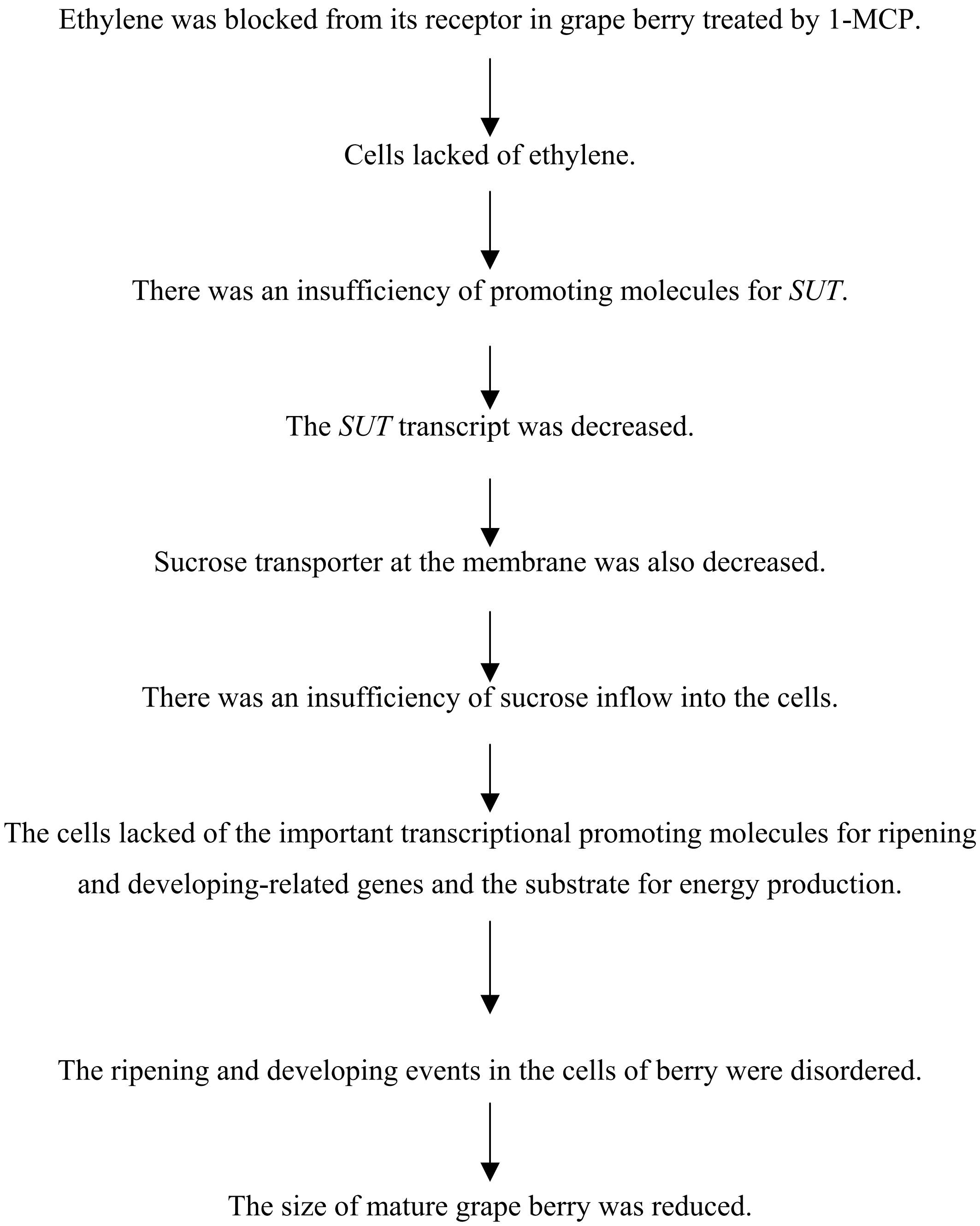
Ethylene is an important PGR that plays important role in fruit ripening and development (Arshad and Frankenberger, 2002; Abeles et al., 1992 and Matto and suttle, 1991). The promoter of a *hexose transpoter* gene (*Vvht1*) in grape contains several potential regulating *cis*-elements, including ethylene boxes (ERELEE4 box). Two ERELEE4 boxes (AWTTCAAA) were found in the positions -1,242 and -1,236 of *Vvht1* promoter. And also was found in the *SUT* gene of grape. The site of this box is shown in the Appendix B. The ERELEE4 boxes had been described as an ethylene-responsive enhancer element of a carnation *glutathione-S-transferase* gene (Fillon et al, 1999).

Ethylene was blocked from its receptor in the berry treated by 1-MCP. So, internal ethylene could not reach its target site. Ethylene hormone was considered to be a promoting factor of *SUT* gene, because there was an ethylene box in the sequence. When ethylene was blocked, the regulation of the genes it employs was also decreased. So, this might cause the lower level of *SUT* gene expression.

Sucrose Transporter protein locates both at the plasma membrane of the phloem tissue and non-phloem tissue such as pollen in *A. thaliana* (Meyer et al., 2000 and Stadler et al., 1999). Its function is about the sucrose transport activity into a cell (Gahrtz, Stolz and Sauer, 1994; Davies and Robinson, 1996; Roblin et al, 1998; Stadler et al., 1999; Meyer et al., 2000 and Ludwig, Stolz and Sauer, 2000). It is an energy-dependent transporter involved to phosphorylation/ dephosporylation activity. In order to activate the transport activity, phosphase group might be cut out from the transporter (Roblin et al, 1998 and Gahrtz, Stolz and Sauer, 1994).

However, sugars are important for transcriptional-control of the expression of many genes such as *patatin*, ploem-specific *rolC* and *Arabidopsis* Leu zipper gene named *ATB2* (Smeekens and Rook, 1997). Since sucrose can be hydrolyzed into glucose and fructose, it is difficult to establish a direct function for the sucrose molecule. Glucose or sucrose could induce the expression of genes encoding extracellular invertase and sucrose synthase (Smeekens and Rook, 1997). Glucose itself is also an essential transcriptional-control molecule. It induced the expression of *HUP1* (*glucose transporter*) gene, *B33* gene (the sugar and amino acid-induced patatin class I) (Smeekens and Rook, 1997). In addition, glucose also drives the feed back regulation to ethylene production by enhancing of the conversion of SAM to ACC and from ACC to ethylene (Matto and Suttle, 1991). Besides, sucrose itself is not just an important transcriptional promoting molecules, but it can also be hydrolyzed into fructose and glucose, another important transcriptional promoting molecules and substrate for energy production and glucose is a very essential substrate for the energy producing metabolism, glycolysis. Because the energy is important to all activities in a cell, so less inflow of sugar into the cell caused an insufficiency to the energy utilization. Remarkable, it is not the actual sucrose concentration but the influx of sucrose into the cell is being sensed to the events of the cell (Smeekens and Rook, 1997).

When the *SUT* transcript was suppressed by the 1-MCP incubation, the amount of plasma membrane sucrose transporter should be decreased, too. This caused the insufficiency of sucrose inflow into the cells of berry. Then, the berry would be insufficient of sucrose. According to the above, genes involve to fruit ripening and developing were also employed by sucrose or glucose. So, lacking of sugars in the cells might effect to the size of mature grape berry. The summarized events were shown in Figure 20.



Ethylene was blocked from its receptor in grape berry treated by 1-MCP.

Cells lacked of ethylene.

There was an insufficiency of promoting molecules for *SUT*.

The *SUT* transcript was decreased.

Sucrose transporter at the membrane was also decreased.

There was an insufficiency of sucrose inflow into the cells.

The cells lacked of the important transcriptional promoting molecules for ripening and developing-related genes and the substrate for energy production.

The ripening and developing events in the cells of berry were disordered.

The size of mature grape berry was reduced.

Figure 20 The summarized events in grape berry cell treated with 1-MCP

CHAPTER IV

CONCLUSION

Grape ripening does not correlate to ethylene hormone, so it is considered to be a non-climacteric fruit. This study aims to find out the relationship between ethylene hormone and the molecular and physiological characteristics of grape berry ripening. 1-MCP was used to block ethylene receptor in grape berry. After total RNA was extracted from sampled berries, the microarray technique and semi-quantitative RT-PCR were done to reveal the level of *SUT* gene expression from 1-MCP treated berry and control berry.

The results from microarray and semi-quantitative RT-PCR showed the lower expression of *sucrose transporter* in 1-MCP treated groups comparing to control groups.

In the presence of 1-MCP, the *SUT* transcript was suppressed because ethylene could not reach its target site. Then the amount of sucrose transporter protein located at plasma membrane should also be decreased. This would make the insufficiency of sucrose inflow into the cells of berry. Sucrose itself is not just an important transcriptional promoting molecules, but it can also be hydrolyzed into fructose and glucose, when the intake of sucrose was reduced, the berry cell would be insufficient to sucrose or (and) fructose and glucose. Glucose is another important transcriptional promoting molecules and a substrate for energy production. Moreover, some genes involve to fruit ripening and developing were also employed by sugars. So, lacking of sugars in the cells might effect to the size of mature grape berry.

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APPENDIX A

Table A The summery normalized data from an Axon Genepix 4000B scanner

Block	Row	Column	Name	ID	Subject	first replication			second replication			average
						Cy5 intensity	Cy3 intensity	Cy5/Cy3 ratio	Cy5 intensity	Cy3 intensity	Cy5/Cy3 ratio	Cy5/Cy3 ratio
1	1	1	cds of gi|1469265|emb|X84846.1|PP111ACNP	luc1#1		28.722	46.000	0.624	11.327	35.000	0.324	0.474
1	1	2	CM001E02	a76couture0400.r#1	>ref|NP_054508.1|| (NC_001879) acetyl-CoA carboxylase beta subunit [Nicotiana tabacum]	1580.935	1700.000	0.930	848.469	1841.000	0.461	0.695
1	1	3	Arabidopsis Control Oligonucleotide	3ara23			13.000	0.000				
1	1	4	GT193E06	a76couture0144.r#1	>ref|NP_200679.1|| (NM_125258) cyclophilin ROC7; protein id: At5g58710.1. supported by	4577.967	4538.000	1.009	3531.857	5307.000	0.666	0.837
1	1	5	CT001H08	a76couture0494.r#1	>ref|NP_085579.1|| (NC_001284) ribosomal protein S7 [Arabidopsis thaliana]	142.359	130.000	1.095	131.801	139.000	0.948	1.022
1	1	6	CM001B05	a76couture0396.r#1	>ref|NP_197954.1|| (NM_122483) putative protein; protein id: At5g25820.1 [Arabidopsis	14.985	24.000	0.624	14.416	23.000	0.627	0.626
1	1	7	ST002E09	a76couture0275.r#1	>sp|P49118|BIP_LYCES Luminal binding protein precursor (BiP) (78 kDa glucose-regulated	1228.783	1596.000	0.770	1353.020	1949.000	0.694	0.732
1	1	8	GT184A02	a76couture0139.r#1	>ref|NP_191327.1|| (NM_115628) D1 CtpA arboxy-terminal protease. putative; protein id:	661.845	837.000	0.791	572.511	782.000	0.732	0.761
1	1	9	CT001G10	a76couture0490.r#1	>gb|AAK73147.1|AC079022_20 (AC079022) putative RING-H2 finger protein [Oryza sativa]	369.634	468.000	0.790	435.561	578.000	0.754	0.772
1	1	10	CM001A05	a76couture0392.r#1	>ref|NP_195884.1|| (NM_120342) putative protein; protein id: At5g02640.1. supported by	124.876	135.000	0.925	217.266	226.000	0.961	0.943
1	1	11	ST005E01	a76couture0269.r#1	>ref|NP_568154.1|| (NM_120609) putative protein; protein id: At5g05270.1 [Arabidopsis	3436.597	3459.000	0.994	3915.933	4308.000	0.909	0.951
1	1	12	GT181D11	a76couture0130.r#1	>ref|NP_566536.1|| (NM_112485) putative L-asparaginase; protein id: At3g16150.1	42.458	58.000	0.732	42.218	59.000	0.716	0.724
1	1	13	CT001E07	a76couture0485.r#1	------	21.229	32.000	0.663	24.713	36.000	0.686	0.675
1	1	14	ST006H09	a76couture0388.r#1	>emb|CAC88085.1| (AJ316582) ribosomal protein L2 [Atropa belladonna]	7209.112	7005.000	1.029	5396.636	6584.000	0.820	0.924
1	1	15	cds of gi|1469265|emb|X84846.1|PP111ACNP	luc2#1		4.995	12.000	0.416	4.119	8.000	0.515	0.466
1	2	1	GB007A08	a76couture0124.r#1	>gb|AAG52090.1|AC012680_1 (AC012680) unknown protein. 5' partial; 69506-67937 [Arabidopsis	3673.862	3962.000	0.927	1724.741	4070.000	0.424	0.676
1	2	2	CT001D01	a76couture0481.r#1	>emb|CAC09928.1| (AJ279066) hypothetical protein [Catharanthus roseus]	1999.270	2772.000	0.721	1247.991	3214.000	0.388	0.555
1	2	3	ST005B09	a76couture0384.r#1	>pir||T07092 Ca+2-binding EF hand protein homolog PM13 - soybean	2897.131	2286.000	1.267	1938.917	2590.000	0.749	1.008
1	2	4	PT012B08	a76couture0258.r#1	>ref|NP_680114.1|| (NM_148861) unknown protein; protein id: At3g48380.1 [Arabidopsis	28.722	38.000	0.756	23.683	39.000	0.607	0.682
1	2	5	CT005G11	a76couture0111.r#1	>pir||T02069 probable DNA-binding protein GBP16 - rice	176.076	184.000	0.957	181.226	218.000	0.831	0.894
1	2	6	CT001B06	a76couture0477.r#1	------	22.478	32.000	0.702	19.564	28.000	0.699	0.701
1	2	7	ST004B04	a76couture0381.r#1	>emb|CAA77432.1| (Z00044) NADH dehydrogenase ND4 subunit [Nicotiana tabacum]	772.985	787.000	0.982	773.302	859.000	0.900	0.941
1	2	8	PT010H01	a76couture0254.r#1	>ref|NP_565568.1|| (NM_127998) putative protein kinase; protein id: At2g24360.1	58.692	64.000	0.917	48.396	57.000	0.849	0.883
1	2	9	CT005A12	a76couture0107.r#1	>ref|NP_182051.1|| (NM_130089) hypothetical protein; protein id: At2g45260.1	1828.190	2081.000	0.879	1950.244	2329.000	0.837	0.858
1	2	10	RT071D07	a76couture0932.r#1	>ref|NP_011800.1|| (NC_001139) ER Vesicle protein of 29 kDa (apparent MW); Erv29p	9.990	16.000	0.624	15.445	19.000	0.813	0.719
1	2	11	RB001D02	a76couture0810.r#1	>gb|AAD55090.1| (AF178653) thaumatin [Vitis riparia]	169.832	227.000	0.748	276.988	369.000	0.751	0.749
1	2	12	ST006A03	a76couture0697.r#1	>gb|AAK96597.1| (AY052693) AT3g52500/F22O6_120 [Arabidopsis thaliana]	415.838	222.000	1.873	504.551	265.000	1.904	1.889
1	2	13	ST001G03	a76couture0599.r#1	>gb|AAL86320.1| (AY080700) putative polyphosphoinositide binding protein	508.247	578.000	0.879	487.046	606.000	0.804	0.842
1	2	14	RT072F05	a76couture0929.r#1	>gb|AAD25942.1|AF085279_15 (AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis	237.265	249.000	0.953	261.543	299.000	0.875	0.914
1	2	15	GT174H03	a76couture0807.r#1	>ref|NP_180776.2|| (NM_128776) hypothetical protein; protein id: At2g32170.1	131.120	141.000	0.930	139.009	161.000	0.863	0.897
1	3	1	ST005H03	a76couture0693.r#1	>ref|NP_199987.1|| (NM_124553) putative protein; protein id: At5g51740.1 [Arabidopsis	445.809	391.000	1.140	257.424	400.000	0.644	0.892
1	3	2	ST001E08	a76couture0596#1	------	44.955	44.000	1.022	41.188	38.000	1.084	1.053
1	3	3	RT072A01	a76couture0925.r#1	------	433.321	485.000	0.893	344.948	562.000	0.614	0.754
1	3	4	RT061A12	a76couture0801.r#1	>dbj|BAB40172.1| (AP002910) putative OsGAI [Oryza sativa (japonica cultivar-group)]	630.626	563.000	1.120	578.689	663.000	0.873	0.996
1	3	5	ST005F01	a76couture0689.r#1	>ref|XP_165264.1|| (XM_165264) hypothetical protein XP_165264 [Mus musculus]	3268.014	2605.000	1.255	2658.675	2764.000	0.962	1.108
1	3	6	ST001C01	a76couture0590.r#1	>ref|NP_172287.1|| (NM_100683) storage protein. putative; protein id: At1g08080.1	294.708	213.000	1.384	266.691	236.000	1.130	1.257
1	3	7	RT071F01	a76couture0921.r#1	>gb|AAK21343.1|AC024594_7 (AC024594) hypothetical protein [Oryza sativa (japonica	68.682	78.000	0.881	74.138	90.000	0.824	0.852
1	3	8	RT033H07	a76couture0795.r#1	------	2636.140	2101.000	1.255	2300.340	2214.000	1.039	1.147
1	3	9	ST005E05	a76couture0685.r#1	>gb|AAG12703.1|AC021046_4 (AC021046) acid phosphatase. putative; 5376-6903 [Arabidopsis	534.471	513.000	1.042	453.066	534.000	0.848	0.945
1	3	10	ST001A09	a76couture0586.r#1	>ref|NP_568535.1|| (NM_123020) transmembrane protein FT27/PFT27-like; protein id:	1065.195	1112.000	0.958	996.746	1171.000	0.851	0.905
1	3	11	TT273D09	a76couture0917.r#1	>ref|NP_175184.1|| (NM_103646) unknown protein; protein id: At1g47530.1. supported by	17.483	30.000	0.583	19.564	33.000	0.593	0.588
1	3	12	RB008D03	a76couture0791.r#1	------	494.510	693.000	0.714	497.343	726.000	0.685	0.699
1	3	13	ST005B03	a76couture0681.r#1	>ref|NP_172042.1|| (NM_100430) hypothetical protein; protein id: At1g05510.1	2597.428	4031.000	0.644	2403.310	3861.000	0.622	0.633
1	3	14	CT006B11	a76couture0582.r#1	>gb|AAM20655.1| (AY099804) unknown protein [Arabidopsis thaliana]	119.881	111.000	1.080	143.128	133.000	1.076	1.078
1	3	15	TT283A04	a76couture0911.r#1	>ref|NP_177230.1|| (NM_105741) putative phosphoglucomutase; protein id: At1g70730.1	163.588	250.000	0.654	233.741	329.000	0.710	0.682
1	4	1	GT204C02	a76couture0786.r#1	>ref|NP_200595.1|| (NM_125172) eukaryotic initiation factor 4. eIF4-like protein;	13.736	22.000	0.624	11.327	26.000	0.436	0.530
1	4	2	ST004H12	a76couture0677.r#1	------	68.682	100.000	0.687	46.336	114.000	0.406	0.547
1	4	3	CT005G07	a76couture0577.r#1	------	92.409	111.000	0.833	73.108	118.000	0.620	0.726
1	4	4	RT062B08	a76couture1387.r#1	>sp|P00051|CYC_CUCMA Cytochrome c >gi|65496|pir||CCPU cytochrome c - cucurbit	1472.292	1118.000	1.317	1176.942	1240.000	0.949	1.133
1	4	5	RB005G02	a76couture1275.r#1	>gb|AAF86340.1|AF277455_1 (AF277455) UMP synthase [Nicotiana plumbaginifolia]	57.443	61.000	0.942	52.514	64.000	0.821	0.881
1	4	6	GT173D09	a76couture1138.r#1	>ref|NP_180571.1|| (NM_128565) putative unknown protein. leucine-rich repeat; protein	253.499	216.000	1.174	199.761	232.000	0.861	1.017
1	4	7	RT091C09	a76couture1023.r#1	>gb|AAF16649.1|AC011661_27 (AC011661) T23J18.3 [Arabidopsis thaliana]	1436.078	1797.000	0.799	1295.357	2038.000	0.636	0.717
1	4	8	RT062B07	a76couture1381.r#1	>pir||T08942 proton pump interactor - Arabidopsis thaliana	2252.769	2039.000	1.105	2091.312	2405.000	0.870	0.987
1	4	9	RB003B02	a76couture1267.r#1	>pir||T07784 AP2 domain protein homolog - potato >gi|1688233|gb|AAC29516.1|	233.519	191.000	1.223	227.563	232.000	0.981	1.102
1	4	10	GT172H10	a76couture1134#1	>ref|NP_191899.1|| (NM_116205) cyclophylin -like protein; protein id: At3g63400.1	144.857	125.000	1.159	162.692	153.000	1.063	1.111
1	4	11	RT084A11	a76couture1020.r#1	------	18.731	29.000	0.646	23.683	32.000	0.740	0.693
1	4	12	RT054E01	a76couture1376.r#1	>pir||T07139 cysteine proteinase inhibitor - soybean >gi|1944319|dbj|BAA19608.1|	206.046	184.000	1.120	224.474	225.000	0.998	1.059
1	4	13	RB001D12	a76couture1263.r#1	>gb|AAD22071.1| (AF124748) putative RNA-binding protein [Larix laricina]	282.221	331.000	0.853	300.671	385.000	0.781	0.817
1	4	14	GT172A10	a76couture1131#1	>sp|P46299|RS4_GOSHI 40S RIBOSOMAL PROTEIN S4 >gi|629496|pir||S45026 ribosomal protein	1232.530	1078.000	1.143	446.888	551.000	0.811	0.977
1	4	15	RT082H10	a76couture1016.r#1	>gb|AAM61117.1| (AY084550) short chain alcohol dehydrogenase-like [Arabidopsis	1343.670	1027.000	1.308	2108.817	1644.000	1.283	1.296
1	5	1	RT054B08	a76couture1372.r#1	>ref|NP_190348.1|| (NM_114632) hypothetical protein; protein id: At3g47640.1	191.061	273.000	0.700	113.267	273.000	0.415	0.557
1	5	2	GT204B12	a76couture1250.r#1	>dbj|BAA34702.1| (AB011797) homolog to plastid-lipid-associated protein [Citrus	640.616	604.000	1.061	477.779	705.000	0.678	0.869
1	5	3	GT171B07	a76couture1126.r#1	>ref|NP_195785.1|| (NM_120243) Macrophage migration inhibitory factor (MIF) family;	2559.965	2853.000	0.897	2216.935	3601.000	0.616	0.756

1	5	4	RT082F08	a76couture1012.r#1	>gb|AAF97835.1|AC034107_18 (AC034107) EST gb|AI997943 comes from this gene. [Arabidopsis	265.987	283.000	0.940	243.008	316.000	0.769	0.854
1	5	5	RT053B06	a76couture1367.r#1	>ref|NP_197725.1|| (NM_122240) putative protein; protein id: At5g23340.1. supported by	308.445	350.000	0.881	263.602	379.000	0.696	0.788
1	5	6	GT203G05	a76couture1245.r#1	>ref|NP_568688.1|| (NM_124152) putative protein; protein id: At5g47780.1. supported by	755.502	681.000	1.109	639.441	703.000	0.910	1.009
1	5	7	GB009F10	a76couture1122.r#1	>ref|NP_568457.1|| (NM_122389) bZIP protein. G/HBF-1-related; protein id: At5g24800.1	106.145	114.000	0.931	109.148	124.000	0.880	0.906
1	5	8	RT082B08	a76couture1008.r#1	>ref|NP_683586.1|| (NM_148744) auxin-regulated protein; protein id: At3g23280.2	383.370	446.000	0.860	365.542	495.000	0.738	0.799
1	5	9	RT052D07	a76couture1363.r#1	>ref|NP_176563.1|| (NM_105053) putative aminopeptidase; protein id: At1g63770.1	787.970	862.000	0.914	647.679	845.000	0.766	0.840
1	5	10	GT203D06	a76couture1241.r#1	>pir||T16995 probable cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - apple tree	1082.678	1335.000	0.811	1001.894	1543.000	0.649	0.730
1	5	11	GB009D03	a76couture1117.r#1	------	253.499	215.000	1.179	270.810	248.000	1.092	1.136
1	5	12	RT081H08	a76couture1004.r#1	------	99.901	123.000	0.812	95.762	124.000	0.772	0.792
1	5	13	GT184F02	a76couture1823.r#1	>gb|AAG08960.1|AF122052_1 (AF122052) tuber-specific and sucrose-responsive element binding	360.893	373.000	0.968	410.849	462.000	0.889	0.928
1	5	14	GT172F08	a76couture1731#1	>sp|O24542|AX2D_PHAAU Auxin-induced protein 22D (Indole-3-acetic acid induced protein	63.687	45.000	1.415	54.574	39.000	1.399	1.407
1	5	15	GB009C03	a76couture1641.r#1	------	159.842	149.000	1.073	229.622	216.000	1.063	1.068
1	6	1	TT282A08	a76couture1508.r#1	>ref|NP_188101.2|| (NM_112344) unknown protein; protein id: At3g14830.1. supported by	47.453	67.000	0.708	28.831	78.000	0.370	0.539
1	6	2	GT191D06	a76couture1819.r#1	>pir||I51237 translation elongation factor EF-1 gamma - African clawed frog	117.384	156.000	0.752	63.841	157.000	0.407	0.580
1	6	3	GT172E07	a76couture1727#1	>emb|CAD12888.1| (AJ421152) hydroxynitrile lyase [Sorghum bicolor]	711.795	640.000	1.112	493.224	730.000	0.676	0.894
1	6	4	GB009A07	a76couture1638.r#1	>ref|NP_174276.1|| (NM_102723) unknown protein; protein id: At1g29830.1 [Arabidopsis	129.871	111.000	1.170	120.474	109.000	1.105	1.138
1	6	5	TT281C12	a76couture1503.r#1	>sp|Q9MB73|LGT_CITUN Limonoid UDP-glucosyltransferase (Limonoid glucosyltransferase)	860.398	932.000	0.923	724.906	941.000	0.770	0.847
1	6	6	GT191A02	a76couture1815.r#1	>gb|AAF79729.1|AC005106_10 (AC005106) T25N20.22 [Arabidopsis thaliana]	369.634	350.000	1.056	334.651	371.000	0.902	0.979
1	6	7	GT172D10	a76couture1725#1	>ref|NP_566842.1|| (NM_113832) pectinesterase family; protein id: At3g29090.1	280.972	269.000	1.045	225.503	268.000	0.841	0.943
1	6	8	GT171A05	a76couture1634.r#1	>ref|NP_200929.1|| (NM_125514) syntaxin SNAP33; protein id: At5g61210.1. supported by	852.906	746.000	1.143	744.470	836.000	0.891	1.017
1	6	9	TT274H08	a76couture1498.r#1	>ref|NP_566559.1|| (NM_112555) expressed protein; protein id: At3g16810.1. supported	46.204	48.000	0.963	50.455	49.000	1.030	0.996
1	6	10	GT184D05	a76couture1811.r#1	>ref|NP_197697.1|| (NM_122212) putative protein; protein id: At5g23060.1. supported by	67.433	66.000	1.022	62.811	73.000	0.860	0.941
1	6	11	GT172B10	a76couture1721#1	------	277.226	249.000	1.113	222.414	234.000	0.950	1.032
1	6	12	GB007G03	a76couture1629.r#1	>ref|NP_171879.1|| (NM_100262) hypothetical protein; protein id: At1g03830.1	82.418	81.000	1.018	77.227	77.000	1.003	1.010
1	6	13	TT274E12	a76couture1493.r#1	>pir||T16995 probable cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - apple tree	79.921	92.000	0.869	77.227	90.000	0.858	0.863
1	6	14	GT182G12	a76couture1807.r#1	>dbj|BAB89792.1| (AP003286) contains ESTs AU077950(C12951).C26744(C12951)~similar to	98.652	107.000	0.922	108.118	126.000	0.858	0.890
1	6	15	GT172B07	a76couture1718.r#1	------	32.468	33.000	0.984	38.099	35.000	1.089	1.036
1	7	1	GB007E05	a76couture1626.r#1	------	212.290	217.000	0.978	145.187	260.000	0.558	0.768
1	7	2	TT274A12	a76couture1485.r#1	>gb|AAK98735.1|AC090485_14 (AC090485) Putative cell death suppressor protein [Oryza sativa]	440.814	710.000	0.621	300.671	816.000	0.368	0.495
1	7	3	GT183H12	a76couture1803.r#1	>ref|NP_197367.1|| (NM_121871) putative protein; protein id: At5g18660.1. supported by	7.493	18.000	0.416	5.148	13.000	0.396	0.406
1	7	4	GT172B03	a76couture1716#1	------	224.777	260.000	0.865	192.553	274.000	0.703	0.784
1	7	5	GB007B02	a76couture1621.r#1	------	8.741	23.000	0.380	5.148	16.000	0.322	0.351
1	7	6	TT273G05	a76couture1481.r#1	------	28.722	42.000	0.684	24.713	39.000	0.634	0.659
1	7	7	RT044D06	a76couture2233.r#1	>ref|NP_190907.1|| (NM_115199) putative protein; protein id: At3g53390.1 [Arabidopsis	430.823	404.000	1.066	383.047	411.000	0.932	0.999
1	7	8	RT032E03	a76couture2133.r#1	>ref|NP_178147.1|| (NM_106680) putative sulfate transporter; protein id: At1g80310.1		13.000	0.000				
1	7	9	RT022B01	a76couture2037#1	>ref|NP_182128.1|| (NM_130167) hypothetical protein; protein id: At2g46040.1	88.662	81.000	1.095	75.168	78.000	0.964	1.029
1	7	10	RB007D11	a76couture1954.r#1	>gb|AAK92832.1| (AY050895) putative glycyl tRNA synthetase [Arabidopsis thaliana]	99.901	98.000	1.019	116.356	120.000	0.970	0.995
1	7	11	RT044B09	a76couture2228.r#1	>sp|Q40089|ATP4_IPOBA ATP synthase delta' chain. mitochondrial precursor	673.084	679.000	0.991	666.213	749.000	0.889	0.940
1	7	12	RT032C12	a76couture2129.r#1	------	1.249	10.000	0.125	3.089	16.000	0.193	0.159
1	7	13	RT022A08	a76couture2034#1	>ref|NP_190343.1|| (NM_114627) putative protein; protein id: At3g47590.1 [Arabidopsis	142.359	148.000	0.962	166.811	181.000	0.922	0.942
1	7	14	RB006D12	a76couture1949.r#1	>gb|AAM66127.1| (AY088598) unknown [Arabidopsis thaliana]	415.838	473.000	0.879	414.967	538.000	0.771	0.825
1	7	15	RT044A02	a76couture2224.r#1	------	93.657	94.000	0.996	95.762	104.000	0.921	0.959
1	8	1	RT031H04	a76couture2125.r#1	>sp|Q42946|HEM6_TOBAC Coproporphyrinogen III oxidase. chloroplast precursor	47.453	80.000	0.593	38.099	98.000	0.389	0.491
1	8	2	RT022B05	a76couture2030#1	>ref|NP_179802.1|| (NM_127780) hypothetical protein; protein id: At2g22120.1	143.608	190.000	0.756	98.851	214.000	0.462	0.609
1	8	3	RB004G03	a76couture1944.r#1	>ref|NP_180277.1|| (NM_128267) hypothetical protein; protein id: At2g27090.1	166.086	208.000	0.798	143.128	221.000	0.648	0.723
1	8	4	RT043F04	a76couture2220.r#1	------	132.369	176.000	0.752	119.445	174.000	0.686	0.719
1	8	5	RT031E08	a76couture2121.r#1	>gb|AAM34777.1|AF509877_1 (AF509877) nam-like protein 14 [Petunia x hybrida]	161.090	191.000	0.843	134.890	182.000	0.741	0.792
1	8	6	RT021G12	a76couture2026#1	>gb|ZP_00082888.1| (NZ_AABA01000030) hypothetical protein [Pseudomonas fluorescens]	766.741	997.000	0.769	791.836	1155.000	0.686	0.727
1	8	7	RB006A08	a76couture1939.r#1	>emb|CAC20728.1| (AJ278767) histidinol phosphate aminotransferase [Nicotiana	72.428	85.000	0.852	66.930	73.000	0.917	0.884
1	8	8	RT043B12	a76couture2217.r#1	>ref|NP_012284.1|| (NC_001141) Required for invasion and pseudohyphae formation in	54.946	58.000	0.947	44.277	53.000	0.835	0.891
1	8	9	RT031C12	a76couture2117.r#1	>gb|AAM91568.1| (AY128365) putative WD-40 repeat protein [Arabidopsis thaliana]	53.697	60.000	0.895	40.158	52.000	0.772	0.834
1	8	10	RT021F11	a76couture2022#1	>gb|AAG16758.1| (AY007560) putative glutathione S-transferase T3 [Lycopersicon	58.692	72.000	0.815	57.663	74.000	0.779	0.797
1	8	11	RB005F02	a76couture1935.r#1	>gb|AAK93948.1|AF284759_1 (AF284759) TatC [Pisum sativum]	178.573	160.000	1.116	178.137	185.000	0.963	1.039
1	8	12	RT041H09	a76couture2212.r#1	------	2888.390	2811.000	1.028	2894.475	3085.000	0.938	0.983
1	8	13	RT031A12	a76couture2114.r#1	>ref|NP_196705.1|| (NM_121182) putative protein; protein id: At5g11440.1 [Arabidopsis	664.342	640.000	1.038	599.283	650.000	0.922	0.980
1	8	14	RT021F02	a76couture2018#1	>emb|CAB55554.1| (AJ010945) auxin binding protein (ABP44); Isovaleryl-CoA	290.962	259.000	1.123	295.523	305.000	0.969	1.046
1	8	15	RB004D01	a76couture1931.r#1	>ref|NP_568368.1|| (NM_121899) putative protein; protein id: At5g18940.1. supported by	113.637	127.000	0.895	93.702	119.000	0.787	0.841
1	9	1	PT002D09	a76couture2659.r#1	------	203.548	259.000	0.786	179.167	331.000	0.541	0.664
1	9	2	TT264C02	a76couture2535.r#1	>ref|NP_197589.1|| (NM_122097) T-complex protein 1. beta subunit; protein id:	1058.951	1474.000	0.718	938.053	1815.000	0.517	0.618
1	9	3	TB007F04	a76couture2432.r#1	>dbj|BAC04594.1| (AK095631) unnamed protein product [Homo sapiens]	157.344	255.000	0.617	146.217	291.000	0.502	0.560
1	9	4	RT061B04	a76couture2322.r#1	>ref|NP_200296.1|| (NM_124866) unknown protein; protein id: At5g54850.1 [Arabidopsis	208.544	261.000	0.799	206.969	297.000	0.697	0.748
1	9	5	PT005B02	a76couture2654.r#1	------	34.965	47.000	0.744	43.247	51.000	0.848	0.796
1	9	6	TT263F04	a76couture2531.r#1	>emb|CAB43599.1| (AJ006940) phosphoribosyl pyrophosphate synthase [Spinacia	122.379	157.000	0.779	124.593	170.000	0.733	0.756
1	9	7	TB006H10	a76couture2426.r#1	>ref|NP_568310.1|| (NM_121526) ribosomal protein L27 - like; protein id: At5g15220.1	172.329	188.000	0.917	140.039	161.000	0.870	0.893
1	9	8	RT054H09	a76couture2318.r#1	>pir||T09294 malate dehydrogenase (EC 1.1.1.37) precursor - alfalfa	54.946	65.000	0.845	46.336	61.000	0.760	0.802
1	9	9	PT002C03	a76couture2650.r#1	------	106.145	109.000	0.974	86.494	94.000	0.920	0.947
1	9	10	TT264G06	a76couture2527.r#1	>ref|NP_196946.1|| (NM_121446) putative protein; protein id: At5g14420.1. supported by	887.871	1132.000	0.784	823.757	1141.000	0.722	0.753
1	9	11	TB006A11	a76couture2421.r#1	>gb|AAL79688.1|AC087599_7 (AC087599) putative phragmoplastin [Oryza sativa]	644.362	647.000	0.996	528.234	613.000	0.862	0.929

1	9	12	Arabidopsis Control Oligonucleotide	3ara23		6.244	18.000	0.347	6.178	12.000	0.515	0.431
1	9	13	PT003G03	a76couture2644.r#1	------	490.764	362.000	1.356	496.313	432.000	1.149	1.252
1	9	14	TT264C09	a76couture2523.r#1	>gb|AAM20730.1| (AY099879) unknown protein [Arabidopsis thaliana]	53.697	56.000	0.959	51.485	61.000	0.844	0.901
1	9	15	TB005G03	a76couture2417.r#1	>ref|NP_566294.1|| (NM_111564) expressed protein; protein id: At3g06840.1. supported	89.911	98.000	0.917	67.960	84.000	0.809	0.863
1	10	1	RT054C02	a76couture2311.r#1	>ref|NP_564266.1|| (NM_102456) expressed protein; protein id: At1g26920.1. supported	619.387	703.000	0.881	463.363	827.000	0.560	0.721
1	10	2	PT009G12	a76couture2640.r#1	>prf||1909359B ribosomal protein L7 [Solanum tuberosum]	434.570	644.000	0.675	423.205	817.000	0.518	0.596
1	10	3	TT263B06	a76couture2519.r#1	>emb|CAA10766.1| (AJ132763) cyclophilin [Pseudotsuga menziesii]	78.672	100.000	0.787	63.841	103.000	0.620	0.703
1	10	4	TB004E09	a76couture2408.r#1	>sp|P29620|KC47_ORYSA CDC2+/CDC28-related protein kinase R2 >gi|82507|pir||S13934 protein	44.955	65.000	0.692	54.574	75.000	0.728	0.710
1	10	5	RT053H05	a76couture2306.r#1	>gb|AAF22526.1|AF123395_1 (AF123395) 26S proteasome AAA-ATPase subunit RPT6a [Arabidopsis	609.397	772.000	0.789	578.689	816.000	0.709	0.749
1	10	6	PT008A02	a76couture2635.r#1	------	549.456	495.000	1.110	460.274	487.000	0.945	1.028
1	10	7	TT261C07	a76couture2515.r#1	------	133.618	166.000	0.805	126.653	168.000	0.754	0.779
1	10	8	TB004D02	a76couture2405.r#1	------	1187.574	1244.000	0.955	1038.963	1191.000	0.872	0.913
1	10	9	RT061E03	a76couture2302.r#1	>ref|NP_197078.1|| (NM_121579) putative protein; protein id: At5g15740.1 [Arabidopsis	103.647	105.000	0.987	107.088	113.000	0.948	0.967
1	10	10	BM436525 TB003H10	couture_a76.111.c1.r#1	>sp|P49198|RS3A_HELAN 40S RIBOSOMAL PROTEIN S3A >gi|7441118|pir||T09301 ribosomal protein	4620.425	3866.000	1.195	3865.478	3794.000	1.019	1.107
1	10	11	RT053C01	a76couture3034.r#1	>ref|NP_194443.1|| (NM_118847) translation initiation factor; protein id: At4g27130.1	4626.669	4095.000	1.130	3873.716	4134.000	0.937	1.033
1	10	12	PT008C06	a76couture2901.r#1	>gb|ZP_00098483.1| (NZ_AABB01000260) hypothetical protein [Desulfitobacterium	32.468	34.000	0.955	35.010	35.000	1.000	0.978
1	10	13	PT002F09	a76couture2761#1	>ref|NP_197514.2|| (NM_122021) putative protein; protein id: At5g20140.1. supported by	101.150	95.000	1.065	91.643	95.000	0.965	1.015
1	10	14	BM437686 RT084E01	couture_a76.105.c1.r#1	>gb|AAD54424.1|AF182079_1 (AF182079) thiol protease [Matricaria chamomilla]	313.440	303.000	1.034	271.840	329.000	0.826	0.930
1	10	15	ST003E01	a76couture3026.r#1	>ref|NP_174569.1|| (NM_103026) Avr9 elicitor response protein. putative; protein id:	52.448	71.000	0.739	40.158	65.000	0.618	0.678
1	11	1	RT083H02	a76couture2898.r#1	>gb|AAM65510.1| (AY087963) 60S ribosomal protein L4-B (L1) [Arabidopsis thaliana]	3138.143	3812.000	0.823	1587.791	3074.000	0.517	0.670
1	11	2	PT012D06	a76couture2757.r#1	------		15.000	0.000				
1	11	3	BE846420 CM002C08	couture_a76.10.c1.r#1	>ref|NP_567441.1|| (NM_117554) Expressed protein; protein id: At4g14710.1. supported	3987.302	5744.000	0.694	3761.479	6314.000	0.596	0.645
1	11	4	RT062G01	a76couture3020.r#1	>dbj|BAB40450.1| (AB030317) long-chain acyl-CoA synthetase [Arabidopsis thaliana]	284.718	279.000	1.020	268.751	304.000	0.884	0.952
1	11	5	CM005a01	a76couture2892.r#1	pir||HSWT41 histone H4 (TH091) - wheat >gi|170747|gb|AAA34292.1|... 162 2e-039	409.594	361.000	1.135	445.858	423.000	1.054	1.094
1	11	6	PT002G10	a76couture2753.r#1	>ref|NP_326292.1|| (NC_002771) conserved hypothetical protein [Mycoplasma pulmonis]	21.229	36.000	0.590	16.475	25.000	0.659	0.624
1	11	7	TB007g07	a76couture3274.r#1	gb|AAF07192.1|AF193846_1 (AF193846) branched-chain amino acid aminotransferase [Solanum	318.435	341.000	0.934	295.523	313.000	0.944	0.939
1	11	8	RT093F06	a76couture3014.r#1	>emb|CAA10494.1| (AJ131733) ubiquitin-conjugating enzyme E2 [Pseudotsuga menziesii]	817.940	959.000	0.853	597.224	794.000	0.752	0.803
1	11	9	CT005H09	a76couture2884.r#1	>ref|NP_565987.1|| (NM_129847) expressed protein; protein id: At2g42860.1. supported	1067.693	1249.000	0.855	801.103	1049.000	0.764	0.809
1	11	10	PT010B02	a76couture2748.r#1	>dbj|BAB01070.1| (AB023041) gene_id:MPE11.24~unknown protein [Arabidopsis thaliana]	211.041	202.000	1.045	164.751	164.000	1.005	1.025
1	11	11	TF004A04C	a76couture3171.r#1	>ref|NP_567115.1|| (NM_116025) putative protein; protein id: At3g61600.1. supported by	133.618	135.000	0.990	98.851	120.000	0.824	0.907
1	11	12	PT003H03	a76couture3009.r#1	>sp|P19950|R141_MAIZE 40S RIBOSOMAL PROTEIN S14 (CLONE MCH1) >gi|82723|pir||A30097	1618.398	1456.000	1.112	1171.794	1245.000	0.941	1.026
1	11	13	GT193F01	a76couture2877.r#1	>sp|Q9ZPN9|TBB2_ELEIN Tubulin beta-2 chain (Beta-2 tubulin) >gi|4415992|gb|AAD20179.1|	3012.018	2981.000	1.010	2568.061	2984.000	0.861	0.936
1	11	14	PT013F12	a76couture2744.r#1	>ref|NP_563961.1|| (NM_101367) 10 kDa chaperonin (CPN10); protein id: At1g14980.1	578.178	349.000	1.657	413.938	341.000	1.214	1.435
1	11	15	MT7REVERS	a76couture3167.r#1	------	169.832	140.000	1.213	136.950	136.000	1.007	1.110
1	12	1	ST004E03	a76couture3003.r#1	>ref|NP_690845.1|| (NC_001144) Transcript Antisense to Ribosomal RNA; Tar1p	8502.831	8769.000	0.970	6548.865	9781.000	0.670	0.820
1	12	2	PT001A09	a76couture2869#1	------	21.229	39.000	0.544	22.653	34.000	0.666	0.605
1	12	3	PT001E05	a76couture2740.r#1	>ref|NP_199109.1|| (NM_123660) putative protein; protein id: At5g42950.1 [Arabidopsis	81.170	114.000	0.712	75.168	120.000	0.626	0.669
1	12	4	BM437059 RT061B01	couture_a76.47.c1.r#1	>emb|CAC82727.1| (AJ301553) monodehydroascorbate reductase [Mesembryanthemum	1087.673	1211.000	0.898	1098.685	1457.000	0.754	0.826
1	12	5	BM437470 BM436947 BM437865 BM437267 GT2	couture_a76.384.c1#1	------	62.438	68.000	0.918	63.841	67.000	0.953	0.936
1	12	6	BM437753 TB005E08	couture_a76.302.c1.r#1	------	2408.865	3157.000	0.763	1989.372	2715.000	0.733	0.748
1	12	7	BG273927 GB000A58 BM437519	couture_a76.209.c1#1	>ref|NP_175098.1|| (NM_103558) unknown protein; protein id: At1g44770.1 [Arabidopsis	499.505	530.000	0.942	446.888	486.000	0.920	0.931
1	12	8	TB007a10 TB007A10	couture_a76.467.c1.r#1	>sp|Q9MB46|VATE_CITUN Vacuolar ATP synthase subunit E (V-ATPase E subunit) (Vacuolar	1740.776	1860.000	0.936	1271.674	1545.000	0.823	0.879
1	12	9	RT022H09 BM436726 BM437622 BM436257 BM	couture_a76.38.c1.r#1	------	5937.871	5621.000	1.056	4843.689	4797.000	1.010	1.033
1	12	10	BG273832 RT062F06	couture_a76.298.c1#1	>gb|AAL47429.1| (AY069873) AT5g45290/K9E15_7 [Arabidopsis thaliana]	2039.231	2592.000	0.787	1795.790	2271.000	0.791	0.789
1	12	11	BM437341 RT093A12	couture_a76.203.c1.r#1	>gb|AAD09518.1| (U64925) NTGP4 [Nicotiana tabacum]	1399.864	1152.000	1.215	819.638	771.000	1.063	1.139
1	12	12	BM437198 TB005A10	couture_a76.463.c1.r#1	>ref|NP_056986.2|| (NM_015902) progestin induced protein; ubiquitin-protein ligase [Homo	651.855	664.000	0.982	549.858	657.000	0.837	0.909
1	12	13	BM437484 BM437598 BM437170 GT162G05	couture_a76.376.c1.r#1	>pir||T07079 leucine-rich repeat protein LRP - tomato	921.588	926.000	0.995	935.994	1110.000	0.843	0.919
1	12	14	RB000A60 BG273742 RT051G12	couture_a76.292.c1.r#1	>ref|NP_197716.1|| (NM_122231) succinyl-CoA synthetase. alpha subunit; protein id:	831.677	724.000	1.149	569.422	626.000	0.910	1.029
1	12	15	BM437490 RT083D03	couture_a76.199.c1#1	>ref|NP_568696.1|| (NM_124213) receptor-like protein kinase; protein id: At5g48380.1	380.873	298.000	1.278	399.522	394.000	1.014	1.146
1	13	1	BM437022 TB001F11	couture_a76.460.c1.r#1	------	28.722	44.000	0.653	17.505	45.000	0.389	0.521
1	13	2	BM436575 GT161G02	couture_a76.373.c1.r#1	>ref|NP_180901.1|| (NM_128903) plastid protein; protein id: At2g33430.1. supported by	511.993	569.000	0.900	411.878	587.000	0.702	0.801
1	13	3	BM437019 RT033B05	couture_a76.288.c1.r#1	>pir||T03793 calmodulin-binding protein TCB60 - common tobacco	283.469	353.000	0.803	229.622	363.000	0.633	0.718
1	13	4	BM437219 BM436853 RT073C01 BM436596 BM	couture_a76.195.c1#1	>ref|NP_177215.1|| (NM_105726) putative alanine aminotransferase; protein id:	1627.139	2293.000	0.710	1375.674	2434.000	0.565	0.637
1	13	5	BG273806 TB000A88	couture_a76.458.c1#1	>ref|NP_197349.2|| (NM_121853) putative protein; protein id: At5g18480.1. supported by	166.086	249.000	0.667	206.969	282.000	0.734	0.700
1	13	6	BM438027 BM436576 GB006F11 BM437978 BM	couture_a76.369.c1#1	>dbj|BAA96146.1| (AP002092) ESTs AU029648(E31187).AU088638(E31187) correspond to a	88.662	152.000	0.583	348.037	484.000	0.719	0.651
1	13	7	BM437207 RT023E10	couture_a76.283.c1.r#1	>ref|NP_197155.1|| (NM_121657) amylogenin; reversibly glycosylatable polypeptide;	173.578	195.000	0.890	191.523	193.000	0.992	0.941
1	13	8	BE846433 TT282E01	couture_a76.190.c1.r#1	>ref|NP_564202.1|| (NM_102223) expressed protein; protein id: At1g23750.1. supported	5153.647	6609.000	0.780	3966.388	5742.000	0.691	0.735
1	13	9	BM438031 RT061G08	couture_a76.454.c1.r#1	>ref|NP_194280.1|| (NM_118682) arginine/serine-rich splicing factor RSp40; protein id:	33.717	43.000	0.784	27.802	32.000	0.869	0.826
1	13	10	GB004A07 BM437349	couture_a76.363.c1.r#1	>ref|NP_194081.1|| (NM_118481) polygalacturonase. putative; protein id: At4g23500.1	96.155	86.000	1.118	78.257	66.000	1.186	1.152
1	13	11	BG273870 GB001e10 RT012B04	couture_a76.278.c1#1	>ref|NP_187728.1|| (NM_111954) putative leucoanthocyanidin dioxygenase; protein id:	7245.326	6172.000	1.174	5708.634	5510.000	1.036	1.105
1	13	12	BM437132 TT284C02	couture_a76.188.c1#1	>ref|NP_190939.1|| (NM_115231) putative protein; protein id: At3g53710.1 [Arabidopsis	13.736	21.000	0.654	10.297	16.000	0.644	0.649
1	13	13	GB007b04 AW707981 AW707980 G515758G VII	couture_a76.sd.87.c1#	>sp|P51615|MAOX_VITVI NADP-DEPENDENT MALIC ENZYME (NADP-ME) >gi|515759|gb|AAA67087.1|	840.418	826.000	1.017	621.936	788.000	0.789	0.903
1	13	14	RB002E08 PT004E06	couture_a76.75.c1.r#1	>pir||T50664 methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5) /	854.154	766.000	1.115	692.985	799.000	0.867	0.991
1	13	15	BM436477 BM437431 CT004B06 BM436606 GB	couture_a76.540.c1.r#1	>gb|AAD48017.1|AF165529_1 (AF165529) chlorophyll a/b binding protein [Rumex palustris]	1722.045	1468.000	1.173	1321.100	1603.000	0.824	0.999
1	14	1	cds of gi|1469265|emb|X84846.1|PP111ACNP	luc1#1		9.990	26.000	0.384	6.178	24.000	0.257	0.321
1	14	2	BG273708 RB000A94	couture_a76.608.c1#1	>dbj|BAA03710.1| (D16139) cytokinin binding protein CBP57 [Nicotiana sylvestris]	523.232	740.000	0.707	374.809	763.000	0.491	0.599
1	14	3	BM436839 PT008F08	couture_a76.510.c1.r#1	------	6.244	17.000	0.367	4.119	13.000	0.317	0.342
1	14	4	PT011C03 VVI318053	couture_a76.sd.28.c1#	>emb|CAC39216.1| (AJ318053) glutamine synthetase [Vitis vinifera]	593.163	878.000	0.676	523.085	956.000	0.547	0.611

1	14	5	RB006E12 RB006E12	couture_a76.607.c2.r#1	>pir||ATSY3 actin - soybean >gi|18532|emb|CAA23728.1| (V00450) actin [Glycine	569.436	719.000	0.792	502.492	673.000	0.747	0.769
1	14	6	BM437092 BM436687 PT004F08	couture_a76.554.c1.r#1	>gb|AAF73016.1|AF262934_1 (AF262934) ubiquitin conjugating protein [Avicennia marina]	970.289	1651.000	0.588	1416.861	2054.000	0.690	0.639
1	14	7	RT043A09 VVADC	couture_a76.sd.75.c1#	>emb|CAA65585.1| (X96791) arginine decarboxylase [Vitis vinifera]	1658.358	1978.000	0.838	1587.791	1857.000	0.855	0.847
1	14	8	BG273703 RB000A99	couture_a76.65.c1.r#1	>ref|NP_196473.1|| (NM_120942) WD-repeat protein-like; protein id: At5g08560.1	574.431	803.000	0.715	514.848	700.000	0.735	0.725
1	14	9	BM437905 BM437077 GT194C07	couture_a76.553.c1.r#1	>gb|AAF73016.1|AF262934_1 (AF262934) ubiquitin conjugating protein [Avicennia marina]	2639.886	3074.000	0.859	2356.974	2738.000	0.861	0.860
1	14	10	BM438125 BG273914 AW707997 BE846437 BG2	couture_a76.sd.16.c1#	>gb|AAK69513.1|AF281656_1 (AF281656) putative transcription factor [Vitis vinifera]	24440.800	25929.000	0.943	23971.319	26136.000	0.917	0.930
1	14	11	RT043A01 PT001H12	couture_a76.598.c1#1	>ref|NP_564165.1|| (NM_102079) protein phosphatase 2C (PP2C). putative; protein id:	171.081	167.000	1.024	114.296	125.000	0.914	0.969
1	14	12	BM437140 PT007B07	couture_a76.526.c1#1	>emb|CAC10358.1| (AJ277086) protein phosphatase 2C [Nicotiana tabacum]	163.588	217.000	0.754	145.187	187.000	0.776	0.765
1	14	13	G18139650 AY070232	couture_a76.sd.15.c1.r	>gb|AAL58535.1| (AY070232) calmodulin [Vitis vinifera]	6.244	16.000	0.390	5.148	11.000	0.468	0.429
1	14	14	GB001e03 GB009D01	couture_a76.543.c1#1	>ref|NP_180489.1|| (NM_128482) putative tropinone reductase; protein id: At2g29260.1	101.150	137.000	0.738	77.227	132.000	0.585	0.662
1	14	15	cds of NM0019271 NM_001927 desmin; DES	des#1		42.458	48.000	0.885	43.247	53.000	0.816	0.850
2	1	1	CM004H03	a76couture0473.r#1	------	262.240	241.000	1.088	261.543	250.000	1.046	1.067
2	1	2	ST002E04	a76couture0377.r#1	>ref|NP_174261.1|| (NM_102708) unknown protein; protein id: At1g29680.1 [Arabidopsis	1351.162	1640.000	0.824	1631.038	1935.000	0.843	0.833
2	1	3	PT010C02	a76couture0250.r#1	>gb|AAF79454.1|AC025808_36 (AC025808) F18O14.5 [Arabidopsis thaliana]	510.744	646.000	0.791	623.996	775.000	0.805	0.798
2	1	4	Arabidopsis Control Oligonucleotide	3ara7		31.219	34.000	0.918	23.683	32.000	0.740	0.829
2	1	5	CM004F10	a76couture0469.r#1	>ref|NP_191358.1|| (NM_115661) putative protein; protein id: At3g57990.1. supported by	563.192	602.000	0.936	588.986	629.000	0.936	0.936
2	1	6	CT005H05	a76couture0371.r#1	------	4866.432	5443.000	0.894	6002.097	5854.000	1.025	0.960
2	1	7	PT007B06	a76couture0245.r#1	>ref|NP_564788.1|| (NM_104873) expressed protein; protein id: At1g61930.1. supported	333.420	440.000	0.758	537.501	565.000	0.951	0.855
2	1	8	CT002A06	a76couture0098.r#1	>ref|NP_175778.1|| (NM_104252) 26S proteasome AAA-ATPase subunit RPT1a; protein id:	374.629	342.000	1.095	498.373	426.000	1.170	1.133
2	1	9	CM004D09	a76couture0465.r#1	>ref|NP_179632.1|| (NM_127601) succinyl-CoA ligase beta subunit; protein id:	308.445	324.000	0.952	380.987	356.000	1.070	1.011
2	1	10	CT002B04	a76couture0367.r#1	>emb|CAB85624.1| (AJ237984) putative proline-rich cell wall protein [Vitis vinifera]	1088.922	1162.000	0.937	1382.882	1291.000	1.071	1.004
2	1	11	PT003G01	a76couture0239.r#1	>gb|AAF34770.1|AF227625_1 (AF227625) proteasome 27 kDa subunit [Euphorbia esula]	558.197	632.000	0.883	748.589	730.000	1.025	0.954
2	1	12	CM005b11	a76couture0094.r#1	none	1469.795	1588.000	0.926	1637.216	1811.000	0.904	0.915
2	1	13	CM004B09	a76couture0461.r#1	>dbj|BAB90138.1| (AP003375) RNA-binding protein-like [Oryza sativa (japonica	914.095	1192.000	0.767	1358.169	1556.000	0.873	0.820
2	1	14	CM004F04	a76couture0363.r#1	>pir||T47748 alpha-galactosidase-like protein - Arabidopsis thaliana	151.100	195.000	0.775	191.523	241.000	0.795	0.785
2	1	15	PT007D05	a76couture0233.r#1	>pir||T50649 elicitor-responsive gene 3 [imported] - rice	1020.240	1113.000	0.917	1232.546	1393.000	0.885	0.901
2	2	1	CM004A03	a76couture0089.r#1	>ref|NP_173666.1|| (NM_102099) RING-H2 zinc finger protein ATL5. putative; protein id:	2376.397	2201.000	1.080	2651.467	2495.000	1.063	1.071
2	2	2	CM003H12	a76couture0457.r#1	>ref|NP_566133.1|| (NM_110982) Expressed protein; protein id: At3g01170.1. supported	239.763	226.000	1.061	267.721	242.000	1.106	1.084
2	2	3	CM002B03	a76couture0359.r#1	------	1343.670	1282.000	1.048	1488.940	1438.000	1.035	1.042
2	2	4	PT010D04	a76couture0228.r#1	>sp|P49199|RS8_ORYSA 40S RIBOSOMAL PROTEIN S8 >gi|7440236|pir||T04082 probable ribosomal	7125.445	5594.000	1.274	6279.085	5726.000	1.097	1.185
2	2	5	CM003A03	a76couture0085.r#1	>pir||C71447 hypothetical protein - Arabidopsis thaliana	1212.549	1754.000	0.691	1458.049	1853.000	0.787	0.739
2	2	6	CM003H04	a76couture0452.r#1	>gb|AAL29212.1|AF354454_1 (AF354454) putative acyl-CoA synthetase [Capsicum annuum]	3357.925	2872.000	1.169	3836.647	2868.000	1.338	1.253
2	2	7	TT273B02	a76couture0355.r#1	>gb|AAG13629.1|AC078840_20 (AC078840) putative steroid membrane binding protein [Oryza sativa	666.840	704.000	0.947	825.816	774.000	1.067	1.007
2	2	8	PT009A07	a76couture0222.r#1	>ref|NP_566456.2|| (NM_112186) expressed protein; protein id: At3g13410.1. supported	1944.325	2397.000	0.811	2324.023	2525.000	0.920	0.866
2	2	9	CM001D10	a76couture0079.r#1	>gb|AAL49875.1| (AY070379) unknown protein [Arabidopsis thaliana]	465.789	525.000	0.887	567.362	521.000	1.089	0.988
2	2	10	TT274C02	a76couture0905.r#1	>ref|NP_564399.1|| (NM_102974) expressed protein; protein id: At1g32400.1. supported	1428.586	1522.000	0.939	1842.126	1566.000	1.176	1.057
2	2	11	GB009E11	a76couture0779.r#1	>sp|Q04960|DNJH_CUCSA DnaJ protein homolog (DNAJ-1) >gi|18260|emb|CAA47925.1| (X67695) cs	1608.407	1484.000	1.084	2433.171	1807.000	1.347	1.215
2	2	12	ST004H03	a76couture0673.r#1	>ref|NP_201151.1|| (NM_125741) unknown protein; protein id: At5g63460.1 [Arabidopsis	87.413	93.000	0.940	101.940	99.000	1.030	0.985
2	2	13	CT005F05	a76couture0574.r#1	>ref|NP_200749.1|| (NM_125332) putative Rab5-interacting protein - like; protein id:	424.580	403.000	1.054	523.085	505.000	1.036	1.045
2	2	14	TT284H10	a76couture0901.r#1	>ref|NP_197108.1|| (NM_121609) UVB-resistance protein-like; protein id: At5g16040.1	19.980	26.000	0.768	24.713	33.000	0.749	0.759
2	2	15	RT074G03	a76couture0773.r#1	>ref|NP_568947.1|| (NM_125590) signal recognition particle - like protein; protein id:	463.291	507.000	0.914	583.838	595.000	0.981	0.948
2	3	1	ST004F09	a76couture0669.r#1	------	12.488	20.000	0.624	15.445	22.000	0.702	0.663
2	3	2	CT005D06	a76couture0569.r#1	>dbj|BAB93194.1| (AP003230) putative serine/threonine protein kinase [Oryza sativa	430.823	413.000	1.043	399.522	408.000	0.979	1.011
2	3	3	RT094D09	a76couture0894.r#1	>pir||S42049 protein kinase (EC 2.7.1.37) cdc2 - Norway spruce	19.980	39.000	0.512	18.535	36.000	0.515	0.514
2	3	4	RT074E07	a76couture0769.r#1	>gb|AAM97010.1| (AY136344) putative protein [Arabidopsis thaliana]	39.960	49.000	0.816	25.742	36.000	0.715	0.765
2	3	5	ST004E05	a76couture0664.r#1	>ref|NP_191528.1|| (NM_115831) putative protein; protein id: At3g59690.1 [Arabidopsis	1316.197	1241.000	1.061	1394.208	1288.000	1.082	1.072
2	3	6	CT005B03	a76couture0565.r#1	------	352.151	371.000	0.949	429.383	411.000	1.045	0.997
2	3	7	TT284A08	a76couture0888.r#1	>ref|NP_195202.1|| (NM_119642) putative auxin-regulated protein; protein id:	3.746	13.000	0.288	7.208	15.000	0.481	0.384
2	3	8	RT074B10	a76couture0764.r#1	>gb|AAG13986.1|AF298827_1 (AF298827) 60S ribosomal protein L24 [Prunus avium]	334.669	298.000	1.123	369.661	282.000	1.311	1.217
2	3	9	ST004D03	a76couture0660.r#1	>pir||T10862 phaseolin G-box binding protein PG2 - kidney bean (fragment)	89.911	82.000	1.096	113.267	86.000	1.317	1.207
2	3	10	CT005A03	a76couture0561.r#1	>gb|AAM65781.1| (AY088240) unknown [Arabidopsis thaliana]	1046.464	1554.000	0.673	1492.029	1642.000	0.909	0.791
2	3	11	RT093G03	a76couture0882.r#1	>ref|NP_565730.1|| (NM_128745) putative poly(ADP-ribose) glycohydrolase; protein id:	72.428	103.000	0.703	126.653	127.000	0.997	0.850
2	3	12	RT073C03	a76couture0759.r#1	>sp|P41090|FL3H_VITVI Naringenin.2-oxoglutarate 3-dioxygenase (Flavonone-3-hydroxylase)	2915.863	3212.000	0.908	4468.880	3952.000	1.131	1.019
2	3	13	ST004B05	a76couture0656.r#1	>dbj|BAB02652.1| (AP002061) gene_id:T21E2.13~pir||T01495~similar to unknown protein	102.399	100.000	1.024	145.187	132.000	1.100	1.062
2	3	14	CT004G06	a76couture0557.r#1	>ref|NP_564919.1|| (NM_105475) F-box protein FKF1/ADO3. AtFBX2a; protein id:	138.613	129.000	1.075	179.167	153.000	1.171	1.123
2	3	15	RT093A07	a76couture0876.r#1	>ref|NP_567999.1|| (NM_119787) Expressed protein; protein id: At4g36195.1. supported	1362.401	1868.000	0.729	1400.386	1893.000	0.740	0.735
2	4	1	RT072G03	a76couture0753.r#1	>ref|NP_568445.1|| (NM_122348) 6-phosphogluconolactonase-like protein; protein id:	2776.001	3005.000	0.924	3470.075	3597.000	0.965	0.944
2	4	2	ST004A02	a76couture0652.r#1	>ref|NP_197794.1|| (NM_122311) putative protein; protein id: At5g24060.1 [Arabidopsis	38.712	60.000	0.645	50.455	70.000	0.721	0.683
2	4	3	CT004E08	a76couture0552.r#1	>gb|AAF26161.1|AC008261_18 (AC008261) unknown protein [Arabidopsis thaliana]	1434.829	1227.000	1.169	1383.911	1233.000	1.122	1.146
2	4	4	RT051H02	a76couture1359.r#1	>pir||T08588 hypothetical protein L23H3.30 - Arabidopsis thaliana	653.103	794.000	0.823	736.233	867.000	0.849	0.836
2	4	5	GT203E07	a76couture1236.r#1	>gb|AAD13216.1| (AF098458) latex-abundant protein [Hevea brasiliensis]	515.739	605.000	0.852	581.778	660.000	0.881	0.867
2	4	6	GB007D08	a76couture1111.r#1	------	8.741	26.000	0.336	12.356	29.000	0.426	0.381
2	4	7	RT083H10	a76couture1000.r#1	>gb|AAM62602.1| (AY085372) unknown [Arabidopsis thaliana]	216.036	271.000	0.797	278.018	290.000	0.959	0.878
2	4	8	RT043G01	a76couture1354.r#1	>gb|AAK81875.1| (AY043232) pectin methylesterase PME1 [Vitis vinifera]	1650.865	1860.000	0.888	2296.222	2274.000	1.010	0.949
2	4	9	GT202C03	a76couture1229.r#1	------	142.359	124.000	1.148	209.028	150.000	1.394	1.271
2	4	10	GB006C12	a76couture1107.r#1	>gb|AAM67048.1| (AY088730) unknown [Arabidopsis thaliana]	3766.271	3753.000	1.004	4918.857	4051.000	1.214	1.109
2	4	11	Arabidopsis Control Oligonucleotide	3ara7		17.483	20.000	0.874	25.742	26.000	0.990	0.932
2	4	12	RT043F05	a76couture1350.r#1	>ref|NP_563880.1|| (NM_100960) putative translation initiation factor; protein id:	344.659	352.000	0.979	553.976	450.000	1.231	1.105

2	4	13	GT201C01	a76couture1220.r#1	>gb|AAF27025.1|AC009177_15 (AC009177) putative branched-chain amino acid aminotransferase	218.534	295.000	0.741	351.126	418.000	0.840	0.790
2	4	14	GB004F02	a76couture1098.r#1	>ref|NP_564555.1|| (NM_103869) expressed protein; protein id: At1g49820.1. supported	636.869	752.000	0.847	754.767	870.000	0.868	0.857
2	4	15	RT083F04	a76couture0995.r#1	>gb|AAL26911.1|AF319167_1 (AF319167) unknown [Prunus persica]	64.936	75.000	0.866	76.197	76.000	1.003	0.934
2	5	1	RT043C10	a76couture1346.r#1	>ref|NP_187098.1|| (NM_111319) unknown protein; protein id: At3g04480.1 [Arabidopsis	36.214	79.000	0.458	40.158	94.000	0.427	0.443
2	5	2	GT202G07	a76couture1214.r#1	>ref|NP_564627.1|| (NM_104210) F-box containing tubby family protein; protein id:	797.960	973.000	0.820	900.984	995.000	0.906	0.863
2	5	3	GB003C04	a76couture1094.r#1	------	101.150	113.000	0.895	129.742	132.000	0.983	0.939
2	5	4	RT083C11	a76couture0990.r#1	>ref|NP_564317.1|| (NM_102645) expressed protein; protein id: At1g29040.1. supported	174.827	186.000	0.940	188.434	204.000	0.924	0.932
2	5	5	RT042G08	a76couture1342.r#1	>ref|NP_171990.2|| (NM_100376) disulfide isomerase-related protein. putative; protein	64.936	98.000	0.663	83.405	112.000	0.745	0.704
2	5	6	GT201A11	a76couture1209.r#1	>ref|NP_566063.1|| (NM_130171) expressed protein; protein id: At2g46080.1. supported	1612.154	1959.000	0.823	1886.403	1887.000	1.000	0.911
2	5	7	GB001A04	a76couture1087.r#1	>gb|AAM63181.1| (AY085971) unknown [Arabidopsis thaliana]	87.413	115.000	0.760	83.405	98.000	0.851	0.806
2	5	8	RT083C06	a76couture0987#1	------	24.975	33.000	0.757	30.891	38.000	0.813	0.785
2	5	9	RT033H10	a76couture1338.r#1	>ref|NP_683417.1|| (NM_148576) hypothetical protein; protein id: At1g51355.1	21.229	37.000	0.574	31.921	43.000	0.742	0.658
2	5	10	GT194C01	a76couture1205.r#1	>ref|NP_191593.1|| (NM_115898) palmitoyl-protein thioesterase precursor - like;	49.951	63.000	0.793	98.851	87.000	1.136	0.965
2	5	11	GB000A86	a76couture1078.r#1	>ref|NP_180873.1|| (NM_128874) 3-ketoacyl-CoA thiolase; protein id: At2g33150.1	1182.579	1677.000	0.705	1800.938	1780.000	1.012	0.858
2	5	12	RT083B08	a76couture0984#1	>dbj|BAB64773.1| (AP003282) hypothetical protein~similar to Arabidopsis thaliana	18.731	38.000	0.493	14.416	33.000	0.437	0.465
2	5	13	GT183E10	a76couture1801#1	------	27.473	30.000	0.916	29.861	31.000	0.963	0.940
2	5	14	GT172A04	a76couture1712#1	>emb|CAA60774.1| (X87332) ribosomal protein L35 [Arabidopsis thaliana]	318.435	381.000	0.836	384.077	400.000	0.960	0.898
2	5	15	GB006F09	a76couture1616.r#1	>pir||S65050 low molecular weight heat shock protein precursor (clone Hsp22.3) -	1136.375	561.000	2.026	1890.522	624.000	3.030	2.528
2	6	1	TT273D01	a76couture1477.r#1	>ref|NP_175482.1|| (NM_103949) unknown protein; protein id: At1g50670.1 [Arabidopsis	27.473	35.000	0.785	31.921	37.000	0.863	0.824
2	6	2	GT182G07	a76couture1797.r#1	>pir||I30010 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Leishmania	34.965	42.000	0.833	54.574	55.000	0.992	0.912
2	6	3	GT171G04	a76couture1708#1	>dbj|BAA87845.1| (AP000815) ESTs AU081301(E20138).C99280(E10593) correspond to a	134.866	161.000	0.838	200.791	218.000	0.921	0.879
2	6	4	GB006D11	a76couture1612.r#1	>ref|NP_389802.1|| (NC_000964) similar to cell wall-binding protein [Bacillus	525.729	547.000	0.961	542.650	560.000	0.969	0.965
2	6	5	TT272F04	a76couture1472.r#1	>gb|AAM63868.1| (AY086820) unknown [Arabidopsis thaliana]	1865.653	2130.000	0.876	2081.015	2099.000	0.991	0.934
2	6	6	GT182A04	a76couture1794.r#1	>ref|NP_566542.1|| (NM_112502) expressed protein; protein id: At3g16310.1. supported	419.585	520.000	0.807	533.382	541.000	0.986	0.896
2	6	7	GT171D09	a76couture1703.r#1	>gb|AAD10836.1| (U52079) P-glycoprotein [Solanum tuberosum]	162.339	225.000	0.722	199.761	214.000	0.933	0.827
2	6	8	GB006B07	a76couture1608.r#1	>ref|NP_200187.1|| (NM_124755) putative protein; protein id: At5g53760.1. supported by	152.349	174.000	0.876	188.434	190.000	0.992	0.934
2	6	9	TT264H11	a76couture1467.r#1	>sp|P52780|SYQ_LUPLU GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)	228.524	208.000	1.099	356.275	247.000	1.442	1.271
2	6	10	GT174C12	a76couture1790.r#1	------	207.295	243.000	0.853	295.523	254.000	1.163	1.008
2	6	11	GT171C03	a76couture1699.r#1	>pir||S52261 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) flavoprotein 1	169.832	229.000	0.742	85.465	98.000	0.872	0.807
2	6	12	GB005H06	a76couture1604.r#1	>ref|NP_567219.1|| (NM_116425) putative NifU-like metallocluster assembly factor;	533.222	538.000	0.991	563.244	510.000	1.104	1.048
2	6	13	TT264F05	a76couture1463.r#1	>ref|NP_198101.1|| (NM_122631) putative protein; protein id: At5g27490.1 [Arabidopsis	579.426	781.000	0.742	748.589	824.000	0.908	0.825
2	6	14	GT174H07	a76couture1785.r#1	>dbj|BAB10377.1| (AB006696) gene_id:MAF19.15~unknown protein [Arabidopsis thaliana]	624.382	816.000	0.765	706.371	775.000	0.911	0.838
2	6	15	GT162G10	a76couture1695.r#1	>gb|AAG60197.1|AC084763_17 (AC084763) hypothetical protein [Oryza sativa]	123.628	105.000	1.177	158.573	120.000	1.321	1.249
2	7	1	GB005F04	a76couture1600.r#1	>ref|NP_564656.1|| (NM_104310) membrane protein common family; protein id:	479.525	525.000	0.913	571.481	629.000	0.909	0.911
2	7	2	TT264H07	a76couture1459.r#1	>ref|NP_191853.1|| (NM_116159) putative protein; protein id: At3g62940.1. supported by	618.138	642.000	0.963	607.521	654.000	0.929	0.946
2	7	3	GT174F07	a76couture1781.r#1	>gb|AAM61103.1| (AY084535) unknown [Arabidopsis thaliana]	1060.200	1210.000	0.876	1216.071	1458.000	0.834	0.855
2	7	4	GT161E12	a76couture1689.r#1	>ref|NP_199598.1|| (NM_124161) putative protein; protein id: At5g47870.1. supported by	73.677	66.000	1.116	78.257	66.000	1.186	1.151
2	7	5	GB005B07	a76couture1596.r#1	>ref|NP_195650.1|| (NM_120100) brassinosteroid insensitive 1 gene (BRI1); protein id:	384.619	490.000	0.785	540.590	516.000	1.048	0.916
2	7	6	TT264E07	a76couture1455.r#1	>ref|NP_199482.1|| (NM_124040) senescence-associated protein 5-like protein; protein	46.204	50.000	0.924	70.019	58.000	1.207	1.066
2	7	7	RT043A11	a76couture2208#1	>gb|AAK49589.1|AF372873_1 (AF372873) At2g26590/T9J22.26 [Arabidopsis thaliana]	64.936	79.000	0.822	81.346	82.000	0.992	0.907
2	7	8	RT024H07	a76couture2108.r#1	>ref|NP_192337.1|| (NM_116666) putative transposon protein; protein id: At4g04280.1	229.772	238.000	0.965	293.463	285.000	1.030	0.998
2	7	9	RT021D10	a76couture2014.r#1	------		11.000	0.000				
2	7	10	RB004A03	a76couture1926.r#1	------	9.990	21.000	0.476	12.356	21.000	0.588	0.532
2	7	11	RT042F03	a76couture2204.r#1	>pir||T14306 glycine-rich protein - carrot (fragment) >gi|1276971|gb|AAB01097.1|	2975.804	3312.000	0.898	4105.397	3746.000	1.096	0.997
2	7	12	RT024D09	a76couture2104.r#1	>ref|NP_175528.1|| (NM_103995) unknown protein; protein id: At1g51160.1 [Arabidopsis	262.240	307.000	0.854	342.889	342.000	1.003	0.928
2	7	13	RT021C10	a76couture2011#1	>ref|NP_192979.1|| (NM_117312) pectinesterase (pectin methylesterase) family; protein	93.657	83.000	1.128	118.415	96.000	1.233	1.181
2	7	14	RB002H04	a76couture1920.r#1	>dbj|BAB92410.1| (AP003293) hypothetical protein [Oryza sativa (japonica	8.741	25.000	0.350	7.208	20.000	0.360	0.355
2	7	15	RT041D10	a76couture2199.r#1	------	4038.501	4084.000	0.989	4026.111	4154.000	0.969	0.979
2	8	1	RT023E01	a76couture2099.r#1	>gb|AAM64391.1| (AY086321) unknown [Arabidopsis thaliana]	74.926	90.000	0.833	64.871	79.000	0.821	0.827
2	8	2	RT021B11	a76couture2007#1	>ref|NP_072983.1|| (NC_000908) conserved hypothetical protein [Mycoplasma genitalium]	117.384	123.000	0.954	153.425	165.000	0.930	0.942
2	8	3	RB002B12	a76couture1913.r#1	>emb|CAB16816.1| (Z99708) putative protein [Arabidopsis thaliana]	354.649	334.000	1.062	474.690	496.000	0.957	1.009
2	8	4	RT041A10	a76couture2195.r#1	>dbj|BAA77682.1| (AB027123) cytochrome c oxidase subunit 5c [Oryza sativa (japonica	7053.017	6718.000	1.050	7466.324	7253.000	1.029	1.040
2	8	5	RT024E11	a76couture2093.r#1	------	24.975	38.000	0.657	33.980	46.000	0.739	0.698
2	8	6	RT021A11	a76couture2003.r#1	>pir||OWASN ornithine carbamoyltransferase (EC 2.1.3.3) precursor - Emericella	22.478	30.000	0.749	30.891	34.000	0.909	0.829
2	8	7	RB001C10	a76couture1908.r#1	>gb|AAL38841.2| (AY065400) unknown protein [Arabidopsis thaliana]	352.151	359.000	0.981	427.324	430.000	0.994	0.987
2	8	8	RT034H09	a76couture2191.r#1	>ref|NP_196202.1|| (NM_120665) putative protein; protein id: At5g05830.1 [Arabidopsis	338.415	469.000	0.722	369.661	497.000	0.744	0.733
2	8	9	RT024C11	a76couture2089.r#1	>dbj|BAB90811.1| (AP004614) putative protein kinase [Oryza sativa (japonica	72.428	88.000	0.823	89.584	99.000	0.905	0.864
2	8	10	RT012F09	a76couture1999.r#1	ef|NP_177413.1|| (NM_105928) unknown protein [Arabidopsis thali... 77 9e-014	76.175	78.000	0.977	101.940	87.000	1.172	1.074
2	8	11	GT204H02	a76couture1887.r#1	>ref|NP_181041.1|| (NM_129048) putative amino acid transporter; protein id:	7.493	17.000	0.441	5.148	13.000	0.396	0.418
2	8	12	RT034G08	a76couture2187.r#1	>ref|NP_568356.1|| (NM_121777) chloroplast GrpE protein; protein id: At5g17710.1	774.233	816.000	0.949	948.350	903.000	1.050	1.000
2	8	13	RT024A08	a76couture2084.r#1	>ref|NP_186881.1|| (NM_111099) putative N2.N2-dimethylguanosine tRNA	430.823	393.000	1.096	593.105	514.000	1.154	1.125
2	8	14	RT012B01	a76couture1995.r#1	------	68.682	74.000	0.928	61.782	71.000	0.870	0.899
2	8	15	GT204E11	a76couture1883.r#1	>gb|AAM47629.1|AC122147_18 (AC122147) Putative non-LTR retroelement reverse transcriptase	197.305	159.000	1.241	207.999	159.000	1.308	1.275
2	9	1	PT008C01	a76couture2631.r#1	------	3.746	13.000	0.288	4.119	7.000	0.588	0.438
2	9	2	TT261A11	a76couture2511.r#1	>gb|AAL58201.1|AC090882_4 (AC090882) putative ATP(GTP)-binding protein [Oryza sativa]	43.707	45.000	0.971	44.277	50.000	0.886	0.928
2	9	3	TB003F08	a76couture2401.r#1	>ref|NP_193723.1|| (NM_118108) putative protein; protein id: At4g19880.1. supported by	1087.673	1033.000	1.053	1218.130	1142.000	1.067	1.060
2	9	4	RT061B03	a76couture2299.r#1	>ref|NP_568487.1|| (NM_122559) putative protein; protein id: At5g26770.1. supported by	14.985	22.000	0.681	3.089	11.000	0.281	0.481
2	9	5	PT008B06	a76couture2627.r#1	------	226.026	174.000	1.299	262.572	212.000	1.239	1.269

<table>
<tr><td>2</td><td>9</td><td>6</td><td>TT261D12</td><td>a76couture2507.r#1</td><td>>pir||T03601 shaggy protein kinase (EC 2.7.1.-) 6 - common tobacco</td><td>57.443</td><td>66.000</td><td>0.870</td><td>78.257</td><td>81.000</td><td>0.966</td><td>0.918</td></tr>
<tr><td>2</td><td>9</td><td>7</td><td>TB003B11</td><td>a76couture2397.r#1</td><td>------</td><td>56.194</td><td>56.000</td><td>1.003</td><td>55.604</td><td>62.000</td><td>0.897</td><td>0.950</td></tr>
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<tr><td>2</td><td>9</td><td>10</td><td>TT261A02</td><td>a76couture2503.r#1</td><td>------</td><td>743.014</td><td>721.000</td><td>1.031</td><td>782.569</td><td>763.000</td><td>1.026</td><td>1.028</td></tr>
<tr><td>2</td><td>9</td><td>11</td><td>TB002H11</td><td>a76couture2393.r#1</td><td>>gb|AAM61570.1| (AY085012) unknown [Arabidopsis thaliana]</td><td>52.448</td><td>50.000</td><td>1.049</td><td>49.425</td><td>43.000</td><td>1.149</td><td>1.099</td></tr>
<tr><td>2</td><td>9</td><td>12</td><td>RT051F12</td><td>a76couture2291.r#1</td><td>>ref|NP_567449.1|| (NM_117579) expressed protein; protein id: At4g14930.1. supported</td><td>359.644</td><td>315.000</td><td>1.142</td><td>430.413</td><td>387.000</td><td>1.112</td><td>1.127</td></tr>
<tr><td>2</td><td>9</td><td>13</td><td>PT006F01</td><td>a76couture2618.r#1</td><td>------</td><td>1329.933</td><td>946.000</td><td>1.406</td><td>1493.059</td><td>1306.000</td><td>1.143</td><td>1.275</td></tr>
<tr><td>2</td><td>9</td><td>14</td><td>TT254E12</td><td>a76couture2499.r#1</td><td>>ref|NP_182110.1|| (NM_130149) hypothetical protein; protein id: At2g45860.1</td><td>255.997</td><td>207.000</td><td>1.237</td><td>267.721</td><td>224.000</td><td>1.195</td><td>1.216</td></tr>
<tr><td>2</td><td>9</td><td>15</td><td>TB001H10</td><td>a76couture2389.r#1</td><td>>ref|NP_565810.1|| (NM_129114) Expressed protein; protein id: At2g35605.1. supported</td><td>138.613</td><td>124.000</td><td>1.118</td><td>159.603</td><td>136.000</td><td>1.174</td><td>1.146</td></tr>
<tr><td>2</td><td>10</td><td>1</td><td>RT053B04</td><td>a76couture2287.r#1</td><td>>ref|NP_566959.1|| (NM_115075) Expressed protein; protein id: At3g52155.1. supported</td><td>51.199</td><td>59.000</td><td>0.868</td><td>44.277</td><td>60.000</td><td>0.738</td><td>0.803</td></tr>
<tr><td>2</td><td>10</td><td>2</td><td>PT010C07</td><td>a76couture2614.r#1</td><td>------</td><td>112.389</td><td>126.000</td><td>0.892</td><td>105.029</td><td>142.000</td><td>0.740</td><td>0.816</td></tr>
<tr><td>2</td><td>10</td><td>3</td><td>TT253D02</td><td>a76couture2494.r#1</td><td>>ref|NP_564389.1|| (NM_102949) expressed protein; protein id: At1g32160.1. supported</td><td>43.707</td><td>55.000</td><td>0.795</td><td>56.633</td><td>72.000</td><td>0.787</td><td>0.791</td></tr>
<tr><td>2</td><td>10</td><td>4</td><td>TB001D03</td><td>a76couture2382.r#1</td><td>>gb|AAM12952.1| (AY090553) auxin-regulated protein [Zinnia elegans]</td><td>726.780</td><td>678.000</td><td>1.072</td><td>830.965</td><td>774.000</td><td>1.074</td><td>1.073</td></tr>
<tr><td>2</td><td>10</td><td>5</td><td>RT052G11</td><td>a76couture2283.r#1</td><td>>ref|NP_189624.1|| (NM_113904) unknown protein; protein id: At3g29780.1 [Arabidopsis</td><td>1312.450</td><td>1416.000</td><td>0.927</td><td>1529.098</td><td>1540.000</td><td>0.993</td><td>0.960</td></tr>
<tr><td>2</td><td>10</td><td>6</td><td>RT064G10</td><td>a76couture2609.r#1</td><td>>gb|AAK50091.1|AF372951_1 (AF372951) At1g78070/F28K19_28 [Arabidopsis thaliana]</td><td>769.238</td><td>897.000</td><td>0.858</td><td>913.340</td><td>1012.000</td><td>0.903</td><td>0.880</td></tr>
<tr><td>2</td><td>10</td><td>7</td><td>TT251H08</td><td>a76couture2490.r#1</td><td>>ref|NP_564248.1|| (NM_102410) expressed protein; protein id: At1g26470.1. supported</td><td>172.329</td><td>176.000</td><td>0.979</td><td>202.850</td><td>221.000</td><td>0.918</td><td>0.949</td></tr>
<tr><td>2</td><td>10</td><td>8</td><td>RT063G07</td><td>a76couture2377.r#1</td><td>>ref|NP_564806.1|| (NM_104978) expressed protein; protein id: At1g63000.1. supported</td><td>4584.211</td><td>3825.000</td><td>1.198</td><td>4257.792</td><td>4457.000</td><td>0.955</td><td>1.077</td></tr>
<tr><td>2</td><td>10</td><td>9</td><td>RT052D11</td><td>a76couture2279.r#1</td><td>>ref|NP_566989.1|| (NM_115238) putative protein; protein id: At3g53780.1 [Arabidopsis</td><td>751.756</td><td>777.000</td><td>0.968</td><td>648.708</td><td>881.000</td><td>0.736</td><td>0.852</td></tr>
<tr><td>2</td><td>10</td><td>10</td><td>GSP6F4AP3</td><td>a76couture3163.r#1</td><td>>ref|NP_564678.1|| (NM_104390) expressed protein; protein id: At1g55170.1. supported</td><td>529.476</td><td>413.000</td><td>1.282</td><td>534.412</td><td>508.000</td><td>1.052</td><td>1.167</td></tr>
<tr><td>2</td><td>10</td><td>11</td><td>TT281B10</td><td>a76couture2998.r#1</td><td>>dbj|BAB89723.1| (AP003269) putative nascent polypeptide associated complex alpha</td><td>89.911</td><td>73.000</td><td>1.232</td><td>107.088</td><td>90.000</td><td>1.190</td><td>1.211</td></tr>
<tr><td>2</td><td>10</td><td>12</td><td>TB007C05</td><td>a76couture2857.r#1</td><td>>sp|O48920|ARF_VIGUN ADP-ribosylation factor >gi|2689631|gb|AAB91395.1| (AF022389)</td><td>6959.359</td><td>6033.000</td><td>1.154</td><td>6662.132</td><td>6812.000</td><td>0.978</td><td>1.066</td></tr>
<tr><td>2</td><td>10</td><td>13</td><td>PT002F01</td><td>a76couture2736.r#1</td><td>>ref|NP_201235.2|| (NM_125826) GTP cyclohydrolase II;</td><td>412.092</td><td>251.000</td><td>1.642</td><td>432.472</td><td>331.000</td><td>1.307</td><td>1.474</td></tr>
<tr><td>2</td><td>10</td><td>14</td><td>FT7F4AP33</td><td>a76couture3140#1</td><td>>pir||T03019 probable ribosomal protein L2 [imported] - rice mitochondrion</td><td>121.130</td><td>88.000</td><td>1.376</td><td>116.356</td><td>107.000</td><td>1.087</td><td>1.232</td></tr>
<tr><td>2</td><td>10</td><td>15</td><td>TT262C09</td><td>a76couture2992.r#1</td><td>>gb|AAG16758.1| (AY007560) putative glutathione S-transferase T3 [Lycopersicon</td><td>26.224</td><td>29.000</td><td>0.904</td><td>27.802</td><td>27.000</td><td>1.030</td><td>0.967</td></tr>
<tr><td>2</td><td>11</td><td>1</td><td>RT043E02</td><td>a76couture2850.r#1</td><td>>sp|P93343|143C_TOBAC 14-3-3-LIKE PROTEIN C (14-3-3-LIKE PROTEIN B)</td><td>53.697</td><td>73.000</td><td>0.736</td><td>52.514</td><td>77.000</td><td>0.682</td><td>0.709</td></tr>
<tr><td>2</td><td>11</td><td>2</td><td>PT004F07</td><td>a76couture2732.r#1</td><td>>ref|NP_191860.1|| (NM_116166) putative protein; protein id: At3g63010.1 [Arabidopsis</td><td>2242.779</td><td>2008.000</td><td>1.117</td><td>2123.233</td><td>2403.000</td><td>0.884</td><td>1.000</td></tr>
<tr><td>2</td><td>11</td><td>3</td><td>40E1PROTE</td><td>a76couture3136.r#1</td><td>>ref|NP_564521.1|| (NM_103710) expressed protein; protein id: At1g48140.1 [Arabidopsis</td><td>167.334</td><td>150.000</td><td>1.116</td><td>156.514</td><td>164.000</td><td>0.954</td><td>1.035</td></tr>
<tr><td>2</td><td>11</td><td>4</td><td>RT082E12</td><td>a76couture2987.r#1</td><td>>ref|NP_567980.1|| (NM_119689) putative protein; protein id: At4g35230.1. supported by</td><td>676.830</td><td>518.000</td><td>1.307</td><td>636.352</td><td>583.000</td><td>1.092</td><td>1.199</td></tr>
<tr><td>2</td><td>11</td><td>5</td><td>PT010H03</td><td>a76couture2843.r#1</td><td>>gb|AAK43709.1|AF358665_1 (AF358665) ribosomal protein L32 [Mercurialis annua]</td><td>2541.234</td><td>2051.000</td><td>1.239</td><td>2337.410</td><td>2070.000</td><td>1.129</td><td>1.184</td></tr>
<tr><td>2</td><td>11</td><td>6</td><td>PT010G10</td><td>a76couture2727.r#1</td><td>>ref|NP_173506.1|| (NM_101935) similar to putative RING zinc finger protein; protein</td><td>319.683</td><td>382.000</td><td>0.837</td><td>377.898</td><td>479.000</td><td>0.789</td><td>0.813</td></tr>
<tr><td>2</td><td>11</td><td>7</td><td>TB007G11</td><td>a76couture3132.r#1</td><td>>gb|AAM66068.1| (AY088535) unknown [Arabidopsis thaliana]</td><td>728.029</td><td>544.000</td><td>1.338</td><td>683.718</td><td>684.000</td><td>1.000</td><td>1.169</td></tr>
<tr><td>2</td><td>11</td><td>8</td><td>GT171G09</td><td>a76couture2983.r#1</td><td>>ref|NP_198129.1|| (NM_122659) 60S ribosomal protein L22 - like; protein id:</td><td>178.573</td><td>116.000</td><td>1.539</td><td>169.900</td><td>133.000</td><td>1.277</td><td>1.408</td></tr>
<tr><td>2</td><td>11</td><td>9</td><td>CT003D06</td><td>a76couture2832.r#1</td><td>>gb|AAM12785.1| (AF492633) unknown [Capsicum annuum]</td><td>6710.855</td><td>4420.000</td><td>1.518</td><td>6601.380</td><td>5376.000</td><td>1.228</td><td>1.373</td></tr>
<tr><td>2</td><td>11</td><td>10</td><td>PT009E08</td><td>a76couture2723.r#1</td><td>>ref|NP_563723.1|| (NM_100374) expressed protein; protein id: At1g04960.1. supported</td><td>1130.131</td><td>915.000</td><td>1.235</td><td>1082.210</td><td>1040.000</td><td>1.041</td><td>1.138</td></tr>
<tr><td>2</td><td>11</td><td>11</td><td>TT284A02</td><td>a76couture3126.r#1</td><td>>emb|CAD20821.1| (AJ420858) alpha tubulin [Zea mays]</td><td>3567.717</td><td>2905.000</td><td>1.228</td><td>3487.580</td><td>3316.000</td><td>1.052</td><td>1.140</td></tr>
<tr><td>2</td><td>11</td><td>12</td><td>GB002B09</td><td>a76couture2975.r#1</td><td>>gb|AAK27802.1|AC022457_5 (AC022457) 60S ribosomal protein L17 [Oryza sativa (japonica</td><td>3459.075</td><td>2022.000</td><td>1.711</td><td>3509.203</td><td>2492.000</td><td>1.408</td><td>1.559</td></tr>
<tr><td>2</td><td>11</td><td>13</td><td>TT264F07</td><td>a76couture2824.r#1</td><td>>dbj|BAA96449.1| (AB021790) metallothionein-like protein [Pyrus pyrifolia]</td><td>648.108</td><td>320.000</td><td>2.025</td><td>604.431</td><td>373.000</td><td>1.620</td><td>1.823</td></tr>
<tr><td>2</td><td>11</td><td>14</td><td>PT007E09</td><td>a76couture2718.r#1</td><td>>ref|NP_569047.1|| (NM_126125) SKP1 interacting partner 2 (SKIP2); protein id:</td><td>342.161</td><td>273.000</td><td>1.253</td><td>369.661</td><td>344.000</td><td>1.075</td><td>1.164</td></tr>
<tr><td>2</td><td>11</td><td>15</td><td>ST005F12</td><td>a76couture3121.r#1</td><td>------</td><td>4.995</td><td>14.000</td><td>0.357</td><td>2.059</td><td>10.000</td><td>0.206</td><td>0.281</td></tr>
<tr><td>2</td><td>12</td><td>1</td><td>GT204B05</td><td>a76couture2968.r#1</td><td>>ref|NP_187210.1|| (NM_111432) putative 60S ribosomal protein L18; protein id:</td><td>1157.604</td><td>747.000</td><td>1.550</td><td>1046.171</td><td>909.000</td><td>1.151</td><td>1.350</td></tr>
<tr><td>2</td><td>12</td><td>2</td><td>PT011G11</td><td>a76couture2819.r#1</td><td>>ref|NP_173854.1|| (NM_102290) putative ribonuclease III; protein id: At1g24450.1</td><td>897.861</td><td>865.000</td><td>1.038</td><td>850.529</td><td>1051.000</td><td>0.809</td><td>0.924</td></tr>
<tr><td>2</td><td>12</td><td>3</td><td>PT005G10</td><td>a76couture2714.r#1</td><td>------</td><td>28.722</td><td>36.000</td><td>0.798</td><td>19.564</td><td>31.000</td><td>0.631</td><td>0.714</td></tr>
<tr><td>2</td><td>12</td><td>4</td><td>BM437704 RT054A06</td><td>couture_a76.451.c1.r#1</td><td>------</td><td>270.982</td><td>194.000</td><td>1.397</td><td>248.157</td><td>209.000</td><td>1.187</td><td>1.292</td></tr>
<tr><td>2</td><td>12</td><td>5</td><td>BM437273 GB009A02</td><td>couture_a76.36.c1.r#1</td><td>>pir||S72544 heat shock protein 17.9 - pearl millet >gi|1122317|emb|CAA63903.1|</td><td>2442.582</td><td>1598.000</td><td>1.529</td><td>2225.173</td><td>1559.000</td><td>1.427</td><td>1.478</td></tr>
<tr><td>2</td><td>12</td><td>6</td><td>RB003C09 RB007E03</td><td>couture_a76.274.c1#1</td><td>>ref|NP_066209.2|| (NC_002545) NADH dehydrogenase subunit 2 [Schistosoma mansoni]</td><td>132.369</td><td>116.000</td><td>1.141</td><td>147.247</td><td>143.000</td><td>1.030</td><td>1.085</td></tr>
<tr><td>2</td><td>12</td><td>7</td><td>BM437379 TT284B05</td><td>couture_a76.184.c1.r#1</td><td>>ref|NP_568280.1|| (NM_121285) putative protein; protein id: At5g12470.1. supported by</td><td>1218.793</td><td>1200.000</td><td>1.016</td><td>1118.250</td><td>1483.000</td><td>0.754</td><td>0.885</td></tr>
<tr><td>2</td><td>12</td><td>8</td><td>BM436593 RT044D01</td><td>couture_a76.449.c1#1</td><td>>ref|NP_179871.1|| (NM_127851) unknown protein; protein id: At2g22860.1. supported by</td><td>189.812</td><td>156.000</td><td>1.217</td><td>190.494</td><td>195.000</td><td>0.977</td><td>1.097</td></tr>
<tr><td>2</td><td>12</td><td>9</td><td>BG273969 GB000A09</td><td>couture_a76.355.c1.r#1</td><td>>ref|NP_181084.1|| (NM_129093) chloroplast RNA-binding protein cp33. putative; protein</td><td></td><td>11.000</td><td>0.000</td><td></td><td></td><td></td><td></td></tr>
<tr><td>2</td><td>12</td><td>10</td><td>BM437441 BM437654 CT006D04</td><td>couture_a76.27.c1.r#1</td><td>>sp|Q43116|PDI_RICCO Protein disulfide isomerase precursor (PDI) >gi|2146797|pir||S62626</td><td>5812.994</td><td>5419.000</td><td>1.073</td><td>5853.821</td><td>6868.000</td><td>0.852</td><td>0.963</td></tr>
<tr><td>2</td><td>12</td><td>11</td><td>RB007B06 BM436661 RT093D04</td><td>couture_a76.180.c1#1</td><td>>gb|AAC49885.1| (U39782) lysine and histidine specific transporter [Arabidopsis</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>2</td><td>12</td><td>12</td><td>BM437298 RT034B04</td><td>couture_a76.442.c1.r#1</td><td>>ref|NP_565783.1|| (NM_128982) Expressed protein; protein id: At2g34310.1. supported</td><td>1921.847</td><td>1422.000</td><td>1.352</td><td>2110.876</td><td>1864.000</td><td>1.132</td><td>1.242</td></tr>
<tr><td>2</td><td>12</td><td>13</td><td>BG273962 GB000A17</td><td>couture_a76.353.c1#1</td><td>>gb|AAM91095.1| (AY128287) At1g68060/T23K23_9 [Arabidopsis thaliana]</td><td>982.777</td><td>767.000</td><td>1.281</td><td>974.092</td><td>930.000</td><td>1.047</td><td>1.164</td></tr>
<tr><td>2</td><td>12</td><td>14</td><td>BG273732 RB000A70</td><td>couture_a76.265.c1#1</td><td>>ref|NP_193961.1|| (NM_118356) putative protein; protein id: At4g22300.1 [Arabidopsis</td><td>397.107</td><td>352.000</td><td>1.128</td><td>399.522</td><td>439.000</td><td>0.910</td><td>1.019</td></tr>
<tr><td>2</td><td>12</td><td>15</td><td>BM436774 RT092C06</td><td>couture_a76.179.c1#1</td><td>>gb|AAF63119.1|AC009526_4 (AC009526) Hypothetical protein [Arabidopsis thaliana]</td><td>1185.077</td><td>899.000</td><td>1.318</td><td>1186.210</td><td>1082.000</td><td>1.096</td><td>1.207</td></tr>
<tr><td>2</td><td>13</td><td>1</td><td>BM437788 RT033A05</td><td>couture_a76.439.c1#1</td><td>>dbj|BAC15528.1| (AP003849) putative asparaginyl-tRNA synthetase</td><td>196.056</td><td>158.000</td><td>1.241</td><td>131.801</td><td>138.000</td><td>0.955</td><td>1.098</td></tr>
<tr><td>2</td><td>13</td><td>2</td><td>BG273956 GB000A23</td><td>couture_a76.350.c1#1</td><td>>dbj|BAA96212.1| (AP002094) EST AU069138(C52375) corresponds to a region of the</td><td>535.720</td><td>374.000</td><td>1.432</td><td>357.304</td><td>379.000</td><td>0.943</td><td>1.188</td></tr>
<tr><td>2</td><td>13</td><td>3</td><td>BG273783 RB000A15 RB000A15</td><td>couture_a76.261.c1.r#1</td><td>>pir||T04814 dihydrolipoamide S-succinyltransferase homolog F10M23.250 -</td><td>36.214</td><td>52.000</td><td>0.696</td><td>28.831</td><td>45.000</td><td>0.641</td><td>0.669</td></tr>
<tr><td>2</td><td>13</td><td>4</td><td>BM437212 RT084F10</td><td>couture_a76.175.c1.r#1</td><td>>ref|NP_195553.1|| (NM_120002) putative pollen allergen; protein id: At4g38400.1</td><td>5069.980</td><td>4769.000</td><td>1.063</td><td>4524.483</td><td>4819.000</td><td>0.939</td><td>1.001</td></tr>
<tr><td>2</td><td>13</td><td>5</td><td>BM437626 BM436617 BM437724 BM436876 BM</td><td>couture_a76.434.c1.r#1</td><td>>sp|Q9FPK7|INO1_MAIZE Myo-inositol-1-phosphate synthase (MI-1-P synthase) (IPS)</td><td>443.311</td><td>361.000</td><td>1.228</td><td>335.681</td><td>335.000</td><td>1.002</td><td>1.115</td></tr>
<tr><td>2</td><td>13</td><td>6</td><td>BG273952 GB000A28</td><td>couture_a76.348.c1#1</td><td>>dbj|BAB11619.1| (AB016875) gene_id:K9D7.6~unknown protein [Arabidopsis thaliana]</td><td>1053.956</td><td>832.000</td><td>1.267</td><td>1258.288</td><td>1134.000</td><td>1.110</td><td>1.188</td></tr>
<tr><td>2</td><td>13</td><td>7</td><td>GB003b10 GT204E02</td><td>couture_a76.259.c1#1</td><td>>ref|NP_180576.1|| (NM_128570) putative glucosyltransferase; protein id: At2g30150.1</td><td>63.687</td><td>47.000</td><td>1.355</td><td>53.544</td><td>48.000</td><td>1.116</td><td>1.235</td></tr>
<tr><td>2</td><td>13</td><td>8</td><td>AW707982 CT006B06</td><td>couture_a76.17.c1.r#1</td><td>>sp|Q39613|CYPH_CATRO Peptidyl-prolyl cis-trans isomerase (PPIase) (Rotamase)</td><td>23846.389</td><td>19135.000</td><td>1.246</td><td>25383.032</td><td>27553.000</td><td>0.921</td><td>1.084</td></tr>
<tr><td>2</td><td>13</td><td>9</td><td>BM437904 GT203B03</td><td>couture_a76.43.c1.r#1</td><td>>sp|O64459|UDPG_PYRPY UTP--glucose-1-phosphate uridylyltransferase (UDP-glucose</td><td>5045.005</td><td>3592.000</td><td>1.405</td><td>5535.645</td><td>4961.000</td><td>1.116</td><td>1.260</td></tr>
<tr><td>2</td><td>13</td><td>10</td><td>BG273944 GB000A39</td><td>couture_a76.345.c1#1</td><td>>gb|AAK49947.1|AF335551_1 (AF335551) TGF-beta receptor-interacting protein 1 [Phaseolus</td><td>859.149</td><td>488.000</td><td>1.761</td><td>1051.319</td><td>771.000</td><td>1.364</td><td>1.562</td></tr>
<tr><td>2</td><td>13</td><td>11</td><td>BM437432 BM437080 BM437759 BM436717 BM</td><td>couture_a76.254.c1.r#1</td><td>>pir||S04125 chlorophyll a/b-binding protein type III precursor - tomato</td><td>124.876</td><td>110.000</td><td>1.135</td><td>182.256</td><td>173.000</td><td>1.054</td><td>1.094</td></tr>
<tr><td>2</td><td>13</td><td>12</td><td>RT081B06 BM436896</td><td>couture_a76.166.c1#1</td><td>>ref|NP_176958.1|| (NM_105461) hypothetical protein; protein id: At1g67910.1</td><td>3494.040</td><td>2682.000</td><td>1.303</td><td>3941.676</td><td>3524.000</td><td>1.119</td><td>1.211</td></tr>
<tr><td>2</td><td>13</td><td>13</td><td>VVU73709 G7271875 AF239617</td><td>couture_a76.sd.60.c1#</td><td>>gb|AAF44667.2|AF239617_1 (AF239617) beta-1.3-glucanase [Vitis vinifera]</td><td>218.534</td><td>182.000</td><td>1.201</td><td>275.958</td><td>264.000</td><td>1.045</td><td>1.123</td></tr>
</table>

2	13	14	BM437235 BG273771 RT092G10	couture_a76.637.c1.r#1	>gb|AAA86689.1| (U15933) ascorbate peroxidase [Nicotiana tabacum]	19925.271	12537.000	1.589	21073.755	17198.000	1.225	1.407
2	13	15	BM437954 PT003H05	couture_a76.515.c1.r#1	>gb|AAM64554.1| (AY086993) unknown [Arabidopsis thaliana]	2347.675	1743.000	1.347	2661.764	2575.000	1.034	1.190
2	14	1	G15824822 AF359521	couture_a76.sd.6.c1#1	>gb|AAL09479.1|AF359521_1 (AF359521) inward rectifying shaker-like K+ channel [Vitis vinifera]	46.204	39.000	1.185	25.742	31.000	0.830	1.008
2	14	2	GB002a07 GT204C03	couture_a76.581.c1#1	>sp|P93338|GAPN_NICPL NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE	573.182	334.000	1.716	546.768	439.000	1.245	1.481
2	14	3	BM437264 BM437439 BM436563 RT064B02	couture_a76.49.c1.r#1	>gb|AAF27918.1|AF220202_1 (AF220202) soluble inorganic pyrophosphatase [Malus x domestica]	1728.289	1512.000	1.143	1341.694	1610.000	0.833	0.988
2	14	4	BM437427 ST007A11	couture_a76.94.c1#1	>gb|AAM63236.1| (AY086026) putative mitochondrial dicarboxylate carrier protein	1297.465	1146.000	1.132	1051.319	1206.000	0.872	1.002
2	14	5	BM437118 RT081G11	couture_a76.580.c1.r#1	>ref|NP_187210.1|| (NM_111432) putative 60S ribosomal protein L18; protein id:	6885.682	4980.000	1.383	4822.066	4473.000	1.078	1.230
2	14	6	BG273848 CT001G03 BG273780 ST002B03	couture_a76.531.c1.r#1	------	40559.840	20246.000	2.003	39324.084	23910.000	1.645	1.824
2	14	7	G7406711 VVI237995	couture_a76.sd.47.c1#	>emb|CAB85635.1| (AJ237995) putative ripening-related P-450 enzyme [Vitis vinifera]	12468.904	10145.000	1.229	12188.510	13052.000	0.934	1.081
2	14	8	TB004a01 RT044B07	couture_a76.625.c1.r#1	>sp|P30707|RL9_PEA 60S ribosomal protein L9 (Gibberellin-regulated protein GA)	6652.163	4195.000	1.586	5902.217	4941.000	1.195	1.390
2	14	9	BM436807 GT202E12	couture_a76.53.c1.r#1	>ref|NP_181285.1|| (NM_129304) unknown protein; protein id: At2g37490.1 [Arabidopsis	1488.526	1127.000	1.321	1354.050	1426.000	0.950	1.135
2	14	10	BE846435 PT011H04	couture_a76.81.c2.r#1	>ref|NP_568707.1|| (NM_124298) expressed protein; protein id: At5g49210.1. supported	228.524	132.000	1.731	234.771	177.000	1.326	1.529
2	14	11	Arabidopsis Control Oligonucleotide	3ara23		58.692	57.000	1.030	71.049	78.000	0.911	0.970
2	14	12	BG273861 TB000A31	couture_a76.499.c1.r#1	>ref|NP_194744.1|| (NM_119161) hypothetical protein; protein id: At4g30150.1	36.214	36.000	1.006	47.366	47.000	1.008	1.007
2	14	13	BE846435 PT011H04	couture_a76.81.c2#1	>ref|NP_568707.1|| (NM_124298) expressed protein; protein id: At5g49210.1. supported	327.176	246.000	1.330	367.601	344.000	1.069	1.199
2	14	14	BM437354 BM437906 BG273976 BM437368 BM4	couture_a76.52.c1.r#1	>sp|Q9SLQ8|PSBP_CUCSA Oxygen-evolving enhancer protein 2. chloroplast precursor (OEE2)	1163.848	960.000	1.212	1324.189	1332.000	0.994	1.103
2	14	15	BM437995 RT092F12 AF220198	couture_a76.sd.63.c1.r	>gb|AAF32354.1|AF220198_1 (AF220198) putative protein [Vitis riparia]	7748.578	6105.000	1.269	7988.380	7813.000	1.022	1.146
3	1	1	CM003G06	a76couture0448.r#1	>gb|AAM62637.1| (AY085410) unknown [Arabidopsis thaliana]	134.866	106.000	1.272	198.731	163.000	1.219	1.246
3	1	2	TB003B08	a76couture0350.r#1	>ref|NP_179984.1|| (NM_127968) putative chloroplast initiation factor 3; protein id:	249.753	232.000	1.077	285.226	286.000	0.997	1.037
3	1	3	RT061F12	a76couture0217.r#1	>dbj|BAC16651.1| (AP004570) putative xylose isomerase [Oryza sativa (japonica	2516.259	3057.000	0.823	2788.416	3625.000	0.769	0.796
3	1	4	CM005f03	a76couture0068.r#1	gb|AAL04507.1|AF406809_1 (AF406809) glutaredoxin [Tilia platyphy... 172 3e-042	9750.346	11907.000	0.819	11969.184	14170.000	0.845	0.832
3	1	5	CM003F08	a76couture0444.r#1	------	866.642	705.000	1.229	980.270	869.000	1.128	1.179
3	1	6	TT274F12	a76couture0343.r#1	>gb|AAF34799.1|AF227979_1 (AF227979) 40S ribosomal protein S16 [Euphorbia esula]	2833.445	2686.000	1.055	3984.923	3465.000	1.150	1.102
3	1	7	RT054D11	a76couture0213.r#1	>pir||T45939 hypothetical protein F5K20.290 - Arabidopsis thaliana	1163.848	1043.000	1.116	1307.714	1184.000	1.104	1.110
3	1	8	CM002E07	a76couture0062.r#1	>dbj|BAB02135.1| (AP000386) gb|AAF15936.1~gene_id:MLD15.10~similar to unknown	5794.263	7651.000	0.757	9099.422	9893.000	0.920	0.839
3	1	9	CM003E03	a76couture0440.r#1	------	33.717	34.000	0.992	36.039	37.000	0.974	0.983
3	1	10	TT264A08	a76couture0338.r#1	>emb|CAC44123.1| (AJ307887) N3 like protein [Medicago truncatula]	10956.651	11902.000	0.921	13646.559	14362.000	0.950	0.935
3	1	11	RT044G07	a76couture0208.r#1	>ref|NP_199196.1|| (NM_123750) aluminum-induced protein-like; protein id: At5g43830.1	4714.082	4844.000	0.973	5232.914	5641.000	0.928	0.950
3	1	12	TF001A01C	a76couture0056.r#1	>gb|AAH19429.1| (BC019429) Unknown (protein for MGC:30371) [Mus musculus]	360.893	352.000	1.025	508.670	481.000	1.058	1.041
3	1	13	CM003B11	a76couture0437#1	------	52.448	59.000	0.889	58.693	63.000	0.932	0.910
3	1	14	TT261E03	a76couture0334.r#1	>sp|Q9SPB3|RL10_VITRI 60S ribosomal protein L10 (QM protein homolog)	3932.356	3078.000	1.278	4806.620	4227.000	1.137	1.207
3	1	15	RT022A05	a76couture0202#1	>gb|AAG01124.1|AF273333_9 (AF273333) BAC19.9 [Lycopersicon esculentum]	69.931	76.000	0.920	92.673	105.000	0.883	0.901
3	2	1	G7264741 reverse complement 1623 bases	a76couture0044.r#1	>gb|AAF44336.1|AF195867_1 (AF195867) alcohol dehydrogenase 7 [Vitis vinifera]	157.344	170.000	0.926	157.543	165.000	0.955	0.940
3	2	2	CM002H10	a76couture0433.r#1	>ref|NP_199553.2|| (NM_124113) putative protein; protein id: At5g47420.1. supported by	258.494	278.000	0.930	288.315	346.000	0.833	0.882
3	2	3	RT084D10	a76couture0325.r#1	>gb|AAM64977.1| (AY087429) putative elongation factor beta-1 [Arabidopsis	2095.425	2059.000	1.018	2643.229	2479.000	1.066	1.042
3	2	4	RB004D12	a76couture0197.r#1	------	292.211	268.000	1.090	323.324	340.000	0.951	1.021
3	2	5	88E3PROTE	a76couture0025#1	>pir||T05989 hypothetical protein F17M5.140 - Arabidopsis thaliana	17.483	19.000	0.920	21.624	24.000	0.901	0.911
3	2	6	CM002G02	a76couture0429.r#1	>ref|NP_564325.1|| (NM_102665) expressed protein; protein id: At1g29250.1. supported	97.404	112.000	0.870	171.959	166.000	1.036	0.953
3	2	7	RT082B02	a76couture0321.r#1	------	37.463	37.000	1.013	32.950	37.000	0.891	0.952
3	2	8	GT201C11	a76couture0190.r#1	>gb|AAF19706.1|AC008047_13 (AC008047) F2K11.19 [Arabidopsis thaliana]	37.463	45.000	0.833	51.485	55.000	0.936	0.884
3	2	9	TT274G06	a76couture0017.r#1	>ref|NP_200952.1|| (NM_125537) thioredoxin-like 3; protein id: At5g61440.1. supported	3038.242	2811.000	1.081	3692.489	3868.000	0.955	1.018
3	2	10	Arabidopsis Control Oligonucleotide	3ara23		19.980	29.000	0.689	9.267	12.000	0.772	0.731
3	2	11	RT072H01	a76couture0748.r#1	>emb|CAA07229.2| (AJ006763) putative beta-amilase [Cicer arietinum]	1572.193	1228.000	1.280	2030.560	1770.000	1.147	1.214
3	2	12	ST003H01	a76couture0648.r#1	>ref|NP_196865.1|| (NM_121364) putative protein; protein id: At5g13610.1. supported by	299.703	298.000	1.006	369.661	371.000	0.996	1.001
3	2	13	CT004C06	a76couture0546.r#1	>ref|NP_003871.1|| (NM_003880) WNT1 inducible signaling pathway protein 3. isoform 1;	265.987	249.000	1.068	323.324	316.000	1.023	1.046
3	2	14	RT092D04	a76couture0868.r#1	>gb|AAG34814.1|AF243379_1 (AF243379) glutathione S-transferase GST 24 [Glycine max]	1016.494	1059.000	0.960	1520.861	1426.000	1.067	1.013
3	2	15	RT072A08	a76couture0743#1	>gb|AAM63723.1| (AY086666) unknown [Arabidopsis thaliana]	17.483	25.000	0.699	16.475	27.000	0.610	0.655
3	3	1	ST003F08	a76couture0644.r#1	------	57.443	62.000	0.927	68.990	67.000	1.030	0.978
3	3	2	CT003G11	a76couture0542.r#1	>pir||T02030 GDP dissociation inhibitor protein - rice	1763.254	2396.000	0.736	2041.887	2658.000	0.768	0.752
3	3	3	RT091E05	a76couture0862.r#1	>dbj|BAA36585.1| (AB014884) adenylyl cyclase associated protein [Gossypium hirsutum]	342.161	441.000	0.776	515.878	558.000	0.925	0.850
3	3	4	ST007G10	a76couture0738.r#1	>ref|NP_196552.1|| (NM_121027) 26S proteasome regulatory subunit (RPN5). putative;	1703.313	1700.000	1.002	1992.461	2008.000	0.992	0.997
3	3	5	ST003D11	a76couture0640.r#1	------	43.707	51.000	0.857	53.544	59.000	0.908	0.882
3	3	6	CT003E12	a76couture0539.r#1	>dbj|BAA95791.1| (AB009885) wound inducive gene [Nicotiana tabacum]	315.937	322.000	0.981	437.621	437.000	1.001	0.991
3	3	7	RT084D11	a76couture0855.r#1	------	458.296	460.000	0.996	541.620	572.000	0.947	0.972
3	3	8	ST007F05	a76couture0734.r#1	>ref|NP_180966.1|| (NM_128970) putative membrane transporter; protein id: At2g34190.1	399.604	424.000	0.942	470.571	481.000	0.978	0.960
3	3	9	ST003C07	a76couture0636.r#1	------	99.901	100.000	0.999	97.821	108.000	0.906	0.952
3	3	10	CT003B04	a76couture0535.r#1	>dbj|BAB43909.1| (AB050473) phosphoenolpyruvate carboxykinase [Flaveria pringlei]	3286.746	2588.000	1.270	3761.479	3299.000	1.140	1.205
3	3	11	RT091A06	a76couture0851.r#1	>ref|NP_564962.1|| (NM_105603) expressed protein; protein id: At1g69360.1. supported by	62.438	53.000	1.178	73.108	68.000	1.075	1.127
3	3	12	ST007E02	a76couture0729.r#1	------	38.712	35.000	1.106	40.158	39.000	1.030	1.068
3	3	13	ST003B02	a76couture0631.r#1	>ref|NP_566655.1|| (NM_112914) expressed protein; protein id: At3g20230.1. supported	102.399	102.000	1.004	119.445	126.000	0.948	0.976
3	3	14	CT003A07	a76couture0532.r#1	>ref|NP_192765.1|| (NM_117095) probable wound-induced protein; protein id:	929.080	717.000	1.296	1114.131	899.000	1.239	1.268
3	3	15	RT082D11	a76couture0846.r#1	>sp|Q9AXJ4|IF5A_MANES Initiation factor 5A (eIF-5A) >gi|14193249|gb|AAK55848.1|AF266464_1	2300.222	2584.000	0.890	3211.621	3654.000	0.879	0.885
3	4	1	ST007C02	a76couture0725.r#1	>gb|AAC72194.1| (AF069910) pyruvate dehydrogenase E1 beta subunit isoform 3 [Zea	31.219	51.000	0.612	44.277	51.000	0.868	0.740
3	4	2	ST002H07	a76couture0627.r#1	>ref|NP_198396.1|| (NM_122937) putative protein; protein id: At5g35460.1. supported by	443.311	565.000	0.785	527.204	594.000	0.888	0.836
3	4	3	CT002H01	a76couture0528.r#1	>ref|NP_195626.1|| (NM_120075) dnaJ-like protein; protein id: At4g39150.1. supported	1141.370	1342.000	0.850	1462.168	1572.000	0.930	0.890
3	4	4	RT033E05	a76couture1333.r#1	------	171.081	160.000	1.069	214.177	204.000	1.050	1.060
3	4	5	Arabidopsis Control Oligonucleotide	3ara23		9.990	11.000	0.908	8.238	10.000	0.824	0.866
3	4	6	TT284F09	a76couture1075.r#1	>sp|Q08069|RS8_MAIZE 40S ribosomal protein S8 >gi|7440237|pir||T04088 ribosomal protein	1101.409	1085.000	1.015	1474.524	1312.000	1.124	1.069

3	4	7	RT083A10	a76couture0980.r#1	>ref|NP_180571.1|| (NM_128565) putative unknown protein. leucine-rich repeat; protein	232.270	220.000	1.056	303.760	279.000	1.089	1.072
3	4	8	RT032C02	a76couture1327.r#1	>pir||S00443 chlorophyll a/b-binding protein type I precursor (cab-6A) - tomato	847.910	924.000	0.918	961.736	1041.000	0.924	0.921
3	4	9	GT192H10	a76couture1194.r#1	>ref|NP_191781.1|| (NM_116087) serine/threonine protein kinase-like protein; protein	628.128	634.000	0.991	659.005	755.000	0.873	0.932
3	4	10	RT094G03	a76couture1071.r#1	>ref|NP_567105.1|| (NM_115947) actin - like protein; protein id: At3g60830.1	31.219	36.000	0.867	29.861	34.000	0.878	0.873
3	4	11	RT081G02	a76couture0975.r#1	>ref|NP_191595.1|| (NM_115900) putative protein; protein id: At3g60360.1. supported by	253.499	225.000	1.127	268.751	251.000	1.071	1.099
3	4	12	RT031B06	a76couture1323.r#1	>ref|NP_565744.1|| (NM_128799) putative ligand-gated ion channel subunit; protein id:	112.389	94.000	1.196	134.890	125.000	1.079	1.137
3	4	13	GT192D04	a76couture1189.r#1	>ref|NP_196742.1|| (NM_121219) putative protein; protein id: At5g11810.1 [Arabidopsis	260.992	273.000	0.956	318.176	380.000	0.837	0.897
3	4	14	TT284G02	a76couture1067.r#1	------	303.450	315.000	0.963	431.443	454.000	0.950	0.957
3	4	15	RT081D09	a76couture0970.r#1	>ref|NP_566224.1|| (NM_111306) expressed protein; protein id: At3g04350.1. supported	142.359	125.000	1.139	198.731	169.000	1.176	1.157
3	5	1	RT022H10	a76couture1319#1	>gb|AAF79297.1|AC068602_20 (AC068602) F14D16.30 [Arabidopsis thaliana]	98.652	100.000	0.987	111.207	104.000	1.069	1.028
3	5	2	GT193C09	a76couture1185.r#1	>ref|NP_173907.1|| (NM_102346) hypothetical protein; protein id: At1g25360.1	41.209	36.000	1.145	50.455	41.000	1.231	1.188
3	5	3	RT094B03	a76couture1063.r#1	>ref|NP_593372.1|| (NC_003424) zinc finger protein [Schizosaccharomyces pombe]	4.995	9.000	0.555	1.030	8.000	0.129	0.342
3	5	4	RT074G12	a76couture0965.r#1	>ref|NP_187361.1|| (NM_111585) putative GTPase; protein id: At3g07050.1 [Arabidopsis	974.036	823.000	1.184	1131.636	987.000	1.147	1.165
3	5	5	RT023H03	a76couture1314.r#1	>emb|CAA09042.1| (AJ010227) 40S ribosomal protein S6 [Cicer arietinum]	328.425	237.000	1.386	377.898	319.000	1.185	1.285
3	5	6	GT192C12	a76couture1181.r#1	>ref|NP_191050.1|| (NM_115347) putative protein; protein id: At3g54900.1. supported by	719.288	683.000	1.053	828.905	845.000	0.981	1.017
3	5	7	RT093F12	a76couture1059.r#1	>sp|O04136|HKL3_MALDO Homeobox protein knotted-1 like 3 (KNAP3) >gi|7488621|pir||T17010	255.997	303.000	0.845	327.443	371.000	0.883	0.864
3	5	8	RT074B11	a76couture0961.r#1	>gb|AAK77908.1|AF397903_1 (AF397903) AAA-metalloprotease FtsH [Pisum sativum]	57.443	61.000	0.942	77.227	77.000	1.003	0.972
3	5	9	RT022H08	a76couture1310#1	>gb|AAF24813.1|AC007592_6 (AC007592) F12K11.9 [Arabidopsis thaliana]	2487.537	2059.000	1.208	2558.794	2463.000	1.039	1.124
3	5	10	GT191F10	a76couture1176.r#1	>gb|AAK49035.1|AF249733_1 (AF249733) putative SR-like splicing factor [Arabidopsis thaliana]	482.023	380.000	1.268	498.373	433.000	1.151	1.210
3	5	11	RT093B12	a76couture1054.r#1	>ref|NP_189085.1|| (NM_113349) unknown protein; protein id: At3g24420.1 [Arabidopsis	8.741	23.000	0.380	8.238	24.000	0.343	0.362
3	5	12	RT073H04	a76couture0957.r#1	>ref|NP_196721.1|| (NM_121198) putative protein; protein id: At5g11600.1 [Arabidopsis	103.647	79.000	1.312	120.474	94.000	1.282	1.297
3	5	13	GT174D12	a76couture1777.r#1	>gb|AAF78493.1|AC012187_13 (AC012187) Contains similarity to AP2/EREBP-like transcription	313.440	388.000	0.808	403.641	504.000	0.801	0.804
3	5	14	GT161B09	a76couture1686.r#1	>gb|AAG51369.1|AC011560_1 (AC011560) putative galactokinase. 5' partial; 97-568 [Arabidopsis	52.448	55.000	0.954	74.138	82.000	0.904	0.929
3	5	15	GB005A04	a76couture1593.r#1	>ref|NP_198099.1|| (NM_122629) seryl-tRNA synthetase; protein id: At5g27470.1	1087.673	987.000	1.102	1399.357	1349.000	1.037	1.070
3	6	1	TT263C05	a76couture1450.r#1	------	630.626	605.000	1.042	835.083	732.000	1.141	1.092
3	6	2	GT174D07	a76couture1774.r#1	------	176.076	153.000	1.151	185.345	152.000	1.219	1.185
3	6	3	GT162E03	a76couture1680.r#1	------	48.702	53.000	0.919	49.425	48.000	1.030	0.974
3	6	4	GB004B10	a76couture1589.r#1	------	298.454	301.000	0.992	294.493	288.000	1.023	1.007
3	6	5	TT262D03	a76couture1446.r#1	>gb|AAL79278.1| (AF479965) unknown [Saccharomyces cerevisiae]	929.080	671.000	1.385	1184.150	838.000	1.413	1.399
3	6	6	GT174A09	a76couture1770.r#1	>ref|NP_179186.2|| (NM_127146) unknown protein; protein id: At2g15860.1. supported by	84.916	99.000	0.858	102.970	112.000	0.919	0.889
3	6	7	GT162B08	a76couture1677.r#1	>ref|NP_565258.1|| (NM_126188) expressed protein; protein id: At2g01270.1. supported	18.731	18.000	1.041	19.564	23.000	0.851	0.946
3	6	8	GB002G09	a76couture1583.r#1	>ref|NP_194200.1|| (NM_118602) putative protein; protein id: At4g24690.1. supported by	3984.804	3758.000	1.060	4661.433	4319.000	1.079	1.070
3	6	9	TT262B04	a76couture1441.r#1	>gb|AAM13050.1| (AY093051) unknown protein [Arabidopsis thaliana]	473.281	460.000	1.029	517.937	525.000	0.987	1.008
3	6	10	GT173G08	a76couture1766.r#1	>gb|AAF08571.1|AC011623_4 (AC011623) unknown protein [Arabidopsis thaliana]	748.009	797.000	0.939	730.054	852.000	0.857	0.898
3	6	11	GT161F09	a76couture1673.r#1	>ref|NP_176860.1|| (NM_105359) protein kinase. putative; protein id: At1g66880.1	3647.638	3812.000	0.957	3991.101	4596.000	0.868	0.913
3	6	12	GB003E08	a76couture1578.r#1	>ref|NP_199380.1|| (NM_123935) FKBP-type peptidyl-prolyl cis-trans isomerase; protein	33.717	37.000	0.911	32.950	36.000	0.915	0.913
3	6	13	RT064D03	a76couture1434.r#1	>dbj|BAB17342.1| (AP002747) putative receptor kinase [Oryza sativa (japonica	178.573	160.000	1.116	196.672	188.000	1.046	1.081
3	6	14	GT173E06	a76couture1762.r#1	------	19.980	25.000	0.799	24.713	28.000	0.883	0.841
3	6	15	GT161C11	a76couture1669.r#1	------	686.820	693.000	0.991	900.984	894.000	1.008	0.999
3	7	1	GB002D12	a76couture1574#1	------	21.229	25.000	0.849	19.564	22.000	0.889	0.869
3	7	2	TT253D04	a76couture1422.r#1	>ref|NP_182083.1|| (NM_130121) putative protein kinase; protein id: At2g45590.1	1262.500	1247.000	1.012	1408.624	1403.000	1.004	1.008
3	7	3	GT173C02	a76couture1758.r#1	>ref|NP_177175.2|| (NM_105686) hypothetical protein; protein id: At1g70180.1	37.463	40.000	0.937	43.247	44.000	0.983	0.960
3	7	4	GB009H04	a76couture1666#1	------	49.951	37.000	1.350	44.277	41.000	1.080	1.215
3	7	5	GB001H07	a76couture1570.r#1	------	992.767	975.000	1.018	1279.912	1280.000	1.000	1.009
3	7	6	TT251G03	a76couture1419#1	>gb|ZP_00111998.1| (NZ_AABC01000200) hypothetical protein [Nostoc punctiforme]	124.876	153.000	0.816	160.633	176.000	0.913	0.864
3	7	7	RT034F02	a76couture2182.r#1	>dbj|BAA94530.2| (AP001800) Similar to Arabidopsis thaliana chromosome 1. BAC							
3	7	8	RT023H08	a76couture2080.r#1	------	439.565	528.000	0.833	619.877	625.000	0.992	0.912
3	7	9	RB008E09	a76couture1992#1	------	2101.669	1653.000	1.271	2675.150	2162.000	1.237	1.254
3	7	10	GT203D08	a76couture1878.r#1	>gb|AAM65279.1| (AY087742) unknown [Arabidopsis thaliana]	228.524	226.000	1.011	297.582	288.000	1.033	1.022
3	7	11	RT034D10	a76couture2178.r#1	>ref|NP_180645.2|| (NM_128640) unknown protein; protein id: At2g30880.1. supported by	31.219	44.000	0.710	38.099	49.000	0.778	0.744
3	7	12	RT023F01	a76couture2074.r#1	------	1951.817	2230.000	0.875	2168.539	2629.000	0.825	0.850
3	7	13	RT012E02	a76couture1989.r#1	>pir||T03216 enoyl-[acyl-carrier-protein] reductase (NADH) (EC 1.3.1.9)	39.960	41.000	0.975	48.396	42.000	1.152	1.063
3	7	14	GT203F11	a76couture1868.r#1	>ref|NP_201021.1|| (NM_125608) putative protein; protein id: At5g62150.1 [Arabidopsis	383.370	437.000	0.877	462.333	528.000	0.876	0.876
3	7	15	RT034D02	a76couture2174#1	>ref|NP_191311.1|| (NM_115612) glycosyl hydrolase family 36; protein id: At3g57520.1	902.856	985.000	0.917	1156.348	1213.000	0.953	0.935
3	8	1	RT023E03	a76couture2071.r#1	>ref|NP_194945.2|| (NM_119370) putative protein; protein id: At4g32180.1. supported by	474.530	440.000	1.078	546.768	505.000	1.083	1.081
3	8	2	RT011G10	a76couture1983.r#1	------	102.399	102.000	1.004	109.148	108.000	1.011	1.007
3	8	3	GT202G02	a76couture1864.r#1	>ref|NP_181999.2|| (NM_130035) RRM-containing protein; protein id: At2g44710.1	1052.708	1059.000	0.994	1211.952	1261.000	0.961	0.978
3	8	4	RT034B03	a76couture2169.r#1	>ref|NP_178122.1|| (NM_106654) adenine phosphoribosyltransferase; protein id:	71.180	56.000	1.271	81.346	64.000	1.271	1.271
3	8	5	RT023C05	a76couture2067.r#1	>ref|NP_186883.1|| (NM_111101) RING zinc-finger protein. putative; protein id:	81.170	90.000	0.902	92.673	101.000	0.918	0.910
3	8	6	RT011D08	a76couture1981#1	>gb|AAH28867.1| (BC028867) Similar to hypothetical protein MGC3180 [Mus musculus]	7.493	12.000	0.624	9.267	14.000	0.662	0.643
3	8	7	GT202D12	a76couture1860.r#1	>ref|NP_566019.1|| (NM_130015) putative heme A:farnesyltransferase; protein id:	194.807	189.000	1.031	246.097	241.000	1.021	1.026
3	8	8	RT033G12	a76couture2164.r#1	------	83.667	92.000	0.909	93.702	99.000	0.946	0.928
3	8	9	RT023B05	a76couture2063.r#1	>ref|NP_175706.1|| (NM_104176) putative GTP-binding protein; protein id: At1g52980.1	866.642	749.000	1.157	1229.457	1103.000	1.115	1.136
3	8	10	RB008H09	a76couture1977.r#1	>ref|NP_200017.1|| (NM_124583) arginine/serine-rich splicing factor RSp41; protein id:	114.886	145.000	0.792	200.791	204.000	0.984	0.888
3	8	11	GT201C10	a76couture1855.r#1	>emb|CAD36515.1| (AJ491323) putative beta-glycosidase [Oryza sativa (japonica	299.703	285.000	1.052	370.690	348.000	1.065	1.058
3	8	12	RT033F11	a76couture2161.r#1	>pir||T01989 calcium-dependent protein kinase (EC 2.7.1.-) 1 - common tobacco	223.529	212.000	1.054	253.305	253.000	1.001	1.028
3	8	13	RT022G04	a76couture2059#1	>ref|NP_191462.1|| (NM_115765) MATE efflux family protein. putative; protein id:	84.916	76.000	1.117	102.970	90.000	1.144	1.131
3	8	14	RB008H01	a76couture1975.r#1	>emb|CAB97476.2| (AL389901) conserved hypothetical protein [Neurospora crassa]		8.000	0.000				

<table>
<tr><td>3</td><td>8</td><td>15</td><td>GT202C01</td><td>a76couture1850.r#1</td><td>>ref|NP_565658.1|| (NM_128335) putative tRNA isopentenylpyrophosphate transferase;</td><td>36.214</td><td>30.000</td><td>1.207</td><td>33.980</td><td>32.000</td><td>1.062</td><td>1.135</td></tr>
<tr><td>3</td><td>9</td><td>1</td><td>RT064D05</td><td>a76couture2605.r#1</td><td>>dbj|BAB67874.1| (AP003231) putative protein kinase AFC1 [Oryza sativa (japonica</td><td>640.616</td><td>663.000</td><td>0.966</td><td>836.113</td><td>899.000</td><td>0.930</td><td>0.948</td></tr>
<tr><td>3</td><td>9</td><td>2</td><td>TT251G09</td><td>a76couture2486#1</td><td>>ref|NP_566231.1|| (NM_111327) expressed protein; protein id: At3g04560.1. supported</td><td>44.955</td><td>43.000</td><td>1.045</td><td>52.514</td><td>50.000</td><td>1.050</td><td>1.048</td></tr>
<tr><td>3</td><td>9</td><td>3</td><td>RT063D08</td><td>a76couture2373.r#1</td><td>>ref|NP_201222.1|| (NM_125813) putative protein; protein id: At5g64170.1. supported by</td><td>1051.459</td><td>1248.000</td><td>0.843</td><td>1314.922</td><td>1512.000</td><td>0.870</td><td>0.856</td></tr>
<tr><td>3</td><td>9</td><td>4</td><td>RT052B12</td><td>a76couture2275.r#1</td><td>>dbj|BAB02241.1| (AP002034) mRNA cap methyltransferase-like protein [Arabidopsis</td><td>335.917</td><td>307.000</td><td>1.094</td><td>394.374</td><td>387.000</td><td>1.019</td><td>1.057</td></tr>
<tr><td>3</td><td>9</td><td>5</td><td>RT064B06</td><td>a76couture2601.r#1</td><td>>ref|NP_176185.1|| (NM_104669) DEAD/DEAH box RNA helicase (HUA ENHANCER2). putative;</td><td>173.578</td><td>159.000</td><td>1.092</td><td>201.820</td><td>182.000</td><td>1.109</td><td>1.100</td></tr>
<tr><td>3</td><td>9</td><td>6</td><td>TT251E03</td><td>a76couture2482#1</td><td>>ref|NP_174808.1|| (NM_103272) 50S ribosomal protein L21 chloroplast precursor (CL21);</td><td>197.305</td><td>175.000</td><td>1.127</td><td>251.246</td><td>217.000</td><td>1.158</td><td>1.143</td></tr>
<tr><td>3</td><td>9</td><td>7</td><td>RT063B07</td><td>a76couture2369.r#1</td><td>>gb|AAM61357.1| (AY084790) unknown [Arabidopsis thaliana]</td><td>92.409</td><td>87.000</td><td>1.062</td><td>114.296</td><td>106.000</td><td>1.078</td><td>1.070</td></tr>
<tr><td>3</td><td>9</td><td>8</td><td>RT051G03</td><td>a76couture2271.r#1</td><td>------</td><td>111.140</td><td>104.000</td><td>1.069</td><td>156.514</td><td>130.000</td><td>1.204</td><td>1.136</td></tr>
<tr><td>3</td><td>9</td><td>9</td><td>RT063H03</td><td>a76couture2597.r#1</td><td>>ref|NP_176681.1|| (NM_105175) hypothetical protein; protein id: At1g65010.1</td><td>412.092</td><td>425.000</td><td>0.970</td><td>557.065</td><td>548.000</td><td>1.017</td><td>0.993</td></tr>
<tr><td>3</td><td>9</td><td>10</td><td>TT251D05</td><td>a76couture2478#1</td><td>>ref|NP_173376.1|| (NM_101800) very-long-chain fatty acid condensing enzyme CUT1</td><td>224.777</td><td>170.000</td><td>1.322</td><td>278.018</td><td>215.000</td><td>1.293</td><td>1.308</td></tr>
<tr><td>3</td><td>9</td><td>11</td><td>RT062F09</td><td>a76couture2362.r#1</td><td>>pir||T09773 myb-related protein - upland cotton >gi|2921340|gb|AAC04720.1|</td><td>464.540</td><td>615.000</td><td>0.755</td><td>576.630</td><td>744.000</td><td>0.775</td><td>0.765</td></tr>
<tr><td>3</td><td>9</td><td>12</td><td>RT051F05</td><td>a76couture2268.r#1</td><td>>ref|NP_567543.1|| (NM_117898) Expressed protein; protein id: At4g17890.1 [Arabidopsis</td><td>959.050</td><td>940.000</td><td>1.020</td><td>1161.497</td><td>1105.000</td><td>1.051</td><td>1.036</td></tr>
<tr><td>3</td><td>9</td><td>13</td><td>RT064F08</td><td>a76couture2573.r#1</td><td>>gb|AAM65866.1| (AY088327) unknown [Arabidopsis thaliana]</td><td>226.026</td><td>244.000</td><td>0.926</td><td>279.048</td><td>269.000</td><td>1.037</td><td>0.982</td></tr>
<tr><td>3</td><td>9</td><td>14</td><td>TT254C01</td><td>a76couture2473.r#1</td><td>>ref|NP_175933.1|| (NM_104412) unknown protein; protein id: At1g55360.1 [Arabidopsis</td><td>561.944</td><td>576.000</td><td>0.976</td><td>664.154</td><td>686.000</td><td>0.968</td><td>0.972</td></tr>
<tr><td>3</td><td>9</td><td>15</td><td>RT062E02</td><td>a76couture2358.r#1</td><td>bj|BAB12433.1| (AB025030) p450 [Coptis japonica] 276 2e-073</td><td>796.711</td><td>970.000</td><td>0.821</td><td>1111.042</td><td>1192.000</td><td>0.932</td><td>0.877</td></tr>
<tr><td>3</td><td>10</td><td>1</td><td>RT053C05</td><td>a76couture2265.r#1</td><td>------</td><td>453.301</td><td>457.000</td><td>0.992</td><td>537.501</td><td>561.000</td><td>0.958</td><td>0.975</td></tr>
<tr><td>3</td><td>10</td><td>2</td><td>TT283B09</td><td>a76couture2568.r#1</td><td>>gb|AAK52144.1|AC084380_17 (AC084380) putative heat shock protein [Oryza sativa]</td><td>33.717</td><td>40.000</td><td>0.843</td><td>32.950</td><td>41.000</td><td>0.804</td><td>0.823</td></tr>
<tr><td>3</td><td>10</td><td>3</td><td>TT253G03</td><td>a76couture2469.r#1</td><td>>gb|AAM29184.1| (AY098940) CDPK-like protein [Solanum tuberosum]</td><td>561.944</td><td>404.000</td><td>1.391</td><td>718.728</td><td>573.000</td><td>1.254</td><td>1.323</td></tr>
<tr><td>3</td><td>10</td><td>4</td><td>RT062B04</td><td>a76couture2354.r#1</td><td>>sp|P28723|FTHS_SPIOL FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE SYNTHETASE</td><td>769.238</td><td>800.000</td><td>0.962</td><td>770.212</td><td>894.000</td><td>0.862</td><td>0.912</td></tr>
<tr><td>3</td><td>10</td><td>5</td><td>RT052F05</td><td>a76couture2262.r#1</td><td>>emb|CAA98186.1| (Z73958) RAB11J [Lotus japonicus]</td><td>122.379</td><td>119.000</td><td>1.028</td><td>128.712</td><td>146.000</td><td>0.882</td><td>0.955</td></tr>
<tr><td>3</td><td>10</td><td>6</td><td>TT283F10</td><td>a76couture2565.r#1</td><td>>gb|AAD16279.1| (AF099096) pulvinus outward-rectifying channel for potassium SPOCK1</td><td>37.463</td><td>37.000</td><td>1.013</td><td>37.069</td><td>39.000</td><td>0.950</td><td>0.981</td></tr>
<tr><td>3</td><td>10</td><td>7</td><td>TT253E03</td><td>a76couture2466.r#1</td><td>>emb|CAA07566.1| (AJ007578) pRIB5 protein [Ribes nigrum]</td><td>302.201</td><td>261.000</td><td>1.158</td><td>444.829</td><td>382.000</td><td>1.164</td><td>1.161</td></tr>
<tr><td>3</td><td>10</td><td>8</td><td>RT062A01</td><td>a76couture2350.r#1</td><td>------</td><td>435.818</td><td>508.000</td><td>0.858</td><td>614.728</td><td>635.000</td><td>0.968</td><td>0.913</td></tr>
<tr><td>3</td><td>10</td><td>9</td><td>RT052A06</td><td>a76couture2258.r#1</td><td>>ref|NP_195572.1|| (NM_120021) putative protein; protein id: At4g38600.1 [Arabidopsis</td><td>118.633</td><td>105.000</td><td>1.130</td><td>171.959</td><td>145.000</td><td>1.186</td><td>1.158</td></tr>
<tr><td>3</td><td>10</td><td>10</td><td>ST004E08</td><td>a76couture3117.r#1</td><td>>sp|Q9SXU1|PSA7_CICAR Proteasome subunit alpha type 7 (20S proteasome alpha subunit D)</td><td>720.537</td><td>614.000</td><td>1.174</td><td>942.172</td><td>855.000</td><td>1.102</td><td>1.138</td></tr>
<tr><td>3</td><td>10</td><td>11</td><td>GT194F08</td><td>a76couture2963.r#1</td><td>>ref|NP_197918.1|| (NM_122445) putative protein; protein id: At5g25360.1 [Arabidopsis</td><td>614.392</td><td>519.000</td><td>1.184</td><td>803.163</td><td>712.000</td><td>1.128</td><td>1.156</td></tr>
<tr><td>3</td><td>10</td><td>12</td><td>PT006A03</td><td>a76couture2815.r#1</td><td>>ref|NP_182109.1|| (NM_130148) putative AT-hook DNA-binding protein; protein id:</td><td>264.738</td><td>206.000</td><td>1.285</td><td>398.492</td><td>296.000</td><td>1.346</td><td>1.316</td></tr>
<tr><td>3</td><td>10</td><td>13</td><td>PT004G09</td><td>a76couture2709.r#1</td><td>>pir||S31083 glycerol-3-phosphate O-acyltransferase (EC 2.3.1.15) precursor -</td><td>47.453</td><td>55.000</td><td>0.863</td><td>61.782</td><td>57.000</td><td>1.084</td><td>0.973</td></tr>
<tr><td>3</td><td>10</td><td>14</td><td>RT061C06</td><td>a76couture3105.r#1</td><td>>ref|NP_565864.1|| (NM_129312) expressed protein; protein id: At2g37570.1. supported</td><td>328.425</td><td>329.000</td><td>0.998</td><td>418.057</td><td>374.000</td><td>1.118</td><td>1.058</td></tr>
<tr><td>3</td><td>10</td><td>15</td><td>GT193E02</td><td>a76couture2959.r#1</td><td>>ref|NP_568742.1|| (NM_124448) 11-beta-hydroxysteroid dehydrogenase-like; protein id:</td><td>1175.087</td><td>1114.000</td><td>1.055</td><td>1209.893</td><td>1159.000</td><td>1.044</td><td>1.049</td></tr>
<tr><td>3</td><td>11</td><td>1</td><td>PT006G05</td><td>a76couture2811.r#1</td><td>>ref|NP_565632.1|| (NM_128257) COP9 complex subunit CSN2. putative; protein id:</td><td>1966.803</td><td>1403.000</td><td>1.402</td><td>2300.340</td><td>1901.000</td><td>1.210</td><td>1.306</td></tr>
<tr><td>3</td><td>11</td><td>2</td><td>PT002A01</td><td>a76couture2704.r#1</td><td>>gb|AAL57633.1| (AY064980) AT3g48690/T8P19_200 [Arabidopsis thaliana]</td><td>81.170</td><td>91.000</td><td>0.892</td><td>96.791</td><td>114.000</td><td>0.849</td><td>0.871</td></tr>
<tr><td>3</td><td>11</td><td>3</td><td>RT061G11</td><td>a76couture3100.r#1</td><td>>sp|Q9FVI1|ADF2_PETHY Actin-depolymerizing factor 2 (ADF 2)</td><td></td><td>5290.000</td><td>0.000</td><td></td><td></td><td></td><td></td></tr>
<tr><td>3</td><td>11</td><td>4</td><td>RT071F03</td><td>a76couture2955.r#1</td><td>>sp|P35135|UBC4_LYCES Ubiquitin-conjugating enzyme E2-17 kDa (Ubiquitin-protein ligase)</td><td>5384.668</td><td>3826.000</td><td>1.407</td><td>5696.277</td><td>4870.000</td><td>1.170</td><td>1.289</td></tr>
<tr><td>3</td><td>11</td><td>5</td><td>PT009F11</td><td>a76couture2807.r#1</td><td>>ref|NP_195818.1|| (NM_120276) putative protein; protein id: At5g01980.1 [Arabidopsis</td><td>82.418</td><td>77.000</td><td>1.070</td><td>76.197</td><td>80.000</td><td>0.952</td><td>1.011</td></tr>
<tr><td>3</td><td>11</td><td>6</td><td>PT012C05</td><td>a76couture2700.r#1</td><td>>gb|AAM12785.1| (AF492633) unknown [Capsicum annuum]</td><td>2798.479</td><td>1615.000</td><td>1.733</td><td>2476.418</td><td>1736.000</td><td>1.427</td><td>1.580</td></tr>
<tr><td>3</td><td>11</td><td>7</td><td>RT024B08</td><td>a76couture3094.r#1</td><td>>sp|P08437|H3_VOLCA Histone H3 >gi|81287|pir||S00940 histone H3 - Volvox carteri</td><td>1015.245</td><td>1017.000</td><td>0.998</td><td>1158.408</td><td>1097.000</td><td>1.056</td><td>1.027</td></tr>
<tr><td>3</td><td>11</td><td>8</td><td>RT051G08</td><td>a76couture2948.r#1</td><td>>dbj|BAB55500.1| (AP002972) putative mitochondrial processing peptidase alpha</td><td>279.723</td><td>285.000</td><td>0.981</td><td>339.800</td><td>322.000</td><td>1.055</td><td>1.018</td></tr>
<tr><td>3</td><td>11</td><td>9</td><td>PT010C05</td><td>a76couture2803.r#1</td><td>>gb|AAM65651.1| (AY088105) Myb-related transcription activator. putative</td><td>841.667</td><td>1094.000</td><td>0.769</td><td>1082.210</td><td>1257.000</td><td>0.861</td><td>0.815</td></tr>
<tr><td>3</td><td>11</td><td>10</td><td>PT001A11</td><td>a76couture2695.r#1</td><td>>ref|NP_051043.1|| (NC_000932) photosystem II protein I [Arabidopsis thaliana]</td><td>1202.559</td><td>587.000</td><td>2.049</td><td>1368.466</td><td>678.000</td><td>2.018</td><td>2.034</td></tr>
<tr><td>3</td><td>11</td><td>11</td><td>PT010F08</td><td>a76couture3088.r#1</td><td>>gb|AAK11229.1|AF327525_1 (AF327525) truncated copper-binding protein CUTA [Arabidopsis</td><td>104.896</td><td>87.000</td><td>1.206</td><td>134.890</td><td>107.000</td><td>1.261</td><td>1.233</td></tr>
<tr><td>3</td><td>11</td><td>12</td><td>GT192E10</td><td>a76couture2939.r#1</td><td>>emb|CAA10231.1| (AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]</td><td>24.975</td><td>30.000</td><td>0.833</td><td>29.861</td><td>31.000</td><td>0.963</td><td>0.898</td></tr>
<tr><td>3</td><td>11</td><td>13</td><td>PT013F01</td><td>a76couture2799.r#1</td><td>>ref|NP_199250.1|| (NM_123804) Na+-dependent inorganic phosphate cotransporter-like</td><td>58.692</td><td>53.000</td><td>1.107</td><td>65.901</td><td>55.000</td><td>1.198</td><td>1.153</td></tr>
<tr><td>3</td><td>11</td><td>14</td><td>PT012E04</td><td>a76couture2690.r#1</td><td>>gb|AAF99731.1|AC004557_10 (AC004557) F17L21.12 [Arabidopsis thaliana]</td><td>8110.719</td><td>8338.000</td><td>0.973</td><td>12462.409</td><td>9570.000</td><td>1.302</td><td>1.137</td></tr>
<tr><td>3</td><td>11</td><td>15</td><td>RT041B02</td><td>a76couture3083.r#1</td><td>>gb|AAM64958.1| (AY087409) unknown [Arabidopsis thaliana]</td><td>8416.666</td><td>8428.000</td><td>0.999</td><td>9360.965</td><td>9329.000</td><td>1.003</td><td>1.001</td></tr>
<tr><td>3</td><td>12</td><td>1</td><td>CT006G04</td><td>a76couture2931.r#1</td><td>------</td><td>2542.483</td><td>2209.000</td><td>1.151</td><td>3656.450</td><td>3910.000</td><td>0.935</td><td>1.043</td></tr>
<tr><td>3</td><td>12</td><td>2</td><td>PT005G02</td><td>a76couture2793.r#1</td><td>>sp|P27806|H1_WHEAT Histone H1</td><td>1018.991</td><td>765.000</td><td>1.332</td><td>1203.714</td><td>1046.000</td><td>1.151</td><td>1.241</td></tr>
<tr><td>3</td><td>12</td><td>3</td><td>PT009A08</td><td>a76couture2686.r#1</td><td>------</td><td>93.657</td><td>64.000</td><td>1.463</td><td>96.791</td><td>67.000</td><td>1.445</td><td>1.454</td></tr>
<tr><td>3</td><td>12</td><td>4</td><td>BM436573 RT012H11</td><td>couture_a76.424.c1.r#1</td><td>------</td><td>2129.142</td><td>1923.000</td><td>1.107</td><td>2308.578</td><td>2360.000</td><td>0.978</td><td>1.043</td></tr>
<tr><td>3</td><td>12</td><td>5</td><td>BG273926 GB000A59</td><td>couture_a76.341.c1#1</td><td>>ref|NP_566308.1|| (NM_111625) expressed protein; protein id: At3g07470.1. supported</td><td>984.026</td><td>834.000</td><td>1.180</td><td>1016.310</td><td>927.000</td><td>1.096</td><td>1.138</td></tr>
<tr><td>3</td><td>12</td><td>6</td><td>BM436537 GT202B05</td><td>couture_a76.251.c1.r#1</td><td>>ref|NP_174376.1|| (NM_102828) hypothetical protein; protein id: At1g30910.1</td><td>1834.434</td><td>1565.000</td><td>1.172</td><td>1883.314</td><td>1824.000</td><td>1.033</td><td>1.102</td></tr>
<tr><td>3</td><td>12</td><td>7</td><td>RB007B05 RT052D10</td><td>couture_a76.162.c1.r#1</td><td>>emb|CAC85667.1| (AJ319762) zeta-carotene desaturase [Citrus sinensis]</td><td>1687.080</td><td>1611.000</td><td>1.047</td><td>1855.512</td><td>1837.000</td><td>1.010</td><td>1.029</td></tr>
<tr><td>3</td><td>12</td><td>8</td><td>BM436931 GT191C07</td><td>couture_a76.42.c1.r#1</td><td>>gb|AAL75812.1| (AY077702) temperature stress-induced lipocalin [Triticum aestivum]</td><td>2345.178</td><td>1255.000</td><td>1.869</td><td>2428.023</td><td>1411.000</td><td>1.721</td><td>1.795</td></tr>
<tr><td>3</td><td>12</td><td>9</td><td>BG273918 GB000A69</td><td>couture_a76.339.c1#1</td><td>>ref|NP_565147.1|| (NM_106351) F-box protein family. AtFBL5; protein id: At1g77000.1</td><td>1988.032</td><td>1782.000</td><td>1.116</td><td>2466.122</td><td>2146.000</td><td>1.149</td><td>1.132</td></tr>
<tr><td>3</td><td>12</td><td>10</td><td>BM436374 BM436822 BM437224 BM436994 GT2</td><td>couture_a76.249.c1.r#1</td><td>>sp|P31336|PSBX_GOSHI Photosystem II 5 kDa protein. chloroplast precursor (PSII-T)</td><td>129.871</td><td>80.000</td><td>1.623</td><td>134.890</td><td>91.000</td><td>1.482</td><td>1.553</td></tr>
<tr><td>3</td><td>12</td><td>11</td><td>BM436755 BM437757 GT184A10</td><td>couture_a76.159.c1.r#1</td><td>>gb|AAB39248.1| (U80912) NADP-isocitrate dehydrogenase [Eucalyptus globulus]</td><td>2830.947</td><td>2877.000</td><td>0.984</td><td>3879.894</td><td>3643.000</td><td>1.065</td><td>1.025</td></tr>
<tr><td>3</td><td>12</td><td>12</td><td>RB002G10 RB002G10</td><td>couture_a76.416.c1.r#1</td><td>>sp|P42495|CAD1_ARACO Cinnamyl-alcohol dehydrogenase 1 (CAD) >gi|474300|dbj|BAA03099.1|</td><td>156.095</td><td>185.000</td><td>0.844</td><td>210.058</td><td>215.000</td><td>0.977</td><td>0.910</td></tr>
<tr><td>3</td><td>12</td><td>13</td><td>BG273910 GB000A80</td><td>couture_a76.334.c1#1</td><td>>ref|NP_179875.1|| (NM_127856) putative amino acid acetyltransferase; protein id:</td><td>8.741</td><td>10.000</td><td>0.874</td><td>11.327</td><td>14.000</td><td>0.809</td><td>0.842</td></tr>
<tr><td>3</td><td>12</td><td>14</td><td>BG273797 GT194G12 TB000A98</td><td>couture_a76.246.c1.r#1</td><td>>pir||T03400 probable transcription factor SF3 - common tobacco</td><td>640.616</td><td>951.000</td><td>0.674</td><td>971.003</td><td>1086.000</td><td>0.894</td><td>0.784</td></tr>
<tr><td>3</td><td>12</td><td>15</td><td>BG273975 RT074D05</td><td>couture_a76.152.c1.r#1</td><td>>gb|AAF66824.1|AF190656_1 (AF190656) poly(A)-binding protein [Nicotiana tabacum]</td><td>1939.330</td><td>2311.000</td><td>0.839</td><td>2591.744</td><td>2667.000</td><td>0.972</td><td>0.905</td></tr>
<tr><td>3</td><td>13</td><td>1</td><td>BM436810 RB001A02</td><td>couture_a76.412.c1.r#1</td><td>>gb|AAL50082.1| (AY070742) AT3g22845/MWI23_22 [Arabidopsis thaliana]</td><td>1226.286</td><td>1035.000</td><td>1.185</td><td>1322.129</td><td>1344.000</td><td>0.984</td><td>1.084</td></tr>
<tr><td>3</td><td>13</td><td>2</td><td>BG273904 GB000A87</td><td>couture_a76.331.c1#1</td><td>------</td><td>222.280</td><td>186.000</td><td>1.195</td><td>266.691</td><td>266.000</td><td>1.003</td><td>1.099</td></tr>
<tr><td>3</td><td>13</td><td>3</td><td>GB001h03 GT193H10</td><td>couture_a76.243.c1#1</td><td>>ref|NP_178453.1|| (NM_126405) putative esterase; protein id: At2g03550.1 [Arabidopsis</td><td>1233.778</td><td>787.000</td><td>1.568</td><td>1305.654</td><td>994.000</td><td>1.314</td><td>1.441</td></tr>
<tr><td>3</td><td>13</td><td>4</td><td>RB001A06 RT072H07</td><td>couture_a76.148.c1#1</td><td>>sp|Q07511|FDH_SOLTU Formate dehydrogenase. mitochondrial precursor (NAD-dependent</td><td>5011.288</td><td>4590.000</td><td>1.092</td><td>5523.288</td><td>5811.000</td><td>0.950</td><td>1.021</td></tr>
<tr><td>3</td><td>13</td><td>5</td><td>BG273752 RB000A49</td><td>couture_a76.409.c1#1</td><td>>gb|AAN05506.1| (AC099399) Putative serine acetyltransferase [Oryza sativa</td><td>68.682</td><td>59.000</td><td>1.164</td><td>66.930</td><td>63.000</td><td>1.062</td><td>1.113</td></tr>
<tr><td>3</td><td>13</td><td>6</td><td>BG273894 GB000A98</td><td>couture_a76.329.c1.r#1</td><td>>ref|NP_199209.1|| (NM_123763) NTF2-containing RNA-binding protein. putative; protein</td><td>8.741</td><td>11.000</td><td>0.795</td><td>12.356</td><td>11.000</td><td>1.123</td><td>0.959</td></tr>
<tr><td>3</td><td>13</td><td>7</td><td>GB003g12 GT193A02</td><td>couture_a76.240.c1#1</td><td>>ref|NP_178108.1|| (NM_106639) mitochondrial carrier protein family; protein id:</td><td>338.415</td><td>279.000</td><td>1.213</td><td>337.740</td><td>313.000</td><td>1.079</td><td>1.146</td></tr>
</table>

3	13	8	BM436269 BM437727 TT273C07	couture_a76.144.c2.r#1	------	89.911	15.000	5.994	125.623	16.000	7.851	6.923
3	13	9	BG273749 RB000A52	couture_a76.407.c1#1	>emb|CAD40551.1| (AL606621) OSJNBa0072K14.7 [Oryza sativa]	288.464	289.000	0.998	341.859	335.000	1.020	1.009
3	13	10	BM436544 BM437748 TT283C08	couture_a76.326.c1.r#1	>ref|NP_510564.1|| (NM_078163) EGF-like domain (3 domains) [Caenorhabditis elegans]	3407.876	2230.000	1.528	4996.084	3195.000	1.564	1.546
3	13	11	BM436292 GT183H09	couture_a76.237.c1.r#1	>emb|CAD33929.1| (AJ489614) microtubule associated protein [Cicer arietinum]	405.848	354.000	1.146	491.165	430.000	1.142	1.144
3	13	12	BM437740 ST003B10	couture_a76.140.c1.r#1	>ref|NP_173692.1|| (NM_102125) putative 40S ribosomal protein S18; protein id:	2361.412	2494.000	0.947	3238.393	2874.000	1.127	1.037
3	13	13	G9957233 AF177590	couture_a76.sd.34.c1#	>gb|AAG09278.1|AF177590_1 (AF177590) ornithine aminotransferase [Vitis vinifera]	128.623	177.000	0.727	185.345	201.000	0.922	0.824
3	13	14	BM437094 BE846423 BM437463 BM436297 RT0	couture_a76.613.c1#1	>emb|CAC16165.1| (AJ291704) pathogenesis-related protein 10 [Vitis vinifera]	4586.709	5289.000	0.867	5972.236	5589.000	1.069	0.968
3	13	15	BM437996 BG273837 TB000A56	couture_a76.493.c1.r#1	>ref|NP_194330.1|| (NM_118733) KH domain protein; protein id: At4g26000.1. supported	17.483	29.000	0.603	30.891	39.000	0.792	0.697
3	14	1	G10732643 AF195868	couture_a76.sd.33.c1#	>gb|AAG22488.1|AF195868_1 (AF195868) pyruvate decarboxylase 1 [Vitis vinifera]	12480.143	7517.000	1.660	13833.963	9612.000	1.439	1.550
3	14	2	BM436971 BM436939 BM436891 TB000A29 BG2	couture_a76.559.c1.r#1	>sp|Q9LEI9|ENO2_HEVBR ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2) (2-PHOSPHO-D-GLYCERATE	3310.472	3085.000	1.073	4470.939	4734.000	0.944	1.009
3	14	3	VVI289866 TI100A01C GB002f12 AF271661	couture_a76.sd.8.c1#1		5500.803	3756.000	1.465	6089.621	4605.000	1.322	1.393
3	14	4	BM436981 63HISTONE	couture_a76.7.c1#1	>ref|NP_195713.1|| (NM_120167) histone H3.3; protein id: At4g40030.1. supported by	5544.510	4254.000	1.303	5453.269	4804.000	1.135	1.219
3	14	5	Arabidopsis Control Oligonucleotide	3ara23		22.478	22.000	1.022	19.564	21.000	0.932	0.977
3	14	6	BG273885 TB000A07	couture_a76.504.c1#1	------	41.209	49.000	0.841	39.128	44.000	0.889	0.865
3	14	7	TB005C09 AY043237	couture_a76.sd.22.c1#	>sp|P35694|BRU1_SOYBN Brassinosteroid-regulated protein BRU1 precursor	2282.740	1031.000	2.214	2405.369	1106.000	2.175	2.194
3	14	8	BM437878 ST007B04 RT064G08	couture_a76.602.c1.r#1	>emb|CAC43286.1| (AJ298137) translation initiation factor eIF-4A1 [Arabidopsis	3414.120	3490.000	0.978	3654.391	3726.000	0.981	0.980
3	14	9	BM437385 BM437590 BG273875 TB000A17 TB0	couture_a76.503.c1#1	>sp|Q02585|UCRB_TOBAC Cytochrome B6-F complex iron-sulfur subunit 2. chloroplast	82.418	91.000	0.906	96.791	95.000	1.019	0.962
3	14	10	BG273840 TB000A52 RB004C08	couture_a76.642.c1#1	ref|NP_405697.1|| (NC_003143) putative membrane protein [Yersini... 35 0.42	11447.415	11694.000	0.979	14690.670	13182.000	1.114	1.047
3	14	11	GB002g04 BM436406 RT041H11	couture_a76.57.c1#1	>gb|AAM64516.1| (AY086953) cytochrome c oxidase subunit. putative [Arabidopsis	516.988	614.000	0.842	749.619	709.000	1.057	0.950
3	14	12	BM437007 TT254D01	couture_a76.478.c1.r#1	>ref|NP_190679.1|| (NM_114970) putative protein; protein id: At3g51100.1 [Arabidopsis	362.141	384.000	0.943	546.768	456.000	1.199	1.071
3	14	13	BG273741 RB000A61 RT084C12	couture_a76.641.c1.r#1	------	2.498	9.000	0.278	7.208	11.000	0.655	0.466
3	14	14	BG273847 TB000A45	couture_a76.495.c1.r#1	>ref|NP_191656.1|| (NM_115961) ABC transporter family protein; protein id: At3g60970.1	750.507	997.000	0.753	1059.557	1115.000	0.950	0.852
3	14	15	G9885273 AF194174	couture_a76.sd.36.c1#	>gb|AAG01382.1|AF194174_1 (AF194174) alcohol dehydrogenase 2 [Vitis vinifera]	1804.463	1961.000	0.920	2431.112	2233.000	1.089	1.004
4	1	1	CM002F05	a76couture0425.r#1	>ref|NP_566360.1|| (NM_111824) expressed protein; protein id: At3g09890.1. supported	761.746	554.000	1.375	956.587	809.000	1.182	1.279
4	1	2	RT094D07	a76couture0314.r#1	>gb|AAG32920.1|AF184232_1 (AF184232) expansin [Lycopersicon esculentum]	19004.933	18455.000	1.030	20702.035	23212.000	0.892	0.961
4	1	3	RT061D10	a76couture0183.r#1	>ref|NP_566443.1|| (NM_112144) Expressed protein; protein id: At3g13062.1. supported	693.064	513.000	1.351	719.757	628.000	1.146	1.249
4	1	4	TT273C06	a76couture0012.r#1	>gb|AAM83226.1| (AY126999) AT4g02450/T14P8_5 [Arabidopsis thaliana]	1863.155	1737.000	1.073	2621.606	2490.000	1.053	1.063
4	1	5	CM002E06	a76couture0421.r#1	------	249.753	246.000	1.015	253.305	306.000	0.828	0.922
4	1	6	RT093H03	a76couture0309.r#1	>ref|NP_190756.1|| (NM_115047) high mobility group protein 2-like; protein id:	5626.929	4467.000	1.260	6483.995	5911.000	1.097	1.178
4	1	7	RT051F02	a76couture0177.r#1	>gb|AAK68836.1| (AY042896) Unknown protein [Arabidopsis thaliana]	1924.345	2262.000	0.851	2556.735	3427.000	0.746	0.798
4	1	8	TT253G04	a76couture0004.r#1	>ref|NP_191227.1|| (NM_115527) putative protein; protein id: At3g56680.1. supported by	3114.416	3027.000	1.029	4273.238	4385.000	0.975	1.002
4	1	9	CM002D03	a76couture0416.r#1	>ref|NP_196958.1|| (NM_121458) putative protein; protein id: At5g14540.1 [Arabidopsis	62.438	68.000	0.918	98.851	113.000	0.875	0.896
4	1	10	RT084F03	a76couture0305#1	>emb|CAB85628.1| (AJ237988) putative ripening-related protein [Vitis vinifera]	1247.515	1104.000	1.130	1522.920	1455.000	1.047	1.088
4	1	11	RT043G05	a76couture0173.r#1	>emb|CAB71135.1| (AJ271668) putative imbibition protein [Cicer arietinum]	8349.233	7150.000	1.168	10323.730	9713.000	1.063	1.115
4	1	12	PT012H11	a76couture2676.r#1	------	34.965	42.000	0.833	5.148	12.000	0.429	0.631
4	1	13	CM002B02	a76couture0412.r#1	>sp|Q9SNW7|PRO1_LILLO Profilin 1 >gi|6425105|gb|AAF08302.1|AF200184_1 (AF200184) profilin	221.031	185.000	1.195	343.918	293.000	1.174	1.184
4	1	14	RT083F11	a76couture0297.r#1	>dbj|BAB60909.1| (AP003213) contains ESTs	8176.904	4829.000	1.693	9825.358	7025.000	1.399	1.546
4	1	15	cds of gi|1469265|emb|X84846.1|PP111ACNP	luc3#1		0.000			13.386	23.000	0.582	0.582
4	2	1	RT012B03	a76couture1986.r#1	>ref|NP_567862.2|| (NM_119241) WRKY family transcription factor; protein id:	458.296	404.000	1.134	632.233	590.000	1.072	1.103
4	2	2	CM001G08	a76couture0407.r#1	>ref|NP_568410.1|| (NM_122125) Expressed protein; protein id: At5g22000.1. supported	733.024	779.000	0.941	922.607	1016.000	0.908	0.925
4	2	3	RT074F06	a76couture0290.r#1	>gb|AAC24586.1| (AF071892) omega-6 fatty acid desaturase [Prunus armeniaca]	169.832	169.000	1.005	161.662	183.000	0.883	0.944
4	2	4	GT201H11	a76couture0162.r#1	>ref|NP_201447.1|| (NM_126044) glycosyl hydrolase family 5/cellulase	154.847	169.000	0.916	167.840	207.000	0.811	0.864
4	2	5	GT174E02	a76couture1145.r#1	>ref|NP_198024.1|| (NM_122553) putative protein; protein id: At5g26718.1 [Arabidopsis	305.947	223.000	1.372	394.374	313.000	1.260	1.316
4	2	6	CM001F01	a76couture0403.r#1	------	339.664	359.000	0.946	395.403	460.000	0.860	0.903
4	2	7	ST006C10	a76couture0284.r#1	>ref|NP_172655.1|| (NM_101062) putative aspartic proteinase; protein id: At1g11910.1	9786.560	9652.000	1.014	9397.004	11562.000	0.813	0.913
4	2	8	RT052H11	a76couture0152.r#1	>gb|AAG29777.1| (AF228333) lipid transfer protein 3 precursor [Gossypium hirsutum]	2835.942	3023.000	0.938	3131.305	3674.000	0.852	0.895
4	2	9	CM005f06	a76couture0510.r#1	none	322.181	294.000	1.096	330.532	344.000	0.961	1.028
4	2	10	RT082B11	a76couture0842.r#1	>ref|NP_568506.1|| (NM_122713) GTL1 - like protein; protein id: At5g28300.1. supported	149.852	148.000	1.013	171.959	192.000	0.896	0.954
4	2	11	ST007A09	a76couture0721.r#1	>gb|AAF15952.1|AF095753_1 (AF095753) thioredoxin x [Arabidopsis thaliana]	144.857	107.000	1.354	181.226	143.000	1.267	1.311
4	2	12	Arabidopsis Control Oligonucleotide	3ara7		23.727	35.000	0.678	22.653	34.000	0.666	0.672
4	2	13	CT002E02	a76couture0524.r#1	>ref|NP_192880.1|| (NM_117212) putative protein; protein id: At4g11410.1 [Arabidopsis	549.456	425.000	1.293	677.540	592.000	1.144	1.219
4	2	14	RT083C04	a76couture0835.r#1	>ref|NP_194149.1|| (NM_118551) thaumatin-like protein; protein id: At4g24180.1	563.192	313.000	1.799	618.847	400.000	1.547	1.673
4	2	15	ST006G12	a76couture0717.r#1	>gb|AAF22517.1|AF118924_1 (AF118924) glutathione S-transferase 1 [Papaver somniferum]	834.174	828.000	1.007	989.538	1160.000	0.853	0.930
4	3	1	CT006F07	a76couture0620.r#1	>ref|XP_085861.1|| (XM_085861) similar to zinc finger protein 216 [Homo sapiens]	98.652	97.000	1.017	133.860	137.000	0.977	0.997
4	3	2	CT002C03	a76couture0520.r#1	>ref|NP_196176.1|| (NM_120639) putative protein; protein id: At5g05570.1 [Arabidopsis	13.736	19.000	0.723	43.247	50.000	0.865	0.794
4	3	3	RT081F10	a76couture0831.r#1	>ref|NP_200364.1|| (NM_124935) putative protein; protein id: At5g55530.1 [Arabidopsis	595.660	575.000	1.036	653.857	763.000	0.857	0.946
4	3	4	ST006G01	a76couture0713.r#1	>ref|NP_042364.1|| (NC_001631) ATP synthase CF0 A chain [Pinus thunbergii]	922.836	820.000	1.125	1132.665	1067.000	1.062	1.093
4	3	5	CT006E06	a76couture0616.r#1	>dbj|BAB64732.1| (AP003236) cullin-like protein [Oryza sativa (japonica	36.214	39.000	0.929	45.307	51.000	0.888	0.908
4	3	6	CM005h02	a76couture0515.r#1	ef|NP_566435.1|| (NM_112110) expressed protein [Arabidopsis tha... 33 3e-004	739.268	934.000	0.792	1172.824	1332.000	0.880	0.836
4	3	7	RT081B03	a76couture0827.r#1	>emb|CAA72330.1| (Y11591) shaggy-like kinase [Ricinus communis]	3341.691	4151.000	0.805	3877.834	5259.000	0.737	0.771
4	3	8	ST006E05	a76couture0709.r#1	------	299.703	349.000	0.859	356.275	444.000	0.802	0.831
4	3	9	ST002G02	a76couture0612.r#1	>ref|NP_196367.1|| (NM_120832) zinc finger transcription factor; protein id:	270.982	96.000	2.823	313.028	127.000	2.465	2.644
4	3	10	CM005f05	a76couture0509.r#1	ref|NP_194391.1|| (NM_118795) putative protein kinase [Arabidops... 313 2e-084	26.224	28.000	0.937	26.772	28.000	0.956	0.946
4	3	11	RT063B10	a76couture0819.r#1	>sp|P34091|RL6_MESCR 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi|280374|pir||S28586	1748.269	1644.000	1.063	2221.054	2016.000	1.102	1.083
4	3	12	ST006C07	a76couture0704.r#1	>gb|AAF47594.1| (AE003473) CG12361-PA [Drosophila melanogaster]	98.652	71.000	1.389	108.118	71.000	1.523	1.456
4	3	13	ST002C05	a76couture0607.r#1	>gb|AAM65108.1| (AY087566) putative LEA protein [Arabidopsis thaliana]	104.896	105.000	0.999	112.237	108.000	1.039	1.019
4	3	14	CM005e03	a76couture0505.r#1	ref|NP_565917.1|| (NM_129549) expressed protein [Arabidopsis tha... 249 2e-065	113.637	114.000	0.997	136.950	148.000	0.925	0.961
4	3	15	RT024C04	a76couture0814.r#1	>ref|NP_568293.1|| (NM_121406) expressed protein; protein id: At5g14030.1. supported	605.650	509.000	1.190	712.550	693.000	1.028	1.109

4	4	1	ST006B06	a76couture0701.r#1	>ref|NP_565699.1|| (NM_128594) TCP1-chaperonin cofactor A isolog; protein id:	51.199	40.000	1.280	73.108	64.000	1.142	1.211
4	4	2	ST002A02	a76couture0603.r#1	>ref|NP_567343.1|| (NM_116967) F-box protein family. AtFBW2; protein id: At4g08980.1	388.365	460.000	0.844	546.768	569.000	0.961	0.903
4	4	3	CM005d01	a76couture0501.r#1	ref|NP_567849.1|| (NM_119210) F-box protein family, AtFBL19 [Ara... 140 2e-032	24.975	24.000	1.041	11.327	18.000	0.629	0.835
4	4	4	RT021G03	a76couture1305#1	>ref|NP_196186.1|| (NM_120649) signal recognition particle receptor beta subunit-like	154.847	136.000	1.139	188.434	171.000	1.102	1.120
4	4	5	GT184B12	a76couture1172.r#1	>ref|NP_191293.1|| (NM_115594) dnaJ-like protein; protein id: At3g57340.1. supported	1466.048	1625.000	0.902	1929.650	2082.000	0.927	0.915
4	4	6	RT092E11	a76couture1050.r#1	>ref|NP_683316.1|| (NM_148475) hypothetical protein; protein id: At1g20925.1	995.265	1025.000	0.971	1299.476	1368.000	0.950	0.960
4	4	7	RT081G01	a76couture0953.r#1	------	694.313	701.000	0.990	856.707	979.000	0.875	0.933
4	4	8	RT021C12	a76couture1301#1	>emb|CAA09177.1| (AJ010423) glyoxalase I [Glycine max]	419.585	382.000	1.098	456.155	515.000	0.886	0.992
4	4	9	GT183A06	a76couture1166.r#1	>ref|NP_193740.1|| (NM_118126) hyuC-like protein; protein id: At4g20070.1 [Arabidopsis	1595.920	1423.000	1.122	1654.721	1680.000	0.985	1.053
4	4	10	RT093H02	a76couture1045.r#1	>ref|NP_563759.1|| (NM_100492) F-box protein family; protein id: At1g06110.1	414.589	408.000	1.016	560.155	571.000	0.981	0.999
4	4	11	RT074E01	a76couture0950.r#1	------	724.283	643.000	1.126	991.597	906.000	1.094	1.110
4	4	12	RT012B06	a76couture1296.r#1	>ref|NP_564960.1|| (NM_105601) expressed protein; protein id: At1g69340.1. supported	252.250	235.000	1.073	305.820	307.000	0.996	1.035
4	4	13	GT184A03	a76couture1159.r#1	>ref|NP_180005.2|| (NM_127990) putative prolylcarboxypeptidase; protein id:	77.423	84.000	0.922	86.494	113.000	0.765	0.844
4	4	14	RT091G07	a76couture1039.r#1	>ref|NP_194641.1|| (NM_119056) putative protein; protein id: At4g29120.1. supported by	1905.613	2160.000	0.882	2123.233	2442.000	0.869	0.876
4	4	15	RT073H11	a76couture0946.r#1	>gb|AAD31056.1|AC007357_5 (AC007357) F3F19.5 [Arabidopsis thaliana]	164.837	136.000	1.212	166.811	159.000	1.049	1.131
4	5	1	RB008D10	a76couture1291.r#1	>gb|AAM63420.1| (AY086418) unknown [Arabidopsis thaliana]	6928.140	6712.000	1.032	8397.169	7798.000	1.077	1.055
4	5	2	GT181D08	a76couture1154.r#1	>ref|NP_191007.1|| (NM_115299) putative protein; protein id: At3g54390.1. supported by	48.702	49.000	0.994	67.960	69.000	0.985	0.989
4	5	3	RT091C03	a76couture1035.r#1	>ref|NP_189367.1|| (NM_113646) esterase. putative; protein id: At3g27320.1	302.201	312.000	0.969	459.244	439.000	1.046	1.007
4	5	4	RT073H03	a76couture0944#1	------	26.224	25.000	1.049	27.802	32.000	0.869	0.959
4	5	5	RB007F08	a76couture1286.r#1	>ref|NP_198151.1|| (NM_122682) putative protein; protein id: At5g27990.1. supported by	452.052	468.000	0.966	626.055	616.000	1.016	0.991
4	5	6	GT174H11	a76couture1150.r#1	>ref|NP_563698.1|| (NM_100285) expressed protein; protein id: At1g04040.1. supported	438.316	403.000	1.088	556.036	507.000	1.097	1.092
4	5	7	RT084H11	a76couture1031.r#1	>ref|NP_192233.1|| (NM_116562) putative frataxin-like protein; protein id: At4g03240.1	322.181	341.000	0.945	430.413	433.000	0.994	0.969
4	5	8	RT073B02	a76couture0940.r#1	>dbj|BAB10077.1| (AB010069) contains similarity to RNA binding	143.608	131.000	1.096	153.425	159.000	0.965	1.031
4	5	9	RB006C07	a76couture1279.r#1	------	186.066	188.000	0.990	213.147	224.000	0.952	0.971
4	5	10	GT174A12	a76couture1143.r#1	>ref|NP_182126.1|| (NM_130165) putative SNF2 subfamily transcriptional activator;	121.130	129.000	0.939	146.217	161.000	0.908	0.924
4	5	11	RT084C09	a76couture1027.r#1	>gb|AAM97085.1| (AY136419) X-Pro dipeptidase-like protein [Arabidopsis thaliana]	365.888	406.000	0.901	428.353	509.000	0.842	0.871
4	5	12	RT072G01	a76couture0937.r#1	>pir||T01743 ribosomal protein L10. chloroplast - common tobacco	49.951	61.000	0.819	43.247	64.000	0.676	0.747
4	5	13	GT172F03	a76couture1754.r#1	>ref|NP_566066.1|| (NM_130184) Expressed protein; protein id: At2g46220.1. supported	247.255	130.000	1.902	254.335	87.000	2.923	2.413
4	5	14	GB009H01	a76couture1663.r#1	>dbj|BAA97098.1| (AP002460) gene_id:F1D9.26~unknown protein [Arabidopsis thaliana]	177.324	101.000	1.756	210.058	137.000	1.533	1.644
4	5	15	GB001C07	a76couture1566.r#1	------	302.201	263.000	1.149	351.126	348.000	1.009	1.079
4	6	1	TT253F06	a76couture1415.r#1	>gb|AAL78741.1| (AY077453) MYB-like transcription factor DIVARICATA [Antirrhinum	524.481	432.000	1.214	694.015	575.000	1.207	1.211
4	6	2	GT171G01	a76couture1750.r#1	>ref|NP_376514.1|| (NC_003106) 945aa long hypothetical leucyl-tRNA synthetase	395.858	231.000	1.714	467.482	290.000	1.612	1.663
4	6	3	GB009G05	a76couture1659.r#1	------	92.409	59.000	1.566	96.791	61.000	1.587	1.576
4	6	4	GB001B03	a76couture1562.r#1	------	9.990	11.000	0.908	11.327	15.000	0.755	0.832
4	6	5	TT251B04	a76couture1411#1	>ref|NP_189306.1|| (NM_113583) glycosyl hydrolase family 38 (alpha-mannosidase);	103.647	103.000	1.006	148.276	134.000	1.107	1.056
4	6	6	GT171A06	a76couture1746.r#1	>ref|NP_180858.1|| (NM_128859) glycosyl hydrolase family 9; protein id: At2g32990.1	49.951	67.000	0.746	72.079	94.000	0.767	0.756
4	6	7	GB009F09	a76couture1656#1	------	24.975	22.000	1.135	25.742	28.000	0.919	1.027
4	6	8	TT283C09	a76couture1527.r#1	>ref|NP_197684.1|| (NM_122199) putative protein; protein id: At5g22930.1 [Arabidopsis	914.095	838.000	1.091	1026.607	1093.000	0.939	1.015
4	6	9	TB007D09	a76couture1407.r#1	>gb|AAL87161.1|AF480496_15 (AF480496) putative ethylene-responsive protein [Oryza sativa	96.155	94.000	1.023	117.385	127.000	0.924	0.974
4	6	10	GT173A06	a76couture1742.r#1	>ref|NP_193312.1|| (NM_117668) hypothetical protein; protein id: At4g15770.1	6.244	15.000	0.416	10.297	15.000	0.686	0.551
4	6	11	GB009E10	a76couture1652.r#1	------	19.980	28.000	0.714	16.475	30.000	0.549	0.631
4	6	12	TT283H06	a76couture1523.r#1	>ref|NP_177346.1|| (NM_105859) unknown protein; protein id: At1g72010.1. supported by	700.556	545.000	1.285	1101.775	796.000	1.384	1.335
4	6	13	TB005E07	a76couture1402.r#1	------	525.729	514.000	1.023	713.579	699.000	1.021	1.022
4	6	14	GT172G08	a76couture1738#1	>sp|P40590|RL34_PEA 60S RIBOSOMAL PROTEIN L34 >gi|2119150|pir||S60476 ribosomal protein	4275.766	2903.000	1.473	4574.939	3574.000	1.280	1.376
4	6	15	GB009E02	a76couture1648.r#1	>ref|NP_176564.1|| (NM_105054) putative U3 small nucleolar ribonucleoprotein protein;	267.235	151.000	1.770	293.463	162.000	1.812	1.791
4	7	1	TT283E07	a76couture1518.r#1	>ref|NP_199774.1|| (NM_124341) amino acid permease 6 (emb CAA65051.1); protein id:	337.166	473.000	0.713	418.057	576.000	0.726	0.719
4	7	2	TB003F04	a76couture1397.r#1	>pir||T09261 JUN kinase-activation-domain-binding protein homolog - alfalfa	664.342	621.000	1.070	852.588	804.000	1.060	1.065
4	7	3	GT172G01	a76couture1735#1	>gb|AAK68782.1| (AY042842) putative RING zinc finger ankyrin protein [Arabidopsis	59.941	51.000	1.175	49.425	48.000	1.030	1.103
4	7	4	GB009D06	a76couture1645.r#1	------	0.000			4.119	6.000	0.686	0.686
4	7	5	TT282H04	a76couture1513.r#1	>ref|NP_197591.1|| (NM_122099) ABI3-interacting protein 2; protein id: At5g20910.1	709.298	771.000	0.920	1071.913	1005.000	1.067	0.993
4	7	6	RT063B12	a76couture1392.r#1	>ref|NP_195696.1|| (NM_120149) putative protein; protein id: At4g39860.1. supported by	96.155	90.000	1.068	149.306	129.000	1.157	1.113
4	7	7	RT033E07	a76couture2157.r#1	>ref|NP_568854.1|| (NM_125117) Expressed protein; protein id: At5g57345.1. supported	465.789	435.000	1.071	739.322	672.000	1.100	1.085
4	7	8	RT022F01	a76couture2056#1	>emb|CAB75429.1| (AJ272011) oligouridylate binding protein [Nicotiana	558.197	508.000	1.099	632.233	670.000	0.944	1.021
4	7	9	RB008G11	a76couture1973.r#1	>gb|AAK62477.1| (AY034092) putative DNA-invertase [Micrococcus sp. 28]	0.000			36.039	37.000	0.974	0.974
4	7	10	GT201H07	a76couture1847#1	------	54.946	61.000	0.901	61.782	72.000	0.858	0.879
4	7	11	RT033C09	a76couture2153.r#1	------	42.458	40.000	1.061	47.366	49.000	0.967	1.014
4	7	12	RT022E04	a76couture2052.r#1	>emb|CAD41399.1| (AL606998) OJ000223_09.11 [Oryza sativa]	21.229	24.000	0.885	11.327	17.000	0.666	0.775
4	7	13	RB008G05	a76couture1971.r#1	>gb|AAF79913.1|AC022472_22 (AC022472) Contains similarity to PRO2134 mRNA from Homo sapiens	47.453	55.000	0.863	60.752	66.000	0.920	0.892
4	7	14	GT194A06	a76couture1843.r#1	>ref|NP_198037.1|| (NM_122567) putative protein; protein id: At5g26850.1 [Arabidopsis	289.713	313.000	0.926	370.690	437.000	0.848	0.887
4	7	15	RT033A02	a76couture2148.r#1	>ref|NP_177812.1|| (NM_106337) Sm-like protein; protein id: At1g76860.1. supported by	262.240	304.000	0.863	342.889	414.000	0.828	0.845
4	8	1	RT022D09	a76couture2050#1	>gb|AAL07535.1| (AF316405) resistance gene analog PU3 [Helianthus annuus]	16.234	27.000	0.601	38.099	50.000	0.762	0.682
4	8	2	RB008F03	a76couture1968#1	------	14.985	20.000	0.749	15.445	24.000	0.644	0.696
4	8	3	GT193F03	a76couture1839.r#1	>ref|NP_197132.1|| (NM_121633) putative protein; protein id: At5g16280.1 [Arabidopsis	285.967	237.000	1.207	315.087	279.000	1.129	1.168
4	8	4	RT032H02	a76couture2144.r#1	>ref|NP_178105.1|| (NM_106636) putative D-isomer specific 2-hydroxyacid dehydrogenase;	1781.986	1694.000	1.052	2277.687	2073.000	1.099	1.075
4	8	5	RT022D02	a76couture2047#1	>gb|AAD25675.1| (AC007020) hypothetical protein [Arabidopsis thaliana]	49.951	52.000	0.961	67.960	64.000	1.062	1.011
4	8	6	RB008D07	a76couture1964.r#1	>ref|NP_566356.1|| (NM_111812) expressed protein; protein id: At3g09770.1. supported	1052.708	1476.000	0.713	1743.275	2024.000	0.861	0.787
4	8	7	GT193B08	a76couture1835#1	------	77.423	57.000	1.358	91.643	73.000	1.255	1.307
4	8	8	RT032F09	a76couture2139.r#1	>dbj|BAB85942.1| (AB071330) qSH-1 [Oryza sativa (indica cultivar-group)]	317.186	353.000	0.899	558.095	533.000	1.047	0.973

4	8	9	RT022C07	a76couture2043#1	>gb|AAL08294.1| (AY056438) AT4g17070/dl4565c [Arabidopsis thaliana]	97.404	86.000	1.133	111.207	111.000	1.002	1.067
4	8	10	RB008D04	a76couture1962#1	>gb|AAF63787.1|AF142406_1 (AF142406) 200 kDa antigen p200 [Babesia bigemina]							
4	8	11	GT194A07	a76couture1831.r#1	>ref|NP_191099.1|| (NM_115397) putative protein; protein id: At3g55390.1. supported by	152.349	140.000	1.088	192.553	176.000	1.094	1.091
4	8	12	RT032E10	a76couture2135.r#1	------	154.847	149.000	1.039	161.662	162.000	0.998	1.019
4	8	13	RT022C03	a76couture2040#1	>gb|AAL31655.1|AC079179_10 (AC079179) Unknown protein [Oryza sativa]	34.965	30.000	1.166	33.980	29.000	1.172	1.169
4	8	14	RB007H04	a76couture1959#1	------	27.473	31.000	0.886	27.802	31.000	0.897	0.892
4	8	15	GT192C07	a76couture1827.r#1	>dbj|BAB02306.1| (AB017071) gene_id:MSJ11.15~unknown protein [Arabidopsis thaliana]	184.817	166.000	1.113	248.157	221.000	1.123	1.118
4	9	1	TT282E02	a76couture2560.r#1	>ref|NP_566802.1|| (NM_113597) expressed protein; protein id: At3g26850.1. supported	91.160	102.000	0.894	134.890	131.000	1.030	0.962
4	9	2	TT253B04	a76couture2462.r#1	>ref|NP_568749.1|| (NM_124480) expressed protein; protein id: At5g51010.1. supported	119.881	87.000	1.378	113.267	78.000	1.452	1.415
4	9	3	RT061G09	a76couture2346.r#1	>ref|NP_567596.1|| (NM_118134) putative protein; protein id: At4g20150.1. supported by	415.838	480.000	0.866	602.372	590.000	1.021	0.944
4	9	4	Arabidopsis Control Oligonucleotide	3ara23		14.985	19.000	0.789	18.535	23.000	0.806	0.797
4	9	5	TT282G10	a76couture2554.r#1	>ref|NP_190446.1|| (NM_114736) hypothetical protein; protein id: At3g48770.1	36.214	44.000	0.823	54.574	61.000	0.895	0.859
4	9	6	TT251B05	a76couture2457#1	>emb|CAA98167.1| (Z73939) RAB5B [Lotus japonicus]	47.453	60.000	0.791	88.554	89.000	0.995	0.893
4	9	7	RT063A11	a76couture2341.r#1	>ref|NP_194836.1|| (NM_119257) putative protein; protein id: At4g31070.1 [Arabidopsis	1.249	6.000	0.208	10.297	12.000	0.858	0.533
4	9	8	RT043H08	a76couture2252.r#1	>ref|NP_565942.1|| (NM_129646) expressed protein; protein id: At2g40830.1. supported	726.780	676.000	1.075	868.034	826.000	1.051	1.063
4	9	9	TT274E06	a76couture2550.r#1	>gb|AAM63845.1| (AY086796) putative signal sequence receptor. alpha subunit	593.163	638.000	0.930	811.400	830.000	0.978	0.954
4	9	10	TT242F12	a76couture2451.r#1	------	213.539	209.000	1.022	286.255	297.000	0.964	0.993
4	9	11	RT062E04	a76couture2336.r#1	none	293.459	242.000	1.213	387.166	337.000	1.149	1.181
4	9	12	RT051B09	a76couture2248.r#1	>ref|NP_565697.1|| (NM_128573) putative malonyl-CoA:Acyl carrier protein transacylase;	26.224	29.000	0.904	15.445	21.000	0.735	0.820
4	9	13	TT274B01	a76couture2546.r#1	------	3431.602	4317.000	0.795	4363.851	5272.000	0.828	0.811
4	9	14	TT241D11	a76couture2447.r#1	>ref|NP_197507.1|| (NM_122014) putative protein; protein id: At5g20070.1. supported by	370.883	385.000	0.963	536.472	543.000	0.988	0.976
4	9	15	RT062B12	a76couture2333.r#1	>gb|AAD56950.1|AF184885_1 (AF184885) LIM domain protein PLIM1 [Nicotiana tabacum]	2541.234	2339.000	1.086	2917.128	3246.000	0.899	0.993
4	10	1	RT044H06	a76couture2245.r#1	>gb|AAK19773.1| (AY015286) maturase K [Frailea phaeodisca]	21.229	17.000	1.249	30.891	29.000	1.065	1.157
4	10	2	TT272G04	a76couture2541.r#1	>ref|NP_199508.1|| (NM_124068) unknown protein; protein id: At5g46970.1 [Arabidopsis	129.871	158.000	0.822	155.484	193.000	0.806	0.814
4	10	3	TT242D02	a76couture2440.r#1	------	12.488	13.000	0.961	11.327	11.000	1.030	0.995
4	10	4	RT061H01	a76couture2330.r#1	------	1407.357	2072.000	0.679	1995.551	2496.000	0.799	0.739
4	10	5	RT044F06	a76couture2241.r#1	>ref|NP_201035.1|| (NM_125623) putative protein; protein id: At5g62290.1. supported by	169.832	131.000	1.296	256.394	181.000	1.417	1.356
4	10	6	TT272D04	a76couture2539#1	------		24.000	0.000				
4	10	7	TT241A11	a76couture2436.r#1	------	4.995	14.000	0.357	8.238	19.000	0.434	0.395
4	10	8	RT061D07	a76couture2326.r#1	>ref|NP_197965.1|| (NM_122494) receptor-like protein kinase - like; protein id:	13.736	16.000	0.859	20.594	28.000	0.735	0.797
4	10	9	RT044E10	a76couture2237.r#1	>gb|EAA00792.1| (AAAB01008986) agCP9495 [Anopheles gambiae str. PEST]	238.514	220.000	1.084	361.423	318.000	1.137	1.110
4	10	10	RT063F08	a76couture3076.r#1	>gb|AAC63273.1| (AF070967) SKP1-like protein [Nicotiana clevelandii]	805.452	788.000	1.022	1301.536	1258.000	1.035	1.028
4	10	11	RT053H01	a76couture2925.r#1	>dbj|BAB21209.1| (AP002913) putative ribosomal protein L26 [Oryza sativa (japonica	1565.949	1459.000	1.073	2617.487	2305.000	1.136	1.104
4	10	12	PT013F09	a76couture2789.r#1	>pir||T04466 hypothetical protein F4D11.200 - Arabidopsis thaliana	154.847	142.000	1.090	217.266	196.000	1.108	1.099
4	10	13	PT002C02	a76couture2683.r#1	>ref|NP_174819.1|| (NM_103283) hypothetical protein; protein id: At1g35830.1	49.951	57.000	0.876	76.197	80.000	0.952	0.914
4	10	14	RT022G05	a76couture3070#1	>ref|NP_191842.1|| (NM_116148) dTDP-glucose 4-6-dehydratase homolog D18; protein id:	665.591	574.000	1.160	883.479	779.000	1.134	1.147
4	10	15	TT272H10	a76couture2922.r#1	>dbj|BAC06946.1| (AP003759) putative GTP-binding protein [Oryza sativa (japonica	926.583	629.000	1.473	1201.655	950.000	1.265	1.369
4	11	1	PT013A07	a76couture2785.r#1	>ref|NP_176646.1|| (NM_105140) unknown protein; protein id: At1g64650.1 [Arabidopsis	434.570	616.000	0.705	549.858	682.000	0.806	0.756
4	11	2	PT002D06	a76couture2679.r#1	------	350.903	339.000	1.035	359.364	372.000	0.966	1.001
4	11	3	RB004H11	a76couture3065.r#1	------	400.853	468.000	0.857	587.956	551.000	1.067	0.962
4	11	4	CT002A07	a76couture2917.r#1	>dbj|BAB89620.1| (AP003258) hypothetical protein~similar to Arabidopsis thaliana	82.418	78.000	1.057	102.970	90.000	1.144	1.100
4	11	5	PT007E12	a76couture2780.r#1	>ref|NP_174170.1|| (NM_102616) glutaredoxin. putative; protein id: At1g28480.1	42.458	32.000	1.327	56.633	44.000	1.287	1.307
4	11	6	PT008E10	a76couture2674.r#1	>dbj|BAA89009.1| (AB027455) anthocyanin 5-O-glucosyltransferase [Petunia x hybrida]	1015.245	766.000	1.325	1206.804	900.000	1.341	1.333
4	11	7	RT074C10	a76couture3057.r#1	>dbj|BAB08256.1| (AB006698) phosphate/triose-phosphate translocator precursor	13.736	17.000	0.808	8.238	20.000	0.412	0.610
4	11	8	PT005F10	a76couture2911.r#1	>sp|Q9AXE3|DCAM_DAUCA S-adenosylmethionine decarboxylase proenzyme (AdoMetDC) (SamDC)	1735.781	1579.000	1.099	1784.463	1705.000	1.047	1.073
4	11	9	PT013F08	a76couture2775.r#1	>gb|AAG00256.1|AC002130_21 (AC002130) F1N21.7 [Arabidopsis thaliana]	1202.559	996.000	1.207	1403.475	1326.000	1.058	1.133
4	11	10	PT001E12	a76couture2670.r#1	------	629.377	717.000	0.878	1152.230	1216.000	0.948	0.913
4	11	11	RT033A10	a76couture3047.r#1	>ref|NP_566976.1|| (NM_115159) pyruvate kinase - like protein; protein id:	258.494	274.000	0.943	405.700	417.000	0.973	0.958
4	11	12	ST007G05	a76couture2908.r#1	>ref|NP_200279.1|| (NM_124849) bHLH protein; protein id: At5g54680.1. supported by	1228.783	1304.000	0.942	1760.780	1798.000	0.979	0.961
4	11	13	PT012G02	a76couture2771.r#1	>gb|AAL47679.1| (AY066012) aminotransferase 1 [Cucumis melo]	474.530	420.000	1.130	616.788	549.000	1.123	1.127
4	11	14	PT004C02	a76couture2666.r#1	------	32.468	36.000	0.902	32.950	40.000	0.824	0.863
4	11	15	RT074D09	a76couture3040.r#1	>dbj|BAA03710.1| (D16139) cytokinin binding protein CBP57 [Nicotiana sylvestris]	1816.951	1697.000	1.071	2273.568	2429.000	0.936	1.003
4	12	1	PT008G07	a76couture2905.r#1	>gb|AAM18755.1|AC099325_11 (AC099325) putatputative ABC transporter [Oryza sativa (japonica	16.234	25.000	0.649	29.861	32.000	0.933	0.791
4	12	2	PT006E02	a76couture2766.r#1	>ref|NP_566713.1|| (NM_113160) expressed protein; protein id: At3g22620.1. supported	27.473	27.000	1.018	23.683	28.000	0.846	0.932
4	12	3	PT009A12	a76couture2663.r#1	>ref|NP_518131.1|| (NC_003295) PUTATIVE ACRIFLAVIN RESISTANCE TRANSMEMBRANE PROTEIN	272.230	259.000	1.051	249.186	254.000	0.981	1.016
4	12	4	BG273730 RB000A72	couture_a76.403.c1.r#1	>dbj|BAA94084.1| (AB025969) NAD-dependent sorbitol dehydrogenase [Prunus persica]	904.105	511.000	1.769	1072.943	651.000	1.648	1.709
4	12	5	BM436826 TT274G11	couture_a76.322.c1.r#1	>gb|AAL68853.1|AF466199_12 (AF466199) gb protein [Sorghum bicolor]	686.820	580.000	1.184	840.232	691.000	1.216	1.200
4	12	6	BE846393 GT184A05	couture_a76.234.c1#1	>ref|NP_197574.1|| (NM_122081) ripening-related protein - like; protein id:	17.483	23.000	0.760	25.742	28.000	0.919	0.840
4	12	7	AW708011 ST001C08	couture_a76.136.c1.r#1	>dbj|BAA84613.1| (AP000492) EST AU078118(E3904) corresponds to a region of the	472.033	445.000	1.061	632.233	576.000	1.098	1.079
4	12	8	BG273951 GB000A29	couture_a76.4.c1.r#1	>pir||S38378 hypothetical protein - Madagascar periwinkle	39.960	44.000	0.908	48.396	55.000	0.880	0.894
4	12	9	BM436776 TT282B09	couture_a76.320.c1#1	>pir||T48530 clathrin binding protein-like - Arabidopsis thaliana	64.936	76.000	0.854	89.584	106.000	0.845	0.850
4	12	10	BM436921 CM004B08	couture_a76.23.c1#1	>ref|NP_200396.1|| (NM_124967) NOI protein. nitrate-induced; protein id: At5g55850.1	5141.160	5790.000	0.888	6525.182	6600.000	0.989	0.938
4	12	11	BM437623 CT002B10	couture_a76.131.c1.r#1	>ref|NP_568820.1|| (NM_124892) putative protein; protein id: At5g55100.1. supported by	153.598	196.000	0.784	188.434	237.000	0.795	0.789
4	12	12	BG273712 RB000A90	couture_a76.398.c1#1	>ref|NP_194929.1|| (NM_119353) similar to putative VP1/ABI3 family regulatory protein;	265.987	247.000	1.077	405.700	346.000	1.173	1.125
4	12	13	TT272H07 BM437320	couture_a76.317.c1#1	>ref|NP_200925.1|| (NM_125510) 40S ribsomal protein S19 - like; protein id:	3223.059	3282.000	0.982	3884.013	3910.000	0.993	0.988
4	12	14	BM437098 GB009D07	couture_a76.226.c1.r#1	>sp|Q9ZNS1|RS7_AVIMR 40S ribosomal protein S7 >gi|3851636|gb|AAC97947.1| (AF098519)	738.019	741.000	0.996	1047.201	1023.000	1.024	1.010
4	12	15	BM436580 CM002D05	couture_a76.127.c1#1	>ref|NP_567901.1|| (NM_119421) Expressed protein; protein id: At4g32690.1. supported	2343.929	1791.000	1.309	3121.008	2594.000	1.203	1.256
4	13	1	BG273795 RB000A03	couture_a76.393.c1#1	>ref|NP_200538.1|| (NM_125110) protein carboxyl methylase-like; protein id:	83.667	82.000	1.020	139.009	124.000	1.121	1.071

4	13	2	BM436503 TT254A07	couture_a76.313.c1.r#1	>gb|AAD27880.2|AF139468_1 (AF139468) photosystem I reaction center subunit III [Vigna	438.316	354.000	1.238	587.956	473.000	1.243	1.241
4	13	3	GB005d01 GB005D01	couture_a76.222.c1.r#1	>ref|NP_188931.1|| (NM_113191) potential calcium-transporting ATPase 13. plasma	171.081	199.000	0.860	189.464	210.000	0.902	0.881
4	13	4	BM436505 TT242A06	couture_a76.123.c1.r#1	>gb|AAD09515.1| (U64917) GMFP7 [Glycine max]	495.759	390.000	1.271	698.134	470.000	1.485	1.378
4	13	5	BM437559 GB002H02	couture_a76.39.c1.r#1	------	11.239	14.000	0.803	15.445	16.000	0.965	0.884
4	13	6	BM437923 GB003H06	couture_a76.31.c1.r#1	>gb|AAB62947.1| (AF007784) LTCOR11 [Lavatera thuringiaca]	15083.815	16583.000	0.910	17967.163	19230.000	0.934	0.922
4	13	7	BM437083 BM437580 BM436925 GB004H02	couture_a76.218.c1.r#1	>pir||T02434 DNA binding protein EREBP-4 - common tobacco	39.960	38.000	1.052	55.604	47.000	1.183	1.117
4	13	8	BM437863 TT283B10	couture_a76.120.c1.r#1	>dbj|BAB86520.1| (AP003381) ribosomal protein L28-like [Oryza sativa (japonica	2828.449	2106.000	1.343	3414.471	2719.000	1.256	1.299
4	13	9	BG273766 RB000A34 BM438127	couture_a76.387.c1#1	------	73.677	60.000	1.228	94.732	79.000	1.199	1.214
4	13	10	BG273855 TB000A37 TB000A37	couture_a76.306.c1.r#1	>pir||T03406 probable isocitrate dehydrogenase (NAD+) (EC 1.1.1.41) precursor -	964.045	868.000	1.111	1470.406	1378.000	1.067	1.089
4	13	11	BG273977 GB000A01	couture_a76.212.c1#1	>ref|NP_180956.1|| (NM_128960) hypothetical protein; protein id: At2g34090.1	17.483	25.000	0.699	14.416	28.000	0.515	0.607
4	13	12	BG273821 TB000A73	couture_a76.117.c1.r#1	>emb|CAC27142.1| (AJ132537) 60S ribosomal protein L13E [Picea abies]	2172.849	2299.000	0.945	3903.577	3552.000	1.099	1.022
4	13	13	TB001c02 BG273887 BG273737 AW707986 BG27	couture_a76.sd.1.c1#1	>gb|AAK51119.1| (AY032600) xyloglucan endo-transglycosylase [Carica papaya]	5890.418	8591.000	0.686	8502.198	11419.000	0.745	0.715
4	13	14	BM436671 BM437246 GB003e12 GB003E12	couture_a76.588.c1.r#1	>ref|NP_567210.1|| (NM_116345) expressed protein; protein id: At4g01150.1. supported	882.876	809.000	1.091	1140.903	1091.000	1.046	1.069
4	13	15	BM437808 G499019E VVF3H	couture_a76.sd.86.c1#	>sp|P41090|FL3H_VITVI Naringenin.2-oxoglutarate 3-dioxygenase (Flavonone-3-hydroxylase)	1279.983	1242.000	1.031	1621.771	1732.000	0.936	0.983
4	14	1	TB003e09 RT082C10	couture_a76.99.c1.r#1	>gb|AAL18930.1|AF429389_1 (AF429389) hydroxymethylglutaryl coenzyme A synthase [Hevea	3315.467	3811.000	0.870	3793.399	4575.000	0.829	0.850
4	14	2	GB001h11 GB001H11	couture_a76.535.c1.r#1	>gb|AAK58693.1|AF273256_1 (AF273256) sinapyl alcohol dehydrogenase [Populus tremuloides]	206.046	184.000	1.120	234.771	227.000	1.034	1.077
4	14	3	AW707965 RT083B07 VVI237986 BG273798 BG	couture_a76.sd.54.c1.r	------	17980.946	16144.000	1.114	20515.660	18992.000	1.080	1.097
4	14	4	AW707955 RT083F08 AW707956 BM437064 AW	couture_a76.630.c1#1	>gb|AAF35901.1|AF230332_1 (AF230332) expansin 2 [Zinnia elegans]	3461.573	3677.000	0.941	4200.129	3880.000	1.083	1.012
4	14	5	TB007h04 ST003B05	couture_a76.558.c1.r#1	>sp|P42896|ENO_RICCO Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate	5181.120	6491.000	0.798	7590.918	7736.000	0.981	0.890
4	14	6	BM437082 BG273812 TB000A82	couture_a76.486.c1#1	>emb|CAD40829.1| (AL606615) OSJNBa0086B14.1 [Oryza sativa]	1725.791	1605.000	1.075	2088.223	1821.000	1.147	1.111
4	14	7	BG273801 ST005G05	couture_a76.89.c1.r#1	>gb|AAK15089.1|AF240006_1 (AF240006) 7S globulin [Sesamum indicum]	2027.992	3014.000	0.673	3303.264	4200.000	0.786	0.730
4	14	8	TT253A08 GT173C03	couture_a76.575.c1#1	>gb|AAN08216.1| (AC090874) ribosomal protein L15 [Oryza sativa (japonica	1217.544	1305.000	0.933	1715.473	1733.000	0.990	0.961
4	14	9	BM437376 RT064D04	couture_a76.485.c1.r#1	>ref|NP_192009.1|| (NM_116328) putative protein; protein id: At4g01000.1. supported by	414.589	499.000	0.831	583.838	612.000	0.954	0.892
4	14	10	BM436433 GB003d07 RT062H05	couture_a76.62.c1#1	>sp|P42027|NUKM_BRAOL NADH-ubiquinone oxidoreductase 20 kDa subunit. mitochondrial	2618.657	2834.000	0.924	2883.148	3394.000	0.849	0.887
4	14	11	RT081H11 PT009G05	couture_a76.549.c1#1	>dbj|BAA96068.1| (AB042856) 60S ribosomal protein L27a [Panax ginseng]	2965.813	2655.000	1.117	4415.336	3697.000	1.194	1.156
4	14	12	G1785612 VVU83274 AF176652 VVPYPOXC	couture_a76.sd.70.c1#	>gb|AAB41022.1| (U83274) polyphenol oxidase [Vitis vinifera]	417.087	1073.000	0.389	622.966	1530.000	0.407	0.398
4	14	13	RB003A11 RB003A11	couture_a76.619.c1.r#1	>sp|P93092|ACP1_CASGL Acyl carrier protein 1. chloroplast precursor (ACP 1)	2276.496	2422.000	0.940	4103.338	3712.000	1.105	1.023
4	14	14	BM436609 TT242E04	couture_a76.471.c1#1	>ref|NP_200949.1|| (NM_125534) ribulose-5-phosphate-3-epimerase; protein id:	549.456	523.000	1.051	785.658	791.000	0.993	1.022
4	14	15	PI103A01C AF141899 AF188844	couture_a76.sd.11.c1#	>gb|AAF80557.1|AF188844_1 (AF188844) plasma membrane aquaporin [Vitis vinifera]	4569.226	4163.000	1.098	6132.868	5959.000	1.029	1.063
5	1	1	CM005a09	a76couture0497.r#1	ef|NP_179145.1|| (NM_127103) DNA-directed RNA polymerase II, th... 84 3e-016	202.300	326.000	0.621	135.920	369.000	0.368	0.494
5	1	2	CM001D02	a76couture0399.r#1	>ref|NP_199554.1|| (NM_124114) DNA-binding protein-like; protein id: At5g47430.1	262.240	380.000	0.690	204.909	416.000	0.493	0.591
5	1	3	ST005D01	a76couture0279.r#1	>ref|NP_671959.1|| (NM_091489) 60S ribosomal protein L7; protein id: At2g44120.2	3120.660	3298.000	0.946	2438.320	3577.000	0.682	0.814
5	1	4	GT192H02	a76couture0143.r#1	>ref|NP_181435.1|| (NM_129459) unknown protein; protein id: At2g39020.1 [Arabidopsis	1383.630	1766.000	0.783	1145.022	2077.000	0.551	0.667
5	1	5	CT001H05	a76couture0493.r#1	>ref|NP_173104.1|| (NM_101520) unknown protein; protein id: At1g16560.1 [Arabidopsis	138.613	194.000	0.714	116.356	194.000	0.600	0.657
5	1	6	CM001B01	a76couture0395.r#1	>ref|NP_200824.1|| (NM_125409) aspartyl aminopeptidase - like protein; protein id:	530.725	644.000	0.824	609.580	702.000	0.868	0.846
5	1	7	ST006A07	a76couture0274.r#1	>pir||T51098 hypothetical protein p85RF [imported] - Prunus armeniaca	1038.971	1335.000	0.778	1273.734	1401.000	0.909	0.844
5	1	8	GT162C10	a76couture0137.r#1	>gb|AAK20050.1|AC025783_10 (AC025783) putative zinc finger protein [Oryza sativa (japonica	262.240	326.000	0.804	331.562	366.000	0.906	0.855
5	1	9	CT001G05	a76couture0489.r#1	>gb|AAB88878.1| (U97530) ethylene-forming-enzyme-like dioxygenase [Prunus	1250.012	1332.000	0.938	1527.039	1558.000	0.980	0.959
5	1	10	ST007F11	a76couture0391.r#1	>ref|NP_194817.1|| (NM_119235) hypothetical protein; protein id: At4g30880.1	526.978	246.000	2.142	489.106	205.000	2.386	2.264
5	1	11	ST005B12	a76couture0268.r#1	>ref|NP_564061.1|| (NM_101730) expressed protein; protein id: At1g18720.1. supported	41.209	42.000	0.981	31.921	28.000	1.140	1.061
5	1	12	GT171C10	a76couture0129.r#1	------	11763.353	10662.000	1.103	10209.434	10303.000	0.991	1.047
5	1	13	CT001E03	a76couture0484.r#1	>ref|NP_181336.1|| (NM_129357) unknown protein; protein id: At2g38000.1. supported by	619.387	686.000	0.903	621.936	738.000	0.843	0.873
5	1	14	ST006H01	a76couture0387.r#1	>gb|AAL88710.1|AF484696_1 (AF484696) 1-cys peroxiredoxin [Xerophyta viscosa]	7323.998	7640.000	0.959	7491.037	8908.000	0.841	0.900
5	1	15	PT012H10	a76couture0262.r#1	>gb|AAF18411.1|AF190652_1 (AF190652) putative integral membrane protein [Phaseolus vulgaris]	1253.759	1029.000	1.218	1164.586	1248.000	0.933	1.076
5	2	1	GT184F01	a76couture0118.r#1	>ref|NP_566563.1|| (NM_112576) E2. ubiquitin-conjugating enzyme. putative; protein id:	1448.566	2117.000	0.684	1099.715	2412.000	0.456	0.570
5	2	2	CT001C12	a76couture0480.r#1	------	28.722	51.000	0.563	24.713	45.000	0.549	0.556
5	2	3	Arabidopsis Control Oligonucleotide	3ara23			12.000	0.000				
5	2	4	PT012H01	a76couture0257.r#1	>ref|NP_566715.1|| (NM_113173) putative selenocysteine methyltransferase; protein id:	134.866	216.000	0.624	94.732	209.000	0.453	0.539
5	2	5	CT005F12	a76couture0110.r#1	>dbj|BAB03143.1| (AP002047) ankyrin-like protein [Arabidopsis thaliana]	941.568	1228.000	0.767	812.430	1353.000	0.600	0.684
5	2	6	CM004H08	a76couture0476.r#1	>ref|NP_566975.1|| (NM_115154) nuclear envelope membrane protein - like; protein id:	173.578	262.000	0.663	176.078	239.000	0.737	0.700
5	2	7	ST004A04	a76couture0380.r#1	>pir||S65051 low molecular weight heat shock protein precursor (clone Hsp22.5)	4511.783	1072.000	4.209	6416.035	1209.000	5.307	4.758
5	2	8	PT006H03	a76couture0253.r#1	>ref|NP_190652.1|| (NM_114943) putative cold acclimation protein; protein id:	3869.918	5398.000	0.717	4986.817	6278.000	0.794	0.756
5	2	9	CT004F08	a76couture0105.r#1	>ref|NP_178935.1|| (NM_126891) unknown protein; protein id: At2g12400.1. supported by	2957.072	4045.000	0.731	3705.875	4708.000	0.787	0.759
5	2	10	RT071B03	a76couture0931.r#1	------	11.239	20.000	0.562	11.327	16.000	0.708	0.635
5	2	11	GT204G08	a76couture0809.r#1	>ref|NP_181042.1|| (NM_129049) putative translation initiation factor eIF-2B epsilon	18.731	25.000	0.749	17.505	20.000	0.875	0.812
5	2	12	ST006A02	a76couture0696.r#1	>ref|NP_564846.1|| (NM_105199) expressed protein; protein id: At1g65260.1. supported	61.189	91.000	0.672	57.663	79.000	0.730	0.701
5	2	13	ST001F02	a76couture0598.r#1	>ref|NP_173551.1|| (NM_101981) hypothetical protein; protein id: At1g21290.1	11.239	25.000	0.450	15.445	22.000	0.702	0.576
5	2	14	RT072E06	a76couture0928#1	>gb|AAF19538.1|AC007190_6 (AC007190) F23N19.10 [Arabidopsis thaliana]	395.858	276.000	1.434	377.898	308.000	1.227	1.331
5	2	15	GT174D01	a76couture0806.r#1	>pir||T07171 subtilisin-like proteinase (EC 3.4.21.-) 1 - tomato	8821.266	6508.000	1.355	8049.132	7515.000	1.071	1.213
5	3	1	ST005F10	a76couture0692.r#1	>ref|NP_176960.1|| (NM_105463) golgi transport complex protein-related; protein id:	56.194	89.000	0.631	35.010	84.000	0.417	0.524
5	3	2	ST001E01	a76couture0595.r#1	>pir||T03812 hypothetical protein (clone NF22) - common tobacco	56.194	97.000	0.579	56.633	116.000	0.488	0.534
5	3	3	RT071H06	a76couture0924.r#1	>dbj|BAB02368.1| (AB022218) gene_id:MJK13.5~unknown protein [Arabidopsis thaliana]	370.883	618.000	0.600	305.820	675.000	0.453	0.527
5	3	4	RT043H03	a76couture0799.r#1	>emb|CAA66109.2| (X97455) specific tissue protein 2 [Cicer arietinum]	78.672	165.000	0.477	62.811	167.000	0.376	0.426
5	3	5	ST005E11	a76couture0688.r#1	>ref|NP_567716.1|| (NM_118649) putative protein; protein id: At4g25170.1. supported by	11.239	29.000	0.388	9.267	21.000	0.441	0.414
5	3	6	ST001B05	a76couture0589.r#1	>ref|NP_196049.1|| (NM_120511) glycine-rich protein; protein id: At5g04290.1	19.980	43.000	0.465	20.594	34.000	0.606	0.535
5	3	7	RT071E02	a76couture0920.r#1	>ref|NP_189152.1|| (NM_113420) ER lumen protein retaining receptor. putative; protein	399.604	600.000	0.666	453.066	592.000	0.765	0.716
5	3	8	RT033A07	a76couture0794.r#1	>ref|NP_566623.1|| (NM_112786) expressed protein; protein id: At3g19000.1. supported	67.433	86.000	0.784	73.108	85.000	0.860	0.822
5	3	9	ST005B11	a76couture0684.r#1	>ref|NP_195274.1|| (NM_119714) ribosomal protein L11 homolog; protein id: At4g35490.1	148.603	185.000	0.803	131.801	157.000	0.839	0.821

5	3	10	ST001A06	a76couture0585.r#1	>dbj|BAA00615.1| (D00710) heat-shock protein [Arabidopsis thaliana]	54.946	70.000	0.785	45.307	54.000	0.839	0.812
5	3	11	TT254H11	a76couture0915.r#1	------	26.224	43.000	0.610	29.861	42.000	0.711	0.660
5	3	12	RB007B11	a76couture0789.r#1	>gb|AAC49776.1| (AF003103) AP2 domain containing protein RAP2.10 [Arabidopsis	433.321	416.000	1.042	415.997	445.000	0.935	0.988
5	3	13	ST005A11	a76couture0680.r#1	>pir||T05262 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) - soybean	1341.172	1045.000	1.283	1245.932	1095.000	1.138	1.211
5	3	14	CT006A11	a76couture0581.r#1	------	78.672	78.000	1.009	84.435	85.000	0.993	1.001
5	3	15	TT282D12	a76couture0909.r#1	>ref|NP_188548.2|| (NM_112804) metalloprotease. putative; protein id: At3g19170.1	414.589	383.000	1.082	336.711	432.000	0.779	0.931
5	4	1	GT192G08	a76couture0784.r#1	>ref|NP_566884.1|| (NM_114513) E2. ubiquitin-conjugating enzyme 13 (UBC13); protein	7471.352	10224.000	0.731	5840.435	11661.000	0.501	0.616
5	4	2	ST004H10	a76couture0676.r#1	------	151.100	232.000	0.651	135.920	280.000	0.485	0.568
5	4	3	CT005G07	a76couture0577#1	------	44.955	67.000	0.671	47.366	81.000	0.585	0.628
5	4	4	RT063E05	a76couture1386#1	>emb|CAB85632.1| (AJ237992) putative ripening-related bZIP protein [Vitis vinifera]	76.175	80.000	0.952	65.901	78.000	0.845	0.899
5	4	5	RB005D09	a76couture1274.r#1	>gb|AAM96979.1| (AY136313) putative protein [Arabidopsis thaliana]	2091.679	2939.000	0.712	2777.090	3945.000	0.704	0.708
5	4	6	GT173D08	a76couture1137.r#1	>gb|AAC17634.1| (AC002131) Contains similarity to vesicle trafficking protein	37.463	72.000	0.520	35.010	58.000	0.604	0.562
5	4	7	RT084G04	a76couture1022.r#1	------	69.931	72.000	0.971	85.465	64.000	1.335	1.153
5	4	8	RT061G06	a76couture1380.r#1	>dbj|BAA96366.1| (AB043974) cytoplasmic ribosomal protein S13 [Panax ginseng]	226.026	266.000	0.850	262.572	254.000	1.034	0.942
5	4	9	RB003A06	a76couture1266.r#1	------	17.483	26.000	0.672	14.416	18.000	0.801	0.737
5	4	10	GT172H04	a76couture1133.r#1	>ref|NP_192113.1|| (NM_116435) hypothetical protein; protein id: At4g02040.1	39.960	46.000	0.869	41.188	45.000	0.915	0.892
5	4	11	RT084A11	a76couture1020#1	------	6.244	21.000	0.297	5.148	12.000	0.429	0.363
5	4	12	RT054D03	a76couture1375.r#1	>dbj|BAB33274.1| (AP003054) putative oxalyl-CoA decarboxylase [Oryza sativa	1361.152	1504.000	0.905	1117.220	1474.000	0.758	0.831
5	4	13	RB001C11	a76couture1262.r#1	>dbj|BAB64646.1| (AP003225) putative splicing factor-like protein [Oryza sativa	586.919	490.000	1.198	524.115	526.000	0.996	1.097
5	4	14	GT172A08	a76couture1130#1	>gb|AAM64433.1| (AY086365) similar to late embryogenesis abundant proteins	4694.102	3929.000	1.195	3678.074	4246.000	0.866	1.030
5	4	15	RT082G09	a76couture1015.r#1	>ref|NP_567154.1|| (NM_116235) putative YABBY3 axial regulator; protein id:	203.548	211.000	0.965	178.137	242.000	0.736	0.850
5	5	1	RT051F07	a76couture1370.r#1	>sp|Q96558|UGDH_SOYBN UDP-GLUCOSE 6-DEHYDROGENASE (UDP-GLC DEHYDROGENASE) (UDP-GLCDH)	2582.443	4513.000	0.572	2172.658	4860.000	0.447	0.510
5	5	2	GT204B07	a76couture1248.r#1	>pir||JC7335 chitinase (EC 3.2.1.14) 1 - cone shell (Conus tulipa)	253.499	407.000	0.623	230.652	477.000	0.484	0.553
5	5	3	GB009G12	a76couture1125.r#1	>gb|ZP_00057740.1| (NZ_AAAQ01000031) hypothetical protein [Thermobifida fusca]	355.898	522.000	0.682	219.325	426.000	0.515	0.598
5	5	4	RT082E04	a76couture1011.r#1	>ref|NP_194549.1|| (NM_118960) putative protein; protein id: At4g28200.1. supported by	124.876	180.000	0.694	97.821	161.000	0.608	0.651
5	5	5	RT053A10	a76couture1366.r#1	>ref|NP_174351.1|| (NM_102800) coatomer-like protein. epsilon subunit; protein id:	1584.681	1982.000	0.800	1851.393	2244.000	0.825	0.812
5	5	6	GT203G03	a76couture1244.r#1	------	88.662	122.000	0.727	124.593	148.000	0.842	0.784
5	5	7	GB009E01	a76couture1121.r#1	------	139.862	182.000	0.768	153.425	171.000	0.897	0.833
5	5	8	RT082B03	a76couture1007.r#1	------	32.468	42.000	0.773	33.980	44.000	0.772	0.773
5	5	9	RT052A10	a76couture1362.r#1	>gb|AAF43231.1|AC012654_15 (AC012654) EST gb|Z37689 comes from this gene. [Arabidopsis	947.812	977.000	0.970	712.550	879.000	0.811	0.890
5	5	10	GT203C09	a76couture1239.r#1	>ref|NP_201209.1|| (NM_125800) photosystem I reaction center subunit PSI-N precursor	260.992	232.000	1.125	204.909	223.000	0.919	1.022
5	5	11	GB009B10	a76couture1115.r#1	>ref|NP_567622.1|| (NM_118238) putative protein; protein id: At4g21190.1. supported by	103.647	102.000	1.016	76.197	87.000	0.876	0.946
5	5	12	RT081G10	a76couture1003.r#1	>ref|NP_567787.1|| (NM_118921) glycosyl hydrolase family 1; protein id: At4g27830.1	399.604	544.000	0.735	339.800	573.000	0.593	0.664
5	5	13	GT184B03	a76couture1822.r#1	>ref|NP_179201.1|| (NM_127162) hypothetical protein; protein id: At2g16030.1	97.404	87.000	1.120	72.079	80.000	0.901	1.010
5	5	14	GT172F07	a76couture1730#1	>ref|NP_569048.1|| (NM_126136) subtilisin-like serine protease ARA12; protein id:	700.556	480.000	1.459	613.699	545.000	1.126	1.293
5	5	15	GB009B07	a76couture1640.r#1	------	1.249	12.000	0.104	2.059	10.000	0.206	0.155
5	6	1	TT281F10	a76couture1507.r#1	>ref|NP_567340.1|| (NM_116949) nitrilase 1 like protein; protein id: At4g08790.1	329.674	469.000	0.703	275.958	547.000	0.504	0.604
5	6	2	GT191C06	a76couture1818.r#1	------	14.985	27.000	0.555	11.327	25.000	0.453	0.504
5	6	3	GT172E03	a76couture1726.r#1	>pir||S14305 chlorophyll a/b-binding protein (cab-11) - tomato	12.488	20.000	0.624	9.267	17.000	0.545	0.585
5	6	4	GB009A05	a76couture1637.r#1	------	1.249	14.000	0.089	0.000			0.089
5	6	5	TT281B04	a76couture1502.r#1	>ref|NP_189306.1|| (NM_113583) glycosyl hydrolase family 38 (alpha-mannosidase); protein	82.418	130.000	0.634	67.960	106.000	0.641	0.638
5	6	6	GT184G05	a76couture1814.r#1	>ref|NP_194093.1|| (NM_118493) putative protein; protein id: At4g23620.1. supported by	47.453	80.000	0.593	58.693	74.000	0.793	0.693
5	6	7	GT172D05	a76couture1724.r#1	>ref|NP_180738.1|| (NM_128737) UDP-glycosyltransferase family; protein id:	244.758	278.000	0.880	303.760	313.000	0.970	0.925
5	6	8	GT171A03	a76couture1633.r#1	>ref|NP_175264.2|| (NM_103727) hypothetical protein; protein id: At1g48300.1	44.955	50.000	0.899	35.010	41.000	0.854	0.877
5	6	9	TT274H02	a76couture1497.r#1	>dbj|BAA97374.1| (AB023044) contains similarity to poly(A)-binding protein	207.295	214.000	0.969	186.375	213.000	0.875	0.922
5	6	10	GT184C06	a76couture1810.r#1	------		25.000	0.000				
5	6	11	GT172B09	a76couture1720#1	>gb|AAB82764.1| (U89511) b-keto acyl reductase [Allium porrum]	865.393	619.000	1.398	721.817	627.000	1.151	1.275
5	6	12	GB007F12	a76couture1628.r#1	>gb|AAM01021.1|AC090488_21 (AC090488) Putative acid cluster protein 33 [Oryza sativa] [Oryza							
5	6	13	TT274B11	a76couture1490.r#1	>ref|NP_176682.1|| (NM_105176) hypothetical protein; protein id: At1g65020.1	61.189	57.000	1.073	42.218	40.000	1.055	1.064
5	6	14	GT182F11	a76couture1806.r#1	>ref|NP_181869.1|| (NM_129902) RRM-containing protein; protein id: At2g43410.1	77.423	88.000	0.880	63.841	85.000	0.751	0.815
5	6	15	GT172B07	a76couture1718#1	------	108.642	100.000	1.086	89.584	102.000	0.878	0.982
5	7	1	GB007E01	a76couture1625.r#1	>ref|NP_195280.1|| (NM_119720) homeodomain - like protein; protein id: At4g35550.1	11.239	17.000	0.661	9.267	23.000	0.403	0.532
5	7	2	TT274A11	a76couture1484.r#1	>ref|NP_174718.1|| (NM_103182) monosaccharide transporter. putative; protein id:	13.736	29.000	0.474	11.327	27.000	0.420	0.447
5	7	3	GT183G10	a76couture1802.r#1	>ref|NP_568698.1|| (NM_124223) expressed protein; protein id: At5g48480.1. supported	114.886	129.000	0.891	95.762	129.000	0.742	0.816
5	7	4	GT172B01	a76couture1715#1	>ref|NP_181797.1|| (NM_129830) putative lipase; protein id: At2g42690.1. supported by	121.130	142.000	0.853	124.593	149.000	0.836	0.845
5	7	5	GB006H10	a76couture1620.r#1	>ref|NP_563779.1|| (NM_100582) expressed protein; protein id: At1g07080.1. supported	238.514	306.000	0.779	259.483	278.000	0.933	0.856
5	7	6	TT273E12	a76couture1480.r#1	>dbj|BAB43907.1| (AB050471) phosphoenolpyruvate carboxykinase [Flaveria trinervia]	3414.120	5394.000	0.633	4926.065	6385.000	0.772	0.702
5	7	7	RT044C06	a76couture2231.r#1	>ref|NP_172088.1|| (NM_100478) hypothetical protein; protein id: At1g05970.1	138.613	142.000	0.976	186.375	179.000	1.041	1.009
5	7	8	RT032D06	a76couture2132.r#1	>pir||S60054 peroxidase (EC 1.11.1.7) A3a precursor - Japanese aspen x	224.777	271.000	0.829	191.523	277.000	0.691	0.760
5	7	9	RT022A12	a76couture2036#1	>gb|AAG60133.1|AC073555_17 (AC073555) hypothetical protein [Arabidopsis thaliana]	204.797	151.000	1.356	189.464	161.000	1.177	1.267
5	7	10	RB007B04	a76couture1953.r#1	>pir||JC7336 zinc-finger protein - Arabidopsis thaliana	69.931	71.000	0.985	39.128	50.000	0.783	0.884
5	7	11	RT044B03	a76couture2227.r#1	>sp|Q9XI05|PS31_ARATH Proteasome subunit beta type 3-1 (20S proteasome alpha subunit C1)	1406.108	1266.000	1.111	1084.270	1363.000	0.796	0.953
5	7	12	RT032C11	a76couture2128.r#1	>ref|NP_630271.1|| (NC_003888) proline rich protein (putative membrane protein)	303.450	329.000	0.922	219.325	304.000	0.721	0.822
5	7	13	RT021F09	a76couture2033#1	>pir||T12180 probable transcription factor - fava bean	3519.016	2658.000	1.324	2998.474	2994.000	1.001	1.163
5	7	14	RB008B03	a76couture1948.r#1	>ref|NP_195785.1|| (NM_120243) Macrophage migration inhibitory factor (MIF) family;	19.980	24.000	0.833	14.416	18.000	0.801	0.817
5	7	15	RT043H06	a76couture2223.r#1	>gb|ZP_00110381.1| (NZ_AABC01000183) hypothetical protein [Nostoc punctiforme]	28.722	37.000	0.776	21.624	27.000	0.801	0.789
5	8	1	RT031F07	a76couture2124.r#1	>gb|AAD14454.1| (AC005275) putative protein phosphatase regulatory subunit	244.758	457.000	0.536	226.533	500.000	0.453	0.494
5	8	2	RT022A04	a76couture2029#1	>gb|AAM08784.1|AC016780_14 (AC016780) Putative epimerase/dehydratase [Oryza sativa]	189.812	279.000	0.680	152.395	283.000	0.538	0.609

5	8	3	RB004E09	a76couture1943.r#1	>ref|NP_177153.1|| (NM_105664) unknown protein; protein id: At1g69950.1 [Arabidopsis	128.623	204.000	0.631	103.999	194.000	0.536	0.583
5	8	4	RT043E11	a76couture2219.r#1	>gb|AAM63014.1| (AY085798) unknown [Arabidopsis thaliana]	6.244	19.000	0.329	5.148	14.000	0.368	0.348
5	8	5	RT031D11	a76couture2120.r#1	>pir||C71407 hypothetical protein - Arabidopsis thaliana	488.267	713.000	0.685	629.144	829.000	0.759	0.722
5	8	6	RT021G11	a76couture2025#1	>ref|NP_193037.1|| (NM_117370) putative protein; protein id: At4g13010.1. supported by	96.155	141.000	0.682	117.385	134.000	0.876	0.779
5	8	7	RB005G05	a76couture1938.r#1	------	11.239	29.000	0.388	7.208	17.000	0.424	0.406
5	8	8	RT043B11	a76couture2216.r#1	>gb|AAL77575.1|L46847_1 (L46847) dehydroquinate synthase [Lycopersicon esculentum]							
5	8	9	RT031C09	a76couture2116.r#1	------	54.946	76.000	0.723	56.633	66.000	0.858	0.791
5	8	10	RT021F08	a76couture2021#1	>dbj|BAA04838.1| (D21814) ORF [Lilium longiflorum]	99.901	69.000	1.448	106.059	68.000	1.560	1.504
5	8	11	RB005F01	a76couture1934.r#1	------	38.712	50.000	0.774	29.861	42.000	0.711	0.743
5	8	12	RT041C05	a76couture2211.r#1	>ref|NP_196080.1|| (NM_120542) RRM-containing protein; protein id: At5g04600.1	59.941	41.000	1.462	65.901	46.000	1.433	1.447
5	8	13	RT031A11	a76couture2113.r#1	>pir||T04562 hypothetical protein T12H17.60 - Arabidopsis thaliana	255.997	234.000	1.094	174.019	199.000	0.874	0.984
5	8	14	RT021E09	a76couture2017.r#1	>ref|XP_129216.1|| (XM_129216) similar to KIAA0020 gene product [Mus musculus]	757.999	664.000	1.142	639.441	735.000	0.870	1.006
5	8	15	RB004C11	a76couture1930.r#1	>ref|NP_195948.1|| (NM_120406) putative protein; protein id: At5g03280.1. supported by	12.488	21.000	0.595	10.297	15.000	0.686	0.641
5	9	1	PT001C07	a76couture2657.r#1	------	53.697	67.000	0.801	44.277	66.000	0.671	0.736
5	9	2	TT264B08	a76couture2534.r#1	>ref|NP_524520.1|| (NM_079796) Ribonuclear protein at 97D [Drosophila melanogaster]	9.990	22.000	0.454	7.208	16.000	0.450	0.452
5	9	3	TB007B03	a76couture2430.r#1	>gb|AAM61449.1| (AY084886) unknown [Arabidopsis thaliana]	295.957	374.000	0.791	260.513	397.000	0.656	0.724
5	9	4	RT061A09	a76couture2321.r#1	>dbj|BAA98203.1| (AP002031) emb|CAB77600.1~gene_id:K3D20.2~similar to unknown protein	992.767	1636.000	0.607	1259.318	2120.000	0.594	0.600
5	9	5	PT008E06	a76couture2653.r#1	>gb|AAM64473.1| (AY086406) unknown [Arabidopsis thaliana]	274.728	322.000	0.853	327.443	353.000	0.928	0.890
5	9	6	TT263E11	a76couture2530.r#1	>ref|NP_174174.1|| (NM_102620) unknown protein; protein id: At1g28520.1 [Arabidopsis	43.707	74.000	0.591	63.841	84.000	0.760	0.675
5	9	7	TB006E08	a76couture2424.r#1	>ref|NP_680222.1|| (NM_147917) hypothetical protein; protein id: At5g25754.1	703.054	805.000	0.873	817.578	883.000	0.926	0.900
5	9	8	RT054H07	a76couture2317.r#1	>ref|NP_568289.2|| (NM_121368) GTP-binding protein typA (tyrosine phosphorylated protein	750.507	774.000	0.970	734.173	907.000	0.809	0.890
5	9	9	PT004E09	a76couture2648.r#1	------	1218.793	963.000	1.266	860.826	864.000	0.996	1.131
5	9	10	TT264F03	a76couture2526.r#1	>ref|NP_565714.1|| (NM_128665) expressed protein; protein id: At2g31090.1. supported	1303.709	1016.000	1.283	1013.221	1053.000	0.962	1.123
5	9	11	TB006A05	a76couture2420.r#1	>ref|NP_181756.1|| (NM_129789) U5 small nuclear ribonucleoprotein helicase. putative;	355.898	245.000	1.453	339.800	285.000	1.192	1.322
5	9	12	RT054C05	a76couture2313.r#1	>ref|NP_179858.1|| (NM_127838) hypothetical protein; protein id: At2g22730.1	112.389	133.000	0.845	116.356	162.000	0.718	0.782
5	9	13	PT001D05	a76couture2643.r#1	------	119.881	104.000	1.153	116.356	127.000	0.916	1.034
5	9	14	TT264B07	a76couture2522.r#1	>ref|NP_186798.1|| (NM_111015) putative protein kinase; protein id: At3g01490.1	2136.634	1685.000	1.268	1955.392	2060.000	0.949	1.109
5	9	15	TB005D07	a76couture2415.r#1	>ref|NP_565868.1|| (NM_129322) expressed protein; protein id: At2g37660.1. supported	1584.681	1091.000	1.453	1620.741	1529.000	1.060	1.256
5	10	1	RT054B10	a76couture2310.r#1	>gb|AAM65302.1| (AY087766) unknown [Arabidopsis thaliana]	375.878	597.000	0.630	342.889	673.000	0.509	0.570
5	10	2	PT009G12	a76couture2640#1	>prf||1909359B ribosomal protein L7 [Solanum tuberosum]	19.980	37.000	0.540	17.505	34.000	0.515	0.527
5	10	3	TT262C07	a76couture2518.r#1	>dbj|BAA95888.1| (AP002071) ESTs AU082563(S20379).D15187(C0226)	1051.459	1494.000	0.704	1014.250	1539.000	0.659	0.681
5	10	4	TB004E04	a76couture2407.r#1	------	484.520	857.000	0.565	648.708	1158.000	0.560	0.563
5	10	5	RT053G11	a76couture2305.r#1	>gb|AAM61711.1| (AY085158) putative prolyl 4-hydroxylase. alpha subunit	1096.414	1558.000	0.704	1430.248	1898.000	0.754	0.729
5	10	6	PT001B09	a76couture2634.r#1	------	24.975	49.000	0.510	28.831	45.000	0.641	0.575
5	10	7	TT261B06	a76couture2514.r#1	>ref|NP_178101.1|| (NM_106632) unknown protein; protein id: At1g79830.1 [Arabidopsis	86.165	102.000	0.845	90.613	104.000	0.871	0.858
5	10	8	TB004C07	a76couture2404.r#1	>ref|NP_187885.1|| (NM_112115) unknown protein; protein id: At3g12790.1 [Arabidopsis	114.886	122.000	0.942	126.653	145.000	0.873	0.908
5	10	9	RT061E03	a76couture2302#1	>ref|NP_197078.1|| (NM_121579) putative protein; protein id: At5g15740.1 [Arabidopsis	27.473	41.000	0.670	24.713	36.000	0.686	0.678
5	10	10	BG273829 TB000A64 BM436533 TT284G03 TB0	couture_a76.110.c1#1	>pir||T10174 hypothetical protein - castor bean >gi|1621268|emb|CAB02653.1|	10410.942	10238.000	1.017	10634.699	13829.000	0.769	0.893
5	10	11	RT083A07	a76couture3032.r#1	>emb|CAC84489.1| (AJ309088) putative translation factor [Pinus pinaster]		19.000	0.000				
5	10	12	Arabidopsis Control Oligonucleotide	3ara23		33.717	47.000	0.717	31.921	47.000	0.679	0.698
5	10	13	PT013C12	a76couture2760.r#1	>dbj|BAA81662.2| (AB029060) F1F0-ATPase inhibitor protein [Oryza sativa (japonica	1269.993	1116.000	1.138	1034.844	1184.000	0.874	1.006
5	10	14	BM437040 RT084E10 GB005f08	couture_a76.104.c1.r#1	>dbj|BAA02729.1| (D13512) cytoplasmic aldolase [Oryza sativa]	19526.916	16335.000	1.195	17216.514	20456.000	0.842	1.019
5	10	15	RT023A12	a76couture3025.r#1	>emb|CAD41089.1| (AL606614) OSJNBb0011N17.6 [Oryza sativa]	44.955	36.000	1.249	49.425	47.000	1.052	1.150
5	11	1	CM002G04	a76couture2895.r#1	>sp|Q38709|THI4_ALNGL Thiazole biosynthetic enzyme. chloroplast precursor (AG6)	430.823	597.000	0.722	368.631	627.000	0.588	0.655
5	11	2	PT006B03	a76couture2756.r#1	>ref|NP_564876.1|| (NM_105322) expressed protein; protein id: At1g66510.1. supported	58.692	72.000	0.815	46.336	65.000	0.713	0.764
5	11	3	BM437875 BM436973 BM437243 BM436711 BM	couture_a76.1.c1.r#1	>gb|AAL07213.1| (AY056134) unknown protein [Arabidopsis thaliana]	3711.325	5284.000	0.702	3409.323	5615.000	0.607	0.655
5	11	4	TT281D04	a76couture3019.r#1	>dbj|BAB86528.1| (AP003381) putative vesicle transport v-SNARE protein [Oryza sativa	1101.409	1886.000	0.584	1169.734	1867.000	0.627	0.605
5	11	5	TT254C02	a76couture2891.r#1	>ref|NP_565372.1|| (NM_127089) expressed protein; protein id: At2g15290.1. supported	272.230	367.000	0.742	316.117	394.000	0.802	0.772
5	11	6	PT012C01	a76couture2752.r#1	>ref|NP_201291.1|| (NM_125884) glycosyl hydrolase family 77	91.160	136.000	0.670	123.563	165.000	0.749	0.710
5	11	7	GB004g07	a76couture3194.r#1	>emb|CAA10231.1| (AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]	43.707	87.000	0.502	45.307	77.000	0.588	0.545
5	11	8	PT009B07	a76couture3013.r#1	>dbj|BAA74802.1| (AB018422) DNA binding zinc finger protein (Pspzf) [Pisum sativum]	29.970	64.000	0.468	32.950	58.000	0.568	0.518
5	11	9	PT011A02	a76couture2883.r#1	>pir||A61144 probable flagellar protein (clone FCH-F8-4) - Trypanosoma cruzi	27.473	54.000	0.509	25.742	50.000	0.515	0.512
5	11	10	PT013E05	a76couture2747.r#1	>pir||T47796 ABC transporter-like protein - Arabidopsis thaliana	826.681	724.000	1.142	671.362	767.000	0.875	1.009
5	11	11	MY003B03C	a76couture3170.r#1	>gb|AAA82943.1| (U39448) MYB-like transcriptional factor MBF1 [Picea mariana]	243.509	237.000	1.027	174.019	221.000	0.787	0.907
5	11	12	PT006E04	a76couture3005.r#1	------	59.941	62.000	0.967	49.425	59.000	0.838	0.902
5	11	13	PT009A09	a76couture2872.r#1	>sp|P49215|RS17_LYCES 40S ribosomal protein S17 >gi|5758304|gb|AAD50774.1|AF161704_1	5438.365	4643.000	1.171	7780.382	7548.000	1.031	1.101
5	11	14	PT007B12	a76couture2743.r#1	>ref|NP_192229.2|| (NM_116556) unknown protein; protein id: At4g03200.1. supported by	410.843	376.000	1.093	324.354	377.000	0.860	0.977
5	11	15	MB001A01C	a76couture3166.r#1	>ref|NP_196342.1|| (NM_120807) membrane protein; protein id: At5g07250.1. supported by	206.046	161.000	1.280	179.167	170.000	1.054	1.167
5	12	1	RB004B01	a76couture3002.r#1	------	27.473	59.000	0.466	23.683	56.000	0.423	0.444
5	12	2	PT007A12	a76couture2867.r#1	>sp|Q96552|METL_CATRO S-adenosylmethionine synthetase 2 (Methionine adenosyltransferase	3078.202	4063.000	0.758	2695.744	4228.000	0.638	0.698
5	12	3	PT008E05	a76couture2739.r#1	>ref|NP_193962.1|| (NM_118357) putative protein; protein id: At4g22310.1. supported by	664.342	847.000	0.784	743.440	993.000	0.749	0.767
5	12	4	AW708006 BM436772 BG273911 GB000A78 GT2	couture_a76.469.c3#1	>sp|O49169|EF1A_MANES ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi|2791834|gb|AAC39447.1|	8466.617	11924.000	0.710	9026.314	11752.000	0.768	0.739
5	12	5	BM436468 BM436690 GT193C03	couture_a76.383.c1.r#1	>gb|AAK82449.1|AC091247_16 (AC091247) putative phospholipase [Oryza sativa]	579.426	868.000	0.668	827.875	1099.000	0.753	0.710
5	12	6	TB004g02 TB004G02	couture_a76.301.c1.r#1	>ref|NP_181526.1|| (NM_129555) 36kDa-peroxisomal membrane protein (PMP36); protein id:	495.759	714.000	0.694	638.411	900.000	0.709	0.702
5	12	7	BG273922 GB000A65	couture_a76.208.c1.r#1	>gb|AAK27801.1|AC022457_4 (AC022457) 60S ribosomal protein L21 [Oryza sativa (japonica	2196.575	2027.000	1.084	2269.450	2298.000	0.988	1.036
5	12	8	TB005f09 TB005F09	couture_a76.466.c1.r#1	>pir||T12180 probable transcription factor - fava bean	3273.009	3076.000	1.064	3053.048	3459.000	0.883	0.973
5	12	9	RT022H09 BM436726 BM437622 BM436257 BM	couture_a76.38.c1#1	------	69.931	73.000	0.958	62.811	72.000	0.872	0.915
5	12	10	TB005a07 RT062E10	couture_a76.297.c1#1	>pir||S39508 alcohol dehydrogenase homolog. ripening-related - tomato	1737.030	1022.000	1.700	1649.573	1241.000	1.329	1.514

5	12	11	BM436824 RT092A07	couture_a76.202.c1.r#1	>ref|NP_199595.1|| (NM_124158) putative protein; protein id: At5g47840.1. supported by	408.346	450.000	0.907	283.166	422.000	0.671	0.789
5	12	12	BM437198 TB005A10	couture_a76.463.c1#1	>ref|NP_056986.2|| (NM_015902) progestin induced protein; ubiquitin-protein ligase [Homo	32.468	38.000	0.854	27.802	33.000	0.842	0.848
5	12	13	BM438114 BM437089 BM437791 GT162E12	couture_a76.375.c1.r#1	>gb|AAG38521.1|AF283536_1 (AF283536) cystatin-like protein [Citrus x paradisi]	22.478	39.000	0.576	19.564	30.000	0.652	0.614
5	12	14	BM436989 BM436326 BM437882 BM436464 RT	couture_a76.290.c1.r#1	>gb|AAK25798.1|AF338237_1 (AF338237) rubisco activase [Zantedeschia aethiopica]	837.920	580.000	1.445	724.906	698.000	1.039	1.242
5	12	15	BM437516 RT083A05	couture_a76.198.c1#1	>ref|NP_172371.1|| (NM_100768) putative transcription factor; protein id: At1g08970.1	681.825	588.000	1.160	563.244	662.000	0.851	1.005
5	13	1	GB001g05 RT052H03	couture_a76.46.c1#1	>gb|AAB47171.1| vacuolar invertase 1. GIN1 [Vitis viniferagrape berries. Sultana	454.550	867.000	0.524	451.007	964.000	0.468	0.496
5	13	2	GB007g07 GB007G07	couture_a76.371.c1.r#1	>ref|NP_566976.1|| (NM_115159) pyruvate kinase - like protein; protein id:	59.941	138.000	0.434	54.574	144.000	0.379	0.407
5	13	3	BM437809 BM437877 TB000A93 BG273802 RT0	couture_a76.287.c1.r#1	>ref|NP_180789.1|| (NM_128789) putative uclacyanin I; protein id: At2g32300.1	450.804	621.000	0.726	505.581	685.000	0.738	0.732
5	13	4	BM437951 RT071E04	couture_a76.194.c1.r#1	>ref|NP_195802.1|| (NM_120260) putative protein; protein id: At5g01820.1. supported by	151.100	181.000	0.835	207.999	216.000	0.963	0.899
5	13	5	BM436765 RT063B02	couture_a76.457.c1.r#1	>ref|NP_187644.1|| (NM_111868) transcription initiation factor IIB (TFIIB); protein	797.960	829.000	0.963	1046.171	1056.000	0.991	0.977
5	13	6	GB006d03 GB006D03	couture_a76.368.c1.r#1	>gb|AAD30584.1|AC007260_15 (AC007260) Very similar to prenyltransferases [Arabidopsis	168.583	177.000	0.952	186.375	215.000	0.867	0.910
5	13	7	BM437612 RT021B01	couture_a76.280.c1#1	>gb|AAF34771.1|AF227626_1 (AF227626) 40S ribosomal protein S11 [Euphorbia esula]	2290.232	2038.000	1.124	2471.270	2286.000	1.081	1.102
5	13	8	BM436513 BM437097 BM437673 BM437161 BM	couture_a76.19.c1.r#1	>gb|AAL67991.1| (AY072821) dehydration-induced protein RD22-like protein [Gossypium	7709.866	9017.000	0.855	8095.469	10598.000	0.764	0.809
5	13	9	BM438031 RT061G08	couture_a76.454.c1#1	>ref|NP_194280.1|| (NM_118682) arginine/serine-rich splicing factor RSp40; protein id:	525.729	424.000	1.240	542.650	501.000	1.083	1.162
5	13	10	GB003g09 GB003G09	couture_a76.362.c1.r#1	>gb|AAK27720.1|AF356004_1 (AF356004) ADP-glucose pyrophosphorylase small subunit CagpS1	1166.345	1193.000	0.978	965.855	1230.000	0.785	0.881
5	13	11	RB003C07 RB008D08	couture_a76.276.c1#1	>ref|NP_190400.1|| (NM_114686) betaine aldehyde dehydrogenase-like protein; protein	282.221	288.000	0.980	272.869	341.000	0.800	0.890
5	13	12	RB004D09 RT094H09	couture_a76.187.c1#1	>pir||T07123 nine-cis-epoxycarotenoid dioxygenase - tomato	374.629	368.000	1.018	336.711	445.000	0.757	0.887
5	13	13	BM437165 PT001G06	couture_a76.74.c1.r#1	>ref|NP_566079.1|| (NM_130219) expressed protein; protein id: At2g46540.1. supported	608.148	478.000	1.272	493.224	559.000	0.882	1.077
5	13	14	RT083H02 ST005A09	couture_a76.561.c1.r#1	>sp|Q9XF97|RL4_PRUAR 60S ribosomal protein L4 (L1) >gi|4887131|gb|AAD32206.1|AF134732_1	5764.293	4460.000	1.292	4989.906	5003.000	0.997	1.145
5	13	15	G499021E VVLDOX	couture_a76.sd.85.c1#	>sp|P51093|LDOX_VITVI LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN	1182.579	1323.000	0.894	738.292	1206.000	0.612	0.753
5	14	1	TB005g10 PT013A01	couture_a76.73.c1.r#1	>emb|CAC10208.1| (AJ299059) cytosolic malate dehydrogenase [Cicer arietinum]	700.556	1245.000	0.563	636.352	1285.000	0.495	0.529
5	14	2	BG273744 CM002G06	couture_a76.534.c1.r#1	>ref|NP_180353.1|| (NM_128345) putative dTDP-glucose 4-6-dehydratase; protein id:	1647.119	2414.000	0.682	1327.278	2430.000	0.546	0.614
5	14	3	BG273919 PT005G09 VVI237987	couture_a76.sd.53.c1#	------	5483.321	9458.000	0.580	6694.053	10778.000	0.621	0.600
5	14	4	BM437739 RT063G05	couture_a76.63.c1.r#1	>pir||T16993 GTP-binding protein Sar1. pollination-induced - apple tree	274.728	452.000	0.608	323.324	485.000	0.667	0.637
5	14	5	BM437252 CM001C01 RT081G03	couture_a76.557.c1.r#1	>emb|CAA98160.1| (Z73932) RAB1C [Lotus japonicus]	543.212	697.000	0.779	808.311	922.000	0.877	0.828
5	14	6	TB000A72 BG273822 GT184B11 AF159123	couture_a76.sd.74.c1#	>sp|Q43111|PME3_PHAVU Pectinesterase 3 precursor (Pectin methylesterase 3) (PE 3)	403.351	337.000	1.197	643.560	566.000	1.137	1.167
5	14	7	BM436319 GB002a05 RT043E07 BM436504	couture_a76.624.c1#1	>pir||S37224 triose phosphate/3-phosphoglycerate/phosphate translocator - common	479.525	664.000	0.722	606.491	866.000	0.700	0.711
5	14	8	TB001e01 TT283A12	couture_a76.529.c1#1	>gb|AAF04147.1| (AF193438) ubiquitin precursor [Hevea brasiliensis]	1628.388	1436.000	1.134	1626.919	1565.000	1.040	1.087
5	14	9	PT006E03 BG273849 VVI237999 AF003007	couture_a76.sd.45.c1#	>emb|CAB85637.1| (AJ237999) putative thaumatin-like protein [Vitis vinifera]	22426.545	22655.000	0.990	26165.601	29062.000	0.900	0.945
5	14	10	PT003H03 RT084A08	couture_a76.597.c1.r#1	>emb|CAD40586.1| (AL662945) oj000126_13.8 [Oryza sativa]	924.085	813.000	1.137	817.578	812.000	1.007	1.072
5	14	11	BG273861 TB000A31	couture_a76.499.c1#1	>ref|NP_194744.1|| (NM_119161) hypothetical protein; protein id: At4g30150.1	78.672	68.000	1.157	82.376	77.000	1.070	1.113
5	14	12	GB000A49 BG273936 PT012C03	couture_a76.80.c1.r#1	>ref|NP_180219.1|| (NM_128208) putative membrane transporter; protein id: At2g26510.1	2682.344	2604.000	1.030	2322.994	2814.000	0.826	0.928
5	14	13	BM436336 BM437696 TT264F04 TB003h06	couture_a76.568.c1.r#1	>pir||T51628 endoplasmatic reticulum retrieval protein Rer1B [validated] -	1012.747	834.000	1.214	915.400	994.000	0.921	1.068
5	14	14	BM437931 BM438107 BM437188 BM437102 PT0	couture_a76.79.c1.r#1	>sp|P43390|MT2_ACTCH Metallothionein-like protein type 2 PKIWI504	309.693	102.000	3.036	286.255	115.000	2.489	2.763
5	14	15	CM005h12 TT261D06	couture_a76.563.c1#1	>emb|CAA05979.1| (AJ003197) adenine nucleotide translocator [Lupinus albus]	2365.158	1800.000	1.314	1936.858	2036.000	0.951	1.133
6	1	1	CM004G12	a76couture0472.r#1	------	514.491	398.000	1.293	376.869	393.000	0.959	1.126
6	1	2	ST002C04	a76couture0374.r#1	>pir||JQ0986 lipid body-associated membrane protein - carrot	8404.179	5677.000	1.480	6968.981	6454.000	1.080	1.280
6	1	3	PT010F10	a76couture0249.r#1	>ref|NP_177947.1|| (NM_106473) unknown protein; protein id: At1g78230.1. supported by	797.960	579.000	1.378	666.213	665.000	1.002	1.190
6	1	4	CT003C12	a76couture0102.r#1	>ref|NP_198460.1|| (NM_123002) cytochrome p450 family; protein id: At5g36110.1	924.085	685.000	1.349	715.639	660.000	1.084	1.217
6	1	5	CM004F03	a76couture0468.r#1	------	3100.680	3155.000	0.983	2519.666	3109.000	0.810	0.897
6	1	6	CT005A06	a76couture0370.r#1	>dbj|BAB78504.1| (AB071016) 26S proteasome regulatory particle triple-A ATPase	3205.576	2713.000	1.182	2489.805	2512.000	0.991	1.086
6	1	7	PT005H10	a76couture0243.r#1	>ref|NP_224038.1|| (NC_000921) putative histidine-rich metal-binding protein	1304.958	846.000	1.543	1192.388	1051.000	1.135	1.339
6	1	8	CT002A05	a76couture0097.r#1	>gb|AAG52266.1|AC019018_3 (AC019018) putative deoxyoctulonosic acid synthetase; 116195-114393	86.165	69.000	1.249	91.643	84.000	1.091	1.170
6	1	9	CM004D08	a76couture0464.r#1	>ref|NP_188875.1|| (NM_113134) alternative oxidase 1b precursor; protein id:	388.365	147.000	2.642	501.462	210.000	2.388	2.515
6	1	10	CT002A11	a76couture0366.r#1	>pir||T00964 hypothetical protein F20D22.14 - Arabidopsis thaliana	4213.328	3636.000	1.159	4988.876	4356.000	1.145	1.152
6	1	11	PT012D10	a76couture0238.r#1	>ref|NP_567797.1|| (NM_118950) expressed protein; protein id: At4g28100.1. supported	333.420	265.000	1.258	377.898	289.000	1.308	1.283
6	1	12	CM004H09	a76couture0093.r#1	>gb|AAK73102.1|AF390556_1 (AF390556) Bax inhibitor 1 [Nicotiana tabacum]	7284.038	4288.000	1.699	8392.021	5879.000	1.427	1.563
6	1	13	CM004B07	a76couture0460.r#1	>ref|NP_680194.1|| (NM_147889) unknown protein; protein id: At5g22080.1 [Arabidopsis	14.985	26.000	0.576	17.505	25.000	0.700	0.638
6	1	14	CM004B01	a76couture0362.r#1	>ref|NP_566945.1|| (NM_114973) putative protein; protein id: At3g51130.1. supported by	277.226	246.000	1.127	318.176	338.000	0.941	1.034
6	1	15	PT012E10	a76couture0232#1	>gb|AAM21344.1|AF373603_1 (AF373603) MADS-box protein 4 [Vitis vinifera]	3334.199	2701.000	1.234	3603.935	3482.000	1.035	1.135
6	2	1	CM003G08	a76couture0088.r#1	>ref|NP_188902.1|| (NM_113162) 20S proteasome beta subunit D (PBD1); protein id:	3537.747	2588.000	1.367	3064.375	2971.000	1.031	1.199
6	2	2	CM003H11	a76couture0456.r#1	>pir||S65675 aspartate transaminase (EC 2.6.1.1) - proso millet	1055.205	993.000	1.063	899.954	1085.000	0.829	0.946
6	2	3	CM002A03	a76couture0358.r#1	>gb|AAM63085.1| (AY085872) putative ubiquinol--cytochrome-c reductase [Arabidopsis	2244.028	1927.000	1.165	1889.492	2114.000	0.894	1.029
6	2	4	Arabidopsis Control Oligonucleotide	3ara7		203.548	146.000	1.394	198.731	166.000	1.197	1.296
6	2	5	CM002H05	a76couture0084.r#1	>ref|NP_175576.1|| (NM_104043) epsilon subunit of mitochondrial F1-ATPase; protein id:	1068.942	759.000	1.408	862.885	801.000	1.077	1.243
6	2	6	CM003H02	a76couture0451.r#1	>ref|NP_566066.1|| (NM_130184) Expressed protein; protein id: At2g46220.1. supported	99.901	52.000	1.921	105.029	65.000	1.616	1.769
6	2	7	TT263F05	a76couture0354.r#1	>ref|NP_201551.1|| (NM_126150) porin-like protein; protein id: At5g67500.1. supported	2608.667	1854.000	1.407	2113.966	2110.000	1.002	1.204
6	2	8	PT001G09	a76couture0221.r#1	------	598.158	345.000	1.734	621.936	474.000	1.312	1.523
6	2	9	CT005D12	a76couture0073.r#1	>ref|NP_200716.1|| (NM_125298) putative protein; protein id: At5g59080.1. supported by	1735.781	1598.000	1.086	2135.589	2244.000	0.952	1.019
6	2	10	TT272G01	a76couture0904.r#1	>pir||T09262 glycine-rich cell wall protein EMB31 - white spruce	679.327	487.000	1.395	1047.201	763.000	1.372	1.384
6	2	11	GB005F12	a76couture0777.r#1	>ref|NP_566396.1|| (NM_111998) VAMP protein SEC22; protein id: At3g11660.1. supported	16.234	25.000	0.649	23.683	31.000	0.764	0.707
6	2	12	ST004G09	a76couture0672.r#1	>ref|NP_196843.1|| (NM_121342) putative protein; protein id: At5g13390.1 [Arabidopsis	748.009	583.000	1.283	803.163	754.000	1.065	1.174
6	2	13	CT005E11	a76couture0573.r#1	>ref|NP_176645.1|| (NM_105139) unknown protein; protein id: At1g64640.1 [Arabidopsis	488.267	365.000	1.338	681.659	650.000	1.049	1.193
6	2	14	TT284A05	a76couture0899.r#1	>gb|AAG50872.1|AC025294_10 (AC025294) tRNA-guaninine transglycosylase. putative [Arabidopsis	805.452	645.000	1.249	954.528	912.000	1.047	1.148
6	2	15	RT074F08	a76couture0772.r#1	>ref|NP_568148.1|| (NM_120590) E2. ubiquitin-conjugating enzyme. putative; protein id:		13.000	0.000				
6	3	1	ST004F05	a76couture0667.r#1	>ref|NP_680760.1|| (NM_148394) putative protein; protein id: At4g33780.2. supported by	211.041	184.000	1.147	183.286	202.000	0.907	1.027
6	3	2	CT005D01	a76couture0568.r#1	------	91.160	88.000	1.036	51.485	61.000	0.844	0.940
6	3	3	RT094C03	a76couture0893.r#1	>emb|CAA66045.1| (X97377) atranbp1a [Arabidopsis thaliana]	34.965	34.000	1.028	24.713	27.000	0.915	0.972

<table>
<tr><td>6</td><td>3</td><td>4</td><td>RT074E05</td><td>a76couture0768.r#1</td><td>>ref|NP_197039.1|| (NM_121539) putative protein; protein id: At5g15350.1. supported by</td><td>1127.633</td><td>896.000</td><td>1.259</td><td>1023.518</td><td>903.000</td><td>1.133</td><td>1.196</td></tr>
<tr><td>6</td><td>3</td><td>5</td><td>ST004E04</td><td>a76couture0663.r#1</td><td>>gb|AAM93209.1|AF527542_1 (AF527542) glyoxysomal malate dehydrogenase [Medicago sativa]</td><td>264.738</td><td>224.000</td><td>1.182</td><td>216.236</td><td>207.000</td><td>1.045</td><td>1.113</td></tr>
<tr><td>6</td><td>3</td><td>6</td><td>CT005B02</td><td>a76couture0564.r#1</td><td>>ref|NP_195833.1|| (NM_120291) putative protein; protein id: At5g02130.1. supported by</td><td>700.556</td><td>755.000</td><td>0.928</td><td>650.768</td><td>786.000</td><td>0.828</td><td>0.878</td></tr>
<tr><td>6</td><td>3</td><td>7</td><td>RT094B12</td><td>a76couture0887.r#1</td><td>>sp|P51118|GLN1_VITVI GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME 1 (GLUTAMATE--AMMONIA</td><td>1496.019</td><td>1051.000</td><td>1.423</td><td>1422.010</td><td>1325.000</td><td>1.073</td><td>1.248</td></tr>
<tr><td>6</td><td>3</td><td>8</td><td>RT074B06</td><td>a76couture0763.r#1</td><td>>emb|CAA69976.1| (Y08726) MtN3 [Medicago truncatula]</td><td>2456.318</td><td>2111.000</td><td>1.164</td><td>2579.388</td><td>2940.000</td><td>0.877</td><td>1.020</td></tr>
<tr><td>6</td><td>3</td><td>9</td><td>ST004C08</td><td>a76couture0659.r#1</td><td>------</td><td>16.234</td><td>22.000</td><td>0.738</td><td>4.119</td><td>13.000</td><td>0.317</td><td>0.527</td></tr>
<tr><td>6</td><td>3</td><td>10</td><td>CT004H07</td><td>a76couture0560.r#1</td><td>>sp|P29060|CHIA_TOBAC ACIDIC ENDOCHITINASE PRECURSOR >gi|82156|pir||S23544 chitinase (EC</td><td>317.186</td><td>281.000</td><td>1.129</td><td>240.949</td><td>312.000</td><td>0.772</td><td>0.951</td></tr>
<tr><td>6</td><td>3</td><td>11</td><td>RT093G02</td><td>a76couture0881.r#1</td><td>>dbj|BAB10407.1| (AB011474) emb|CAB63010.1~gene_id:K2A18.9~strong similarity to</td><td>189.812</td><td>151.000</td><td>1.257</td><td>218.296</td><td>205.000</td><td>1.065</td><td>1.161</td></tr>
<tr><td>6</td><td>3</td><td>12</td><td>RT073B07</td><td>a76couture0758.r#1</td><td>>sp|Q42962|PGKY_TOBAC Phosphoglycerate kinase. cytosolic >gi|7434547|pir||T03661</td><td>2187.834</td><td>1715.000</td><td>1.276</td><td>3043.781</td><td>2957.000</td><td>1.029</td><td>1.153</td></tr>
<tr><td>6</td><td>3</td><td>13</td><td>ST004A10</td><td>a76couture0655.r#1</td><td>>ref|NP_190965.1|| (NM_115257) putative protein; protein id: At3g53970.1. supported by</td><td>728.029</td><td>522.000</td><td>1.395</td><td>909.221</td><td>806.000</td><td>1.128</td><td>1.261</td></tr>
<tr><td>6</td><td>3</td><td>14</td><td>CT004F12</td><td>a76couture0556.r#1</td><td>------</td><td>3.746</td><td>16.000</td><td>0.234</td><td>3.089</td><td>12.000</td><td>0.257</td><td>0.246</td></tr>
<tr><td>6</td><td>3</td><td>15</td><td>RT092H01</td><td>a76couture0875.r#1</td><td>>ref|NP_566305.1|| (NM_111616) expressed protein; protein id: At3g07370.1. supported</td><td>66.184</td><td>60.000</td><td>1.103</td><td>81.346</td><td>73.000</td><td>1.114</td><td>1.109</td></tr>
<tr><td>6</td><td>4</td><td>1</td><td>RT072D03</td><td>a76couture0752.r#1</td><td>>gb|AAC36698.1| (AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum</td><td>104.896</td><td>97.000</td><td>1.081</td><td>87.524</td><td>96.000</td><td>0.912</td><td>0.997</td></tr>
<tr><td>6</td><td>4</td><td>2</td><td>ST003H11</td><td>a76couture0651.r#1</td><td>>dbj|BAB40150.1| (AP002910) hypothetical protein [Oryza sativa (japonica</td><td>9.990</td><td>23.000</td><td>0.434</td><td>8.238</td><td>19.000</td><td>0.434</td><td>0.434</td></tr>
<tr><td>6</td><td>4</td><td>3</td><td>CT004E07</td><td>a76couture0551.r#1</td><td>>ref|NP_186792.1|| (NM_111009) hypothetical protein; protein id: At3g01430.1</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>6</td><td>4</td><td>4</td><td>RT051E06</td><td>a76couture1357.r#1</td><td>>ref|NP_199592.1|| (NM_124155) pyrophosphate-fructose-6-phosphate</td><td>1250.012</td><td>1447.000</td><td>0.864</td><td>1223.279</td><td>1502.000</td><td>0.814</td><td>0.839</td></tr>
<tr><td>6</td><td>4</td><td>5</td><td>GT202H11</td><td>a76couture1235.r#1</td><td>>ref|NP_180811.1|| (NM_128811) putative carboxymethylenebutenolidase; protein id:</td><td>6073.986</td><td>5229.000</td><td>1.162</td><td>5048.599</td><td>5476.000</td><td>0.922</td><td>1.042</td></tr>
<tr><td>6</td><td>4</td><td>6</td><td>GB007A12</td><td>a76couture1110.r#1</td><td>------</td><td>83.667</td><td>148.000</td><td>0.565</td><td>90.613</td><td>171.000</td><td>0.530</td><td>0.548</td></tr>
<tr><td>6</td><td>4</td><td>7</td><td>RT083H07</td><td>a76couture0999.r#1</td><td>>ref|NP_187643.1|| (NM_111867) unknown protein; protein id: At3g10320.1 [Arabidopsis</td><td>985.274</td><td>678.000</td><td>1.453</td><td>966.884</td><td>873.000</td><td>1.108</td><td>1.280</td></tr>
<tr><td>6</td><td>4</td><td>8</td><td>RT051B07</td><td>a76couture1353.r#1</td><td>>ref|NP_568694.1|| (NM_124198) acetyl-CoA C-acetyltransferase; protein id:</td><td>4896.402</td><td>3213.000</td><td>1.524</td><td>5788.950</td><td>5103.000</td><td>1.134</td><td>1.329</td></tr>
<tr><td>6</td><td>4</td><td>9</td><td>GT201H04</td><td>a76couture1226.r#1</td><td>>ref|NP_566324.1|| (NM_111670) expressed protein; protein id: At3g07910.1. supported</td><td>454.550</td><td>311.000</td><td>1.462</td><td>491.165</td><td>430.000</td><td>1.142</td><td>1.302</td></tr>
<tr><td>6</td><td>4</td><td>10</td><td>GB006C03</td><td>a76couture1106.r#1</td><td>>ref|NP_198815.1|| (NM_123362) N-acetylglucosaminyltransferase family</td><td>419.585</td><td>299.000</td><td>1.403</td><td>610.610</td><td>526.000</td><td>1.161</td><td>1.282</td></tr>
<tr><td>6</td><td>4</td><td>11</td><td>RT083G08</td><td>a76couture0997.r#1</td><td>>ref|NP_201182.1|| (NM_125772) diacylglycerol kinase; protein id: At5g63770.1</td><td>529.476</td><td>538.000</td><td>0.984</td><td>626.055</td><td>798.000</td><td>0.785</td><td>0.884</td></tr>
<tr><td>6</td><td>4</td><td>12</td><td>RT043E05</td><td>a76couture1349.r#1</td><td>>ref|NP_192112.1|| (NM_116434) hypothetical protein; protein id: At4g02030.1</td><td>676.830</td><td>481.000</td><td>1.407</td><td>779.480</td><td>702.000</td><td>1.110</td><td>1.259</td></tr>
<tr><td>6</td><td>4</td><td>13</td><td>GT201B07</td><td>a76couture1219.r#1</td><td>>ref|NP_567038.1|| (NM_115507) protein kinase C inhibitor-like protein; protein id:</td><td>6886.931</td><td>5226.000</td><td>1.318</td><td>8732.850</td><td>8372.000</td><td>1.043</td><td>1.180</td></tr>
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<tr><td>6</td><td>4</td><td>15</td><td>RT083F02</td><td>a76couture0994.r#1</td><td>>gb|AAF26772.1|AC007396_21 (AC007396) T4O12.5 [Arabidopsis thaliana]</td><td>254.748</td><td>214.000</td><td>1.190</td><td>328.473</td><td>299.000</td><td>1.099</td><td>1.144</td></tr>
<tr><td>6</td><td>5</td><td>1</td><td>RT042C12</td><td>a76couture1345.r#1</td><td>>ref|NP_179558.1|| (NM_127526) copia-like retroelement pol polyprotein; protein id:</td><td>1776.991</td><td>1353.000</td><td>1.313</td><td>1565.138</td><td>1581.000</td><td>0.990</td><td>1.152</td></tr>
<tr><td>6</td><td>5</td><td>2</td><td>GT202D06</td><td>a76couture1212.r#1</td><td>>ref|NP_568775.1|| (NM_124635) putative protein; protein id: At5g52560.1. supported by</td><td>1478.536</td><td>1176.000</td><td>1.257</td><td>1227.397</td><td>1328.000</td><td>0.924</td><td>1.091</td></tr>
<tr><td>6</td><td>5</td><td>3</td><td>GB003B08</td><td>a76couture1093.r#1</td><td>>ref|NP_567067.1|| (NM_115713) DEAD/DEAH box RNA helicase protein. putative; protein</td><td>380.873</td><td>288.000</td><td>1.322</td><td>351.126</td><td>336.000</td><td>1.045</td><td>1.184</td></tr>
<tr><td>6</td><td>5</td><td>4</td><td>RT083C10</td><td>a76couture0989.r#1</td><td>>pir||PQ0446 DNA-binding protein B2F - common tobacco (fragment)</td><td>479.525</td><td>396.000</td><td>1.211</td><td>478.809</td><td>437.000</td><td>1.096</td><td>1.153</td></tr>
<tr><td>6</td><td>5</td><td>5</td><td>RT042C06</td><td>a76couture1341.r#1</td><td>>dbj|BAC15484.1| (AP003833) contains ESTs AU091627(C0596).D15410(C0596A)~similar to</td><td>2004.266</td><td>2047.000</td><td>0.979</td><td>1680.464</td><td>2124.000</td><td>0.791</td><td>0.885</td></tr>
<tr><td>6</td><td>5</td><td>6</td><td>GT194C12</td><td>a76couture1208#1</td><td>------</td><td>83.667</td><td>63.000</td><td>1.328</td><td>96.791</td><td>76.000</td><td>1.274</td><td>1.301</td></tr>
<tr><td>6</td><td>5</td><td>7</td><td>GB001D04</td><td>a76couture1086.r#1</td><td>>ref|NP_565659.1|| (NM_128337) Expressed protein; protein id: At2g27775.1. supported</td><td>328.425</td><td>224.000</td><td>1.466</td><td>328.473</td><td>272.000</td><td>1.208</td><td>1.337</td></tr>
<tr><td>6</td><td>5</td><td>8</td><td>RT083C03</td><td>a76couture0986.r#1</td><td>>ref|NP_173030.1|| (NM_101446) hypothetical protein; protein id: At1g15780.1</td><td>280.972</td><td>223.000</td><td>1.260</td><td>274.929</td><td>296.000</td><td>0.929</td><td>1.094</td></tr>
<tr><td>6</td><td>5</td><td>9</td><td>RT034F07</td><td>a76couture1336.r#1</td><td>>ref|NP_568377.1|| (NM_121965) putative protein; protein id: At5g19600.1. supported by</td><td>715.542</td><td>487.000</td><td>1.469</td><td>969.973</td><td>867.000</td><td>1.119</td><td>1.294</td></tr>
<tr><td>6</td><td>5</td><td>10</td><td>GT193H08</td><td>a76couture1203.r#1</td><td>>ref|NP_195215.1|| (NM_119655) xanthine dehydrogenase - like protein; protein id:</td><td>490.764</td><td>348.000</td><td>1.410</td><td>480.868</td><td>425.000</td><td>1.131</td><td>1.271</td></tr>
<tr><td>6</td><td>5</td><td>11</td><td>Arabidopsis Control Oligonucleotide</td><td>3ara7</td><td></td><td>9.990</td><td>17.000</td><td>0.588</td><td>18.535</td><td>18.000</td><td>1.030</td><td>0.809</td></tr>
<tr><td>6</td><td>5</td><td>12</td><td>RT083B05</td><td>a76couture0983.r#1</td><td>>ref|NP_566369.1|| (NM_111856) expressed protein; protein id: At3g10210.1. supported</td><td>608.148</td><td>501.000</td><td>1.214</td><td>704.312</td><td>674.000</td><td>1.045</td><td>1.129</td></tr>
<tr><td>6</td><td>5</td><td>13</td><td>GT183D05</td><td>a76couture1800.r#1</td><td>>ref|XP_159060.1|| (XM_159060) hypothetical protein XP_159060 [Mus musculus]</td><td>81.170</td><td>70.000</td><td>1.160</td><td>165.781</td><td>132.000</td><td>1.256</td><td>1.208</td></tr>
<tr><td>6</td><td>5</td><td>14</td><td>GT172A02</td><td>a76couture1711#1</td><td>>emb|CAC84143.2| (AJ309009) thioredoxin peroxidase [Nicotiana tabacum]</td><td>410.843</td><td>261.000</td><td>1.574</td><td>620.907</td><td>530.000</td><td>1.172</td><td>1.373</td></tr>
<tr><td>6</td><td>5</td><td>15</td><td>GB006F02</td><td>a76couture1615.r#1</td><td>>ref|NP_568659.1|| (NM_123992) expressed protein; protein id: At5g46230.1. supported</td><td>694.313</td><td>674.000</td><td>1.030</td><td>1137.814</td><td>1110.000</td><td>1.025</td><td>1.028</td></tr>
<tr><td>6</td><td>6</td><td>1</td><td>TT273B06</td><td>a76couture1476.r#1</td><td>>dbj|BAB17667.1| (AB037538) PEX14 [Arabidopsis thaliana]</td><td>1688.328</td><td>1298.000</td><td>1.301</td><td>1518.801</td><td>1515.000</td><td>1.003</td><td>1.152</td></tr>
<tr><td>6</td><td>6</td><td>2</td><td>GT182G02</td><td>a76couture1796.r#1</td><td>------</td><td>43.707</td><td>52.000</td><td>0.841</td><td>43.247</td><td>60.000</td><td>0.721</td><td>0.781</td></tr>
<tr><td>6</td><td>6</td><td>3</td><td>GT171E03</td><td>a76couture1706.r#1</td><td>>ref|NP_178637.1|| (NM_126593) glycosyl hydrolase family 17; protein id: At2g05790.1</td><td>379.624</td><td>509.000</td><td>0.746</td><td>313.028</td><td>536.000</td><td>0.584</td><td>0.665</td></tr>
<tr><td>6</td><td>6</td><td>4</td><td>GB006D05</td><td>a76couture1611.r#1</td><td>>ref|NP_173559.1|| (NM_101989) hypothetical protein; protein id: At1g21370.1</td><td>41.209</td><td>43.000</td><td>0.958</td><td>43.247</td><td>43.000</td><td>1.006</td><td>0.982</td></tr>
<tr><td>6</td><td>6</td><td>5</td><td>TT274D09</td><td>a76couture1471.r#1</td><td>>ref|NP_179220.1|| (NM_127181) leucine-rich repeat transmembrane protein kinase</td><td>24.975</td><td>30.000</td><td>0.833</td><td>20.594</td><td>27.000</td><td>0.763</td><td>0.798</td></tr>
<tr><td>6</td><td>6</td><td>6</td><td>GT182A02</td><td>a76couture1793.r#1</td><td>>ref|NP_196756.1|| (NM_121233) lysine decarboxylase - like protein; protein id:</td><td>242.260</td><td>186.000</td><td>1.302</td><td>275.958</td><td>246.000</td><td>1.122</td><td>1.212</td></tr>
<tr><td>6</td><td>6</td><td>7</td><td>GT171D08</td><td>a76couture1702.r#1</td><td>>ref|NP_566700.1|| (NM_113117) aminotransferase. putative; protein id: At3g22200.1</td><td>806.701</td><td>769.000</td><td>1.049</td><td>876.271</td><td>1079.000</td><td>0.812</td><td>0.931</td></tr>
<tr><td>6</td><td>6</td><td>8</td><td>GB006B06</td><td>a76couture1607.r#1</td><td>------</td><td>598.158</td><td>466.000</td><td>1.284</td><td>580.748</td><td>603.000</td><td>0.963</td><td>1.123</td></tr>
<tr><td>6</td><td>6</td><td>9</td><td>TT264H04</td><td>a76couture1466.r#1</td><td>>ref|NP_194945.2|| (NM_119370) putative protein; protein id: At4g32180.1. supported by</td><td>29.970</td><td>43.000</td><td>0.697</td><td>37.069</td><td>53.000</td><td>0.699</td><td>0.698</td></tr>
<tr><td>6</td><td>6</td><td>10</td><td>GT174C01</td><td>a76couture1789.r#1</td><td>------</td><td>1431.083</td><td>1074.000</td><td>1.332</td><td>1415.832</td><td>1296.000</td><td>1.092</td><td>1.212</td></tr>
<tr><td>6</td><td>6</td><td>11</td><td>GT171A11</td><td>a76couture1698.r#1</td><td>>gb|AAF34801.1|AF227981_1 (AF227981) F21J9.20-like protein [Euphorbia esula]</td><td>48.702</td><td>53.000</td><td>0.919</td><td>63.841</td><td>69.000</td><td>0.925</td><td>0.922</td></tr>
<tr><td>6</td><td>6</td><td>12</td><td>GB005C02</td><td>a76couture1603.r#1</td><td>>ref|NP_563952.1|| (NM_101312) expressed protein; protein id: At1g14450.1. supported</td><td>1207.554</td><td>1228.000</td><td>0.983</td><td>1564.108</td><td>1809.000</td><td>0.865</td><td>0.924</td></tr>
<tr><td>6</td><td>6</td><td>13</td><td>TT263C11</td><td>a76couture1462.r#1</td><td>>ref|NP_173682.1|| (NM_102115) hypothetical protein; protein id: At1g22680.1</td><td>1749.518</td><td>1754.000</td><td>0.997</td><td>2282.836</td><td>2604.000</td><td>0.877</td><td>0.937</td></tr>
<tr><td>6</td><td>6</td><td>14</td><td>GT174H06</td><td>a76couture1784.r#1</td><td>>gb|AAK56254.1|AF367265_1 (AF367265) At1g01540/F22L4_6 [Arabidopsis thaliana]</td><td>531.973</td><td>316.000</td><td>1.683</td><td>824.786</td><td>524.000</td><td>1.574</td><td>1.629</td></tr>
<tr><td>6</td><td>6</td><td>15</td><td>GT162F02</td><td>a76couture1693.r#1</td><td>>gb|AAM62839.1| (AY085618) putative splicing factor [Arabidopsis thaliana]</td><td>1409.854</td><td>1184.000</td><td>1.191</td><td>1562.049</td><td>1402.000</td><td>1.114</td><td>1.152</td></tr>
<tr><td>6</td><td>7</td><td>1</td><td>GB005E10</td><td>a76couture1599.r#1</td><td>>gb|AAG49030.1|AF204783_1 (AF204783) ripening regulated protein DDTFR8 [Lycopersicon</td><td>455.799</td><td>219.000</td><td>2.081</td><td>471.601</td><td>294.000</td><td>1.604</td><td>1.843</td></tr>
<tr><td>6</td><td>7</td><td>2</td><td>TT264H03</td><td>a76couture1458.r#1</td><td>>ref|NP_565962.1|| (NM_129754) putative CCCH-type zinc finger protein; protein id:</td><td>58.692</td><td>111.000</td><td>0.529</td><td>676.510</td><td>726.000</td><td>0.932</td><td>0.730</td></tr>
<tr><td>6</td><td>7</td><td>3</td><td>GT174F03</td><td>a76couture1780.r#1</td><td>>dbj|BAB33412.1| (AB049714) putative senescence-associated protein [Pisum sativum]</td><td>1438.576</td><td>1506.000</td><td>0.955</td><td>1301.536</td><td>1608.000</td><td>0.809</td><td>0.882</td></tr>
<tr><td>6</td><td>7</td><td>4</td><td>GT161D09</td><td>a76couture1688.r#1</td><td>>ref|NP_197714.1|| (NM_122229) putative protein; protein id: At5g23230.1 [Arabidopsis</td><td>169.832</td><td>114.000</td><td>1.490</td><td>178.137</td><td>133.000</td><td>1.339</td><td>1.415</td></tr>
<tr><td>6</td><td>7</td><td>5</td><td>GB005B06</td><td>a76couture1595.r#1</td><td>>gb|AAM97080.1| (AY136414) cytoplasmic aconitate hydratase [Arabidopsis thaliana]</td><td>2652.374</td><td>2447.000</td><td>1.084</td><td>2328.142</td><td>2893.000</td><td>0.805</td><td>0.944</td></tr>
<tr><td>6</td><td>7</td><td>6</td><td>TT264B05</td><td>a76couture1453.r#1</td><td>>ref|NP_189335.1|| (NM_113613) hypothetical protein; protein id: At3g26990.1</td><td>289.713</td><td>236.000</td><td>1.228</td><td>305.820</td><td>272.000</td><td>1.124</td><td>1.176</td></tr>
<tr><td>6</td><td>7</td><td>7</td><td>RT043A04</td><td>a76couture2207.r#1</td><td>>ref|NP_567001.1|| (NM_115311) ABC transporter family protein; protein id: At3g54540.1</td><td>1040.220</td><td>797.000</td><td>1.305</td><td>1037.933</td><td>991.000</td><td>1.047</td><td>1.176</td></tr>
<tr><td>6</td><td>7</td><td>8</td><td>RT024H07</td><td>a76couture2108#1</td><td>>ref|NP_192337.1|| (NM_116666) putative transposon protein; protein id: At4g04280.1</td><td>13.736</td><td>21.000</td><td>0.654</td><td>11.327</td><td>20.000</td><td>0.566</td><td>0.610</td></tr>
<tr><td>6</td><td>7</td><td>9</td><td>RT021D10</td><td>a76couture2014#1</td><td>------</td><td>82.418</td><td>78.000</td><td>1.057</td><td>127.682</td><td>116.000</td><td>1.101</td><td>1.079</td></tr>
<tr><td>6</td><td>7</td><td>10</td><td>RB003C11</td><td>a76couture1924.r#1</td><td>------</td><td>583.173</td><td>420.000</td><td>1.389</td><td>716.668</td><td>639.000</td><td>1.122</td><td>1.255</td></tr>
<tr><td>6</td><td>7</td><td>11</td><td>RT042D07</td><td>a76couture2203.r#1</td><td>------</td><td>26.224</td><td>28.000</td><td>0.937</td><td>52.514</td><td>48.000</td><td>1.094</td><td>1.015</td></tr>
</table>

6	7	12	RT024B07	a76couture2103.r#1	>ref|NP_563728.1|| (NM_100386) expressed protein; protein id: At1g05070.1. supported	1776.991	1417.000	1.254	2311.667	2022.000	1.143	1.199
6	7	13	RT021C05	a76couture2010#1	>gb|AAG43411.1| (AF175964) JAB [Lycopersicon esculentum]	194.807	140.000	1.391	364.512	269.000	1.355	1.373
6	7	14	RB002H01	a76couture1919.r#1	>gb|ZP_00081263.1| (NZ_AAAS01000009) hypothetical protein [Geobacter metallireducens]	66.184	59.000	1.122	120.474	110.000	1.095	1.108
6	7	15	RT041C12	a76couture2198.r#1	>ref|NP_649438.1|| (NM_141181) CG1107 gene product [Drosophila melanogaster]	253.499	232.000	1.093	348.037	316.000	1.101	1.097
6	8	1	RT024G01	a76couture2096.r#1	>ref|NP_199565.1|| (NM_124127) putative protein; protein id: At5g47540.1 [Arabidopsis	43.707	52.000	0.841	41.188	52.000	0.792	0.816
6	8	2	RT021B08	a76couture2006#1	>ref|NP_567956.1|| (NM_119578) putative protein; protein id: At4g34150.1. supported by	192.310	124.000	1.551	184.316	155.000	1.189	1.370
6	8	3	RB002B02	a76couture1912.r#1	------	2260.262	2040.000	1.108	2112.936	2533.000	0.834	0.971
6	8	4	RT041A05	a76couture2194.r#1	>gb|AAM63612.1| (AY086548) unknown [Arabidopsis thaliana]	484.520	434.000	1.116	493.224	533.000	0.925	1.021
6	8	5	RT024E09	a76couture2092.r#1	>dbj|BAB92460.1| (AP003297) putative SnRK1-interacting protein 1 [Oryza sativa	154.847	148.000	1.046	121.504	143.000	0.850	0.948
6	8	6	RT021A11	a76couture2003#1	>pir||OWASN ornithine carbamoyltransferase (EC 2.1.3.3) precursor - Emericella	28.722	37.000	0.776	29.861	41.000	0.728	0.752
6	8	7	RB001B09	a76couture1907.r#1	>ref|NP_171806.1|| (NM_100189) putative glutamate/aspartate-binding peptide; protein	1753.264	701.000	2.501	1792.700	966.000	1.856	2.178
6	8	8	RT034H07	a76couture2190.r#1	>gb|AAL32632.1| (AY062554) nuclear receptor binding factor-like protein	77.423	86.000	0.900	93.702	114.000	0.822	0.861
6	8	9	RT024C08	a76couture2088.r#1	>ref|NP_177231.1|| (NM_105742) putative protein kinase; protein id: At1g70740.1	97.404	75.000	1.299	170.930	137.000	1.248	1.273
6	8	10	RT012F07	a76couture1998.r#1	------	1733.284	1123.000	1.543	2065.570	1552.000	1.331	1.437
6	8	11	GT204G10	a76couture1886.r#1	------	6.244	15.000	0.416	9.267	11.000	0.842	0.629
6	8	12	RT034G04	a76couture2186.r#1	>ref|NP_196176.1|| (NM_120639) putative protein; protein id: At5g05570.1 [Arabidopsis	198.553	153.000	1.298	239.919	213.000	1.126	1.212
6	8	13	RT024A04	a76couture2083.r#1	>gb|AAG46169.1|AC018727_21 (AC018727) unknown protein [Oryza sativa]	1439.824	1303.000	1.105	2065.570	2016.000	1.025	1.065
6	8	14	RT011G05	a76couture1994.r#1	>gb|AAK52587.1|AC079685_18 (AC079685) Putative NADPH-dependent oxidoreductase [Oryza sativa]	277.226	265.000	1.046	385.106	422.000	0.913	0.979
6	8	15	GT204E08	a76couture1882.r#1	>ref|NP_187396.1|| (NM_111619) hypothetical protein; protein id: At3g07400.1	118.633	98.000	1.211	150.336	125.000	1.203	1.207
6	9	1	PT002B05	a76couture2630.r#1	------	123.628	111.000	1.114	113.267	118.000	0.960	1.037
6	9	2	TT261A08	a76couture2510.r#1	>gb|AAM20600.1| (AY099749) putative protein [Arabidopsis thaliana]	3760.027	2883.000	1.304	3423.739	3410.000	1.004	1.154
6	9	3	TB003E02	a76couture2400.r#1	>ref|NP_194954.1|| (NM_119379) hypothetical protein; protein id: At4g32270.1	66.184	61.000	1.085	61.782	65.000	0.950	1.018
6	9	4	RT054H11	a76couture2298.r#1	>gb|AAK50125.1|AC087797_10 (AC087797) unknown protein [Oryza sativa]	36.214	41.000	0.883	38.099	52.000	0.733	0.808
6	9	5	PT013H05	a76couture2626.r#1	------	282.221	246.000	1.147	345.978	359.000	0.964	1.055
6	9	6	TT261B10	a76couture2506.r#1	>ref|NP_190001.2|| (NM_114283) putative protein; protein id: At3g44150.1. supported by	1890.628	1648.000	1.147	2146.916	2025.000	1.060	1.104
6	9	7	TB003B06	a76couture2396.r#1	------	36.214	43.000	0.842	46.336	59.000	0.785	0.814
6	9	8	RT054B12	a76couture2294.r#1	>sp|P27608|AROF_TOBAC Phospho-2-dehydro-3-deoxyheptonate aldolase 1. chloroplast	324.679	180.000	1.804	528.234	328.000	1.610	1.707
6	9	9	PT011D09	a76couture2621.r#1	------	465.789	353.000	1.320	854.648	674.000	1.268	1.294
6	9	10	TT254H12	a76couture2502.r#1	>gb|AAM12880.1|AF495716_1 (AF495716) GTP-binding protein [Helianthus annuus]	1764.503	1575.000	1.120	2162.361	2137.000	1.012	1.066
6	9	11	TB002F12	a76couture2392.r#1	>ref|NP_566070.1|| (NM_130196) arabinogalactan-protein (AGP16); protein id:	505.749	361.000	1.401	572.511	456.000	1.256	1.328
6	9	12	RT053E01	a76couture2290.r#1	>ref|NP_191557.1|| (NM_115861) putative protein; protein id: At3g59980.1. supported by	297.206	253.000	1.175	399.522	378.000	1.057	1.116
6	9	13	PT010E10	a76couture2617.r#1	>ref|NP_084801.1|| (NC_002694) ATP synthase CF0 C chain [Lotus japonicus]	1478.536	1155.000	1.280	2218.995	1893.000	1.172	1.226
6	9	14	TT254E05	a76couture2498.r#1	>gb|AAC36698.1| (AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum	1013.996	875.000	1.159	1347.872	1328.000	1.015	1.087
6	9	15	TB001H07	a76couture2388.r#1	>emb|CAD22254.1| (AJ429358) maturase [Kaliphora madagascariensis]	584.421	494.000	1.183	786.688	674.000	1.167	1.175
6	10	1	RT053A09	a76couture2286.r#1	>emb|CAC01441.1| (AJ292770) putative fatty acid elongase [Zea mays]	2181.590	1777.000	1.228	1957.452	2170.000	0.902	1.065
6	10	2	PT003A01	a76couture2613.r#1	>dbj|BAB84111.1| (AB066274) chalcone synthase [Vitis vinifera]	2235.287	1508.000	1.482	2308.578	2159.000	1.069	1.276
6	10	3	TT251H11	a76couture2492#1	>sp|P55876|IF5_MAIZE Eukaryotic translation initiation factor 5 (eIF-5)	177.324	128.000	1.385	186.375	170.000	1.096	1.241
6	10	4	TB001C08	a76couture2381.r#1	------	22.478	29.000	0.775	26.772	35.000	0.765	0.770
6	10	5	RT052G10	a76couture2282.r#1	>pir||T50603 ubiquitin-conjugating enzyme [imported] - Prunus armeniaca	264.738	200.000	1.324	313.028	269.000	1.164	1.244
6	10	6	RT064F11	a76couture2608.r#1	------	2970.808	3016.000	0.985	3348.571	3865.000	0.866	0.926
6	10	7	TT251H04	a76couture2489#1	>gb|AAF23822.1|AF219223_1 (AF219223) homocysteine S-methyltransferase AtHMT-2 [Arabidopsis	59.941	49.000	1.223	58.693	53.000	1.107	1.165
6	10	8	RT063G03	a76couture2376.r#1	>pir||T47924 hypothetical protein T20K12.220 - Arabidopsis thaliana	283.469	152.000	1.865	320.235	195.000	1.642	1.754
6	10	9	RT052D06	a76couture2278.r#1	------	189.812	172.000	1.104	313.028	295.000	1.061	1.082
6	10	10	G9885271 reverse complement 1355 bases	a76couture3160.r#1	>gb|AAB65840.1| (U36586) alcohol dehydrogenase [Vitis vinifera]	4769.028	4589.000	1.039	5772.475	6268.000	0.921	0.980
6	10	11	RT043B09	a76couture2995.r#1	>pir||S49847 aconitate hydratase (EC 4.2.1.3) - Arabidopsis thaliana (fragment)	39.960	56.000	0.714	65.901	78.000	0.845	0.779
6	10	12	GT194B08	a76couture2856.r#1	>ref|NP_191788.1|| (NM_116094) ADP-ribosylation factor-like protein; protein id:	4304.488	2564.000	1.679	6550.925	4313.000	1.519	1.599
6	10	13	PT013H10	a76couture2735.r#1	>pir||T50023 hypothetical protein T31P16.180 - Arabidopsis thaliana	49.951	48.000	1.041	71.049	61.000	1.165	1.103
6	10	14	CT7F4AP24	a76couture3139.r#1	------	17.483	28.000	0.624	28.831	38.000	0.759	0.692
6	10	15	GT183C09	a76couture2991.r#1	>sp|Q9XHE4|R37A_GOSHI 60S RIBOSOMAL PROTEIN L37A >gi|4741896|gb|AAD28753.1|AF127042_1	1022.737	510.000	2.005	1505.415	824.000	1.827	1.916
6	11	1	GB009G03	a76couture2848.r#1	>gb|AAL79826.1|AF440310_1 (AF440310) actin depolymerizing factor [Vitis vinifera]	3392.891	3147.000	1.078	3282.670	4048.000	0.811	0.945
6	11	2	PT003A12	a76couture2730.r#1	>ref|NP_566876.2|| (NM_114393) serine/threonine-protein kinase-like protein; protein	93.657	54.000	1.734	96.791	70.000	1.383	1.559
6	11	3	VVOPT1H 3	a76couture3135.r#1		89.911	81.000	1.110	84.435	94.000	0.898	1.004
6	11	4	ST006D02	a76couture2986.r#1	>ref|NP_568463.1|| (NM_122400) cytochrome p450. putative; protein id: At5g24910.1	153.598	142.000	1.082	168.870	178.000	0.949	1.015
6	11	5	CM003D09	a76couture2839.r#1	>sp|P93257|MTD_MESCR Probable mannitol dehydrogenase (NAD-dependent mannitol	2420.104	1277.000	1.895	2878.000	1861.000	1.546	1.721
6	11	6	PT003E12	a76couture2726.r#1	>pir||T03627 GTP-binding protein Rab6 - common tobacco >gi|623586|gb|AAA74117.1|	711.795	581.000	1.225	699.163	671.000	1.042	1.134
6	11	7	TT274C10	a76couture3131.r#1	>ref|NP_191376.1|| (NM_115679) putative protein; protein id: At3g58170.1. supported by	705.551	528.000	1.336	676.510	730.000	0.927	1.131
6	11	8	GB009G07	a76couture2982.r#1	>ref|NP_175683.1|| (NM_104152) putative histone H2A; protein id: At1g52740.1	374.629	306.000	1.224	631.204	522.000	1.209	1.217
6	11	9	CT001G03	a76couture2829.r#1	------	24300.939	11559.000	2.102	43973.160	24774.000	1.775	1.939
6	11	10	PT007E08	a76couture2721.r#1	>gb|AAG51892.1|AC016162_13 (AC016162) ARE1-like protein; 78992-73047 [Arabidopsis thaliana]	194.807	192.000	1.015	301.701	301.000	1.002	1.008
6	11	11	RT083H06	a76couture3125.r#1	>gb|AAL87158.1|AF480496_12 (AF480496) putative ring box-1 protein [Oryza sativa (japonica	785.472	593.000	1.325	1051.319	873.000	1.204	1.264
6	11	12	RT053F09	a76couture2973.r#1	>sp|P27985|RBS2_BRANA Ribulose bisphosphate carboxylase small chain F1. chloroplast	8761.325	5329.000	1.644	10054.980	6928.000	1.451	1.548
6	11	13	RT021E11 reverse complement 681 bases 22	a76couture2822.r#1	>ref|NP_175683.1|| (NM_104152) putative histone H2A; protein id: At1g52740.1	1684.582	1192.000	1.413	2127.352	1687.000	1.261	1.337
6	11	14	PT013C03	a76couture2717.r#1	>ref|NP_174556.1|| (NM_103013) RNA-binding protein. putative; protein id: At1g32790.1	1082.678	872.000	1.242	1314.922	1109.000	1.186	1.214
6	11	15	ST003F12	a76couture3120.r#1	>sp|P46280|EFT2_SOYBN ELONGATION FACTOR TU. CHLOROPLAST PRECURSOR (EF-TU)	309.693	251.000	1.234	443.799	368.000	1.206	1.220
6	12	1	GT202G01	a76couture2966.r#1	>gb|AAF17691.1|AC009243_18 (AC009243) F28K19.29 [Arabidopsis thaliana]	322.181	299.000	1.078	245.068	307.000	0.798	0.938
6	12	2	PT012H08	a76couture2818.r#1	>sp|P19684|ROC5_NICSY 33 kDa ribonucleoprotein. chloroplast precursor	142.359	99.000	1.438	126.653	116.000	1.092	1.265
6	12	3	PT002A08	a76couture2713.r#1	>ref|NP_199757.1|| (NM_124323) ATP citrate lyase; protein id: At5g49460.1. supported	2838.440	2038.000	1.393	2732.813	2705.000	1.010	1.202
6	12	4	BM437350 RT052B01	couture_a76.450.c1.r#1	>dbj|BAB19758.1| (AB052786) putative nitrate transporter NRT1-3 [Glycine max]	21.229	16.000	1.327	25.742	19.000	1.355	1.341

<table>
<tr><td>6</td><td>12</td><td>5</td><td>BG273974 GB000A04 GB000A04</td><td>couture_a76.358.c1#1</td><td>>pir||S51376 sucrose cleavage protein - potato >gi|707001|gb|AAB33256.1|</td><td>1622.144</td><td>1311.000</td><td>1.237</td><td>1995.551</td><td>1964.000</td><td>1.016</td><td>1.127</td></tr>
<tr><td>6</td><td>12</td><td>6</td><td>RB001H10 RB006D10</td><td>couture_a76.273.c1.r#1</td><td>>ref|NP_194175.1|| (NM_118577) transcription factor IIA small subunit; protein id:</td><td>934.075</td><td>836.000</td><td>1.117</td><td>997.775</td><td>991.000</td><td>1.007</td><td>1.062</td></tr>
<tr><td>6</td><td>12</td><td>7</td><td>BM437270 RT094A11</td><td>couture_a76.183.c1.r#1</td><td>>sp|Q43433|VAB2_GOSHI Vacuolar ATP synthase subunit B isoform 2 (V-ATPase B subunit 2)</td><td>313.440</td><td>247.000</td><td>1.269</td><td>626.055</td><td>621.000</td><td>1.008</td><td>1.139</td></tr>
<tr><td>6</td><td>12</td><td>8</td><td>BM437056 BM438106 RT043B10</td><td>couture_a76.448.c1.r#1</td><td>>gb|AAN14410.1| (AF264146) bifunctional lysine-ketoglutarate reductase/saccharopine</td><td>825.433</td><td>862.000</td><td>0.958</td><td>1241.813</td><td>1318.000</td><td>0.942</td><td>0.950</td></tr>
<tr><td>6</td><td>12</td><td>9</td><td>BG273969 GB000A09</td><td>couture_a76.355.c1#1</td><td>>ref|NP_181084.1|| (NM_129093) chloroplast RNA-binding protein cp33. putative; protein</td><td>51.199</td><td>40.000</td><td>1.280</td><td>72.079</td><td>55.000</td><td>1.311</td><td>1.295</td></tr>
<tr><td>6</td><td>12</td><td>10</td><td>RB004A11 RB004A11</td><td>couture_a76.269.c1.r#1</td><td>>emb|CAB52797.1| (AJ245862) putative external rotenone-insensitive NADH</td><td>515.739</td><td>479.000</td><td>1.077</td><td>805.222</td><td>791.000</td><td>1.018</td><td>1.047</td></tr>
<tr><td>6</td><td>12</td><td>11</td><td>CT006D07 BM436601</td><td>couture_a76.18.c1#1</td><td>>ref|NP_566108.1|| (NM_130339) expressed protein; protein id: At2g47710.1. supported</td><td>3215.566</td><td>2292.000</td><td>1.403</td><td>4960.045</td><td>3724.000</td><td>1.332</td><td>1.367</td></tr>
<tr><td>6</td><td>12</td><td>12</td><td>BM437298 RT034B04</td><td>couture_a76.442.c1#1</td><td>>ref|NP_565783.1|| (NM_128982) Expressed protein; protein id: At2g34310.1. supported</td><td>77.423</td><td>79.000</td><td>0.980</td><td>108.118</td><td>114.000</td><td>0.948</td><td>0.964</td></tr>
<tr><td>6</td><td>12</td><td>13</td><td>BG273960 GB000A19 GB000A19</td><td>couture_a76.352.c1.r#1</td><td>>ref|NP_565998.1|| (NM_129903) putative sterol dehydrogenase; protein id: At2g43420.1</td><td>428.326</td><td>333.000</td><td>1.286</td><td>616.788</td><td>490.000</td><td>1.259</td><td>1.273</td></tr>
<tr><td>6</td><td>12</td><td>14</td><td>BM437399 GT204F07</td><td>couture_a76.264.c1.r#1</td><td>>ref|NP_525084.1|| (NM_080345) rhomboid-4; Rho-related [10C6] [Drosophila</td><td>71.180</td><td>56.000</td><td>1.271</td><td>117.385</td><td>93.000</td><td>1.262</td><td>1.267</td></tr>
<tr><td>6</td><td>12</td><td>15</td><td>BM437419 RT092A03</td><td>couture_a76.178.c1.r#1</td><td>>ref|NP_565671.1|| (NM_128397) expressed protein; protein id: At2g28370.1. supported</td><td>860.398</td><td>778.000</td><td>1.106</td><td>1046.171</td><td>950.000</td><td>1.101</td><td>1.104</td></tr>
<tr><td>6</td><td>13</td><td>1</td><td>BM437394 RT032G02</td><td>couture_a76.437.c1.r#1</td><td>>ref|NP_173863.2|| (NM_102299) putative myosin heavy chain; protein id: At1g24560.1</td><td>492.013</td><td>390.000</td><td>1.262</td><td>405.700</td><td>428.000</td><td>0.948</td><td>1.105</td></tr>
<tr><td>6</td><td>13</td><td>2</td><td>GB005f06 GB005F06</td><td>couture_a76.35.c1.r#1</td><td>>ref|NP_172022.1|| (NM_100409) putative zinc transporter; protein id: At1g05300.1</td><td>166.086</td><td>146.000</td><td>1.138</td><td>159.603</td><td>185.000</td><td>0.863</td><td>1.000</td></tr>
<tr><td>6</td><td>13</td><td>3</td><td>BM438041 BM437631 GT204G11</td><td>couture_a76.260.c1.r#1</td><td>>ref|NP_200265.1|| (NM_124834) putative protein; protein id: At5g54540.1. supported by</td><td>96.155</td><td>45.000</td><td>2.137</td><td>113.267</td><td>49.000</td><td>2.312</td><td>2.224</td></tr>
<tr><td>6</td><td>13</td><td>4</td><td>RB002C09 RT082E02</td><td>couture_a76.173.c1#1</td><td>>ref|NP_565544.1|| (NM_127855) Expressed protein; protein id: At2g22900.1. supported</td><td>1918.101</td><td>1823.000</td><td>1.052</td><td>2692.655</td><td>2891.000</td><td>0.931</td><td>0.992</td></tr>
<tr><td>6</td><td>13</td><td>5</td><td>BM438000 RT023G02</td><td>couture_a76.433.c1.r#1</td><td>>gb|AAM66002.1| (AY088466) unknown [Arabidopsis thaliana]</td><td>116.135</td><td>119.000</td><td>0.976</td><td>130.771</td><td>149.000</td><td>0.878</td><td>0.927</td></tr>
<tr><td>6</td><td>13</td><td>6</td><td>BG273948 GB000A35</td><td>couture_a76.347.c1.r#1</td><td>>ref|NP_172388.1|| (NM_100786) putative protein phosphatase 2C; protein id:</td><td>289.713</td><td>256.000</td><td>1.132</td><td>335.681</td><td>369.000</td><td>0.910</td><td>1.021</td></tr>
<tr><td>6</td><td>13</td><td>7</td><td>BG273858 GT204B11</td><td>couture_a76.257.c1.r#1</td><td>>ref|NP_564683.1|| (NM_104401) Expressed protein; protein id: At1g55265.1. supported</td><td>11794.572</td><td>9368.000</td><td>1.259</td><td>13358.244</td><td>12219.000</td><td>1.093</td><td>1.176</td></tr>
<tr><td>6</td><td>13</td><td>8</td><td>TB001a02 RT081A11</td><td>couture_a76.169.c1#1</td><td>>gb|AAF04193.1|AF053638_1 (AF053638) short-chain alcohol dehydrogenase [Pisum sativum]</td><td>10585.769</td><td>8581.000</td><td>1.234</td><td>12984.464</td><td>11444.000</td><td>1.135</td><td>1.184</td></tr>
<tr><td>6</td><td>13</td><td>9</td><td>BM437177 BM436972 RT023G06</td><td>couture_a76.429.c1.r#1</td><td>>emb|CAA04703.1| (AJ001370) cytochome b5 [Olea europaea]</td><td>556.949</td><td>400.000</td><td>1.392</td><td>716.668</td><td>557.000</td><td>1.287</td><td>1.340</td></tr>
<tr><td>6</td><td>13</td><td>10</td><td>BG273942 GB000A42</td><td>couture_a76.344.c1#1</td><td>>dbj|BAB85235.1| (AP003247) similar to SET1 [Oryza sativa (japonica cultivar-group)]</td><td>591.914</td><td>349.000</td><td>1.696</td><td>972.033</td><td>635.000</td><td>1.531</td><td>1.613</td></tr>
<tr><td>6</td><td>13</td><td>11</td><td>BM436953 GT202D07</td><td>couture_a76.253.c1.r#1</td><td>>dbj|BAB08888.1| (AB012243) gene_id:MIJ24.6~ref|NP_013897.1~similar to unknown</td><td>0.000</td><td></td><td></td><td>11622.177</td><td>11904.000</td><td>0.976</td><td>0.976</td></tr>
<tr><td>6</td><td>13</td><td>12</td><td>BM436758 BE846411 RT031D09 BM436840</td><td>couture_a76.165.c1.r#1</td><td>>ref|NP_191670.1|| (NM_115975) ribosomal protein S27; protein id: At3g61110.1</td><td>598.158</td><td>365.000</td><td>1.639</td><td>875.241</td><td>567.000</td><td>1.544</td><td>1.591</td></tr>
<tr><td>6</td><td>13</td><td>13</td><td>BM437775 RT063C08</td><td>couture_a76.636.c1.r#1</td><td>>gb|AAC49770.1| (AF003097) AP2 domain containing protein RAP2.4 [Arabidopsis</td><td>1985.534</td><td>1977.000</td><td>1.004</td><td>2750.318</td><td>2893.000</td><td>0.951</td><td>0.977</td></tr>
<tr><td>6</td><td>13</td><td>14</td><td>BE846400 ST007F01</td><td>couture_a76.54.c2.r#1</td><td>>gb|AAG51879.1|AC079678_9 (AC079678) cytochrome P-450. 3' partial; 38886-39601 [Arabidopsis</td><td>10151.199</td><td>4922.000</td><td>2.062</td><td>13761.885</td><td>6764.000</td><td>2.035</td><td>2.048</td></tr>
<tr><td>6</td><td>13</td><td>15</td><td>G7271882 AF239740</td><td>couture_a76.sd.59.c1#</td><td>>gb|AAF44672.1|AF239740_1 (AF239740) caffeic acid O-methyltransferase [Vitis vinifera]</td><td>1317.446</td><td>1767.000</td><td>0.746</td><td>1443.634</td><td>1840.000</td><td>0.785</td><td>0.765</td></tr>
<tr><td>6</td><td>14</td><td>1</td><td>RT054H08 ST005A08</td><td>couture_a76.635.c1.r#1</td><td>>sp|P50346|RLA0_SOYBN 60S ACIDIC RIBOSOMAL PROTEIN P0 >gi|7440740|pir||T07106 acidic</td><td>5139.911</td><td>3700.000</td><td>1.389</td><td>4509.038</td><td>4485.000</td><td>1.005</td><td>1.197</td></tr>
<tr><td>6</td><td>14</td><td>2</td><td>BM436714 BM436483 RT042H12</td><td>couture_a76.51.c1.r#1</td><td>>ref|NP_190930.1|| (NM_115222) inorganic pyrophosphatase -like protein; protein id:</td><td>1960.559</td><td>1695.000</td><td>1.157</td><td>1704.147</td><td>2051.000</td><td>0.831</td><td>0.994</td></tr>
<tr><td>6</td><td>14</td><td>3</td><td>G14764485 AY039034</td><td>couture_a76.sd.27.c1#</td><td>>gb|AAK72100.1| (AY039034) beta-glucosidase [Vitis vinifera]</td><td>32.468</td><td>45.000</td><td>0.722</td><td>42.218</td><td>64.000</td><td>0.660</td><td>0.691</td></tr>
<tr><td>6</td><td>14</td><td>4</td><td>Arabidopsis Control Oligonucleotide</td><td>3ara7</td><td></td><td>94.906</td><td>97.000</td><td>0.978</td><td>121.504</td><td>136.000</td><td>0.893</td><td>0.936</td></tr>
<tr><td>6</td><td>14</td><td>5</td><td>BM437197 RT071A03 BM438036</td><td>couture_a76.533.c2.r#1</td><td>>gb|AAK55703.1|AF378900_1 (AF378900) At2g04520/T1O3.7 [Arabidopsis thaliana]</td><td>11226.384</td><td>10545.000</td><td>1.065</td><td>10277.394</td><td>12092.000</td><td>0.850</td><td>0.957</td></tr>
<tr><td>6</td><td>14</td><td>6</td><td>TT264D11 AY043238</td><td>couture_a76.sd.21.c1#</td><td>>gb|AAC09388.1| (L46792) xyloglucan endotransglycosylase precursor [Actinidia</td><td>589.416</td><td>574.000</td><td>1.027</td><td>669.302</td><td>798.000</td><td>0.839</td><td>0.933</td></tr>
<tr><td>6</td><td>14</td><td>7</td><td>BM437028 RT042F09</td><td>couture_a76.600.c1.r#1</td><td>>ref|NP_564255.1|| (NM_102430) v-SNARE protein AtVTI1b. putative; protein id:</td><td>444.560</td><td>356.000</td><td>1.249</td><td>673.421</td><td>547.000</td><td>1.231</td><td>1.240</td></tr>
<tr><td>6</td><td>14</td><td>8</td><td>BG273873 TB000A19</td><td>couture_a76.502.c1.r#1</td><td>>gb|AAF98216.1|AC007152_12 (AC007152) Unknown protein [Arabidopsis thaliana]</td><td>902.856</td><td>679.000</td><td>1.330</td><td>1449.812</td><td>1181.000</td><td>1.228</td><td>1.279</td></tr>
<tr><td>6</td><td>14</td><td>9</td><td>BM436621 BM436585 BM436304 G19070129 AF</td><td>couture_a76.sd.2.c1#1</td><td>>gb|AAL83720.1|AF236127_1 (AF236127) catalase [Vitis vinifera]</td><td>7627.448</td><td>6909.000</td><td>1.104</td><td>10636.758</td><td>10596.000</td><td>1.004</td><td>1.054</td></tr>
<tr><td>6</td><td>14</td><td>10</td><td>BG273958 GB000A21</td><td>couture_a76.569.c1.r#1</td><td>>ref|NP_198801.1|| (NM_123348) 40S ribosomal protein S9-like; protein id: At5g39850.1</td><td>4584.211</td><td>3711.000</td><td>1.235</td><td>6120.512</td><td>5314.000</td><td>1.152</td><td>1.194</td></tr>
<tr><td>6</td><td>14</td><td>11</td><td>BM436899 TT251B07</td><td>couture_a76.475.c1#1</td><td>>ref|NP_198897.1|| (NM_123446) cytochrome c1 precursor; protein id: At5g40810.1</td><td>1251.261</td><td>839.000</td><td>1.491</td><td>1781.374</td><td>1348.000</td><td>1.321</td><td>1.406</td></tr>
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<tr><td>6</td><td>14</td><td>14</td><td>BM436901 ST005C10</td><td>couture_a76.639.c2#1</td><td>------</td><td>944.065</td><td>433.000</td><td>2.180</td><td>1251.080</td><td>579.000</td><td>2.161</td><td>2.171</td></tr>
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<tr><td>7</td><td>1</td><td>4</td><td>CM003D02</td><td>a76couture0065.r#1</td><td>>dbj|BAA92988.1| (AP001550) ESTs AU069293(C53946).AU077613(E20660) correspond to a</td><td>4299.493</td><td>2864.000</td><td>1.501</td><td>4657.314</td><td>3485.000</td><td>1.336</td><td>1.419</td></tr>
<tr><td>7</td><td>1</td><td>5</td><td>CM003E11</td><td>a76couture0443.r#1</td><td>>dbj|BAB63862.1| (AP003687) hypothetical protein~similar to GABA permease [Oryza</td><td>384.619</td><td>350.000</td><td>1.099</td><td>493.224</td><td>479.000</td><td>1.030</td><td>1.064</td></tr>
<tr><td>7</td><td>1</td><td>6</td><td>TT274E08</td><td>a76couture0342.r#1</td><td>>emb|CAC27145.1| (AJ132540) glutamate-cysteine ligase [Picea abies]</td><td>18.731</td><td>25.000</td><td>0.749</td><td>29.861</td><td>34.000</td><td>0.878</td><td>0.814</td></tr>
<tr><td>7</td><td>1</td><td>7</td><td>RT052D12</td><td>a76couture0212.r#1</td><td>>ref|NP_187342.1|| (NM_111566) fatty acid multifunctional protein (AtMFP2); protein id:</td><td>2209.063</td><td>2580.000</td><td>0.856</td><td>2666.912</td><td>3121.000</td><td>0.855</td><td>0.855</td></tr>
<tr><td>7</td><td>1</td><td>8</td><td>WK001A01C</td><td>a76couture0060.r#1</td><td>>emb|CAB97004.1| (AJ278507) WRKY DNA binding protein [Solanum tuberosum]</td><td>559.446</td><td>603.000</td><td>0.928</td><td>614.728</td><td>661.000</td><td>0.930</td><td>0.929</td></tr>
<tr><td>7</td><td>1</td><td>9</td><td>CM003E02</td><td>a76couture0439.r#1</td><td>>ref|NP_175965.1|| (NM_104445) Phosphatidylinositol Transfer Protein. putative;</td><td>338.415</td><td>313.000</td><td>1.081</td><td>409.819</td><td>356.000</td><td>1.151</td><td>1.116</td></tr>
<tr><td>7</td><td>1</td><td>10</td><td>TT264H09</td><td>a76couture0337.r#1</td><td>>emb|CAC86383.1| (AJ313514) carboxypeptidase type III [Theobroma cacao]</td><td>9928.919</td><td>9241.000</td><td>1.074</td><td>11531.564</td><td>10716.000</td><td>1.076</td><td>1.075</td></tr>
<tr><td>7</td><td>1</td><td>11</td><td>RT034H12</td><td>a76couture0206.r#1</td><td>>pir||T47665 beta-N-acetylhexosaminidase-like protein - Arabidopsis thaliana</td><td>589.416</td><td>607.000</td><td>0.971</td><td>704.312</td><td>720.000</td><td>0.978</td><td>0.975</td></tr>
<tr><td>7</td><td>1</td><td>12</td><td>MY004B04C</td><td>a76couture0053.r#1</td><td>>gb|AAK19611.1|AF336278_1 (AF336278) BNLGHi233 [Gossypium hirsutum]</td><td>646.860</td><td>650.000</td><td>0.995</td><td>778.450</td><td>690.000</td><td>1.128</td><td>1.062</td></tr>
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<tr><td>7</td><td>1</td><td>15</td><td>RT021D09</td><td>a76couture0200#1</td><td>>ref|NP_195822.1|| (NM_120280) putative protein; protein id: At5g02020.1. supported by</td><td>129.871</td><td>108.000</td><td>1.203</td><td>189.464</td><td>146.000</td><td>1.298</td><td>1.250</td></tr>
<tr><td>7</td><td>2</td><td>1</td><td>G499017E reverse complement 1315 bases</td><td>a76couture0037.r#1</td><td>>sp|P51110|DFRA_VITVI DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL 4-REDUCTASE)</td><td>543.212</td><td>450.000</td><td>1.207</td><td>652.827</td><td>613.000</td><td>1.065</td><td>1.136</td></tr>
<tr><td>7</td><td>2</td><td>2</td><td>CM002H06</td><td>a76couture0432.r#1</td><td>>ref|NP_176516.1|| (NM_105006) ABC transporter family protein; protein id: At1g63270.1</td><td>52.448</td><td>47.000</td><td>1.116</td><td>80.316</td><td>72.000</td><td>1.116</td><td>1.116</td></tr>
<tr><td>7</td><td>2</td><td>3</td><td>RT084B11</td><td>a76couture0324.r#1</td><td>>ref|NP_191121.1|| (NM_115420) eukaryotic translation initiation factor 6 (EIF-6) -</td><td>976.533</td><td>824.000</td><td>1.185</td><td>1349.931</td><td>1153.000</td><td>1.171</td><td>1.178</td></tr>
<tr><td>7</td><td>2</td><td>4</td><td>RB004C05</td><td>a76couture0196.r#1</td><td>>emb|CAC43323.1| (AJ291738) putative alpha7 proteasome subunit [Nicotiana tabacum]</td><td>1166.345</td><td>961.000</td><td>1.214</td><td>1580.583</td><td>1385.000</td><td>1.141</td><td>1.177</td></tr>
<tr><td>7</td><td>2</td><td>5</td><td>3B1PROTEI</td><td>a76couture0022.r#1</td><td>>ref|NP_195819.1|| (NM_120277) putative protein; protein id: At5g01990.1 [Arabidopsis</td><td>551.953</td><td>560.000</td><td>0.986</td><td>706.371</td><td>713.000</td><td>0.991</td><td>0.988</td></tr>
<tr><td>7</td><td>2</td><td>6</td><td>CM002F11</td><td>a76couture0428.r#1</td><td>>ref|NP_191027.1|| (NM_115324) structural maintenance of chromosomes (SMC) - like</td><td>307.196</td><td>225.000</td><td>1.365</td><td>306.849</td><td>256.000</td><td>1.199</td><td>1.282</td></tr>
<tr><td>7</td><td>2</td><td>7</td><td>TT283H10</td><td>a76couture0319.r#1</td><td>>ref|NP_567979.1|| (NM_119688) putative protein; protein id: At4g35220.1. supported by</td><td>10385.966</td><td>11217.000</td><td>0.926</td><td>11427.564</td><td>13733.000</td><td>0.832</td><td>0.879</td></tr>
<tr><td>7</td><td>2</td><td>8</td><td>RT064H02</td><td>a76couture0189.r#1</td><td>>pir||T01029 hypothetical protein YUP8H12R.12 - Arabidopsis thaliana</td><td>333.420</td><td>300.000</td><td>1.111</td><td>412.908</td><td>363.000</td><td>1.137</td><td>1.124</td></tr>
<tr><td>7</td><td>2</td><td>9</td><td>RT052H02</td><td>a76couture0015.r#1</td><td>>gb|AAK58564.1|AF265562_1 (AF265562) MAD-box transcripion factor [Vitis vinifera]</td><td>673.084</td><td>796.000</td><td>0.846</td><td>859.796</td><td>930.000</td><td>0.925</td><td>0.885</td></tr>
<tr><td>7</td><td>2</td><td>10</td><td>RT092F01</td><td>a76couture0871.r#1</td><td>>ref|NP_565118.1|| (NM_106231) expressed protein; protein id: At1g75810.1. supported</td><td>1381.132</td><td>1196.000</td><td>1.155</td><td>1446.723</td><td>1376.000</td><td>1.051</td><td>1.103</td></tr>
<tr><td>7</td><td>2</td><td>11</td><td>RT072F08</td><td>a76couture0747#1</td><td>>sp|Q43070|GAE1_PEA UDP-glucose 4-epimerase (Galactowaldenase) (UDP-galactose</td><td></td><td>35.000</td><td>0.000</td><td></td><td></td><td></td><td></td></tr>
<tr><td>7</td><td>2</td><td>12</td><td>ST003G10</td><td>a76couture0647.r#1</td><td>>ref|NP_201520.1|| (NM_126119) TINY-like protein; protein id: At5g67190.1 [Arabidopsis</td><td>219.782</td><td>255.000</td><td>0.862</td><td>250.216</td><td>223.000</td><td>1.122</td><td>0.992</td></tr>
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<table>
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<tr><td>7</td><td>3</td><td>3</td><td>RT091D12</td><td>a76couture0861.r#1</td><td>>ref|NP_172940.1|| (NM_101356) unknown protein; protein id: At1g14870.1. supported by</td><td>17.483</td><td>25.000</td><td>0.699</td><td>19.564</td><td>27.000</td><td>0.725</td><td>0.712</td></tr>
<tr><td>7</td><td>3</td><td>4</td><td>ST007G04</td><td>a76couture0737.r#1</td><td>>gb|AAG24455.1|AF311746_1 (AF311746) 19 kDa oleosin [Perilla frutescens]</td><td>86.165</td><td>107.000</td><td>0.805</td><td>180.197</td><td>176.000</td><td>1.024</td><td>0.915</td></tr>
<tr><td>7</td><td>3</td><td>5</td><td>ST003D10</td><td>a76couture0639.r#1</td><td>>ref|NP_191007.1|| (NM_115299) putative protein; protein id: At3g54390.1. supported by</td><td>7.493</td><td>14.000</td><td>0.535</td><td>8.238</td><td>16.000</td><td>0.515</td><td>0.525</td></tr>
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<tr><td>7</td><td>3</td><td>10</td><td>Arabidopsis Control Oligonucleotide</td><td>3ara23</td><td></td><td>14.985</td><td>15.000</td><td>0.999</td><td>10.297</td><td>16.000</td><td>0.644</td><td>0.821</td></tr>
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<tr><td>7</td><td>3</td><td>12</td><td>ST007D11</td><td>a76couture0728.r#1</td><td>------</td><td>52.448</td><td>46.000</td><td>1.140</td><td>52.514</td><td>42.000</td><td>1.250</td><td>1.195</td></tr>
<tr><td>7</td><td>3</td><td>13</td><td>ST003A09</td><td>a76couture0630.r#1</td><td>>pir||S26981 pvs protein 1 - kidney bean mitochondrion >gi|169320|gb|AAB01584.1|</td><td>374.629</td><td>255.000</td><td>1.469</td><td>428.353</td><td>258.000</td><td>1.660</td><td>1.565</td></tr>
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<tr><td>7</td><td>4</td><td>2</td><td>ST002H05</td><td>a76couture0626.r#1</td><td>>ref|NP_177592.1|| (NM_106112) AtHVA22a; protein id: At1g74520.1. supported by cDNA:</td><td>53.697</td><td>45.000</td><td>1.193</td><td>70.019</td><td>52.000</td><td>1.347</td><td>1.270</td></tr>
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<tr><td>7</td><td>4</td><td>6</td><td>TT284B04</td><td>a76couture1074.r#1</td><td>>ref|NP_199675.1|| (NM_124240) cyclin C-like protein; protein id: At5g48640.1</td><td>490.764</td><td>469.000</td><td>1.046</td><td>574.570</td><td>582.000</td><td>0.987</td><td>1.017</td></tr>
<tr><td>7</td><td>4</td><td>7</td><td>RT083A06</td><td>a76couture0979.r#1</td><td>>ref|NP_566144.1|| (NM_111030) expressed protein; protein id: At3g01640.1. supported</td><td>58.692</td><td>60.000</td><td>0.978</td><td>91.643</td><td>83.000</td><td>1.104</td><td>1.041</td></tr>
<tr><td>7</td><td>4</td><td>8</td><td>RT032A06</td><td>a76couture1326.r#1</td><td>------</td><td>73.677</td><td>77.000</td><td>0.957</td><td>100.910</td><td>91.000</td><td>1.109</td><td>1.033</td></tr>
<tr><td>7</td><td>4</td><td>9</td><td>GT192H07</td><td>a76couture1193.r#1</td><td>>gb|AAF72556.1|AF130425_1 (AF130425) cryptochrome 2 [Lycopersicon esculentum]</td><td>277.226</td><td>258.000</td><td>1.075</td><td>373.780</td><td>376.000</td><td>0.994</td><td>1.034</td></tr>
<tr><td>7</td><td>4</td><td>10</td><td>RT094E12</td><td>a76couture1070.r#1</td><td>>gb|AAF21428.1|AF165422_1 (AF165422) suppressor of K+ transport growth defect-like protein</td><td>2365.158</td><td>2636.000</td><td>0.897</td><td>2535.111</td><td>2710.000</td><td>0.935</td><td>0.916</td></tr>
<tr><td>7</td><td>4</td><td>11</td><td>RT081F03</td><td>a76couture0974.r#1</td><td>>sp|Q10710|STA_RICCO Sugar carrier protein A >gi|7446730|pir||T10150 sugar transport</td><td>392.112</td><td>425.000</td><td>0.923</td><td>373.780</td><td>403.000</td><td>0.927</td><td>0.925</td></tr>
<tr><td>7</td><td>4</td><td>12</td><td>RT031A06</td><td>a76couture1322.r#1</td><td>>gb|AAM66084.1| (AY088552) thioredoxin [Arabidopsis thaliana]</td><td>792.965</td><td>863.000</td><td>0.919</td><td>712.550</td><td>740.000</td><td>0.963</td><td>0.941</td></tr>
<tr><td>7</td><td>4</td><td>13</td><td>GT194D06</td><td>a76couture1188.r#1</td><td>>ref|NP_187906.2|| (NM_112137) hypothetical protein; protein id: At3g13000.1</td><td>44.955</td><td>51.000</td><td>0.881</td><td>59.722</td><td>57.000</td><td>1.048</td><td>0.965</td></tr>
<tr><td>7</td><td>4</td><td>14</td><td>TT284G01</td><td>a76couture1066.r#1</td><td>------</td><td>107.394</td><td>111.000</td><td>0.968</td><td>114.296</td><td>102.000</td><td>1.121</td><td>1.044</td></tr>
<tr><td>7</td><td>4</td><td>15</td><td>RT081B02</td><td>a76couture0969.r#1</td><td>>ref|NP_198135.1|| (NM_122665) putative protein; protein id: At5g27830.1. supported by</td><td>37.463</td><td>49.000</td><td>0.765</td><td>62.811</td><td>56.000</td><td>1.122</td><td>0.943</td></tr>
<tr><td>7</td><td>5</td><td>1</td><td>RT024D04</td><td>a76couture1318.r#1</td><td>>ref|NP_190956.1|| (NM_115248) aldo/keto reductase family; protein id: At3g53880.1</td><td>1017.742</td><td>790.000</td><td>1.288</td><td>1327.278</td><td>1169.000</td><td>1.135</td><td>1.212</td></tr>
<tr><td>7</td><td>5</td><td>2</td><td>GT193A08</td><td>a76couture1184.r#1</td><td>>ref|NP_196822.1|| (NM_121321) NAM-like protein; protein id: At5g13180.1. supported by</td><td>521.983</td><td>370.000</td><td>1.411</td><td>568.392</td><td>454.000</td><td>1.252</td><td>1.331</td></tr>
<tr><td>7</td><td>5</td><td>3</td><td>RT094A01</td><td>a76couture1062.r#1</td><td>>dbj|BAC06208.1| (AP003227) contains EST AU081354(R0069)~similar to Arabidopsis</td><td>249.753</td><td>174.000</td><td>1.435</td><td>428.353</td><td>299.000</td><td>1.433</td><td>1.434</td></tr>
<tr><td>7</td><td>5</td><td>4</td><td>RT074E06</td><td>a76couture0964.r#1</td><td>>gb|AAL36305.1| (AY063949) unknown protein [Arabidopsis thaliana]</td><td>305.947</td><td>298.000</td><td>1.027</td><td>482.927</td><td>471.000</td><td>1.025</td><td>1.026</td></tr>
<tr><td>7</td><td>5</td><td>5</td><td>Arabidopsis Control Oligonucleotide</td><td>3ara23</td><td></td><td>12.488</td><td>18.000</td><td>0.694</td><td>17.505</td><td>18.000</td><td>0.972</td><td>0.833</td></tr>
<tr><td>7</td><td>5</td><td>6</td><td>GT192C03</td><td>a76couture1180.r#1</td><td>------</td><td>37.463</td><td>33.000</td><td>1.135</td><td>54.574</td><td>43.000</td><td>1.269</td><td>1.202</td></tr>
<tr><td>7</td><td>5</td><td>7</td><td>RT093E10</td><td>a76couture1058.r#1</td><td>>ref|NP_180911.2|| (NM_128913) putative serine carboxypeptidase II; protein id:</td><td>56.194</td><td>44.000</td><td>1.277</td><td>66.930</td><td>49.000</td><td>1.366</td><td>1.322</td></tr>
<tr><td>7</td><td>5</td><td>8</td><td>RT074B04</td><td>a76couture0960.r#1</td><td>>ref|NP_179721.1|| (NM_127697) mannose 6-phosphate reductase (NADPH-dependent)</td><td>1394.869</td><td>1105.000</td><td>1.262</td><td>1511.593</td><td>1257.000</td><td>1.203</td><td>1.232</td></tr>
<tr><td>7</td><td>5</td><td>9</td><td>RT022H01</td><td>a76couture1309#1</td><td>>ref|NP_197368.1|| (NM_121872) glycosyl hydrolase family 14 (beta-amylase); protein</td><td>3646.390</td><td>2825.000</td><td>1.291</td><td>4117.754</td><td>3124.000</td><td>1.318</td><td>1.304</td></tr>
<tr><td>7</td><td>5</td><td>10</td><td>GT191C09</td><td>a76couture1175.r#1</td><td>------</td><td>13.736</td><td>17.000</td><td>0.808</td><td>14.416</td><td>17.000</td><td>0.848</td><td>0.828</td></tr>
<tr><td>7</td><td>5</td><td>11</td><td>RT093B05</td><td>a76couture1053.r#1</td><td>>ref|NP_565294.1|| (NM_126363) expressed protein; protein id: At2g03120.1. supported</td><td>3552.732</td><td>3057.000</td><td>1.162</td><td>3179.701</td><td>2834.000</td><td>1.122</td><td>1.142</td></tr>
<tr><td>7</td><td>5</td><td>12</td><td>RT073G01</td><td>a76couture0956.r#1</td><td>>ref|NP_563856.1|| (NM_100861) expressed protein; protein id: At1g09870.1. supported</td><td>39.960</td><td>48.000</td><td>0.833</td><td>27.802</td><td>31.000</td><td>0.897</td><td>0.865</td></tr>
<tr><td>7</td><td>5</td><td>13</td><td>GT174D10</td><td>a76couture1776.r#1</td><td>>gb|AAC00091.1| (AF028198) cytochrome c oxidase subunit I [Otocyon megalotis]</td><td>857.901</td><td>770.000</td><td>1.114</td><td>790.806</td><td>710.000</td><td>1.114</td><td>1.114</td></tr>
<tr><td>7</td><td>5</td><td>14</td><td>GB009A04</td><td>a76couture1684.r#1</td><td>>gb|AAB63650.1| (AC001645) Myb-related transcription activator (MybSt1) isolog</td><td>561.944</td><td>504.000</td><td>1.115</td><td>678.570</td><td>551.000</td><td>1.232</td><td>1.173</td></tr>
<tr><td>7</td><td>5</td><td>15</td><td>GB004H07</td><td>a76couture1592.r#1</td><td>>ref|NP_647646.1|| (NM_139389) CG12011 gene product [Drosophila melanogaster]</td><td>89.911</td><td>106.000</td><td>0.848</td><td>136.950</td><td>115.000</td><td>1.191</td><td>1.020</td></tr>
<tr><td>7</td><td>6</td><td>1</td><td>TT263C01</td><td>a76couture1449.r#1</td><td>>ref|NP_188031.1|| (NM_112271) glycolate oxidase. putative; protein id: At3g14150.1</td><td>318.435</td><td>384.000</td><td>0.829</td><td>404.670</td><td>543.000</td><td>0.745</td><td>0.787</td></tr>
<tr><td>7</td><td>6</td><td>2</td><td>GT174D05</td><td>a76couture1773.r#1</td><td>>pir||T30560 resistance protein RGC20 - garden lettuce (fragment)</td><td>61.189</td><td>45.000</td><td>1.360</td><td>87.524</td><td>59.000</td><td>1.483</td><td>1.422</td></tr>
<tr><td>7</td><td>6</td><td>3</td><td>GT162D05</td><td>a76couture1679.r#1</td><td>------</td><td>1196.315</td><td>1168.000</td><td>1.024</td><td>1690.761</td><td>1428.000</td><td>1.184</td><td>1.104</td></tr>
<tr><td>7</td><td>6</td><td>4</td><td>GB004B03</td><td>a76couture1587.r#1</td><td>------</td><td></td><td>12.000</td><td>0.000</td><td></td><td></td><td></td><td></td></tr>
<tr><td>7</td><td>6</td><td>5</td><td>TT262C10</td><td>a76couture1445.r#1</td><td>------</td><td>343.410</td><td>286.000</td><td>1.201</td><td>478.809</td><td>369.000</td><td>1.298</td><td>1.249</td></tr>
<tr><td>7</td><td>6</td><td>6</td><td>GT174A08</td><td>a76couture1769.r#1</td><td>>ref|XP_131191.1|| (XM_131191) hypothetical protein XP_131191 [Mus musculus]</td><td>101.150</td><td>76.000</td><td>1.331</td><td>144.157</td><td>109.000</td><td>1.323</td><td>1.327</td></tr>
<tr><td>7</td><td>6</td><td>7</td><td>GT162B08</td><td>a76couture1677#1</td><td>>ref|NP_565258.1|| (NM_126188) expressed protein; protein id: At2g01270.1. supported</td><td>23.727</td><td>27.000</td><td>0.879</td><td>36.039</td><td>37.000</td><td>0.974</td><td>0.926</td></tr>
<tr><td>7</td><td>6</td><td>8</td><td>GB003H04</td><td>a76couture1582.r#1</td><td>>ref|NP_186824.1|| (NM_111041) hypothetical protein; protein id: At3g01750.1</td><td>1161.350</td><td>1080.000</td><td>1.075</td><td>1380.822</td><td>1209.000</td><td>1.142</td><td>1.109</td></tr>
<tr><td>7</td><td>6</td><td>9</td><td>TT262A12</td><td>a76couture1440.r#1</td><td>>gb|AAL85017.1| (AY080650) putative DNA-binding protein [Arabidopsis thaliana]</td><td>42.458</td><td>35.000</td><td>1.213</td><td>39.128</td><td>33.000</td><td>1.186</td><td>1.199</td></tr>
<tr><td>7</td><td>6</td><td>10</td><td>GT173G04</td><td>a76couture1765.r#1</td><td>>gb|ZP_00043120.1| (NZ_AAAN01000125) hypothetical protein [Magnetococcus sp. MC-1]</td><td>283.469</td><td>317.000</td><td>0.894</td><td>308.909</td><td>327.000</td><td>0.945</td><td>0.919</td></tr>
<tr><td>7</td><td>6</td><td>11</td><td>GT161F04</td><td>a76couture1672.r#1</td><td>>ref|NP_192086.1|| (NM_116407) hypothetical protein; protein id: At4g01770.1</td><td>333.420</td><td>342.000</td><td>0.975</td><td>343.918</td><td>312.000</td><td>1.102</td><td>1.039</td></tr>
<tr><td>7</td><td>6</td><td>12</td><td>GB003B07</td><td>a76couture1577.r#1</td><td>>ref|NP_193728.1|| (NM_118113) putative protein; protein id: At4g19950.1 [Arabidopsis</td><td>144.857</td><td>169.000</td><td>0.857</td><td>146.217</td><td>134.000</td><td>1.091</td><td>0.974</td></tr>
<tr><td>7</td><td>6</td><td>13</td><td>RT064B10</td><td>a76couture1433.r#1</td><td>>ref|NP_199011.1|| (NM_123561) unknown protein; protein id: At5g41960.1 [Arabidopsis</td><td>127.374</td><td>124.000</td><td>1.027</td><td>119.445</td><td>97.000</td><td>1.231</td><td>1.129</td></tr>
<tr><td>7</td><td>6</td><td>14</td><td>GT173D06</td><td>a76couture1761.r#1</td><td>>dbj|BAB86920.1| (AB070745) glucosyltransferase-2 [Vigna angularis]</td><td>23.727</td><td>27.000</td><td>0.879</td><td>28.831</td><td>26.000</td><td>1.109</td><td>0.994</td></tr>
<tr><td>7</td><td>6</td><td>15</td><td>GB009H10</td><td>a76couture1668.r#1</td><td>------</td><td>0.000</td><td></td><td></td><td>5.148</td><td>8.000</td><td>0.644</td><td>0.644</td></tr>
<tr><td>7</td><td>7</td><td>1</td><td>GB002C06</td><td>a76couture1572.r#1</td><td>>gb|AAF63167.1|AC010657_3 (AC010657) T5E21.7 [Arabidopsis thaliana]</td><td>352.151</td><td>266.000</td><td>1.324</td><td>592.075</td><td>439.000</td><td>1.349</td><td>1.336</td></tr>
<tr><td>7</td><td>7</td><td>2</td><td>TT253B01</td><td>a76couture1421.r#1</td><td>>gb|AAK44146.1|AF370331_1 (AF370331) unknown protein [Arabidopsis thaliana]</td><td>8064.515</td><td>5677.000</td><td>1.421</td><td>13271.750</td><td>9104.000</td><td>1.458</td><td>1.439</td></tr>
<tr><td>7</td><td>7</td><td>3</td><td>GT173B12</td><td>a76couture1757.r#1</td><td>>ref|NP_187319.1|| (NM_111543) unknown protein; protein id: At3g66654.1 [Arabidopsis</td><td>526.978</td><td>408.000</td><td>1.292</td><td>855.677</td><td>652.000</td><td>1.312</td><td>1.302</td></tr>
<tr><td>7</td><td>7</td><td>4</td><td>GB009H03</td><td>a76couture1665.r#1</td><td>------</td><td>11.239</td><td>18.000</td><td>0.624</td><td>15.445</td><td>18.000</td><td>0.858</td><td>0.741</td></tr>
<tr><td>7</td><td>7</td><td>5</td><td>GB001G09</td><td>a76couture1569.r#1</td><td>>ref|NP_671876.1|| (NM_147338) hypothetical protein; protein id: At2g24395.1</td><td>16.234</td><td>18.000</td><td>0.902</td><td>16.475</td><td>20.000</td><td>0.824</td><td>0.863</td></tr>
</table>

7	7	6	TT251F04	a76couture1418#1	>ref|NP_564834.1|| (NM_105116) Expressed protein; protein id: At1g64405.1. supported	353.400	389.000	0.908	557.065	505.000	1.103	1.006
7	7	7	RT034F01	a76couture2181.r#1	>dbj|BAB64115.1| (AP003235) putative aspartate aminotransferase [Oryza sativa							
7	7	8	RT023G10	a76couture2078.r#1	------	503.252	567.000	0.888	704.312	663.000	1.062	0.975
7	7	9	RB008C08	a76couture1991.r#1	>dbj|BAB78478.1| (AB062669) preproMP73 [Cucurbita maxima]	7.493	10.000	0.749	16.475	14.000	1.177	0.963
7	7	10	GT203C05	a76couture1877.r#1	------	221.031	195.000	1.133	288.315	231.000	1.248	1.191
7	7	11	RT034D08	a76couture2177.r#1	------	62.438	80.000	0.780	84.435	98.000	0.862	0.821
7	7	12	RT023F01	a76couture2074#1	------	73.677	99.000	0.744	72.079	86.000	0.838	0.791
7	7	13	RT012C04	a76couture1987.r#1	>ref|NP_188170.1|| (NM_112419) putative jasmonic acid regulatory protein; protein id:	1070.190	1028.000	1.041	1208.863	899.000	1.345	1.193
7	7	14	GT202H08	a76couture1867.r#1	>ref|NP_178480.1|| (NM_126432) putative snRNP splicing factor; protein id:	1567.198	1619.000	0.968	1780.344	1552.000	1.147	1.058
7	7	15	RT034C05	a76couture2173.r#1	>ref|NP_201202.2|| (NM_125793) putative protein; protein id: At5g63970.1. supported by							
7	8	1	RT023D12	a76couture2070.r#1	>gb|AAK63247.1|AF367433_1 (AF367433) phosphatidylinositol transfer-like protein III [Lotus	1603.412	1371.000	1.170	2278.717	1998.000	1.140	1.155
7	8	2	RT011G10	a76couture1983#1	------	27.473	23.000	1.194	28.831	28.000	1.030	1.112
7	8	3	GT202F09	a76couture1863.r#1	>ref|NP_566732.1|| (NM_113263) expressed protein; protein id: At3g23600.1. supported	422.082	462.000	0.914	597.224	583.000	1.024	0.969
7	8	4	RT034A09	a76couture2167.r#1	>ref|NP_188660.2|| (NM_112916) pumilio-family RNA-binding protein. putative; protein id:	119.881	125.000	0.959	212.117	188.000	1.128	1.044
7	8	5	RT023C02	a76couture2066.r#1	>ref|NP_197045.1|| (NM_121545) cyclic nucleotide-regulated ion channel (CNGC2);	98.652	68.000	1.451	141.068	86.000	1.640	1.546
7	8	6	RT011C05	a76couture1980.r#1	>ref|NP_566562.1|| (NM_112571) dihydrolipoamide dehydrogenase. putative; protein id:	81.170	72.000	1.127	149.306	116.000	1.287	1.207
7	8	7	GT202D08	a76couture1859.r#1	>pir||T07844 BURP domain-containing protein - rape >gi|3098571|gb|AAC15700.1|	93.657	131.000	0.715	124.593	145.000	0.859	0.787
7	8	8	RT033G12	a76couture2164#1	------	18.731	27.000	0.694	30.891	32.000	0.965	0.830
7	8	9	RT023A03	a76couture2062#1	>ref|NP_194186.1|| (NM_118588) clathrin coat assembly like protein; protein id:	24.975	25.000	0.999	43.247	31.000	1.395	1.197
7	8	10	RB008H08	a76couture1976.r#1	------	33.717	34.000	0.992	84.435	61.000	1.384	1.188
7	8	11	GT201C03	a76couture1853.r#1	>ref|NP_564640.1|| (NM_104245) transcriptional regulator. putative; protein id:	372.132	386.000	0.964	567.362	461.000	1.231	1.097
7	8	12	RT033F10	a76couture2160.r#1	>ref|NP_199373.1|| (NM_123928) putative protein; protein id: At5g45600.1. supported by	26.224	47.000	0.558	33.980	45.000	0.755	0.657
7	8	13	RT022F10	a76couture2058#1	>ref|NP_182033.1|| (NM_130071) putative transport protein SEC61 beta-subunit; protein	124.876	157.000	0.795	133.860	128.000	1.046	0.921
7	8	14	RB008H01	a76couture1975#1	>emb|CAB97476.2| (AL389901) conserved hypothetical protein [Neurospora crassa]	36.214	45.000	0.805	44.277	50.000	0.886	0.845
7	8	15	GT202A10	a76couture1849.r#1	------	354.649	274.000	1.294	480.868	301.000	1.598	1.446
7	9	1	RT064C10	a76couture2604.r#1	>gb|AAM47602.1|AF513859_1 (AF513859) ovule/fiber cell elongation protein Ghfe1 [Gossypium	3325.457	2793.000	1.191	4324.722	3582.000	1.207	1.199
7	9	2	TT251F11	a76couture2485#1	>pir||T02195 hypothetical protein F14M4.25 - Arabidopsis thaliana	144.857	145.000	0.999	230.652	204.000	1.131	1.065
7	9	3	RT063D05	a76couture2372.r#1	>gb|AAF65513.1| (AF108896) GTP-binding protein [Capsicum annuum]	1051.459	934.000	1.126	1619.712	1391.000	1.164	1.145
7	9	4	RT052B03	a76couture2274.r#1	>ref|NP_568128.1|| (NM_120469) auxin-regulated protein; protein id: At5g03880.1	270.982	228.000	1.189	324.354	278.000	1.167	1.178
7	9	5	RT064B01	a76couture2600.r#1	>ref|NP_181861.2|| (NM_129894) putative membrane transporter; protein id: At2g43330.1	317.186	279.000	1.137	453.066	409.000	1.108	1.122
7	9	6	TT251E02	a76couture2481#1	>sp|P93841|ISPE_LYCES 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase. chloroplast	107.394	98.000	1.096	170.930	134.000	1.276	1.186
7	9	7	RT063B04	a76couture2368.r#1	>ref|NP_177267.1|| (NM_105780) hypothetical protein; protein id: At1g71110.1	94.906	116.000	0.818	145.187	152.000	0.955	0.887
7	9	8	RT051G03	a76couture2271#1	------	22.478	33.000	0.681	27.802	25.000	1.112	0.897
7	9	9	TB000A03	a76couture2595.r#1	------	959.050	937.000	1.024	1610.444	1124.000	1.433	1.228
7	9	10	TT254C08	a76couture2477.r#1	>dbj|BAB78487.1| (AB037150) 26S proteasome regulatory particle non-ATPase subunit8	1765.752	1782.000	0.991	2628.813	1977.000	1.330	1.160
7	9	11	RT062F02	a76couture2361.r#1	------	299.703	298.000	1.006	497.343	376.000	1.323	1.164
7	9	12	RT051F01	a76couture2267.r#1	>ref|NP_499380.1|| (NM_066979) Y39A1B.2.p [Caenorhabditis elegans]	149.852	158.000	0.948	228.592	177.000	1.291	1.120
7	9	13	RT064E10	a76couture2572.r#1	>ref|NP_224038.1|| (NC_000921) putative histidine-rich metal-binding protein	718.039	627.000	1.145	836.113	711.000	1.176	1.161
7	9	14	TT254B08	a76couture2472.r#1	>gb|AAM65894.1| (AY088355) unknown [Arabidopsis thaliana]	127.374	136.000	0.937	164.751	153.000	1.077	1.007
7	9	15	RT062D08	a76couture2357.r#1	ref|NP_191462.1|| (NM_115765) putative protein [Arabidopsis thal... 191 1e-047	123.628	143.000	0.865	215.206	184.000	1.170	1.017
7	10	1	RT053C05	a76couture2265#1	------	36.214	55.000	0.658	44.277	57.000	0.777	0.718
7	10	2	TT283A08	a76couture2567.r#1	>ref|NP_197901.1|| (NM_122428) ethylene-responsive element - like protein; protein id:	1092.668	816.000	1.339	1279.912	937.000	1.366	1.353
7	10	3	TT253G03	a76couture2469#1	>gb|AAM29184.1| (AY098940) CDPK-like protein [Solanum tuberosum]	19.980	22.000	0.908	25.742	23.000	1.119	1.014
7	10	4	RT062A09	a76couture2353.r#1	>ref|NP_567969.1|| (NM_119632) putative protein; protein id: At4g34660.1. supported by	302.201	260.000	1.162	515.878	431.000	1.197	1.180
7	10	5	RT052E05	a76couture2261.r#1	>ref|NP_565249.1|| (NM_106743) expressed protein; protein id: At1g80950.1. supported	407.097	375.000	1.086	580.748	484.000	1.200	1.143
7	10	6	TT283D12	a76couture2564.r#1	------	72.428	60.000	1.207	121.504	89.000	1.365	1.286
7	10	7	TT253D07	a76couture2465.r#1	------	184.817	144.000	1.283	241.979	169.000	1.432	1.358
7	10	8	RT061H10	a76couture2349.r#1	>emb|CAA05278.1| (AJ002236) loxc homologue [Lycopersicon pimpinellifolium]	6868.200	6239.000	1.101	9509.241	7758.000	1.226	1.163
7	10	9	RT051D12	a76couture2257.r#1	------	13.736	15.000	0.916	20.594	19.000	1.084	1.000
7	10	10	ST002B09	a76couture3111.r#1	>gb|AAF65770.1|AF242312_1 (AF242312) cyclophilin [Euphorbia esula]	9174.666	9772.000	0.939	14767.898	10925.000	1.352	1.145
7	10	11	PT012G01	a76couture2962.r#1	>ref|NP_191429.1|| (NM_115732) ribosomal protein L11 -like; protein id: At3g58700.1	4163.378	3338.000	1.247	6393.381	4027.000	1.588	1.417
7	10	12	PT005G07	a76couture2814.r#1	------	574.431	564.000	1.018	985.419	742.000	1.328	1.173
7	10	13	PT008C12	a76couture2708.r#1	>dbj|BAB86225.1| (AP003922) putative hydroxymethyltransferase [Oryza sativa	253.499	284.000	0.893	372.750	337.000	1.106	0.999
7	10	14	RT054H08	a76couture3104.r#1	>sp|P50346|RLA0_SOYBN 60S ACIDIC RIBOSOMAL PROTEIN P0 >gi|7440740|pir||T07106 acidic	1973.046	2098.000	0.940	2722.516	2318.000	1.175	1.057
7	10	15	GT192H06	a76couture2958.r#1	>sp|P48495|TPIS_PETHY Triosephosphate isomerase. cytosolic (TIM)	5581.973	5130.000	1.088	7736.105	6603.000	1.172	1.130
7	11	1	PT013E08	a76couture2810.r#1	>gb|AAK51682.1| (AF297617) NADH dehydrogenase subunit 2 [Echinococcus granulosus]	990.269	722.000	1.372	1298.446	897.000	1.448	1.410
7	11	2	PT003F04	a76couture2703.r#1	>ref|NP_191779.1|| (NM_116085) putative protein; protein id: At3g62200.1 [Arabidopsis	373.380	268.000	1.393	455.126	307.000	1.482	1.438
7	11	3	RT041D11	a76couture3099.r#1	>sp|Q9FVI1|ADF2_PETHY Actin-depolymerizing factor 2 (ADF 2)	28.722	30.000	0.957	45.307	41.000	1.105	1.031
7	11	4	GT194D07	a76couture2953.r#1	>dbj|BAB33422.1| (AB049724) putative senescence-associated protein [Pisum sativum]	5269.782	4291.000	1.228	7506.483	5614.000	1.337	1.283
7	11	5	PT007A04	a76couture2806.r#1	>ref|NP_051079.1|| (NC_000932) photosystem I subunit IX [Arabidopsis thaliana]	3869.918	2511.000	1.541	5830.138	3605.000	1.617	1.579
7	11	6	PT001F10	a76couture2699.r#1	------	236.016	245.000	0.963	385.106	315.000	1.223	1.093
7	11	7	RT023C11	a76couture3092.r#1	------	24.975	28.000	0.892	40.158	38.000	1.057	0.974
7	11	8	GT182E05	a76couture2947.r#1	>dbj|BAB62405.1| (AB049578) mitochondrial processing peptidase alpha subunit [Morus	1886.882	1870.000	1.009	2305.489	1959.000	1.177	1.093
7	11	9	PT010G05	a76couture2802.r#1	>ref|NP_181990.1|| (NM_130026) acyl carrier protein; protein id: At2g44620.1	9.990	25.000	0.400	17.505	35.000	0.500	0.450
7	11	10	PT005C06	a76couture2694.r#1	>ref|NP_680213.1|| (NM_147908) Expressed protein; protein id: At5g23575.1. supported	34.965	55.000	0.636	54.574	66.000	0.827	0.731
7	11	11	ST007D08	a76couture3087.r#1	>ref|NP_194842.1|| (NM_119263) putative protein; protein id: At4g31130.1. supported by	9022.317	8683.000	1.039	12803.238	9406.000	1.361	1.200
7	11	12	GT192A08	a76couture2937.r#1	>ref|NP_198801.1|| (NM_123348) 40S ribosomal protein S9-like; protein id: At5g39850.1	2512.512	1925.000	1.305	3958.151	2240.000	1.767	1.536
7	11	13	PT011B01	a76couture2798.r#1	>ref|NP_200962.1|| (NM_125547) glycosylasparaginase - like protein; protein id:	224.777	255.000	0.881	441.740	334.000	1.323	1.102

7	11	14	PT001B07	a76couture2689.r#1	------	352.151	339.000	1.039	609.580	485.000	1.257	1.148
7	11	15	PT012F06	a76couture3082.r#1	>pir||T51098 hypothetical protein p85RF [imported] - Prunus armeniaca	454.550	440.000	1.033	588.986	528.000	1.116	1.074
7	12	1	CT004H12	a76couture2929.r#1	>dbj|BAB84324.1| (AB079022) ras-related protein RAB8-3 [Nicotiana tabacum]	1043.966	831.000	1.256	1246.962	934.000	1.335	1.296
7	12	2	PT009G08	a76couture2792.r#1	>sp|O22518|RSP4_SOYBN 40S RIBOSOMAL PROTEIN SA (P40) >gi|7441124|pir||T05733	6713.353	5675.000	1.183	10092.049	7071.000	1.427	1.305
7	12	3	PT009A08	a76couture2686#1	------	3692.594	3141.000	1.176	4997.114	3760.000	1.329	1.252
7	12	4	RB007G08 RB007G08	couture_a76.423.c1.r#1	>emb|CAC12882.1| (AJ295005) O-linked GlcNAc transferase like [Nicotiana tabacum]	971.538	859.000	1.131	1450.841	1182.000	1.227	1.179
7	12	5	BG273924 GB000A63 GB000A63	couture_a76.340.c1.r#1	>gb|AAD38147.1|AF139500_1 (AF139500) unknown [Prunus armeniaca]	188.563	197.000	0.957	280.077	247.000	1.134	1.046
7	12	6	GB003e11 GT202A11	couture_a76.250.c1#1	>ref|NP_190383.1|| (NM_114669) aldehyde dehydrogenase (NAD+)-like protein; protein id:	872.886	991.000	0.881	1240.783	1130.000	1.098	0.989
7	12	7	BM436748 BM437829 RT042C09	couture_a76.161.c1.r#1	>sp|P48418|C751_PETHY Flavonoid 3'.5'-hydroxylase 1 (F3'5'H) (Cytochrome P450 75A1)	3771.266	4307.000	0.876	6215.244	5716.000	1.087	0.981
7	12	8	RB006B03 RB006B03	couture_a76.419.c1.r#1	>gb|AAL75899.1| (AY074846) At2g43020/MFL8.12 [Arabidopsis thaliana]	1459.805	1759.000	0.830	2103.669	1957.000	1.075	0.952
7	12	9	BG273917 GB000A70	couture_a76.338.c1#1	>ref|NP_565101.1|| (NM_106166) expressed protein; protein id: At1g75100.1. supported	233.519	184.000	1.269	333.621	209.000	1.596	1.433
7	12	10	BM436374 BM436822 BM437224 BM436994 GT	couture_a76.249.c1#1	>sp|P31336|PSBX_GOSHI Photosystem II 5 kDa protein. chloroplast precursor (PSII-T)	999.011	1028.000	0.972	1713.414	1273.000	1.346	1.159
7	12	11	BM437247 BM437714 BM436489 GT173E07	couture_a76.157.c1.r#1	>ref|NP_191706.1|| (NM_116012) light-harvesting chlorophyll a/b binding protein;	631.874	758.000	0.834	1036.904	946.000	1.096	0.965
7	12	12	BM436371 RB001F02	couture_a76.415.c1.r#1	>ref|NP_567775.1|| (NM_118880) putative protein; protein id: At4g27450.1. supported by	867.891	865.000	1.003	2044.976	1297.000	1.577	1.290
7	12	13	BG273908 GB000A82	couture_a76.333.c1#1	>ref|NP_568300.1|| (NM_121441) putative protein; protein id: At5g14370.1. supported by	8.741	22.000	0.397	23.683	31.000	0.764	0.581
7	12	14	RB000A92 BG273710 GT194F05	couture_a76.245.c1.r#1	>ref|NP_176968.1|| (NM_105471) hydroxypyruvate reductase (HPR); protein id:	399.604	568.000	0.704	972.033	845.000	1.150	0.927
7	12	15	RB005B09 RT073H01	couture_a76.151.c1.r#1	>gb|AAK30204.1|AF349963_1 (AF349963) endoxyloglucan transferase [Daucus carota]	1072.688	1150.000	0.933	1594.999	1554.000	1.026	0.980
7	13	1	BG273757 RB000A44	couture_a76.411.c1#1	>ref|NP_188856.2|| (NM_113114) far-red impaired response protein. putative; protein	191.061	166.000	1.151	273.899	216.000	1.268	1.210
7	13	2	BG273897 GB000A95	couture_a76.330.c1.r#1	>gb|AAM47506.1| (AY100447) iron-stress related protein [Citrus junos]	56.194	65.000	0.865	76.197	80.000	0.952	0.908
7	13	3	GB002b07 GT193E10	couture_a76.242.c1#1	>gb|AAL25647.1|AF197330_1 (AF197330) calcineurin-like protein [Eucalyptus grandis]	520.734	397.000	1.312	698.134	486.000	1.436	1.374
7	13	4	BM436997 BM437358 RT071G11	couture_a76.147.c1.r#1	>ref|NP_563636.1|| (NM_100065) expressed protein; protein id: At1g01820.1. supported	1221.291	1088.000	1.123	1574.405	1266.000	1.244	1.183
7	13	5	BG273751 RB000A50	couture_a76.408.c1#1	>ref|NP_198903.1|| (NM_123452) uridine kinase-like protein; protein id: At5g40870.1	701.805	739.000	0.950	1086.329	916.000	1.186	1.068
7	13	6	BG273894 GB000A98	couture_a76.329.c1#1	>ref|NP_199209.1|| (NM_123763) NTF2-containing RNA-binding protein. putative; protein	475.779	468.000	1.017	704.312	578.000	1.219	1.118
7	13	7	BM436515 CT002C11	couture_a76.24.c1.r#1	>gb|AAF31705.1|AF221856_1 (AF221856) heat-shock protein 80 [Euphorbia esula]	6263.798	5740.000	1.091	9615.300	7301.000	1.317	1.204
7	13	8	BM436424 BM437715 BM437969 BM436719 ST0	couture_a76.144.c1.r#1	>pir||T03958 heat shock protein 18p - common tobacco >gi|558606|emb|CAA50022.1|	13841.295	2645.000	5.233	24655.037	3945.000	6.250	5.741
7	13	9	BG273746 RB000A55	couture_a76.406.c1#1	>ref|NP_187193.1|| (NM_111415) unknown protein; protein id: At3g05420.1 [Arabidopsis	370.883	337.000	1.101	600.313	436.000	1.377	1.239
7	13	10	TB001c03 TT282B03	couture_a76.325.c1#1	>sp|O82147|SPDE_COFAR Spermidine synthase (Putrescine aminopropyltransferase) (SPDSY)	1595.920	1396.000	1.143	2452.735	1689.000	1.452	1.298
7	13	11	BM437650 BM436300 GT182H11	couture_a76.236.c1#1	>ref|NP_680180.1|| (NM_147875) unknown protein; protein id: At5g21920.1 [Arabidopsis	143.608	164.000	0.876	285.226	231.000	1.235	1.055
7	13	12	BM436875 CT004B05	couture_a76.14.c1.r#1	>sp|P47920|NDKB_FLABI NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B)	7975.853	8309.000	0.960	14304.534	10569.000	1.353	1.157
7	13	13	BM436778 RT054H10	couture_a76.612.c1.r#1	>gb|AAM22747.1| (AY090539) pyruvate kinase-like [Deschampsia antarctica]	214.787	305.000	0.704	596.194	524.000	1.138	0.921
7	13	14	BM436630 PT001C06	couture_a76.514.c1.r#1	>ref|NP_564614.1|| (NM_104150) expressed protein; protein id: At1g52720.1. supported	290.962	358.000	0.813	659.005	509.000	1.295	1.054
7	13	15	G1030069 VVCHIT1MR	couture_a76.sd.32.c1#	>sp|P51613|CHIB_VITVI BASIC ENDOCHITINASE PRECURSOR >gi|1030070|emb|CAA90970.1| (Z54234)	83.667	124.000	0.675	125.623	172.000	0.730	0.703
7	14	1	BM436847 BM436870 RT054H06	couture_a76.611.c1.r#1	>sp|P35135|UBC4_LYCES Ubiquitin-conjugating enzyme E2-17 kDa (Ubiquitin-protein ligase)	1898.121	1724.000	1.101	2953.168	2358.000	1.252	1.177
7	14	2	BG273820 TB000A74 TB000A74	couture_a76.489.c1.r#1	>ref|NP_177412.1|| (NM_105927) putative cinnamyl-alcohol dehydrogenase; protein id:	571.934	530.000	1.079	910.251	725.000	1.256	1.167
7	14	3	BM436698 ST005G07	couture_a76.93.c1.r#1	>gb|AAD41409.1|AF159562_1 (AF159562) cytosolic class II low molecular weight heat shock	1413.600	493.000	2.867	1990.402	641.000	3.105	2.986
7	14	4	TT263C10 BG273753 RT083A07	couture_a76.606.c1#1	>emb|CAC84489.1| (AJ309088) putative translation factor [Pinus pinaster]	2849.678	2394.000	1.190	4324.722	3083.000	1.403	1.297
7	14	5	BM437818 BM436825 PT003B04	couture_a76.509.c1.r#1	>gb|AAM65892.1| (AY088353) unknown [Arabidopsis thaliana]	189.812	199.000	0.954	476.749	371.000	1.285	1.119
7	14	6	BG273882 TB000A10 BM436295 ST003H12	couture_a76.87.c1.r#1	>dbj|BAB20799.1| (AB045710) sucrose synthase 1 [Pyrus pyrifolia]	2939.589	2715.000	1.083	4748.957	3714.000	1.279	1.181
7	14	7	GB004c08 GB009D04	couture_a76.574.c1#1	>sp|P51850|DCP1_PEA Pyruvate decarboxylase isozyme 1 (PDC) >gi|2146786|pir||S65470	108.642	160.000	0.679	188.434	222.000	0.849	0.764
7	14	8	TT282G09 BM437782	couture_a76.484.c1.r#1	>dbj|BAB02198.1| (AP001298) contains similarity to alpha	668.089	774.000	0.863	992.627	923.000	1.075	0.969
7	14	9	AW707967 ST003E04	couture_a76.86.c1.r#1	>emb|CAA55009.1| (X78119) prunin [Prunus dulcis]	10589.515	5319.000	1.991	16349.510	6426.000	2.544	2.268
7	14	10	RB005F04 RT093H05	couture_a76.547.c1#1	>gb|AAD48485.1|AF170798_1 (AF170798) S-adenosyl-L-methionine synthetase [Petunia x hybrida]	9573.021	7967.000	1.202	14618.592	9906.000	1.476	1.339
7	14	11	G8699607 AF271662	couture_a76.sd.7.c1#1	>gb|AAF78759.1|AF271662_1 (AF271662) putative aquaporin TIP2 [Vitis berlandieri x Vitis	19.980	24.000	0.833	36.039	31.000	1.163	0.998
7	14	12	BM436855 BG273758 RB000A43	couture_a76.618.c1.r#1	>sp|P46280|EFT2_SOYBN ELONGATION FACTOR TU. CHLOROPLAST PRECURSOR (EF-TU)	193.558	190.000	1.019	332.592	244.000	1.363	1.191
7	14	13	BM437832 PT008G06	couture_a76.523.c1#1	>ref|NP_194120.1|| (NM_118521) putative protein; protein id: At4g23890.1. supported by	169.832	145.000	1.171	287.285	195.000	1.473	1.322
7	14	14	AJ430532 RT082E10	couture_a76.614.c1.r#1	>pir||S54172 inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco	2721.056	3579.000	0.760	5577.862	4901.000	1.138	0.949
7	14	15	BM436330 BM438063 BM437706 GT192B08	couture_a76.542.c1.r#1	>ref|NP_191788.1|| (NM_116094) ADP-ribosylation factor-like protein; protein id:	2701.076	2275.000	1.187	5022.856	3226.000	1.557	1.372
8	1	1	CM002F02	a76couture0424.r#1	>ref|NP_567701.1|| (NM_118571) putative protein; protein id: At4g24380.1. supported by	2029.241	1992.000	1.019	2645.289	2283.000	1.159	1.089
8	1	2	RT093A06	a76couture0313.r#1	>ref|NP_194153.1|| (NM_118555) putative protein; protein id: At4g24220.1. supported by	4516.778	3438.000	1.314	5297.785	4008.000	1.322	1.318
8	1	3	RT052H09	a76couture0181.r#1	>sp|O82531|PSB1_PETHY Proteasome subunit beta type 1 (20S proteasome alpha subunit F)	680.576	771.000	0.883	847.440	909.000	0.932	0.907
8	1	4	RT093F08	a76couture0009.r#1	>ref|NP_039864.1|| (NC_001345) major outer envelope glycoprotein [Human herpesvirus 4]	21427.534	19077.000	1.123	26850.348	21745.000	1.235	1.179
8	1	5	CM002E05	a76couture0420.r#1	>ref|NP_196885.1|| (NM_121384) putative protein; protein id: At5g13810.1. supported by	212.290	183.000	1.160	194.613	155.000	1.256	1.208
8	1	6	RT092A08	a76couture0308.r#1	>dbj|BAB18760.1| (AB027000) beta-cyanoalanine synthase [Solanum tuberosum]	228.524	223.000	1.025	396.433	319.000	1.243	1.134
8	1	7	RT053A12	a76couture0176.r#1	>sp|Q9FUM1|EF1G_PRUAV Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma)	1770.747	1691.000	1.047	2435.231	2079.000	1.171	1.109
8	1	8	GT204B03	a76couture2997.r#1	>sp|P29766|RL2_LYCES 60S RIBOSOMAL PROTEIN L2 (L8) (RIBOSOMAL PROTEIN TL2)	827.930	755.000	1.097	985.419	950.000	1.037	1.067
8	1	9	CM002C04	a76couture0415.r#1	>gb|AAK91459.1| (AY050444) At5g65691/F16M2.160 [Arabidopsis thaliana]	57.443	55.000	1.044	76.197	73.000	1.044	1.044
8	1	10	RT084G09	a76couture0303.r#1	>pir||JC4321 gibberellin responsive protein LRG11 - garden lettuce	1499.765	1972.000	0.761	2375.508	2918.000	0.814	0.787
8	1	11	RT041F09	a76couture0171.r#1	>dbj|BAB09481.1| (AB012246) contains similarity to transcription	72.428	78.000	0.929	115.326	109.000	1.058	0.993
8	1	12	PT001D08	a76couture2658.r#1	------	144.857	127.000	1.141	166.811	128.000	1.303	1.222
8	1	13	CM002A07	a76couture0411.r#1	------	56.194	62.000	0.906	83.405	86.000	0.970	0.938
8	1	14	RT083F01	a76couture0296.r#1	>ref|NP_187867.1|| (NM_112096) DNA-damage-repair/toleration protein. putative	5016.283	5769.000	0.870	8913.047	9932.000	0.897	0.883
8	1	15	GT204D03	a76couture0166.r#1	>gb|AAN03626.1|AF406702_1 (AF406702) BEL1-related homeotic protein 29 [Solanum tuberosum]	4605.440	4682.000	0.984	6974.130	7133.000	0.978	0.981
8	2	1	GT181C10	a76couture1787.r#1	------	43.707	53.000	0.825	89.584	84.000	1.066	0.946
8	2	2	CM001G05	a76couture0406.r#1	------	68.682	53.000	1.296	70.019	54.000	1.297	1.296
8	2	3	ST006G06	a76couture0287.r#1	------	355.898	378.000	0.942	439.680	442.000	0.995	0.968
8	2	4	RT033H06	a76couture0159.r#1	>gb|AAM65725.1| (AY088182) putative dehydrogenase [Arabidopsis thaliana]	1201.311	936.000	1.283	1384.941	998.000	1.388	1.336
8	2	5	RT074D01	a76couture0949.r#1	>ref|NP_180196.1|| (NM_128185) unknown protein; protein id: At2g26280.1 [Arabidopsis	1058.951	950.000	1.115	1272.704	1006.000	1.265	1.190
8	2	6	CM001E06	a76couture0402.r#1	>emb|CAA73220.1| (Y12689) isoflavone reductase-like protein [Citrus x paradisi]	511.993	865.000	0.592	788.747	1022.000	0.772	0.682

8	2	7	ST006C06	a76couture0283.r#1	>ref|NP_190647.1|| (NM_114938) putative protein; protein id: At3g50780.1 [Arabidopsis	231.021	229.000	1.009	291.404	276.000	1.056	1.032
8	2	8	RT051A05	a76couture0150.r#1	>dbj|BAA95845.1| (AP002070) Similar to Arabidopsis thaliana low temperature and salt	13556.577	12173.000	1.114	14007.982	12320.000	1.137	1.125
8	2	9	CM003H09	a76couture0454.r#1	>dbj|BAA88530.1| (AP000969) ESTs AU070430(S15424). AU082086(E11580) correspond to a	133.618	138.000	0.968	177.108	175.000	1.012	0.990
8	2	10	RT083G05	a76couture0839.r#1	>gb|AAM92707.1| (AY123417) putative glycine decarboxylase subunit [Triticum	126.125	122.000	1.034	157.543	151.000	1.043	1.039
8	2	11	ST006H10	a76couture0720.r#1	>dbj|BAA83711.1| (AB014484) heat shock factor [Nicotiana tabacum]	362.141	357.000	1.014	530.293	491.000	1.080	1.047
8	2	12	CT006G11	a76couture0623.r#1	------	184.817	166.000	1.113	230.652	176.000	1.311	1.212
8	2	13	CT002D10	a76couture0523.r#1	>dbj|BAB63782.1| (AP003607) putative cinnamoyl CoA reductase [Oryza sativa (japonica	575.680	538.000	1.070	741.381	674.000	1.100	1.085
8	2	14	RT083B01	a76couture0834.r#1	>emb|CAA10608.1| (AJ132228) amino acid carrier [Ricinus communis]	1613.403	1984.000	0.813	2225.173	2942.000	0.756	0.785
8	2	15	ST006G10	a76couture0716.r#1	>pir||T17459 polyprotein - tomato >gi|4235644|gb|AAD13304.1| (AF119040)	112.389	79.000	1.423	128.712	99.000	1.300	1.361
8	3	1	CT006F01	a76couture0619.r#1	------	108.642	120.000	0.905	175.048	157.000	1.115	1.010
8	3	2	CT002B11	a76couture0519.r#1	------	325.927	365.000	0.893	376.869	385.000	0.979	0.936
8	3	3	RT081F04	a76couture0830.r#1	>gb|AAM91528.1| (AY128325) putative casein kinase [Arabidopsis thaliana]	2126.644	1870.000	1.137	2192.222	1927.000	1.138	1.137
8	3	4	ST006F06	a76couture0712.r#1	>ref|NP_176633.1|| (NM_105127) 26S proteasome regulatory subunit (RPN12). putative;	39.960	44.000	0.908	53.544	53.000	1.010	0.959
8	3	5	CT006E05	a76couture0615.r#1	>ref|NP_190075.1|| (NM_114358) RP19 gene for chloroplast ribosomal protein CL9;	78.672	69.000	1.140	91.643	70.000	1.309	1.225
8	3	6	CM005g06	a76couture0514.r#1	ef|NP_189282.1|| (NM_113558) unknown protein [Arabidopsis thali... 46 7e-005	67.433	76.000	0.887	92.673	93.000	0.996	0.942
8	3	7	RT074H11	a76couture0823.r#1	>gb|AAK76703.1| (AY046029) unknown protein [Arabidopsis thaliana]	2698.578	4609.000	0.586	4504.919	5724.000	0.787	0.686
8	3	8	ST006E03	a76couture0708.r#1	>ref|NP_177021.1|| (NM_105525) putative reductase; protein id: At1g68540.1	14.985	17.000	0.881	14.416	21.000	0.686	0.784
8	3	9	ST002F05	a76couture0610.r#1	>pir||T06023 squalene monooxygenase (EC 1.14.99.7) - Arabidopsis thaliana	43.707	53.000	0.825	74.138	83.000	0.893	0.859
8	3	10	CM005e12	a76couture0508.r#1	p|Q9XGY5|IM13_ORYSA Mitochondrial import inner membrane translo... 92 2e-018	29.970	38.000	0.789	41.188	49.000	0.841	0.815
8	3	11	RT062F05	a76couture0818.r#1	>gb|AAM64382.1| (AY086310) unknown [Arabidopsis thaliana]	440.814	490.000	0.900	705.342	688.000	1.025	0.962
8	3	12	Arabidopsis Control Oligonucleotide	3ara7		17.483	21.000	0.833	21.624	25.000	0.865	0.849
8	3	13	ST002B07	a76couture0606.r#1	>dbj|BAA96982.1| (AB023037) 11-beta-hydroxysteroid dehydrogenase-like [Arabidopsis	17.483	28.000	0.624	20.594	27.000	0.763	0.694
8	3	14	CM005e02	a76couture0504.r#1	sp|P49299|CYSZ_CUCMA CITRATE SYNTHASE, GLYOXYSOMAL PRECURSOR (GC... 279 2e-074	724.283	639.000	1.133	1027.636	908.000	1.132	1.133
8	3	15	RT022E11	a76couture0813#1	>ref|NP_568343.1|| (NM_121727) putative protein; protein id: At5g17210.1. supported by	460.794	457.000	1.008	776.391	726.000	1.069	1.039
8	4	1	ST006B02	a76couture0700.r#1	>gb|AAD42942.1|AF091840_1 (AF091840) 15 kDa oleosin [Sesamum indicum]	11.239	14.000	0.803	27.802	22.000	1.264	1.033
8	4	2	ST001H11	a76couture0602.r#1	>pir||T05290 hypothetical protein T4L20.280 - Arabidopsis thaliana	784.224	877.000	0.894	818.608	803.000	1.019	0.957
8	4	3	CM005c04	a76couture0500.r#1	none	61.189	63.000	0.971	61.782	65.000	0.950	0.961
8	4	4	RT021E12	a76couture1304#1	>sp|P26301|ENO1_MAIZE Enolase 1 (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate	3807.480	3985.000	0.955	5474.893	4511.000	1.214	1.085
8	4	5	GT184B01	a76couture1170.r#1	>ref|NP_524119.1|| (NM_079395) Disabled [Drosophila melanogaster]	0.000			4.119	7.000	0.588	0.588
8	4	6	RT092C10	a76couture1048.r#1	------	18.731	28.000	0.669	25.742	35.000	0.735	0.702
8	4	7	RT081G01	a76couture0953#1	------	76.175	87.000	0.876	103.999	99.000	1.050	0.963
8	4	8	RT021A06	a76couture1299#1	>gb|AAG29594.1|AF196287_1 (AF196287) Ser/Thr specific protein phosphatase 2A A regulatory	234.768	219.000	1.072	316.117	266.000	1.188	1.130
8	4	9	GT182F07	a76couture1164.r#1	>ref|NP_191580.1|| (NM_115884) chloroplast chaperonin 10. putative; protein id:	168.583	124.000	1.360	214.177	173.000	1.238	1.299
8	4	10	RT093C11	a76couture1044.r#1	>dbj|BAB03145.1| (AP002047) actin-like protein [Arabidopsis thaliana]	92.409	87.000	1.062	139.009	124.000	1.121	1.092
8	4	11	RT074E01	a76couture0950#1	------	344.659	368.000	0.937	526.175	537.000	0.980	0.958
8	4	12	RT012F03	a76couture1295.r#1	>ref|NP_174485.1|| (NM_102939) secretory carrier membrane protein. putative; protein	1359.904	1443.000	0.942	2199.430	2017.000	1.090	1.016
8	4	13	GT183C07	a76couture1157.r#1	>gb|AAK44165.1|AF370350_1 (AF370350) unknown protein [Arabidopsis thaliana]	1198.813	1049.000	1.143	1656.781	1425.000	1.163	1.153
8	4	14	RT091F12	a76couture1038.r#1	>ref|NP_005270.1|| (NM_005279) G protein-coupled receptor 1 [Homo sapiens]	1153.858	1194.000	0.966	1603.236	1722.000	0.931	0.949
8	4	15	RT073H08	a76couture0945.r#1	>dbj|BAB90317.1| (AP003447) contains ESTs AU078053(R10920).AU078052(R10920)~unknown	4158.383	2475.000	1.680	5543.882	3566.000	1.555	1.617
8	5	1	RB008D09	a76couture1290.r#1	>emb|CAA75593.1| (Y15371) MtN5 [Medicago truncatula]	384.619	466.000	0.825	541.620	525.000	1.032	0.929
8	5	2	GT181D01	a76couture1153.r#1	>gb|AAM90848.1|AF481952_1 (AF481952) hairy meristem [Petunia x hybrida]	498.257	520.000	0.958	713.579	588.000	1.214	1.086
8	5	3	RT091C01	a76couture1034.r#1	------							
8	5	4	RT073E01	a76couture0943.r#1	------	38.712	50.000	0.774	57.663	67.000	0.861	0.817
8	5	5	RB007F06	a76couture1285.r#1	>ref|NP_188538.1|| (NM_112794) hypothetical protein; protein id: At3g19080.1							
8	5	6	GT174H02	a76couture1149.r#1	>gb|AAM64685.1| (AY087127) unknown [Arabidopsis thaliana]	13.736	10.000	1.374	18.535	14.000	1.324	1.349
8	5	7	RT084F04	a76couture1030.r#1	>ref|NP_568037.1|| (NM_119984) Expressed protein; protein id: At4g38225.1. supported	171.081	154.000	1.111	253.305	221.000	1.146	1.129
8	5	8	RT072H10	a76couture0939.r#1	>pir||T07050 hypothetical protein R1 - potato >gi|3287270|emb|CAA70725.1| (Y09533)	2797.230	2322.000	1.205	3082.909	2729.000	1.130	1.167
8	5	9	RB008B02	a76couture1278.r#1	>pir||T50822 ribosomal protein S26. cytosolic [imported] - garden pea	5880.428	3941.000	1.492	7327.316	4963.000	1.476	1.484
8	5	10	GT174A10	a76couture1142.r#1	>ref|NP_568187.1|| (NM_120890) syntaxin SYP132; protein id: At5g08080.1. supported by	1422.342	1355.000	1.050	1916.264	1801.000	1.064	1.057
8	5	11	RT084C03	a76couture1026.r#1	>ref|NP_187172.1|| (NM_111394) putative nucleotide repair protein; protein id:	179.822	174.000	1.033	229.622	213.000	1.078	1.056
8	5	12	RT072E12	a76couture0936.r#1	------	153.598	164.000	0.937	283.166	231.000	1.226	1.081
8	5	13	GT172F03	a76couture1754#1	>ref|NP_566066.1|| (NM_130184) Expressed protein; protein id: At2g46220.1. supported	372.132	390.000	0.954	580.748	550.000	1.056	1.005
8	5	14	GB009G09	a76couture1662.r#1	------	19.980	26.000	0.768	14.416	20.000	0.721	0.745
8	5	15	GB001C03	a76couture1565.r#1	>ref|NP_194555.1|| (NM_118966) putative protein; protein id: At4g28260.1 [Arabidopsis	153.598	160.000	0.960	213.147	214.000	0.996	0.978
8	6	1	TT253A10	a76couture1414.r#1	>gb|AAM63624.1| (AY086561) DnaJ protein. putative [Arabidopsis thaliana]	87.413	73.000	1.197	154.454	87.000	1.775	1.486
8	6	2	GT171C01	a76couture1749.r#1	>ref|NP_564756.1|| (NM_104729) expressed protein; protein id: At1g60420.1. supported	4239.552	4041.000	1.049	5445.032	4384.000	1.242	1.146
8	6	3	GB009G04	a76couture1658.r#1	------	14.985	19.000	0.789	10.297	16.000	0.644	0.716
8	6	4	GB001B02	a76couture1561.r#1	>ref|NP_194380.1|| (NM_118783) putative protein; protein id: At4g26500.1. supported by	179.822	166.000	1.083	270.810	198.000	1.368	1.225
8	6	5	TT251A12	a76couture1410#1	>ref|NP_565702.1|| (NM_128610) putative C3HC4 zinc finger protein; protein id:	314.688	450.000	0.699	479.838	510.000	0.941	0.820
8	6	6	GT173B06	a76couture1745.r#1	------	839.169	779.000	1.077	1199.596	995.000	1.206	1.141
8	6	7	GB009F08	a76couture1655.r#1	>pir||T09845 L-ascorbate peroxidase (EC 1.11.1.11). glyoxysomal - upland cotton	82.418	82.000	1.005	118.415	108.000	1.096	1.051
8	6	8	TT283C02	a76couture1526.r#1	>ref|NP_563946.1|| (NM_101300) RRM-containing protein; protein id: At1g14340.1	1010.250	1467.000	0.689	1475.554	1873.000	0.788	0.738
8	6	9	TB007B11	a76couture1406.r#1	>gb|AAB61100.1| (AC002062) ESTs gb|R30459.gb|N38441 come from this gene.	1553.462	1592.000	0.976	2081.015	2082.000	1.000	0.988
8	6	10	GT173A05	a76couture1741.r#1	>dbj|BAB10214.1| (AB010077) contains similarity to unknown	1974.295	1697.000	1.163	2784.298	2502.000	1.113	1.138
8	6	11	GB009E06	a76couture1651.r#1	>gb|AAH12382.1|AAH12382 (BC012382) Unknown (protein for MGC:21495) [Homo sapiens]	38.712	44.000	0.880	27.802	39.000	0.713	0.796
8	6	12	TT283G10	a76couture1522.r#1	------	484.520	518.000	0.935	733.143	707.000	1.037	0.986
8	6	13	TB005D04	a76couture1401.r#1	>ref|NP_564078.1|| (NM_101788) expressed protein; protein id: At1g19310.1. supported	163.588	180.000	0.909	249.186	245.000	1.017	0.963
8	6	14	GT172G06	a76couture1737#1	>ref|NP_179828.1|| (NM_127806) putative peroxidase; protein id: At2g22420.1. supported	91.160	118.000	0.773	162.692	183.000	0.889	0.831

8	6	15	GB009D11	a76couture1647.r#1	------	41.209	43.000	0.958	26.772	33.000	0.811	0.885
8	7	1	TT283C10	a76couture1517.r#1	>gb|AAD29845.1|AF064697_1 (AF064697) O-methyltransferase; Omt II;THATU;5 [Thalictrum	196.056	250.000	0.784	355.245	319.000	1.114	0.949
8	7	2	TB002C04	a76couture1395.r#1	>ref|NP_182115.1|| (NM_130154) putative protein kinase; protein id: At2g45910.1	167.334	150.000	1.116	216.236	165.000	1.311	1.213
8	7	3	GT172F12	a76couture1734#1	>ref|NP_176133.1|| (NM_104617) glycosyl hydrolase family 10; protein id: At1g58370.1	82.418	72.000	1.145	79.287	66.000	1.201	1.173
8	7	4	GB009C11	a76couture1644.r#1	------	18.731	27.000	0.694	29.861	37.000	0.807	0.750
8	7	5	TT282F09	a76couture1512.r#1	>gb|AAD44161.1|AF130423_1 (AF130423) cryptochrome 1 [Lycopersicon esculentum]	66.184	87.000	0.761	103.999	101.000	1.030	0.895
8	7	6	RT063A01	a76couture1391.r#1	>ref|NP_172953.1|| (NM_101369) serine carboxypeptidase precursor. putative; protein	122.379	158.000	0.775	164.751	192.000	0.858	0.816
8	7	7	RT033E06	a76couture2156#1	>ref|NP_176009.1|| (NM_104491) receptor-like protein kinase. putative; protein id:	8.741	13.000	0.672	9.267	15.000	0.618	0.645
8	7	8	RT022E10	a76couture2055#1	>ref|NP_181210.2|| (NM_129227) putative PHD-type zinc finger protein; protein id:	16.234	19.000	0.854	20.594	25.000	0.824	0.839
8	7	9	RB008G11	a76couture1973#1	>gb|AAK62477.1| (AY034092) putative DNA-invertase [Micrococcus sp. 28]	6.244	16.000	0.390	17.505	30.000	0.583	0.487
8	7	10	GT201C06	a76couture1846.r#1	>ref|NP_563737.1|| (NM_100418) Expressed protein; protein id: At1g05385.1. supported	31.219	29.000	1.077	49.425	40.000	1.236	1.156
8	7	11	RT033C02	a76couture2152.r#1	>gb|AAG52346.1|AC011663_25 (AC011663) hypothetical protein; 66431-64463 [Arabidopsis thaliana]	97.404	109.000	0.894	111.207	127.000	0.876	0.885
8	7	12	RT022E04	a76couture2052#1	>emb|CAD41399.1| (AL606998) OJ000223_09.11 [Oryza sativa]	19.980	20.000	0.999	23.683	20.000	1.184	1.092
8	7	13	RB008F12	a76couture1970#1	>pir||S51911 cryptogene protein G5(ND3) - Leishmania tarentolae (strain LEM125)	11.239	24.000	0.468	16.475	25.000	0.659	0.564
8	7	14	GT193H01	a76couture1842.r#1	>ref|NP_201416.1|| (NM_126013) glycosyl hydrolase family 38 (alpha-mannosidase); protein	173.578	230.000	0.755	260.513	318.000	0.819	0.787
8	7	15	RT032A03	a76couture2147.r#1	------	1188.823	1379.000	0.862	1939.947	2205.000	0.880	0.871
8	8	1	RT022D08	a76couture2049#1	>gb|AAM97127.1| (AY136462) unknown protein [Arabidopsis thaliana]	41.209	44.000	0.937	56.633	49.000	1.156	1.046
8	8	2	RB008F01	a76couture1967#1	------	18.731	26.000	0.720	27.802	34.000	0.818	0.769
8	8	3	GT193E07	a76couture1838.r#1	>ref|NP_171775.1|| (NM_100155) hypothetical protein; protein id: At1g02750.1	514.491	564.000	0.912	705.342	624.000	1.130	1.021
8	8	4	RT032H01	a76couture2143.r#1	>pir||T06299 potassium transport protein homolog T9E8.160 - Arabidopsis thaliana	1023.986	1027.000	0.997	1579.553	1258.000	1.256	1.126
8	8	5	RT022D01	a76couture2046#1	>pir||T49962 hypothetical protein F8M21.160 - Arabidopsis thaliana	97.404	96.000	1.015	209.028	145.000	1.442	1.228
8	8	6	RB008D05	a76couture1963.r#1	------	89.911	80.000	1.124	122.534	96.000	1.276	1.200
8	8	7	GT193A05	a76couture1834.r#1	>ref|NP_567407.1|| (NM_117427) putative protein; protein id: At4g13530.1. supported by	1126.385	1170.000	0.963	1782.403	1659.000	1.074	1.019
8	8	8	RT032F03	a76couture2138.r#1	>ref|NP_563676.1|| (NM_100196) expressed protein; protein id: At1g03140.1. supported	489.515	482.000	1.016	676.510	662.000	1.022	1.019
8	8	9	RT022C06	a76couture2042.r#1	>ref|NP_194708.1|| (NM_119125) putative protein; protein id: At4g29790.1. supported by	9.990	14.000	0.714	23.683	35.000	0.677	0.695
8	8	10	RB008C03	a76couture1961.r#1	>dbj|BAB16432.1| (AB041520) WRKY transcription factor Nt-SubD48 [Nicotiana tabacum]	7.493	16.000	0.468	5.148	16.000	0.322	0.395
8	8	11	GT192G12	a76couture1830#1	------	31.219	30.000	1.041	12.356	14.000	0.883	0.962
8	8	12	RT032E10	a76couture2135#1	------	53.697	44.000	1.220	66.930	53.000	1.263	1.242
8	8	13	RT022B11	a76couture2039#1	>gb|AAD46419.1|AF100770_1 (AF100770) receptor-like kinase [Hordeum vulgare]	16.234	21.000	0.773	23.683	25.000	0.947	0.860
8	8	14	RB007H01	a76couture1958.r#1	>gb|AAK54616.1|AF374474_1 (AF374474) CK2 alpha subunit [Nicotiana tabacum]	751.756	661.000	1.137	1155.319	991.000	1.166	1.152
8	8	15	GT192C05	a76couture1826.r#1	------	46.204	51.000	0.906	71.049	78.000	0.911	0.908
8	9	1	TT281G05	a76couture2557.r#1	>pir||T04773 hypothetical protein F10M10.40 - Arabidopsis thaliana	132.369	196.000	0.675	179.167	209.000	0.857	0.766
8	9	2	TT253A07	a76couture2461.r#1	------	121.130	128.000	0.946	193.583	187.000	1.035	0.991
8	9	3	RT063E11	a76couture2344.r#1	>ref|NP_568774.1|| (NM_124634) putative protein; protein id: At5g52550.1. supported by	112.389	117.000	0.961	148.276	128.000	1.158	1.059
8	9	4	RT044D12	a76couture2254.r#1	>gb|AAK53759.1|AF367865_1 (AF367865) potassium transporter HAK2p [Mesembryanthemum	400.853	385.000	1.041	583.838	465.000	1.256	1.148
8	9	5	TT282C11	a76couture2553.r#1	>dbj|BAB59127.1| (AB062682) hypothetical protein [Arabidopsis thaliana]	203.548	238.000	0.855	315.087	308.000	1.023	0.939
8	9	6	TT251A07	a76couture2455#1	>gb|AAF97353.1|AC021045_10 (AC021045) Putative GTL1 [Arabidopsis thaliana]	147.354	138.000	1.068	227.563	184.000	1.237	1.152
8	9	7	RT062H06	a76couture2339#1	>ref|NP_195899.1|| (NM_120357) In2-1 protein. putative; protein id: At5g02790.1	327.176	385.000	0.850	604.431	568.000	1.064	0.957
8	9	8	RT043G10	a76couture2251.r#1	>emb|CAD31715.1| (AJ487039) hypothetical protein [Cicer arietinum]	1520.994	1583.000	0.961	1970.838	2037.000	0.968	0.964
8	9	9	TT274E03	a76couture2549.r#1	------	319.683	452.000	0.707	657.976	734.000	0.896	0.802
8	9	10	TT242C11	a76couture2450.r#1	>gb|AAM62675.1| (AY085449) 50S ribosomal protein L27 [Arabidopsis thaliana]	223.529	220.000	1.016	390.255	342.000	1.141	1.079
8	9	11	RT062D04	a76couture2335.r#1	ef|NP_566889.1|| (NM_114573) FtsH protease, putative [Arabidops... 249 1e-068	172.329	187.000	0.922	278.018	261.000	1.065	0.993
8	9	12	RT051A10	a76couture2247.r#1	>ref|NP_192854.1|| (NM_117186) translation initiation factor IF-2. putative; protein	149.852	136.000	1.102	240.949	190.000	1.268	1.185
8	9	13	TT274A07	a76couture2545.r#1	>ref|NP_195437.1|| (NM_119883) thiol-disulfide interchange like protein; protein id:	354.649	354.000	1.002	660.035	570.000	1.158	1.080
8	9	14	TT242G05	a76couture2445.r#1	>ref|NP_186877.1|| (NM_111095) putative NADPH-ferrihemoprotein reductase; protein id:	149.852	182.000	0.823	324.354	318.000	1.020	0.922
8	9	15	RT062B01	a76couture2332.r#1	------	162.339	196.000	0.828	283.166	302.000	0.938	0.883
8	10	1	RT044G10	a76couture2244.r#1	------	34.965	39.000	0.897	66.930	60.000	1.116	1.006
8	10	2	TT273H01	a76couture2540.r#1	------	7.493	15.000	0.500	35.010	36.000	0.972	0.736
8	10	3	TT242C02	a76couture2439.r#1	>ref|NP_218310.1|| (NC_000962) embC [Mycobacterium tuberculosis H37Rv]	218.534	220.000	0.993	319.206	260.000	1.228	1.111
8	10	4	RT061G03	a76couture2329.r#1	>ref|NP_195581.1|| (NM_120030) putative protein; protein id: At4g38690.1. supported by	123.628	204.000	0.606	214.177	260.000	0.824	0.715
8	10	5	RT044F05	a76couture2240.r#1	>gb|AAK60545.1|AF382146_1 (AF382146) putative 3-keto-acyl-ACP dehydratase [Brassica napus]	278.474	315.000	0.884	494.254	450.000	1.098	0.991
8	10	6	TT272C06	a76couture2538.r#1	>ref|NP_197125.2|| (NM_121626) putative protein; protein id: At5g16210.1. supported by	352.151	360.000	0.978	598.253	503.000	1.189	1.084
8	10	7	TT241A06	a76couture2435.r#1	------	518.237	550.000	0.942	856.707	741.000	1.156	1.049
8	10	8	RT061D05	a76couture2325.r#1	>pir||T11855 DnaJ protein homolog - kidney bean (fragment)	31.219	34.000	0.918	44.277	44.000	1.006	0.962
8	10	9	RT044E06	a76couture2236#1	>dbj|BAB07966.1| (AP002524) putative t-SNARE SED5 [Oryza sativa (japonica	129.871	122.000	1.065	198.731	177.000	1.123	1.094
8	10	10	RT051D10	a76couture3075.r#1	>gb|AAD34458.1| (AF135596) Skp1 [Medicago sativa]	320.932	285.000	1.126	461.304	402.000	1.148	1.137
8	10	11	CT003F11	a76couture2924.r#1	>ref|NP_190560.1|| (NM_114851) 60S RIBOSOMAL PROTEIN - like; protein id: At3g49910.1	203.548	246.000	0.827	393.344	374.000	1.052	0.940
8	10	12	PT012F04	a76couture2788.r#1	>dbj|BAB93108.1| (AB075902) betaine/proline transporter [Avicennia marina]	534.471	613.000	0.872	872.152	955.000	0.913	0.893
8	10	13	PT001F08	a76couture2682.r#1	------	22.478	41.000	0.548	24.713	51.000	0.485	0.516
8	10	14	RT012D05	a76couture3069.r#1	>ref|NP_194457.1|| (NM_118861) quinone reductase family; protein id: At4g27270.1	2085.435	1612.000	1.294	3777.954	2681.000	1.409	1.351
8	10	15	CT002D05	a76couture2921.r#1	>dbj|BAC06946.1| (AP003759) putative GTP-binding protein [Oryza sativa (japonica	143.608	154.000	0.933	295.523	261.000	1.132	1.032
8	11	1	PT011E02	a76couture2784.r#1	------	39.960	38.000	1.052	79.287	66.000	1.201	1.126
8	11	2	PT001B11	a76couture2678.r#1	------	22.478	24.000	0.937	66.930	68.000	0.984	0.960
8	11	3	RT023G05	a76couture3064.r#1	>ref|NP_189295.2|| (NM_113572) Eukaryotic peptide chain release factor subunit 1	1131.380	1388.000	0.815	1792.700	1806.000	0.993	0.904
8	11	4	Arabidopsis Control Oligonucleotide	3ara7		41.209	69.000	0.597	68.990	91.000	0.758	0.678
8	11	5	PT009E11	a76couture2779.r#1	>ref|NP_563744.1|| (NM_100437) Expressed protein; protein id: At1g05575.1. supported	39.960	51.000	0.784	67.960	61.000	1.114	0.949
8	11	6	PT011C08	a76couture2673.r#1	------	521.983	558.000	0.935	1088.388	877.000	1.241	1.088
8	11	7	RT081E03	a76couture3056.r#1	>ref|NP_564937.1|| (NM_105538) expressed protein; protein id: At1g68660.1. supported	769.238	810.000	0.950	1244.902	1117.000	1.115	1.032

8	11	8	CT001H09	a76couture2910.r#1	>emb|CAD30058.1| (AJ457824) replication enhancer protein [Malvastrum begomovirus]	79.921	74.000	1.080	112.237	90.000	1.247	1.164
8	11	9	PT004F04	a76couture2774.r#1	>ref|NP_564563.1|| (NM_103909) chloroplast FtsH protease; protein id: At1g50250.1	1828.190	1741.000	1.050	2569.091	2425.000	1.059	1.055
8	11	10	PT005C02	a76couture2669.r#1	------	243.509	254.000	0.959	406.730	358.000	1.136	1.047
8	11	11	RT022E07	a76couture3044#1	>emb|CAD21849.1| (AJ420195) ethylene responsive element binding protein [Fagus	1645.870	1439.000	1.144	2812.099	2410.000	1.167	1.155
8	11	12	RB008B10	a76couture2907.r#1	------	66.184	69.000	0.959	99.880	101.000	0.989	0.974
8	11	13	PT010G01	a76couture2770.r#1	------	267.235	246.000	1.086	539.561	426.000	1.267	1.176
8	11	14	PT004C02	a76couture2666#1	------	47.453	58.000	0.818	84.435	96.000	0.880	0.849
8	11	15	RT082C09	a76couture3038.r#1	>ref|NP_177693.1|| (NM_106215) vacuolar ATP synthase. putative; protein id:	3034.495	3241.000	0.936	4239.258	3780.000	1.121	1.029
8	12	1	PT008B10	a76couture2904.r#1	>ref|NP_566068.1|| (NM_130186) expressed protein; protein id: At2g46230.1. supported	2156.615	1990.000	1.084	2925.366	2209.000	1.324	1.204
8	12	2	PT009E07	a76couture2765.r#1	>ref|NP_191111.1|| (NM_115409) FKBP-type peptidyl-prolyl cis-trans isomerase	295.957	318.000	0.931	482.927	427.000	1.131	1.031
8	12	3	PT006D06	a76couture2662.r#1	------	558.197	470.000	1.188	775.361	591.000	1.312	1.250
8	12	4	BG273728 RB000A74	couture_a76.402.c1#1	>gb|AAF22455.1| (AF060880) MADS box protein [Paulownia kawakamii]	183.568	156.000	1.177	324.354	224.000	1.448	1.312
8	12	5	BM436826 TT274G11	couture_a76.322.c1#1	>gb|AAL68853.1|AF466199_12 (AF466199) gb protein [Sorghum bicolor]	73.677	89.000	0.828	115.326	123.000	0.938	0.883
8	12	6	BM437145 GT183D04	couture_a76.233.c1.r#1	>sp|P32811|PHSH_SOLTU ALPHA-GLUCAN PHOSPHORYLASE. H ISOZYME (STARCH PHOSPHORYLASE H)	343.410	503.000	0.683	569.422	666.000	0.855	0.769
8	12	7	BM436570 CT005D07	couture_a76.134.c1.r#1	>ref|NP_191370.1|| (NM_115673) putative protein; protein id: At3g58110.1 [Arabidopsis	211.041	211.000	1.000	402.611	318.000	1.266	1.133
8	12	8	BG273715 RB000A87	couture_a76.399.c1.r#1	>pir||T04458 hypothetical protein F4D11.120 - Arabidopsis thaliana	92.409	116.000	0.797	159.603	169.000	0.944	0.871
8	12	9	BG273949 GB000A32 BM436409	couture_a76.32.c1#1	>gb|AAC32121.1| (AF051217) probable 40S ribosomal protein S15 [Picea mariana]	2945.833	2913.000	1.011	4161.001	3800.000	1.095	1.053
8	12	10	BM437746 BM436808 GT173E05	couture_a76.229.c1.r#1	>gb|AAM94337.2| (AF529237) phosphoribulokinase precursor [Oryza sativa (indica	161.090	163.000	0.988	279.048	293.000	0.952	0.970
8	12	11	BM437222 CT002A04	couture_a76.130.c1#1	>ref|NP_176904.1|| (NM_105404) stress related protein. putative; protein id:	5415.888	3344.000	1.620	8953.205	5247.000	1.706	1.663
8	12	12	BG273706 RB000A96	couture_a76.397.c1.r#1	>ref|NP_567599.2|| (NM_118157) zinc-finger protein Lsd1; protein id: At4g20380.1	892.866	1164.000	0.767	1790.641	1943.000	0.922	0.844
8	12	13	TB004d07 TT264D10	couture_a76.315.c1#1	>gb|AAM91028.1| (AY134619) calcineurin B [Pisum sativum]	1006.503	1212.000	0.830	1839.037	1863.000	0.987	0.909
8	12	14	BG273808 GB009C02	couture_a76.225.c1.r#1	------	2016.753	2072.000	0.973	4018.903	3407.000	1.180	1.076
8	12	15	BM437461 CM001G11	couture_a76.126.c1.r#1	>sp|Q38732|DAG_ANTMA DAG PROTEIN. CHLOROPLAST PRECURSOR >gi|7489296|pir||S71747 DAG	72.428	90.000	0.805	127.682	136.000	0.939	0.872
8	13	1	BG273790 RB000A08	couture_a76.392.c1#1	>dbj|BAB89639.1| (AP003260) hypothetical protein~similar to Arabidopsis thaliana	72.428	83.000	0.873	132.831	124.000	1.071	0.972
8	13	2	TB000A49 BG273843 TB000A49	couture_a76.312.c1.r#1	>pir||T02301 aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) 2A precursor	566.939	782.000	0.725	835.083	808.000	1.034	0.879
8	13	3	BM438047 GB005C12	couture_a76.221.c1.r#1	>ref|NP_568804.1|| (NM_124791) membrane associated protein; protein id: At5g54110.1	173.578	137.000	1.267	233.741	176.000	1.328	1.298
8	13	4	TB001g08 TB001G08	couture_a76.122.c1.r#1	>ref|NP_181277.1|| (NM_129296) putative protein translocase; protein id: At2g37410.1	1705.811	1670.000	1.021	2579.388	2270.000	1.136	1.079
8	13	5	BG273776 RB000A24	couture_a76.389.c1.r#1	>dbj|BAB17342.1| (AP002747) putative receptor kinase [Oryza sativa (japonica	11.239	15.000	0.749	15.445	15.000	1.030	0.889
8	13	6	BG273869 TB000A23 TB000A23	couture_a76.309.c1.r#1	>gb|AAF70823.1|AF154422_1 (AF154422) beta-galactosidase [Lycopersicon esculentum]	229.772	214.000	1.074	397.463	309.000	1.286	1.180
8	13	7	BM437499 GB002G08 BM438073	couture_a76.215.c1.r#1	>gb|AAM65773.1| (AY088232) putative RING zinc finger protein [Arabidopsis thaliana]	2795.982	2329.000	1.201	4244.406	3148.000	1.348	1.274
8	13	8	BM437977 BG273836 CM004D01	couture_a76.12.c1#1	>gb|AAB88876.1| (U93273) putative auxin-repressed protein [Prunus armeniaca]	136.115	140.000	0.972	197.702	181.000	1.092	1.032
8	13	9	BM436820 BM436293 GT204G07	couture_a76.386.c1.r#1	>ref|NP_188991.1|| (NM_113252) cyanate lyase (CYN); protein id: At3g23490.1. supported	283.469	272.000	1.042	402.611	385.000	1.046	1.044
8	13	10	BG273845 TB000A47	couture_a76.305.c1.r#1	>dbj|BAA92699.1| (AB039918) type 2A protein phosphatase-3 [Vicia faba]	288.464	291.000	0.991	457.185	424.000	1.078	1.035
8	13	11	BG273973 GB000A05	couture_a76.211.c1.r#1	>ref|NP_564425.1|| (NM_103074) expressed protein; protein id: At1g33490.1. supported	635.621	683.000	0.931	1019.399	1022.000	0.997	0.964
8	13	12	TB007c12 TB007C12 TB001d08	couture_a76.115.c1#1	------	73.677	99.000	0.744	134.890	154.000	0.876	0.810
8	13	13	TB006a01 BM436920 RT052C02	couture_a76.587.c1#1	>ref|NP_567210.1|| (NM_116345) expressed protein; protein id: At4g01150.1. supported	187.315	200.000	0.937	316.117	315.000	1.004	0.970
8	13	14	BG273835 TB000A58	couture_a76.492.c1#1	>ref|NP_192996.1|| (NM_117329) putative protein; protein id: At4g12590.1. supported by	1102.658	1056.000	1.044	1967.749	1729.000	1.138	1.091
8	13	15	RB004H08 RT081C12	couture_a76.98.c1#1	>emb|CAC91565.1| (AJ414400) hydroperoxide lyase [Nicotiana attenuata]	109.891	130.000	0.845	275.958	284.000	0.972	0.909
8	14	1	BM437647 TT281D02	couture_a76.586.c1.r#1	>pir||S47082 dnaK-type molecular chaperone hsp70.4 - maize (fragment)	2202.819	2996.000	0.735	2804.891	3360.000	0.835	0.785
8	14	2	BG273782 RT083H11 VVU97522 VVU97521	couture_a76.sd.79.c1#	>gb|AAB65777.1| (U97522) class IV endochitinase [Vitis vinifera]	5183.618	5589.000	0.927	8190.201	6521.000	1.256	1.092
8	14	3	BM436653 RT052G12	couture_a76.69.c1.r#1	>ref|NP_200236.1|| (NM_124805) cyclic nucleotide-regulated ion channel (CNGC4);	1846.921	3162.000	0.584	3070.553	4299.000	0.714	0.649
8	14	4	TB005b01 GT192H06	couture_a76.579.c1#1	>sp|P48495|TPIS_PETHY Triosephosphate isomerase. cytosolic (TIM)	3467.816	3584.000	0.968	5041.391	4629.000	1.089	1.028
8	14	5	BG273818 TB000A76	couture_a76.488.c1.r#1	>ref|NP_180926.1|| (NM_128928) protein phosphatase 2C (PP2C); protein id: At2g33700.1	52.448	62.000	0.846	111.207	93.000	1.196	1.021
8	14	6	BM436741 44BIAAAU	couture_a76.646.c1.r#1	>emb|CAC84706.1| (AJ306825) aux/IAA protein [Populus tremula x Populus tremuloides]	599.407	617.000	0.971	869.063	795.000	1.093	1.032
8	14	7	BM436506 GT192E04	couture_a76.552.c1.r#1	>dbj|BAB39951.1| (AP003018) putative tubulin beta-4 chain [Oryza sativa (japonica	2642.384	3802.000	0.695	4254.703	4677.000	0.910	0.802
8	14	8	CT003A08 AF159125	couture_a76.sd.73.c1#	>gb|AAD46483.1| (AF128266) polygalacturonase PG1 [Glycine max]	28.722	52.000	0.552	49.425	72.000	0.686	0.619
8	14	9	BM437067 TB002h02 TT264C04	couture_a76.645.c1#1	>emb|CAC83750.1| (AJ292078) reversibly glycosylated polypeptide [Gossypium hirsutum]	2950.828	3213.000	0.918	3916.963	4324.000	0.906	0.912
8	14	10	BM437241 BM437373 BM437497 BM436543 BM	couture_a76.525.c1.r#1	>emb|CAB51533.1| (AJ237693) galactinol synthase. isoform GolS-1 [Ajuga reptans]	79.921	98.000	0.816	135.920	153.000	0.888	0.852
8	14	11	GB005a03 BM436377 AF192308 G7739778 AF25	couture_a76.sd.41.c1#	>gb|AAF69010.1|AF257777_1 (AF257777) H+-pyrophosphatase [Vitis vinifera]	1841.926	2250.000	0.819	3436.095	3997.000	0.860	0.839
8	14	12	PT001G04 RT053G06	couture_a76.596.c1.r#1	>ref|NP_173290.1|| (NM_101713) kinesin-related protein; protein id: At1g18550.1	12.488	17.000	0.735	22.653	22.000	1.030	0.882
8	14	13	BG273859 TB000A33	couture_a76.498.c1#1	>ref|NP_201454.1|| (NM_126051) apospory-associated protein C-like; protein id:	679.327	683.000	0.995	1023.518	977.000	1.048	1.021
8	14	14	BM436266 RT052B10	couture_a76.59.c1.r#1	>ref|NP_567130.1|| (NM_116123) putative membrane protein; protein id: At3g62580.1	2031.738	2225.000	0.913	3559.658	3592.000	0.991	0.952
8	14	15	BM437475 PT012D01	couture_a76.519.c1.r#1	>ref|NP_179752.1|| (NM_127729) 40S ribosomal protein S25; protein id: At2g21580.1	5088.711	5143.000	0.989	6490.173	6155.000	1.054	1.022
9	1	1	CM005a04	a76couture0496.r#1	none	526.978	929.000	0.567	593.105	1077.000	0.551	0.559
9	1	2	CM001C10	a76couture0398.r#1	>ref|NP_195791.1|| (NM_120249) putative protein; protein id: At5g01710.1. supported by	269.733	319.000	0.846	244.038	355.000	0.687	0.766
9	1	3	ST005A07	a76couture0278.r#1	>gb|AAM63491.1| (AY086489) putative kinesin light chain [Arabidopsis thaliana]	899.110	1351.000	0.666	998.805	1466.000	0.681	0.673
9	1	4	GT184H07	a76couture0142.r#1	>ref|NP_179079.1|| (NM_127036) spot 3 protein and vacuolar sorting receptor homolog	16.234	30.000	0.541	14.416	17.000	0.848	0.695
9	1	5	CT001H04	a76couture0492.r#1	>ref|NP_189092.1|| (NM_113356) hypothetical protein; protein id: At3g24490.1	143.608	161.000	0.892	185.345	197.000	0.941	0.916
9	1	6	CM001A10	a76couture0394.r#1	>ref|NP_566810.1|| (NM_113634) blue copper protein. putative; protein id: At3g27200.1	42.458	48.000	0.885	50.455	58.000	0.870	0.877
9	1	7	ST005H01	a76couture0272.r#1	>pir||T01984 late-embryogenesis protein lea5 - common tobacco	14057.331	11191.000	1.256	17459.523	13820.000	1.263	1.260
9	1	8	GB005F09	a76couture0135.r#1	>sp|Q9M573|RL31_PERFR 60S ribosomal protein L31 >gi|7229709|gb|AAF42953.1|AF237624_1	3602.683	2963.000	1.216	4442.108	3652.000	1.216	1.216
9	1	9	CT001F03	a76couture0487.r#1	>ref|NP_201045.1|| (NM_125633) KED - like protein; protein id: At5g62390.1. supported	1053.956	1387.000	0.760	1103.834	1467.000	0.752	0.756
9	1	10	ST007D09	a76couture0390.r#1	>sp|P10973|NLTA_RICCO NONSPECIFIC LIPID-TRANSFER PROTEIN A (NS-LTP A) (PHOSPHOLIPID	18324.356	19117.000	0.959	15548.407	19503.000	0.797	0.878
9	1	11	PT005H08	a76couture0265.r#1	>ref|NP_566516.1|| (NM_112416) expressed protein; protein id: At3g15480.1. supported	63.687	56.000	1.137	57.663	53.000	1.088	1.113
9	1	12	GB009F02	a76couture0128.r#1	>sp|P11796|SODM_NICPL Superoxide dismutase [Mn]. mitochondrial precursor	8843.743	6612.000	1.338	8789.484	8203.000	1.071	1.205
9	1	13	CT001D10	a76couture0483.r#1	>ref|NP_566942.1|| (NM_114961) expressed protein; protein id: At3g51010.1. supported	17.483	25.000	0.699	25.742	27.000	0.953	0.826
9	1	14	ST005H09	a76couture0386.r#1	>sp|P10973|NLTA_RICCO NONSPECIFIC LIPID-TRANSFER PROTEIN A (NS-LTP A) (PHOSPHOLIPID	12776.100	5675.000	2.251	14787.462	8328.000	1.776	2.013
9	1	15	PT013A09	a76couture0261.r#1	>ref|NP_566004.1|| (NM_129959) VirF-interacting protein FIP1; protein id: At2g43970.1	2818.459	2110.000	1.336	2874.911	2766.000	1.039	1.188

9	2	1	CT006H11	a76couture0114.r#1	>pir||S71223 xyloglucan endo-1.4-beta-D-glucanase (EC 3.2.1.-) XTR-4 -	1429.834	2556.000	0.559	1281.971	2681.000	0.478	0.519
9	2	2	CT001B12	a76couture0479.r#1	>ref|NP_198861.1|| (NM_123409) putative protein; protein id: At5g40450.1 [Arabidopsis	26.224	58.000	0.452	25.742	52.000	0.495	0.474
9	2	3	ST005B06	a76couture0383.r#1	>gb|AAD42942.1|AF091840_1 (AF091840) 15 kDa oleosin [Sesamum indicum]	3803.734	3685.000	1.032	4643.928	4387.000	1.059	1.045
9	2	4	PT012A09	a76couture0256.r#1	>dbj|BAB09378.1| (AB010694) gene_id:K3K3.14~unknown protein [Arabidopsis thaliana]	404.599	403.000	1.004	427.324	464.000	0.921	0.962
9	2	5	CT005E05	a76couture0109.r#1	>gb|AAK58690.1|AF272860_1 (AF272860) receptor-like kinase Xa21-binding protein 3 [Oryza	764.243	1102.000	0.694	807.282	1288.000	0.627	0.660
9	2	6	CM004H07	a76couture0475.r#1	>ref|NP_180524.1|| (NM_128517) putative thiamin biosynthesis protein; protein id:	965.294	1207.000	0.800	1110.012	1523.000	0.729	0.764
9	2	7	ST003H09	a76couture0379.r#1	>gb|AAF37268.1|AF220407_1 (AF220407) dehydrin-like protein [Vitis riparia]	1332.431	1911.000	0.697	1519.831	2087.000	0.728	0.713
9	2	8	PT009B05	a76couture0252.r#1	>emb|CAD29693.1| (AJ441311) putative glycine rich protein [Rumex obtusifolius]	169.832	111.000	1.530	306.849	204.000	1.504	1.517
9	2	9	CT004C11	a76couture0104.r#1	>ref|NP_200661.1|| (NM_125239) putative protein; protein id: At5g58530.1 [Arabidopsis	259.743	263.000	0.988	294.493	302.000	0.975	0.981
9	2	10	RT073B05	a76couture0930.r#1	------	358.395	302.000	1.187	320.235	334.000	0.959	1.073
9	2	11	GT201H05	a76couture0808.r#1	>ref|NP_186814.1|| (NM_111031) unknown protein; protein id: At3g01650.1 [Arabidopsis	196.056	159.000	1.233	193.583	184.000	1.052	1.143
9	2	12	ST005H08	a76couture0695.r#1	>ref|NP_182147.1|| (NM_130187) hypothetical protein; protein id: At2g46240.1	223.529	87.000	2.569	180.197	81.000	2.225	2.397
9	2	13	ST001F01	a76couture0597.r#1	>gb|AAG50081.1|AF333344_1 (AF333344) SPEC3-like protein [Sterkiella histriomuscorum]	199.802	145.000	1.378	174.019	162.000	1.074	1.226
9	2	14	RT072C01	a76couture0927.r#1	>gb|AAM34266.1|AF508793_1 (AF508793) VTC2 [Arabidopsis thaliana]	1005.255	830.000	1.211	913.340	1007.000	0.907	1.059
9	2	15	GT173H02	a76couture0805.r#1	>ref|NP_189916.1|| (NM_114198) guanine nucleotide-exchange - like protein; protein id:	538.217	410.000	1.313	521.026	544.000	0.958	1.135
9	3	1	ST005F08	a76couture0691.r#1	>ref|NP_563819.1|| (NM_100721) expressed protein; protein id: At1g08480.1. supported	3637.648	4854.000	0.749	2586.596	4850.000	0.533	0.641
9	3	2	ST001D02	a76couture0593.r#1	>gb|AAG31326.1| (AF178575) putative serine/threonine kinase GDBrPK [Vitis vinifera]	237.265	397.000	0.598	226.533	439.000	0.516	0.557
9	3	3	RT071G10	a76couture0923.r#1	>ref|NP_568103.1|| (NM_120336) putative protein; protein id: At5g02580.1. supported by	22.478	36.000	0.624	20.594	33.000	0.624	0.624
9	3	4	RT041G10	a76couture0797.r#1	>emb|CAB95829.1| (AJ404639) hypothetical protein [Cicer arietinum]	6557.257	6439.000	1.018	7470.443	8477.000	0.881	0.950
9	3	5	ST005E09	a76couture0687.r#1	>ref|NP_192272.1|| (NM_116601) putative nodulin; protein id: At4g03630.1 [Arabidopsis	126.125	142.000	0.888	170.930	208.000	0.822	0.855
9	3	6	ST001B04	a76couture0588.r#1	>ref|NP_191426.1|| (NM_115729) putative protein; protein id: At3g58670.1. supported by	146.105	178.000	0.821	177.108	238.000	0.744	0.782
9	3	7	RT071D11	a76couture0919.r#1	>dbj|BAA77836.1| (AB027456) extensive homology to FT (FLOWERING LOCUS T. AB027504)	88.662	95.000	0.933	75.168	87.000	0.864	0.899
9	3	8	RT031A10	a76couture0793.r#1	------	3000.779	2317.000	1.295	3790.310	3052.000	1.242	1.269
9	3	9	ST005B10	a76couture0683.r#1	>ref|NP_505575.1|| (NM_073174) K08H10.1.p [Caenorhabditis elegans]	56.194	68.000	0.826	60.752	82.000	0.741	0.784
9	3	10	CT006D03	a76couture0584.r#1	>ref|NP_194819.2|| (NM_119237) hypothetical protein; protein id: At4g30900.1	578.178	570.000	1.014	553.976	658.000	0.842	0.928
9	3	11	TT242F03	a76couture0913.r#1	>emb|CAB65284.1| (AJ248337) putative wound-induced protein [Medicago sativa subsp. x	1101.409	1153.000	0.955	1198.566	1507.000	0.795	0.875
9	3	12	RB001F12	a76couture0788.r#1	------	1886.882	1359.000	1.388	1905.967	1800.000	1.059	1.224
9	3	13	ST005A06	a76couture0679.r#1	>gb|AAD41078.1|AF141204_1 (AF141204) Nramp2 [Arabidopsis thaliana]	449.555	389.000	1.156	449.977	516.000	0.872	1.014
9	3	14	CT006A04	a76couture0579.r#1	------	44.955	40.000	1.124	35.010	38.000	0.921	1.023
9	3	15	TT282A05	a76couture0908.r#1	>dbj|BAA83471.1| (AB008848) Csf-3 [Cucumis sativus]	2406.367	1468.000	1.639	1838.007	1583.000	1.161	1.400
9	4	1	GT183E05	a76couture0782.r#1	>ref|NP_196647.1|| (NM_121124) putative protein; protein id: At5g10860.1. supported by	1248.764	1961.000	0.637	1226.368	2246.000	0.546	0.591
9	4	2	ST004H08	a76couture0675.r#1	>pir||S27757 embryonic abundant protein. 59K - soybean >gi|170010|gb|AAA33985.1|	2391.382	4376.000	0.546	3265.165	5477.000	0.596	0.571
9	4	3	CT005F09	a76couture0576.r#1	>ref|NP_175905.2|| (NM_104382) hypothetical protein; protein id: At1g55080.1	31.219	66.000	0.473	33.980	65.000	0.523	0.498
9	4	4	RT063C10	a76couture1385.r#1	>ref|NP_029426.1|| (NM_128399) expressed protein; protein id: At2g28390.1. supported	177.324	220.000	0.806	164.751	205.000	0.804	0.805
9	4	5	RB004E03	a76couture1271.r#1	>emb|CAA07567.1| (AJ007579) cysteine proteinase [Ribes nigrum]	4197.094	5737.000	0.732	4633.631	7030.000	0.659	0.695
9	4	6	GT171H11	a76couture1136.r#1	>dbj|BAB16429.1| (AB041517) elicitor inducible gene Nt-SA1-1 [Nicotiana tabacum]	18.731	29.000	0.646	22.653	34.000	0.666	0.656
9	4	7	RT084G04	a76couture1022#1	------	68.682	82.000	0.838	94.732	118.000	0.803	0.820
9	4	8	RT054G09	a76couture1378.r#1	>ref|NP_181837.1|| (NM_129870) 3-isopropylmalate dehydratase. small subunit; protein	2817.211	3537.000	0.796	2884.178	3928.000	0.734	0.765
9	4	9	RB002H03	a76couture1265.r#1	------	151.100	170.000	0.889	149.306	175.000	0.853	0.871
9	4	10	GT172H04	a76couture1133#1	>ref|NP_192113.1|| (NM_116435) hypothetical protein; protein id: At4g02040.1	4677.868	4546.000	1.029	4267.060	4638.000	0.920	0.975
9	4	11	RT083G04	a76couture1019.r#1	>sp|O65759|H2A_CICAR Histone H2A >gi|3204129|emb|CAA07234.1| (AJ006768) histone H2A	360.893	267.000	1.352	375.839	323.000	1.164	1.258
9	4	12	RT053H11	a76couture1374.r#1	>pir||T02073 hypothetical protein S25-PR6 - common tobacco	971.538	718.000	1.353	916.429	877.000	1.045	1.199
9	4	13	GT204H10	a76couture1259.r#1	------	398.356	325.000	1.226	377.898	392.000	0.964	1.095
9	4	14	GT171G08	a76couture1128.r#1	>dbj|BAB71853.1| (AB065100) phosphoenolpyruvate carboxylase kinase [Flaveria	951.558	550.000	1.730	783.599	639.000	1.226	1.478
9	4	15	RT082G04	a76couture1014.r#1	>ref|NP_196552.1|| (NM_121027) 26S proteasome regulatory subunit (RPN5). putative;	906.602	538.000	1.685	892.746	698.000	1.279	1.482
9	5	1	RT053F05	a76couture1369.r#1	>dbj|BAB11508.1| (AB015469) gb|AAD39327.1~gene_id:K19B1.19~similar to unknown	417.087	951.000	0.439	467.482	1127.000	0.415	0.427
9	5	2	GT204A02	a76couture1247.r#1	>gb|AAK93585.2| (AY050908) unknown protein [Arabidopsis thaliana]	18.731	35.000	0.535	19.564	33.000	0.593	0.564
9	5	3	GB009H09	a76couture1124.r#1	>ref|NP_196563.1|| (NM_121039) hypothetical protein; protein id: At5g10010.1	814.194	1227.000	0.664	1126.487	1550.000	0.727	0.695
9	5	4	RT082C05	a76couture1010.r#1	>sp|P22177|PCNA_SOYBN PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) (CYCLIN)	52.448	58.000	0.904	67.960	72.000	0.944	0.924
9	5	5	RT053A07	a76couture1365.r#1	>pir||T00641 hypothetical protein F3I6.4 - Arabidopsis thaliana	213.539	289.000	0.739	244.038	346.000	0.705	0.722
9	5	6	GT203E03	a76couture1243.r#1	>dbj|BAC10905.1| (AB071966) Moco containing protein [Oryza sativa (japonica	1327.436	1399.000	0.949	1378.763	1526.000	0.904	0.926
9	5	7	GB009D08	a76couture1120.r#1	>dbj|BAA92902.1| (AP001539) hypothetical protein [Oryza sativa (japonica	1178.833	1433.000	0.823	1197.536	1509.000	0.794	0.808
9	5	8	RT082A07	a76couture1006.r#1	------	208.544	227.000	0.919	207.999	226.000	0.920	0.920
9	5	9	RT052A05	a76couture1361.r#1	>sp|P13708|SUSY_SOYBN Sucrose synthase (Sucrose-UDP glucosyltransferase) (Nodulin-100)	605.650	598.000	1.013	562.214	544.000	1.033	1.023
9	5	10	GT203B07	a76couture1238.r#1	>ref|NP_191362.2|| (NM_115665) putative protein; protein id: At3g58030.1. supported by	309.693	398.000	0.778	329.503	437.000	0.754	0.766
9	5	11	GB009B09	a76couture1114.r#1	>gb|AAL67133.1| (AY074520) unknown protein [Arabidopsis thaliana]	186.066	180.000	1.034	176.078	192.000	0.917	0.975
9	5	12	RT081G08	a76couture1002.r#1	>ref|NP_179503.1|| (NM_127470) putative receptor-like protein kinase; protein id:	239.763	191.000	1.255	251.246	254.000	0.989	1.122
9	5	13	GT191G01	a76couture1821.r#1	>ref|NP_196844.1|| (NM_121343) peptide transporter - like protein; protein id:	32.468	44.000	0.738	21.624	31.000	0.698	0.718
9	5	14	GT172E12	a76couture1729#1	>ref|NP_187568.1|| (NM_111791) unknown protein; protein id: At3g09570.1 [Arabidopsis	1664.602	1206.000	1.380	1466.287	1400.000	1.047	1.214
9	5	15	GB009B07	a76couture1640#1	------	8.741	17.000	0.514	12.356	15.000	0.824	0.669
9	6	1	TT281E10	a76couture1505.r#1	>gb|AAK55708.1|AF380627_1 (AF380627) AT5g53330/K19E1_13 [Arabidopsis thaliana]	183.568	316.000	0.581	166.811	307.000	0.543	0.562
9	6	2	GT191C02	a76couture1817.r#1	>ref|NP_058298.1|| (NC_002305) IS10 transposase [Salmonella typhi]	4.995	17.000	0.294	6.178	14.000	0.441	0.368
9	6	3	Arabidopsis Control Oligonucleotide	3ara23			12.000	0.000				
9	6	4	GB009A03	a76couture1636.r#1	------	19.980	29.000	0.689	21.624	31.000	0.698	0.693
9	6	5	TT281B02	a76couture1501.r#1	>ref|NP_196958.1|| (NM_121458) putative protein; protein id: At5g14540.1 [Arabidopsis	303.450	344.000	0.882	361.423	410.000	0.882	0.882
9	6	6	GT184G01	a76couture1813.r#1	>gb|AAM61053.1| (AY084482) AtPH1-like protein [Arabidopsis thaliana]	157.344	175.000	0.899	167.840	194.000	0.865	0.882
9	6	7	GT172C08	a76couture1723#1	>gb|AAK07610.1|AF319771_2 (AF319771) prohibitin 1-like protein [Brassica napus]	492.013	457.000	1.077	423.205	422.000	1.003	1.040
9	6	8	GT171A02	a76couture1632.r#1	>ref|NP_179485.2|| (NM_127452) hypothetical protein; protein id: At2g18950.1	129.871	136.000	0.955	126.653	136.000	0.931	0.943

9	6	9	TT274F08	a76couture1495.r#1	>gb|AAL15887.1|AF417299_1 (AF417299) putative germin [Castanea sativa]	27.473	34.000	0.808	22.653	34.000	0.666	0.737
9	6	10	GT183H07	a76couture1809.r#1	>ref|NP_181397.1|| (NM_129420) unknown protein; protein id: At2g38630.1 [Arabidopsis	804.204	816.000	0.986	785.658	872.000	0.901	0.943
9	6	11	GT172B08	a76couture1719.r#1	>dbj|BAB64669.1| (AP003296) contains EST AU082313(E2215)~unknown protein [Oryza	22.478	28.000	0.803	19.564	27.000	0.725	0.764
9	6	12	GB007F08	a76couture1627.r#1	------	1098.912	995.000	1.104	1070.884	1189.000	0.901	1.003
9	6	13	TT274B10	a76couture1489.r#1	>ref|NP_193218.1|| (NM_117568) hypothetical protein; protein id: At4g14820.1	32.468	32.000	1.015	27.802	24.000	1.158	1.087
9	6	14	GT182E11	a76couture1805.r#1	>ref|NP_566302.1|| (NM_111611) expressed protein; protein id: At3g07310.1. supported	268.484	258.000	1.041	283.166	339.000	0.835	0.938
9	6	15	GT172B04	a76couture1717.r#1	>ref|NP_194449.1|| (NM_118853) disease resistance protein (NBS-LRR class). putative;	22.478	23.000	0.977	15.445	16.000	0.965	0.971
9	7	1	GB007D04	a76couture1624.r#1	>gb|AAD19957.1| (AF109156) thiosulfate sulfurtransferase [Datisca glomerata]	545.710	1075.000	0.508	735.203	1276.000	0.576	0.542
9	7	2	TT273H07	a76couture1483.r#1	>ref|NP_200011.1|| (NM_124577) putative protein; protein id: At5g51980.1 [Arabidopsis	241.011	466.000	0.517	328.473	548.000	0.599	0.558
9	7	3	GT183E10	a76couture1801.r#1	------	63.687	128.000	0.498	75.168	132.000	0.569	0.534
9	7	4	GT172A07	a76couture1714#1	>ref|NP_176788.1|| (NM_105285) C2H2-type zinc finger protein. putative; protein id:	163.588	207.000	0.790	199.761	256.000	0.780	0.785
9	7	5	GB006G08	a76couture1619.r#1	>ref|NP_565013.1|| (NM_105786) putative dehydrogenase; protein id: At1g71170.1	423.331	523.000	0.809	469.541	613.000	0.766	0.788
9	7	6	TT273E09	a76couture1479.r#1	------	153.598	186.000	0.826	166.811	194.000	0.860	0.843
9	7	7	RT044C01	a76couture2230.r#1	>gb|AAF49313.1| (AE003523) CG6064-PA [Drosophila melanogaster]	269.733	283.000	0.953	267.721	292.000	0.917	0.935
9	7	8	RT032D03	a76couture2131.r#1	>ref|NP_175103.1|| (NM_103563) aminoacylase. putative; protein id: At1g44820.1							
9	7	9	RT022A09	a76couture2035.r#1	>ref|NP_175010.2|| (NM_103470) heterogeneous nuclear ribonucleoprotein (hnRNP)	43.707	45.000	0.971	47.366	45.000	1.053	1.012
9	7	10	RB007A09	a76couture1952.r#1	>ref|NP_199785.1|| (NM_124352) FRO1-like protein; NADPH oxidase-like; protein id:	88.662	76.000	1.167	81.346	80.000	1.017	1.092
9	7	11	RT044A05	a76couture2226.r#1	>ref|NP_567660.1|| (NM_118359) putative protein; protein id: At4g22330.1. supported by	222.280	185.000	1.202	189.464	177.000	1.070	1.136
9	7	12	RT032C09	a76couture2127.r#1	>gb|AAK62030.1| (AY036011) phenylalanine ammonia-lyase 1 [Manihot esculenta]	293.459	266.000	1.103	326.414	342.000	0.954	1.029
9	7	13	RT021E05	a76couture2032#1	>sp|P49299|CYSZ_CUCMA CITRATE SYNTHASE. GLYOXYSOMAL PRECURSOR (GCS)	609.397	593.000	1.028	648.708	727.000	0.892	0.960
9	7	14	RB008A05	a76couture1946.r#1	------	337.166	307.000	1.098	292.434	343.000	0.853	0.975
9	7	15	RT043H05	a76couture2222.r#1	>ref|NP_201491.1|| (NM_126089) disease resistance protein (CC-NBS-LRR class). putative;	88.662	70.000	1.267	87.524	86.000	1.018	1.142
9	8	1	RT031F04	a76couture2123.r#1	>pir||T50856 response regulator 5 [imported] - Arabidopsis thaliana	8.741	25.000	0.350	14.416	27.000	0.534	0.442
9	8	2	RT021H04	a76couture2028#1	>gb|AAL06842.1| (AY054181) AT3g16650/MGL6_10 [Arabidopsis thaliana]	77.423	144.000	0.538	114.296	178.000	0.642	0.590
9	8	3	RB006B09	a76couture1942.r#1	------	2.498	15.000	0.167	3.089	9.000	0.343	0.255
9	8	4	RT043D12	a76couture2218.r#1	------	113.637	146.000	0.778	130.771	182.000	0.719	0.748
9	8	5	RT031D08	a76couture2119.r#1	>ref|NP_566564.1|| (NM_112578) expressed protein; protein id: At3g17020.1. supported	573.182	715.000	0.802	590.016	792.000	0.745	0.773
9	8	6	RT021G05	a76couture2024#1	>ref|NP_178393.1|| (NM_126345) unknown protein; protein id: At2g02910.1 [Arabidopsis	146.105	145.000	1.008	127.682	143.000	0.893	0.950
9	8	7	RB005F10	a76couture1937.r#1	------	59.941	103.000	0.582	60.752	110.000	0.552	0.567
9	8	8	RT042G04	a76couture2214.r#1	>dbj|BAA83368.1| (AP000391) ESTs AU029348(E30206).C74035(E30206) correspond to a	99.901	127.000	0.787	83.405	117.000	0.713	0.750
9	8	9	RT031B09	a76couture2115.r#1	------	43.707	34.000	1.285	39.128	36.000	1.087	1.186
9	8	10	RT021F07	a76couture2020#1	>ref|NP_191101.1|| (NM_115399) 2-oxoglutarate dehydrogenase. E1 subunit - like protein;	218.534	217.000	1.007	193.583	198.000	0.978	0.992
9	8	11	RB004H10	a76couture1933.r#1	>pir||T12286 L-ascorbate peroxidase (EC 1.11.1.11) precursor. stromal - common	3224.307	3583.000	0.900	3110.711	3969.000	0.784	0.842
9	8	12	RT041B10	a76couture2210.r#1	>ref|NP_567627.1|| (NM_118265) putative membrane associated protein; protein id:							
9	8	13	RT031A05	a76couture2111.r#1	>ref|NP_190069.1|| (NM_114352) putative protein; protein id: At3g44830.1 [Arabidopsis	54.946	71.000	0.774	47.366	65.000	0.729	0.751
9	8	14	RT021E07	a76couture2016#1	------	1617.149	1307.000	1.237	1794.760	1759.000	1.020	1.129
9	8	15	RB004B12	a76couture1929.r#1	>ref|NP_567334.1|| (NM_116886) inositol 1.3.4-trisphosphate 5/6-kinase-like protein;	2245.277	2060.000	1.090	2245.767	2664.000	0.843	0.966
9	9	1	PT012H09	a76couture2656.r#1	------	2311.461	4565.000	0.506	3063.345	5259.000	0.582	0.544
9	9	2	TT264A05	a76couture2533.r#1	>ref|NP_190048.1|| (NM_114330) protein-tyrosine-phosphatase-like protein; protein id:	71.180	141.000	0.505	81.346	146.000	0.557	0.531
9	9	3	TB006H01	a76couture2428.r#1	>ref|NP_190998.1|| (NM_115290) synaptobrevin -like protein; protein id: At3g54300.1	418.336	693.000	0.604	681.659	986.000	0.691	0.647
9	9	4	RT061A06	a76couture2320.r#1	>ref|NP_173069.1|| (NM_101485) unknown protein; protein id: At1g16180.1 [Arabidopsis	469.535	592.000	0.793	471.601	709.000	0.665	0.729
9	9	5	PT011D03	a76couture2652.r#1	------	32.468	45.000	0.722	29.861	43.000	0.694	0.708
9	9	6	TT263E04	a76couture2529.r#1	>ref|NP_190882.1|| (NM_115174) O-diphenol-O-methyl transferase. putative; protein id:	700.556	925.000	0.757	707.401	1006.000	0.703	0.730
9	9	7	TB006C05	a76couture2423.r#1	>pir||T17104 translation initiation factor eIF-2 beta chain - apple tree	339.664	444.000	0.765	324.354	422.000	0.769	0.767
9	9	8	RT054G01	a76couture2315.r#1	>gb|AAG34804.1|AF243369_1 (AF243369) glutathione S-transferase GST 14 [Glycine max]	639.367	459.000	1.393	543.679	460.000	1.182	1.287
9	9	9	PT002F02	a76couture2647.r#1	------	213.539	198.000	1.078	205.939	225.000	0.915	0.997
9	9	10	TT264E02	a76couture2525.r#1	>gb|AAD16139.1| (AF096299) DNA-binding protein 2 [Nicotiana tabacum]	1167.594	986.000	1.184	1082.210	1023.000	1.058	1.121
9	9	11	TB006A03	a76couture2419.r#1	------	79.921	96.000	0.833	70.019	95.000	0.737	0.785
9	9	12	RT054C04	a76couture2312.r#1	>ref|XP_066808.2|| (XM_066808) similar to ARYLSULFATASE D PRECURSOR (ASD) [Homo	16.234	27.000	0.601	18.535	29.000	0.639	0.620
9	9	13	PT003E03	a76couture2642.r#1	------	136.115	133.000	1.023	103.999	125.000	0.832	0.928
9	9	14	TT264B03	a76couture2521.r#1	>dbj|BAC10123.1| (AP004309) gag-pol polyprotein -like [Oryza sativa (japonica	97.404	103.000	0.946	72.079	91.000	0.792	0.869
9	9	15	TB004H11	a76couture2411.r#1	------	302.201	246.000	1.228	248.157	244.000	1.017	1.123
9	10	1	RT054B09	a76couture2309.r#1	>ref|NP_199233.1|| (NM_123787) nuclear cap binding protein CBP20; protein id:	265.987	381.000	0.698	324.354	470.000	0.690	0.694
9	10	2	PT007B03	a76couture2639.r#1	------	142.359	260.000	0.548	189.464	316.000	0.600	0.574
9	10	3	TT262B02	a76couture2517.r#1	>ref|NP_195766.1|| (NM_120224) putative protein; protein id: At5g01460.1. supported by	29.970	55.000	0.545	52.514	80.000	0.656	0.601
9	10	4	TB004E04	a76couture2407#1	------	38.712	64.000	0.605	40.158	65.000	0.618	0.611
9	10	5	RT053G05	a76couture2304.r#1	>dbj|BAC15996.1| (AP004300) putative MSP1(mitochondrial sorting of proteins) protein	62.438	76.000	0.822	64.871	81.000	0.801	0.811
9	10	6	PT007F07	a76couture2633.r#1	------	540.715	763.000	0.709	506.610	784.000	0.646	0.677
9	10	7	TT261B05	a76couture2513.r#1	>ref|NP_565875.1|| (NM_129350) expressed protein; protein id: At2g37940.1. supported	650.606	747.000	0.871	703.282	844.000	0.833	0.852
9	10	8	TB004C01	a76couture2403.r#1	------	82.418	93.000	0.886	83.405	99.000	0.842	0.864
9	10	9	RT061D08	a76couture2301.r#1	>ref|NP_194814.1|| (NM_119232) putative protein; protein id: At4g30850.1 [Arabidopsis	8.741	20.000	0.437	8.238	20.000	0.412	0.424
9	10	10	BM437835 CM004A05	couture_a76.11.c1.r#1	>ref|NP_178207.1|| (NM_106740) J8-like protein; protein id: At1g80920.1. supported by	1878.140	1979.000	0.949	1630.008	2077.000	0.785	0.867
9	10	11	PT011A11	a76couture3029.r#1	>gb|AAL38253.1| (AY065077) putative ribosomal protein L10 [Arabidopsis thaliana]	2172.849	2031.000	1.070	1979.075	1961.000	1.009	1.040
9	10	12	CT001B11	a76couture2900.r#1	>gb|AAN07899.1| (AY135174) 20S proteasome alpha 6 subunit [Nicotiana benthamiana]	979.031	1027.000	0.953	899.954	1019.000	0.883	0.918
9	10	13	PT007D04	a76couture2759.r#1	>dbj|BAB08314.1| (AB018107) ADP-ribosylation factor-like protein [Arabidopsis	228.524	216.000	1.058	196.672	208.000	0.946	1.002
9	10	14	AW707998 RT083H01	couture_a76.103.c1.r#1	>gb|AAL15885.1|AF417297_1 (AF417297) putative gamma-thionin [Castanea sativa]	3909.879	2817.000	1.388	3494.788	2941.000	1.188	1.288
9	10	15	RT034A02	a76couture3024.r#1	>gb|AAM66053.1| (AY088519) copia-like retroelement pol polyprotein [Arabidopsis	1813.205	1976.000	0.918	1695.909	2150.000	0.789	0.853
9	11	1	RT052G05	a76couture2894.r#1	>sp|O23787|THI4_CITSI Thiazole biosynthetic enzyme. chloroplast precursor	1759.508	3063.000	0.574	1795.790	2869.000	0.626	0.600

9	11	2	PT003G09	a76couture2755.r#1	------	83.667	166.000	0.504	112.237	174.000	0.645	0.575
9	11	3	BM437287 BM436309 BM437120 RB001G12 BM	couture_a76.0.c1#1	>gb|AAF35186.1|AF195865_1 (AF195865) lipid transfer protein precursor [Gossypium hirsutum]	3015.764	4694.000	0.642	4443.138	6616.000	0.672	0.657
9	11	4	RT062G12	a76couture3016.r#1	>emb|CAA65634.1| (X96932) PS60 [Nicotiana tabacum]	224.777	381.000	0.590	259.483	419.000	0.619	0.605
9	11	5	CM001C01	a76couture2888.r#1	>emb|CAA98160.1| (Z73932) RAB1C [Lotus japonicus]	1240.022	1557.000	0.796	1346.842	1826.000	0.738	0.767
9	11	6	PT010H12	a76couture2751.r#1	>ref|NP_567747.1|| (NM_118784) putative uracil phosphoribosyl transferase; protein id:	239.763	300.000	0.799	245.068	336.000	0.729	0.764
9	11	7	WK002A02C	a76couture3175.r#1	>gb|AAD16139.1| (AF096299) DNA-binding protein 2 [Nicotiana tabacum]	116.135	159.000	0.730	114.296	163.000	0.701	0.716
9	11	8	PT001H12	a76couture3011.r#1	>ref|NP_564165.1|| (NM_102079) protein phosphatase 2C (PP2C). putative; protein id:	841.667	783.000	1.075	922.607	927.000	0.995	1.035
9	11	9	RT082H05	a76couture2881.r#1	>gb|AAF73016.1|AF262934_1 (AF262934) ubiquitin conjugating protein [Avicennia marina]	2795.982	2370.000	1.180	2430.082	2313.000	1.051	1.115
9	11	10	PT011A10	a76couture2746.r#1	>dbj|BAB86220.1| (AP003922) contains ESTs AU093915(E1276).AU162319(E60301)~similar	741.766	570.000	1.301	777.420	653.000	1.191	1.246
9	11	11	MY002B02C	a76couture3169.r#1	>gb|AAK19611.1|AF336278_1 (AF336278) BNLGHi233 [Gossypium hirsutum]	305.947	283.000	1.081	254.335	244.000	1.042	1.062
9	11	12	Arabidopsis Control Oligonucleotide	3ara7		8.741	9.000	0.971	6.178	8.000	0.772	0.872
9	11	13	RT081H11	a76couture2871.r#1	------	699.308	566.000	1.236	633.263	567.000	1.117	1.176
9	11	14	PT002A09	a76couture2742.r#1	>ref|NP_197089.1|| (NM_121590) Zinc finger protein CONSTANS-LIKE 1 (COL1); protein id:	32.468	40.000	0.812	25.742	34.000	0.757	0.784
9	11	15	K4T7REVER	a76couture3165.r#1	------	362.141	322.000	1.125	333.621	344.000	0.970	1.047
9	12	1	RT053A03	a76couture3001.r#1	>ref|NP_177742.2|| (NM_106264) hypothetical protein; protein id: At1g76150.1	54.946	115.000	0.478	72.079	129.000	0.559	0.518
9	12	2	GT181C12	a76couture2864.r#1	>gb|AAF79822.1|AC026875_2 (AC026875) T6D22.2 [Arabidopsis thaliana]	2229.043	4112.000	0.542	2177.807	3365.000	0.647	0.595
9	12	3	PT002G01	a76couture2738.r#1	>ref|NP_189309.2|| (NM_113586) bHLH protein; protein id: At3g26744.1. supported by	143.608	173.000	0.830	177.108	192.000	0.922	0.876
9	12	4	BM436447 BE846434 GT202E10	couture_a76.469.c2#1	>gb|AAD27590.1|AF121261_1 (AF121261) elongation factor 1-alpha 1; EF-1-alpha1 [Lilium	2804.723	3737.000	0.751	3394.907	4567.000	0.743	0.747
9	12	5	BM437017 GT171H10	couture_a76.381.c1.r#1	>ref|NP_200196.1|| (NM_124764) putative protein; protein id: At5g53850.1 [Arabidopsis	825.433	884.000	0.934	864.944	1085.000	0.797	0.865
9	12	6	BG273844 BG273770 BM437800 BM437011 BM4	couture_a76.30.c1.r#1	>sp|Q9ZSW9|TCTP_HEVBR Translationally controlled tumor protein homolog (TCTP)	6000.309	6004.000	0.999	5512.991	6475.000	0.851	0.925
9	12	7	BM436481 RT093D11	couture_a76.205.c1.r#1	>ref|NP_192705.1|| (NM_117035) AX110P -like protein; protein id: At4g09670.1	1040.220	1086.000	0.958	1052.349	1247.000	0.844	0.901
9	12	8	TB003g06 BM436861 TB003G06	couture_a76.465.c1.r#1	>dbj|BAB40974.1| (AB049816) isopentenyl diphosphate isomerase 2 [Nicotiana tabacum]	5214.837	6595.000	0.791	5494.457	7692.000	0.714	0.753
9	12	9	RT024C02 BM437107 GT172A02	couture_a76.378.c1#1	>emb|CAC84143.2| (AJ309009) thioredoxin peroxidase [Nicotiana tabacum]	455.799	446.000	1.022	434.532	481.000	0.903	0.963
9	12	10	BG273934 RT062D07	couture_a76.296.c1#1	>ref|NP_564289.1|| (NM_102517) expressed protein; protein id: At1g27530.1. supported	1022.737	710.000	1.440	1050.290	886.000	1.185	1.313
9	12	11	BM436331 RT083E02 BM438074 BM436636 BM	couture_a76.201.c1.r#1	>emb|CAB75430.1| (AJ272037) putative 16kDa membrane protein [Nicotiana tabacum]	89.911	105.000	0.856	70.019	94.000	0.745	0.801
9	12	12	TB004g05 TB004G05	couture_a76.462.c1.r#1	>gb|AAF20003.1|AF213937_1 (AF213937) 1-acyl-sn-glycerol-3-phosphate acyltransferase [Prunus	894.115	1163.000	0.769	754.767	1108.000	0.681	0.725
9	12	13	BM438114 BM437089 BM437791 GT162E12	couture_a76.375.c1#1	>gb|AAG38521.1|AF283536_1 (AF283536) cystatin-like protein [Citrus x paradisi]	450.804	499.000	0.903	434.532	515.000	0.844	0.874
9	12	14	BG273899 BM437251 GB009F06	couture_a76.29.c1#1	>gb|AAM83095.1|AF525402_1 (AF525402) SOS2-like protein kinase [Glycine max]	8487.846	8183.000	1.037	8469.248	8921.000	0.949	0.993
9	12	15	BM437756 RT081D12	couture_a76.197.c1.r#1	>emb|CAD12767.2| (AJ420902) LHY protein [Phaseolus vulgaris]	8.741	16.000	0.546	6.178	16.000	0.386	0.466
9	13	1	BM436419 TB001E04	couture_a76.459.c1.r#1	>dbj|BAB86225.1| (AP003922) putative hydroxymethyltransferase [Oryza sativa	132.369	315.000	0.420	181.226	352.000	0.515	0.468
9	13	2	RT084H07 BE846422 GB007B06	couture_a76.370.c1.r#1	------	157.344	377.000	0.417	205.939	413.000	0.499	0.458
9	13	3	BM437001 RT032C02 BM436396 BM436922 BM	couture_a76.286.c1#1	>pir||S00443 chlorophyll a/b-binding protein type I precursor (cab-6A) - tomato	87.413	215.000	0.407	103.999	232.000	0.448	0.427
9	13	4	BM436907 TT273C11	couture_a76.193.c1#1	>dbj|BAA77508.1| (AB026909) F1-ATP synthase delta subunit [Ipomoea batatas]	2076.694	3105.000	0.669	2631.903	3972.000	0.663	0.666
9	13	5	BM437036 RT062H01	couture_a76.456.c1.r#1	>ref|NP_565885.1|| (NM_129383) expressed protein; protein id: At2g38270.1. supported	400.853	500.000	0.802	417.027	549.000	0.760	0.781
9	13	6	GB004b08 GB004B08	couture_a76.365.c1.r#1	>gb|AAK84008.1|AF393847_1 (AF393847) beta-amylase PCT-BMYI [Solanum tuberosum]	694.313	999.000	0.695	606.491	1013.000	0.599	0.647
9	13	7	GB001f05 GB001F05	couture_a76.28.c1.r#1	>gb|AAM91875.1| (AC051632) putative transcription factor [Oryza sativa (japonica	5889.169	5418.000	1.087	5984.592	5937.000	1.008	1.047
9	13	8	BM437316 TT274E04	couture_a76.189.c1.r#1	>dbj|BAA88264.1| (AB008017) similar to ribosomal protein S2 [Arabidopsis thaliana]	5910.398	5914.000	0.999	4011.695	4747.000	0.845	0.922
9	13	9	BM437741 RT062H12	couture_a76.453.c1.r#1	>pir||T09622 protein kinase MMK4 (EC 2.7.1.-). cold- and drought-induced -	550.705	608.000	0.906	503.521	587.000	0.858	0.882
9	13	10	BM436737 BM437474 GB002E05	couture_a76.361.c1.r#1	------	47.453	58.000	0.818	36.039	54.000	0.667	0.743
9	13	11	RB007F04 RB007F04	couture_a76.275.c1.r#1	>emb|CAA70330.1| (Y09113) dioxygenase [Marah macrocarpus]	126.125	123.000	1.025	116.356	130.000	0.895	0.960
9	13	12	BM436313 RT094G06	couture_a76.186.c1.r#1	>ref|NP_194940.2|| (NM_119365) hypothetical protein; protein id: At4g32130.1	665.591	660.000	1.008	615.758	652.000	0.944	0.976
9	13	13	BG273876 CM003D03	couture_a76.560.c1#1	>ref|NP_175635.1|| (NM_104104) dynein light chain. putative; protein id: At1g52250.1	2461.313	3698.000	0.666	2609.249	3370.000	0.774	0.720
9	13	14	G499025E VVPAL	couture_a76.sd.84.c1#	>sp|P45735|PALY_VITVI Phenylalanine ammonia-lyase >gi|1345583|emb|CAA53581.1| (X75967)	262.240	140.000	1.873	189.464	101.000	1.876	1.875
9	13	15	BM436932 PT013D12 BM438108	couture_a76.72.c1.r#1	>sp|P26585|HMGL_SOYBN HMG1/2-LIKE PROTEIN (SB11 PROTEIN) >gi|99914|pir||S22309 high	670.586	570.000	1.176	626.055	565.000	1.108	1.142
9	14	1	BM437975 CT003C03	couture_a76.537.c1.r#1	>ref|NP_188300.1|| (NM_112551) putative ribosomal protein; protein id: At3g16780.1	1448.566	2483.000	0.583	1746.364	2472.000	0.706	0.645
9	14	2	BM437325 BM437549 BM437422 BM437333 BM	couture_a76.sd.78.c1#	>gb|AAB72091.1| (AF020709) chalcone synthase [Vitis vinifera]	991.518	1887.000	0.525	1190.328	1853.000	0.642	0.584
9	14	3	BM436895 RT032H04	couture_a76.68.c1.r#1	>sp|Q9M4T8|PSA5_SOYBN Proteasome subunit alpha type 5 (20S proteasome alpha subunit E)	325.927	776.000	0.420	368.631	707.000	0.521	0.471
9	14	4	ST002F02 CT006A09	couture_a76.556.c1.r#1	------	19.980	31.000	0.645	26.772	33.000	0.811	0.728
9	14	5	G3063642 AF056622	couture_a76.sd.77.c1#	>sp|O65199|SODP_VITVI Superoxide dismutase [Cu-Zn]. chloroplast precursor	328.425	475.000	0.691	366.572	565.000	0.649	0.670
9	14	6	RB003C06 RT044C08	couture_a76.623.c1#1	>emb|CAD31838.1| (AJ487465) putative quinone oxidoreductase [Cicer arietinum]	1826.941	2898.000	0.630	1477.614	2606.000	0.567	0.599
9	14	7	BM436347 CM002H09	couture_a76.528.c1.r#1	>dbj|BAA88898.1| (AB020961) cysteine protease component of protease-inhibitor	4303.239	6488.000	0.663	3713.083	6097.000	0.609	0.636
9	14	8	G7547006 AF243474	couture_a76.sd.44.c1#	>gb|AAF63755.1|AF243474_1 (AF243474) putative ethylene receptor [Vitis vinifera]	183.568	253.000	0.726	197.702	286.000	0.691	0.708
9	14	9	RB001A05 RB004F03	couture_a76.621.c1.r#1	>emb|CAA67923.1| (X99609) ubiquitin-like protein [Arabidopsis thaliana]	1097.663	1071.000	1.025	1008.072	1215.000	0.830	0.927
9	14	10	BM437104 TT251B03	couture_a76.474.c1.r#1	>ref|NP_174304.1|| (NM_102751) pyruvate dehydrogenase E1 beta subunit. putative;	94.906	102.000	0.930	66.930	84.000	0.797	0.864
9	14	11	BM436854 TB001b11 BM437891 RT084G01	couture_a76.640.c1.r#1	>ref|NP_569012.1|| (NM_125941) 14-3-3 protein GF14 kappa (grf8); protein id:	3211.820	3149.000	1.020	2229.291	2572.000	0.867	0.943
9	14	12	BM436572 BM438016 BM436284 BM436995 BM	couture_a76.545.c1#1	>gb|AAD02175.1| (AF039662) ferredoxin-like protein [Capsicum annuum]	2825.952	2593.000	1.090	2154.124	2233.000	0.965	1.027
9	**14**	**13**	**G6434830 AF021809**	**couture_a76.sd.65.c1#**	**>gb|AAF08330.1|AF021809_1 (AF021809) putative sucrose transporter [Vitis vinifera]**	**227.275**	**255.000**	**0.891**	**174.019**	**219.000**	**0.795**	**0.843**
9	14	14	BM437217 BG273842 TB000A50	couture_a76.494.c1.r#1	------	19.980	32.000	0.624	19.564	31.000	0.631	0.628
9	14	15	GB005d08 BM437910 GT204A12	couture_a76.sd.10.c1.r	>gb|AAF71820.1|AF141900_1 (AF141900) putative aquaporin PIP2-2 [Vitis berlandieri x Vitis	48.702	61.000	0.798	41.188	56.000	0.735	0.767
10	1	1	CM004G02	a76couture0471.r#1	>ref|NP_194405.1|| (NM_118809) putative protein; protein id: At4g26750.1. supported by	123.628	91.000	1.359	150.336	132.000	1.139	1.249
10	1	2	ST001H03	a76couture0373.r#1	------	825.433	513.000	1.609	794.925	704.000	1.129	1.369
10	1	3	PT007B04	a76couture0248.r#1	>gb|AAL90751.1| (AF483268) peroxiredoxin [Populus tremula x Populus tremuloides]	8444.139	7416.000	1.139	7341.731	9484.000	0.774	0.956
10	1	4	CT002G05	a76couture0101.r#1	------	13484.149	11724.000	1.150	12981.375	14796.000	0.877	1.014
10	1	5	CM004E08	a76couture0467.r#1	>gb|AAM67182.1| (AY088876) unknown [Arabidopsis thaliana]	79.921	70.000	1.142	65.901	84.000	0.785	0.963
10	1	6	CT004G10	a76couture0369.r#1	>pir||D75542 hypothetical protein - Deinococcus radiodurans (strain R1)	405.848	459.000	0.884	424.235	644.000	0.659	0.771
10	1	7	PT009D11	a76couture0241.r#1	>ref|NP_187709.1|| (NM_111935) unknown protein; protein id: At3g10980.1 [Arabidopsis	154.847	128.000	1.210	337.740	201.000	1.680	1.445
10	1	8	CT002A02	a76couture0096.r#1	>pir||S27762 Sip1 protein - barley >gi|167100|gb|AAA32975.1| (M77475) seed	724.283	887.000	0.817	1142.962	1262.000	0.906	0.861
10	1	9	CM004C12	a76couture0463.r#1	------	1147.614	836.000	1.373	1637.216	1089.000	1.503	1.438

10	1	10	CM005h07	a76couture0365.r#1	none	23.727	25.000	0.949	37.069	31.000	1.196	1.072
10	1	11	PT001A02	a76couture0236.r#1	>ref|NP_200396.1|| (NM_124967) NOI protein. nitrate-induced; protein id: At5g55850.1	1414.849	1095.000	1.292	2170.599	1693.000	1.282	1.287
10	1	12	CM004G10	a76couture0092.r#1	>ref|NP_197190.1|| (NM_121694) TOM (target of myb1) -like protein; protein id:	769.238	634.000	1.213	987.478	836.000	1.181	1.197
10	1	13	CM004A07	a76couture0459.r#1	------	33.717	35.000	0.963	54.574	48.000	1.137	1.050
10	1	14	CM003E06	a76couture0361.r#1	>gb|AAD22104.1| (AF130978) B12D protein [Ipomoea batatas]	801.706	679.000	1.181	1256.229	969.000	1.296	1.239
10	1	15	PT011B11	a76couture0231.r#1	>sp|P49043|VPE_CITSI Vacuolar processing enzyme precursor (VPE) >gi|1076563|pir||S51117	5566.988	6293.000	0.885	8808.018	8757.000	1.006	0.945
10	2	1	CM003G02	a76couture0087.r#1	>gb|AAL09767.1| (AY057527) AT5g03040/F15A17_70 [Arabidopsis thaliana]	619.387	454.000	1.364	526.175	538.000	0.978	1.171
10	2	2	CM003H10	a76couture0455.r#1	>dbj|BAB83948.1| (AB046419) CIG1 [Nicotiana tabacum]	384.619	273.000	1.409	322.295	327.000	0.986	1.197
10	2	3	CM001H02	a76couture0357.r#1	>gb|AAM65577.1| (AY088031) globulin-like protein [Arabidopsis thaliana]	7965.863	7617.000	1.046	7772.144	9873.000	0.787	0.917
10	2	4	PT011F02	a76couture0226.r#1	>ref|NP_567466.1|| (NM_117636) Expressed protein; protein id: At4g15470.1. supported	12137.982	11128.000	1.091	13182.166	15618.000	0.844	0.967
10	2	5	CM001F07	a76couture0081.r#1	------	736.770	885.000	0.833	637.382	1038.000	0.614	0.723
10	2	6	CM003G12	a76couture0450.r#1	------	849.159	750.000	1.132	1035.874	1062.000	0.975	1.054
10	2	7	TT262C11	a76couture0353.r#1	>ref|NP_197516.1|| (NM_122023) ribosomal protein L7Ae-like; protein id: At5g20160.1	766.741	708.000	1.083	1494.089	949.000	1.574	1.329
10	2	8	RT064A10	a76couture0219.r#1	>ref|NP_177894.1|| (NM_106420) unknown protein; protein id: At1g77710.1. supported by	10625.729	7687.000	1.382	18392.427	10659.000	1.726	1.554
10	2	9	CT004E05	a76couture0072.r#1	>gb|AAL76261.1|AF466824_1 (AF466824) putative permease 1 [Arabidopsis thaliana]	1082.678	859.000	1.260	1682.523	1195.000	1.408	1.334
10	2	10	TT264F09	a76couture0903.r#1	>dbj|BAB01470.1| (AP000731) gb|AAD31369.1~gene_id:F16J14.11~similar to unknown	3710.077	3355.000	1.106	4525.513	4258.000	1.063	1.084
10	2	11	GB001E12	a76couture0776.r#1	>ref|NP_564336.1|| (NM_102725) expressed protein; protein id: At1g29850.1. supported	4868.929	4297.000	1.133	5707.604	5169.000	1.104	1.119
10	2	12	ST004G06	a76couture0671.r#1	>ref|NP_175665.1|| (NM_104134) chloroplast-localized small heat shock protein	2265.257	1250.000	1.812	3198.235	1610.000	1.986	1.899
10	2	13	CT005E10	a76couture0572.r#1	>ref|NP_051116.1|| (NC_000932) ribosomal protein S15 [Arabidopsis thaliana]	1663.353	1108.000	1.501	2180.896	1320.000	1.652	1.577
10	2	14	RT094H05	a76couture0897.r#1	------	3913.625	3245.000	1.206	5619.050	4148.000	1.355	1.280
10	2	15	RT074F05	a76couture0771.r#1	>gb|AAM61146.1| (AY084581) unknown [Arabidopsis thaliana]	29.970	46.000	0.652	40.158	56.000	0.717	0.684
10	3	1	ST004F03	a76couture0666.r#1	>ref|NP_027543.1|| (NM_126399) expressed protein; protein id: At2g03480.1 [Arabidopsis	387.117	356.000	1.087	344.948	440.000	0.784	0.936
10	3	2	CT005C11	a76couture0567.r#1	------	86.165	73.000	1.180	66.930	71.000	0.943	1.062
10	3	3	TT284H05	a76couture0892.r#1	>gb|AAF43225.1|AC012654_9 (AC012654) Contains S1 RNA binding domain PF|00575. EST	48.702	47.000	1.036	33.980	46.000	0.739	0.887
10	3	4	RT074C08	a76couture0766.r#1	------	821.686	632.000	1.300	698.134	699.000	0.999	1.149
10	3	5	ST004E01	a76couture0662.r#1	>dbj|BAB63567.1| (AP003224) putative receptor protein kinase-like protein [Oryza	23.727	30.000	0.791	11.327	22.000	0.515	0.653
10	3	6	CT005B01	a76couture0563.r#1	>emb|CAC88035.1| (AJ316582) RNA polymerase beta I subunit [Atropa belladonna]	162.339	187.000	0.868	303.760	284.000	1.070	0.969
10	3	7	RT094B04	a76couture0886.r#1	>ref|NP_564346.1|| (NM_102746) expressed protein; protein id: At1g30070.1. supported	2211.560	2221.000	0.996	4466.821	3090.000	1.446	1.221
10	3	8	RT073H02	a76couture0762.r#1	>gb|AAK70805.1| (AY040533) leucine-rich repeat resistance protein-like protein	226.026	194.000	1.165	443.799	323.000	1.374	1.270
10	3	9	ST004C03	a76couture0658.r#1	>ref|NP_195586.1|| (NM_120035) hypothetical protein; protein id: At4g38750.1	172.329	132.000	1.306	283.166	187.000	1.514	1.410
10	3	10	CT004H06	a76couture0559.r#1	>ref|NP_568013.1|| (NM_119865) putative protein; protein id: At4g37020.1 [Arabidopsis	168.583	154.000	1.095	237.860	205.000	1.160	1.127
10	3	11	RT093F09	a76couture0879.r#1	>gb|AAM67368.1| (AY087211) unknown [Arabidopsis thaliana]	500.754	449.000	1.115	698.134	580.000	1.204	1.159
10	3	12	RT072H03	a76couture0755.r#1	------	1371.142	1105.000	1.241	1822.562	1443.000	1.263	1.252
10	3	13	ST004A09	a76couture0654.r#1	------	46.204	44.000	1.050	86.494	73.000	1.185	1.117
10	3	14	CT004F04	a76couture0554.r#1	>gb|AAM63274.1| (AY086067) unknown [Arabidopsis thaliana]	3452.831	3150.000	1.096	5214.380	4168.000	1.251	1.174
10	3	15	RT093A01	a76couture0874.r#1	>ref|NP_565468.1|| (NM_127582) expressed protein; protein id: At2g20230.1. supported	388.365	462.000	0.841	562.214	570.000	0.986	0.913
10	4	1	RT072A04	a76couture0751.r#1	>ref|NP_198391.1|| (NM_122932) serine/threonine protein kinase SOS2 (gb|AAF62923.1);	1383.630	1315.000	1.052	1124.428	1494.000	0.753	0.902
10	4	2	ST003H10	a76couture0650.r#1	------	1009.001	608.000	1.660	784.628	704.000	1.115	1.387
10	4	3	CT004D08	a76couture0548.r#1	>dbj|BAB86462.1| (AP003240) rac-GTP binding protein -like [Oryza sativa (japonica	163.588	163.000	1.004	131.801	178.000	0.740	0.872
10	4	4	RT052G06	a76couture1356.r#1	>gb|AAL27503.1|AF439832_1 (AF439832) At2g47010/F14M4.16 [Arabidopsis thaliana]	499.505	542.000	0.922	484.987	693.000	0.700	0.811
10	4	5	GT202D10	a76couture1233.r#1	>ref|NP_566831.1|| (NM_113723) expressed protein; protein id: At3g28050.1. supported	805.452	727.000	1.108	704.312	925.000	0.761	0.935
10	4	6	GB007A03	a76couture1109.r#1	------	14.985	22.000	0.681	9.267	20.000	0.463	0.572
10	4	7	RT083H05	a76couture0998.r#1	>ref|NP_198395.1|| (NM_122936) disease resistance protein (CC-NBS-LRR class). putative;	0.000			6.178	15.000	0.412	0.412
10	4	8	RT044F08	a76couture1352.r#1	>ref|NP_198035.1|| (NM_122565) threonyl-tRNA synthetase; protein id: At5g26830.1	101.150	89.000	1.137	211.088	132.000	1.599	1.368
10	4	9	GT201E04	a76couture1223.r#1	>gb|AAG24946.1| (AF195887) dehydroascorbate reductase [Arabidopsis thaliana]	94.906	94.000	1.010	141.068	123.000	1.147	1.078
10	4	10	GB005F10	a76couture1105.r#1	>ref|NP_565750.1|| (NM_128830) Kip-related protein 4; protein id: At2g32710.1	404.599	253.000	1.599	473.660	290.000	1.633	1.616
10	4	11	RT083G01	a76couture0996.r#1	------	2348.924	2048.000	1.147	3136.453	2488.000	1.261	1.204
10	4	12	RT043D11	a76couture1348.r#1	>ref|NP_568912.1|| (NM_125363) putative protein; protein id: At5g59710.1. supported by	68.682	71.000	0.967	102.970	104.000	0.990	0.979
10	4	13	GT194H01	a76couture1218.r#1	>ref|NP_176268.1|| (NM_104752) auxin-induced protein. putative; protein id:	784.224	1022.000	0.767	1223.279	1353.000	0.904	0.836
10	4	14	GB004C01	a76couture1096.r#1	>ref|NP_189093.1|| (NM_113358) ethylene-responsive transcriptional coactivator	977.782	590.000	1.657	1384.941	738.000	1.877	1.767
10	4	15	RT083D12	a76couture0993.r#1	>ref|NP_566244.1|| (NM_111373) expressed protein; protein id: At3g05010.1. supported	483.271	510.000	0.948	836.113	729.000	1.147	1.047
10	5	1	RT041H10	a76couture1344.r#1	>ref|NP_568436.1|| (NM_122281) expressed protein; protein id: At5g23760.1. supported	1630.885	1019.000	1.600	1339.634	1116.000	1.200	1.400
10	5	2	GT202D04	a76couture1211.r#1	------	57.443	88.000	0.653	39.128	79.000	0.495	0.574
10	5	3	GB002A09	a76couture1090.r#1	>ref|NP_566657.1|| (NM_112920) expressed protein; protein id: At3g20290.1. supported	679.327	726.000	0.936	570.451	878.000	0.650	0.793
10	5	4	RT083C09	a76couture0988.r#1	>ref|NP_175627.1|| (NM_104096) HD-Zip transcription factor; protein id: At1g52150.1	136.115	141.000	0.965	130.771	173.000	0.756	0.861
10	5	5	RT041F03	a76couture1340.r#1	>gb|AAC98455.1| (AC005851) hypothetical protein [Arabidopsis thaliana]	969.041	838.000	1.156	897.895	986.000	0.911	1.034
10	5	6	GT194C06	a76couture1207.r#1	>ref|NP_194716.1|| (NM_119133) putative protein; protein id: At4g29870.1. supported by	1446.068	1569.000	0.922	2402.280	2302.000	1.044	0.983
10	5	7	GB001C05	a76couture1085.r#1	>ref|NP_194229.1|| (NM_118631) expressed protein; protein id: At4g24990.1. supported	530.725	589.000	0.901	894.806	812.000	1.102	1.002
10	5	8	RT083C02	a76couture0985.r#1	>pir||T51100 protein phosphatase 2C homolog [imported] - common ice plant	122.379	118.000	1.037	275.958	226.000	1.221	1.129
10	5	9	RT034C07	a76couture1335.r#1	>dbj|BAB64114.1| (AP003235) putative zinc finger protein [Oryza sativa (japonica	463.291	391.000	1.185	643.560	489.000	1.316	1.250
10	5	10	GT193F04	a76couture1202.r#1	>emb|CAA10101.1| (AJ012653) ribosomal protein S28 [Prunus persica]	2664.861	2124.000	1.255	4300.010	2934.000	1.466	1.360
10	5	11	TT253H06	a76couture1077.r#1	------	398.356	401.000	0.993	572.511	518.000	1.105	1.049
10	5	12	RT083B04	a76couture0982.r#1	>ref|NP_199582.1|| (NM_124145) putative protein; protein id: At5g47710.1. supported by	644.362	681.000	0.946	940.112	871.000	1.079	1.013
10	5	13	GT183D01	a76couture1799.r#1	>pir||T09820 fiber protein 1 [imported] - upland cotton	182.319	209.000	0.872	258.454	261.000	0.990	0.931
10	5	14	GT171H09	a76couture1710.r#1	>ref|NP_200428.1|| (NM_124999) putative protein; protein id: At5g56170.1 [Arabidopsis	720.537	789.000	0.913	1122.368	1030.000	1.090	1.001
10	5	15	GB006E12	a76couture1614.r#1	>ref|NP_176040.1|| (NM_104523) 20S proteasome beta subunit G1 (PBG1); protein id:	1844.424	1827.000	1.010	2342.558	2068.000	1.133	1.071
10	6	1	TT273A10	a76couture1475.r#1	>emb|CAC21424.1| (AJ278332) 12-oxophytodienoate reductase 3 [Lycopersicon	999.011	824.000	1.212	864.944	927.000	0.933	1.073
10	6	2	GT182G02	a76couture1796#1	------	7.493	25.000	0.300	8.238	23.000	0.358	0.329

10	6	3	GT171E01	a76couture1705.r#1	>dbj|BAB63707.1| (AP003289) putative G10 protein [Oryza sativa (japonica	634.372	563.000	1.127	524.115	691.000	0.758	0.943
10	6	4	Arabidopsis Control Oligonucleotide	3ara7		97.404	93.000	1.047	85.465	105.000	0.814	0.931
10	6	5	TT273F04	a76couture1470.r#1	>ref|NP_182291.1|| (NM_130337) unknown protein; protein id: At2g47690.1 [Arabidopsis	691.815	657.000	1.053	731.084	889.000	0.822	0.938
10	6	6	GT181A09	a76couture1792.r#1	>pir||T49263 hypothetical protein F12M12.190 - Arabidopsis thaliana	333.420	267.000	1.249	410.849	326.000	1.260	1.255
10	6	7	GT171C11	a76couture1701.r#1	>dbj|BAB03441.1| (AP002817) ESTs AU078742(C11888).C26225(C11888) correspond to a	4.995	13.000	0.384	11.327	16.000	0.708	0.546
10	6	8	GB005H11	a76couture1606.r#1	>dbj|BAB09848.1| (AB005246) gene_id:MUP24.17~pir||S76167~similar to unknown protein	152.349	192.000	0.793	236.830	247.000	0.959	0.876
10	6	9	TT264G03	a76couture1465.r#1	>ref|NP_192177.1|| (NM_116502) hypothetical protein; protein id: At4g02680.1	342.161	404.000	0.847	504.551	507.000	0.995	0.921
10	6	10	GT173F01	a76couture1788.r#1	>ref|NP_197498.1|| (NM_122005) lipophosphoglycan biosynthetic protein - like; protein	53.697	60.000	0.895	96.791	100.000	0.968	0.931
10	6	11	GT162H05	a76couture1697.r#1	>ref|NP_175919.1|| (NM_104396) unknown protein; protein id: At1g55230.1 [Arabidopsis	1321.192	1566.000	0.844	1791.671	2014.000	0.890	0.867
10	6	12	GB004D02	a76couture1602.r#1	>pir||T05663 hypothetical protein F22I13.120 - Arabidopsis thaliana	754.253	916.000	0.823	1093.537	1142.000	0.958	0.890
10	6	13	TT262H03	a76couture1461.r#1	>gb|AAM22708.1|AC098693_13 (AC098693) Putative ubiquitin protein [Oryza sativa (japonica	535.720	551.000	0.972	799.044	704.000	1.135	1.054
10	6	14	GT174G04	a76couture1783.r#1	>dbj|BAB78667.1| (AP003434) contains EST AU064167(E4058)~similar to Arabidopsis	358.395	336.000	1.067	562.214	462.000	1.217	1.142
10	6	15	GT161H12	a76couture1691.r#1	>gb|AAM61528.1| (AY084967) unknown [Arabidopsis thaliana]	33.717	34.000	0.992	46.336	38.000	1.219	1.106
10	7	1	GB005C07	a76couture1598.r#1	>ref|NP_567418.1|| (NM_117476) expressed protein; protein id: At4g14010.1. supported	51.199	47.000	1.089	43.247	44.000	0.983	1.036
10	7	2	TT264G09	a76couture1457.r#1	>gb|AAF18502.1|AC010924_15 (AC010924) ESTs gb|AI992787. gb|T20398 come from this gene.	36.214	37.000	0.979	22.653	28.000	0.809	0.894
10	7	3	GT174F01	a76couture1779.r#1	>ref|NP_566990.1|| (NM_115245) putative protein; protein id: At3g53850.1. supported by	144.857	119.000	1.217	107.088	133.000	0.805	1.011
10	7	4	GT161C04	a76couture1687.r#1	>ref|NP_568245.1|| (NM_121158) DEAD/DEAH box RNA helicase. putative; protein id:	425.828	366.000	1.163	428.353	469.000	0.913	1.038
10	7	5	GB005B06	a76couture1595#1	>gb|AAM97080.1| (AY136414) cytoplasmic aconitate hydratase [Arabidopsis thaliana]	28.722	48.000	0.598	37.069	56.000	0.662	0.630
10	7	6	TT264A12	a76couture1452.r#1	>ref|NP_564753.1|| (NM_104698) expressed protein; protein id: At1g60060.1. supported	96.155	119.000	0.808	125.623	143.000	0.878	0.843
10	7	7	RT042H06	a76couture2206.r#1	------	18.731	22.000	0.851	32.950	35.000	0.941	0.896
10	7	8	RT024H06	a76couture2107.r#1	>ref|NP_191365.1|| (NM_115668) putative protein; protein id: At3g58060.1 [Arabidopsis	28.722	36.000	0.798	49.425	50.000	0.989	0.893
10	7	9	RT021D07	a76couture2013#1	>pir||T02877 probable chlorophyll a/b-binding protein - rice	133.618	167.000	0.800	222.414	227.000	0.980	0.890
10	7	10	RB003B01	a76couture1922.r#1	>gb|AAM34774.1|AF509874_1 (AF509874) nam-like protein 11 [Petunia x hybrida]	698.059	863.000	0.809	954.528	1050.000	0.909	0.859
10	7	11	RT042D01	a76couture2202.r#1	>ref|XP_139140.1|| (XM_139140) similar to seven in absentia 2 [Mus musculus]	4418.125	4189.000	1.055	8098.558	6043.000	1.340	1.197
10	7	12	RT024B03	a76couture2102.r#1	>ref|NP_196663.1|| (NM_121140) ser/thr specific protein kinase-like protein; protein	551.953	826.000	0.668	872.152	1036.000	0.842	0.755
10	7	13	RT021C02	a76couture2008#1	>ref|NP_568187.1|| (NM_120890) syntaxin SYP132; protein id: At5g08080.1. supported by	398.356	348.000	1.145	674.451	488.000	1.382	1.263
10	7	14	RB002G07	a76couture1917.r#1	>dbj|BAA97100.1| (AB040471) bZIP transcriptional activator RSG [Nicotiana tabacum]	1563.452	1450.000	1.078	2202.519	1846.000	1.193	1.136
10	7	15	RT041B12	a76couture2197.r#1	>ref|NP_187383.1|| (NM_111607) GTP cyclohydrolase I; protein id: At3g07270.1	68.682	81.000	0.848	119.445	106.000	1.127	0.987
10	8	1	RT024F08	a76couture2095.r#1	>gb|AAB61680.1| (L22203) S-adenosyl-L-methionine:trans-caffeoyl-CoA	5063.736	4802.000	1.055	4162.031	5472.000	0.761	0.908
10	8	2	RT021B05	a76couture2005#1	>gb|AAF02882.1|AC009525_16 (AC009525) Similar to beta-glucosidases [Arabidopsis thaliana]	749.258	549.000	1.365	584.867	624.000	0.937	1.151
10	8	3	RB001H06	a76couture1911.r#1	>ref|NP_565950.1|| (NM_129712) UDP-GlcNAc:dolichol phosphate	1103.907	1026.000	1.076	947.320	1234.000	0.768	0.922
10	8	4	RT034B01	a76couture2193.r#1	>gb|AAF79607.1|AC027665_8 (AC027665) F5M15.12 [Arabidopsis thaliana]	11.239	22.000	0.511	7.208	18.000	0.400	0.456
10	8	5	RT024D07	a76couture2091.r#1	>emb|CAB41041.1| (AJ132222) polyketide synthase [Streptomyces natalensis]	18.731	37.000	0.506	28.831	47.000	0.613	0.560
10	8	6	RT021A08	a76couture2002#1	>gb|AAN05325.1| (AC105364) Putative beta-1.3-glucanase [Oryza sativa (japonica	56.194	62.000	0.906	57.663	58.000	0.994	0.950
10	8	7	RB001A04	a76couture1906.r#1	>pir||T02019 callus-associated protein - common tobacco (fragment)	89.911	96.000	0.937	128.712	129.000	0.998	0.967
10	8	8	RT034H06	a76couture2189.r#1	>ref|NP_187791.1|| (NM_112018) hypothetical protein; protein id: At3g11850.1	0.000			828.905	739.000	1.122	1.122
10	8	9	RT024C05	a76couture2087.r#1	------	83.667	82.000	1.020	148.276	124.000	1.196	1.108
10	8	10	RT012F05	a76couture1997.r#1	>ref|NP_564750.1|| (NM_104658) expressed protein; protein id: At1g59650.1. supported	272.230	299.000	0.910	422.175	416.000	1.015	0.963
10	8	11	GT204F08	a76couture1885.r#1	>ref|NP_200104.1|| (NM_124670) pyruvate kinase; protein id: At5g52920.1. supported by	1573.442	1602.000	0.982	2088.223	1848.000	1.130	1.056
10	8	12	RT034G03	a76couture2185.r#1	>ref|NP_564308.1|| (NM_102607) Expressed protein; protein id: At1g28395.1. supported	31.219	39.000	0.800	50.455	51.000	0.989	0.895
10	8	13	RT023H10	a76couture2082.r#1	>gb|AAM65231.1| (AY087694) unknown [Arabidopsis thaliana]	193.558	216.000	0.896	297.582	273.000	1.090	0.993
10	8	14	RT011F03	a76couture1993.r#1	>gb|AAK38502.1|AC087181_18 (AC087181) putative basic protein [Oryza sativa]	236.016	260.000	0.908	394.374	363.000	1.086	0.997
10	8	15	GT204A11	a76couture1881.r#1	>ref|NP_201244.2|| (NM_125835) KH domain protein; protein id: At5g64390.1 [Arabidopsis	392.112	493.000	0.795	616.788	654.000	0.943	0.869
10	9	1	PT001D07	a76couture2629.r#1	------	482.023	396.000	1.217	389.225	451.000	0.863	1.040
10	9	2	TT262A02	a76couture2509.r#1	>ref|NP_192453.1|| (NM_116783) D123 -like protein; protein id: At4g05440.1	93.657	75.000	1.249	72.079	81.000	0.890	1.069
10	9	3	TB003D02	a76couture2399.r#1	>ref|NP_568349.1|| (NM_121758) root cap 1 (RCP1); protein id: At5g17520.1. supported		10.000	0.000				
10	9	4	RT054E12	a76couture2297.r#1	>gb|AAK02020.2|AC074283_1 (AC074283) Putative gag-pol polyprotein [Oryza sativa]	31.219	39.000	0.800	24.713	40.000	0.618	0.709
10	9	5	PT005E01	a76couture2625.r#1	------	901.607	1088.000	0.829	1293.298	1385.000	0.934	0.881
10	9	6	TT261B04	a76couture2505.r#1	>gb|AAF17705.1|AF033562_1 (AF033562) ornithine carbamoyltransferase; OCTase [Canavalia	353.400	381.000	0.928	446.888	446.000	1.002	0.965
10	9	7	TB001B02	a76couture2395.r#1	------	134.866	153.000	0.881	227.563	211.000	1.078	0.980
10	9	8	RT054A11	a76couture2293.r#1	>ref|NP_201297.1|| (NM_125891) COP1-interacting protein CIP8; protein id: At5g64920.1	0.000			202.850	226.000	0.898	0.898
10	9	9	PT013F04	a76couture2620.r#1	>sp|Q9LTF2|R103_ARATH 40S ribosomal protein S10-3 >gi|8953720|dbj|BAA98083.1| (AB025606)	419.585	390.000	1.076	822.727	650.000	1.266	1.171
10	9	10	TT254H08	a76couture2501.r#1	>pir||T05497 hypothetical protein T19K4.180 - Arabidopsis thaliana	94.906	110.000	0.863	136.950	140.000	0.978	0.920
10	9	11	TB002C06	a76couture2391.r#1	>ref|NP_194186.1|| (NM_118588) clathrin coat assembly like protein; protein id:	232.270	323.000	0.719	373.780	445.000	0.840	0.780
10	9	12	RT053D10	a76couture2289.r#1	>emb|CAB81057.1| (AL161502) putative protein [Arabidopsis thaliana]	698.059	783.000	0.892	1235.635	1105.000	1.118	1.005
10	9	13	PT012D03	a76couture2616.r#1	------	43.707	45.000	0.971	82.376	64.000	1.287	1.129
10	9	14	TT254D06	a76couture2497.r#1	>gb|AAK28315.1|AF224705_1 (AF224705) receptor-like protein kinase 4 [Arabidopsis thaliana]	161.090	187.000	0.861	297.582	284.000	1.048	0.955
10	9	15	TB001G07	a76couture2386.r#1	>gb|AAL66964.1| (AY074267) unknown protein [Arabidopsis thaliana]	77.423	74.000	1.046	120.474	100.000	1.205	1.126
10	10	1	RT053A02	a76couture2285.r#1	>ref|NP_567799.1|| (NM_118959) expressed protein; protein id: At4g28190.1. supported	816.691	618.000	1.322	700.193	711.000	0.985	1.153
10	10	2	PT005D02	a76couture2611.r#1	------	3546.488	2532.000	1.401	2927.425	3133.000	0.934	1.168
10	10	3	TT251H09	a76couture2491.r#1	>dbj|BAB61258.1| (AP003315) contains ESTs C71872(E0508).C72452(E1641)~similar to	131.120	108.000	1.214	107.088	115.000	0.931	1.073
10	10	4	TB001A10	a76couture2380.r#1	>ref|NP_565899.1|| (NM_129462) expressed protein; protein id: At2g39050.1. supported	1739.528	1532.000	1.135	1489.970	2147.000	0.694	0.915
10	10	5	RT052F11	a76couture2281#1	>ref|NP_176296.1|| (NM_104781) unknown protein; protein id: At1g61000.1 [Arabidopsis	279.723	204.000	1.371	306.849	248.000	1.237	1.304
10	10	6	RT064E09	a76couture2607.r#1	>ref|NP_563668.1|| (NM_100168) expressed protein; protein id: At1g02870.1. supported	192.310	142.000	1.354	273.899	181.000	1.513	1.434
10	10	7	TT251H03	a76couture2488#1	>ref|NP_196024.1|| (NM_120486) expressed protein; protein id: At5g04040.1 [Arabidopsis	133.618	119.000	1.123	175.048	140.000	1.250	1.187
10	10	8	RT063F09	a76couture2375.r#1	>gb|AAD03398.1| (AF015782) blight-associated protein p12 precursor [Citrus	0.000			250.216	330.000	0.758	0.758
10	10	9	RT052D03	a76couture2277.r#1	>ref|NP_565984.1|| (NM_129839) expressed protein; protein id: At2g42780.1. supported	88.662	96.000	0.924	119.445	124.000	0.963	0.943
10	10	10	G18152532 reverse complement 879 bases 1	a76couture3147.r#1	>emb|CAD20741.1| (AJ427634) S-adenosyl-L-methionine decarboxylase [Vitis vinifera]	1113.897	1019.000	1.093	1756.661	1379.000	1.274	1.183

10	10	11	GT192D11	a76couture2994.r#1	>sp|P49608|ACOC_CUCMA ACONITATE HYDRATASE. CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE)	142.359	90.000	1.582	246.097	130.000	1.893	1.737
10	10	12	TT262B12	a76couture2855.r#1	>gb|AAF65512.1| (AF108891) ADP-ribosylation factor [Capsicum annuum]	566.939	641.000	0.884	1011.161	936.000	1.080	0.982
10	10	13	PT007C05	a76couture2734.r#1	>ref|NP_194730.1|| (NM_119147) putative protein; protein id: At4g30010.1. supported by	280.972	319.000	0.881	539.561	505.000	1.068	0.975
10	10	14	CT7F4AP24	a76couture3139#1	------	64.936	68.000	0.955	120.474	99.000	1.217	1.086
10	10	15	TB005B10	a76couture2990.r#1	>sp|Q9XHE4|R37A_GOSHI 60S RIBOSOMAL PROTEIN L37A >gi|4741896|gb|AAD28753.1|AF127042_1	991.518	784.000	1.265	1644.424	1095.000	1.502	1.383
10	11	1	CT003D04	a76couture2845.r#1	>dbj|BAA92495.1| (AB038598) cysteine protease [Vigna mungo]	2201.570	2632.000	0.836	2002.758	2911.000	0.688	0.762
10	11	2	PT002B12	a76couture2729.r#1	>gb|AAM61395.1| (AY084830) putative P-protein: chorismate mutase. prephenate	143.608	117.000	1.227	116.356	123.000	0.946	1.087
10	11	3	1B3PROTEI	a76couture3134.r#1	>ref|NP_199010.1|| (NM_123560) putative protein; protein id: At5g41950.1. supported by	831.677	724.000	1.149	587.956	848.000	0.693	0.921
10	11	4	GT173G09	a76couture2985.r#1	>ref|NP_568463.1|| (NM_122400) cytochrome p450. putative; protein id: At5g24910.1	52.448	42.000	1.249	42.218	38.000	1.111	1.180
10	11	5	CM001F03	a76couture2837.r#1	>sp|P29766|RL2_LYCES 60S RIBOSOMAL PROTEIN L2 (L8) (RIBOSOMAL PROTEIN TL2)	8360.472	5691.000	1.469	8456.892	6859.000	1.233	1.351
10	11	6	PT001E03	a76couture2725.r#1	>ref|NP_191881.1|| (NM_116187) Kelch repeat containing F-box protein family; protein	227.275	170.000	1.337	260.513	198.000	1.316	1.326
10	11	7	TT274D06	a76couture3128.r#1	>ref|NP_195447.1|| (NM_119894) putative protein; protein id: At4g37300.1. supported by	3008.271	2435.000	1.235	4793.234	3844.000	1.247	1.241
10	11	8	RT034D03	a76couture2980.r#1	>pir||T07398 myb-related transcription factor THM6 - tomato	407.097	450.000	0.905	697.104	704.000	0.990	0.947
10	11	9	CM004B03	a76couture2828.r#1	>ref|NP_567247.1|| (NM_116523) polyubiquitin (UBQ14); protein id: At4g02890.1	2062.957	1981.000	1.041	3124.097	2651.000	1.178	1.110
10	11	10	PT001C05	a76couture2720.r#1	------	16.234	23.000	0.706	12.356	24.000	0.515	0.610
10	11	11	RT083A08	a76couture3124.r#1	>emb|CAB39974.1| (AJ133422) glyceraldehyde-3-phosphate dehydrogenase [Nicotiana	4008.531	2777.000	1.443	6297.620	3751.000	1.679	1.561
10	11	12	RT023C12	a76couture2971.r#1	>sp|P93338|GAPN_NICPL NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE	179.822	185.000	0.972	263.602	233.000	1.131	1.052
10	11	13	PT005C10	a76couture2821.r#1	>ref|NP_188797.1|| (NM_113055) unknown protein; protein id: At3g21600.1 [Arabidopsis	121.130	138.000	0.878	188.434	174.000	1.083	0.980
10	11	14	PT007B09	a76couture2716.r#1	------	76.175	80.000	0.952	115.326	109.000	1.058	1.005
10	11	15	ST004B09	a76couture3119.r#1	>dbj|BAB91330.1| (AB061226) NADH dehydrogenase subunit 4 [Beta vulgaris]	1297.465	1019.000	1.273	2220.024	1494.000	1.486	1.380
10	12	1	RT021B09	a76couture2965#1	>gb|AAG39002.1|AF213399_1 (AF213399) SLT1 protein [Nicotiana tabacum]	173.578	160.000	1.085	178.137	186.000	0.958	1.021
10	12	2	PT006G06	a76couture2817.r#1	>gb|AAM67294.1| (AY084860) NAM-like protein [Arabidopsis thaliana]	148.603	148.000	1.004	156.514	197.000	0.794	0.899
10	12	3	PT011A05	a76couture2711.r#1	------	344.659	322.000	1.070	234.771	349.000	0.673	0.872
10	12	4	BM437283 RT041F12	couture_a76.45.c1.r#1	>ref|NP_199687.1|| (NM_124253) 60S ribosomal protein L13a; protein id: At5g48760.1	4296.995	2959.000	1.452	4300.010	3639.000	1.182	1.317
10	12	5	BG273971 GB000A07	couture_a76.357.c1.r#1	>gb|AAF64313.1|AF250923_1 (AF250923) plastid ribosomal protein PRPL5 [Spinacia oleracea]	872.886	714.000	1.223	844.351	758.000	1.114	1.168
10	12	6	RB004G11 RB004G11	couture_a76.271.c1.r#1	>pir||T06127 probable sugar transport protein F23E12.140 - Arabidopsis thaliana	8436.647	8480.000	0.995	8749.325	9628.000	0.909	0.952
10	12	7	BM437054 RT093H06	couture_a76.182.c1#1	>ref|NP_563622.1|| (NM_100006) expressed protein; protein id: At1g01230.1. supported	2134.137	2117.000	1.008	2351.825	2518.000	0.934	0.971
10	12	8	BM436548 RT042A08 BM436984	couture_a76.445.c1.r#1	>dbj|BAA87823.1| (AP000815) ESTs D47452(S12946).C23573(S10086).C19173(E10057)	1575.940	1297.000	1.215	1656.781	1420.000	1.167	1.191
10	12	9	BG273964 GB000A15 BM437742	couture_a76.354.c1#1	>ref|NP_200803.1|| (NM_125388) RNA and export factor binding protein. putative;	478.276	406.000	1.178	603.402	491.000	1.229	1.203
10	12	10	BM437735 RB004A09	couture_a76.268.c1.r#1	>ref|NP_174405.1|| (NM_102858) hypothetical protein; protein id: At1g31200.1	1226.286	1354.000	0.906	1903.908	1786.000	1.066	0.986
10	12	11	Arabidopsis Control Oligonucleotide	3ara7		21.229	24.000	0.885	36.039	35.000	1.030	0.957
10	12	12	BM438087 RT034B02	couture_a76.441.c1.r#1	------	2713.563	2816.000	0.964	4461.672	3838.000	1.162	1.063
10	12	13	BG273960 GB000A19 GB000A19	couture_a76.352.c1#1	>ref|NP_565998.1|| (NM_129903) putative sterol dehydrogenase; protein id: At2g43420.1	16.234	23.000	0.706	79.287	68.000	1.166	0.936
10	12	14	BM436948 GT204D08	couture_a76.263.c1#1	>pir||T10078 hypothetical protein - castor bean >gi|1632831|emb|CAA89698.1|	660.596	744.000	0.888	1079.121	976.000	1.106	0.997
10	12	15	BG273929 BM437662 RT091B12	couture_a76.177.c1.r#1	>ref|NP_201350.2|| (NM_125945) putative protein; protein id: At5g65470.1. supported by	3056.973	3347.000	0.913	4798.383	4496.000	1.067	0.990
10	13	1	BM437230 RT031A07	couture_a76.436.c1.r#1	>ref|NP_189047.1|| (NM_113310) GATA transcription factor 1 (AtGATA-1); protein id:	204.797	206.000	0.994	204.909	244.000	0.840	0.917
10	13	2	BG273955 GB000A25	couture_a76.349.c1#1	>ref|NP_565410.1|| (NM_127278) expressed protein; protein id: At2g17240.1. supported	370.883	328.000	1.131	364.512	389.000	0.937	1.034
10	13	3	BM438041 BM437631 GT204G11	couture_a76.260.c1#1	>ref|NP_200265.1|| (NM_124834) putative protein; protein id: At5g54540.1. supported by	1183.828	940.000	1.259	1003.953	1199.000	0.837	1.048
10	13	4	BM436317 RT081H02 BM437294	couture_a76.172.c1.r#1	>gb|AAF27100.1|AC011809_9 (AC011809) Putative phospatase 2A inhibitor [Arabidopsis thaliana]	675.581	379.000	1.783	761.975	503.000	1.515	1.649
10	13	5	BM436348 RT024G06	couture_a76.432.c1.r#1	------	201.051	185.000	1.087	198.731	212.000	0.937	1.012
10	13	6	BG273948 GB000A35	couture_a76.347.c1#1	>ref|NP_172388.1|| (NM_100786) putative protein phosphatase 2C; protein id:	79.921	80.000	0.999	80.316	83.000	0.968	0.983
10	13	7	BG273858 GT204B11	couture_a76.257.c1#1	>ref|NP_564683.1|| (NM_104401) Expressed protein; protein id: At1g55265.1. supported	42.458	42.000	1.011	43.247	43.000	1.006	1.008
10	13	8	BM436559 RT081A06 BM437506 BM436657	couture_a76.168.c1.r#1	>pir||S16294 chlorophyll a/b-binding protein type I precursor - tomato	925.334	859.000	1.077	997.775	940.000	1.061	1.069
10	13	9	RT073B01 BM436812 RT022A04	couture_a76.426.c1#1	>ref|NP_198236.1|| (NM_122767) epimerase/dehydratase - like protein; protein id:	2224.048	2417.000	0.920	2736.932	2962.000	0.924	0.922
10	13	10	BG273939 GB000A46	couture_a76.343.c1#1	>ref|NP_191160.1|| (NM_115459) putative protein; protein id: At3g56010.1. supported by	219.782	193.000	1.139	246.097	212.000	1.161	1.150
10	13	11	GB001e08 GT202C08	couture_a76.252.c1#1	>emb|CAD20577.1| (AJ427453) putative potassium transporter [Vicia faba]	173.578	204.000	0.851	237.860	251.000	0.948	0.899
10	13	12	BM436703 RT063H07	couture_a76.164.c1.r#1	>sp|O23755|EF2_BETVU Elongation factor 2 (EF-2) >gi|7443464|pir||T14579 translation	2100.420	2033.000	1.033	3161.166	2535.000	1.247	1.140
10	13	13	GB003c08 BM436604 GT203H09	couture_a76.539.c1#1	>pir||T09838 chlorophyll a/b binding protein precursor - upland cotton	98.652	103.000	0.958	169.900	146.000	1.164	1.061
10	13	14	VVI237983 BG273874 RB005D10 RT054A08	couture_a76.sd.57.c1#	>emb|CAB85623.1| (AJ237983) putative proline-rich cell wall protein [Vitis vinifera]	10821.785	14522.000	0.745	13852.498	15740.000	0.880	0.813
10	13	15	RT041D11 RT061G11 BM436339 BM436498 TT2	couture_a76.633.c1.r#1	>sp|Q9FVI1|ADF2_PETHY Actin-depolymerizing factor 2 (ADF 2)	7415.158	6524.000	1.137	10140.445	7811.000	1.298	1.217
10	14	1	BM436654 BM437457 BM437997 BM438100 BM	couture_a76.511.c1.r#1	------	5091.209	3475.000	1.465	3667.777	3154.000	1.163	1.314
10	14	2	BG273841 BG273867 BG273705 CT006G12 BG27	couture_a76.sd.51.c1#	grip22	36322.785	35221.000	1.031	35005.539	38773.000	0.903	0.967
10	14	3	BM436321 RT054D02	couture_a76.629.c1.r#1	>pir||T51098 hypothetical protein p85RF [imported] - Prunus armeniaca	3752.534	3733.000	1.005	3564.807	3906.000	0.913	0.959
10	14	4	BM436789 CT004H09	couture_a76.533.c1#1	>gb|AAK55703.1|AF378900_1 (AF378900) At2g04520/T1O3.7 [Arabidopsis thaliana]	2109.162	2132.000	0.989	2605.130	2899.000	0.899	0.944
10	14	5	G18693181 VVI430780	couture_a76.sd.5.c1#1	>emb|CAD23545.1| (AJ430780) putative callose synthase [Vitis vinifera]	525.729	472.000	1.114	545.739	549.000	0.994	1.054
10	14	6	BM437130 BM436383 BM436970 RT061D03	couture_a76.60.c1.r#1	>dbj|BAB64536.1| (AB062755) ferritin [Glycine max]	601.904	775.000	0.777	612.669	822.000	0.745	0.761
10	14	7	BG273866 TB000A26	couture_a76.500.c1#1	>ref|NP_200119.1|| (NM_124686) putative protein; protein id: At5g53070.1 [Arabidopsis	955.304	661.000	1.445	919.518	681.000	1.350	1.398
10	14	8	G13172311 AF305093	couture_a76.sd.18.c1#	>gb|AAK14075.1|AF305093_1 (AF305093) polygalacturonase inhibiting protein [Vitis vinifera]	12762.364	9631.000	1.325	13480.778	9319.000	1.447	1.386
10	14	9	BE846408 ST004H09	couture_a76.6.c1#1	>ref|NP_171821.1|| (NM_100204) unknown protein; protein id: At1g03220.1. supported by	17174.245	9681.000	1.774	12629.219	7493.000	1.685	1.730
10	14	10	RT082A04 AF195654	couture_a76.sd.66.c1#	>gb|AAF06347.1|AF195654_1 (AF195654) SCUTL2 [Vitis vinifera]	6001.558	6229.000	0.963	6940.150	6348.000	1.093	1.028
10	14	11	BM437682 RT062G05	couture_a76.617.c1.r#1	>ref|NP_564937.1|| (NM_105538) expressed protein; protein id: At1g68660.1. supported	407.097	379.000	1.074	550.887	464.000	1.187	1.131
10	14	12	BM437100 PT002B06	couture_a76.522.c1.r#1	>gb|AAG51484.1|AC069471_15 (AC069471) unknown protein [Arabidopsis thaliana]	148.603	179.000	0.830	236.830	231.000	1.025	0.928
10	14	13	BM437813 RT063G09 BM436272 AF440310	couture_a76.sd.4.c1#1	>gb|AAL79826.1|AF440310_1 (AF440310) actin depolymerizing factor [Vitis vinifera]	2164.107	2518.000	0.859	3756.330	3515.000	1.069	0.964
10	14	14	TT242D09 BM438093	couture_a76.470.c1.r#1	>ref|NP_197854.1|| (NM_122375) putative protein; protein id: At5g24660.1. supported by	505.749	402.000	1.258	756.826	517.000	1.464	1.361
10	14	15	BM436466 PT003B03 BM437853 BM438055 BM	couture_a76.77.c1#1	>gb|AAD27878.1|AF139466_1 (AF139466) chlorophyll a/b binding protein CP29 [Vigna radiata]	1016.494	1272.000	0.799	1513.653	1624.000	0.932	0.866
11	1	1	CM003F10	a76couture0446.r#1	------	362.141	293.000	1.236	534.412	379.000	1.410	1.323
11	1	2	TB001G03	a76couture0347.r#1	>ref|NP_174468.1|| (NM_102922) unknown protein; protein id: At1g31850.1 [Arabidopsis	8025.803	6470.000	1.240	10336.087	7399.000	1.397	1.319
11	1	3	RT061E02	a76couture0215.r#1	>gb|AAM63420.1| (AY086418) unknown [Arabidopsis thaliana]	305.947	334.000	0.916	528.234	440.000	1.201	1.058

11	1	4	CM003B06	a76couture0064.r#1	>emb|CAA07232.1| (AJ006766) putative Pi starvation-induced protein [Cicer arietinum]	3931.108	4202.000	0.936	5691.129	5346.000	1.065	1.000
11	1	5	CM003E10	a76couture0442.r#1	------	423.331	283.000	1.496	662.094	363.000	1.824	1.660
11	1	6	TT273H04	a76couture0341.r#1	>gb|AAM65623.1| (AY088077) unknown [Arabidopsis thaliana]	1901.867	2191.000	0.868	2760.615	2546.000	1.084	0.976
11	1	7	RT044H02	a76couture0210.r#1	>sp|Q02921|NO93_SOYBN EARLY NODULIN 93 (N-93) >gi|486679|pir||S34801 nodulin N93 -	26351.408	27764.000	0.949	39826.575	34966.000	1.139	1.044
11	1	8	TI300A01C	a76couture0059.r#1	>gb|AAF78757.1|AF271660_1 (AF271660) putative aquaporin TIP3 [Vitis berlandieri x Vitis	6366.197	4883.000	1.304	10083.811	6439.000	1.566	1.435
11	1	9	CM003D05	a76couture0438.r#1	------	49.951	58.000	0.861	97.821	88.000	1.112	0.986
11	1	10	TT262G09	a76couture0336.r#1	>pir||T03680 plasma membrane protein - common tobacco	1577.188	1148.000	1.374	2354.914	1396.000	1.687	1.530
11	1	11	RT032H06	a76couture0205.r#1	>gb|AAM65209.1| (AY087672) unknown [Arabidopsis thaliana]	3937.351	3067.000	1.284	5834.257	3709.000	1.573	1.428
11	1	12	KT7+SP6F1	a76couture0052.r#1	>pir||T07171 subtilisin-like proteinase (EC 3.4.21.-) 1 - tomato	588.168	437.000	1.346	975.122	581.000	1.678	1.512
11	1	13	CM003A07	a76couture0435.r#1	>dbj|BAB90110.1| (AP003345) putative Nuclear transport factor 2 [Oryza sativa	1404.859	1460.000	0.962	2125.292	1834.000	1.159	1.061
11	1	14	RT094C05	a76couture0328.r#1	>ref|NP_200865.1|| (NM_125450) putative protein; protein id: At5g60570.1 [Arabidopsis	723.034	684.000	1.057	1344.783	979.000	1.374	1.215
11	1	15	RT021C11	a76couture0199#1	>ref|NP_174273.1|| (NM_102720) unknown protein; protein id: At1g29800.1 [Arabidopsis	333.420	320.000	1.042	737.262	479.000	1.539	1.291
11	2	1	CS001A01C	a76couture0027.r#1	>gb|AAD39534.2| (AF150630) cellulose synthase catalytic subunit [Gossypium hirsutum]	601.904	446.000	1.350	806.252	534.000	1.510	1.430
11	2	2	CM002H01	a76couture0431.r#1	>gb|AAF79701.1|AC020889_9 (AC020889) T1N15.16 [Arabidopsis thaliana]	31.219	28.000	1.115	44.277	28.000	1.581	1.348
11	2	3	RT081H07	a76couture0323.r#1	>ref|NP_176568.1|| (NM_105058) unknown protein; protein id: At1g63830.1. supported by	1476.039	1514.000	0.975	2358.003	1980.000	1.191	1.083
11	2	4	GT204D06	a76couture0193.r#1	>gb|AAM61483.1| (AY084921) unknown [Arabidopsis thaliana]	293.459	406.000	0.723	512.789	501.000	1.024	0.873
11	2	5	60BTRAN 3	a76couture0021.r#1		805.452	864.000	0.932	1296.387	1074.000	1.207	1.070
11	2	6	CM002F09	a76couture0427.r#1	>gb|AAF70196.1|AF255711_1 (AF255711) putative histone deacetylase HD2 [Oryza sativa]	52.448	62.000	0.846	83.405	83.000	1.005	0.925
11	2	7	TT273A08	a76couture0318.r#1	>ref|NP_191420.1|| (NM_115723) ketol-acid reductoisomerase; protein id: At3g58610.1	5241.061	5204.000	1.007	8581.485	6800.000	1.262	1.135
11	2	8	RT063B11	a76couture0185.r#1	>ref|NP_196822.1|| (NM_121321) NAM-like protein; protein id: At5g13180.1. supported by	817.940	594.000	1.377	1688.701	914.000	1.848	1.612
11	2	9	RT022B07	a76couture0014#1	>ref|NP_172695.1|| (NM_101103) putative serine/threonine kinase; protein id:	1518.496	1476.000	1.029	2796.654	2144.000	1.304	1.167
11	2	10	RT092D12	a76couture0870.r#1	>sp|P93162|CHLI_SOYBN Magnesium-chelatase subunit chlI. chloroplast precursor	136.115	178.000	0.765	291.404	257.000	1.134	0.949
11	2	11	RT072F07	a76couture0746.r#1	>gb|AAK18619.1|AF352797_1 (AF352797) ankyrin-repeat protein HBP1 [Nicotiana tabacum]	7054.265	6838.000	1.032	10339.176	8158.000	1.267	1.149
11	2	12	ST003G08	a76couture0646.r#1	>ref|NP_191695.1|| (NM_116000) putative protein; protein id: At3g61360.1. supported by	76.175	64.000	1.190	110.177	84.000	1.312	1.251
11	2	13	CT004A11	a76couture0544.r#1	>ref|NP_190386.1|| (NM_114672) putative protein; protein id: At3g48030.1 [Arabidopsis	845.413	896.000	0.944	1466.287	1186.000	1.236	1.090
11	2	14	RT092E12	a76couture0865.r#1	>gb|AAF79405.1|AC068197_15 (AC068197) F16A14.22 [Arabidopsis thaliana]	1173.838	1303.000	0.901	2216.935	1726.000	1.284	1.093
11	2	15	ST007H11	a76couture0741.r#1	>gb|AAF54394.3| (AE003683) CG9381-PC [Drosophila melanogaster]	103.647	98.000	1.058	193.583	134.000	1.445	1.251
11	3	1	ST003E07	a76couture0642.r#1	>ref|NP_197047.1|| (NM_121547) putative protein; protein id: At5g15430.1 [Arabidopsis	52.448	49.000	1.070	79.287	63.000	1.259	1.164
11	3	2	CT003F05	a76couture0540.r#1	------	2315.208	2023.000	1.144	3506.114	2491.000	1.408	1.276
11	3	3	RT091C08	a76couture0860.r#1	>gb|AAM65603.1| (AY088057) transmembrane protein. putative [Arabidopsis thaliana]	2272.750	2378.000	0.956	3442.273	3082.000	1.117	1.036
11	3	4	ST007G03	a76couture0736.r#1	>ref|NP_568525.1|| (NM_122899) putative protein; protein id: At5g35080.1. supported by	861.647	693.000	1.243	1311.832	994.000	1.320	1.282
11	3	5	ST003D05	a76couture0638.r#1	>ref|NP_508698.1|| (NM_076297) F09F9.2.p [Caenorhabditis elegans]	24.975	27.000	0.925	31.921	31.000	1.030	0.977
11	3	6	CT003C10	a76couture0537.r#1	>gb|AAF24938.1|AC012375_1 (AC012375) T22C5.2 [Arabidopsis thaliana]	137.364	155.000	0.886	222.414	196.000	1.135	1.010
11	3	7	RT091G10	a76couture0853.r#1	------	3.746	13.000	0.288	9.267	15.000	0.618	0.453
11	3	8	ST007F02	a76couture0732.r#1	>ref|NP_054486.1|| (NC_001879) RNA polymerase beta" chain [Nicotiana tabacum]	144.857	143.000	1.013	273.899	190.000	1.442	1.227
11	3	9	ST003B07	a76couture0633.r#1	>ref|NP_191210.1|| (NM_115509) putative protein; protein id: At3g56510.1 [Arabidopsis	500.754	428.000	1.170	703.282	501.000	1.404	1.287
11	3	10	CT003B01	a76couture0534.r#1	>pir||T01712 hypothetical protein A_IG002N01.21 - Arabidopsis thaliana	2094.176	2158.000	0.970	3304.294	2721.000	1.214	1.092
11	3	11	RT082H04	a76couture0849.r#1	>ref|NP_567583.1|| (NM_118059) putative protein; protein id: At4g19390.1. supported by	228.524	223.000	1.025	333.621	281.000	1.187	1.106
11	3	12	ST007D06	a76couture0727.r#1	>sp|P46804|SPD2_NEPCL Spidroin 2 (Dragline silk fibroin 2) >gi|345426|pir||A44112	1241.271	331.000	3.750	1940.977	420.000	4.621	4.186
11	3	13	ST003A06	a76couture0629.r#1	>sp|P03291|Y215_ADE02 HYPOTHETICAL PROTEIN F-215 >gi|76760|pir||A03863 hypothetical	32.468	35.000	0.928	59.722	46.000	1.298	1.113
11	3	14	CT002H07	a76couture0530.r#1	>emb|CAD21002.1| (AJ427981) putative potasium transporter [Oryza sativa (japonica	18.731	21.000	0.892	36.039	30.000	1.201	1.047
11	3	15	RT082D08	a76couture0844.r#1	>gb|AAD00119.1| (U64926) NTGP5 [Nicotiana tabacum]	475.779	527.000	0.903	911.281	715.000	1.275	1.089
11	4	1	ST007B09	a76couture0723.r#1	>gb|AAD16138.1| (AF096298) DNA-binding protein 1 [Nicotiana tabacum]	345.908	334.000	1.036	475.719	401.000	1.186	1.111
11	4	2	CT006H06	a76couture0625.r#1	>gb|AAK57563.1| (AF290565) plastid-lipid associated protein PAP3 [Brassica rapa]	69.931	74.000	0.945	114.296	107.000	1.068	1.007
11	4	3	CT002G02	a76couture0526.r#1	>ref|NP_032002.1|| (NM_007976) coagulation factor V [Mus musculus]	241.011	206.000	1.170	343.918	256.000	1.343	1.257
11	4	4	RT032F01	a76couture1330.r#1	>sp|Q43593|STAD_OLEEU Acyl-[acyl-carrier protein] desaturase. chloroplast precursor	465.789	546.000	0.853	736.233	712.000	1.034	0.944
11	4	5	GT193A11	a76couture1197.r#1	>pir||S19701 hypothetical protein H1flk - Arabidopsis thaliana (fragment)	2062.957	1640.000	1.258	2702.952	1986.000	1.361	1.309
11	4	6	RT094H11	a76couture1073.r#1	>ref|NP_190880.1|| (NM_115172) putative protein; protein id: At3g53120.1 [Arabidopsis	2132.888	1983.000	1.076	2689.566	2306.000	1.166	1.121
11	4	7	RT082H06	a76couture0977.r#1	>ref|NP_196569.1|| (NM_121045) putative protein; protein id: At5g10070.1 [Arabidopsis	108.642	101.000	1.076	166.811	128.000	1.303	1.189
11	4	8	RT031H12	a76couture1325.r#1	>ref|NP_196487.1|| (NM_120961) putative transcriptional co-activator (KIWI); protein	734.273	583.000	1.259	1161.497	823.000	1.411	1.335
11	4	9	GT192G11	a76couture1192.r#1	>dbj|BAB90170.1| (AP003379) contains ESTs D40498(S2523).AU033072(S2523)~similar to	338.415	272.000	1.244	431.443	302.000	1.429	1.336
11	4	10	RT094C09	a76couture1069.r#1	>gb|AAK39571.1|AC025296_6 (AC025296) putative gamma-lyase [Oryza sativa]	18.731	18.000	1.041	32.950	27.000	1.220	1.131
11	4	11	RT081E07	a76couture0973.r#1	------	295.957	228.000	1.298	504.551	302.000	1.671	1.484
11	4	12	RT024H10	a76couture1321.r#1	>ref|NP_192755.1|| (NM_117085) putative protein; protein id: At4g10170.1 [Arabidopsis	497.008	446.000	1.114	679.599	527.000	1.290	1.202
11	4	13	GT194A11	a76couture1187.r#1	>ref|NP_566033.1|| (NM_130066) expressed protein; protein id: At2g45010.1. supported	728.029	640.000	1.138	1048.230	764.000	1.372	1.255
11	4	14	TT284D03	a76couture1065.r#1	>ref|NP_192386.1|| (NM_116715) putative ABC transporter; protein id: At4g04770.1	1086.424	1032.000	1.053	1654.721	1259.000	1.314	1.184
11	4	15	RT081A08	a76couture0968.r#1	>gb|AAG52185.1|AC012329_12 (AC012329) putative splicing factor; 53460-55514 [Arabidopsis	720.537	672.000	1.072	1319.040	895.000	1.474	1.273
11	5	1	RT024C03	a76couture1317#1	>ref|NP_566854.1|| (NM_113938) expressed protein; protein id: At3g30390.1. supported	524.481	602.000	0.871	856.707	770.000	1.113	0.992
11	5	2	GT192G06	a76couture1183.r#1	>ref|NP_181134.1|| (NM_129149) hypothetical protein; protein id: At2g35900.1	152.349	107.000	1.424	165.781	110.000	1.507	1.465
11	5	3	RT093G09	a76couture1061.r#1	------	423.331	361.000	1.173	537.501	428.000	1.256	1.214
11	5	4	RT074D11	a76couture0963.r#1	------	28.722	33.000	0.870	42.218	43.000	0.982	0.926
11	5	5	RT023D10	a76couture1311.r#1	------	171.081	143.000	1.196	270.810	193.000	1.403	1.300
11	5	6	GT191H03	a76couture1178.r#1	>ref|NP_565089.1|| (NM_106126) Exostosin family; protein id: At1g74680.1. supported by	289.713	236.000	1.228	405.700	284.000	1.429	1.328
11	5	7	RT093C04	a76couture1056.r#1	>ref|NP_193466.1|| (NM_117839) putative protein; protein id: At4g17350.1 [Arabidopsis	309.693	357.000	0.867	481.898	479.000	1.006	0.937
11	5	8	RT074A11	a76couture0959.r#1	>gb|AAF23836.1|AC007234_8 (AC007234) F1E22.16 [Arabidopsis thaliana]	118.633	123.000	0.964	194.613	168.000	1.158	1.061
11	5	9	RT021B10	a76couture1308#1	>ref|NP_198663.1|| (NM_123208) DNA repair protein RAD23 homolog; protein id:	1514.750	1564.000	0.969	2251.945	1887.000	1.193	1.081
11	5	10	GT191B07	a76couture1174.r#1	>ref|NP_680800.1|| (NC_004113) ORF_ID:tll0009~unknown protein [Thermosynechococcus	49.951	47.000	1.063	119.445	86.000	1.389	1.226
11	5	11	RT093A02	a76couture1052.r#1	>gb|AAF43926.1|AC012188_3 (AC012188) Contains similarity to a hypothetical protein from	47.453	39.000	1.217	103.999	77.000	1.351	1.284

11	5	12	RT073F06	a76couture0955.r#1	>gb|AAM98179.1| (AY140038) Ca2+-dependent lipid-binding protein. putative	226.026	252.000	0.897	373.780	313.000	1.194	1.046
11	5	13	GT174D10	a76couture1776#1	>gb|AAC00091.1| (AF028198) cytochrome c oxidase subunit I [Otocyon megalotis]	42.458	51.000	0.833	86.494	71.000	1.218	1.025
11	5	14	GT171A01	a76couture1683.r#1	>ref|NP_182056.1|| (NM_130094) putative nucleotide sugar epimerase; protein id:	158.593	142.000	1.117	291.404	189.000	1.542	1.329
11	5	15	GB004E06	a76couture1591.r#1	>ref|NP_565270.1|| (NM_126225) expressed protein; protein id: At2g01640.1. supported	159.842	187.000	0.855	356.275	266.000	1.339	1.097
11	6	1	TT263B07	a76couture1448.r#1	>gb|AAL79796.1|AC079874_19 (AC079874) unknown protein [Oryza sativa]	285.967	301.000	0.950	506.610	426.000	1.189	1.070
11	6	2	GT174C11	a76couture1772.r#1	------	231.021	224.000	1.031	311.998	263.000	1.186	1.109
11	6	3	GT162D05	a76couture1679#1	------	49.951	50.000	0.999	80.316	69.000	1.164	1.082
11	6	4	GB004B01	a76couture1586.r#1	------	169.832	189.000	0.899	232.711	212.000	1.098	0.998
11	6	5	TT262A05	a76couture1444.r#1	>dbj|BAB10995.1| (AB024029) gene_id:K21L19.3~unknown protein [Arabidopsis thaliana]	661.845	648.000	1.021	1055.438	858.000	1.230	1.126
11	6	6	GT173H06	a76couture1768.r#1	>ref|NP_200098.1|| (NM_124664) ABC transporter family protein; protein id: At5g52860.1	92.409	101.000	0.915	177.108	137.000	1.293	1.104
11	6	7	GT162A04	a76couture1676.r#1	>gb|AAA29596.1| (L27592) erythrocyte membrane antigen 1 [Plasmodium chabaudi]	419.585	495.000	0.848	798.014	728.000	1.096	0.972
11	6	8	GB003F12	a76couture1580.r#1	>gb|AAA34296.1| (M95819) initiation factor (iso)4F p28 subunit [Triticum aestivum]	1186.325	1222.000	0.971	2029.530	1630.000	1.245	1.108
11	6	9	TT262A11	a76couture1439.r#1	>emb|CAC82998.1| (AJ344154) calcium-dependent protein kinase 2 [Nicotiana tabacum]	255.997	244.000	1.049	517.937	402.000	1.288	1.169
11	6	10	GT173F09	a76couture1764.r#1	>ref|NP_175873.1|| (NM_104350) hypothetical protein; protein id: At1g54740.1							
11	6	11	GT161E11	a76couture1671.r#1	>ref|NP_195319.1|| (NM_119761) putative protein; protein id: At4g35940.1 [Arabidopsis	1723.294	1606.000	1.073	2564.972	2059.000	1.246	1.159
11	6	12	GB002H08	a76couture1576.r#1	------	280.972	279.000	1.007	531.323	378.000	1.406	1.206
11	6	13	RT064A05	a76couture1424.r#1	>gb|AAD55473.1|AC009322_13 (AC009322) Hypothetical protein [Arabidopsis thaliana]	4094.696	2787.000	1.469	6230.689	3487.000	1.787	1.628
11	6	14	GT173C08	a76couture1760.r#1	>ref|NP_563816.1|| (NM_100718) calreticulin. putative; protein id: At1g08450.1	639.367	614.000	1.041	991.597	775.000	1.279	1.160
11	6	15	GB009H05	a76couture1667.r#1	------	6.244	9.000	0.694	9.267	9.000	1.030	0.862
11	7	1	GB002A11	a76couture1571.r#1	------							
11	7	2	TT251G06	a76couture1420#1	>gb|AAF66242.1|AF243180_1 (AF243180) dicyanin [Lycopersicon esculentum]	1257.505	1007.000	1.249	1799.908	1226.000	1.468	1.358
11	7	3	GT173B05	a76couture1756.r#1	------	102.399	132.000	0.776	183.286	195.000	0.940	0.858
11	7	4	GB009H02	a76couture1664.r#1	------	1.249	8.000	0.156	5.148	9.000	0.572	0.364
11	7	5	GB001C12	a76couture1568.r#1	>ref|NP_566310.1|| (NM_111629) expressed protein; protein id: At3g07510.1. supported	302.201	319.000	0.947	540.590	445.000	1.215	1.081
11	7	6	TT253H07	a76couture1417.r#1	------	149.852	156.000	0.961	269.780	226.000	1.194	1.077
11	7	7	RT034E03	a76couture2180.r#1	>sp|Q40588|ASO_TOBAC L-ASCORBATE OXIDASE PRECURSOR (ASCORBASE) (ASO)	322.181	480.000	0.671	608.550	675.000	0.902	0.786
11	7	8	RT023G03	a76couture2076.r#1	------	314.688	236.000	1.333	505.581	331.000	1.527	1.430
11	7	9	RB008C08	a76couture1991#1	>dbj|BAB78478.1| (AB062669) preproMP73 [Cucurbita maxima]	67.433	68.000	0.992	135.920	118.000	1.152	1.072
11	7	10	Arabidopsis Control Oligonucleotide	3ara23								
11	7	11	RT034D06	a76couture2176.r#1	>dbj|BAB02515.1| (AB026645) transporter-like protein [Arabidopsis thaliana]	611.894	416.000	1.471	815.519	497.000	1.641	1.556
11	7	12	RT023E11	a76couture2073.r#1	>ref|NP_187250.1|| (NM_111473) hypothetical protein; protein id: At3g05990.1	52.448	57.000	0.920	119.445	102.000	1.171	1.046
11	7	13	RT012A05	a76couture1985.r#1	------	108.642	110.000	0.988	197.702	153.000	1.292	1.140
11	7	14	GT202G09	a76couture1866.r#1	------	116.135	162.000	0.717	199.761	212.000	0.942	0.830
11	7	15	RT034B12	a76couture2172.r#1	>ref|NP_193202.1|| (NM_117548) RNA polymerase II fifth largest subunit like protein;	448.306	406.000	1.104	859.796	540.000	1.592	1.348
11	8	1	RT023D04	a76couture2069.r#1	>ref|NP_172814.1|| (NM_101227) F-box protein; protein id: At1g13570.1 [Arabidopsis	584.421	451.000	1.296	824.786	571.000	1.444	1.370
11	8	2	RT011E06	a76couture1982.r#1	------	43.707	38.000	1.150	84.435	61.000	1.384	1.267
11	8	3	GT202F02	a76couture1862.r#1	------	1393.620	1860.000	0.749	2060.421	2393.000	0.861	0.805
11	8	4	RT033H11	a76couture2166.r#1	>dbj|BAB59066.1| (AB048260) pectate lyase [Salix gilgiana]	2551.224	2642.000	0.966	4130.110	3701.000	1.116	1.041
11	8	5	RT023B09	a76couture2065.r#1	>gb|AAM63025.1| (AY085809) unknown [Arabidopsis thaliana]	996.513	1009.000	0.988	1850.363	1660.000	1.115	1.051
11	8	6	RT011A09	a76couture1979.r#1	>ref|NP_188137.1|| (NM_112382) 30S ribosomal protein S20; protein id: At3g15190.1	317.186	381.000	0.833	607.521	553.000	1.099	0.966
11	8	7	GT201F06	a76couture1857.r#1	>ref|NP_176762.1|| (NM_105259) disease resistance response protein-related/ dirigent	79.921	73.000	1.095	136.950	103.000	1.330	1.212
11	8	8	RT033G05	a76couture2163.r#1	>ref|NP_173980.1|| (NM_102420) hypothetical protein; protein id: At1g26580.1	111.140	124.000	0.896	191.523	180.000	1.064	0.980
11	8	9	RT022G12	a76couture2061#1	>pir||T05707 phosphate transport protein G7. mitochondrial - soybean	971.538	772.000	1.258	1734.008	1080.000	1.606	1.432
11	8	10	RB008H08	a76couture1976#1	------	6.244	15.000	0.416	9.267	16.000	0.579	0.498
11	8	11	GT194H11	a76couture1852.r#1	------	13.736	18.000	0.763	29.861	31.000	0.963	0.863
11	8	12	RT033F09	a76couture2159.r#1	>gb|AAM64677.1| (AY087119) putative HesB-like protein [Arabidopsis thaliana]	841.667	650.000	1.295	1623.830	1066.000	1.523	1.409
11	8	13	RT022F09	a76couture2057.r#1	>gb|AAL07213.1| (AY056134) unknown protein [Arabidopsis thaliana]	18.731	26.000	0.720	37.069	35.000	1.059	0.890
11	8	14	RB008G12	a76couture1974.r#1	>ref|NP_149129.1|| (NM_033138) caldesmon 1 isoform 1; H-CAD; L-CAD [Homo sapiens]	39.960	44.000	0.908	84.435	68.000	1.242	1.075
11	8	15	GT202A04	a76couture1848.r#1	>gb|AAM62498.1| (AY085266) unknown [Arabidopsis thaliana]	103.647	116.000	0.894	150.336	122.000	1.232	1.063
11	9	1	RT064C05	a76couture2603.r#1	>ref|NP_566181.1|| (NM_111138) expressed protein; protein id: At3g02700.1. supported	1799.468	1970.000	0.913	2980.969	2633.000	1.132	1.023
11	9	2	TT251F02	a76couture2484#1	------	1849.419	1647.000	1.123	2668.972	2055.000	1.299	1.211
11	9	3	RT063C11	a76couture2371.r#1	>ref|NP_567226.1|| (NM_116459) putative GTP pyrophosphokinase; protein id: At4g02260.1	369.634	353.000	1.047	517.937	434.000	1.193	1.120
11	9	4	RT051H10	a76couture2273.r#1	>ref|NP_180118.1|| (NM_128105) unknown protein; protein id: At2g25480.1 [Arabidopsis	269.733	306.000	0.881	423.205	417.000	1.015	0.948
11	9	5	RT064A09	a76couture2599.r#1	>ref|NP_175129.1|| (NM_103589) hypothetical protein; protein id: At1g45150.1	201.051	193.000	1.042	304.790	265.000	1.150	1.096
11	9	6	TT251E01	a76couture2480#1	>ref|NP_181780.1|| (NM_129813) DEAD/DEAH box RNA helicase. putative; protein id:	43.707	58.000	0.754	89.584	91.000	0.984	0.869
11	9	7	RT062H08	a76couture2366.r#1	>ref|NP_175027.1|| (NM_103487) sterol glucosyltransferase. putative; protein id:	14.985	28.000	0.535	14.416	30.000	0.481	0.508
11	9	8	RT051G01	a76couture2270.r#1	------	540.715	531.000	1.018	1115.161	987.000	1.130	1.074
11	9	9	TB000A06	a76couture2594.r#1	>gb|ZP_00091595.1| (NZ_AAAD01000089) hypothetical protein [Azotobacter vinelandii]	104.896	117.000	0.897	193.583	170.000	1.139	1.018
11	9	10	TT254C07	a76couture2476.r#1	>ref|NP_567405.1|| (NM_117417) putative protein; protein id: At4g13430.1. supported by	756.751	766.000	0.988	1255.199	1070.000	1.173	1.081
11	9	11	RT062F01	a76couture2360.r#1	>ref|NP_181401.1|| (NM_129424) putative phospholipid cytidylyltransferase; protein id:	534.471	681.000	0.785	978.211	976.000	1.002	0.894
11	9	12	RT053C12	a76couture2266.r#1	------	149.852	123.000	1.218	284.196	184.000	1.545	1.381
11	9	13	RT064D02	a76couture2570.r#1	>ref|NP_180871.1|| (NM_128872) putative synaptobrevin; protein id: At2g33120.1	1232.530	1211.000	1.018	2073.807	1712.000	1.211	1.115
11	9	14	TT254B02	a76couture2471.r#1	>gb|AAM64614.1| (AY087053) Isp4-like protein [Arabidopsis thaliana]	640.616	603.000	1.062	1081.181	816.000	1.325	1.194
11	9	15	RT062D01	a76couture2356.r#1	pir||T51739 RNA helicase RH5 [imported] - Arabidopsis thaliana ... 283 2e-075	1060.200	1140.000	0.930	1578.524	1261.000	1.252	1.091
11	10	1	RT053B05	a76couture2264.r#1	>ref|NP_197447.2|| (NM_121951) putative protein; protein id: At5g19460.1. supported by	149.852	128.000	1.171	202.850	159.000	1.276	1.223
11	10	2	TT283H09	a76couture2566.r#1	>ref|NP_196376.1|| (NM_120841) WD-repeat protein-like; protein id: At5g07590.1	212.290	177.000	1.199	308.909	218.000	1.417	1.308
11	10	3	TT253F12	a76couture2468.r#1	>gb|AAK19883.1| (U24241) soraphen polyketide synthase A [Polyangium cellulosum]	129.871	102.000	1.273	175.048	131.000	1.336	1.305
11	10	4	RT062A08	a76couture2352.r#1	>ref|NP_565922.1|| (NM_129566) expressed protein; protein id: At2g40080.1. supported	447.057	389.000	1.149	568.392	463.000	1.228	1.188

11	10	5	RT052B08	a76couture2260.r#1	------	676.830	562.000	1.204	1281.971	843.000	1.521	1.363
11	10	6	TT283A09	a76couture2563.r#1	------	97.404	88.000	1.107	134.890	106.000	1.273	1.190
11	10	7	TT253D06	a76couture2464.r#1	>ref|NP_565585.1|| (NM_128068) expressed protein; protein id: At2g25110.1. supported	186.066	191.000	0.974	304.790	265.000	1.150	1.062
11	10	8	RT061H08	a76couture2348.r#1	>gb|AAF44708.1|AF242849_1 (AF242849) wound-inducible carboxypeptidase [Lycopersicon	118.633	168.000	0.706	248.157	289.000	0.859	0.782
11	10	9	RT051C04	a76couture2256.r#1	>ref|NP_174998.1|| (NM_103458) bZIP family transcription factor; protein id:	1286.226	1210.000	1.063	2369.330	1840.000	1.288	1.175
11	10	10	PT013F02	a76couture3109.r#1	>sp|P48493|TPIS_LACSA Triosephosphate isomerase. cytosolic (TIM)	335.917	357.000	0.941	803.163	650.000	1.236	1.088
11	10	11	GT193E05	a76couture2961.r#1	>ref|NP_191429.1|| (NM_115732) ribosomal protein L11 -like; protein id: At3g58700.1	2261.511	1721.000	1.314	3566.866	2381.000	1.498	1.406
11	10	12	PT005C11	a76couture2813.r#1	>ref|NP_182103.1|| (NM_130142) putative phosphomannomutase; protein id: At2g45790.1	1137.624	1025.000	1.110	1991.432	1557.000	1.279	1.194
11	10	13	PT001C10	a76couture2706.r#1	>gb|AAG43551.1|AF211533_1 (AF211533) Avr9/Cf-9 rapidly elicited protein 146 [Nicotiana	138.613	154.000	0.900	285.226	281.000	1.015	0.958
11	10	14	TT282G12	a76couture3102.r#1	>sp|P46297|RS23_FRAAN 40S RIBOSOMAL PROTEIN S23 (S12) >gi|1362041|pir||S56673 ribosomal	462.043	384.000	1.203	717.698	505.000	1.421	1.312
11	10	15	GT192F06	a76couture2957.r#1	>pir||S24602 cysteine proteinase tpp (EC 3.4.22.-) - garden pea	3392.891	4100.000	0.828	5151.568	5044.000	1.021	0.924
11	11	1	PT013F05	a76couture2809.r#1	>ref|NP_565460.1|| (NM_127546) expressed protein; protein id: At2g19880.1. supported	1230.032	1294.000	0.951	2062.481	1772.000	1.164	1.057
11	11	2	PT001A04	a76couture2702.r#1	------	2285.237	2476.000	0.923	3552.451	3219.000	1.104	1.013
11	11	3	TT254C10	a76couture3097.r#1	>gb|AAB65777.1| (U97522) class IV endochitinase [Vitis vinifera]	21.229	30.000	0.708	29.861	40.000	0.747	0.727
11	11	4	RB007F10	a76couture2952.r#1	------	1424.839	1493.000	0.954	2185.015	1850.000	1.181	1.068
11	11	5	PT006D12	a76couture2805.r#1	>gb|AAM62895.1| (AY085676) unknown [Arabidopsis thaliana]	142.359	143.000	0.996	229.622	185.000	1.241	1.118
11	11	6	PT008B05	a76couture2697.r#1	>pir||T45819 villin 3 homolog F28O9.260 - Arabidopsis thaliana (fragment)	1048.961	876.000	1.197	1577.494	1137.000	1.387	1.292
11	11	7	TT281E02	a76couture3091.r#1	>emb|CAB91554.1| (AJ277900) beta 1-3 glucanase [Vitis vinifera]	14027.361	16903.000	0.830	20019.346	20865.000	0.959	0.895
11	11	8	TT283D05	a76couture2946.r#1	>ref|NP_047285.1|| (NC_001948) 28 kDa coat protein [Rupestris stem pitting associated	2210.311	2324.000	0.951	4956.956	3961.000	1.251	1.101
11	11	9	PT011H03	a76couture2801.r#1	>gb|AAG12703.1|AC021046_4 (AC021046) acid phosphatase. putative; 5376-6903 [Arabidopsis	127.374	137.000	0.930	200.791	189.000	1.062	0.996
11	11	10	PT008B07	a76couture2692.r#1	------	1966.803	2166.000	0.908	2353.885	1916.000	1.229	1.068
11	11	11	RT062E03	a76couture3086.r#1	ref|NP_190228.1|| (NM_114511) dTDP-glucose 4-6-dehydratases-like... 334 2e-093	5768.039	6142.000	0.939	8574.277	7591.000	1.130	1.034
11	11	12	ST007G02	a76couture2934.r#1	>dbj|BAB93248.1| (AP003246) hypothetical protein~similar to Arabidopsis thaliana	6.244	7.000	0.892	16.475	14.000	1.177	1.034
11	11	13	PT012D04	a76couture2797.r#1	>gb|AAK55780.1|AC079038_14 (AC079038) Putative 40S ribosomal protein; contains C-terminal	6504.809	5175.000	1.257	11147.487	7715.000	1.445	1.351
11	11	14	PT001A10	a76couture2688.r#1	>gb|AAK61315.1|AF306499_1 (AF306499) NBS-LRR resistance-like protein B8 [Phaseolus vulgaris]	218.534	135.000	1.619	383.047	194.000	1.974	1.797
11	11	15	TT241C01	a76couture3080.r#1	>sp|P51133|UCR3_TOBAC UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 3	1161.350	1200.000	0.968	1755.631	1553.000	1.130	1.049
11	12	1	GT174G11	a76couture2928.r#1	>dbj|BAB84326.1| (AB079024) ras-related protein RAB8-5 [Nicotiana tabacum]	464.540	476.000	0.976	803.163	721.000	1.114	1.045
11	12	2	PT011B09	a76couture2791.r#1	>ref|NP_171991.1|| (NM_100377) unknown protein; protein id: At1g04985.1 [Arabidopsis	2531.244	2322.000	1.090	5251.449	4149.000	1.266	1.178
11	12	3	PT008D10	a76couture2685.r#1	>sp|P15710|PHO4_NEUCR PHOSPHATE-REPRESSIBLE PHOSPHATE PERMEASE >gi|83785|pir||JQ0116	12.488	14.000	0.892	18.535	18.000	1.030	0.961
11	12	4	RB007A01 RB007A01	couture_a76.421.c1.r#1	>ref|NP_192016.1|| (NM_116337) putative flavonol glucosyltransferase; protein id:	52.448	51.000	1.028	75.168	59.000	1.274	1.151
11	12	5	Arabidopsis Control Oligonucleotide	3ara23		388.365	321.000	1.210	586.927	422.000	1.391	1.300
11	12	6	BM437469 CT005A08	couture_a76.25.c1.r#1	>ref|NP_564765.1|| (NM_104768) expressed protein; protein id: At1g60870.1. supported	3064.466	3077.000	0.996	4391.653	4148.000	1.059	1.027
11	12	7	BM436730 BM437058 GT202F07	couture_a76.160.c1.r#1	>gb|AAM14957.1| (AC004482) hypothetical protein [Arabidopsis thaliana]	4885.163	7007.000	0.697	7296.425	8416.000	0.867	0.782
11	12	8	RB003D09 RB003D09	couture_a76.418.c1.r#1	>ref|NP_196949.1|| (NM_121449) early nodule-specific protein - like; protein id:	300.952	362.000	0.831	505.581	541.000	0.935	0.883
11	12	9	BG273915 GB000A73	couture_a76.336.c1#1	>ref|NP_565761.1|| (NM_128881) expressed protein; protein id: At2g33220.1. supported	964.045	917.000	1.051	1709.295	1381.000	1.238	1.145
11	12	10	BM437966 GT201F08	couture_a76.248.c1.r#1	>gb|AAL59935.1| (AY072113) putative nitrilase [Arabidopsis thaliana]	74.926	68.000	1.102	157.543	113.000	1.394	1.248
11	12	11	GB003a12 GB009C01	couture_a76.155.c1#1	>ref|NP_563900.1|| (NM_101095) expressed protein; protein id: At1g12230.1. supported	674.332	939.000	0.718	1127.517	1206.000	0.935	0.827
11	12	12	BG273711 RB000A91	couture_a76.414.c1.r#1	------	464.540	287.000	1.619	869.063	476.000	1.826	1.722
11	12	13	BG273907 GB000A83 BM437879	couture_a76.332.c1#1	>ref|NP_564781.1|| (NM_104844) expressed protein; protein id: At1g61620.1. supported	417.087	404.000	1.032	699.163	622.000	1.124	1.078
11	12	14	GB003b05 GT202D09	couture_a76.244.c1#1	>sp|Q9LNQ4|ALA4_ARATH Potential phospholipid-transporting ATPase 4 (Aminophospholipid	194.807	188.000	1.036	288.315	233.000	1.237	1.137
11	12	15	BG273722 CT004D04	couture_a76.15.c1.r#1	>ref|NP_188674.1|| (NM_112930) translational inhibitor protein. putative; protein id:	2835.942	3026.000	0.937	5041.391	4332.000	1.164	1.050
11	13	1	BG273755 RB000A46	couture_a76.410.c1.r#1	>ref|NP_172716.1|| (NM_101126) hypothetical protein; protein id: At1g12550.1	161.090	159.000	1.013	241.979	210.000	1.152	1.083
11	13	2	BG273897 GB000A95	couture_a76.330.c1#1	>gb|AAM47506.1| (AY100447) iron-stress related protein [Citrus junos]	2470.054	2458.000	1.005	3632.767	3028.000	1.200	1.102
11	13	3	BE846396 GT193C04	couture_a76.241.c1.r#1	>ref|NP_182147.1|| (NM_130187) hypothetical protein; protein id: At2g46240.1	16974.443	5958.000	2.849	21091.260	6522.000	3.234	3.041
11	13	4	BM437898 RT072D10	couture_a76.146.c1.r#1	>ref|NP_176998.1|| (NM_105502) unknown protein; protein id: At1g68310.1 [Arabidopsis	67.433	71.000	0.950	132.831	119.000	1.116	1.033
11	13	5	BG273749 RB000A52	couture_a76.407.c1.r#1	>emb|CAD40551.1| (AL606621) OSJNBa0072K14.7 [Oryza sativa]	9.990	15.000	0.666	9.267	13.000	0.713	0.689
11	13	6	BG273893 GB000A99 GB000A99	couture_a76.328.c1.r#1	>sp|P32980|ATPD_TOBAC ATP synthase delta chain. chloroplast precursor	28.722	32.000	0.898	50.455	43.000	1.173	1.035
11	13	7	BM436665 GB004a02 GT192D07	couture_a76.239.c1.r#1	>sp|P22243|STAD_CARTI Acyl-[acyl-carrier protein] desaturase. chloroplast precursor	794.214	678.000	1.171	1130.606	847.000	1.335	1.253
11	13	8	BM437168 ST006D08	couture_a76.143.c1.r#1	>ref|NP_054502.1|| (NC_001879) NADH dehydrogenase subunit J [Nicotiana tabacum]	380.873	248.000	1.536	741.381	415.000	1.786	1.661
11	13	9	BG273738 BM437050 RB000A64	couture_a76.405.c1.r#1	>gb|AAM83095.1|AF525402_1 (AF525402) SOS2-like protein kinase [Glycine max]	1060.200	896.000	1.183	1723.711	1193.000	1.445	1.314
11	13	10	TB002b06 TT281F09	couture_a76.324.c1#1	>gb|AAD25602.1|AC005287_4 (AC005287) Putative dihyrdolipoamide acetyltransferase [Arabidopsis	1002.757	955.000	1.050	1639.276	1277.000	1.284	1.167
11	13	11	BM437876 GT181H12	couture_a76.235.c1.r#1	>gb|AAM62950.1| (AY085732) unknown [Arabidopsis thaliana]	349.654	383.000	0.913	604.431	547.000	1.105	1.009
11	13	12	BM437421 ST002F07	couture_a76.138.c1.r#1	>gb|AAM67046.1| (AY088728) unknown [Arabidopsis thaliana]	1088.922	1056.000	1.031	1467.317	1297.000	1.131	1.081
11	13	13	BM437447 PT006G01 BM437624	couture_a76.512.c1.r#1	------	1025.235	834.000	1.229	1406.565	1062.000	1.324	1.277
11	13	14	G1150685 VVCHIT3	couture_a76.sd.31.c1#	>sp|P51614|CHIA_VITVI ACIDIC ENDOCHITINASE PRECURSOR >gi|1150686|emb|CAA92207.1| (Z68123)	27.473	210.000	0.131	43.247	287.000	0.151	0.141
11	13	15	BM436624 RT022E07 RT044H04	couture_a76.610.c1.r#1	>emb|CAD21849.1| (AJ420195) ethylene responsive element binding protein [Fagus	4421.872	5213.000	0.848	6671.399	6857.000	0.973	0.911
11	14	1	BG273827 TB000A66	couture_a76.490.c1.r#1	>dbj|BAB08527.1| (AB009052) emb|CAB87783.1~gene_id:MNF13.9~similar to unknown	168.583	171.000	0.986	241.979	206.000	1.175	1.080
11	14	2	RB007C05 RB008E04 AY043231	couture_a76.sd.26.c1#	>gb|AAK81874.1| (AY043231) putative beta-galactosidase BG1 [Vitis vinifera]	363.390	514.000	0.707	560.155	669.000	0.837	0.772
11	14	3	TT254A12 PT011A11	couture_a76.605.c1#1	>gb|AAL38253.1| (AY065077) putative ribosomal protein L10 [Arabidopsis thaliana]	945.314	870.000	1.087	1367.436	1168.000	1.171	1.129
11	14	4	BG273890 TB000A02	couture_a76.507.c1#1	>ref|NP_566924.1|| (NM_114832) expressed protein; protein id: At3g49720.1. supported	365.888	374.000	0.978	553.976	470.000	1.179	1.078
11	14	5	TB001b08 G15081599 AY043233	couture_a76.sd.25.c1#	>gb|AAK81876.1| (AY043233) polygalacturonase PG1 [Vitis vinifera]	318.435	458.000	0.695	430.413	551.000	0.781	0.738
11	14	6	BM437502 RT022G08	couture_a76.573.c1.r#1	>gb|AAF69802.1|AF195869_1 (AF195869) malate dehydrogenase [Vitis vinifera]	498.257	381.000	1.308	627.085	451.000	1.390	1.349
11	14	7	BM436399 TT282B05	couture_a76.483.c1.r#1	>dbj|BAB20860.1| (AB029483) cyclin dependent kinase inhibitor [Pisum sativum]	121.130	98.000	1.236	192.553	129.000	1.493	1.364
11	14	8	BM437342 PT006E06	couture_a76.84.c1#1	>dbj|BAB92011.1| (AB075550) pleiotropic drug resistance like protein [Nicotiana	33.717	46.000	0.733	64.871	60.000	1.081	0.907
11	14	9	BG273901 GB000A90	couture_a76.572.c1#1	>ref|NP_568059.1|| (NM_120099) putative protein; protein id: At4g39390.1. supported by	262.240	277.000	0.947	399.522	357.000	1.119	1.033
11	14	10	GB003a08 BM437880 G7798705 AF195869	couture_a76.sd.40.c1#	>gb|AAF69802.1|AF195869_1 (AF195869) malate dehydrogenase [Vitis vinifera]	348.405	294.000	1.185	569.422	428.000	1.330	1.258
11	14	11	PT001G04 RT053G06	couture_a76.596.c1#1	>ref|NP_173290.1|| (NM_101713) kinesin-related protein; protein id: At1g18550.1	16.234	20.000	0.812	26.772	29.000	0.923	0.867
11	14	12	BG273852 TB000A40	couture_a76.497.c1.r#1	>gb|AAF16869.1|AF109693_1 (AF109693) allergen-like protein BRSn20 [Sambucus nigra]	2613.662	2639.000	0.990	3342.393	3145.000	1.063	1.027

<table>
<tr><td>11</td><td>14</td><td>13</td><td>AF141642 BM437196 BM437643 TB006e02 PI20</td><td>couture_a76.sd.13.c1.r</td><td>gi|8071620|gb|AAF71816.1|AF141642_1 putative aquaporin PIP2-1 [Vitis berlandieri x Vitis rupestris]</td><td>2547.478</td><td>2782.000</td><td>0.916</td><td>3644.094</td><td>3964.000</td><td>0.919</td><td>0.917</td></tr>
<tr><td>11</td><td>14</td><td>14</td><td>G7141242 AF220405</td><td>couture_a76.sd.62.c1#</td><td>>gb|AAF37266.1|AF220405_1 (AF220405) transcription factor [Vitis riparia]</td><td>132.369</td><td>138.000</td><td>0.959</td><td>224.474</td><td>212.000</td><td>1.059</td><td>1.009</td></tr>
<tr><td>11</td><td>14</td><td>15</td><td>cds of NM0019271 NM_001927 desmin; DES</td><td>des#1</td><td></td><td>267.235</td><td>274.000</td><td>0.975</td><td>384.077</td><td>370.000</td><td>1.038</td><td>1.007</td></tr>
<tr><td>12</td><td>1</td><td>1</td><td>CM002F01</td><td>a76couture0423.r#1</td><td>>ref|NP_194979.1|| (NM_119405) H+-transporting ATPase - like protein; protein id:</td><td>59.941</td><td>77.000</td><td>0.778</td><td>136.950</td><td>116.000</td><td>1.181</td><td>0.980</td></tr>
<tr><td>12</td><td>1</td><td>2</td><td>RT093A05</td><td>a76couture0312.r#1</td><td>>ref|NP_566436.1|| (NM_112112) expressed protein; protein id: At3g12760.1. supported</td><td>2659.866</td><td>2110.000</td><td>1.261</td><td>3582.312</td><td>2895.000</td><td>1.237</td><td>1.249</td></tr>
<tr><td>12</td><td>1</td><td>3</td><td>RT052D04</td><td>a76couture0180.r#1</td><td>>gb|AAM61664.1| (AY085110) unknown [Arabidopsis thaliana]</td><td>1939.330</td><td>1616.000</td><td>1.200</td><td>2124.262</td><td>1866.000</td><td>1.138</td><td>1.169</td></tr>
<tr><td>12</td><td>1</td><td>4</td><td>TT284C01</td><td>a76couture0008.r#1</td><td>>sp|Q96551|METK_CATRO S-adenosylmethionine synthetase 1 (Methionine adenosyltransferase</td><td>1246.266</td><td>1310.000</td><td>0.951</td><td>1951.274</td><td>1784.000</td><td>1.094</td><td>1.023</td></tr>
<tr><td>12</td><td>1</td><td>5</td><td>CM002E03</td><td>a76couture0419.r#1</td><td>>gb|AAM97033.1| (AY136367) putative protein [Arabidopsis thaliana]</td><td>49.951</td><td>52.000</td><td>0.961</td><td>78.257</td><td>73.000</td><td>1.072</td><td>1.016</td></tr>
<tr><td>12</td><td>1</td><td>6</td><td>RT091F02</td><td>a76couture0307.r#1</td><td>>gb|AAF14244.1|AF110228_1 (AF110228) nuclear RNA binding protein A [Spinacia oleracea]</td><td>8.741</td><td>12.000</td><td>0.728</td><td>8.238</td><td>11.000</td><td>0.749</td><td>0.739</td></tr>
<tr><td>12</td><td>1</td><td>7</td><td>RT044C12</td><td>a76couture0175.r#1</td><td>>ref|NP_191685.1|| (NM_115990) putative DNA-binding protein; protein id: At3g61260.1</td><td>6007.801</td><td>6285.000</td><td>0.956</td><td>9548.369</td><td>8749.000</td><td>1.091</td><td>1.024</td></tr>
<tr><td>12</td><td>1</td><td>8</td><td>PT010F02</td><td>a76couture2712.r#1</td><td>>gb|AAG17888.1| (AF295339) dihydrolipoamide dehydrogenase precursor [Solanum</td><td>875.383</td><td>917.000</td><td>0.955</td><td>1406.565</td><td>1288.000</td><td>1.092</td><td>1.023</td></tr>
<tr><td>12</td><td>1</td><td>9</td><td>CM002B08</td><td>a76couture0414.r#1</td><td>>ref|NP_181964.1|| (NM_129999) unknown protein; protein id: At2g44360.1 [Arabidopsis</td><td>14.985</td><td>21.000</td><td>0.714</td><td>19.564</td><td>25.000</td><td>0.783</td><td>0.748</td></tr>
<tr><td>12</td><td>1</td><td>10</td><td>RT082D05</td><td>a76couture0300.r#1</td><td>>ref|NP_565895.1|| (NM_129431) expressed protein; protein id: At2g38740.1. supported</td><td>500.754</td><td>500.000</td><td>1.002</td><td>687.837</td><td>689.000</td><td>0.998</td><td>1.000</td></tr>
<tr><td>12</td><td>1</td><td>11</td><td>RT032C08</td><td>a76couture0170.r#1</td><td>>pir||T07139 cysteine proteinase inhibitor - soybean >gi|1944319|dbj|BAA19608.1|</td><td>12.488</td><td>19.000</td><td>0.657</td><td>22.653</td><td>27.000</td><td>0.839</td><td>0.748</td></tr>
<tr><td>12</td><td>1</td><td>12</td><td>TT253D01</td><td>a76couture2493.r#1</td><td>>ref|NP_187384.1|| (NM_111608) unknown protein; protein id: At3g07280.1 [Arabidopsis</td><td>0.000</td><td></td><td></td><td>2.059</td><td>6.000</td><td>0.343</td><td>0.343</td></tr>
<tr><td>12</td><td>1</td><td>13</td><td>CM002A05</td><td>a76couture0410.r#1</td><td>>pir||I46413 keratin KAP5.5 - sheep (fragment) >gi|313722|emb|CAA51830.1|</td><td>13.736</td><td>16.000</td><td>0.859</td><td>20.594</td><td>27.000</td><td>0.763</td><td>0.811</td></tr>
<tr><td>12</td><td>1</td><td>14</td><td>RT081F07</td><td>a76couture0294.r#1</td><td>>ref|NP_680135.1|| (NM_147830) expressed protein; protein id: At5g01750.2. supported</td><td>69.931</td><td>74.000</td><td>0.945</td><td>120.474</td><td>116.000</td><td>1.039</td><td>0.992</td></tr>
<tr><td>12</td><td>1</td><td>15</td><td>GT204D05</td><td>a76couture0165.r#1</td><td>>ref|NP_177551.1|| (NM_106071) cytochrome p450 family; protein id: At1g74110.1</td><td>134.866</td><td>146.000</td><td>0.924</td><td>168.870</td><td>135.000</td><td>1.251</td><td>1.087</td></tr>
<tr><td>12</td><td>2</td><td>1</td><td>RT023G07</td><td>a76couture1313.r#1</td><td>>ref|NP_565477.1|| (NM_127618) 26S proteasome regulatory subunit S2 (RPN1); protein id:</td><td>138.613</td><td>216.000</td><td>0.642</td><td>408.789</td><td>360.000</td><td>1.136</td><td>0.889</td></tr>
<tr><td>12</td><td>2</td><td>2</td><td>CM001G01</td><td>a76couture0405.r#1</td><td>>gb|AAN03470.1| (AF532623) RING-H2 finger protein [Glycine max]</td><td>524.481</td><td>628.000</td><td>0.835</td><td>746.529</td><td>954.000</td><td>0.783</td><td>0.809</td></tr>
<tr><td>12</td><td>2</td><td>3</td><td>ST006E07</td><td>a76couture0286.r#1</td><td>>gb|AAL57648.1| (AY065000) AT4g23460/F16G20_160 [Arabidopsis thaliana]</td><td>1324.938</td><td>1436.000</td><td>0.923</td><td>1710.325</td><td>1809.000</td><td>0.945</td><td>0.934</td></tr>
<tr><td>12</td><td>2</td><td>4</td><td>RT053G08</td><td>a76couture0154.r#1</td><td>>ref|NP_565256.1|| (NM_126180) expressed protein; protein id: At2g01190.1. supported by</td><td>9832.764</td><td>10141.000</td><td>0.970</td><td>13580.658</td><td>11854.000</td><td>1.146</td><td>1.058</td></tr>
<tr><td>12</td><td>2</td><td>5</td><td>CT006A07</td><td>a76couture0580.r#1</td><td>>ref|NP_175488.1|| (NM_103955) hypothetical protein; protein id: At1g50730.1</td><td>317.186</td><td>336.000</td><td>0.944</td><td>475.719</td><td>456.000</td><td>1.043</td><td>0.994</td></tr>
<tr><td>12</td><td>2</td><td>6</td><td>CM001E04</td><td>a76couture0401.r#1</td><td>------</td><td>99.901</td><td>108.000</td><td>0.925</td><td>157.543</td><td>150.000</td><td>1.050</td><td>0.988</td></tr>
<tr><td>12</td><td>2</td><td>7</td><td>ST005F03</td><td>a76couture0281.r#1</td><td>>emb|CAB85633.1| (AJ237993) putative ripening-related protein [Vitis vinifera]</td><td>1548.467</td><td>1634.000</td><td>0.948</td><td>2451.706</td><td>2405.000</td><td>1.019</td><td>0.984</td></tr>
<tr><td>12</td><td>2</td><td>8</td><td>RT011E11</td><td>a76couture0148.r#1</td><td>>gb|AAF73932.1|AF230703_1 (AF230703) MADS box transcription factor TM6 [Hydrangea</td><td>1281.231</td><td>972.000</td><td>1.318</td><td>1848.304</td><td>1377.000</td><td>1.342</td><td>1.330</td></tr>
<tr><td>12</td><td>2</td><td>9</td><td>RT074F01</td><td>a76couture0320.r#1</td><td>>ref|NP_567476.1|| (NM_117672) Expressed protein; protein id: At4g15800.1. supported</td><td>142.359</td><td>135.000</td><td>1.055</td><td>180.197</td><td>188.000</td><td>0.958</td><td>1.007</td></tr>
<tr><td>12</td><td>2</td><td>10</td><td>RT083F03</td><td>a76couture0838.r#1</td><td>>dbj|BAB39438.1| (AP003338) putative receptor kinase [Oryza sativa (japonica</td><td>194.807</td><td>151.000</td><td>1.290</td><td>227.563</td><td>181.000</td><td>1.257</td><td>1.274</td></tr>
<tr><td>12</td><td>2</td><td>11</td><td>ST006H06</td><td>a76couture0719.r#1</td><td>>gb|AAK52557.1|AC079853_10 (AC079853) Putative calmodulin-like protein [Oryza sativa]</td><td>64.936</td><td>56.000</td><td>1.160</td><td>91.643</td><td>78.000</td><td>1.175</td><td>1.167</td></tr>
<tr><td>12</td><td>2</td><td>12</td><td>CT006G02</td><td>a76couture0622.r#1</td><td>>ref|NP_060531.1|| (NM_018061) hypothetical protein FLJ10330 [Homo sapiens]</td><td>153.598</td><td>126.000</td><td>1.219</td><td>198.731</td><td>160.000</td><td>1.242</td><td>1.231</td></tr>
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<tr><td>12</td><td>2</td><td>15</td><td>ST006G05</td><td>a76couture0715.r#1</td><td>------</td><td>221.031</td><td>287.000</td><td>0.770</td><td>330.532</td><td>401.000</td><td>0.824</td><td>0.797</td></tr>
<tr><td>12</td><td>3</td><td>1</td><td>CT006E08</td><td>a76couture0618.r#1</td><td>>ref|NP_563982.1|| (NM_101449) expressed protein; protein id: At1g15810.1. supported</td><td>69.931</td><td>86.000</td><td>0.813</td><td>144.157</td><td>122.000</td><td>1.182</td><td>0.997</td></tr>
<tr><td>12</td><td>3</td><td>2</td><td>CT002B11</td><td>a76couture0519#1</td><td>------</td><td>17.483</td><td>20.000</td><td>0.874</td><td>46.336</td><td>40.000</td><td>1.158</td><td>1.016</td></tr>
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<tr><td>12</td><td>3</td><td>5</td><td>CT006D12</td><td>a76couture0614.r#1</td><td>>emb|CAB57220.1| (AJ249866) GTP binding protein [Cichorium intybus x Cichorium</td><td>683.074</td><td>896.000</td><td>0.762</td><td>1155.319</td><td>1231.000</td><td>0.939</td><td>0.850</td></tr>
<tr><td>12</td><td>3</td><td>6</td><td>CM005g04</td><td>a76couture0513.r#1</td><td>ref|NP_175036.1|| (NM_103496) histidine decarboxylase, putative ... 124 3e-028</td><td>570.685</td><td>657.000</td><td>0.869</td><td>811.400</td><td>861.000</td><td>0.942</td><td>0.906</td></tr>
<tr><td>12</td><td>3</td><td>7</td><td>RT074H08</td><td>a76couture0822.r#1</td><td>>gb|AAM12880.1|AF495716_1 (AF495716) GTP-binding protein [Helianthus annuus]</td><td>4112.178</td><td>3683.000</td><td>1.117</td><td>7927.628</td><td>5946.000</td><td>1.333</td><td>1.225</td></tr>
<tr><td>12</td><td>3</td><td>8</td><td>ST006D05</td><td>a76couture0706.r#1</td><td>------</td><td>345.908</td><td>321.000</td><td>1.078</td><td>511.759</td><td>430.000</td><td>1.190</td><td>1.134</td></tr>
<tr><td>12</td><td>3</td><td>9</td><td>ST002D05</td><td>a76couture0609.r#1</td><td>>sp|P17815|MASY_RICCO MALATE SYNTHASE. GLYOXYSOMAL >gi|68219|pir||SYCSM2 malate synthase</td><td>564.441</td><td>658.000</td><td>0.858</td><td>884.509</td><td>930.000</td><td>0.951</td><td>0.904</td></tr>
<tr><td>12</td><td>3</td><td>10</td><td>CM005e06</td><td>a76couture0507.r#1</td><td>ref|NP_565534.1|| (NM_127802) expressed protein [Arabidopsis tha... 189 3e-047</td><td>42.458</td><td>45.000</td><td>0.944</td><td>38.099</td><td>43.000</td><td>0.886</td><td>0.915</td></tr>
<tr><td>12</td><td>3</td><td>11</td><td>RT044H12</td><td>a76couture0817.r#1</td><td>>emb|CAA63894.1| (X94184) aspartate aminotransferase [Lotus japonicus]</td><td>16.234</td><td>25.000</td><td>0.649</td><td>27.802</td><td>38.000</td><td>0.732</td><td>0.690</td></tr>
<tr><td>12</td><td>3</td><td>12</td><td>ST006B12</td><td>a76couture0703.r#1</td><td>>sp|Q02028|HS7S_PEA Stromal 70 kDa heat shock-related protein. chloroplast precursor</td><td>2446.328</td><td>2497.000</td><td>0.980</td><td>3386.670</td><td>3150.000</td><td>1.075</td><td>1.027</td></tr>
<tr><td>12</td><td>3</td><td>13</td><td>ST002B06</td><td>a76couture0605.r#1</td><td>>ref|NP_568286.1|| (NM_121322) putative protein; protein id: At5g13190.1. supported by</td><td>586.919</td><td>690.000</td><td>0.851</td><td>975.122</td><td>991.000</td><td>0.984</td><td>0.917</td></tr>
<tr><td>12</td><td>3</td><td>14</td><td>CM005e01</td><td>a76couture0503.r#1</td><td>gb|AAL68641.1|AF458765_1 (AF458765) polyprotein [Oryza sativa] [... 175 2e-043</td><td>52.448</td><td>75.000</td><td>0.699</td><td>81.346</td><td>109.000</td><td>0.746</td><td>0.723</td></tr>
<tr><td>12</td><td>3</td><td>15</td><td>RB003B05</td><td>a76couture0812.r#1</td><td>>gb|AAG50909.1|AC069159_10 (AC069159) receptor protein kinase. putative [Arabidopsis thaliana]</td><td>111.140</td><td>104.000</td><td>1.069</td><td>177.108</td><td>174.000</td><td>1.018</td><td>1.043</td></tr>
<tr><td>12</td><td>4</td><td>1</td><td>ST006A12</td><td>a76couture0699.r#1</td><td>>gb|AAD41409.1|AF159562_1 (AF159562) cytosolic class II low molecular weight heat shock</td><td>3276.756</td><td>3084.000</td><td>1.063</td><td>6990.605</td><td>4813.000</td><td>1.452</td><td>1.257</td></tr>
<tr><td>12</td><td>4</td><td>2</td><td>ST001H09</td><td>a76couture0601.r#1</td><td>------</td><td>17.483</td><td>27.000</td><td>0.648</td><td>33.980</td><td>43.000</td><td>0.790</td><td>0.719</td></tr>
<tr><td>12</td><td>4</td><td>3</td><td>CM005c02</td><td>a76couture0499.r#1</td><td>ref|NP_195062.1|| (NM_119490) putative protein [Arabidopsis thal... 266 2e-070</td><td>89.911</td><td>94.000</td><td>0.956</td><td>165.781</td><td>141.000</td><td>1.176</td><td>1.066</td></tr>
<tr><td>12</td><td>4</td><td>4</td><td>RT021E02</td><td>a76couture1303#1</td><td>>gb|AAF99779.1|AC003981_29 (AC003981) F22O13.12 [Arabidopsis thaliana]</td><td>62.438</td><td>75.000</td><td>0.833</td><td>109.148</td><td>106.000</td><td>1.030</td><td>0.931</td></tr>
<tr><td>12</td><td>4</td><td>5</td><td>GT183H11</td><td>a76couture1169.r#1</td><td>>dbj|BAB41199.1| (AB024509) TMV response-related gene product [Nicotiana tabacum]</td><td>48.702</td><td>43.000</td><td>1.133</td><td>59.722</td><td>58.000</td><td>1.030</td><td>1.081</td></tr>
<tr><td>12</td><td>4</td><td>6</td><td>RT092B12</td><td>a76couture1047.r#1</td><td>>sp|P37900|HS7M_PEA HEAT SHOCK 70 KD PROTEIN. MITOCHONDRIAL PRECURSOR</td><td>489.515</td><td>480.000</td><td>1.020</td><td>848.469</td><td>691.000</td><td>1.228</td><td>1.124</td></tr>
<tr><td>12</td><td>4</td><td>7</td><td>RT081E12</td><td>a76couture0952.r#1</td><td>>pir||T48123 hypothetical protein F16M2.190 - Arabidopsis thaliana</td><td>23.727</td><td>25.000</td><td>0.949</td><td>42.218</td><td>36.000</td><td>1.173</td><td>1.061</td></tr>
<tr><td>12</td><td>4</td><td>8</td><td>RT012E08</td><td>a76couture1298.r#1</td><td>>gb|AAL01675.1| (AF321408) homeodomain protein Otx5 [Erpetoichthys calabaricus]</td><td>156.095</td><td>158.000</td><td>0.988</td><td>330.532</td><td>264.000</td><td>1.252</td><td>1.120</td></tr>
<tr><td>12</td><td>4</td><td>9</td><td>GT182D12</td><td>a76couture1163.r#1</td><td>>emb|CAA73620.1| (Y13177) multicatalytic endopeptidase [Arabidopsis thaliana]</td><td>1388.625</td><td>1440.000</td><td>0.964</td><td>2035.709</td><td>1753.000</td><td>1.161</td><td>1.063</td></tr>
<tr><td>12</td><td>4</td><td>10</td><td>RT093B02</td><td>a76couture1043.r#1</td><td>>ref|NP_030274.1|| (NM_129280) expressed protein; protein id: At2g37240.1. supported</td><td>71.180</td><td>82.000</td><td>0.868</td><td>79.287</td><td>90.000</td><td>0.881</td><td>0.875</td></tr>
<tr><td>12</td><td>4</td><td>11</td><td>RT074B01</td><td>a76couture0948.r#1</td><td>------</td><td>4535.509</td><td>4225.000</td><td>1.073</td><td>6790.844</td><td>6113.000</td><td>1.111</td><td>1.092</td></tr>
<tr><td>12</td><td>4</td><td>12</td><td>RT012D11</td><td>a76couture1294.r#1</td><td>>gb|AAF75749.1|AF261139_1 (AF261139) dehydration-induced protein ERD15 [Lycopersicon</td><td>303.450</td><td>343.000</td><td>0.885</td><td>490.135</td><td>543.000</td><td>0.903</td><td>0.894</td></tr>
<tr><td>12</td><td>4</td><td>13</td><td>GT181E07</td><td>a76couture1156.r#1</td><td>>ref|NP_564859.1|| (NM_105239) step II splicing factor. putative; protein id:</td><td>308.445</td><td>309.000</td><td>0.998</td><td>542.650</td><td>469.000</td><td>1.157</td><td>1.078</td></tr>
<tr><td>12</td><td>4</td><td>14</td><td>RT091F05</td><td>a76couture1037.r#1</td><td>>ref|NP_176113.1|| (NM_104598) disease resistance response protein-related/ dirigent</td><td>255.997</td><td>278.000</td><td>0.921</td><td>498.373</td><td>431.000</td><td>1.156</td><td>1.039</td></tr>
<tr><td>12</td><td>4</td><td>15</td><td>RT073H08</td><td>a76couture0945#1</td><td>>dbj|BAB90317.1| (AP003447) contains ESTs AU078053(R10920).AU078052(R10920)~unknown</td><td>680.576</td><td>328.000</td><td>2.075</td><td>875.241</td><td>450.000</td><td>1.945</td><td>2.010</td></tr>
<tr><td>12</td><td>5</td><td>1</td><td>RB006D02</td><td>a76couture1288.r#1</td><td>>gb|AAD34673.1|AC006341_1 (AC006341) ESTs gb|T04357 and gb|AA595092 come from this gene.</td><td>236.016</td><td>244.000</td><td>0.967</td><td>436.591</td><td>290.000</td><td>1.505</td><td>1.236</td></tr>
<tr><td>12</td><td>5</td><td>2</td><td>GT181B12</td><td>a76couture1152.r#1</td><td>>ref|NP_199763.1|| (NM_124329) WRKY family transcription factor; protein id:</td><td>1110.151</td><td>1230.000</td><td>0.903</td><td>2224.143</td><td>1571.000</td><td>1.416</td><td>1.159</td></tr>
<tr><td>12</td><td>5</td><td>3</td><td>RT091B01</td><td>a76couture1033.r#1</td><td>>ref|XP_138948.1|| (XM_138948) hypothetical protein XP_138948 [Mus musculus]</td><td>2478.796</td><td>2983.000</td><td>0.831</td><td>6039.166</td><td>4447.000</td><td>1.358</td><td>1.095</td></tr>
<tr><td>12</td><td>5</td><td>4</td><td>RT073E01</td><td>a76couture0943#1</td><td>------</td><td>41.209</td><td>73.000</td><td>0.565</td><td>51.485</td><td>89.000</td><td>0.578</td><td>0.571</td></tr>
<tr><td>12</td><td>5</td><td>5</td><td>RB007E11</td><td>a76couture1283.r#1</td><td>------</td><td>122.379</td><td>112.000</td><td>1.093</td><td>186.375</td><td>163.000</td><td>1.143</td><td>1.118</td></tr>
</table>

12	5	6	GT174G08	a76couture1148.r#1	>dbj|BAB62108.1| (AB066279) GDP-D-mannose pyrophosphorylase [Nicotiana tabacum]	679.327	551.000	1.233	869.063	747.000	1.163	1.198
12	5	7	RT084E09	a76couture1029.r#1	>ref|NP_195169.2|| (NM_119608) putative protein; protein id: At4g34430.1. supported by	27.473	44.000	0.624	25.742	47.000	0.548	0.586
12	5	8	RT072G05	a76couture0938.r#1	>pir||T11672 quinone oxidoreductase homolog - cowpea >gi|1617036|emb|CAA69914.1|	17.483	29.000	0.603	19.564	32.000	0.611	0.607
12	5	9	RB006B02	a76couture1277.r#1	------	71.180	91.000	0.782	142.098	138.000	1.030	0.906
12	5	10	GT174A06	a76couture1141.r#1	>pir||T02941 CP12 protein precursor. chloroplast - common tobacco	740.517	841.000	0.881	1335.515	1174.000	1.138	1.009
12	5	11	RT084A09	a76couture1025.r#1	>sp|Q01402|NDK2_SPIOL Nucleoside diphosphate kinase II. chloroplast precursor (NDK II)	136.115	150.000	0.907	184.316	193.000	0.955	0.931
12	5	12	RT072D07	a76couture0935.r#1	>ref|NP_565640.1|| (NM_128281) expressed protein; protein id: At2g27230.1. supported	89.911	110.000	0.817	134.890	157.000	0.859	0.838
12	5	13	GT172E01	a76couture1753#1	>ref|NP_193123.1|| (NM_117461) putative protein; protein id: At4g13870.1 [Arabidopsis	37.463	34.000	1.102	59.722	60.000	0.995	1.049
12	5	14	GB009G08	a76couture1661.r#1	------	69.931	88.000	0.795	130.771	154.000	0.849	0.822
12	5	15	GB001C01	a76couture1564.r#1	>ref|NP_194617.2|| (NM_119032) protein kinase - like protein; protein id: At4g28880.1	690.566	782.000	0.883	993.656	1099.000	0.904	0.894
12	6	1	TT251C03	a76couture1413#1	>gb|AAG13988.1|AF298829_1 (AF298829) putative protein disulfide-isomerase [Prunus avium]	3233.049	3550.000	0.911	5551.090	4240.000	1.309	1.110
12	6	2	GT171B12	a76couture1748.r#1	>ref|NP_194941.1|| (NM_119366) putative protein; protein id: At4g32140.1. supported by	339.664	291.000	1.167	686.807	430.000	1.597	1.382
12	6	3	GB009G02	a76couture1657.r#1	>gb|AAK84884.1|AF402603_1 (AF402603) NAC domain protein NAC2 [Phaseolus vulgaris]	379.624	378.000	1.004	766.094	583.000	1.314	1.159
12	6	4	GB000A72	a76couture1538.r#1	>ref|NP_567830.1|| (NM_119111) putative protein; protein id: At4g29660.1. supported by	106.145	116.000	0.915	244.038	164.000	1.488	1.202
12	6	5	TB007G10	a76couture1409.r#1	>gb|AAF40306.1|AF156667_1 (AF156667) RNA helicase [Vigna radiata]	558.197	529.000	1.055	828.905	759.000	1.092	1.074
12	6	6	GT173B04	a76couture1744.r#1	>ref|NP_195729.1|| (NM_120187) lectin - like protein; protein id: At5g01090.1	102.399	77.000	1.330	142.098	107.000	1.328	1.329
12	6	7	GB009F04	a76couture1654.r#1	>gb|AAC78100.1| (AF093628) protochlorophyllide reductase homolog [Oryza sativa]	519.486	601.000	0.864	724.906	769.000	0.943	0.904
12	6	8	TT282H11	a76couture1525.r#1	>ref|NP_201090.1|| (NM_125679) putative protein; protein id: At5g62840.1. supported by	29.970	39.000	0.768	44.277	51.000	0.868	0.818
12	6	9	TB007A12	a76couture1405.r#1	>ref|NP_199281.1|| (NM_123835) putative protein; protein id: At5g44680.1. supported by	338.415	348.000	0.972	454.096	437.000	1.039	1.006
12	6	10	GT172H12	a76couture1740#1	------							
12	6	11	GB009E05	a76couture1650.r#1	>sp|Q42908|PMGI_MESCR 2.3-bisphosphoglycerate-independent phosphoglycerate mutase	4258.284	3826.000	1.113	5846.613	5063.000	1.155	1.134
12	6	12	TT283F11	a76couture1521.r#1	>gb|AAK63942.1|AC084282_23 (AC084282) putative protein phosphatase [Oryza sativa (japonica	349.654	425.000	0.823	465.423	532.000	0.875	0.849
12	6	13	TB005D02	a76couture1400.r#1	------	704.303	908.000	0.776	1065.735	1312.000	0.812	0.794
12	6	14	GT172G04	a76couture1736.r#1	------	6.244	16.000	0.390	15.445	27.000	0.572	0.481
12	6	15	GB009D09	a76couture1646.r#1	>ref|NP_012089.1|| (NC_001140) Hypothetical ORF; Yhr217cp [Saccharomyces cerevisiae]	329.674	256.000	1.288	437.621	359.000	1.219	1.253
12	7	1	TT283A10	a76couture1515.r#1	>ref|NP_564972.1|| (NM_105636) expressed protein; protein id: At1g69680.1. supported	71.180	72.000	0.989	114.296	92.000	1.242	1.115
12	7	2	TB001G02	a76couture1394.r#1	>ref|NP_178009.1|| (NM_106536) hypothetical protein; protein id: At1g78880.1	899.110	1105.000	0.814	1902.878	1627.000	1.170	0.992
12	7	3	GT172F11	a76couture1733#1	>pir||T14319 protein AX110P - carrot >gi|285739|dbj|BAA03455.1| (D14605) AX110P	217.285	202.000	1.076	451.007	322.000	1.401	1.238
12	7	4	GB009C07	a76couture1643.r#1	>ref|NP_565390.1|| (NM_127222) actin depolymerizing factor 5; protein id: At2g16700.1	57.443	78.000	0.736	183.286	147.000	1.247	0.992
12	7	5	TT282C05	a76couture1511.r#1	>ref|NP_177172.2|| (NM_105683) unknown protein; protein id: At1g70150.1 [Arabidopsis	19.980	28.000	0.714	20.594	28.000	0.735	0.725
12	7	6	RT062H10	a76couture1390.r#1	>ref|NP_565192.1|| (NM_106535) E2. ubiquitin-conjugating enzyme. putative; protein id:	113.637	100.000	1.136	169.900	146.000	1.164	1.150
12	7	7	RT033C12	a76couture2155.r#1	------	413.341	476.000	0.868	555.006	620.000	0.895	0.882
12	7	8	RT022E09	a76couture2054#1	>gb|AAN03471.1| (AF532624) unknown protein [Glycine max]	408.346	509.000	0.802	670.332	704.000	0.952	0.877
12	7	9	RB008G09	a76couture1972.r#1	------	26.224	29.000	0.904	50.455	53.000	0.952	0.928
12	7	10	GT201B02	a76couture1845.r#1	------	762.995	780.000	0.978	1281.971	1103.000	1.162	1.070
12	7	11	RT033B12	a76couture2151.r#1	>ref|NP_197617.1|| (NM_122130) CCR4-associated factor-like protein; protein id:	895.363	1236.000	0.724	1707.236	1949.000	0.876	0.800
12	7	12	Arabidopsis Control Oligonucleotide	3ara7		17.483	20.000	0.874	35.010	37.000	0.946	0.910
12	7	13	RB008F08	a76couture1969.r#1	------	417.087	216.000	1.931	709.460	356.000	1.993	1.962
12	7	14	GT193G10	a76couture1841.r#1	>emb|CAC00654.1| (AJ224640) FKBP-like [Arabidopsis thaliana]	147.354	148.000	0.996	237.860	225.000	1.057	1.026
12	7	15	RT031G02	a76couture2146.r#1	>ref|NP_566574.1|| (NM_112615) Expressed protein; protein id: At3g17365.1 [Arabidopsis	1217.544	1268.000	0.960	1875.076	1871.000	1.002	0.981
12	8	1	RT022D05	a76couture2048.r#1	------	4.995	12.000	0.416	13.386	17.000	0.787	0.602
12	8	2	RB008E12	a76couture1966.r#1	>gb|AAG23444.1|AC084165_10 (AC084165) unknown protein [Arabidopsis thaliana]	102.399	104.000	0.985	182.256	152.000	1.199	1.092
12	8	3	GT193E03	a76couture1837.r#1	>ref|NP_197702.1|| (NM_122217) putative protein; protein id: At5g23110.1 [Arabidopsis	257.245	228.000	1.128	527.204	363.000	1.452	1.290
12	8	4	RT032G11	a76couture2142.r#1	>emb|CAC37356.1| (AJ309300) putative membrane protein [Solanum tuberosum]	97.404	68.000	1.432	170.930	92.000	1.858	1.645
12	8	5	RT022C12	a76couture2045#1	>dbj|BAB86118.1| (AP003437) putative dynamin-like protein ADL2 [Oryza sativa	29.970	25.000	1.199	47.366	29.000	1.633	1.416
12	8	6	RB008D05	a76couture1963#1	------	6.244	11.000	0.568	10.297	14.000	0.735	0.652
12	8	7	GT192H04	a76couture1833.r#1	>ref|NP_174575.1|| (NM_103032) ribosomal protein L11. putative; protein id:	168.583	162.000	1.041	221.385	216.000	1.025	1.033
12	8	8	RT032F02	a76couture2137.r#1	>pir||T08816 choline kinase (EC 2.7.1.32) CK2 - soybean	465.789	611.000	0.762	683.718	806.000	0.848	0.805
12	8	9	RT022C06	a76couture2042#1	>ref|NP_194708.1|| (NM_119125) putative protein; protein id: At4g29790.1. supported by	96.155	95.000	1.012	167.840	139.000	1.207	1.110
12	8	10	RB008A04	a76couture1960.r#1	------	22.478	25.000	0.899	6.178	10.000	0.618	0.758
12	8	11	GT192G07	a76couture1829.r#1	>ref|NP_178029.1|| (NM_106559) hypothetical protein; protein id: At1g79080.1	46.204	58.000	0.797	99.880	98.000	1.019	0.908
12	8	12	RT032E04	a76couture2134.r#1	>ref|NP_172069.1|| (NM_100458) unknown protein; protein id: At1g05780.1 [Arabidopsis	776.731	727.000	1.068	990.567	949.000	1.044	1.056
12	8	13	RT022B02	a76couture2038#1	>ref|NP_568147.1|| (NM_120583) coatomer delta subunit (delta-coat protein)	631.874	529.000	1.194	810.371	714.000	1.135	1.165
12	8	14	RB007E08	a76couture1956.r#1	>gb|AAF24563.1|AC007764_5 (AC007764) F22C12.10 [Arabidopsis thaliana]	1627.139	2205.000	0.738	2164.421	2792.000	0.775	0.757
12	8	15	GT191G11	a76couture1825.r#1	>ref|NP_565511.1|| (NM_127710) Expressed protein; protein id: At2g21385.1. supported	44.955	51.000	0.881	59.722	67.000	0.891	0.886
12	9	1	TT274H03	a76couture2556.r#1	>ref|NP_178660.1|| (NM_126617) hypothetical protein; protein id: At2g06030.1	136.115	136.000	1.001	237.860	179.000	1.329	1.165
12	9	2	TT253A06	a76couture2460.r#1	>dbj|BAB01731.1| (AB026648) gene_id:MLJ15.6~unknown protein [Arabidopsis thaliana]	169.832	207.000	0.820	273.899	250.000	1.096	0.958
12	9	3	RT063B01	a76couture2343.r#1	>ref|NP_177399.1|| (NM_105914) putative phenylalanyl-tRNA synthetase beta-subunit;	144.857	135.000	1.073	214.177	171.000	1.252	1.163
12	9	4	RT044B04	a76couture2253.r#1	>ref|NP_186921.1|| (NM_111140) expressed protein; protein id: At3g02720.1 [Arabidopsis	17.483	26.000	0.672	41.188	43.000	0.958	0.815
12	9	5	TT281D08	a76couture2552.r#1	>dbj|BAB90185.1| (AP003407) putative allyl alcohol dehydrogenase [Oryza sativa	93.657	78.000	1.201	174.019	114.000	1.526	1.364
12	9	6	TT251A06	a76couture2454#1	>ref|NP_201447.1|| (NM_126044) glycosyl hydrolase family 5/cellulase	1995.524	2528.000	0.789	2482.597	3288.000	0.755	0.772
12	9	7	RT062F10	a76couture2338#1	>gb|AAM28618.1|AF503760_1 (AF503760) adenosine monophosphate binding protein 1 AMPBP1	77.423	89.000	0.870	107.088	120.000	0.892	0.881
12	9	8	RT051C12	a76couture2250.r#1	>ref|NP_198552.1|| (NM_123095) putative protein; protein id: At5g37360.1. supported by	24.975	34.000	0.735	46.336	50.000	0.927	0.831
12	9	9	TT274D08	a76couture2548.r#1	>ref|NP_194974.1|| (NM_119400) putative protein; protein id: At4g32480.1. supported by	749.258	629.000	1.191	983.360	794.000	1.238	1.215
12	9	10	TT242B09	a76couture2449.r#1	------	564.441	659.000	0.857	776.391	815.000	0.953	0.905
12	9	11	RT062D03	a76couture2334.r#1	none	463.291	558.000	0.830	610.610	716.000	0.853	0.842
12	9	12	RT051A03	a76couture2246.r#1	------	575.680	622.000	0.926	940.112	849.000	1.107	1.016
12	9	13	TT273B10	a76couture2543.r#1	------	69.931	79.000	0.885	94.732	96.000	0.987	0.936

12	9	14	TT242F11	a76couture2444.r#1	>ref|NP_201430.1|| (NM_126027) unknown protein; protein id: At5g66290.1 [Arabidopsis	122.379	109.000	1.123	184.316	169.000	1.091	1.107
12	9	15	RT062B01	a76couture2332#1	------	39.960	48.000	0.833	26.772	37.000	0.724	0.778
12	10	1	RT044G05	a76couture2243.r#1	>emb|CAC34506.1| (AL589883) mannosyltransferase-like protein [Arabidopsis thaliana]	154.847	153.000	1.012	241.979	202.000	1.198	1.105
12	10	2	TT273H01	a76couture2540#1	------	304.698	194.000	1.571	424.235	271.000	1.565	1.568
12	10	3	TT241E04	a76couture2438.r#1	------	161.090	175.000	0.921	356.275	282.000	1.263	1.092
12	10	4	RT061F04	a76couture2328.r#1	>dbj|BAA82387.1| (AP000367) Similar to SEC7 protein. Saccharomyces cerevisiae	18.731	26.000	0.720	43.247	36.000	1.201	0.961
12	10	5	RT044F04	a76couture2239.r#1	>ref|NP_174466.1|| (NM_102920) amino acid permease. putative; protein id: At1g31830.1	283.469	343.000	0.826	524.115	475.000	1.103	0.965
12	10	6	TT264G12	a76couture2537.r#1	------	3.746	16.000	0.234	5.148	13.000	0.396	0.315
12	10	7	TB007H09	a76couture2434.r#1	>gb|AAD27590.1|AF121261_1 (AF121261) elongation factor 1-alpha 1; EF-1-alpha1 [Lilium	7.493	12.000	0.624	11.327	16.000	0.708	0.666
12	10	8	RT061D02	a76couture2324.r#1	>ref|NP_566902.1|| (NM_114697) putative protein; protein id: At3g48360.1. supported by	152.349	207.000	0.736	212.117	282.000	0.752	0.744
12	10	9	RT044E05	a76couture2235.r#1	>ref|NP_173589.1|| (NM_102019) putative transcriptional regulatory protein; protein	243.509	267.000	0.912	338.770	340.000	0.996	0.954
12	10	10	TT273F09	a76couture3074.r#1	>sp|P30707|RL9_PEA 60S ribosomal protein L9 (Gibberellin-regulated protein GA)	2662.364	2641.000	1.008	4247.495	3716.000	1.143	1.076
12	10	11	CT002E09	a76couture2923.r#1	>ref|NP_179742.1|| (NM_127719) putative ubiquitin activating enzyme; protein id:	127.374	125.000	1.019	200.791	172.000	1.167	1.093
12	10	12	PT005A12	a76couture2787.r#1	>gb|AAN06846.1| (AC099401) Hypothetical protein [Oryza sativa (japonica	295.957	277.000	1.068	539.561	431.000	1.252	1.160
12	10	13	PT009C08	a76couture2681.r#1	------	58.692	61.000	0.962	94.732	94.000	1.008	0.985
12	10	14	RT033F03	a76couture3067.r#1	>gb|AAM96891.1| (AY129669) auxin-responsive protein IAA1; MjAux/IAA1 [Mirabilis	354.649	357.000	0.993	453.066	496.000	0.913	0.953
12	10	15	CT002C06	a76couture2920.r#1	------	3942.347	3573.000	1.103	7028.704	6156.000	1.142	1.123
12	11	1	PT010F06	a76couture2783.r#1	>ref|NP_502221.1|| (NM_069820) protein-tyrosine-phosphatase like [Caenorhabditis	118.633	123.000	0.964	178.137	165.000	1.080	1.022
12	11	2	PT007F01	a76couture2677.r#1	------	2505.020	1985.000	1.262	3415.501	2461.000	1.388	1.325
12	11	3	RT021A05 reverse complement 685 bases 15	a76couture3060.r#1	b|AAD46394.1|AF083950_1 (AF083950) acyl carrier protein [Corian... 160 8e-039	1808.210	1752.000	1.032	3050.989	2293.000	1.331	1.181
12	11	4	Arabidopsis Control Oligonucleotide	3ara23		23.727	34.000	0.698	51.485	46.000	1.119	0.909
12	11	5	PT011D11	a76couture2778.r#1	>ref|NP_200311.1|| (NM_124882) FH protein interacting protein FIP2 (gb|AAF14550.1);	452.052	464.000	0.974	792.866	641.000	1.237	1.106
12	11	6	PT009F04	a76couture2672.r#1	------	400.853	396.000	1.012	682.688	530.000	1.288	1.150
12	11	7	RT072C06	a76couture3052.r#1	>gb|AAF07192.1|AF193846_1 (AF193846) branched-chain amino acid aminotransferase [Solanum	350.903	332.000	1.057	406.730	436.000	0.933	0.995
12	11	8	CT001H09	a76couture2910#1	>emb|CAD30058.1| (AJ457824) replication enhancer protein [Malvastrum begomovirus]	9.990	15.000	0.666	8.238	15.000	0.549	0.608
12	11	9	PT009F01	a76couture2773.r#1	>ref|NP_173960.1|| (NM_102400) hypothetical protein; protein id: At1g26360.1	19.980	43.000	0.465	28.831	52.000	0.554	0.510
12	11	10	PT011G01	a76couture2668.r#1	------	516.988	550.000	0.940	617.817	643.000	0.961	0.950
12	11	11	TT283D01	a76couture3042.r#1	>ref|NP_198706.1|| (NM_123252) frnE protein - like; protein id: At5g38900.1. supported	277.226	251.000	1.104	460.274	417.000	1.104	1.104
12	11	12	RB008B10	a76couture2907#1	------	14.985	15.000	0.999	23.683	23.000	1.030	1.014
12	11	13	PT004D09	a76couture2769.r#1	>emb|CAA69348.1| (Y08155) pectin methylesterase [Silene latifolia subsp. alba]	63.687	83.000	0.767	73.108	113.000	0.647	0.707
12	11	14	PT008E02	a76couture2665.r#1	>gb|AAC04693.1| (AF026150) beta-ketoacyl-ACP synthase IIIA [Perilla frutescens]	413.341	485.000	0.852	538.531	653.000	0.825	0.838
12	11	15	RT063H12	a76couture3037.r#1	>ref|NP_177693.1|| (NM_106215) vacuolar ATP synthase. putative; protein id:	3105.675	2642.000	1.176	4360.762	3895.000	1.120	1.148
12	12	1	PT002H10	a76couture2903.r#1	------	588.168	531.000	1.108	830.965	677.000	1.227	1.168
12	12	2	PT005B01	a76couture2764.r#1	>pir||T04125 protein kinase PK12 (EC 2.7.1.-). ethylene-induced - common tobacco	201.051	188.000	1.069	265.662	214.000	1.241	1.155
12	12	3	PT009H02	a76couture2661.r#1	>sp|O65759|H2A_CICAR Histone H2A >gi|3204129|emb|CAA07234.1| (AJ006768) histone H2A	1674.592	1633.000	1.025	2378.597	1878.000	1.267	1.146
12	12	4	BG273720 RB000A82 BM436605	couture_a76.400.c1#1	>ref|NP_565645.1|| (NM_128288) expressed protein; protein id: At2g27290.1. supported	186.066	222.000	0.838	380.987	318.000	1.198	1.018
12	12	5	TB006c01 TT282D04	couture_a76.321.c1#1	>dbj|BAB01172.1| (AP000414) phosphatidic acid phosphatase-like protein [Arabidopsis	454.550	443.000	1.026	812.430	593.000	1.370	1.198
12	12	6	BM437915 BM437730 GT174E05	couture_a76.232.c1.r#1	>ref|NP_190227.1|| (NM_114510) putative protein; protein id: At3g46430.1 [Arabidopsis	1677.089	1845.000	0.909	2965.524	2390.000	1.241	1.075
12	12	7	BM437828 CT004E06	couture_a76.133.c1.r#1	------	22.478	28.000	0.803	31.921	34.000	0.939	0.871
12	12	8	BG273715 RB000A87	couture_a76.399.c1#1	>pir||T04458 hypothetical protein F4D11.120 - Arabidopsis thaliana	226.026	316.000	0.715	321.265	426.000	0.754	0.735
12	12	9	BG273828 TT274B04	couture_a76.319.c1#1	>gb|AAG40343.1|AF324991_1 (AF324991) AT4g13930 [Arabidopsis thaliana]	1221.291	1310.000	0.932	1852.423	1784.000	1.038	0.985
12	12	10	BM436674 GB005e12 GT171H05	couture_a76.228.c1.r#1	>ref|NP_174144.1|| (NM_102588) purine permease; protein id: At1g28230.1. supported by	92.409	95.000	0.973	136.950	127.000	1.078	1.026
12	12	11	BM437709 CM005f10	couture_a76.129.c1.r#1		167.334	161.000	1.039	259.483	242.000	1.072	1.056
12	12	12	BM436757 BM437641 GT203E06 BM437078 BM4	couture_a76.395.c1.r#1	>ref|NP_565335.1|| (NM_126649) expressed protein; protein id: At2g06520.1. supported	516.988	407.000	1.270	746.529	533.000	1.401	1.335
12	12	13	BM437582 TT262A04	couture_a76.314.c1.r#1	>ref|NP_567574.1|| (NM_118030) kinase-like protein; protein id: At4g19110.1. supported	1441.073	2289.000	0.630	1825.651	3030.000	0.603	0.616
12	12	14	BG273808 GB009C02	couture_a76.225.c1#1	------	39.960	49.000	0.816	85.465	96.000	0.890	0.853
12	12	15	AW708012 ST002C11	couture_a76.125.c1#1	>ref|NP_567895.1|| (NM_119404) glycine hydroxymethyltransferase (EC 2.1.2.1) - like	314.688	371.000	0.848	460.274	482.000	0.955	0.902
12	13	1	BG273781 RB000A18	couture_a76.391.c1#1	>emb|CAD41094.1| (AL606614) OSJNBb0011N17.11 [Oryza sativa]	1287.475	1048.000	1.229	1754.602	1321.000	1.328	1.278
12	13	2	BG273912 RT064E08	couture_a76.311.c1.r#1	>ref|NP_172076.1|| (NM_100466) glycosyl hydrolase family 19 (chitinase); protein id:	2377.646	1946.000	1.222	3405.204	2560.000	1.330	1.276
12	13	3	BM437448 GB005B09	couture_a76.220.c1.r#1	>sp|Q41228|PSE1_NICSY PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E A)	777.980	696.000	1.118	1076.032	830.000	1.296	1.207
12	13	4	TB001g08 TB001G08	couture_a76.122.c1#1	>ref|NP_181277.1|| (NM_129296) putative protein translocase; protein id: At2g37410.1	192.310	193.000	0.996	489.106	331.000	1.478	1.237
12	13	5	BG273776 RB000A24	couture_a76.389.c1#1	>dbj|BAB17342.1| (AP002747) putative receptor kinase [Oryza sativa (japonica	51.199	64.000	0.800	91.643	85.000	1.078	0.939
12	13	6	BG273856 BG273864 TB000A28	couture_a76.308.c1.r#1	>ref|NP_197969.1|| (NM_122498) putative protein; protein id: At5g25970.1 [Arabidopsis	1607.159	2480.000	0.648	2595.863	3080.000	0.843	0.745
12	13	7	GB002d06 GB002D06	couture_a76.214.c1.r#1	>ref|NP_190357.2|| (NM_114641) ABC transporter family protein; protein id: At3g47730.1	22.478	27.000	0.833	38.099	37.000	1.030	0.931
12	13	8	BM436938 TT273D11	couture_a76.119.c1.r#1	>prf||1909359A ribosomal protein S19 [Solanum tuberosum]	26.224	33.000	0.795	29.861	38.000	0.786	0.790
12	13	9	BM437020 BM437345 BM437487 BM437780 BM	couture_a76.385.c1.r#1	>ref|NP_191183.1|| (NM_115482) copper homeostasis factor; protein id: At3g56240.1	3623.912	3086.000	1.174	5077.430	4252.000	1.194	1.184
12	13	10	BG273823 TB000A71 TB000A71	couture_a76.304.c1.r#1	>pir||S71454 farnesyl-pyrophosphate synthetase - Para rubber tree	526.978	628.000	0.839	829.935	869.000	0.955	0.897
12	13	11	BG273945 GB000A38	couture_a76.210.c1.r#1	>ref|NP_201231.1|| (NM_125822) phi-1-like protein; protein id: At5g64260.1. supported	630.626	484.000	1.303	750.648	606.000	1.239	1.271
12	13	12	BM437185 TB001B01	couture_a76.114.c1.r#1	>ref|NP_566608.1|| (NM_112726) expressed protein; protein id: At3g18410.1. supported	3431.602	3299.000	1.040	5058.896	4642.000	1.090	1.065
12	13	13	BG273833 TB000A60	couture_a76.491.c1.r#1	>ref|NP_200854.1|| (NM_125439) protein transport protein subunit - like; protein id:	372.132	323.000	1.152	425.264	396.000	1.074	1.113
12	13	14	BM436355 RT074G09	couture_a76.97.c1.r#1	>ref|NP_197314.1|| (NM_121818) putative protein; protein id: At5g18130.1. supported by	3938.600	4006.000	0.983	3827.379	4304.000	0.889	0.936
12	13	15	TB007a04 TB007A04	couture_a76.584.c1.r#1	>gb|AAC32130.1| (AF051229) 60S ribosomal protein L17 [Picea mariana]	1924.345	1515.000	1.270	2804.891	2197.000	1.277	1.273
12	14	1	G499035E VVCHI	couture_a76.sd.83.c1#	>sp|P51117|CFI_VITVI CHALCONE--FLAVONONE ISOMERASE (CHALCONE ISOMERASE)	4450.593	4104.000	1.084	5394.576	4469.000	1.207	1.146
12	14	2	GB004g09 ST003B09	couture_a76.92.c1.r#1	>sp|O82702|VAG1_TOBAC Vacuolar ATP synthase subunit G 1 (V-ATPase G subunit 1) (Vacuolar	6784.532	6746.000	1.006	9106.630	7617.000	1.196	1.101
12	14	3	AW707964 RT022E12	couture_a76.578.c1#1	>ref|NP_198790.1|| (NM_123336) ribosomal protein L5 - like; protein id: At5g39740.1	1693.323	1050.000	1.613	2112.936	1222.000	1.729	1.671
12	14	4	BG273815 TB000A79	couture_a76.487.c1#1	>sp|Q43621|GSHR_PEA GLUTATHIONE REDUCTASE. CYTOSOLIC (GR) (GRASE) (GOR2)	1173.838	1120.000	1.048	1953.333	1359.000	1.437	1.243
12	14	5	AW708001 ST005H11	couture_a76.91.c1.r#1	>sp|P36907|CHIX_PEA ENDOCHITINASE PRECURSOR >gi|2118033|pir||S59947 chitinase (EC	26135.372	16525.000	1.582	40341.423	19351.000	2.085	1.833
12	14	6	BG273813 PT007G09	couture_a76.551.c1.r#1	>ref|NP_179097.1|| (NM_127055) unknown protein; protein id: At2g14910.1. supported by	835.423	905.000	0.923	1315.951	1169.000	1.126	1.024

12	14	7	G4585616 VVI5686	couture_a76.sd.72.c1#	>emb|CAB40834.1| (AJ005686) pyrroline-5-carboxylate synthetase [Vitis vinifera]	568.187	1054.000	0.539	1283.001	1779.000	0.721	0.630
12	14	8	TB004d01 TB004D01	couture_a76.644.c1.r#1	>emb|CAC83750.1| (AJ292078) reversibly glycosylated polypeptide [Gossypium hirsutum]	566.939	505.000	1.123	564.273	660.000	0.855	0.989
12	14	9	TB003g08 BM437086 PT006D03	couture_a76.550.c1#1	>pir||T09015 transketolase (EC 2.2.1.1) precursor. chloroplast - spinach	1150.111	1295.000	0.888	1550.722	1691.000	0.917	0.903
12	14	10	GB001H01 GB001h01 BM437767 G18152532 VVI	couture_a76.sd.14.c1#	>sp|Q9M6K1|DCAM_IPOBA S-adenosylmethionine decarboxylase proenzyme (AdoMetDC) (SamDC)	1367.396	1421.000	0.962	1920.383	1945.000	0.987	0.975
12	14	11	GB005b03 GT194C11	couture_a76.567.c1#1	>dbj|BAB16908.1| (AP002863) putative Rer1A protein (AtRer1A) [Oryza sativa (japonica	1066.444	908.000	1.174	1373.614	1196.000	1.149	1.162
12	14	12	BM437375 TT242H08	couture_a76.473.c1.r#1	------	68.682	73.000	0.941	94.732	100.000	0.947	0.944
12	14	13	RB001B10 TT264D05	couture_a76.8.c2#1	>pir||T09781 glutathione transferase (EC 2.5.1.18) - papaya	3650.136	3827.000	0.954	5144.360	4684.000	1.098	1.026
12	14	14	G9885275 gi|9885275|gb|AF194175.1|AF1941	couture_a76.sd.35.c1#	>gb|AAG01383.1|AF194175_1 (AF194175) alcohol dehydrogenase 3 [Vitis vinifera]	1260.002	1447.000	0.871	1419.951	1755.000	0.809	0.840
12	14	15	BG273959 BG273950 BE846427 AW707958 BE84	couture_a76.639.c1#1	>gb|EAA12742.1| (AAAB01008964) agCP10966 [Anopheles gambiae str. PEST]	3643.892	2190.000	1.664	3664.687	2183.000	1.679	1.671
13	1	1	CM005a03	a76couture0495.r#1	none	337.166	562.000	0.600	395.403	602.000	0.657	0.628
13	1	2	CM001C02	a76couture0397.r#1	>ref|NP_187081.1|| (NM_111302) hypothetical protein; protein id: At3g04310.1	217.285	451.000	0.482	274.929	461.000	0.596	0.539
13	1	3	ST004H07	a76couture0277.r#1	>gb|AAM64789.1| (AY087233) unknown [Arabidopsis thaliana]	280.972	511.000	0.550	484.987	731.000	0.663	0.607
13	1	4	GT191F09	a76couture0141.r#1	>ref|NP_200638.1|| (NM_125215) leucine-rich repeat transmembrane protein kinase	49.951	92.000	0.543	48.396	78.000	0.620	0.582
13	1	5	CT001G11	a76couture0491.r#1	------	520.734	567.000	0.918	521.026	575.000	0.906	0.912
13	1	6	CM001A09	a76couture0393.r#1	>gb|AAK92787.2| (AY050852) putative RNA binding protein [Arabidopsis thaliana]	589.416	677.000	0.871	627.085	752.000	0.834	0.852
13	1	7	ST005E03	a76couture0270.r#1	>ref|NP_189909.1|| (NM_114191) putative protein; protein id: At3g43230.1. supported by	119.881	132.000	0.908	114.296	138.000	0.828	0.868
13	1	8	GT193B04	a76couture0131.r#1	>ref|NP_027545.1|| (NM_126401) expressed protein; protein id: At2g03510.1. supported	619.387	793.000	0.781	688.867	920.000	0.749	0.765
13	1	9	CT001E08	a76couture0486.r#1	>ref|NP_563879.1|| (NM_100959) expressed protein; protein id: At1g10830.1. supported	123.628	135.000	0.916	94.732	127.000	0.746	0.831
13	1	10	ST007D05	a76couture0389.r#1	>gb|AAM46847.1|AF498264_1 (AF498264) steroleosin-B [Sesamum indicum]	122.379	106.000	1.155	100.910	105.000	0.961	1.058
13	1	11	PT005E06	a76couture0263.r#1	>emb|CAC33000.1| (AJ272523) urease accessory protein G [Solanum tuberosum]	227.275	250.000	0.909	205.939	261.000	0.789	0.849
13	1	12	GB009D10	a76couture0127.r#1	>ref|NP_565409.1|| (NM_127277) expressed protein; protein id: At2g17230.1. supported	1991.778	2026.000	0.983	1930.680	2163.000	0.893	0.938
13	1	13	CT001D08	a76couture0482.r#1	------	254.748	306.000	0.833	281.107	329.000	0.854	0.843
13	1	14	ST005F07	a76couture0385.r#1	>sp|P04929|HRPX_PLALO HISTIDINE-RICH GLYCOPROTEIN PRECURSOR >gi|72400|pir||KGZQHL	669.337	334.000	2.004	584.867	327.000	1.789	1.896
13	1	15	PT007C09	a76couture0260.r#1	>ref|NP_187593.1|| (NM_111817) putative adenosine kinase; protein id: At3g09820.1	7819.757	7598.000	1.029	6774.369	7894.000	0.858	0.944
13	2	1	CT005H01	a76couture0112.r#1	>pir||T01932 RNA binding protein homolog - common tobacco (fragment)	811.696	1453.000	0.559	1050.290	1531.000	0.686	0.622
13	2	2	CT001B10	a76couture0478.r#1	>ref|NP_568923.1|| (NM_125451) putative protein; protein id: At5g60580.1. supported by	34.965	95.000	0.368	36.039	72.000	0.501	0.434
13	2	3	ST004B06	a76couture0382.r#1	>ref|NP_188045.1|| (NM_112286) unknown protein; protein id: At3g14280.1 [Arabidopsis	51.199	87.000	0.588	48.396	75.000	0.645	0.617
13	2	4	PT012B02	a76couture0255.r#1	>gb|AAM62786.1| (AY085564) 2C-methyl-D-erythritol 2.4-cyclodiphosphate synthase	246.006	406.000	0.606	262.572	388.000	0.677	0.641
13	2	5	CT005B12	a76couture0108.r#1	>ref|NP_179896.1|| (NM_127879) putative metal ion transporter (NRAMP); protein id:	415.838	573.000	0.726	576.630	768.000	0.751	0.738
13	2	6	CM004H04	a76couture0474.r#1	>ref|NP_191004.1|| (NM_115296) RING finger - like protein; protein id: At3g54360.1	13.736	24.000	0.572	9.267	15.000	0.618	0.595
13	2	7	ST002H01	a76couture0378.r#1	------	227.275	128.000	1.776	214.177	142.000	1.508	1.642
13	2	8	PT005E10	a76couture0251.r#1	>gb|AAD56411.1|AF185269_1 (AF185269) bHLH transcription factor GBOF-1 [Tulipa gesneriana]	1293.719	1554.000	0.833	1083.240	1481.000	0.731	0.782
13	2	9	CT004A10	a76couture0103.r#1	>ref|NP_196075.1|| (NM_120537) putative protein; protein id: At5g04550.1. supported by	1338.675	1111.000	1.205	1079.121	1147.000	0.941	1.073
13	2	10	RT073B05	a76couture0930#1	------	18.731	27.000	0.694	16.475	26.000	0.634	0.664
13	2	11	GT201H05	a76couture0808#1	>ref|NP_186814.1|| (NM_111031) unknown protein; protein id: At3g01650.1 [Arabidopsis	199.802	222.000	0.900	203.880	235.000	0.868	0.884
13	2	12	ST005H06	a76couture0694.r#1	>ref|NP_188039.1|| (NM_112280) unknown protein; protein id: At3g14225.1 [Arabidopsis	1308.704	1595.000	0.821	1351.991	1799.000	0.752	0.786
13	2	13	ST001E08	a76couture0596.r#1	------	28.722	29.000	0.990	33.980	32.000	1.062	1.026
13	2	14	RT072A10	a76couture0926.r#1	>dbj|BAC07052.1| (AP004006) hypothetical protein~similar to Arabidopsis thaliana	68.682	101.000	0.680	65.901	94.000	0.701	0.691
13	2	15	RT063F02	a76couture0803.r#1	>dbj|BAB10162.1| (AB016880) auxin response factor-like protein [Arabidopsis	1004.006	1265.000	0.794	883.479	1298.000	0.681	0.737
13	3	1	ST005F02	a76couture0690.r#1	>ref|NP_054486.1|| (NC_001879) RNA polymerase beta" chain [Nicotiana tabacum]	137.364	262.000	0.524	145.187	215.000	0.675	0.600
13	3	2	ST001C02	a76couture0591.r#1	>gb|AAL77445.1|L78468_1 (L78468) acyl-ACP thioesterase [Perilla frutescens]	12.488	30.000	0.416	9.267	30.000	0.309	0.363
13	3	3	RT071F08	a76couture0922.r#1	------	131.120	228.000	0.575	130.771	207.000	0.632	0.603
13	3	4	RT034G12	a76couture0796.r#1	>gb|AAM61533.1| (AY084973) unknown [Arabidopsis thaliana]	457.047	672.000	0.680	469.541	588.000	0.799	0.739
13	3	5	ST005E06	a76couture0686.r#1	>ref|NP_188317.1|| (NM_112568) glycosyl hydrolase family 19 (chitinase); protein id:	121.130	104.000	1.165	135.920	105.000	1.294	1.230
13	3	6	ST001B02	a76couture0587.r#1	------	413.341	578.000	0.715	466.452	628.000	0.743	0.729
13	3	7	RT071D01	a76couture0918.r#1	>ref|NP_197565.1|| (NM_122072) putative protein; protein id: At5g20650.1. supported by	1168.843	1396.000	0.837	1141.933	1450.000	0.788	0.812
13	3	8	RT023B03	a76couture0792.r#1	>ref|NP_563648.1|| (NM_100111) Expressed protein; protein id: At1g02305.1. supported	3002.028	3685.000	0.815	2421.845	3333.000	0.727	0.771
13	3	9	ST005B04	a76couture0682.r#1	>ref|NP_195436.1|| (NM_119882) tubulin-like protein; protein id: At4g37190.1	16.234	23.000	0.706	14.416	18.000	0.801	0.753
13	3	10	CT006C05	a76couture0583.r#1	>gb|ZP_00045864.1| (NZ_AAAB01000001) hypothetical protein [Lactobacillus gasseri]	2082.938	2002.000	1.040	1559.989	1821.000	0.857	0.949
13	3	11	TB005C12	a76couture0912.r#1	>gb|AAM91571.1| (AY128368) unknown protein [Arabidopsis thaliana]	429.575	442.000	0.972	387.166	454.000	0.853	0.912
13	3	12	RB001B03	a76couture0787.r#1	------	309.693	295.000	1.050	260.513	292.000	0.892	0.971
13	3	13	ST005A03	a76couture0678.r#1	>ref|NP_187354.1|| (NM_111578) DEAD/DEAH box RNA helicase protein. putative; protein id:	171.081	145.000	1.180	167.840	158.000	1.062	1.121
13	3	14	CT006A03	a76couture0578.r#1	------	2137.883	2017.000	1.060	1682.523	1901.000	0.885	0.973
13	3	15	TT281F05	a76couture0907.r#1	>dbj|BAA76734.1| (AB024575) ethylene responsive element binding factor [Nicotiana	44.955	36.000	1.249	40.158	39.000	1.030	1.139
13	4	1	GT174C03	a76couture0781.r#1	>sp|Q41387|PSBW_SPIOL Photosystem II reaction center W protein. chloroplast precursor	720.537	1243.000	0.580	991.597	1434.000	0.691	0.636
13	4	2	ST004H05	a76couture0674.r#1	>dbj|BAA96367.1| (AB043975) ribosomal protein L27 [Panax ginseng]	6125.185	10315.000	0.594	6836.151	9779.000	0.699	0.646
13	4	3	CT005F07	a76couture0575.r#1	------	33.717	53.000	0.636	41.188	55.000	0.749	0.693
13	4	4	RT063C03	a76couture1384.r#1	>ref|NP_198741.1|| (NM_123287) F-box protein family; protein id: At5g39250.1	634.372	1195.000	0.531	724.906	1176.000	0.616	0.574
13	4	5	RB003D01	a76couture1268.r#1	>ref|NP_191056.2|| (NM_115353) protein disulfide-isomerase-like protein; protein id:	410.843	584.000	0.703	458.215	682.000	0.672	0.688
13	4	6	GT171F11	a76couture1135.r#1	>ref|NP_680721.1|| (NM_148355) similar to 26S proteasome regulatory subunit (RPN9)	108.642	119.000	0.913	130.771	145.000	0.902	0.907
13	4	7	RT084B03	a76couture1021.r#1	>ref|NP_566951.1|| (NM_115002) strictosidine synthase-related; protein id:	711.795	811.000	0.878	558.095	732.000	0.762	0.820
13	4	8	RT054G04	a76couture1377.r#1	>ref|NP_564318.1|| (NM_102646) expressed protein; protein id: At1g29050.1. supported	1513.501	2658.000	0.569	1325.219	2517.000	0.527	0.548
13	4	9	RB001G09	a76couture1264.r#1	>ref|NP_565087.1|| (NM_106122) expressed protein; protein id: At1g74640.1. supported	1557.208	2080.000	0.749	1381.852	2208.000	0.626	0.687
13	4	10	GT172C04	a76couture1132#1	>dbj|BAA96068.1| (AB042856) 60S ribosomal protein L27a [Panax ginseng]	29.970	50.000	0.599	23.683	44.000	0.538	0.569
13	4	11	RT083E05	a76couture1018.r#1	>ref|NP_200286.1|| (NM_124856) transport protein particle component Bet3p-like	779.228	800.000	0.974	653.857	762.000	0.858	0.916
13	4	12	RT053H09	a76couture1373.r#1	>dbj|BAA88535.1| (AP000969) ESTs D39011(R0609). AU032023(R3215) correspond to a	315.937	344.000	0.918	246.097	302.000	0.815	0.867
13	4	13	GT204D02	a76couture1255.r#1	>ref|NP_567498.1|| (NM_117741) Expressed protein; protein id: At4g16444.1. supported	295.957	300.000	0.987	251.246	301.000	0.835	0.911
13	4	14	GT171C08	a76couture1127.r#1	>ref|NP_180450.1|| (NM_128443) putative RING zinc finger ankyrin protein; protein id:	223.529	218.000	1.025	188.434	207.000	0.910	0.968

13	4	15	RT082G01	a76couture1013.r#1	>ref|NP_194630.1|| (NM_119045) AIM1 protein; protein id: At4g29010.1. supported by	171.081	155.000	1.104	149.306	163.000	0.916	1.010
13	5	1	RT053B11	a76couture1368.r#1	>ref|NP_569038.1|| (NM_126066) dolichyl-di-phosphooligosaccharide-protein	528.227	1133.000	0.466	627.085	1143.000	0.549	0.507
13	5	2	GT203H05	a76couture1246.r#1	>ref|NP_181243.2|| (NM_129262) putative CCAAT-box binding trancription factor; protein	262.240	659.000	0.398	330.532	655.000	0.505	0.451
13	5	3	GB009F11	a76couture1123.r#1	>ref|NP_567349.1|| (NM_117068) putative protein; protein id: At4g10000.1. supported by	8.741	26.000	0.336	10.297	23.000	0.448	0.392
13	5	4	RT082C03	a76couture1009.r#1	------	6.244	16.000	0.390	8.238	16.000	0.515	0.453
13	5	5	RT052H01	a76couture1364.r#1	>sp|P93798|SNAA_VITVI Alpha-soluble NSF attachment protein (Alpha-SNAP)	4724.073	4901.000	0.964	4792.204	5157.000	0.929	0.947
13	5	6	GT203D07	a76couture1242.r#1	>ref|NP_196772.1|| (NM_121249) elongation factor 1B alpha-subunit (emb|CAB64729.1);	3583.951	3388.000	1.058	3875.775	4130.000	0.938	0.998
13	5	7	GB009D05	a76couture1118.r#1	>ref|NP_565190.1|| (NM_106529) Expressed protein; protein id: At1g78815.1. supported	959.050	940.000	1.020	829.935	962.000	0.863	0.941
13	5	8	RT081H12	a76couture1005.r#1	>gb|AAL85984.1| (AY080638) unknown protein [Arabidopsis thaliana]	397.107	403.000	0.985	364.512	428.000	0.852	0.919
13	5	9	RT052A02	a76couture1360.r#1	>ref|NP_683570.1|| (NM_148728) hypothetical protein; protein id: At3g16565.1	640.616	615.000	1.042	593.105	682.000	0.870	0.956
13	5	10	GT203H12	a76couture1237.r#1	>dbj|BAB90560.1| (AP003794) contains ESTs C73990(E30106).AU029295(E30106)~unknown	293.459	240.000	1.223	217.266	215.000	1.011	1.117
13	5	11	GB007D10	a76couture1112.r#1	>ref|NP_568828.1|| (NM_124946) expressed protein; protein id: At5g55640.1. supported	328.425	384.000	0.855	303.760	414.000	0.734	0.794
13	5	12	RT081G05	a76couture1001.r#1	>sp|P41099|RLA2_PARAR 60S ACIDIC RIBOSOMAL PROTEIN P2 >gi|551267|emb|CAA55047.1| (X78213)	1527.238	1218.000	1.254	1297.417	1172.000	1.107	1.180
13	5	13	GT191F12	a76couture1820.r#1	------	72.428	74.000	0.979	63.841	72.000	0.887	0.933
13	5	14	GT172E08	a76couture1728.r#1	>ref|NP_568715.1|| (NM_124372) Expressed protein; protein id: At5g49940.1. supported	39.960	30.000	1.332	35.010	34.000	1.030	1.181
13	5	15	GB009B05	a76couture1639.r#1	>ref|NP_193721.1|| (NM_118106) putative protein; protein id: At4g19860.1 [Arabidopsis	1237.525	1209.000	1.024	1107.953	1263.000	0.877	0.950
13	6	1	TT281E05	a76couture1504.r#1	>emb|CAD33925.1| (AJ489610) proline rich protein 3 [Cicer arietinum]	292.211	433.000	0.675	340.829	435.000	0.784	0.729
13	6	2	GT191B02	a76couture1816.r#1	>dbj|BAB09300.1| (AB011476) contains similarity to actin~gene_id:MDA7.24	109.891	243.000	0.452	143.128	264.000	0.542	0.497
13	6	3	GT172E03	a76couture1726#1	>pir||S14305 chlorophyll a/b-binding protein (cab-11) - tomato	29.970	53.000	0.565	35.010	47.000	0.745	0.655
13	6	4	GB009A01	a76couture1635.r#1	------	9.990	26.000	0.384	10.297	24.000	0.429	0.407
13	6	5	TT281A03	a76couture1499.r#1	>ref|NP_179383.1|| (NM_127347) hypothetical protein; protein id: At2g17930.1	69.931	101.000	0.692	71.049	98.000	0.725	0.709
13	6	6	GT184E02	a76couture1812.r#1	>gb|AAF02155.1|AC009853_15 (AC009853) unknown protein [Arabidopsis thaliana]	409.594	588.000	0.697	545.739	696.000	0.784	0.740
13	6	7	GT172C01	a76couture1722#1	>dbj|BAB09738.1| (AB015476) gene_id:MNC6.16~unknown protein [Arabidopsis thaliana]	209.792	180.000	1.166	127.682	140.000	0.912	1.039
13	6	8	GB007G08	a76couture1631.r#1	>ref|NP_178443.1|| (NM_126395) unknown protein; protein id: At2g03440.1 [Arabidopsis	2086.684	2628.000	0.794	1527.039	2312.000	0.660	0.727
13	6	9	TT274F04	a76couture1494.r#1	>gb|AAB63613.1| (AC002343) unknown protein [Arabidopsis thaliana]	1078.932	1396.000	0.773	879.360	1373.000	0.640	0.707
13	6	10	GT183D08	a76couture1808.r#1	>ref|NP_586651.1|| (NC_003242) hypothetical protein [Encephalitozoon cuniculi]	41.209	46.000	0.896	31.921	44.000	0.725	0.811
13	6	11	GT172B08	a76couture1719#1	>dbj|BAB64669.1| (AP003296) contains EST AU082313(E2215)~unknown protein [Oryza	37.463	32.000	1.171	33.980	34.000	0.999	1.085
13	6	12	GB007F08	a76couture1627#1	------	6.244	9.000	0.694	12.356	13.000	0.950	0.822
13	6	13	TT274B07	a76couture1488.r#1	>ref|NP_181056.1|| (NM_129064) unknown protein; protein id: At2g35110.1 [Arabidopsis	112.389	144.000	0.780	91.643	142.000	0.645	0.713
13	6	14	GT184A08	a76couture1804.r#1	>gb|AAF02163.1|AC009853_23 (AC009853) unknown protein [Arabidopsis thaliana]	561.944	837.000	0.671	452.036	779.000	0.580	0.626
13	6	15	GT172B04	a76couture1717#1	>ref|NP_194449.1|| (NM_118853) disease resistance protein (NBS-LRR class). putative;	282.221	317.000	0.890	225.503	311.000	0.725	0.808
13	7	1	GB007D01	a76couture1623.r#1	------	44.955	107.000	0.420	59.722	109.000	0.548	0.484
13	7	2	TT273G09	a76couture1482.r#1	>emb|CAC10212.1| (AJ299063) putative mitochondrial glyoxalase II [Cicer arietinum]	550.705	1251.000	0.440	701.223	1281.000	0.547	0.494
13	7	3	Arabidopsis Control Oligonucleotide	3ara23		8.741	19.000	0.460	6.178	15.000	0.412	0.436
13	7	4	GT172A05	a76couture1713#1	>ref|NP_191372.1|| (NM_115675) putative protein; protein id: At3g58130.1 [Arabidopsis	53.697	100.000	0.537	46.336	92.000	0.504	0.520
13	7	5	GB006G02	a76couture1618.r#1	>gb|AAN03474.1| (AF532627) syntaxin [Glycine max]	762.995	1220.000	0.625	723.876	1173.000	0.617	0.621
13	7	6	TT273D12	a76couture1478.r#1	>ref|NP_191899.1|| (NM_116205) cyclophylin -like protein; protein id: At3g63400.1	991.518	1190.000	0.833	1102.804	1394.000	0.791	0.812
13	7	7	RT044B10	a76couture2229.r#1	>gb|AAM13167.1| (AY093168) unknown protein [Arabidopsis thaliana]	103.647	120.000	0.864	95.762	120.000	0.798	0.831
13	7	8	RT032D01	a76couture2130.r#1	>ref|NP_198419.2|| (NM_122960) putative protein; protein id: At5g35690.1. supported by	59.941	53.000	1.131	51.485	52.000	0.990	1.061
13	7	9	RT022A09	a76couture2035#1	>ref|NP_175010.2|| (NM_103470) heterogeneous nuclear ribonucleoprotein (hnRNP)	12.488	17.000	0.735	11.327	17.000	0.666	0.700
13	7	10	RB006H10	a76couture1950.r#1	>dbj|BAB09318.1| (AB016870) ubiquitin activating enzyme E1-like protein [Arabidopsis	84.916	105.000	0.809	63.841	97.000	0.658	0.733
13	7	11	RT044A03	a76couture2225.r#1	>ref|NP_566652.1|| (NM_112887) expressed protein; protein id: At3g19970.1. supported	39.960	30.000	1.332	23.683	26.000	0.911	1.121
13	7	12	RT032C05	a76couture2126.r#1	>ref|NP_179920.1|| (NM_127903) hypothetical protein; protein id: At2g23390.1	56.194	60.000	0.937	44.277	63.000	0.703	0.820
13	7	13	RT021D01	a76couture2031#1	>ref|NP_198777.1|| (NM_123323) NAM / CUC2 - like protein; protein id: At5g39610.1	173.578	144.000	1.205	136.950	145.000	0.944	1.075
13	7	14	RB006A07	a76couture1945.r#1	>ref|NP_178534.1|| (NM_126486) putative protein phosphatase; protein id: At2g04550.1	413.341	464.000	0.891	332.592	461.000	0.721	0.806
13	7	15	RT043F07	a76couture2221.r#1	------	550.705	522.000	1.055	456.155	515.000	0.886	0.970
13	8	1	RT031E11	a76couture2122.r#1	>ref|NP_564507.1|| (NM_103640) expressed protein; protein id: At1g47480.1. supported	34.965	81.000	0.432	42.218	79.000	0.534	0.483
13	8	2	RT021H03	a76couture2027#1	>pir||T07712 probable ABC-type transport protein T23J7.60 - Arabidopsis thaliana	44.955	105.000	0.428	52.514	97.000	0.541	0.485
13	8	3	RB006B04	a76couture1941.r#1	>ref|NP_565668.1|| (NM_128389) expressed protein; protein id: At2g28305.1. supported	353.400	624.000	0.566	334.651	606.000	0.552	0.559
13	8	4	RT043D12	a76couture2218#1	------	4.995	13.000	0.384	4.119	9.000	0.458	0.421
13	8	5	RT031D02	a76couture2118.r#1	>gb|AAF03471.1|AC009327_10 (AC009327) hypothetical protein [Arabidopsis thaliana]	44.955	60.000	0.749	51.485	63.000	0.817	0.783
13	8	6	RT021G02	a76couture2023#1	>gb|AAL07080.1| (AY056231) unknown protein [Arabidopsis thaliana]	103.647	146.000	0.710	123.563	176.000	0.702	0.706
13	8	7	RB005F03	a76couture1936.r#1	------	64.936	56.000	1.160	46.336	43.000	1.078	1.119
13	8	8	RT042F04	a76couture2213.r#1	>gb|AAL31888.1|AF419556_1 (AF419556) At2g32080/F22D22.17 [Arabidopsis thaliana]	634.372	735.000	0.863	471.601	635.000	0.743	0.803
13	8	9	RT031B09	a76couture2115#1	------	8.741	9.000	0.971	9.267	11.000	0.842	0.907
13	8	10	RT021F03	a76couture2019#1	>gb|AAF63202.1|AF240679_1 (AF240679) poly(A)-binding protein [Cucumis sativus]	655.601	563.000	1.164	517.937	537.000	0.965	1.064
13	8	11	RB004D02	a76couture1932.r#1	>ref|NP_196482.2|| (NM_120952) GTP-binding protein LepA. putative; protein id:	303.450	274.000	1.107	225.503	255.000	0.884	0.996
13	8	12	RT041B01	a76couture2209.r#1	>ref|NP_189514.1|| (NM_113793) hypothetical protein; protein id: At3g28720.1	571.934	590.000	0.969	547.798	651.000	0.841	0.905
13	8	13	RT024H08	a76couture2109.r#1	>ref|NP_683425.1|| (NM_148584) expressed protein; protein id: At1g52870.2. supported	1332.431	1136.000	1.173	1057.498	1122.000	0.943	1.058
13	8	14	RT021E04	a76couture2015#1	>ref|NP_568019.1|| (NM_119884) putative protein; protein id: At4g37210.1 [Arabidopsis	636.869	751.000	0.848	610.610	804.000	0.759	0.804
13	8	15	RB004C07	a76couture1928.r#1	------	302.201	326.000	0.927	275.958	332.000	0.831	0.879
13	9	1	PT002D07	a76couture2655.r#1	------	77.423	196.000	0.395	106.059	204.000	0.520	0.457
13	9	2	TT263G10	a76couture2532.r#1	>gb|AAL91367.2|AF441241_1 (AF441241) chimera1 [synthetic construct]	674.332	1471.000	0.458	1008.072	1625.000	0.620	0.539
13	9	3	TB006B04	a76couture2427.r#1	>ref|NP_568996.1|| (NM_125878) Expressed protein; protein id: At5g64813.1 [Arabidopsis	104.896	197.000	0.532	116.356	197.000	0.591	0.562
13	9	4	RT061A03	a76couture2319.r#1	>dbj|BAB90655.1| (AP004223) contains EST C26216(C11870)~similar to Arabidopsis	49.951	73.000	0.684	54.574	72.000	0.758	0.721
13	9	5	PT001C01	a76couture2651.r#1	------	2.498	15.000	0.167	3.089	14.000	0.221	0.194
13	9	6	TT263D04	a76couture2528.r#1	>ref|NP_564404.1|| (NM_102985) expressed protein; protein id: At1g32500.1. supported	108.642	121.000	0.898	123.563	155.000	0.797	0.848
13	9	7	TB006B06	a76couture2422.r#1	------	1958.061	2164.000	0.905	1627.949	2106.000	0.773	0.839

13	9	8	RT054E10	a76couture2314.r#1	------	147.354	150.000	0.982	146.217	157.000	0.931	0.957
13	9	9	PT013C09	a76couture2646.r#1	------	254.748	207.000	1.231	209.028	209.000	1.000	1.115
13	9	10	TT264D01	a76couture2524.r#1	>gb|AAF75749.1|AF261139_1 (AF261139) dehydration-induced protein ERD15 [Lycopersicon	3466.568	4984.000	0.696	3205.443	5283.000	0.607	0.651
13	9	11	TB005H08	a76couture2418.r#1	------	370.883	383.000	0.968	286.255	361.000	0.793	0.881
13	9	12	Arabidopsis Control Oligonucleotide	3ara7		77.423	104.000	0.744	60.752	99.000	0.614	0.679
13	9	13	PT001G03	a76couture2641.r#1	------	2137.883	1718.000	1.244	1655.751	1637.000	1.011	1.128
13	9	14	TT263E01	a76couture2520.r#1	------	260.992	299.000	0.873	216.236	294.000	0.735	0.804
13	9	15	TB004F08	a76couture2409.r#1	------	63.687	50.000	1.274	51.485	48.000	1.073	1.173
13	10	1	RT053H06	a76couture2307.r#1	------	48.702	110.000	0.443	71.049	121.000	0.587	0.515
13	10	2	PT008G11	a76couture2637.r#1	------	29.970	55.000	0.545	36.039	56.000	0.644	0.594
13	10	3	TT261G10	a76couture2516.r#1	>ref|NP_189034.1|| (NM_113297) glycosyl hydrolase family 14 (beta-amylase); protein	2718.558	3723.000	0.730	2935.663	3845.000	0.764	0.747
13	10	4	TB004E03	a76couture2406.r#1	>emb|CAB61883.1| (AJ249998) aminoacylase-1 [Lycopersicon esculentum]	723.034	1153.000	0.627	814.489	1333.000	0.611	0.619
13	10	5	RT061F11	a76couture2303.r#1	>dbj|BAB19757.1| (AB052785) nitrate transporter NRT1-2 [Glycine max]	161.090	169.000	0.953	240.949	255.000	0.945	0.949
13	10	6	PT001C12	a76couture2632.r#1	------	325.927	541.000	0.602	417.027	629.000	0.663	0.633
13	10	7	TT261B03	a76couture2512.r#1	>ref|NP_196024.1|| (NM_120486) expressed protein; protein id: At5g04040.1 [Arabidopsis	219.782	245.000	0.897	210.058	268.000	0.784	0.840
13	10	8	TB003H09	a76couture2402.r#1	>gb|AAF79444.1|AC025808_26 (AC025808) F18O14.26 [Arabidopsis thaliana]	553.202	669.000	0.827	464.393	669.000	0.694	0.761
13	10	9	RT061B05	a76couture2300.r#1	>ref|NP_200527.1|| (NM_125099) Macrophage migration inhibitory factor (MIF) family;	188.563	188.000	1.003	154.454	187.000	0.826	0.914
13	10	10	BG273719 RB000A83 RB000A83 BM437268 BM	couture_a76.107.c1.r#1	>pir||S68805 pectin acetylesterase (EC 3.1.1.-) precursor - mung bean	2984.545	3260.000	0.916	2696.773	3571.000	0.755	0.835
13	10	11	PT013A12	a76couture3028.r#1	>pir||T05707 phosphate transport protein G7. mitochondrial - soybean	4772.774	4096.000	1.165	3825.320	3874.000	0.987	1.076
13	10	12	CT001B03	a76couture2899.r#1	>ref|NP_196322.1|| (NM_120787) MtN21 nodulin protein-like; protein id: At5g07050.1	77.423	71.000	1.090	62.811	68.000	0.924	1.007
13	10	13	PT013C05	a76couture2758.r#1	>ref|NP_186955.1|| (NM_111175) putative cellulose synthase catalytic subunit; protein	1384.879	1372.000	1.009	1076.032	1390.000	0.774	0.892
13	10	14	BG273793 RT083H09	couture_a76.102.c1#1	>dbj|BAA95794.1| (AB009888) DC1.2 homologue [Nicotiana tabacum]	9501.842	8191.000	1.160	6742.448	7391.000	0.912	1.036
13	10	15	ST007B04	a76couture3022.r#1	>emb|CAC43286.1| (AJ298137) translation initiation factor eIF-4A1 [Arabidopsis	4682.863	4870.000	0.962	3336.214	4316.000	0.773	0.867
13	11	1	PT013C04	a76couture2893.r#1	>dbj|BAB30189.1| (AK016310) data source:MGD. source key:MGI:96099	774.233	1477.000	0.524	949.380	1497.000	0.634	0.579
13	11	2	PT003A08	a76couture2754.r#1	>ref|NP_201433.1|| (NM_126030) GATA zinc finger protein; protein id: At5g66320.1	51.199	100.000	0.512	64.871	107.000	0.606	0.559
13	11	3	TB002d06	a76couture3332.r#1	>dbj|BAB11219.1| (AB011480) contains similarity to unknown	462.043	972.000	0.475	566.333	1127.000	0.503	0.489
13	11	4	PT004B02	a76couture3015.r#1	>ref|NP_565110.1|| (NM_106198) E2. ubiquitin-conjugating enzyme 16 (UBC16); protein	21.229	48.000	0.442	19.564	44.000	0.445	0.443
13	11	5	ST002F02	a76couture2886.r#1	>ref|NP_142215.1|| (NC_000961) hypothetical protein [Pyrococcus horikoshii]	370.883	436.000	0.851	395.403	485.000	0.815	0.833
13	11	6	PT003H08	a76couture2750.r#1	>pir||T06264 3-dehydroquinate dehydratase (EC 4.2.1.10) / shikimate	410.843	526.000	0.781	453.066	631.000	0.718	0.750
13	11	7	TK001A01C	a76couture3172.r#1	>pir||T10449 probable serine/threonine-specific protein kinase (EC 2.7.1.-) -	1316.197	1255.000	1.049	998.805	1172.000	0.852	0.950
13	11	8	RT033G10	a76couture3010.r#1	>sp|Q9XEK6|RS14_TORRU 40S ribosomal protein S14 >gi|4574240|gb|AAD23964.1|AF108724_1	1843.175	1510.000	1.221	1344.783	1361.000	0.988	1.104
13	11	9	PT007H07	a76couture2878.r#1	>ref|NP_568959.1|| (NM_125664) tubulin beta-2/beta-3 chain (sp|P29512); protein id:	29.970	48.000	0.624	21.624	46.000	0.470	0.547
13	11	10	PT003D09	a76couture2745.r#1	>ref|NP_200788.1|| (NM_125372) putative protein; protein id: At5g59800.1 [Arabidopsis	172.329	138.000	1.249	147.247	149.000	0.988	1.118
13	11	11	MY001B01C	a76couture3168.r#1	>pir||S26605 myb-related protein 1 - garden petunia >gi|20563|emb|CAA78386.1|	48.702	61.000	0.798	40.158	60.000	0.669	0.734
13	11	12	PT005H09	a76couture3004.r#1	------	7063.007	5919.000	1.193	5060.955	5493.000	0.921	1.057
13	11	13	PT001A09	a76couture2869.r#1	------	27.473	49.000	0.561	20.594	45.000	0.458	0.509
13	11	14	PT012G05	a76couture2741.r#1	>emb|CAB44316.1| (AJ242659) serine palmitoyltransferase [Solanum tuberosum]	2081.689	2089.000	0.997	1700.028	2183.000	0.779	0.888
13	11	15	GT7F4AP93	a76couture3164.r#1	------	1358.655	855.000	1.589	1034.844	856.000	1.209	1.399
13	12	1	PT002G02	a76couture2999.r#1	>ref|NP_190516.1|| (NM_114807) alpha NAC-like protein; protein id: At3g49470.1	94.906	193.000	0.492	129.742	208.000	0.624	0.558
13	12	2	GT182E03	a76couture2861.r#1	>sp|O65731|RS5_CICAR 40S RIBOSOMAL PROTEIN S5 >gi|3043428|emb|CAA06491.1| (AJ005346) 40S	2172.849	2860.000	0.760	2256.064	2893.000	0.780	0.770
13	12	3	PT003D05	a76couture2737.r#1	>pir||F71446 hypothetical protein - Arabidopsis thaliana	4456.837	5213.000	0.855	5281.310	5509.000	0.959	0.907
13	12	4	TB007e11 TB007E11	couture_a76.468.c1.r#1	>ref|NP_200887.1|| (NM_125472) ABC transporter family protein; protein id: At5g60790.1	1318.694	3346.000	0.394	1559.989	3456.000	0.451	0.423
13	12	5	PT010E04 BM437953 GT172C08	couture_a76.380.c1#1	>gb|AAK07610.1|AF319771_2 (AF319771) prohibitin 1-like protein [Brassica napus]	300.952	388.000	0.776	308.909	399.000	0.774	0.775
13	12	6	BM436917 TB002H08	couture_a76.299.c1.r#1	>ref|NP_195664.1|| (NM_120114) shikimate kinase - like protein; protein id:	801.706	974.000	0.823	747.559	1049.000	0.713	0.768
13	12	7	BM437725 RT092C12	couture_a76.204.c1.r#1	none	1794.473	2041.000	0.879	1420.980	1958.000	0.726	0.802
13	12	8	TB005a11 TB005A11	couture_a76.464.c1.r#1	>ref|NP_200761.1|| (NM_125345) 1-aminocyclopropane-1-carboxylate oxidase - like	178.573	150.000	1.190	133.860	142.000	0.943	1.067
13	12	9	BM436727 GT171F05	couture_a76.377.c1.r#1	>ref|NP_565629.1|| (NM_128237) putative hydroxymethylglutaryl-CoA lyase; protein id:	473.281	461.000	1.027	407.760	470.000	0.868	0.947
13	12	10	BM437043 RT061A11	couture_a76.294.c1#1	>pir||G71445 hypothetical protein - Arabidopsis thaliana	1361.152	1563.000	0.871	1130.606	1592.000	0.710	0.791
13	12	11	BM437726 CM001G12	couture_a76.20.c1.r#1	>sp|O04905|UMPK_ARATH URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)	5013.786	4488.000	1.117	3355.779	3845.000	0.873	0.995
13	12	12	AW708005 BM436507 BM437678 TB001H02	couture_a76.461.c1.r#1	>ref|NP_199045.1|| (NM_123595) ubiquitin-like protein; protein id: At5g42300.1	8004.574	7065.000	1.133	7150.208	7234.000	0.988	1.061
13	12	13	BE846431 GT162H12	couture_a76.374.c1#1	>gb|AAK70910.1|AC087551_9 (AC087551) hypothetical protein [Oryza sativa]	660.596	625.000	1.057	522.056	637.000	0.820	0.938
13	12	14	BM436833 RT041A03	couture_a76.289.c1.r#1	>emb|CAC17628.1| (AJ270955) putative phospholipid hydroperoxide glutathione	1073.937	983.000	1.093	755.797	910.000	0.831	0.962
13	12	15	BM437312 RT081A04	couture_a76.196.c1.r#1	>gb|AAK27733.1| (AY028704) thermicin [Thermoanaerobacter yonseiensis]	332.171	319.000	1.041	285.226	346.000	0.824	0.933
13	13	1	BG273806 TB000A88	couture_a76.458.c1.r#1	>ref|NP_197349.2|| (NM_121853) putative protein; protein id: At5g18480.1. supported by	11.239	39.000	0.288	10.297	37.000	0.278	0.283
13	13	2	BM437348 BM436565 GB009A09	couture_a76.37.c1.r#1	>sp|Q40459|PSBO_TOBAC Oxygen-evolving enhancer protein 1. chloroplast precursor (OEE1)	16.234	32.000	0.507	20.594	36.000	0.572	0.540
13	13	3	RB004A08 RT024B06	couture_a76.284.c1.r#1	>emb|CAC84903.1| (AJ306961) aldehyde dehydrogenase [Arabidopsis thaliana]	932.826	1969.000	0.474	1089.418	1921.000	0.567	0.520
13	13	4	TT254H04 BM437660	couture_a76.192.c1.r#1	------	177.324	230.000	0.771	187.405	231.000	0.811	0.791
13	13	5	BM436387 RT062G10	couture_a76.455.c1.r#1	>ref|NP_568863.1|| (NM_125149) CONSTANS-like B-box zinc finger protein-like; protein	919.090	1086.000	0.846	992.627	1169.000	0.849	0.848
13	13	6	BM436260 GB004A08	couture_a76.364.c1.r#1	>gb|AAM64577.1| (AY087016) putative nitrilase-associated protein [Arabidopsis	730.527	956.000	0.764	775.361	1067.000	0.727	0.745
13	13	7	BM437571 RT021C06	couture_a76.279.c1.r#1	>sp|P37218|H1_LYCES HISTONE H1 >gi|629668|pir||S45662 histone H1 - tomato	126.125	89.000	1.417	98.851	100.000	0.989	1.203
13	13	8	BM437132 TT284C02	couture_a76.188.c1.r#1	>ref|NP_190939.1|| (NM_115231) putative protein; protein id: At3g53710.1 [Arabidopsis	4413.130	4181.000	1.056	3476.253	4019.000	0.865	0.960
13	13	9	BM437633 RT054G02	couture_a76.452.c1.r#1	>gb|AAC09468.2| (AF002698) putative NADPH-cytochrome P450 reductase [Pisum sativum]	4037.253	3309.000	1.220	3068.494	3293.000	0.932	1.076
13	13	10	GB002D08 BM437941	couture_a76.360.c1#1	>dbj|BAA94084.1| (AB025969) NAD-dependent sorbitol dehydrogenase [Prunus persica]	13.736	12.000	1.145	13.386	14.000	0.956	1.050
13	13	11	RB003C09 RB007E03	couture_a76.274.c1.r#1	>ref|NP_066209.2|| (NC_002545) NADH dehydrogenase subunit 2 [Schistosoma mansoni]	355.898	359.000	0.991	298.612	352.000	0.848	0.920
13	13	12	BM436402 TT284F02 BM437705	couture_a76.185.c1.r#1	>gb|AAF25968.1|AC017118_5 (AC017118) F6N18.8 [Arabidopsis thaliana]	1954.315	2184.000	0.895	1293.298	1863.000	0.694	0.795
13	13	13	AW707985 VVI237984 BG273760 RT052C11 BE	couture_a76.sd.56.c1.r	>emb|CAB85624.1| (AJ237984) putative proline-rich cell wall protein [Vitis vinifera]	22375.345	24254.000	0.923	16778.894	22640.000	0.741	0.832
13	13	14	BM437672 BM436531 BM436366 BM437912 RT	couture_a76.631.c1#1	>ref|NP_195713.1|| (NM_120167) histone H3.3; protein id: At4g40030.1. supported by	1458.556	1002.000	1.456	1150.170	977.000	1.177	1.316
13	13	15	AW707963 TT273G08	couture_a76.536.c1#1	>ref|NP_171777.1|| (NM_100157) ribosomal protein L19. putative; protein id:	5173.627	3782.000	1.368	4546.107	3994.000	1.138	1.253

13	14	1	cds of gi|1469265|emb|X84846.1|PP111ACNP	luc2#1		1.249	13.000	0.096	7.208	20.000	0.360	0.228
13	14	2	BM437143 RT021G07	couture_a76.67.c1#1	>ref|NP_564560.1|| (NM_103884) ATP-dependent Clp protease proteolytic subunit (ClpR1);	262.240	401.000	0.654	365.542	469.000	0.779	0.717
13	14	3	GB004e08 GB004E08	couture_a76.554.c2.r#1	>gb|AAF73016.1|AF262934_1 (AF262934) ubiquitin conjugating protein [Avicennia marina]	658.098	1089.000	0.604	771.242	1114.000	0.692	0.648
13	14	4	BM437734 VVHT1HEXO VVHEXTRAN	couture_a76.sd.76.c1#	>emb|CAA70777.1| (Y09590) hexose transporter [Vitis vinifera]	62.438	111.000	0.563	87.524	133.000	0.658	0.610
13	14	5	BG273721 RB000A81	couture_a76.66.c1.r#1	>gb|AAM65587.1| (AY088041) unknown [Arabidopsis thaliana]	339.664	450.000	0.755	395.403	519.000	0.762	0.758
13	14	6	BG273966 BM436927 CM002C11	couture_a76.527.c1.r#1	>sp|Q39511|MT1_CASGL Metallothionein-like protein 1 >gi|7441824|pir||T09587	217.285	289.000	0.752	231.682	342.000	0.677	0.715
13	14	7	G7547008 gi|7547008|gb|AF243475.1|AF2434	couture_a76.sd.43.c1#	>gb|AAF63756.1|AF243475_1 (AF243475) pectate lyase [Vitis vinifera]	79.921	56.000	1.427	66.930	59.000	1.134	1.281
13	14	8	RB007A05 BM437471 BM437415 RT092F08	couture_a76.620.c1#1	>emb|CAB60728.1| (AJ012717) SUMO protein [Lycopersicon esculentum]	1448.566	1262.000	1.148	1064.705	1166.000	0.913	1.030
13	14	9	BG273966 BM436927 CM002C11	couture_a76.527.c1#1	>sp|Q39511|MT1_CASGL Metallothionein-like protein 1 >gi|7441824|pir||T09587	2608.667	2551.000	1.023	2014.085	2490.000	0.809	0.916
13	14	10	BG273762 RB000A39	couture_a76.64.c1#1	>gb|AAF79435.1|AC025808_17 (AC025808) F18O14.34 [Arabidopsis thaliana]	510.744	445.000	1.148	424.235	453.000	0.937	1.042
13	14	11	TB004h03 TT281H03	couture_a76.544.c1#1	>ref|NP_189967.1|| (NM_114249) calmodulin 7; protein id: At3g43810.1. supported by	1578.437	1417.000	1.114	1079.121	1243.000	0.868	0.991
13	14	12	gi|6434832|gb|AF021810.1|AF021810 G64348	couture_a76.sd.64.c1.r	Vitis vinifera putative sucrose transporter (VvSUC27) mRNA	262.240	300.000	0.874	227.563	306.000	0.744	0.809
13	14	13	BM436901 ST005C10	couture_a76.639.c2.r#1	------	3593.942	2172.000	1.655	2489.805	1959.000	1.271	1.463
13	14	14	BM436627 BM436370 RT031B12	couture_a76.613.c2.r#1	>emb|CAC16166.1| (AJ291705) pathogenesis-related protein 10 [Vitis vinifera]	2798.479	935.000	2.993	2522.755	995.000	2.535	2.764
13	14	15	BM437968 PT001H07	couture_a76.517.c1.r#1	>dbj|BAB63699.1| (AP003289) hypothetical protein~similar to Arabidopsis thaliana	792.965	652.000	1.216	560.155	603.000	0.929	1.073
14	1	1	CM004F11	a76couture0470.r#1	>ref|NP_174463.1|| (NM_102917) hypothetical protein; protein id: At1g31814.1	203.548	220.000	0.925	186.375	241.000	0.773	0.849
14	1	2	ST001G10	a76couture0372.r#1	>ref|NP_054996.1|| (NC_002202) ycf1 protein [Spinacia oleracea]	1684.582	973.000	1.731	1838.007	1210.000	1.519	1.625
14	1	3	PT013A02	a76couture0246.r#1	>emb|CAB90633.1| (AJ277743) protein phpsphatase 2C (PP2C) [Fagus sylvatica]	3494.040	3535.000	0.988	3491.699	3236.000	1.079	1.034
14	1	4	CT002C01	a76couture0099.r#1	>ref|NP_200764.1|| (NM_125348) putative protein; protein id: At5g59560.1. supported by	79.921	67.000	1.193	57.663	57.000	1.012	1.102
14	1	5	CM004E02	a76couture0466.r#1	------	449.555	341.000	1.318	290.374	296.000	0.981	1.150
14	1	6	CT004D12	a76couture0368.r#1	>sp|Q9SP55|VATG_CITLI Vacuolar ATP synthase subunit G (V-ATPase G subunit) (Vacuolar	7703.622	4921.000	1.565	4271.178	3543.000	1.206	1.385
14	1	7	PT010G04	a76couture0240.r#1	>pir||T09262 glycine-rich cell wall protein EMB31 - white spruce	37680.191	17719.000	2.127	24284.346	14475.000	1.678	1.902
14	1	8	CM005d02	a76couture0095.r#1	sp|Q96499|RL44_GOSHI 60S RIBOSOMAL PROTEIN L44 >gi|2119128|pir||... 194 5e-049	7754.822	4547.000	1.705	6266.729	3770.000	1.662	1.684
14	1	9	CM004C04	a76couture0462.r#1	>ref|NP_193556.1|| (NM_117932) putative protein; protein id: At4g18220.1 [Arabidopsis	179.822	165.000	1.090	166.811	164.000	1.017	1.053
14	1	10	CM005d08	a76couture0364.r#1	ef|NP_085475.1|| (NC_001284) orf107a [Arabidopsis thaliana] >gi... 104 2e-022	1020.240	615.000	1.659	751.678	533.000	1.410	1.535
14	1	11	PT004C05	a76couture0235.r#1	>dbj|BAA96072.1| (AB042860) ribosomal protein L29 [Panax ginseng]	13074.554	6890.000	1.898	12435.637	6860.000	1.813	1.855
14	1	12	CM004E10	a76couture0091.r#1	>gb|AAK83088.1|AF290200_1 (AF290200) Pin1-type peptidyl-prolyl cis/trans isomerase [Malus x	678.079	686.000	0.988	1019.399	776.000	1.314	1.151
14	1	13	CM004A02	a76couture0458.r#1	>ref|NP_193012.1|| (NM_117345) hypothetical protein; protein id: At4g12760.1	114.886	114.000	1.008	128.712	91.000	1.414	1.211
14	1	14	CM002C06	a76couture0360.r#1	>ref|NP_296498.1|| (NC_002620) hypothetical protein [Chlamydia muridarum]	297.206	339.000	0.877	443.799	419.000	1.059	0.968
14	1	15	PT006C05	a76couture0229#1	>pir||T02995 unspecific monooxygenase (EC 1.14.14.1) - common tobacco	801.706	514.000	1.560	1069.854	563.000	1.900	1.730
14	2	1	CM003F06	a76couture0086.r#1	>gb|AAG12692.1|AC025814_16 (AC025814) cytosolic IMP-GMP specific 5'-nucleotidase. putative;	265.987	296.000	0.899	235.800	324.000	0.728	0.813
14	2	2	CM003H06	a76couture0453.r#1	>gb|AAF04257.1| (AF139114) subtilisin-like serine protease [Neospora caninum]	729.278	757.000	0.963	752.708	841.000	0.895	0.929
14	2	3	CM001G04	a76couture0356.r#1	------	91.160	90.000	1.013	89.584	85.000	1.054	1.033
14	2	4	PT002H04	a76couture0223.r#1	>dbj|BAB33421.1| (AB049723) putative senescence-associated protein [Pisum sativum]	4957.591	3180.000	1.559	3956.091	3145.000	1.258	1.408
14	2	5	CM001E11	a76couture0080.r#1	>ref|NP_187939.1|| (NM_112176) DnaJ protein. putative; protein id: At3g13310.1	4113.427	2826.000	1.456	2801.802	2700.000	1.038	1.247
14	2	6	CM003G09	a76couture0449.r#1	>ref|NP_567185.1|| (NM_116301) F-box protein family; protein id: At4g00755.1	661.845	417.000	1.587	434.532	391.000	1.111	1.349
14	2	7	TT251D10	a76couture0352#1	>ref|NP_564725.1|| (NM_104574) expressed protein; protein id: At1g57790.1. supported	655.601	402.000	1.631	443.799	367.000	1.209	1.420
14	2	8	RT063B08	a76couture0218.r#1	>ref|NP_568713.1|| (NM_124360) putative protein; protein id: At5g49820.1. supported by	790.467	504.000	1.568	673.421	460.000	1.464	1.516
14	2	9	CT003G06	a76couture0069.r#1	>emb|CAC44032.1| (AJ320185) snakin-1 [Solanum tuberosum]	20058.889	16038.000	1.251	14642.275	12757.000	1.148	1.199
14	2	10	TT253D12	a76couture0902.r#1	>sp|Q43317|CYSK_CITLA Cysteine synthase (O-acetylserine sulfhydrylase) (O-acetylserine	3051.978	2287.000	1.334	2645.289	2345.000	1.128	1.231
14	2	11	RB008G08	a76couture0775.r#1	>gb|AAL30426.1|AF435089_1 (AF435089) beta-1.3-glucanase [Prunus persica]	43.707	31.000	1.410	37.069	35.000	1.059	1.235
14	2	12	ST004G02	a76couture0670.r#1	>gb|ZP_00092247.1| (NZ_AAAD01000091) hypothetical protein [Azotobacter vinelandii]	1899.369	1367.000	1.389	1999.669	1868.000	1.070	1.230
14	2	13	CT005D09	a76couture0571.r#1	>ref|NP_084748.1|| (NC_002693) hypothetical protein [Oenothera elata subsp. hookeri]	156.095	202.000	0.773	216.236	223.000	0.970	0.871
14	2	14	RT094H03	a76couture0896.r#1	>ref|NP_190758.1|| (NM_115049) sulfate transporter ATST1; protein id: At3g51895.1	12.488	14.000	0.892	44.277	33.000	1.342	1.117
14	2	15	RT074E10	a76couture0770.r#1	>dbj|BAC16095.1| (AP004382) contains EST AU082117(E11611)~unknown protein [Oryza	18.731	28.000	0.669	33.980	34.000	0.999	0.834
14	3	1	ST004F01	a76couture0665.r#1	>gb|AAF08159.1| (AF130203) NADH dehydrogenase subunit F [Hedera helix]	2.498	13.000	0.192	4.119	15.000	0.275	0.233
14	3	2	CT005B05	a76couture0566.r#1	------	51.199	62.000	0.826	41.188	57.000	0.723	0.774
14	3	3	TT284H01	a76couture0891.r#1	>ref|NP_564310.1|| (NM_102617) syntaxin SYP6 family; protein id: At1g28490.1	937.821	932.000	1.006	1105.893	973.000	1.137	1.071
14	3	4	RT074C07	a76couture0765.r#1	>ref|NP_191262.1|| (NM_115562) strictosidine synthase-related; protein id: At3g57030.1	876.632	785.000	1.117	597.224	685.000	0.872	0.994
14	3	5	ST004D11	a76couture0661.r#1	------	52.448	46.000	1.140	8.238	12.000	0.686	0.913
14	3	6	CT005A10	a76couture0562.r#1	------	88.662	78.000	1.137	53.544	64.000	0.837	0.987
14	3	7	RT094A04	a76couture0884.r#1	>pir||T07172 subtilisin-like proteinase (EC 3.4.21.-) 2 - tomato	73.677	53.000	1.390	46.336	47.000	0.986	1.188
14	3	8	RT073C06	a76couture0760.r#1	>ref|NP_568660.1|| (NM_123994) RRM-containing protein; protein id: At5g46250.1	4454.340	2895.000	1.539	1224.308	1172.000	1.045	1.292
14	3	9	ST004B12	a76couture0657.r#1	>ref|NP_196000.1|| (NM_120461) putative protein; protein id: At5g03800.1 [Arabidopsis	753.004	488.000	1.543	519.996	409.000	1.271	1.407
14	3	10	CT004G09	a76couture0558.r#1	>sp|Q99090|CPR2_PETCR Light-inducible protein CPRF-2 >gi|1806261|emb|CAA41453.1| (X58577)	76.175	64.000	1.190	43.247	40.000	1.081	1.136
14	3	11	RT093D12	a76couture0878.r#1	------		8.000	0.000				
14	3	12	RT072G06	a76couture0754.r#1	>emb|CAB63803.1| (AJ251868) heat shock factor 7 [Arabidopsis thaliana]	12.488	12.000	1.041	11.327	7.000	1.618	1.329
14	3	13	ST004A05	a76couture0653.r#1	>sp|P13983|EXTN_TOBAC Extensin precursor (Cell wall hydroxyproline-rich glycoprotein)	1442.322	965.000	1.495	754.767	501.000	1.507	1.501
14	3	14	CT004F02	a76couture0553.r#1	>ref|NP_568038.1|| (NM_119988) putative protein; protein id: At4g38260.1. supported by	7.493	10.000	0.749	11.327	13.000	0.871	0.810
14	3	15	RT092F09	a76couture0872.r#1	>sp|P10357|V70K_TYMV 69 KD PROTEIN >gi|94380|pir||S01955 hypothetical protein. 69K -	57.443	60.000	0.957	72.079	63.000	1.144	1.051
14	4	1	RT071E08	a76couture0749.r#1	>ref|NP_197221.1|| (NM_121725) putative protein; protein id: At5g17190.1. supported by	1491.024	1513.000	0.985	943.201	1095.000	0.861	0.923
14	4	2	ST003H06	a76couture0649.r#1	>gb|AAG26110.1| (AF123777) ribosomal protein S7 [Dioscorea bulbifera]	1067.693	1348.000	0.792	945.261	1337.000	0.707	0.750
14	4	3	CT004D02	a76couture0547.r#1	>pir||T02996 N-ethylmaleimide sensitive fusion protein NSF - common tobacco	187.315	163.000	1.149	186.375	181.000	1.030	1.089
14	4	4	RT044H08	a76couture1355.r#1	>emb|CAA74966.1| (Y14616) Importin alpha-like protein [Arabidopsis thaliana]	1075.185	838.000	1.283	784.628	657.000	1.194	1.239
14	4	5	GT202C11	a76couture1231.r#1	>ref|NP_200876.1|| (NM_125461) putative protein; protein id: At5g60680.1. supported by	1133.877	986.000	1.150	1225.338	1170.000	1.047	1.099
14	4	6	GB006D10	a76couture1108.r#1	>ref|NP_567832.1|| (NM_119119) Expressed protein; protein id: At4g29735.1. supported	689.317	415.000	1.661	404.670	344.000	1.176	1.419
14	4	7	RT083H05	a76couture0998#1	>ref|NP_198395.1|| (NM_122936) disease resistance protein (CC-NBS-LRR class). putative;	49.951	43.000	1.162	43.247	42.000	1.030	1.096
14	4	8	RT044E12	a76couture1351.r#1	>gb|AAF79338.1|AC002304_31 (AC002304) F14J16.10 [Arabidopsis thaliana]	1215.047	853.000	1.424	836.113	733.000	1.141	1.283

14	4	9	GT201D07	a76couture1221.r#1	>ref|NP_195035.2|| (NM_119463) aminopeptidase- like protein; protein id: At4g33090.1	5991.568	4607.000	1.301	5204.083	5044.000	1.032	1.166
14	4	10	GB005D09	a76couture1104.r#1	>ref|NP_187494.1|| (NM_111716) unknown protein; protein id: At3g08820.1 [Arabidopsis	54.946	34.000	1.616	33.980	25.000	1.359	1.488
14	4	11	RT083G01	a76couture0996#1	------	131.120	101.000	1.298	121.504	100.000	1.215	1.257
14	4	12	RT043D09	a76couture1347.r#1	>emb|CAA68993.1| (Y07721) glutathione S-transferase [Petunia x hybrida]	1713.304	1140.000	1.503	780.509	636.000	1.227	1.365
14	4	13	GT194F07	a76couture1216.r#1	>ref|NP_567871.1|| (NM_119278) unknown protein; protein id: At4g31290.1. supported by	182.319	64.000	2.849	154.454	62.000	2.491	2.670
14	4	14	GB003F08	a76couture1095.r#1	>pir||E71440 GTP-binding protein RAB2A - Arabidopsis thaliana	966.543	999.000	0.968	1501.297	1119.000	1.342	1.155
14	4	15	RT083D02	a76couture0991.r#1	>gb|AAM44275.1| (AF506518) receptor-like kinase RHG4 [Glycine max]	137.364	112.000	1.226	201.820	137.000	1.473	1.350
14	5	1	RT043B07	a76couture1343.r#1	>dbj|BAB03357.1| (AP002486) ESTs AU097577(C62003).C28669(C62003) correspond to a	203.548	210.000	0.969	170.930	180.000	0.950	0.959
14	5	2	GT201G05	a76couture1210.r#1	>ref|NP_565878.1|| (NM_129356) expressed protein; protein id: At2g37990.1. supported	43.707	47.000	0.930	23.683	32.000	0.740	0.835
14	5	3	GB001H09	a76couture1089.r#1	>ref|NP_564507.1|| (NM_103640) expressed protein; protein id: At1g47480.1. supported	231.021	156.000	1.481	149.306	144.000	1.037	1.259
14	5	4	RT083C06	a76couture0987.r#1	------	318.435	270.000	1.179	292.434	283.000	1.033	1.106
14	5	5	RT041D12	a76couture1339.r#1	>ref|NP_176896.1|| (NM_105396) glyoxalase I. putative (lactoylglutathione lyase);	673.084	481.000	1.399	530.293	458.000	1.158	1.279
14	5	6	GT194C04	a76couture1206.r#1	>emb|CAC09348.1| (AL442007) putative phosphoglycerate dehydrogenase [Oryza sativa]	874.134	575.000	1.520	668.273	568.000	1.177	1.348
14	5	7	GB001A11	a76couture1084.r#1	>ref|NP_200579.1|| (NM_125154) 101 kDa heat shock protein; HSP101-like protein; protein	0.000			7.208	6.000	1.201	1.201
14	5	8	RT083B08	a76couture0984.r#1	>dbj|BAB64773.1| (AP003282) hypothetical protein~similar to Arabidopsis thaliana	68.682	43.000	1.597	47.366	37.000	1.280	1.439
14	5	9	RT034C06	a76couture1334.r#1	>gb|AAM94348.1| (AY128951) pyruvate kinase [Glycine max]	4908.890	3328.000	1.475	6166.848	5070.000	1.216	1.346
14	5	10	GT193F02	a76couture1201.r#1	>pir||JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating)	724.283	685.000	1.057	628.114	665.000	0.945	1.001
14	5	11	TT284H07	a76couture1076.r#1	------	207.295	148.000	1.401	149.306	122.000	1.224	1.312
14	5	12	RT083A12	a76couture0981.r#1	>ref|NP_171839.1|| (NM_100222) putative 1-aminocyclopropane-1-carboxylate oxidase;	473.281	372.000	1.272	384.077	355.000	1.082	1.177
14	5	13	GT182H06	a76couture1798.r#1	------	46.204	54.000	0.856	27.802	43.000	0.647	0.751
14	5	14	GT171H03	a76couture1709.r#1	>ref|NP_631562.1|| (NC_003888) putative integral membrane protein [Streptomyces	26.224	20.000	1.311	18.535	24.000	0.772	1.042
14	5	15	GB006E10	a76couture1613.r#1	>gb|AAM63342.1| (AY086137) heat shock protein. putative [Arabidopsis thaliana]	282.221	275.000	1.026	417.027	352.000	1.185	1.105
14	6	1	TT273A01	a76couture1473.r#1	>dbj|BAB40710.1| (AB003038) BY-2 kinesin-like protein 10 [Nicotiana tabacum]	84.916	81.000	1.048	68.990	80.000	0.862	0.955
14	6	2	GT182D10	a76couture1795.r#1	>ref|NP_566473.2|| (NM_112261) subtilisin-like serine protease. putative; protein id:	1499.765	2651.000	0.566	1247.991	2686.000	0.465	0.515
14	6	3	GT171D12	a76couture1704.r#1	>gb|AAF78417.1|AC009273_23 (AC009273) Contains similarity to a retinal short-chain	58.692	92.000	0.638	33.980	54.000	0.629	0.634
14	6	4	GB006B11	a76couture1609.r#1	>ref|NP_175364.1|| (NM_103829) flavonol synthase. putative; protein id: At1g49390.1	432.072	285.000	1.516	207.999	161.000	1.292	1.404
14	6	5	TT273B12	a76couture1469.r#1	>ref|NP_564342.1|| (NM_102735) unknown protein; protein id: At1g29950.1 [Arabidopsis	1366.147	938.000	1.456	842.291	742.000	1.135	1.296
14	6	6	GT174H09	a76couture1791.r#1	------	173.578	132.000	1.315	121.504	123.000	0.988	1.151
14	6	7	GT171C05	a76couture1700.r#1	>gb|AAK98703.1|AC069158_15 (AC069158) Putative PAP-specific phosphatase [Oryza sativa] [Oryza	32.468	29.000	1.120	26.772	30.000	0.892	1.006
14	6	8	GB005H10	a76couture1605.r#1	>ref|NP_566418.1|| (NM_112066) expressed protein; protein id: At3g12300.1. supported	118.633	100.000	1.186	108.118	101.000	1.070	1.128
14	6	9	TT264G01	a76couture1464.r#1	>ref|NP_172172.2|| (NM_100564) unknown protein; protein id: At1g06890.1. supported by	769.238	572.000	1.345	588.986	507.000	1.162	1.253
14	6	10	GT181B04	a76couture1786.r#1	>ref|NP_194113.1|| (NM_118513) polygalacturonase. putative; protein id: At4g23820.1	982.777	970.000	1.013	952.469	1020.000	0.934	0.973
14	6	11	GT162H04	a76couture1696.r#1	>emb|CAD18921.1| (AJ421780) RNA-binding protein precursor [Persea americana]	1765.752	1215.000	1.453	1561.019	1202.000	1.299	1.376
14	6	12	GB005H02	a76couture1601.r#1	>ref|NP_565648.1|| (NM_128294) expressed protein; protein id: At2g27350.1. supported	1454.810	1245.000	1.169	1238.724	1251.000	0.990	1.079
14	6	13	TT272A06	a76couture1460.r#1	>ref|NP_195483.1|| (NM_119931) expressed protein; protein id: At4g37680.1. supported	369.634	270.000	1.369	323.324	272.000	1.189	1.279
14	6	14	GT174G03	a76couture1782.r#1	------	1071.439	756.000	1.417	850.529	735.000	1.157	1.287
14	6	15	GT161H06	a76couture1690.r#1	------	47.453	51.000	0.930	52.514	41.000	1.281	1.106
14	7	1	GB005C01	a76couture1597.r#1	>emb|CAB85635.1| (AJ237995) putative ripening-related P-450 enzyme [Vitis vinifera]	11.239	14.000	0.803	6.178	14.000	0.441	0.622
14	7	2	TT264E09	a76couture1456.r#1	>ref|NP_200424.1|| (NM_124995) putative protein; protein id: At5g56130.1. supported by	182.319	161.000	1.132	162.692	170.000	0.957	1.045
14	7	3	GT174E06	a76couture1778.r#1	>ref|NP_189431.2|| (NM_113709) DegP protease; protein id: At3g27925.1 [Arabidopsis	98.652	82.000	1.203	79.287	96.000	0.826	1.014
14	7	4	Arabidopsis Control Oligonucleotide	3ara7		131.120	92.000	1.425	53.544	62.000	0.864	1.144
14	7	5	GB005A09	a76couture1594.r#1	>pir||T07079 leucine-rich repeat protein LRP - tomato	4544.251	2831.000	1.605	2832.693	2284.000	1.240	1.423
14	7	6	TT263G04	a76couture1451.r#1	>ref|NP_564085.1|| (NM_101804) Expressed protein; protein id: At1g19480.1. supported	541.963	349.000	1.553	384.077	322.000	1.193	1.373
14	7	7	RT042F07	a76couture2205.r#1	>pir||T10055 probable 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41)	26.224	25.000	1.049	19.564	23.000	0.851	0.950
14	7	8	RT024E02	a76couture2105.r#1	------	528.227	418.000	1.264	397.463	369.000	1.077	1.170
14	7	9	RT021D04	a76couture2012#1	------	1093.917	813.000	1.346	830.965	759.000	1.095	1.220
14	7	10	RB003A01	a76couture1921.r#1	>gb|AAM63137.1| (AY085925) TINY-like protein [Arabidopsis thaliana]	39.960	25.000	1.598	44.277	26.000	1.703	1.651
14	7	11	RT041H05	a76couture2200.r#1	>ref|NP_193444.1|| (NM_117815) hypothetical protein; protein id: At4g17110.1		9.000	0.000				
14	7	12	RT023F09	a76couture2100.r#1	>ref|NP_566241.1|| (NM_111360) DNA-damage-repair/toleration protein DRT102; protein	1076.434	768.000	1.402	1553.811	1397.000	1.112	1.257
14	7	13	RT021B11	a76couture2007.r#1	>ref|NP_072983.1|| (NC_000908) conserved hypothetical protein [Mycoplasma genitalium]	12.488	8.000	1.561	21.624	22.000	0.983	1.272
14	7	14	RB000A83	a76couture1915#1	>pir||S68805 pectin acetylesterase (EC 3.1.1.-) precursor - mung bean	1028.981	926.000	1.111	808.311	852.000	0.949	1.030
14	7	15	RT041B03	a76couture2196.r#1	>ref|XP_127033.1|| (XM_127033) RIKEN cDNA 2610027O18 [Mus musculus]	84.916	83.000	1.023	125.623	112.000	1.122	1.072
14	8	1	RT024F03	a76couture2094.r#1	>ref|NP_563680.1|| (NM_100207) expressed protein; protein id: At1g03250.1. supported	202.300	180.000	1.124	166.811	173.000	0.964	1.044
14	8	2	RT021B04	a76couture2004#1	>ref|NP_179895.1|| (NM_127878) hypothetical protein; protein id: At2g23140.1	77.423	64.000	1.210	51.485	51.000	1.010	1.110
14	8	3	RB001F06	a76couture1910.r#1	>gb|AAK68825.1| (AY042885) putative protein [Arabidopsis thaliana]	1145.116	1213.000	0.944	947.320	1143.000	0.829	0.886
14	8	4	RT033C11	a76couture2192.r#1	>ref|NP_445658.1|| (NC_002179) conserved hypothetical protein [Chlamydophila	1361.152	970.000	1.403	164.751	195.000	0.845	1.124
14	8	5	RT024C12	a76couture2090.r#1	>ref|NP_180436.1|| (NM_128429) legumin-like protein; protein id: At2g28680.1	3495.289	3363.000	1.039	1253.140	1642.000	0.763	0.901
14	8	6	RT021A04	a76couture2001#1	>ref|NP_182075.1|| (NM_130113) cytochrome p450. putative; protein id: At2g45510.1	41.209	28.000	1.472	27.802	23.000	1.209	1.340
14	8	7	RB000A75	a76couture1893.r#1	>ref|NP_199062.1|| (NM_123612) brain and reproductive organ-expressed protein-like;	131.120	87.000	1.507	85.465	75.000	1.140	1.323
14	8	8	RT034H02	a76couture2188.r#1	------	177.324	151.000	1.174	129.742	135.000	0.961	1.068
14	8	9	RT024A09	a76couture2085.r#1	>ref|NP_188898.1|| (NM_113158) unknown protein; protein id: At3g22590.1. supported by	1050.210	797.000	1.318	743.440	690.000	1.077	1.198
14	8	10	RT012D08	a76couture1996.r#1	------	22.478	18.000	1.249	13.386	15.000	0.892	1.071
14	8	11	GT204F06	a76couture1884.r#1	>gb|AAF66603.1|AF141942_1 (AF141942) phytochrome C [Oryza sativa] [Oryza sativa (indica	58.692	47.000	1.249	50.455	53.000	0.952	1.100
14	8	12	RT034F05	a76couture2183.r#1	>ref|NP_187413.1|| (NM_111635) hypothetical protein; protein id: At3g07565.1	112.389	74.000	1.519	97.821	78.000	1.254	1.386
14	8	13	RT023H09	a76couture2081.r#1	------	1358.655	946.000	1.436	1066.765	922.000	1.157	1.297
14	8	14	RB008E09	a76couture1992.r#1	------	17.483	22.000	0.795	11.327	14.000	0.809	0.802
14	8	15	GT204A07	a76couture1880.r#1	>dbj|BAB89236.1| (AP004231) putative LRR [Oryza sativa (japonica cultivar-group)]	128.623	75.000	1.715	110.177	74.000	1.489	1.602
14	9	1	PT001E07	a76couture2628.r#1	------	13.736	11.000	1.249	11.327	13.000	0.871	1.060

14	9	2	TT261F11	a76couture2508.r#1	>gb|AAL91256.1| (AY090351) At1g15070/F9L1_1 [Arabidopsis thaliana]	19.980	26.000	0.768	14.416	22.000	0.655	0.712
14	9	3	TB003C01	a76couture2398.r#1	>ref|NP_172353.1|| (NM_100750) unknown protein; protein id: At1g08760.1. supported by	88.662	116.000	0.764	61.782	94.000	0.657	0.711
14	9	4	RT054C12	a76couture2296.r#1	>pir||T40204 probable transcription factor tfIIh - fission yeast	9.990	18.000	0.555	5.148	13.000	0.396	0.476
14	9	5	PT003B05	a76couture2624.r#1	------	2617.408	1648.000	1.588	1628.979	1380.000	1.180	1.384
14	9	6	TT261A05	a76couture2504.r#1	------	609.397	402.000	1.516	404.670	352.000	1.150	1.333
14	9	7	TB003A01	a76couture2394.r#1	>ref|NP_564163.1|| (NM_102077) Expressed protein; protein id: At1g22270.1. supported	251.001	169.000	1.485	156.514	129.000	1.213	1.349
14	9	8	RT053G12	a76couture2292.r#1	>ref|NP_196699.1|| (NM_121176) 1-D-deoxyxylulose 5-phosphate synthase - like protein;	193.558	140.000	1.383	134.890	119.000	1.134	1.258
14	9	9	PT007A06	a76couture2619.r#1	>dbj|BAB02414.1| (AB024033) chloroplast nucleoid DNA binding protein-like	855.403	639.000	1.339	643.560	606.000	1.062	1.200
14	9	10	TT254F05	a76couture2500.r#1	>ref|NP_567619.1|| (NM_118229) Expressed protein; protein id: At4g21105.1. supported	1131.380	901.000	1.256	927.756	880.000	1.054	1.155
14	9	11	TB002C02	a76couture2390.r#1	>ref|NP_187278.2|| (NM_111502) protein phosphatase 2C (PP2C); protein id: At3g06270.1	77.423	65.000	1.191	67.960	66.000	1.030	1.110
14	9	12	RT053C07	a76couture2288.r#1	>gb|AAK00441.1|AC060755_11 (AC060755) unknown protein [Oryza sativa]	6049.011	5459.000	1.108	4903.412	4938.000	0.993	1.051
14	9	13	PT003D03	a76couture2615.r#1	>ref|NP_187257.1|| (NM_111481) unknown protein; protein id: At3g06060.1 [Arabidopsis	278.474	210.000	1.326	233.741	217.000	1.077	1.202
14	9	14	TT254A10	a76couture2495.r#1	>gb|AAD24540.1|AF113545_1 (AF113545) vacuole-associated annexin VCaB42 [Nicotiana tabacum]	5159.891	5632.000	0.916	3760.449	4871.000	0.772	0.844
14	9	15	TB001F02	a76couture2384.r#1	>ref|NP_190069.1|| (NM_114352) putative protein; protein id: At3g44830.1 [Arabidopsis	1117.643	1189.000	0.940	831.994	1042.000	0.798	0.869
14	10	1	RT052H08	a76couture2284.r#1	>gb|AAM76761.1| (AY102556) hypothetical protein [Arabidopsis thaliana]	51.199	54.000	0.948	46.336	62.000	0.747	0.848
14	10	2	RT064G12	a76couture2610.r#1	>ref|NP_197669.1|| (NM_122183) alpha-adaptin; protein id: At5g22770.1. supported by	399.604	472.000	0.847	230.652	307.000	0.751	0.799
14	10	3	TT251H09	a76couture2491#1	>dbj|BAB61258.1| (AP003315) contains ESTs C71872(E0508).C72452(E1641)~similar to	8.741	12.000	0.728	5.148	8.000	0.644	0.686
14	10	4	TB001A07	a76couture2379.r#1	>ref|NP_187161.1|| (NM_111382) hypothetical protein; protein id: At3g05100.1	6.244	12.000	0.520	7.208	11.000	0.655	0.588
14	10	5	RT052E11	a76couture2280.r#1	>emb|CAB72441.1| (AJ271889) alternative oxidase [Populus tremula x Populus	223.529	73.000	3.062	150.336	62.000	2.425	2.743
14	10	6	RT064D11	a76couture2606.r#1	>ref|NP_192750.1|| (NM_117080) sucrose-phosphate synthase - like protein; protein id:	88.662	87.000	1.019	74.138	92.000	0.806	0.912
14	10	7	TT251H02	a76couture2487#1	>ref|NP_195692.1|| (NM_120145) hypothetical protein; protein id: At4g39820.1	392.112	298.000	1.316	321.265	315.000	1.020	1.168
14	10	8	RT063F01	a76couture2374.r#1	------	1046.464	730.000	1.434	801.103	699.000	1.146	1.290
14	10	9	RT052C05	a76couture2276.r#1	>gb|AAL18931.1|AF429985_1 (AF429985) arabinosidase ARA-1 [Lycopersicon esculentum]	889.120	864.000	1.029	612.669	689.000	0.889	0.959
14	10	10	FT7F4AP92	a76couture3141.r#1	>emb|CAB56294.1| (AJ249397) putative protein translation factor [Phleum pratense]	2485.039	1188.000	2.092	1823.591	1100.000	1.658	1.875
14	10	11	TT263F07	a76couture2993.r#1	>gb|AAH06040.1| (BC006040) Unknown (protein for MGC:7642) [Mus musculus]	1449.814	871.000	1.665	1101.775	792.000	1.391	1.528
14	10	12	GT171C07	a76couture2853.r#1	>ref|NP_198236.1|| (NM_122767) epimerase/dehydratase - like protein; protein id:	3595.190	4113.000	0.874	3013.920	4057.000	0.743	0.808
14	10	13	PT012F11	a76couture2733.r#1	------	143.608	120.000	1.197	113.267	114.000	0.994	1.095
14	10	14	B1REVERSE	a76couture3138.r#1	------	62.438	42.000	1.487	50.455	43.000	1.173	1.330
14	10	15	GT182G06	a76couture2989.r#1	>ref|NP_197288.1|| (NM_121792) potassium-dependent sodium-calcium exchanger - like	400.853	241.000	1.663	328.473	242.000	1.357	1.510
14	11	1	CT003C11	a76couture2844.r#1	>gb|AAK43709.1|AF358665_1 (AF358665) ribosomal protein L32 [Mercurialis annua]	1136.375	775.000	1.466	812.430	693.000	1.172	1.319
14	11	2	PT001H06	a76couture2728.r#1	>ref|NP_565722.1|| (NM_128695) salt tolerance-like protein; protein id: At2g31380.1	78.672	60.000	1.311	39.128	29.000	1.349	1.330
14	11	3	CT001E04	a76couture3133.r#1	------	31.219	30.000	1.041	20.594	22.000	0.936	0.988
14	11	4	RT052H12	a76couture2984.r#1	>ref|NP_187207.1|| (NM_111429) putative 60S ribosomal protein L22; protein id:	2169.102	1926.000	1.126	939.083	905.000	1.038	1.082
14	11	5	TT283E06	a76couture2833.r#1	>pir||T12440 mipC protein - common ice plant >gi|1657948|gb|AAB18227.1| (U73466)	7773.553	11215.000	0.693	2515.547	4267.000	0.590	0.641
14	11	6	PT012E08	a76couture2724.r#1	>ref|NP_564153.1|| (NM_102036) expressed protein; protein id: At1g21880.1. supported	157.344	132.000	1.192	96.791	119.000	0.813	1.003
14	11	7	RT084H07	a76couture3127.r#1	>sp|P46259|TBA1_PEA TUBULIN ALPHA-1 CHAIN >gi|2119270|pir||S60233 tubulin alpha-1 chain	11870.746	11058.000	1.073	6533.420	7558.000	0.864	0.969
14	11	8	TT283E11	a76couture2977.r#1	>dbj|BAA34919.1| (AB012716) heat shock protein 70 cognate [Salix gilgiana]	11772.094	8399.000	1.402	7504.423	7453.000	1.007	1.204
14	11	9	RT092F06	a76couture2827.r#1	>gb|AAA34124.1| (M74156) pentameric polyubiquitin [Nicotiana sylvestris]	4493.051	3462.000	1.298	1495.118	1522.000	0.982	1.140
14	11	10	PT009B01	a76couture2719.r#1	>ref|NP_177125.1|| (NM_105635) E3 ubiquitin ligase SCF complex subunit Cullin	1547.218	1125.000	1.375	1256.229	1151.000	1.091	1.233
14	11	11	ST005H12	a76couture3122.r#1	>emb|CAD23919.1| (AJ429656) ATP synthase epsilon subunit [Pterostyrax hispidus]	2381.392	1376.000	1.731	1908.026	1335.000	1.429	1.580
14	11	12	PT008G05	a76couture2969.r#1	>gb|AAK70908.1|AC087551_7 (AC087551) cytoplasmic ribosomal protein L18 [Oryza sativa]	1418.595	950.000	1.493	1125.458	907.000	1.241	1.367
14	11	13	PT012A12	a76couture2820.r#1	>ref|NP_567241.1|| (NM_116484) putative glycosyltransferase; protein id: At4g02500.1	101.150	85.000	1.190	83.405	81.000	1.030	1.110
14	11	14	PT011F09	a76couture2715.r#1	>gb|AAM91894.1| (AC051632) hypothetical protein [Oryza sativa (japonica	429.575	359.000	1.197	373.780	375.000	0.997	1.097
14	11	15	ST002A07	a76couture3118.r#1	>sp|O24030|PSA7_LYCES Proteasome subunit alpha type 7 (20S proteasome alpha subunit D)	2010.509	2213.000	0.908	1262.407	1213.000	1.041	0.975
14	12	1	GT201G10	a76couture2964.r#1	>gb|AAG39002.1|AF213399_1 (AF213399) SLT1 protein [Nicotiana tabacum]	578.178	498.000	1.161	499.402	563.000	0.887	1.024
14	12	2	PT006A05	a76couture2816.r#1	>ref|NP_566335.1|| (NM_111719) expressed protein; protein id: At3g08850.1. supported by	670.586	616.000	1.089	459.244	470.000	0.977	1.033
14	12	3	PT010D08	a76couture2710.r#1	>ref|NP_566384.1|| (NM_111933) expressed protein; protein id: At3g10960.1. supported	1127.633	908.000	1.242	702.253	672.000	1.045	1.143
14	12	4	BM436593 RT044D01	couture_a76.449.c1.r#1	>ref|NP_179871.1|| (NM_127851) unknown protein; protein id: At2g22860.1. supported by	374.629	177.000	2.117	291.404	163.000	1.788	1.952
14	12	5	BG273970 GB000A08 BM438026	couture_a76.356.c1#1	>ref|NP_199009.1|| (NM_123559) GTPase activator protein of Rab-like small GTPases-like	1911.857	1899.000	1.007	796.985	720.000	1.107	1.057
14	12	6	BM437090 RB004E12	couture_a76.270.c1.r#1	>ref|NP_197312.1|| (NM_121816) eukaryotic cap-binding protein (gb|AAC17220.1); protein	279.723	259.000	1.080	271.840	257.000	1.058	1.069
14	12	7	BE846398 BM437521 RT093F10 RB007F07	couture_a76.181.c1.r#1	>emb|CAC84547.1| (AJ311778) dicarboxylate/tricarboxylate carrier [Nicotiana tabacum]	4662.883	3925.000	1.188	2908.891	3589.000	0.811	0.999
14	12	8	BM436872 RT034F11	couture_a76.443.c1#1	>ref|NP_181174.1|| (NM_129190) hypothetical protein; protein id: At2g36330.1	794.214	669.000	1.187	690.926	753.000	0.918	1.052
14	12	9	BG273962 GB000A17	couture_a76.353.c1.r#1	>gb|AAM91095.1| (AY128287) At1g68060/T23K23_9 [Arabidopsis thaliana]	62.438	61.000	1.024	50.455	63.000	0.801	0.912
14	12	10	BG273714 BM437557 BM436603 BM436344 RB0	couture_a76.266.c1.r#1	>ref|NP_565834.1|| (NM_129165) E2. ubiquitin-conjugating enzyme. putative; protein id:	9647.947	6477.000	1.490	7708.303	6779.000	1.137	1.313
14	12	11	BM436774 RT092C06	couture_a76.179.c1.r#1	>gb|AAF63119.1|AC009526_4 (AC009526) Hypothetical protein [Arabidopsis thaliana]	97.404	66.000	1.476	89.584	85.000	1.054	1.265
14	12	12	BM437902 BG273784 RB000A14	couture_a76.44.c1#1	>ref|NP_194094.1|| (NM_118494) putative protein; protein id: At4g23630.1. supported by	9580.514	7813.000	1.226	7942.044	7472.000	1.063	1.145
14	12	13	BG273957 GB000A22	couture_a76.351.c1#1	>dbj|BAB02486.1| (AB025629) DNA topoisomerase VI subunit B-like protein [Arabidopsis	54.946	54.000	1.018	40.158	46.000	0.873	0.945
14	12	14	GB001g03 GT204C04	couture_a76.262.c1#1	>emb|CAB61759.1| (AJ251302) putative aminopropyltransferase [Oryza sativa (japonica	320.932	308.000	1.042	302.731	287.000	1.055	1.048
14	12	15	BG273723 RB000A79 RT084H09	couture_a76.176.c1.r#1	>sp|O22060|SPS1_CITUN SUCROSE-PHOSPHATE SYNTHASE 1 (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE	1482.282	1347.000	1.100	1624.860	1497.000	1.085	1.093
14	13	1	BM436484 RT031A01	couture_a76.435.c1.r#1	>ref|NP_187919.1|| (NM_112151) 30S ribosomal protein S10. putative; protein id:	373.380	348.000	1.073	328.473	394.000	0.834	0.953
14	13	2	BG273952 GB000A28	couture_a76.348.c1.r#1	>ref|NP_199169.1|| (NM_123722) unknown protein; protein id: At5g43560.1. supported by	73.677	73.000	1.009	122.534	156.000	0.785	0.897
14	13	3	GB003b10 GT204E02	couture_a76.259.c1.r#1	>ref|NP_180576.1|| (NM_128570) putative glucosyltransferase; protein id: At2g30150.1	73.677	76.000	0.969	55.604	72.000	0.772	0.871
14	13	4	RB006F10 RT083E08	couture_a76.170.c1#1	>gb|AAL36933.1|AF213481_1 (AF213481) gamma-tocopherol methyltransferase [Perilla frutescens]	676.830	665.000	1.018	671.362	733.000	0.916	0.967
14	13	5	RT023G12 BM436426	couture_a76.430.c1#1	>ref|NP_193652.1|| (NM_118036) 9-cis-epoxycarotenoid dioxygenase (neoxanthin cleavage	84.916	87.000	0.976	76.197	84.000	0.907	0.942
14	13	6	BG273947 GB000A36	couture_a76.346.c1#1	>ref|NP_568616.1|| (NM_123657) putative protein; protein id: At5g42920.1. supported by	383.370	321.000	1.194	214.177	230.000	0.931	1.063
14	13	7	BM437858 BM437540 GT203D02	couture_a76.255.c1#1	>ref|NP_200275.1|| (NM_124845) histone H2A (gb|AAF64418.1); protein id: At5g54640.1	885.373	816.000	1.085	1200.625	1179.000	1.018	1.052
14	13	8	BM437472 BM436889 TB001d09 RT081A05	couture_a76.167.c1.r#1	>sp|P17340|PLAS_LYCES Plastocyanin. chloroplast precursor >gi|100238|pir||S05303	1513.501	880.000	1.720	1289.179	1135.000	1.136	1.428
14	13	9	BM436286 RT021C03	couture_a76.425.c1#1	>ref|NP_201242.1|| (NM_125833) beta-ureidopropionase; protein id: At5g64370.1	104.896	75.000	1.399	124.593	99.000	1.259	1.329

14	13	10	BG273930 GB000A55	couture_a76.342.c1#1	>ref|NP_566429.1|| (NM_112098) expressed protein; protein id: At3g12630.1 [Arabidopsis	807.950	511.000	1.581	640.471	542.000	1.182	1.381
14	13	11	Arabidopsis Control Oligonucleotide	3ara7		13.736	7.000	1.962	13.386	16.000	0.837	1.399
14	13	12	BG273877 RT062D02	couture_a76.163.c1.r#1	>sp|O24076|GBLP_MEDSA GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN	4533.012	3053.000	1.485	3491.699	2756.000	1.267	1.376
14	13	13	VVUFGT G2564111 AF000371	couture_a76.sd.30.c1#	>gb|AAB81682.1| (AF000371) UDP glucose:flavonoid 3-o-glucosyltransferase [Vitis	468.286	378.000	1.239	429.383	367.000	1.170	1.204
14	13	14	BM436475 BM437909 RT063C12	couture_a76.61.c1.r#1	>gb|AAB97142.1| (U93166) cysteine protease [Prunus armeniaca]	11448.664	11783.000	0.972	11090.854	12075.000	0.918	0.945
14	13	15	BG273827 TB000A66	couture_a76.490.c1#1	>dbj|BAB08527.1| (AB009052) emb|CAB87783.1~gene_id:MNF13.9~similar to unknown	181.071	164.000	1.104	270.810	236.000	1.148	1.126
14	14	1	TB005h10 TT274B02 AF236126	couture_a76.sd.3.c1#1	>gb|AAL83719.1|AF236126_1 (AF236126) PEP carboxylase [Vitis vinifera]	762.995	900.000	0.848	767.123	971.000	0.790	0.819
14	14	2	GB006c05 RT054C07	couture_a76.628.c1#1	>ref|NP_196848.1|| (NM_121347) ubiquinol--cytochrome-c reductase - like protein;	3103.177	2923.000	1.062	2678.239	2970.000	0.902	0.982
14	14	3	BM436462 BM436302 BM437468 BM436724 BM	couture_a76.532.c1.r#1	gb|AAL32038.1|AF439279_1 (AF439279) early light-induced protein-... 191 4e-048	3199.332	2167.000	1.476	5068.163	3427.000	1.479	1.478
14	14	4	RT072B04 VVI237994	couture_a76.sd.48.c1#	>emb|CAB85634.1| (AJ237994) putative ripening-related protein [Vitis vinifera]	30467.333	22632.000	1.346	21237.477	19267.000	1.102	1.224
14	14	5	RB003A08 TT263A04	couture_a76.627.c1.r#1	>gb|AAF78757.1|AF271660_1 (AF271660) putative aquaporin TIP3 [Vitis berlandieri x Vitis	2500.025	2934.000	0.852	3299.145	3417.000	0.966	0.909
14	14	6	BG273726 RB000A76	couture_a76.50.c1.r#1	>gb|AAF68624.1|AF254072_1 (AF254072) histone deacetylase 2 isoform b [Zea mays]	2413.860	1705.000	1.416	1391.119	1353.000	1.028	1.222
14	14	7	G499023E VVLSTSYM S63227 AF274281 S6322	couture_a76.sd.17.c1#	>emb|CAA54221.1| (X76892) Stilbene synthase [Vitis vinifera]	2156.615	261.000	8.263	1094.567	180.000	6.081	7.172
14	14	8	TB003f11 TB006F03	couture_a76.599.c1.r#1	>gb|AAL09733.1| (AY057492) At1g76160/T23E18_10 [Arabidopsis thaliana]	869.139	878.000	0.990	306.849	413.000	0.743	0.866
14	14	9	BE846395 BM436556 RT094E08	couture_a76.5.c1.r#1	>gb|AAK25768.1|AF336307_1 (AF336307) auxin-repressed protein like-protein [Malus x domestica]	805.452	603.000	1.336	1682.523	1501.000	1.121	1.228
14	14	10	RT072F01 RT041D07	couture_a76.616.c1.r#1	------	58.692	58.000	1.012	55.604	62.000	0.897	0.954
14	14	11	BM437228 PT011E12	couture_a76.521.c1.r#1	>ref|NP_565417.1|| (NM_127304) expressed protein; protein id: At2g17500.1. supported	2678.598	2431.000	1.102	2511.428	1985.000	1.265	1.184
14	14	12	AF196485 BM437459 RT082F04	couture_a76.sd.38.c1.r	>pir||JC2511 beta-tubulin R2242 - rice	1384.879	1432.000	0.967	1603.236	1499.000	1.070	1.018
14	14	13	RT072F01 RT041D07	couture_a76.616.c1#1	------	1955.564	1928.000	1.014	2125.292	1928.000	1.102	1.058
14	14	14	GT174G10 RT082E12	couture_a76.589.c1#1	>ref|NP_567980.1|| (NM_119689) putative protein; protein id: At4g35230.1. supported by	483.271	424.000	1.140	522.056	442.000	1.181	1.160
14	14	15	BM437217 BG273842 TB000A50	couture_a76.494.c1#1	------	2220.302	1134.000	1.958	2701.922	1345.000	2.009	1.983
15	1	1	CM003F09	a76couture0445.r#1	>ref|NP_567820.1|| (NM_119050) Expressed protein; protein id: At4g29060.1. supported by	151.100	130.000	1.162	196.672	155.000	1.269	1.216
15	1	2	TB001A11	a76couture0346.r#1	>sp|Q9SQL5|SODC_ANACO Superoxide dismutase [Cu-Zn] >gi|6273423|emb|CAB60191.1| (AJ250667)	9448.145	10117.000	0.934	11017.745	10773.000	1.023	0.978
15	1	3	RT054G08	a76couture0214.r#1	>dbj|BAA83469.1| (AB008846) Csf-1 [Cucumis sativus]	932.826	650.000	1.435	1139.873	800.000	1.425	1.430
15	1	4	CM003A12	a76couture0063.r#1	>gb|AAM64870.1| (AY087320) putative microtubule-associated protein [Arabidopsis	2559.965	2324.000	1.102	3465.956	2901.000	1.195	1.148
15	1	5	CM003E09	a76couture0441.r#1	------	2428.845	1995.000	1.217	3063.345	2503.000	1.224	1.221
15	1	6	TT272D07	a76couture0339.r#1	>dbj|BAA76734.1| (AB024575) ethylene responsive element binding factor [Nicotiana	1258.754	1261.000	0.998	1720.622	1565.000	1.099	1.049
15	1	7	RT051A11	a76couture0209.r#1	>gb|AAF34800.1|AF227980_1 (AF227980) 60S ribosomal protein L35 [Euphorbia esula]	2699.827	2365.000	1.142	3841.795	2939.000	1.307	1.224
15	1	8	TF003A03C	a76couture0057.r#1	>pir||T47952 hypothetical protein F2A19.200 - Arabidopsis thaliana	668.089	738.000	0.905	1013.221	957.000	1.059	0.982
15	1	9	CM003B11	a76couture0437.r#1	------	88.662	76.000	1.167	134.890	108.000	1.249	1.208
15	1	10	TT262F07	a76couture0335.r#1	>sp|P35016|ENPL_CATRO Endoplasmin homolog precursor (GRP94 homolog) >gi|542022|pir||S39558	3600.185	3837.000	0.938	5263.805	4969.000	1.059	0.999
15	1	11	RT032B10	a76couture0203.r#1	>dbj|BAB84438.1| (AP003292) S-adenosylmethionine:2-demethylmenaquinone	6723.343	6054.000	1.111	9967.456	8134.000	1.225	1.168
15	1	12	G7801383 reverse complement 1038 bases	a76couture0049.r#1	>emb|CAB91554.1| (AJ277900) beta 1-3 glucanase [Vitis vinifera]	227.275	820.000	0.277	316.117	1056.000	0.299	0.288
15	1	13	CM003A01	a76couture0434.r#1	------	275.977	181.000	1.525	350.097	244.000	1.435	1.480
15	1	14	RT093A09	a76couture0326.r#1	>ref|NP_192861.1|| (NM_117193) putative protein; protein id: At4g11220.1. supported by	2102.918	1806.000	1.164	2653.526	2330.000	1.139	1.152
15	1	15	RB007E04	a76couture0198.r#1	>ref|NP_568900.1|| (NM_125304) elongin - like protein; protein id: At5g59140.1	1491.024	1335.000	1.117	2015.115	1714.000	1.176	1.146
15	2	1	88E3PROTE	a76couture0025.r#1	>pir||T05989 hypothetical protein F17M5.140 - Arabidopsis thaliana	730.527	609.000	1.200	924.667	693.000	1.334	1.267
15	2	2	CM002G12	a76couture0430.r#1	>ref|NP_174746.1|| (NM_103210) phosphate-induced (phi-1) protein. putative; protein	4169.622	2282.000	1.827	6114.334	2902.000	2.107	1.967
15	2	3	RT081G07	a76couture0322.r#1	>gb|AAF04915.1|AF011555_1 (AF011555) jasmonic acid 2 [Lycopersicon esculentum]	469.535	463.000	1.014	698.134	617.000	1.131	1.073
15	2	4	GT203G02	a76couture0191.r#1	>ref|NP_567875.1|| (NM_119291) putative zinc finger protein; protein id: At4g31420.1	1027.732	814.000	1.263	1262.407	944.000	1.337	1.300
15	2	5	PT012H03	a76couture0018.r#1	>ref|XP_156927.1|| (XM_156927) hypothetical protein XP_156927 [Mus musculus]	2461.313	1961.000	1.255	3146.750	2395.000	1.314	1.285
15	2	6	CM002F07	a76couture0426.r#1	>dbj|BAC16401.1| (AP003749) selenium-binding protein-like [Oryza sativa (japonica	16.234	16.000	1.015	23.683	20.000	1.184	1.099
15	2	7	TT263B09	a76couture0317.r#1	>ref|NP_179778.1|| (NM_127756) putative ATP synthase; protein id: At2g21870.1	790.467	912.000	0.867	1067.795	1111.000	0.961	0.914
15	2	8	RT061G01	a76couture0184.r#1	>ref|NP_178224.1|| (NM_126176) putative aldolase; protein id: At2g01140.1. supported	3018.262	3121.000	0.967	4268.089	4004.000	1.066	1.017
15	2	9	GT192C11	a76couture0013.r#1	>emb|CAA51821.1| (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]	2591.184	2207.000	1.174	3946.824	3044.000	1.297	1.235
15	2	10	RT092D06	a76couture0869.r#1	>gb|AAM63790.1| (AY086739) unknown [Arabidopsis thaliana]	504.500	489.000	1.032	703.282	596.000	1.180	1.106
15	2	11	RT072A08	a76couture0743.r#1	>gb|AAM63723.1| (AY086666) unknown [Arabidopsis thaliana]	37.463	48.000	0.780	59.722	67.000	0.891	0.836
15	2	12	ST003G06	a76couture0645.r#1	>ref|NP_198579.1|| (NM_123122) chromosome condensation protein -like; protein id:	7.493	13.000	0.576	11.327	15.000	0.755	0.666
15	2	13	CT003H06	a76couture0543.r#1	>gb|AAM63118.1| (AY085906) unknown [Arabidopsis thaliana]	989.021	848.000	1.166	1305.654	1077.000	1.212	1.189
15	2	14	RT091F03	a76couture0863.r#1	>ref|NP_172736.1|| (NM_101146) unknown protein; protein id: At1g12760.1 [Arabidopsis	57.443	69.000	0.833	89.584	102.000	0.878	0.855
15	2	15	ST007H09	a76couture0740.r#1	>ref|NP_196329.1|| (NM_120794) putative protein; protein id: At5g07120.1 [Arabidopsis	9.990	23.000	0.434	10.297	24.000	0.429	0.432
15	3	1	ST003E05	a76couture0641.r#1	------	13.736	29.000	0.474	11.327	27.000	0.420	0.447
15	3	2	CT003F05	a76couture0540#1	------	51.199	46.000	1.113	106.059	72.000	1.473	1.293
15	3	3	RT091A05	a76couture0858.r#1	>emb|CAA10285.1| (AJ131045) protein phosphatase [Cicer arietinum]	1091.419	1095.000	0.997	1584.702	1449.000	1.094	1.045
15	3	4	ST007F07	a76couture0735.r#1	>ref|NP_177175.2|| (NM_105686) hypothetical protein; protein id: At1g70180.1	31.219	35.000	0.892	45.307	50.000	0.906	0.899
15	3	5	ST003D03	a76couture0637.r#1	>dbj|BAA76348.1| (AB025102) protoporphyrinogen IX oxidase [Glycine max]	26.224	24.000	1.093	21.624	24.000	0.901	0.997
15	3	6	CT003C05	a76couture0536.r#1	>ref|NP_566216.1|| (NM_111260) auxin-regulated protein; protein id: At3g03890.1	23.727	31.000	0.765	33.980	38.000	0.894	0.830
15	3	7	RT091B08	a76couture0852.r#1	>sp|P09469|VATA_DAUCA Vacuolar ATP synthase catalytic subunit A (V-ATPase A subunit)	2808.469	3514.000	0.799	3856.211	4184.000	0.922	0.860
15	3	8	ST007E12	a76couture0730.r#1	------	32.468	27.000	1.203	65.901	46.000	1.433	1.318
15	3	9	ST003B03	a76couture0632.r#1	>ref|NP_173670.1|| (NM_102103) oligopeptide transporter. putative; protein id:	959.050	884.000	1.085	1403.475	1144.000	1.227	1.156
15	3	10	CT003A10	a76couture0533.r#1	>dbj|BAA92697.1| (AB039916) type 2A protein phosphatase-1 [Vicia faba]	1347.416	1305.000	1.033	2095.431	1740.000	1.204	1.118
15	3	11	RT082G07	a76couture0848.r#1	>ref|NP_186875.1|| (NM_111093) unknown protein; protein id: At3g02260.1 [Arabidopsis	633.123	466.000	1.359	943.201	614.000	1.536	1.447
15	3	12	ST007C05	a76couture0726.r#1	>sp|P38550|RPOD_TOBAC DNA-directed RNA polymerase beta" chain	213.539	127.000	1.681	263.602	149.000	1.769	1.725
15	3	13	ST002H08	a76couture0628.r#1	>ref|NP_196498.1|| (NM_120972) laccase (diphenol oxidase) family; protein id:	42.458	21.000	2.022	50.455	23.000	2.194	2.108
15	3	14	CT002H04	a76couture0529.r#1	>ref|NP_188127.1|| (NM_112371) zinc-binding dehydrogenase. putative; protein id:	156.095	111.000	1.406	202.850	138.000	1.470	1.438
15	3	15	RT082D07	a76couture0843.r#1	>dbj|BAB89512.1| (AP003242) hypothetical protein [Oryza sativa (japonica	2159.112	1497.000	1.442	2727.664	1884.000	1.448	1.445
15	4	1	ST007A12	a76couture0722.r#1	------	786.721	718.000	1.096	1071.913	929.000	1.154	1.125
15	4	2	CT006H04	a76couture0624.r#1	>ref|NP_193735.1|| (NM_118121) DAG-like protein; protein id: At4g20020.1 [Arabidopsis	94.906	78.000	1.217	136.950	90.000	1.522	1.369

15	4	3	CT002E08	a76couture0525.r#1	------	221.031	156.000	1.417	320.235	233.000	1.374	1.396
15	4	4	RT032C07	a76couture1328.r#1	>gb|AAG38521.1|AF283536_1 (AF283536) cystatin-like protein [Citrus x paradisi]	1851.916	1683.000	1.100	2470.240	2039.000	1.211	1.156
15	4	5	GT193A04	a76couture1196.r#1	>ref|NP_191906.1|| (NM_116212) serin carboxypeptidase - like protein; protein id:	2947.082	2406.000	1.225	3642.034	2821.000	1.291	1.258
15	4	6	RT094G07	a76couture1072.r#1	>pir||T09217 protein sam2B - spinach >gi|2253092|emb|CAA74590.1| (Y14198)	454.550	454.000	1.001	697.104	622.000	1.121	1.061
15	4	7	RT081H01	a76couture0976.r#1	>ref|NP_196504.1|| (NM_120979) putative subunit of TOC complex; protein id:	107.394	77.000	1.395	135.920	95.000	1.431	1.413
15	4	8	RT031B08	a76couture1324.r#1	>ref|NP_171656.1|| (NM_100031) expressed protein; protein id: At1g01490.1. supported	2718.558	2732.000	0.995	4035.378	3601.000	1.121	1.058
15	4	9	GT192G09	a76couture1191.r#1	>pir||S71237 probable peptidylprolyl isomerase (EC 5.2.1.8) FKBP15-1 -	1825.692	1899.000	0.961	2520.695	2384.000	1.057	1.009
15	4	10	RT094A07	a76couture1068.r#1	>gb|AAK68073.1|AF384969_1 (AF384969) somatic embryogenesis receptor-like kinase 2	703.054	767.000	0.917	985.419	1017.000	0.969	0.943
15	4	11	RT081D10	a76couture0971.r#1	>emb|CAA12646.1| (AJ225806) potassium channel beta subunit [Egeria densa]	1391.123	1355.000	1.027	1984.224	1741.000	1.140	1.083
15	4	12	RT023C07	a76couture1320.r#1	>dbj|BAC06941.1| (AP003759) contains ESTs AU070849(R10361).D23619(C3104)~similar to	811.696	878.000	0.924	1183.121	1077.000	1.099	1.012
15	4	13	GT193H06	a76couture1186.r#1	------	422.082	516.000	0.818	559.125	658.000	0.850	0.834
15	4	14	RT094E03	a76couture1064.r#1	>sp|P41380|IF43_NICPL Eukaryotic initiation factor 4A-3 (eIF-4A-3) (eIF4A-3)	1240.022	1126.000	1.101	1671.196	1521.000	1.099	1.100
15	4	15	RT074H03	a76couture0966.r#1	------	8391.691	9211.000	0.911	9760.487	11332.000	0.861	0.886
15	5	1	RT024B11	a76couture1316.r#1	>ref|NP_565590.1|| (NM_128085) expressed protein; protein id: At2g25280.1. supported	2430.094	2898.000	0.839	3101.444	3366.000	0.921	0.880
15	5	2	GT192D05	a76couture1182.r#1	------	204.797	203.000	1.009	260.513	237.000	1.099	1.054
15	5	3	RT093G05	a76couture1060.r#1	>ref|NP_175980.1|| (NM_104461) polyphosphoinositide binding protein. putative; protein	801.706	696.000	1.152	1024.547	883.000	1.160	1.156
15	5	4	RT074C12	a76couture0962.r#1	>sp|P42553|S1FA_ORYSA DNA BINDING PROTEIN S1FA	899.110	844.000	1.065	1167.675	1038.000	1.125	1.095
15	5	5	RT023D10	a76couture1311#1	------	19.980	24.000	0.833	29.861	30.000	0.995	0.914
15	5	6	GT191G08	a76couture1177.r#1	>ref|NP_565408.1|| (NM_127276) putative protein kinase; protein id: At2g17220.1	402.102	289.000	1.391	525.145	364.000	1.443	1.417
15	5	7	RT093C02	a76couture1055.r#1	>gb|AAC78332.1| (AF095454) PII protein [Ricinus communis]	159.842	131.000	1.220	211.088	162.000	1.303	1.262
15	5	8	RT074A05	a76couture0958.r#1	>ref|NP_195607.2|| (NM_120056) CONSTANS B-box zinc finger family protein; protein id:	516.988	425.000	1.216	738.292	551.000	1.340	1.278
15	5	9	RT021G09	a76couture1306#1	>ref|NP_565294.1|| (NM_126363) expressed protein; protein id: At2g03120.1. supported	912.846	805.000	1.134	1210.922	1002.000	1.209	1.171
15	5	10	GT184E04	a76couture1173.r#1	>emb|CAB76913.1| (AJ276270) hypothetical protein [Cicer arietinum]							
15	5	11	RT092F02	a76couture1051.r#1	------	124.876	125.000	0.999	175.048	152.000	1.152	1.075
15	5	12	RT073E04	a76couture0954.r#1	>ref|NP_172724.2|| (NM_101134) unknown protein; protein id: At1g12640.1. supported by	648.108	534.000	1.214	829.935	687.000	1.208	1.211
15	5	13	GT174D08	a76couture1775.r#1	>dbj|BAB86453.1| (AP003240) putative AAA-metalloprotease [Oryza sativa (japonica	102.399	105.000	0.975	148.276	141.000	1.052	1.013
15	5	14	GT162G07	a76couture1681.r#1	>gb|ZP_00007276.1| (NZ_AAAE01000150) hypothetical protein [Rhodobacter sphaeroides]	393.361	301.000	1.307	501.462	390.000	1.286	1.296
15	5	15	GB004E04	a76couture1590.r#1	>ref|NP_191316.1|| (NM_115617) hypothetical protein; protein id: At3g57570.1	52.448	40.000	1.311	72.079	55.000	1.311	1.311
15	6	1	TT263A05	a76couture1447.r#1	------	6.244	11.000	0.568	13.386	11.000	1.217	0.892
15	6	2	GT174B09	a76couture1771.r#1	>gb|AAF58666.2| (AE003826) CG13209-PA [Drosophila melanogaster]							
15	6	3	GT162C12	a76couture1678.r#1	------	33.717	38.000	0.887	63.841	61.000	1.047	0.967
15	6	4	GB004B01	a76couture1586#1	------	13.736	16.000	0.859	12.356	12.000	1.030	0.944
15	6	5	TT262F06	a76couture1442.r#1	>dbj|BAB02424.1| (AB024033) oxidoreductase. short-chain dehydrogenase/reductase	111.140	94.000	1.182	153.425	131.000	1.171	1.177
15	6	6	GT173G12	a76couture1767.r#1	>ref|NP_564049.1|| (NM_101684) expressed protein; protein id: At1g18260.1. supported	564.441	451.000	1.252	705.342	567.000	1.244	1.248
15	6	7	GT161H09	a76couture1675.r#1	>pir||T00396 hypothetical protein T13E15.2 - Arabidopsis thaliana	62.438	85.000	0.735	91.643	107.000	0.856	0.796
15	6	8	GB003F10	a76couture1579.r#1	>ref|NP_568446.1|| (NM_122355) putative protein; protein id: At5g24470.1. supported by	280.972	366.000	0.768	394.374	477.000	0.827	0.797
15	6	9	TT254B11	a76couture1438.r#1	>sp|P35100|CLPA_PEA ATP-dependent clp protease ATP-binding subunit clpA homolog	591.914	582.000	1.017	835.083	790.000	1.057	1.037
15	6	10	GT173E11	a76couture1763.r#1	>ref|XP_145241.1|| (XM_145241) similar to T-cell receptor beta chain precursor V-D-J	217.285	213.000	1.020	295.523	264.000	1.119	1.070
15	6	11	GT161D11	a76couture1670.r#1	>ref|NP_568497.1|| (NM_122638) putative protein; protein id: At5g27560.1. supported by	44.955	42.000	1.070	51.485	45.000	1.144	1.107
15	6	12	GB002D12	a76couture1574.r#1	------	651.855	622.000	1.048	922.607	821.000	1.124	1.086
15	6	13	RT063G11	a76couture1423.r#1	>ref|NP_568778.1|| (NM_124662) expressed protein; protein id: At5g52840.1. supported	1158.853	1246.000	0.930	1619.712	1634.000	0.991	0.961
15	6	14	GT173C06	a76couture1759.r#1	>pir||T12634 homeotic protein - common sunflower >gi|349379|gb|AAA63765.1|	723.034	615.000	1.176	865.974	728.000	1.190	1.183
15	6	15	GB009H04	a76couture1666.r#1	------	78.672	69.000	1.140	92.673	84.000	1.103	1.122
15	7	1	GB002A11	a76couture1571#1	------	47.453	57.000	0.833	56.633	71.000	0.798	0.815
15	7	2	TT251G03	a76couture1419.r#1	>gb|ZP_00111998.1| (NZ_AABC01000200) hypothetical protein [Nostoc punctiforme]	16.234	19.000	0.854	30.891	32.000	0.965	0.910
15	7	3	GT172H05	a76couture1755#1	>ref|NP_187425.1|| (NM_111647) putative coated vesicle membrane protein; protein id:	414.589	431.000	0.962	635.322	578.000	1.099	1.031
15	7	4	GB009H02	a76couture1664#1	------	0.000			9.267	12.000	0.772	0.772
15	7	5	GB001C09	a76couture1567.r#1	>ref|NP_563633.1|| (NM_100055) Expressed protein; protein id: At1g01725.1. supported	317.186	273.000	1.162	476.749	394.000	1.210	1.186
15	7	6	TT253H02	a76couture1416.r#1	>ref|NP_196751.2|| (NM_121228) putative protein; protein id: At5g11900.1. supported by	274.728	263.000	1.045	316.117	305.000	1.036	1.041
15	7	7	RT034E01	a76couture2179.r#1	>ref|NP_201483.1|| (NM_126081) unknown protein; protein id: At5g66820.1 [Arabidopsis	437.067	401.000	1.090	563.244	490.000	1.149	1.120
15	7	8	RT023F10	a76couture2075.r#1	>pir||T46190 hypothetical protein T8H10.140 - Arabidopsis thaliana	5096.204	5399.000	0.944	5921.781	6130.000	0.966	0.955
15	7	9	RT012F06	a76couture1990.r#1	------	203.548	212.000	0.960	292.434	264.000	1.108	1.034
15	7	10	RB000A34	a76couture1870.r#1	------	684.322	620.000	1.104	916.429	795.000	1.153	1.128
15	7	11	RT034D05	a76couture2175.r#1	>emb|CAC29435.1| (AJ310523) P-type H+-ATPase [Vicia faba]	3936.103	3171.000	1.241	5237.033	3887.000	1.347	1.294
15	7	12	RT023E07	a76couture2072.r#1	>ref|NP_201244.2|| (NM_125835) KH domain protein; protein id: At5g64390.1 [Arabidopsis	96.155	93.000	1.034	150.336	142.000	1.059	1.046
15	7	13	RT011H04	a76couture1984.r#1	------	11.239	15.000	0.749	16.475	15.000	1.098	0.924
15	7	14	GT202G06	a76couture1865.r#1	>ref|NP_565040.1|| (NM_105892) putative alanine aminotransferase; protein id:	5017.532	5021.000	0.999	6211.125	6513.000	0.954	0.976
15	7	15	RT034B06	a76couture2171.r#1	>gb|AAM67229.1| (AY088923) E2. ubiquitin-conjugating enzyme. putative [Arabidopsis	609.397	544.000	1.120	721.817	665.000	1.085	1.103
15	8	1	RT023D02	a76couture2068.r#1	>ref|NP_176878.1|| (NM_105377) phosphomannose isomerase. putative; protein id:	1660.856	1665.000	0.998	1745.334	1786.000	0.977	0.987
15	8	2	RT011D08	a76couture1981.r#1	>gb|AAH28867.1| (BC028867) Similar to hypothetical protein MGC3180 [Mus musculus]	156.095	148.000	1.055	193.583	156.000	1.241	1.148
15	8	3	GT202E11	a76couture1861.r#1	------	738.019	770.000	0.958	1011.161	970.000	1.042	1.000
15	8	4	RT033H08	a76couture2165.r#1	>ref|NP_175460.1|| (NM_103926) sterol delta7 reductase; protein id: At1g50430.1	4513.031	4214.000	1.071	5396.636	5048.000	1.069	1.070
15	8	5	RT023B06	a76couture2064.r#1	>ref|NP_195936.1|| (NM_120394) putative protein; protein id: At5g03160.1. supported by	711.795	666.000	1.069	835.083	836.000	0.999	1.034
15	8	6	RT011A06	a76couture1978.r#1	>ref|NP_568986.1|| (NM_125812) expressed protein; protein id: At5g64160.1. supported	234.768	207.000	1.134	283.166	246.000	1.151	1.143
15	8	7	GT201E12	a76couture1856.r#1	>gb|AAM13204.1| (AY093205) putative serine protease-like protein [Arabidopsis	32.468	38.000	0.854	40.158	40.000	1.004	0.929
15	8	8	RT033G04	a76couture2162.r#1	>emb|CAC05308.1| (AL391629) serine/proline rich protein [Leishmania major]	531.973	556.000	0.957	505.581	509.000	0.993	0.975
15	8	9	RT022G11	a76couture2060#1	>ref|NP_566370.1|| (NM_111860) expressed protein; protein id: At3g10250.1. supported	201.051	202.000	0.995	258.454	238.000	1.086	1.041
15	8	10	Arabidopsis Control Oligonucleotide	3ara23								

15	8	11	GT194G08	a76couture1851.r#1	>ref|NP_187752.1|| (NM_111978) putative cell division related protein; protein id:	427.077	397.000	1.076	480.868	443.000	1.085	1.081
15	8	12	RT033E12	a76couture2158.r#1	>ref|NP_177234.1|| (NM_105745) unknown protein; protein id: At1g70770.1 [Arabidopsis	242.260	207.000	1.170	344.948	293.000	1.177	1.174
15	8	13	RT022F09	a76couture2057#1	>gb|AAL07213.1| (AY056134) unknown protein [Arabidopsis thaliana]	631.874	551.000	1.147	865.974	696.000	1.244	1.195
15	8	14	RB008G12	a76couture1974#1	>ref|NP_149129.1|| (NM_033138) caldesmon 1 isoform 1; H-CAD; L-CAD [Homo sapiens]	12.488	18.000	0.694	13.386	17.000	0.787	0.741
15	8	15	GT201H07	a76couture1847.r#1	------	1337.426	1145.000	1.168	1588.821	1427.000	1.113	1.141
15	9	1	RT064C02	a76couture2602.r#1	>ref|NP_567929.1|| (NM_119519) expressed protein; protein id: At4g33630.1. supported	618.138	607.000	1.018	685.777	640.000	1.072	1.045
15	9	2	TT251E11	a76couture2483#1	>emb|CAB52246.1| (AJ245478) alpha galactosyltransferase [Trigonella foenum-graecum]	1451.063	1368.000	1.061	1805.057	1582.000	1.141	1.101
15	9	3	RT063C02	a76couture2370.r#1	>dbj|BAA97517.1| (AB026634) gene_id:F24B18.6~unknown protein [Arabidopsis thaliana]	318.435	336.000	0.948	420.116	427.000	0.984	0.966
15	9	4	RT051H05	a76couture2272.r#1	>dbj|BAB90349.1| (AP003535) hypothetical protein [Oryza sativa (japonica	38.712	52.000	0.744	59.722	77.000	0.776	0.760
15	9	5	RT064A01	a76couture2598.r#1	>ref|NP_193403.1|| (NM_117771) decarboxylase like protein; protein id: At4g16700.1	64.936	73.000	0.890	75.168	82.000	0.917	0.903
15	9	6	TT251D11	a76couture2479#1	>ref|NP_199691.1|| (NM_124257) non-phototropic hypocotyl-like protein; protein id:	109.891	96.000	1.145	139.009	126.000	1.103	1.124
15	9	7	RT062F12	a76couture2363.r#1	>ref|NP_568258.1|| (NM_121258) dihydropyrimidinase; protein id: At5g12200.1. supported	345.908	386.000	0.896	475.719	500.000	0.951	0.924
15	9	8	RT051F08	a76couture2269.r#1	>emb|CAA69305.1| (Y08067) mitochondrial single-subunit DNA-dependent RNA polymerase	32.468	36.000	0.902	43.247	41.000	1.055	0.978
15	9	9	TB000A56	a76couture2582.r#1	>ref|NP_194330.1|| (NM_118733) KH domain protein; protein id: At4g26000.1. supported	1215.047	1246.000	0.975	1752.542	1576.000	1.112	1.044
15	9	10	TT254C05	a76couture2475.r#1	>ref|NP_566111.1|| (NM_130346) expressed protein; protein id: At2g47790.1. supported	101.150	81.000	1.249	139.009	113.000	1.230	1.239
15	9	11	RT062E05	a76couture2359.r#1	>gb|AAM22751.1| (AY090544) one helix protein [Deschampsia antarctica]	709.298	542.000	1.309	835.083	634.000	1.317	1.313
15	9	12	RT053C12	a76couture2266#1	------	8.741	15.000	0.583	10.297	15.000	0.686	0.635
15	9	13	TT283E04	a76couture2569.r#1	>ref|NP_566440.1|| (NM_112132) Expressed protein; protein id: At3g12955.1. supported	645.611	666.000	0.969	767.123	774.000	0.991	0.980
15	9	14	TT254A08	a76couture2470.r#1	>ref|NP_181874.1|| (NM_129907) 60S ribosomal protein L38; protein id: At2g43460.1	3570.215	2711.000	1.317	4272.208	3322.000	1.286	1.301
15	9	15	RT062C07	a76couture2355.r#1	>gb|AAM14036.1| (AY091014) unknown protein [Arabidopsis thaliana]	14.985	18.000	0.833	26.772	29.000	0.923	0.878
15	10	1	RT053A11	a76couture2263.r#1	------	452.052	341.000	1.326	494.254	382.000	1.294	1.310
15	10	2	TT283H09	a76couture2566#1	>ref|NP_196376.1|| (NM_120841) WD-repeat protein-like; protein id: At5g07590.1	121.130	113.000	1.072	123.563	114.000	1.084	1.078
15	10	3	TT253F02	a76couture2467.r#1	>dbj|BAB86135.1| (AP003451) hypothetical protein [Oryza sativa (japonica	77.423	67.000	1.156	76.197	70.000	1.089	1.122
15	10	4	RT062A05	a76couture2351.r#1	>ref|NP_191819.1|| (NM_116125) putative protein; protein id: At3g62600.1. supported by	1240.022	1368.000	0.906	1519.831	1668.000	0.911	0.909
15	10	5	RT052B08	a76couture2260#1	------	52.448	46.000	1.140	63.841	56.000	1.140	1.140
15	10	6	TT283A03	a76couture2562.r#1	------	1308.704	1094.000	1.196	1791.671	1554.000	1.153	1.175
15	10	7	TT253D03	a76couture2463.r#1	------	506.998	571.000	0.888	593.105	679.000	0.873	0.881
15	10	8	RT061H06	a76couture2347.r#1	>ref|NP_196376.1|| (NM_120841) WD-repeat protein-like; protein id: At5g07590.1	109.891	109.000	1.008	126.653	123.000	1.030	1.019
15	10	9	RT044E09	a76couture2255.r#1	>ref|NP_196275.1|| (NM_120740) putative protein; protein id: At5g06570.1 [Arabidopsis	33.717	33.000	1.022	46.336	43.000	1.078	1.050
15	10	10	RT064H04	a76couture3107.r#1	>gb|AAA86689.1| (U15933) ascorbate peroxidase [Nicotiana tabacum]	1743.274	1418.000	1.229	2267.390	1755.000	1.292	1.261
15	10	11	RT053F06	a76couture2960.r#1	>ref|NP_568742.1|| (NM_124448) 11-beta-hydroxysteroid dehydrogenase-like; protein id:	0.000			7.208	11.000	0.655	0.655
15	10	12	PT011D08	a76couture2812.r#1	>pir||T07139 cysteine proteinase inhibitor - soybean >gi|1944319|dbj|BAA19608.1|	6093.966	4993.000	1.221	6890.724	6005.000	1.147	1.184
15	10	13	PT002C09	a76couture2705.r#1	------	166.086	136.000	1.221	217.266	176.000	1.234	1.228
15	10	14	RT043D04	a76couture3101.r#1	>sp|P46297|RS23_FRAAN 40S RIBOSOMAL PROTEIN S23 (S12) >gi|1362041|pir||S56673 ribosomal	3586.449	2339.000	1.533	4231.020	3038.000	1.393	1.463
15	10	15	GT203E11	a76couture2956.r#1	>sp|P35135|UBC4_LYCES Ubiquitin-conjugating enzyme E2-17 kDa (Ubiquitin-protein ligase)	3198.083	1948.000	1.642	3734.707	2336.000	1.599	1.620
15	11	1	PT004D10	a76couture2808.r#1	>ref|NP_565703.1|| (NM_128611) WRKY family transcription factor; protein id:	101.150	72.000	1.405	92.673	67.000	1.383	1.394
15	11	2	PT001F01	a76couture2701.r#1	>ref|XP_164718.1|| (XM_164718) hypothetical protein XP_164718 [Mus musculus]	648.108	398.000	1.628	682.688	411.000	1.661	1.645
15	11	3	RT033D07	a76couture3096.r#1	>gb|AAB65777.1| (U97522) class IV endochitinase [Vitis vinifera]	114.886	108.000	1.064	136.950	126.000	1.087	1.075
15	11	4	RT024A03	a76couture2950.r#1	>gb|AAG23847.1| (AY004247) RUB1 conjugating enzyme [Lycopersicon esculentum]	320.932	251.000	1.279	330.532	277.000	1.193	1.236
15	11	5	PT011G05	a76couture2804.r#1	>ref|NP_191365.1|| (NM_115668) putative protein; protein id: At3g58060.1 [Arabidopsis	553.202	441.000	1.254	687.837	585.000	1.176	1.215
15	11	6	PT005H12	a76couture2696.r#1	------	67.433	51.000	1.322	71.049	62.000	1.146	1.234
15	11	7	RB008C12	a76couture3090.r#1	>emb|CAB85630.1| (AJ237990) putative metallothionein-like protein [Vitis vinifera]	11.239	11.000	1.022	16.475	15.000	1.098	1.060
15	11	8	GT173C03	a76couture2944.r#1	>gb|AAN08216.1| (AC090874) ribosomal protein L15 [Oryza sativa (japonica	663.093	446.000	1.487	781.539	557.000	1.403	1.445
15	11	9	PT009C01	a76couture2800.r#1	>ref|NP_680755.1|| (NM_148389) hypothetical protein; protein id: At4g32175.1	397.107	345.000	1.151	468.512	389.000	1.204	1.178
15	11	10	PT010D02	a76couture2691.r#1	>ref|NP_178168.1|| (NM_106701) nodulin-like protein; protein id: At1g80530.1	483.271	408.000	1.184	563.244	480.000	1.173	1.179
15	11	11	RT064A02	a76couture3085.r#1	>ref|NP_180443.1|| (NM_128436) putative nucleotide-sugar dehydratase; protein id:	1023.986	1040.000	0.985	1298.446	1290.000	1.007	0.996
15	11	12	GT182H12	a76couture2933.r#1	>gb|AAK62600.1| (AY039545) AT3g62770/F26K9_200 [Arabidopsis thaliana]	541.963	521.000	1.040	732.114	718.000	1.020	1.030
15	11	13	PT012D02	a76couture2795.r#1	>gb|AAL87190.1|AF480497_18 (AF480497) putative pelota [Oryza sativa (japonica cultivar-group)]	738.019	429.000	1.720	744.470	517.000	1.440	1.580
15	11	14	PT012H12	a76couture2687.r#1	>ref|NP_220817.1|| (NC_000963) unknown [Rickettsia prowazekii]	1393.620	1166.000	1.195	1588.821	1394.000	1.140	1.167
15	11	15	TT284E04	a76couture3077.r#1	>gb|AAC06237.1| (AF052570) AGAMOUS homolog [Populus balsamifera subsp. trichocarpa]	2667.359	2188.000	1.219	3258.987	2720.000	1.198	1.209
15	12	1	TT264B11	a76couture2927.r#1	>dbj|BAB84322.1| (AB079020) ras-related protein RAB8-1 [Nicotiana tabacum]	1893.126	1726.000	1.097	1616.622	1627.000	0.994	1.045
15	12	2	PT010G11	a76couture2790.r#1	>gb|AAL18927.1|AF429386_1 (AF429386) mevalonate disphosphate decarboxylase [Hevea	909.100	797.000	1.141	956.587	806.000	1.187	1.164
15	12	3	PT001G12	a76couture2684.r#1	------	2548.726	2351.000	1.084	2548.497	2494.000	1.022	1.053
15	12	4	BM437108 BM436831 RB008A06	couture_a76.420.c1.r#1	>gb|AAK25760.1|AF334840_1 (AF334840) ribosomal protein L33 [Castanea sativa]	4403.140	3184.000	1.383	5353.389	3677.000	1.456	1.419
15	12	5	BM437645 GB005F01	couture_a76.34.c1.r#1	>emb|CAA10123.1| (AJ012681) hypothetical protein [Cicer arietinum]	2603.672	2409.000	1.081	2789.446	2801.000	0.996	1.038
15	12	6	BM437469 CT005A08	couture_a76.25.c1#1	>ref|NP_564765.1|| (NM_104768) expressed protein; protein id: At1g60870.1. supported	0.000			28.831	30.000	0.961	0.961
15	12	7	BM437384 CT006A02	couture_a76.16.c1.r#1	>sp|P43187|ALL3_BETVE Calcium-binding allergen Bet v 3 (Bet v III) >gi|629480|pir||S45011	1627.139	1134.000	1.435	1692.820	1289.000	1.313	1.374
15	12	8	RB003B06 RB003B06	couture_a76.417.c1.r#1	>ref|NP_196793.1|| (NM_121292) glucosyltransferase -like protein; protein id:	193.558	160.000	1.210	238.889	203.000	1.177	1.193
15	12	9	GB000A76 BG273913 GB000A76	couture_a76.335.c1.r#1	>emb|CAA54308.1| (X77012) 1.4-alpha-glucan branching enzyme [Manihot esculenta]	894.115	985.000	0.908	1006.013	1173.000	0.858	0.883
15	12	10	BM437983 GT201D10	couture_a76.247.c1.r#1	>ref|NP_175963.1|| (NM_104443) photosystem I subunit V precursor. putative; protein	67.433	62.000	1.088	81.346	71.000	1.146	1.117
15	12	11	BM437390 RB003C04 RT043C07	couture_a76.153.c1.r#1	>gb|AAC24001.1| (AF071477) isoflavone reductase related protein [Pyrus communis]	174.827	163.000	1.073	247.127	228.000	1.084	1.078
15	12	12	RB001D09 RB001D09	couture_a76.413.c1.r#1	>ref|NP_179660.1|| (NM_127632) glycosyl hydrolase family 5/cellulase	995.265	788.000	1.263	1199.596	1039.000	1.155	1.209
15	12	13	BG273904 GB000A87	couture_a76.331.c1.r#1	------	27.473	28.000	0.981	32.950	32.000	1.030	1.005
15	12	14	GB001h03 GT193H10	couture_a76.243.c1.r#1	>ref|NP_178453.1|| (NM_126405) putative esterase; protein id: At2g03550.1 [Arabidopsis	18.731	30.000	0.624	17.505	27.000	0.648	0.636
15	12	15	BM437857 BM437795 BM437921 BM437240 BM	couture_a76.149.c1#1	>sp|Q40519|PSBR_TOBAC Photosystem II 10 kDa polypeptide. chloroplast precursor (PII10)	733.024	767.000	0.956	937.023	953.000	0.983	0.969
15	13	1	BM437213 GB005g02 GB005G02	couture_a76.41.c1.r#1	>dbj|BAB64345.1| (AB063192) EIN3-like protein [Cucumis melo]	2352.671	2363.000	0.996	2977.880	3266.000	0.912	0.954
15	13	2	GB001b01 GB001B01	couture_a76.33.c1.r#1	>sp|P38385|S61G_ORYSA PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT	8204.377	6960.000	1.179	7972.935	6913.000	1.153	1.166
15	13	3	BE846396 GT193C04	couture_a76.241.c1#1	>ref|NP_182147.1|| (NM_130187) hypothetical protein; protein id: At2g46240.1	46.204	31.000	1.490	70.019	48.000	1.459	1.475

15	13	4	BM437924 RT072A11	couture_a76.145.c1.r#1	>ref|NP_562388.1|| (NC_003366) hypothetical protein [Clostridium perfringens]	1389.874	1270.000	1.094	1780.344	1698.000	1.048	1.071
15	13	5	Arabidopsis Control Oligonucleotide	3ara23								
15	13	6	TB002g03 BM436323 TT283F09	couture_a76.327.c1#1	>gb|AAM65485.1| (AY087937) putative GDSL-motif lipase/hydrolase [Arabidopsis	312.191	312.000	1.001	389.225	398.000	0.978	0.989
15	13	7	BM437830 GT184D09	couture_a76.238.c1.r#1	>ref|NP_192588.1|| (NM_116917) putative mitogen-activated protein kinase; protein id:	686.820	667.000	1.030	775.361	800.000	0.969	0.999
15	13	8	AW707959 ST004F07	couture_a76.141.c1.r#1	>dbj|BAB92670.1| (AP003433) cysteine proteinase inhibitor Scb-like protein [Oryza	4970.079	2370.000	2.097	5796.158	2905.000	1.995	2.046
15	13	9	BG273736 RB000A66	couture_a76.404.c1#1	>gb|AAF99846.1|AC051629_13 (AC051629) Unknown protein [Arabidopsis thaliana]	157.344	169.000	0.931	218.296	224.000	0.975	0.953
15	13	10	TB005g09 TT281A10	couture_a76.323.c1#1	>gb|AAF16414.1|AF126550_1 (AF126550) mannosyl-oligosaccharide 1.2-alpha-mannosidase [Glycine	855.403	733.000	1.167	900.984	846.000	1.065	1.116
15	13	11	BE846393 GT184A05	couture_a76.234.c1.r#1	>ref|NP_197574.1|| (NM_122081) ripening-related protein - like; protein id:	1387.376	1098.000	1.264	1682.523	1443.000	1.166	1.215
15	13	12	BM436990 BM437594 ST001D09	couture_a76.137.c1.r#1	>emb|CAB88668.1| (AJ400863) histone H2B [Cicer arietinum]	1436.078	887.000	1.619	1749.453	1197.000	1.462	1.540
15	13	13	BG273796 RT081D01	couture_a76.96.c1#1	>gb|AAF16869.1|AF109693_1 (AF109693) allergen-like protein BRSn20 [Sambucus nigra]	9335.756	7944.000	1.175	10742.817	9892.000	1.086	1.131
15	13	14	BG273895 GB000A97	couture_a76.582.c1#1	>ref|NP_568396.1|| (NM_122064) ring-box protein - like; protein id: At5g20570.1	558.197	518.000	1.078	630.174	632.000	0.997	1.037
15	13	15	G1561773 VVU67426	couture_a76.sd.82.c1#	>gb|AAB08874.1| (U67426) malate dehydrogenase [Vitis vinifera]	1612.154	1519.000	1.061	1945.095	1933.000	1.006	1.034
15	14	1	BM436762 RT074D04	couture_a76.95.c1.r#1	>dbj|BAB89033.1| (AP003243) contains ESTs AU031041(E60654).AU095214(E60654)~similar	2303.969	1757.000	1.311	2605.130	2240.000	1.163	1.237
15	14	2	BM437604 BM438082 PT012G03	couture_a76.604.c1.r#1	>emb|CAA06925.1| (AJ006228) Avr9 elicitor response protein [Nicotiana tabacum]	1614.651	1630.000	0.991	1830.799	1865.000	0.982	0.986
15	14	3	BG273885 TB000A07	couture_a76.504.c1.r#1	------	152.349	193.000	0.789	480.868	454.000	1.059	0.924
15	14	4	BE846418 AY043234 CHIMPECLY	couture_a76.sd.24.c1#	>gb|AAK66161.1| (AF339025) pectate lyase [Fragaria x ananassa]	601.904	521.000	1.155	705.342	665.000	1.061	1.108
15	14	5	BM437776 BM436937 BM437733 PT012G06	couture_a76.603.c1.r#1	------	2664.861	2247.000	1.186	2878.000	2621.000	1.098	1.142
15	14	6	BM438113 TT281H09	couture_a76.482.c1#1	>ref|NP_567578.1|| (NM_118035) putative protein; protein id: At4g19160.1 [Arabidopsis	424.580	459.000	0.925	525.145	599.000	0.877	0.901
15	14	7	BM437986 PT004B09	couture_a76.82.c1.r#1	>ref|NP_566590.1|| (NM_112667) expressed protein; protein id: At3g17860.1. supported	2396.377	2270.000	1.056	2185.015	2092.000	1.044	1.050
15	14	8	BM437916 RT042A03	couture_a76.571.c1.r#1	>emb|CAA10231.1| (AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]	658.098	293.000	2.246	844.351	404.000	2.090	2.168
15	14	9	BM437546 BG273938 AW707957 RT063A05	couture_a76.48.c1#1	>gb|AAG50831.1|AC074395_5 (AC074395) unknown protein. 5' partial [Arabidopsis thaliana]	15463.439	16835.000	0.919	5837.346	6687.000	0.873	0.896
15	14	10	BM438042 PT008A04	couture_a76.594.c1#1	>sp|Q43636|THIH_RICCO Thioredoxin H-type (TRX-H) >gi|7430846|pir||T10170 thioredoxin -	32181.886	18127.000	1.775	26175.898	17793.000	1.471	1.623
15	14	11	BM436427 BG273851 TB000A41	couture_a76.496.c1#1	>ref|NP_568041.1|| (NM_120008) protein kinase like protein; protein id: At4g38470.1	387.117	280.000	1.383	462.333	349.000	1.325	1.354
15	14	12	BG273777 BG273928 BG273769 RB000A23 BG27	couture_a76.sd.11.c3#	>gb|AAF71819.1|AF141899_1 (AF141899) putative aquaporin PIP1-3 [Vitis berlandieri x Vitis	7983.345	6148.000	1.299	10570.857	8949.000	1.181	1.240
15	14	13	TB004g04 RT043E08	couture_a76.593.c1.r#1	>dbj|BAA97478.1| (AB025604) oxysterol-binding protein [Arabidopsis thaliana]	1318.694	1228.000	1.074	1609.415	1649.000	0.976	1.025
15	14	14	GT173G02 PT005F10	couture_a76.562.c1#1	>sp|Q9AXE3|DCAM_DAUCA S-adenosylmethionine decarboxylase proenzyme (AdoMetDC) (SamDC)	114.886	84.000	1.368	164.751	116.000	1.420	1.394
15	14	15	TT242D09 BM438093	couture_a76.470.c1#1	>ref|NP_197854.1|| (NM_122375) putative protein; protein id: At5g24660.1. supported by	111.140	57.000	1.950	95.762	72.000	1.330	1.640
16	1	1	CM002E08	a76couture0422.r#1	------	1381.132	1015.000	1.361	1722.681	1244.000	1.385	1.373
16	1	2	RT092G12	a76couture0310.r#1	>sp|P12372|PSAD_LYCES Photosystem I reaction center subunit II. chloroplast precursor	4438.106	3939.000	1.127	5976.355	5091.000	1.174	1.150
16	1	3	RT052B04	a76couture0178.r#1	>dbj|BAB63467.1| (AP002903) putative aspartate transaminase [Oryza sativa (japonica	2592.433	2314.000	1.120	3384.610	2822.000	1.199	1.160
16	1	4	GT203C06	a76couture0006.r#1	>ref|NP_193866.1|| (NM_118255) putative protein; protein id: At4g21350.1 [Arabidopsis	1883.135	2963.000	0.636	3785.162	3790.000	0.999	0.817
16	1	5	CM002D06	a76couture0418.r#1	>ref|NP_563683.1|| (NM_100217) expressed protein; protein id: At1g03350.1. supported	1087.673	1070.000	1.017	1900.819	1345.000	1.413	1.215
16	1	6	RT091A02	a76couture0306.r#1	>gb|AAN03468.1| (AF532621) bZIP transcription factor ATB2 [Glycine max]	974.036	1026.000	0.949	1961.571	1424.000	1.378	1.163
16	1	7	RT051B04	a76couture0174.r#1	>dbj|BAC10549.1| (AB080191) nine-cis-epoxycarotenoid dioxygenase1 [Pisum sativum]	3919.869	4760.000	0.824	7301.573	6621.000	1.103	0.963
16	1	8	PT002G05	a76couture2693.r#1	>ref|NP_584708.1|| (NC_003231) ATP-DEPENDENT RNA HELICASE (DEAD box family)	166.086	170.000	0.977	407.760	321.000	1.270	1.124
16	1	9	CM002B04	a76couture0413.r#1	------	1277.485	1518.000	0.842	2500.101	2741.000	0.912	0.877
16	1	10	RT082C12	a76couture0299.r#1	>pir||S48032 cim1 protein - soybean >gi|555616|gb|AAA50175.1| (U03860) cytokinin	2789.738	4476.000	0.623	3888.131	6090.000	0.638	0.631
16	1	11	GT204F01	a76couture0167.r#1	>ref|NP_177392.1|| (NM_105907) unknown protein; protein id: At1g72480.1 [Arabidopsis	413.341	392.000	1.054	565.303	540.000	1.047	1.051
16	1	12	RT012E01	a76couture1988.r#1	>ref|NP_197890.1|| (NM_122417) putative protein; protein id: At5g25080.1. supported by	359.644	329.000	1.093	522.056	444.000	1.176	1.134
16	1	13	CM001H09	a76couture0409.r#1	>pir||T05882 hypothetical protein F6H11.10 - Arabidopsis thaliana	6.244	14.000	0.446	8.238	18.000	0.458	0.452
16	1	14	RT081C12	a76couture0293.r#1	>emb|CAC91565.1| (AJ414400) hydroperoxide lyase [Nicotiana attenuata]	3984.804	5288.000	0.754	4212.486	5475.000	0.769	0.761
16	1	15	GT202G08	a76couture0164.r#1	>gb|AAM64912.1| (AY087362) unknown [Arabidopsis thaliana]	188.563	201.000	0.938	214.177	228.000	0.939	0.939
16	2	1	GT204F02	a76couture1257.r#1	>gb|AAM67318.1| (AY086508) unknown [Arabidopsis thaliana]	2935.843	2561.000	1.146	4217.634	3379.000	1.248	1.197
16	2	2	CM001F08	a76couture0404.r#1	>ref|NP_175816.1|| (NM_104292) transcriptional activation factor TAFII32. putative;	303.450	291.000	1.043	498.373	428.000	1.164	1.104
16	2	3	ST006C12	a76couture0285.r#1	>pir||S72485 peptidylprolyl isomerase (EC 5.2.1.8) ROF1 - Arabidopsis thaliana	6439.874	3929.000	1.639	8005.885	4864.000	1.646	1.643
16	2	4	RT051E03	a76couture0153.r#1	>ref|NP_180566.1|| (NM_128560) G-protein beta family; protein id: At2g30050.1	2794.733	2689.000	1.039	5577.862	3634.000	1.535	1.287
16	2	5	CT004D10	a76couture0549.r#1	------	11.239	17.000	0.661	24.713	25.000	0.989	0.825
16	2	6	CM001E04	a76couture0401#1	------	149.852	165.000	0.908	331.562	263.000	1.261	1.084
16	2	7	ST005D08	a76couture0280.r#1	>ref|NP_568813.1|| (NM_124867) Expressed protein; protein id: At5g54855.1. supported	32.468	35.000	0.928	67.960	57.000	1.192	1.060
16	2	8	GT193F11	a76couture0145.r#1	>gb|AAC17617.1| (AC002131) Similar to hypothetical protein F09E5.8 gb|U37429 from	1202.559	1196.000	1.005	2317.845	1711.000	1.355	1.180
16	2	9	GT171B08	a76couture0138.r#1	>sp|Q9ZNS1|RS7_AVIMR 40S ribosomal protein S7 >gi|3851636|gb|AAC97947.1| (AF098519)	3390.393	3249.000	1.044	5472.833	4133.000	1.324	1.184
16	2	10	RT083E11	a76couture0837.r#1	>ref|NP_568449.1|| (NM_122366) expressed protein; protein id: At5g24580.1. supported	3455.329	4588.000	0.753	4638.780	5616.000	0.826	0.790
16	2	11	ST006H03	a76couture0718.r#1	>ref|NP_055692.1|| (NM_014877) helicase KIAA0054 [Homo sapiens]	18.731	19.000	0.986	20.594	24.000	0.858	0.922
16	2	12	CT006F08	a76couture0621.r#1	------	11.239	20.000	0.562	21.624	29.000	0.746	0.654
16	2	13	CT002C05	a76couture0521.r#1	>emb|CAB85628.1| (AJ237988) putative ripening-related protein [Vitis vinifera]	482.023	700.000	0.689	736.233	988.000	0.745	0.717
16	2	14	RT082C01	a76couture0832.r#1	>pir||S63668 phragmoplastin 5 - soybean >gi|1218004|gb|AAC49183.1| (U36430)	1471.043	1707.000	0.862	1925.531	2150.000	0.896	0.879
16	2	15	ST006G02	a76couture0714.r#1	------	118.633	132.000	0.899	125.623	153.000	0.821	0.860
16	3	1	CT006E07	a76couture0617.r#1	>sp|P07816|RR19_SOYBN Chloroplast 30S ribosomal protein S19 >gi|71027|pir||R3SY19	152.349	147.000	1.036	162.692	161.000	1.011	1.023
16	3	2	CT002A03	a76couture0516.r#1	------	24.975	27.000	0.925	44.277	40.000	1.107	1.016
16	3	3	RT081B08	a76couture0828.r#1	>gb|AAF75794.1|AF272710_1 (AF272710) putative 7-transmembrane G-protein-coupled receptor	380.873	579.000	0.658	743.440	910.000	0.817	0.737
16	3	4	ST006E08	a76couture0710.r#1	------	127.374	76.000	1.676	166.811	108.000	1.545	1.610
16	3	5	CT006D09	a76couture0613.r#1	>ref|NP_196026.1|| (NM_120488) putative protein; protein id: At5g04060.1. supported by	202.300	276.000	0.733	370.690	365.000	1.016	0.874
16	3	6	CM005f11	a76couture0512.r#1	mb|CAC80377.1| (AJ246013) glyceraldehyde-3-phosphate dehydrogen... 109 9e-026	353.400	259.000	1.364	778.450	465.000	1.674	1.519
16	3	7	RT064D12	a76couture0820.r#1	>ref|NP_566957.1|| (NM_115071) gamma response I protein; protein id: At3g52120.1	415.838	523.000	0.795	846.410	750.000	1.129	0.962
16	3	8	ST006C08	a76couture0705.r#1	------	8.741	18.000	0.486	44.277	44.000	1.006	0.746
16	3	9	ST002C10	a76couture0608.r#1	>ref|NP_242447.1|| (NC_002570) two-component sensor histidine kinase [Bacillus	84.916	80.000	1.061	157.543	112.000	1.407	1.234
16	3	10	CM005e04	a76couture0506.r#1	gb|AAD18030.1| (AF118129) Tsi1-interacting protein TSIP1 [Nicoti... 181 8e-045	18.731	20.000	0.937	19.564	22.000	0.889	0.913
16	3	11	RT034F09	a76couture0816.r#1	------	1.249	11.000	0.114	1.030	13.000	0.079	0.096

16	3	12	ST006B08	a76couture0702.r#1	>gb|AAM20488.1| (AY099637) putative protein [Arabidopsis thaliana]	22.478	22.000	1.022	31.921	33.000	0.967	0.995
16	3	13	ST002A06	a76couture0604.r#1	>ref|NP_566677.1|| (NM_113014) expressed protein; protein id: At3g21190.1. supported	196.056	174.000	1.127	313.028	260.000	1.204	1.165
16	3	14	CM005d03	a76couture0502.r#1	none	274.728	332.000	0.827	341.859	387.000	0.883	0.855
16	3	15	RB002A06	a76couture0811.r#1	------	555.700	685.000	0.811	677.540	887.000	0.764	0.788
16	4	1	ST006A06	a76couture0698.r#1	>pir||T46237 hypothetical protein T9C5.190 - Arabidopsis thaliana	6.244	16.000	0.390	3.089	13.000	0.238	0.314
16	4	2	ST001G12	a76couture0600.r#1	>emb|CAC19877.1| (AJ401089) long chain acyl-CoA synthetase [Brassica napus]	207.295	154.000	1.346	273.899	210.000	1.304	1.325
16	4	3	CM005a12	a76couture0498.r#1	ref|NP_051038.1|| (NC_000932) ribosomal protein S12 [Arabidopsis... 71 1e-011	1511.004	1628.000	0.928	2639.110	2387.000	1.106	1.017
16	4	4	RT021D03	a76couture1302#1	>ref|NP_566326.1|| (NM_111674) expressed protein; protein id: At3g07950.1. supported	716.790	671.000	1.068	1085.299	864.000	1.256	1.162
16	4	5	GT183D07	a76couture1167.r#1	------	51.199	38.000	1.347	103.999	63.000	1.651	1.499
16	4	6	RT092B06	a76couture1046.r#1	>gb|AAK91377.1| (AY050360) AT5g25110/T11H3_120 [Arabidopsis thaliana]	1809.458	1391.000	1.301	2876.970	1859.000	1.548	1.424
16	4	7	RT074G11	a76couture0951.r#1	>ref|NP_199752.1|| (NM_124318) putative protein; protein id: At5g49410.1. supported by	333.420	325.000	1.026	562.214	442.000	1.272	1.149
16	4	8	RT012D03	a76couture1297.r#1	>emb|CAD30274.1| (AJ458442) IAA16 protein [Gossypium hirsutum]	3025.754	1910.000	1.584	5370.893	3076.000	1.746	1.665
16	4	9	GT181G08	a76couture1161.r#1	>dbj|BAB89594.1| (AP003252) hypothetical protein~similar to Arabidopsis thaliana	840.418	663.000	1.268	1268.585	850.000	1.492	1.380
16	4	10	RT092A01	a76couture1040.r#1	>gb|AAK84474.1| (AF275345) suppressor-like protein [Lycopersicon esculentum]	463.291	349.000	1.327	573.541	471.000	1.218	1.273
16	4	11	RT073H12	a76couture0947.r#1	>ref|NP_197629.1|| (NM_122142) putative protein; protein id: At5g22370.1 [Arabidopsis	290.962	236.000	1.233	327.443	287.000	1.141	1.187
16	4	12	RT011F02	a76couture1292.r#1	>gb|AAG38144.1| (AY004240) unknown [Glycine max]	137.364	155.000	0.886	196.672	214.000	0.919	0.903
16	4	13	GT181E03	a76couture1155.r#1	>gb|AAL26909.1|AF319165_1 (AF319165) dehydration-responsive protein RD22 [Prunus persica]	187.315	179.000	1.046	299.641	236.000	1.270	1.158
16	4	14	RT091C06	a76couture1036.r#1	>ref|NP_195447.1|| (NM_119894) putative protein; protein id: At4g37300.1. supported by	1002.757	819.000	1.224	1336.545	1053.000	1.269	1.247
16	4	15	RT073H03	a76couture0944.r#1	------	139.862	132.000	1.060	163.722	158.000	1.036	1.048
16	5	1	RB007G05	a76couture1287.r#1	>pir||T12197 immunophilin - fava bean >gi|2104959|gb|AAB57848.1| (U96925)							
16	5	2	GT181B09	a76couture1151.r#1	>gb|AAM61228.1| (AY084666) unknown [Arabidopsis thaliana]	628.128	595.000	1.056	895.835	815.000	1.099	1.077
16	5	3	RT091A10	a76couture1032.r#1	>ref|NP_564277.1|| (NM_102495) unknown protein; protein id: At1g27330.1 [Arabidopsis	52.448	85.000	0.617	50.455	86.000	0.587	0.602
16	5	4	RT073C05	a76couture0942.r#1	>ref|NP_566176.1|| (NM_111123) Expressed protein; protein id: At3g02555.1. supported	1220.042	930.000	1.312	1784.463	1188.000	1.502	1.407
16	5	5	RB007E09	a76couture1282#1	>ref|NP_563834.1|| (NM_100773) expressed protein; protein id: At1g09020.1. supported	255.997	228.000	1.123	348.037	275.000	1.266	1.194
16	5	6	GT174G01	a76couture1147.r#1	------	383.370	337.000	1.138	689.896	497.000	1.388	1.263
16	5	7	RT084D12	a76couture1028.r#1	------	4254.537	3956.000	1.075	5952.672	4462.000	1.334	1.205
16	5	8	RT072G05	a76couture0938#1	>pir||T11672 quinone oxidoreductase homolog - cowpea >gi|1617036|emb|CAA69914.1|	224.777	181.000	1.242	345.978	246.000	1.406	1.324
16	5	9	RB005H05	a76couture1276.r#1	------	32.468	32.000	1.015	36.039	31.000	1.163	1.089
16	5	10	GT173H10	a76couture1140.r#1	>emb|CAA98170.1| (Z73942) RAB7C [Lotus japonicus]	2661.115	2659.000	1.001	3302.235	3361.000	0.983	0.992
16	5	11	RT091D07	a76couture1024.r#1	>ref|NP_567837.1|| (NM_119142) expressed protein; protein id: At4g29960.1. supported	260.992	278.000	0.939	362.453	370.000	0.980	0.959
16	5	12	RT071F12	a76couture0934.r#1	>ref|NP_196963.2|| (NM_121463) isocitrate dehydrogenase - like protein; protein id:	850.408	775.000	1.097	978.211	906.000	1.080	1.089
16	5	13	GT171H01	a76couture1751.r#1	>ref|NP_179672.2|| (NM_127644) unknown protein; protein id: At2g20790.1. supported by	207.295	244.000	0.850	259.483	295.000	0.880	0.865
16	5	14	GB009G06	a76couture1660.r#1	------	9.990	19.000	0.526	15.445	33.000	0.468	0.497
16	5	15	GB001B11	a76couture1563.r#1	------	37.463	50.000	0.749	30.891	47.000	0.657	0.703
16	6	1	TT251B06	a76couture1412#1	>ref|NP_175250.1|| (NM_103712) signal recognition particle 19 kDa protein subunit	1689.577	1472.000	1.148	2126.322	1755.000	1.212	1.180
16	6	2	GT171B11	a76couture1747.r#1	------	146.105	139.000	1.051	206.969	179.000	1.156	1.104
16	6	3	GB009F09	a76couture1656.r#1	------	36.214	39.000	0.929	18.535	25.000	0.741	0.835
16	6	4	TT283F12	a76couture1528.r#1	>dbj|BAA97380.1| (AB023044) gene_id:MWD22.12~pir||T00623~similar to unknown protein	746.761	705.000	1.059	952.469	802.000	1.188	1.123
16	6	5	TB007F12	a76couture1408.r#1	>gb|AAM64310.1| (AY086234) unknown [Arabidopsis thaliana]	1443.571	955.000	1.512	1838.007	1209.000	1.520	1.516
16	6	6	GT173A07	a76couture1743.r#1	>ref|NP_196554.1|| (NM_121029) 15.9 kDa subunit of RNA polymerase II (gb|AAB95261.1);							
16	6	7	GB009E12	a76couture1653.r#1	------	18.731	20.000	0.937	33.980	33.000	1.030	0.983
16	6	8	TT283H07	a76couture1524.r#1	>pir||S34448 small nuclear ribonucleoprotein U2B" - potato	109.891	86.000	1.278	188.434	134.000	1.406	1.342
16	6	9	TB005G12	a76couture1404.r#1	------	32.468	53.000	0.613	29.861	51.000	0.586	0.599
16	6	10	GT172G10	a76couture1739#1	>ref|NP_197494.1|| (NM_122001) putative protein; protein id: At5g19940.1. supported by	93.657	81.000	1.156	118.415	105.000	1.128	1.142
16	6	11	GB009E03	a76couture1649.r#1	>gb|AAM61605.1| (AY085048) unknown [Arabidopsis thaliana]	397.107	395.000	1.005	428.353	469.000	0.913	0.959
16	6	12	TT283F06	a76couture1519.r#1	>ref|NP_189058.1|| (NM_113321) type 1 membrane protein. putative; protein id:	3487.797	3818.000	0.914	4087.892	4483.000	0.912	0.913
16	6	13	TB003H05	a76couture1398.r#1	------	452.052	404.000	1.119	686.807	578.000	1.188	1.154
16	6	14	GT172G04	a76couture1736#1	------	8.741	10.000	0.874	16.475	17.000	0.969	0.922
16	6	15	GB009D09	a76couture1646#1	>ref|NP_012089.1|| (NC_001140) Hypothetical ORF; Yhr217cp [Saccharomyces cerevisiae]	72.428	93.000	0.779	77.227	107.000	0.722	0.750
16	7	1	TT283A07	a76couture1514.r#1	>ref|NP_179734.1|| (NM_127711) coatomer alpha subunit; protein id: At2g21390.1	304.698	368.000	0.828	544.709	586.000	0.930	0.879
16	7	2	TB001F06	a76couture1393.r#1	>sp|Q9SSK9|ML28_ARATH MLP-like protein 28 >gi|5902396|gb|AAD55498.1|AC008148_8 (AC008148)	216.036	178.000	1.214	414.967	284.000	1.461	1.337
16	7	3	GT172F09	a76couture1732#1	>ref|NP_187119.1|| (NM_111340) unknown protein; protein id: At3g04680.1. supported by	164.837	139.000	1.186	215.206	158.000	1.362	1.274
16	7	4	GB009C06	a76couture1642.r#1	------	3.746	7.000	0.535	3.089	7.000	0.441	0.488
16	7	5	TT282B01	a76couture1509.r#1	>ref|NP_194749.1|| (NM_119166) putative protein; protein id: At4g30200.1. supported by	663.093	507.000	1.308	736.233	568.000	1.296	1.302
16	7	6	RT062C09	a76couture1388.r#1	------	718.039	553.000	1.298	794.925	627.000	1.268	1.283
16	7	7	RT033C10	a76couture2154.r#1	>ref|NP_564128.1|| (NM_101953) expressed protein; protein id: At1g21000.1. supported	1588.427	1412.000	1.125	1894.640	1525.000	1.242	1.184
16	7	8	RT022E08	a76couture2053#1	>ref|NP_174489.1|| (NM_102943) hypothetical protein; protein id: At1g32090.1	445.809	564.000	0.790	705.342	784.000	0.900	0.845
16	7	9	RB008G09	a76couture1972#1	------	23.727	29.000	0.818	23.683	28.000	0.846	0.832
16	7	10	GT194D01	a76couture1844.r#1	------	148.603	160.000	0.929	160.633	185.000	0.868	0.899
16	7	11	RT033A03	a76couture2149.r#1	>ref|NP_568817.1|| (NM_124875) putative protein; protein id: At5g54930.1. supported by	244.758	231.000	1.060	263.602	277.000	0.952	1.006
16	7	12	RT022D10	a76couture2051#1	>ref|NP_195496.1|| (NM_119944) putative protein; protein id: At4g37830.1. supported by	1227.535	1331.000	0.922	1708.265	1713.000	0.997	0.960
16	7	13	RB008F03	a76couture1968.r#1	------	8.741	13.000	0.672	24.713	29.000	0.852	0.762
16	7	14	GT193F06	a76couture1840.r#1	>pir||S21495 tomato leucine zipper-containing protein - tomato	395.858	498.000	0.795	620.907	715.000	0.868	0.832
16	7	15	RT031F02	a76couture2145.r#1	>ref|NP_190276.1|| (NM_114559) protein kinase - like protein; protein id: At3g46920.1	32.468	39.000	0.833	12.356	21.000	0.588	0.710
16	8	1	RT022D05	a76couture2048#1	------	17.483	25.000	0.699	24.713	28.000	0.883	0.791
16	8	2	RB008E10	a76couture1965.r#1	>ref|NP_563975.1|| (NM_101409) expressed protein; protein id: At1g15400.1. supported	16.234	21.000	0.773	15.445	18.000	0.858	0.816
16	8	3	GT193B08	a76couture1835.r#1	------	136.115	138.000	0.986	207.999	187.000	1.112	1.049
16	8	4	RT032G03	a76couture2141.r#1	>ref|NP_192573.1|| (NM_116902) putative protein; protein id: At4g08330.1 [Arabidopsis	375.878	385.000	0.976	568.392	528.000	1.077	1.026

16	8	5	RT022C11	a76couture2044.r#1	>ref|NP_568364.1|| (NM_121863) putative protein; protein id: At5g18580.1. supported by	849.159	917.000	0.926	1100.745	1010.000	1.090	1.008
16	8	6	RB008D04	a76couture1962.r#1	>gb|AAF63787.1|AF142406_1 (AF142406) 200 kDa antigen p200 [Babesia bigemina]	123.628	104.000	1.189	166.811	138.000	1.209	1.199
16	8	7	GT192D01	a76couture1832.r#1	>gb|AAA81668.1| (U38184) ATPase subunit 6 [Trypanosoma cruzi]	9.990	6.000	1.665	15.445	11.000	1.404	1.535
16	8	8	RT032E11	a76couture2136.r#1	>gb|AAD25755.1|AC007060_13 (AC007060) T5I8.13 [Arabidopsis thaliana]	136.115	100.000	1.361	148.276	129.000	1.149	1.255
16	8	9	RT022C05	a76couture2041#1	>emb|CAB77245.1| (AJ133148) putative seed imbibition protein [Persea americana]	779.228	628.000	1.241	761.975	680.000	1.121	1.181
16	8	10	RB008A04	a76couture1960#1	------	13.736	16.000	0.859	15.445	19.000	0.813	0.836
16	8	11	GT192F10	a76couture1828.r#1	>ref|NP_567509.2|| (NM_117766) growth regulator like protein; protein id: At4g16650.1	457.047	397.000	1.151	438.650	432.000	1.015	1.083
16	8	12	Arabidopsis Control Oligonucleotide	3ara7		32.468	32.000	1.015	36.039	39.000	0.924	0.969
16	8	13	RT022B01	a76couture2037.r#1	>ref|NP_182128.1|| (NM_130167) hypothetical protein; protein id: At2g46040.1	26.224	33.000	0.795	36.039	46.000	0.783	0.789
16	8	14	RB007D12	a76couture1955.r#1	>dbj|BAB83170.1| (AB038798) twin LOV protein 1 [Arabidopsis thaliana]	403.351	411.000	0.981	467.482	475.000	0.984	0.983
16	8	15	GT191D12	a76couture1824.r#1	>ref|NP_030474.1|| (NM_147392) similar to putative adenylate kinase; protein id:	457.047	552.000	0.828	663.124	818.000	0.811	0.819
16	9	1	TT274E11	a76couture2555#1	>ref|NP_187002.1|| (NM_111223) unknown protein; protein id: At3g03520.1. supported by	255.997	199.000	1.286	393.344	260.000	1.513	1.400
16	9	2	TT251B11	a76couture2459#1	>gb|AAG16977.1|AF184076_1 (AF184076) ACC synthase [Prunus armeniaca]	121.130	117.000	1.035	111.207	105.000	1.059	1.047
16	9	3	RT063A12	a76couture2342.r#1	>dbj|BAA97293.1| (AB019236) gb|AAF03448.1~gene_id:MXK3.3~similar to unknown protein	136.115	142.000	0.959	244.038	207.000	1.179	1.069
16	9	4	Arabidopsis Control Oligonucleotide	3ara7		37.463	35.000	1.070	52.514	45.000	1.167	1.119
16	9	5	TT274G05	a76couture2551.r#1	>ref|NP_186854.1|| (NM_111071) putative potassium transporter; protein id: At3g02050.1	668.089	725.000	0.922	890.687	872.000	1.021	0.971
16	9	6	TT242H09	a76couture2453.r#1	>gb|AAM61622.1| (AY085066) unknown [Arabidopsis thaliana]	1632.134	1743.000	0.936	2310.637	2175.000	1.062	0.999
16	9	7	RT062F04	a76couture2337.r#1	>ref|NP_194708.1|| (NM_119125) putative protein; protein id: At4g29790.1. supported by	649.357	595.000	1.091	695.045	654.000	1.063	1.077
16	9	8	RT051C05	a76couture2249.r#1	>ref|NP_178939.1|| (NM_126895) hypothetical protein; protein id: At2g12550.1	124.876	104.000	1.201	177.108	170.000	1.042	1.121
16	9	9	TT274C04	a76couture2547.r#1	>ref|NP_196820.1|| (NM_121319) protein kinase-like; protein id: At5g13160.1. supported	437.067	433.000	1.009	472.630	520.000	0.909	0.959
16	9	10	TT241E10	a76couture2448.r#1	>ref|NP_198235.1|| (NM_122766) putative protein; protein id: At5g28830.1 [Arabidopsis	741.766	688.000	1.078	652.827	651.000	1.003	1.040
16	9	11	RT062D03	a76couture2334#1	none	43.707	43.000	1.016	48.396	53.000	0.913	0.965
16	9	12	RT051A03	a76couture2246#1	------	9.990	13.000	0.768	6.178	14.000	0.441	0.605
16	9	13	TT273A11	a76couture2542.r#1	>ref|NP_188938.1|| (NM_113198) elongation factor Tu family protein; protein id:	543.212	521.000	1.043	625.025	570.000	1.097	1.070
16	9	14	TT242D04	a76couture2441.r#1	>sp|P93348|TF2D_TOBAC Transcription initiation factor TFIID (TATA-box factor) (TATA	149.852	169.000	0.887	198.731	207.000	0.960	0.923
16	9	15	RT061H03	a76couture2331.r#1	>gb|AAN05420.1| (AY129244) putative RING protein [Populus x canescens]	498.257	433.000	1.151	561.184	551.000	1.018	1.085
16	10	1	RT044G04	a76couture2242.r#1	>ref|NP_564513.1|| (NM_103667) expressed protein; protein id: At1g47740.1. supported	99.901	105.000	0.951	134.890	127.000	1.062	1.007
16	10	2	TT272D04	a76couture2539.r#1	------	28.722	46.000	0.624	56.633	68.000	0.833	0.729
16	10	3	TT241D04	a76couture2437.r#1	>ref|NP_200165.1|| (NM_124733) vacuolar sorting protein-like; embryogenesis protein H	280.972	218.000	1.289	369.661	281.000	1.316	1.302
16	10	4	RT061E10	a76couture2327.r#1	>ref|NP_193160.1|| (NM_117501) hypothetical protein; protein id: At4g14240.1	349.654	293.000	1.193	540.590	420.000	1.287	1.240
16	10	5	RT044E11	a76couture2238.r#1	>dbj|BAB84370.1| (AP003223) contains ESTs C71809(E0380).C98539(E0380)~unknown	154.847	156.000	0.993	214.177	194.000	1.104	1.048
16	10	6	TT264C07	a76couture2536.r#1	------	74.926	53.000	1.414	80.316	59.000	1.361	1.387
16	10	7	TB007G12	a76couture2433.r#1	>ref|NP_176363.1|| (NM_104852) RNA polymerase II subunit (hsRPB10). putative; protein	2598.677	2066.000	1.258	2705.011	2317.000	1.167	1.213
16	10	8	RT061C07	a76couture2323.r#1	>ref|NP_181528.1|| (NM_129557) 26S proteasome regulatory subunit; protein id:	1203.808	1091.000	1.103	1120.309	1188.000	0.943	1.023
16	10	9	RT044E02	a76couture2234.r#1	------	433.321	488.000	0.888	494.254	629.000	0.786	0.837
16	10	10	RT092G07	a76couture3071.r#1	>emb|CAA71883.1| (Y10992) osmotin-like protein [Vitis vinifera]	3185.596	4103.000	0.776	3474.194	4960.000	0.700	0.738
16	10	11	CT002E09	a76couture2923#1	>ref|NP_179742.1|| (NM_127719) putative ubiquitin activating enzyme; protein id:	28.722	29.000	0.990	35.010	34.000	1.030	1.010
16	10	12	PT008H01	a76couture2786.r#1	>gb|AAK14411.1|AC087851_3 (AC087851) unknown protein [Oryza sativa]	795.462	747.000	1.065	1083.240	1022.000	1.060	1.062
16	10	13	PT009D02	a76couture2680.r#1	------	1708.309	1441.000	1.186	2181.925	1832.000	1.191	1.188
16	10	14	RB005C10	a76couture3066.r#1	>gb|AAD32146.1|AF123508_1 (AF123508) Nt-iaa28 deduced protein [Nicotiana tabacum]	2072.947	1151.000	1.801	2103.669	1381.000	1.523	1.662
16	10	15	RT082E11	a76couture2918.r#1	>dbj|BAB89620.1| (AP003258) hypothetical protein~similar to Arabidopsis thaliana	126.125	140.000	0.901	106.059	140.000	0.758	0.829
16	11	1	PT008A11	a76couture2781.r#1	>ref|NP_197752.1|| (NM_122268) cation-transporting ATPase; protein id: At5g23630.1	460.794	397.000	1.161	587.956	483.000	1.217	1.189
16	11	2	PT002B04	a76couture2675.r#1	------	755.502	641.000	1.179	865.974	751.000	1.153	1.166
16	11	3	RB008D02	a76couture3058.r#1	>gb|AAC33732.1| (AF061329) PR-4 type protein [Vitis vinifera]	706.800	539.000	1.311	1194.447	924.000	1.293	1.302
16	11	4	TT261D06	a76couture2914.r#1	>emb|CAA05979.1| (AJ003197) adenine nucleotide translocator [Lupinus albus]	4997.552	4526.000	1.104	6035.047	5000.000	1.207	1.156
16	11	5	PT011B02	a76couture2776.r#1	>ref|NP_567224.1|| (NM_116454) hypothetical protein identical to T10M13.21; protein	11.239	12.000	0.937	14.416	15.000	0.961	0.949
16	11	6	PT009D05	a76couture2671.r#1	------	258.494	200.000	1.292	267.721	243.000	1.102	1.197
16	11	7	RT074G04	a76couture3050.r#1	>ref|NP_566522.1|| (NM_112436) expressed protein; protein id: At3g15660.1. supported	14209.680	9131.000	1.556	14108.892	10996.000	1.283	1.420
16	11	8	ST002D09	a76couture2909.r#1	>sp|O04066|ACBP_RICCO ACYL-COA-BINDING PROTEIN (ACBP) >gi|7441625|pir||T09844	18094.584	15512.000	1.166	16637.825	16321.000	1.019	1.093
16	11	9	PT003B11	a76couture2772.r#1	>gb|AAL09731.1| (AY057490) At2g32240/F22D22.1 [Arabidopsis thaliana]	1334.928	1182.000	1.129	1435.396	1435.000	1.000	1.065
16	11	10	PT005H11	a76couture2667.r#1	------	1269.993	693.000	1.833	1246.962	855.000	1.458	1.646
16	11	11	RT043H04	a76couture3041.r#1	>ref|NP_172473.1|| (NM_100876) unknown protein; protein id: At1g10020.1 [Arabidopsis	594.411	316.000	1.881	617.817	358.000	1.726	1.803
16	11	12	PT010E09	a76couture2906.r#1	------	18050.877	19997.000	0.903	18330.645	21124.000	0.868	0.885
16	11	13	PT011C12	a76couture2768.r#1	>ref|NP_190540.1|| (NM_114831) putative protein; protein id: At3g49710.1 [Arabidopsis	67.433	70.000	0.963	83.405	88.000	0.948	0.956
16	11	14	PT001B10	a76couture2664.r#1	------	407.097	384.000	1.060	287.285	357.000	0.805	0.932
16	11	15	RT081H04	a76couture3035.r#1	>dbj|BAA21108.1| (D88414) actin [Gossypium hirsutum]	7435.138	8318.000	0.894	7406.602	8171.000	0.906	0.900
16	12	1	RB008H04	a76couture2902.r#1	------	49.951	63.000	0.793	46.336	57.000	0.813	0.803
16	12	2	PT006C06	a76couture2762.r#1	------	506.998	458.000	1.107	570.451	503.000	1.134	1.121
16	12	3	PT011H08	a76couture2660.r#1	------	87.413	69.000	1.267	77.227	57.000	1.355	1.311
16	12	4	GB003e05 GB003E05	couture_a76.40.c1.r#1	>gb|AAA81891.1| (U02496) epoxide hydrolase [Solanum tuberosum]	61.189	78.000	0.784	58.693	69.000	0.851	0.818
16	12	5	BM436776 TT282B09	couture_a76.320.c1.r#1	>pir||T48530 clathrin binding protein-like - Arabidopsis thaliana	1334.928	1319.000	1.012	1530.128	1648.000	0.928	0.970
16	12	6	BM437258 GT174C09	couture_a76.231.c1.r#1	>ref|NP_567534.1|| (NM_117875) expressed protein; protein id: At4g17670.1. supported	3809.978	4018.000	0.948	3823.261	4503.000	0.849	0.899
16	12	7	BM437828 CT004E06	couture_a76.133.c1#1	------	413.341	390.000	1.060	395.403	421.000	0.939	1.000
16	12	8	BG273712 RB000A90	couture_a76.398.c1.r#1	>ref|NP_194929.1|| (NM_119353) similar to putative VP1/ABI3 family regulatory protein;	42.458	42.000	1.011	37.069	48.000	0.772	0.892
16	12	9	TB003c11 TT273A09	couture_a76.318.c1#1	>pir||T09153 glucose-6-phosphate isomerase (EC 5.3.1.9) precursor. chloroplast -	887.871	922.000	0.963	898.924	1019.000	0.882	0.923
16	12	10	PT009D01 BM437527 BM437488 GT171B07	couture_a76.227.c1#1	>ref|NP_195785.1|| (NM_120243) Macrophage migration inhibitory factor (MIF) family;	368.385	262.000	1.406	280.077	298.000	0.940	1.173
16	12	11	BM437595 CT001F05	couture_a76.128.c1.r#1	------	1010.250	1016.000	0.994	933.934	1067.000	0.875	0.935
16	12	12	BM436757 BM437641 GT203E06 BM437078 BM	couture_a76.395.c1#1	>ref|NP_565335.1|| (NM_126649) expressed protein; protein id: At2g06520.1. supported	37.463	40.000	0.937	42.218	49.000	0.862	0.899

16	12	13	BM437582 TT262A04	couture_a76.314.c1#1	>ref|NP_567574.1|| (NM_118030) kinase-like protein; protein id: At4g19110.1. supported	148.603	150.000	0.991	134.890	153.000	0.882	0.936
16	12	14	GB007f04 GB007F04	couture_a76.224.c1.r#1	>ref|NP_173259.1|| (NM_101681) calcium-binding protein. putative; protein id:	8364.218	8037.000	1.041	7990.440	9045.000	0.883	0.962
16	12	15	BE846392 ST002C06	couture_a76.124.c1.r#1	>gb|AAK58599.1|AF269158_1 (AF269158) ethylene-induced esterase [Citrus sinensis]	2678.598	2496.000	1.073	2966.554	3280.000	0.904	0.989
16	13	1	BG273779 RB000A20	couture_a76.390.c1#1	>gb|AAK72889.1|AC091123_8 (AC091123) unknown protein [Oryza sativa]	71.180	73.000	0.975	114.296	111.000	1.030	1.002
16	13	2	BG273891 TB000A01 BM436851	couture_a76.310.c1#1	>dbj|BAB32914.1| (AP003047) contains ESTs AU029632(E31167).AU162277(E31167)~similar	787.970	721.000	1.093	1204.744	1017.000	1.185	1.139
16	13	3	GB005a07 GB005A07	couture_a76.219.c1.r#1	>ref|NP_566182.1|| (NM_111147) expressed protein; protein id: At3g02790.1. supported	558.197	578.000	0.966	951.439	1035.000	0.919	0.943
16	13	4	BM437093 TT283G06	couture_a76.121.c1.r#1	>gb|AAK63967.1| (AY039863) AT4g11600/T5C23_30 [Arabidopsis thaliana]	6598.467	5884.000	1.121	6757.894	6953.000	0.972	1.047
16	13	5	BG273767 RB000A33	couture_a76.388.c1#1	>gb|AAF13742.1|AF108438_1 (AF108438) putative NADPH-dependent oxidoreductase [Papaver	581.924	519.000	1.121	617.817	565.000	1.093	1.107
16	13	6	BG273857 TB000A35	couture_a76.307.c1.r#1	>ref|NP_199558.1|| (NM_124120) nodulin-like protein; protein id: At5g47470.1	2793.484	2790.000	1.001	3045.840	3151.000	0.967	0.984
16	13	7	GB001H08 BM437870	couture_a76.213.c1#1	>ref|NP_197460.1|| (NM_121964) putative protein; protein id: At5g19590.1 [Arabidopsis	2179.092	2255.000	0.966	2355.944	2523.000	0.934	0.950
16	13	8	BG273884 TB000A08	couture_a76.118.c1#1	>ref|NP_188633.1|| (NM_112889) hypothetical protein; protein id: At3g19990.1	4551.743	3922.000	1.161	4962.104	4628.000	1.072	1.116
16	13	9	BM437470 BM436947 BM437865 BM437267 GT2	couture_a76.384.c1.r#1	------	696.810	492.000	1.416	688.867	550.000	1.252	1.334
16	13	10	BG273816 TB000A78 TB000A78	couture_a76.303.c1#1	>ref|NP_566800.1|| (NM_113593) transport inhibitor response 1 (TIR1). putative;	877.881	1079.000	0.814	816.549	1049.000	0.778	0.796
16	13	11	BG273965 CM005a02	couture_a76.21.c1#1	emb|CAB61630.1| (AJ251317) putative protein phosphatase [Rubus i... 250 1e-065	2718.558	2063.000	1.318	1891.551	1778.000	1.064	1.191
16	13	12	RT094B09 BM436597	couture_a76.113.c1.r#1	>ref|NP_563969.1|| (NM_101396) expressed protein; protein id: At1g15270.1. supported	197.305	160.000	1.233	185.345	178.000	1.041	1.137
16	13	13	BM437076 PT005B12	couture_a76.71.c1.r#1	>ref|NP_567476.1|| (NM_117672) Expressed protein; protein id: At4g15800.1. supported	5477.077	4221.000	1.298	3325.918	3263.000	1.019	1.158
16	13	14	BM437520 BM436322 BM436911 RT032B03	couture_a76.56.c1.r#1	>dbj|BAB91740.1| (AP003284) putative nifU-like protein [Oryza sativa (japonica	5850.457	5508.000	1.062	5200.994	6064.000	0.858	0.960
16	13	15	AW707988 BG273733 BG273860 RT061C10 BG2	couture_a76.sd.55.c1#	>emb|CAB85625.1| (AJ237985) putative ripening-related protein [Vitis vinifera]	15701.953	14673.000	1.070	21946.937	24652.000	0.890	0.980
16	14	1	BM436566 RT064C03 BM437356	couture_a76.70.c1.r#1	>sp|P37707|B2_DAUCA B2 PROTEIN >gi|322726|pir||S32124 B2 protein - carrot	7104.216	5218.000	1.361	9651.339	7402.000	1.304	1.333
16	14	2	RB007F10 GT184H02	couture_a76.577.c1.r#1	>ref|NP_196488.1|| (NM_120962) putative protein; protein id: At5g09260.1 [Arabidopsis	576.929	493.000	1.170	538.531	608.000	0.886	1.028
16	14	3	BM437082 BG273812 TB000A82	couture_a76.486.c1.r#1	>emb|CAD40829.1| (AL606615) OSJNBa0086B14.1 [Oryza sativa]	252.250	262.000	0.963	252.275	298.000	0.847	0.905
16	14	4	BG273791 RB000A07 HK001A01C	couture_a76.9.c1.r#1	>gb|AAG28503.1|AF196966_1 (AF196966) hexokinase [Citrus sinensis]	946.563	744.000	1.272	950.409	817.000	1.163	1.218
16	14	5	BM437012 GT181G07	couture_a76.576.c1.r#1	>gb|AAF19827.1|AF202771_1 (AF202771) RUB1 conjugating enzyme [Arabidopsis thaliana]	1588.427	1750.000	0.908	1658.840	1854.000	0.895	0.901
16	14	6	G5802952 AF178989	couture_a76.sd.71.c1#	>gb|AAD51853.1|AF178989_1 (AF178989) pectin methylesterase [Vitis riparia]	34.965	35.000	0.999	3.089	3.000	1.030	1.014
16	14	7	BM437162 BM437276 BM437575 AW707973 BM	couture_a76.643.c1.r#1	>ref|NP_172801.1|| (NM_101214) glyceraldehyde-3-phosphate dehydrogenase. putative;	12026.842	10089.000	1.192	10060.128	10095.000	0.997	1.094
16	14	8	RB007C03 RB007C03	couture_a76.55.c1.r#1	>dbj|BAB84111.1| (AB066274) chalcone synthase [Vitis vinifera]	5099.950	3651.000	1.397	3719.261	3290.000	1.130	1.264
16	14	9	VVSUT2SUC AF182445 gi|6434828|gb|AF02180	couture_a76.sd.42.c1#	>gb|AAD55269.1|AF182445_1 (AF182445) sucrose transporter [Vitis vinifera]	1158.853	995.000	1.165	1014.250	945.000	1.073	1.119
16	14	10	AW707969 TT284F08	couture_a76.564.c1.r#1	>sp|O82572|PRO1_RICCO Profilin 1 >gi|3694872|gb|AAC62482.1| (AF092547) profilin [Ricinus	4726.570	4850.000	0.975	4929.154	5459.000	0.903	0.939
16	14	11	BM437027 TT242G12	couture_a76.472.c1.r#1	>gb|AAG35782.1|AF280060_1 (AF280060) tonneau 1 [Oryza sativa] [Oryza sativa (japonica	556.949	456.000	1.221	431.443	410.000	1.052	1.137
16	14	12	TB004a10 BE846410 BE846409 72F1GLUTA	couture_a76.8.c1.r#1	sp|P49332|GTXC_TOBAC PROBABLE GLUTATHIONE S-TRANSFERASE PARC (AUXIN-REGULATED PROTEIN	4394.399	3703.000	1.187	4745.868	4609.000	1.030	1.108
16	14	13	BM437658 BM437344 BM437630 RT061A04	couture_a76.563.c2.r#1	>emb|CAC27140.1| (AJ132535) ADP. ATP carrier protein precursor [Picea abies]	2835.942	2795.000	1.015	1709.295	2179.000	0.784	0.900
16	14	14	TB005d10 GT173A09 RT043E02	couture_a76.541.c1#1	>sp|P46266|1433_PEA 14-3-3-LIKE PROTEIN >gi|555974|gb|AAA85817.1| (U15036) 14-3-3-like	202.300	216.000	0.937	161.662	220.000	0.735	0.836

Table B The summery normalized data of *V.vinifera* genes from Table A

Block	Row	Column	Name	ID	Subject	first replication			second replication			average
						Cy5 intensity	Cy3 intensity	Cy5/Cy3 ratio	Cy5 intensity	Cy3 intensity	Cy5/Cy3 ratio	Cy5/Cy3 ratio
1	14	4	PT011C03 VVI318053	couture_a76.sd.28.c1#1	>emb|CAC39216.1| (AJ318053) glutamine synthetase [Vitis vinifera]	593.163	878.000	0.676	523.085	956.000	0.547	0.611
1	14	7	RT043A09 VVADC	couture_a76.sd.75.c1#1	>emb|CAA65585.1| (X96791) arginine decarboxylase [Vitis vinifera]	1658.358	1978.000	0.838	1587.791	1857.000	0.855	0.847
1	14	10	BM438125 BG273914 AW707997 BE846437 BG27	couture_a76.sd.16.c1#1	>gb|AAK69513.1|AF281656_1 (AF281656) putative transcription factor [Vitis vinifera]	24440.800	25929.000	0.943	23971.319	26136.000	0.917	0.930
1	14	13	G18139650 AY070232	couture_a76.sd.15.c1.r#1	>gb|AAL58535.1| (AY070232) calmodulin [Vitis vinifera]	6.244	16.000	0.390	5.148	11.000	0.468	0.429
2	1	10	CT002B04	a76couture0367.r#1	>emb|CAB85624.1| (AJ237984) putative proline-rich cell wall protein [Vitis vinifera]	1088.922	1162.000	0.937	1382.882	1291.000	1.071	1.004
2	4	8	RT043G01	a76couture1354.r#1	>gb|AAK81875.1| (AY043232) pectin methylesterase PME1 [Vitis vinifera]	1650.865	1860.000	0.888	2296.222	2274.000	1.010	0.949
2	13	13	VVU73709 G7271875 AF239617	couture_a76.sd.60.c1#1	>gb|AAF44667.2|AF239617_1 (AF239617) beta-1.3-glucanase [Vitis vinifera]	218.534	182.000	1.201	275.958	264.000	1.045	1.123
2	14	1	G15824822 AF359521	couture_a76.sd.6.c1#1	>gb|AAL09479.1|AF359521_1 (AF359521) inward rectifying shaker-like K+ channel [Vitis vinifera]	46.204	39.000	1.185	25.742	31.000	0.830	1.008
2	14	7	G7406711 VVI237995	couture_a76.sd.47.c1#1	>emb|CAB85635.1| (AJ237995) putative ripening-related P-450 enzyme [Vitis vinifera]	12468.904	10145.000	1.229	12188.510	13052.000	0.934	1.081
3	2	1	G7264741 reverse complement 1623 bases	a76couture0044.r#1	>gb|AAF44336.1|AF195867_1 (AF195867) alcohol dehydrogenase 7 [Vitis vinifera]	157.344	170.000	0.926	157.543	165.000	0.955	0.940
3	13	13	G9957233 AF177590	couture_a76.sd.34.c1#1	>gb|AAG09278.1|AF177590_1 (AF177590) ornithine aminotransferase [Vitis vinifera]	128.623	177.000	0.727	185.345	201.000	0.922	0.824
3	13	14	BM437094 BE846423 BM437463 BM436297 RT06	couture_a76.613.c1#1	>emb|CAC16165.1| (AJ291704) pathogenesis-related protein 10 [Vitis vinifera]	4586.709	5289.000	0.867	5972.236	5589.000	1.069	0.968
3	14	1	G10732643 AF195868	couture_a76.sd.33.c1#1	>gb|AAG22488.1|AF195868_1 (AF195868) pyruvate decarboxylase 1 [Vitis vinifera]	12480.143	7517.000	1.660	13833.963	9612.000	1.439	1.550
3	14	15	G9885273 AF194174	couture_a76.sd.36.c1#1	>gb|AAG01382.1|AF194174_1 (AF194174) alcohol dehydrogenase 2 [Vitis vinifera]	1804.463	1961.000	0.920	2431.112	2233.000	1.089	1.004
4	1	10	RT084F03	a76couture0305#1	>emb|CAB85628.1| (AJ237988) putative ripening-related protein [Vitis vinifera]	1247.515	1104.000	1.130	1522.920	1455.000	1.047	1.088
4	14	12	G1785612 VVU83274 AF176652 VVPYPOXC	couture_a76.sd.70.c1#1	>gb|AAB41022.1| (U83274) polyphenol oxidase [Vitis vinifera]	417.087	1073.000	0.389	622.966	1530.000	0.407	0.398
4	14	15	PI103A01C AF141899 AF188844	couture_a76.sd.11.c1#1	>gb|AAF80557.1|AF188844_1 (AF188844) plasma membrane aquaporin [Vitis vinifera]	4569.226	4163.000	1.098	6132.868	5959.000	1.029	1.063
5	4	4	RT063E05	a76couture1386#1	>emb|CAB85632.1| (AJ237992) putative ripening-related bZIP protein [Vitis vinifera]	76.175	80.000	0.952	65.901	78.000	0.845	0.899
5	13	1	GB001g05 RT052H03	couture_a76.46.c1#1	>gb|AAB47171.1| vacuolar invertase 1. GIN1 [Vitis viniferagrape berries. Sultana	454.550	867.000	0.524	451.007	964.000	0.468	0.496
5	14	9	PT006E03 BG273849 VVI237999 AF003007	couture_a76.sd.45.c1#1	>emb|CAB85637.1| (AJ237999) putative thaumatin-like protein [Vitis vinifera]	22426.545	22655.000	0.990	26165.601	29062.000	0.900	0.945
6	1	15	PT012E10	a76couture0232#1	>gb|AAM21344.1|AF373603_1 (AF373603) MADS-box protein 4 [Vitis vinifera]	3334.199	2701.000	1.234	3603.935	3482.000	1.035	1.135
6	10	2	PT003A01	a76couture2613.r#1	>dbj|BAB84111.1| (AB066274) chalcone synthase [Vitis vinifera]	2235.287	1508.000	1.482	2308.578	2159.000	1.069	1.276
6	10	10	G9885271 reverse complement 1355 bases	a76couture3160.r#1	>gb|AAB65840.1| (U36586) alcohol dehydrogenase [Vitis vinifera]	4769.028	4589.000	1.039	5772.475	6268.000	0.921	0.980
6	11	1	GB009G03	a76couture2848.r#1	>gb|AAL79826.1|AF440310_1 (AF440310) actin depolymerizing factor [Vitis vinifera]	3392.891	3147.000	1.078	3282.670	4048.000	0.811	0.945
6	13	15	G7271882 AF239740	couture_a76.sd.59.c1#1	>gb|AAF44672.1|AF239740_1 (AF239740) caffeic acid O-methyltransferase [Vitis vinifera]	1317.446	1767.000	0.746	1443.634	1840.000	0.785	0.765
6	14	3	G14764485 AY039034	couture_a76.sd.27.c1#1	>gb|AAK72100.1| (AY039034) beta-glucosidase [Vitis vinifera]	32.468	45.000	0.722	42.218	64.000	0.660	0.691
6	14	9	BM436621 BM436585 BM436304 G19070129 AF2	couture_a76.sd.2.c1#1	>gb|AAL83720.1|AF236127_1 (AF236127) catalase [Vitis vinifera]	7627.448	6909.000	1.104	10636.758	10596.000	1.004	1.054
7	2	9	RT052H02	a76couture0015.r#1	>gb|AAK58564.1|AF265562_1 (AF265562) MAD-box transcripion factor [Vitis vinifera]	673.084	796.000	0.846	859.796	930.000	0.925	0.885
8	14	2	BG273782 RT083H11 VVU97522 VVU97521	couture_a76.sd.79.c1#1	>gb|AAB65777.1| (U97522) class IV endochitinase [Vitis vinifera]	5183.618	5589.000	0.927	8190.201	6521.000	1.256	1.092
8	14	11	GB005a03 BM436377 AF192308 G7739778 AF25	couture_a76.sd.41.c1#1	>gb|AAF69010.1|AF257777_1 (AF257777) H+-pyrophosphatase [Vitis vinifera]	1841.926	2250.000	0.819	3436.095	3997.000	0.860	0.839
9	3	2	ST001D02	a76couture0593.r#1	>gb|AAG31326.1| (AF178575) putative serine/threonine kinase GDBrPK [Vitis vinifera]	237.265	397.000	0.598	226.533	439.000	0.516	0.557
9	14	2	BM437325 BM437549 BM437422 BM437333 BM43	couture_a76.sd.78.c1#1	>gb|AAB72091.1| (AF020709) chalcone synthase [Vitis vinifera]	991.518	1887.000	0.525	1190.328	1853.000	0.642	0.584
9	14	8	G7547006 AF243474	couture_a76.sd.44.c1#1	>gb|AAF63755.1|AF243474_1 (AF243474) putative ethylene receptor [Vitis vinifera]	183.568	253.000	0.726	197.702	286.000	0.691	0.708
9	**14**	**13**	**G6434830 AF021809**	**couture_a76.sd.65.c1#1**	**>gb|AAF08330.1|AF021809_1 (AF021809) putative sucrose transporter [Vitis vinifera]**	**227.275**	**255.000**	**0.891**	**174.019**	**219.000**	**0.795**	$\boxed{\textbf{0.843}}$
10	10	10	G18152532 reverse complement 879 bases 1	a76couture3147.r#1	>emb|CAD20741.1| (AJ427634) S-adenosyl-L-methionine decarboxylase [Vitis vinifera]	1113.897	1019.000	1.093	1756.661	1379.000	1.274	1.183
10	13	14	VVI237983 BG273874 RB005D10 RT054A08	couture_a76.sd.57.c1#1	>emb|CAB85623.1| (AJ237983) putative proline-rich cell wall protein [Vitis vinifera]	10821.785	14522.000	0.745	13852.498	15740.000	0.880	0.813
10	14	5	G18693181 VVI430780	couture_a76.sd.5.c1#1	>emb|CAD23545.1| (AJ430780) putative callose synthase [Vitis vinifera]	525.729	472.000	1.114	545.739	549.000	0.994	1.054
10	14	8	G13172311 AF305093	couture_a76.sd.18.c1#1	>gb|AAK14075.1|AF305093_1 (AF305093) polygalacturonase inhibiting protein [Vitis vinifera]	12762.364	9631.000	1.325	13480.778	9319.000	1.447	1.386
10	14	10	RT082A04 AF195654	couture_a76.sd.66.c1#1	>gb|AAF06347.1|AF195654_1 (AF195654) SCUTL2 [Vitis vinifera]	6001.558	6229.000	0.963	6940.150	6348.000	1.093	1.028

<table>
<tr><td>10</td><td>14</td><td>13</td><td>BM437813 RT063G09 BM436272 AF440310</td><td>couture_a76.sd.4.c1#1</td><td>>gb|AAL79826.1|AF440310_1 (AF440310) actin depolymerizing factor [Vitis vinifera]</td><td>2164.107</td><td>2518.000</td><td>0.859</td><td>3756.330</td><td>3515.000</td><td>1.069</td><td>0.964</td></tr>
<tr><td>11</td><td>11</td><td>3</td><td>TT254C10</td><td>a76couture3097.r#1</td><td>>gb|AAB65777.1| (U97522) class IV endochitinase [Vitis vinifera]</td><td>21.229</td><td>30.000</td><td>0.708</td><td>29.861</td><td>40.000</td><td>0.747</td><td>0.727</td></tr>
<tr><td>11</td><td>11</td><td>7</td><td>TT281E02</td><td>a76couture3091.r#1</td><td>>emb|CAB91554.1| (AJ277900) beta 1-3 glucanase [Vitis vinifera]</td><td>14027.361</td><td>16903.000</td><td>0.830</td><td>20019.346</td><td>20865.000</td><td>0.959</td><td>0.895</td></tr>
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<tr><td>11</td><td>14</td><td>5</td><td>TB001b08 G15081599 AY043233</td><td>couture_a76.sd.25.c1#1</td><td>>gb|AAK81876.1| (AY043233) polygalacturonase PG1 [Vitis vinifera]</td><td>318.435</td><td>458.000</td><td>0.695</td><td>430.413</td><td>551.000</td><td>0.781</td><td>0.738</td></tr>
<tr><td>11</td><td>14</td><td>6</td><td>BM437502 RT022G08</td><td>couture_a76.573.c1.r#1</td><td>>gb|AAF69802.1|AF195869_1 (AF195869) malate dehydrogenase [Vitis vinifera]</td><td>498.257</td><td>381.000</td><td>1.308</td><td>627.085</td><td>451.000</td><td>1.390</td><td>1.349</td></tr>
<tr><td>11</td><td>14</td><td>10</td><td>GB003a08 BM437880 G7798705 AF195869</td><td>couture_a76.sd.40.c1#1</td><td>>gb|AAF69802.1|AF195869_1 (AF195869) malate dehydrogenase [Vitis vinifera]</td><td>348.405</td><td>294.000</td><td>1.185</td><td>569.422</td><td>428.000</td><td>1.330</td><td>1.258</td></tr>
<tr><td>12</td><td>2</td><td>7</td><td>ST005F03</td><td>a76couture0281.r#1</td><td>>emb|CAB85633.1| (AJ237993) putative ripening-related protein [Vitis vinifera]</td><td>1548.467</td><td>1634.000</td><td>0.948</td><td>2451.706</td><td>2405.000</td><td>1.019</td><td>0.984</td></tr>
<tr><td>12</td><td>14</td><td>7</td><td>G4585616 VVI5686</td><td>couture_a76.sd.72.c1#1</td><td>>emb|CAB40834.1| (AJ005686) pyrroline-5-carboxylate synthetase [Vitis vinifera]</td><td>568.187</td><td>1054.000</td><td>0.539</td><td>1283.001</td><td>1779.000</td><td>0.721</td><td>0.630</td></tr>
<tr><td>12</td><td>14</td><td>14</td><td>G9885275 gi|9885275|gb|AF194175.1|AF1941</td><td>couture_a76.sd.35.c1#1</td><td>>gb|AAG01383.1|AF194175_1 (AF194175) alcohol dehydrogenase 3 [Vitis vinifera]</td><td>1260.002</td><td>1447.000</td><td>0.871</td><td>1419.951</td><td>1755.000</td><td>0.809</td><td>0.840</td></tr>
<tr><td>13</td><td>13</td><td>13</td><td>AW707985 VVI237984 BG273760 RT052C11 BE8</td><td>couture_a76.sd.56.c1.r#1</td><td>>emb|CAB85624.1| (AJ237984) putative proline-rich cell wall protein [Vitis vinifera]</td><td>22375.345</td><td>24254.000</td><td>0.923</td><td>16778.894</td><td>22640.000</td><td>0.741</td><td>0.832</td></tr>
<tr><td>13</td><td>14</td><td>4</td><td>BM437734 VVHT1HEXO VVHEXTRAN</td><td>couture_a76.sd.76.c1#1</td><td>>emb|CAA70777.1| (Y09590) hexose transporter [Vitis vinifera]</td><td>62.438</td><td>111.000</td><td>0.563</td><td>87.524</td><td>133.000</td><td>0.658</td><td>0.610</td></tr>
<tr><td>13</td><td>14</td><td>7</td><td>G7547008 gi|7547008|gb|AF243475.1|AF2434</td><td>couture_a76.sd.43.c1#1</td><td>>gb|AAF63756.1|AF243475_1 (AF243475) pectate lyase [Vitis vinifera]</td><td>79.921</td><td>56.000</td><td>1.427</td><td>66.930</td><td>59.000</td><td>1.134</td><td>1.281</td></tr>
<tr><td>13</td><td>14</td><td>12</td><td>gi|6434832|gb|AF021810.1|AF021810 G64348</td><td>couture_a76.sd.64.c1.r#1</td><td>Vitis vinifera putative sucrose transporter (VvSUC27) mRNA</td><td>262.240</td><td>300.000</td><td>0.874</td><td>227.563</td><td>306.000</td><td>0.744</td><td>0.809</td></tr>
<tr><td>13</td><td>14</td><td>14</td><td>BM436627 BM436370 RT031B12</td><td>couture_a76.613.c2.r#1</td><td>>emb|CAC16166.1| (AJ291705) pathogenesis-related protein 10 [Vitis vinifera]</td><td>2798.479</td><td>935.000</td><td>2.993</td><td>2522.755</td><td>995.000</td><td>2.535</td><td>2.764</td></tr>
<tr><td>14</td><td>7</td><td>1</td><td>GB005C01</td><td>a76couture1597.r#1</td><td>>emb|CAB85635.1| (AJ237995) putative ripening-related P-450 enzyme [Vitis vinifera]</td><td>11.239</td><td>14.000</td><td>0.803</td><td>6.178</td><td>14.000</td><td>0.441</td><td>0.622</td></tr>
<tr><td>14</td><td>13</td><td>13</td><td>VVUFGT G2564111 AF000371</td><td>couture_a76.sd.30.c1#1</td><td>>gb|AAB81682.1| (AF000371) UDP glucose:flavonoid 3-o-glucosyltransferase [Vitis</td><td>468.286</td><td>378.000</td><td>1.239</td><td>429.383</td><td>367.000</td><td>1.170</td><td>1.204</td></tr>
<tr><td>14</td><td>14</td><td>1</td><td>TB005h10 TT274B02 AF236126</td><td>couture_a76.sd.3.c1#1</td><td>>gb|AAL83719.1|AF236126_1 (AF236126) PEP carboxylase [Vitis vinifera]</td><td>762.995</td><td>900.000</td><td>0.848</td><td>767.123</td><td>971.000</td><td>0.790</td><td>0.819</td></tr>
<tr><td>14</td><td>14</td><td>4</td><td>RT072B04 VVI237994</td><td>couture_a76.sd.48.c1#1</td><td>>emb|CAB85634.1| (AJ237994) putative ripening-related protein [Vitis vinifera]</td><td>30467.333</td><td>22632.000</td><td>1.346</td><td>21237.477</td><td>19267.000</td><td>1.102</td><td>1.224</td></tr>
<tr><td>14</td><td>14</td><td>7</td><td>G499023E VVLSTSYM S63227 AF274281 S63225</td><td>couture_a76.sd.17.c1#1</td><td>>emb|CAA54221.1| (X76892) Stilbene synthase [Vitis vinifera]</td><td>2156.615</td><td>261.000</td><td>8.263</td><td>1094.567</td><td>180.000</td><td>6.081</td><td>7.172</td></tr>
<tr><td>15</td><td>1</td><td>12</td><td>G7801383 reverse complement 1038 bases</td><td>a76couture0049.r#1</td><td>>emb|CAB91554.1| (AJ277900) beta 1-3 glucanase [Vitis vinifera]</td><td>227.275</td><td>820.000</td><td>0.277</td><td>316.117</td><td>1056.000</td><td>0.299</td><td>0.288</td></tr>
<tr><td>15</td><td>11</td><td>3</td><td>RT033D07</td><td>a76couture3096.r#1</td><td>>gb|AAB65777.1| (U97522) class IV endochitinase [Vitis vinifera]</td><td>114.886</td><td>108.000</td><td>1.064</td><td>136.950</td><td>126.000</td><td>1.087</td><td>1.075</td></tr>
<tr><td>15</td><td>11</td><td>7</td><td>RB008C12</td><td>a76couture3090.r#1</td><td>>emb|CAB85630.1| (AJ237990) putative metallothionein-like protein [Vitis vinifera]</td><td>11.239</td><td>11.000</td><td>1.022</td><td>16.475</td><td>15.000</td><td>1.098</td><td>1.060</td></tr>
<tr><td>15</td><td>13</td><td>15</td><td>G1561773 VVU67426</td><td>couture_a76.sd.82.c1#1</td><td>>gb|AAB08874.1| (U67426) malate dehydrogenase [Vitis vinifera]</td><td>1612.154</td><td>1519.000</td><td>1.061</td><td>1945.095</td><td>1933.000</td><td>1.006</td><td>1.034</td></tr>
<tr><td>16</td><td>2</td><td>13</td><td>CT002C05</td><td>a76couture0521.r#1</td><td>>emb|CAB85628.1| (AJ237988) putative ripening-related protein [Vitis vinifera]</td><td>482.023</td><td>700.000</td><td>0.689</td><td>736.233</td><td>988.000</td><td>0.745</td><td>0.717</td></tr>
<tr><td>16</td><td>10</td><td>10</td><td>RT092G07</td><td>a76couture3071.r#1</td><td>>emb|CAA71883.1| (Y10992) osmotin-like protein [Vitis vinifera]</td><td>3185.596</td><td>4103.000</td><td>0.776</td><td>3474.194</td><td>4960.000</td><td>0.700</td><td>0.738</td></tr>
<tr><td>16</td><td>11</td><td>3</td><td>RB008D02</td><td>a76couture3058.r#1</td><td>>gb|AAC33732.1| (AF061329) PR-4 type protein [Vitis vinifera]</td><td>706.800</td><td>539.000</td><td>1.311</td><td>1194.447</td><td>924.000</td><td>1.293</td><td>1.302</td></tr>
<tr><td>16</td><td>13</td><td>15</td><td>AW707988 BG273733 BG273860 RT061C10 BG27</td><td>couture_a76.sd.55.c1#1</td><td>>emb|CAB85625.1| (AJ237985) putative ripening-related protein [Vitis vinifera]</td><td>15701.953</td><td>14673.000</td><td>1.070</td><td>21946.937</td><td>24652.000</td><td>0.890</td><td>0.980</td></tr>
<tr><td>16</td><td>14</td><td>8</td><td>RB007C03 RB007C03</td><td>couture_a76.55.c1.r#1</td><td>>dbj|BAB84111.1| (AB066274) chalcone synthase [Vitis vinifera]</td><td>5099.950</td><td>3651.000</td><td>1.397</td><td>3719.261</td><td>3290.000</td><td>1.130</td><td>1.264</td></tr>
<tr><td>16</td><td>14</td><td>9</td><td>VVSUT2SUC AF182445 gi|6434828|gb|AF02180</td><td>couture_a76.sd.42.c1#1</td><td>>gb|AAD55269.1|AF182445_1 (AF182445) sucrose transporter [Vitis vinifera]</td><td>1158.853</td><td>995.000</td><td>1.165</td><td>1014.250</td><td>945.000</td><td>1.073</td><td>1.119</td></tr>
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Table C The summery normalized data of ethylene related genes from Table A

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<tr><td>3</td><td>5</td><td>13</td><td>GT174D12</td><td>a76couture1777.r#1</td><td>>gb|AAF78493.1|AC012187_13 (AC012187) Contains similarity to AP2/EREBP-like transcription</td><td>313.440</td><td>388.000</td><td>0.808</td><td>403.641</td><td>504.000</td><td>0.801</td><td>0.804</td></tr>
<tr><td>4</td><td>13</td><td>7</td><td>BM437083 BM437580 BM436925 GB004H02</td><td>couture_a76.218.c1.r#1</td><td>>pir||T02434 DNA binding protein EREBP-4 - common tobacco</td><td>39.960</td><td>38.000</td><td>1.052</td><td>55.604</td><td>47.000</td><td>1.183</td><td>1.117</td></tr>
<tr><td>8</td><td>11</td><td>11</td><td>RT022E07</td><td>a76couture3044#1</td><td>>emb|CAD21849.1| (AJ420195) ethylene responsive element binding protein [Fagus sp.]</td><td>1645.870</td><td>1439.000</td><td>1.144</td><td>2812.099</td><td>2410.000</td><td>1.167</td><td>1.155</td></tr>
<tr><td>9</td><td>14</td><td>8</td><td>G7547006 AF243474</td><td>couture_a76.sd.44.c1#1</td><td>>gb|AAF63755.1|AF243474_1 (AF243474) putative ethylene receptor [Vitis vinifera]</td><td>183.568</td><td>253.000</td><td>0.726</td><td>197.702</td><td>286.000</td><td>0.691</td><td>0.708</td></tr>
<tr><td>11</td><td>13</td><td>15</td><td>BM436624 RT022E07 RT044H04</td><td>couture_a76.610.c1.r#1</td><td>>emb|CAD21849.1| (AJ420195) ethylene responsive element binding protein [Fagus sp.]</td><td>4421.872</td><td>5213.000</td><td>0.848</td><td>6671.399</td><td>6857.000</td><td>0.973</td><td>0.911</td></tr>
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</table>

Table D The summery normalized data of controls for microarray and RT-PCR

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<tr><th rowspan="2">Block</th><th rowspan="2">Row</th><th rowspan="2">Column</th><th rowspan="2">Name</th><th rowspan="2">ID</th><th rowspan="2">Subject</th><th colspan="3">first replication</th><th colspan="3">second replication</th><th>average</th></tr>
<tr><th>Cy5 intensity</th><th>Cy3 intensity</th><th>Cy5/Cy3 ratio</th><th>Cy5 intensity</th><th>Cy3 intensity</th><th>Cy5/Cy3 ratio</th><th>Cy5/Cy3 ratio</th></tr>
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<tr><td>4</td><td>1</td><td>15</td><td>cds of gi|1469265|emb|X84846.1|PP111ACNP</td><td>luc3#1</td><td>-</td><td>0.000</td><td>-</td><td>-</td><td>13.386</td><td>23.000</td><td>0.582</td><td>0.582</td></tr>
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<tr><td>13</td><td>3</td><td>9</td><td>ST005B04</td><td>a76couture0682.r#1</td><td>>ref|NP_195436.1|| (NM_119882) tubulin-like protein; protein id: At4g37190.1</td><td>16.234</td><td>23.000</td><td>0.706</td><td>14.416</td><td>18.000</td><td>0.801</td><td>0.753</td></tr>
<tr><td>13</td><td>11</td><td>9</td><td>PT007H07</td><td>a76couture2878.r#1</td><td>>ref|NP_568959.1|| (NM_125664) tubulin beta-2/beta-3 chain (sp|P29512); protein id:</td><td>29.970</td><td>48.000</td><td>0.624</td><td>21.624</td><td>46.000</td><td>0.470</td><td>0.547</td></tr>
<tr><td>14</td><td>14</td><td>12</td><td>AF196485 BM437459 RT082F04</td><td>couture_a76.sd.38.c1.r#1</td><td>>pir||JC2511 beta-tubulin R2242 - rice</td><td>1384.879</td><td>1432.000</td><td>0.967</td><td>1603.236</td><td>1499.000</td><td>1.070</td><td>1.018</td></tr>
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APPENDIX B

Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy

Search Nucleotide for Go Clear

Limits Preview/Index History Clipboard Deta

Display default Show: 20 Send to File Get Subsequence

☐ **1:** AF439321. Reports Vitis vinifera su...[gi:16930708] Links

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VERSION     AF439321.1  GI:16930708
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  TITLE     Sucrose transporter VvSUT2 is expressed during grape berry ripening
  JOURNAL   Unpublished
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  AUTHORS   Picaud,S., Ageorges,A. and Delrot,S.
  TITLE     Direct Submission
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 721 atacctttta gtttcatccc ttagtcatga aagcccacac nttgggtaag tcctttccat
 781 tctagttaag ccataaacaa gatcctttat atcaatgtac taagaaacct ccttaacctc
 841 gctagaagca aagaagaaag atattgttga acaagtgaga acataccaat ccacatctta
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 961 actactgtct taatgttgag gcatgaaaga tagcactacc aattagtgtc aagcctatca
1021 atttgtctaa taccatcatg atattattaa tgatgacaaa ttttggtctc attagaagaa
1081 tcacttattt aaatggttaa acaaattgag gccttttcaa gtctatgaaa gataaaaatg
1141 ccttaaaaag taagggaaga gccagctaag ttgctactac aagatctcca ctaaaagaaa
1201 atccttccta tggtgctaag gcttgaaggg tgcaagatcc tcctaaaaaa tctttaagtt
1261 tcttcaaacg atcgagtcaa tttttattag ttggctaaag ggaattcatc tcaaatcttt
1321 caaaagaaaa agatgaaagt gatttgctat ccctctaaac ttaagcatag ccttactcat
1381 agaagaaaat attgaaatat atattgagaa tgcctttagg ttttcaagat tcgaaatttc
1441 aattgagaaa ggcaccataa ggcatatatc aattgagcca agcaaacaaa ttgttgtaag
1501 tttactaatt atcatctcat ttgggatgag ccatccttat cctgataagt attaattatt
1561 tacacaacct ccaccatcat tttcattact tcttttaaaa ttttaaaatc ccatattctt
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1681 tcttcatctt ttgagtggtt ttaaataaag aaatttgaat agggcaatga ttcttgtgtt
1741 ttccttggtg ggaaatcata tttgaaaggg ctatggaaga tgtctccttg tacatatcta
1801 caaacttact cattactttt aatttcattt gcagctcaaa tataatcttc atatacccag
1861 attctccata attcaagcag cgtggagaag atatgacccc aaattctccg tgcaaaccgt
1921 tctctattat atcctctctt tctcaaacac tcagccgtaa cctcacctca aggatggttg
1981 gacgtaaatc tctcctctcc ctctctcttt acctcatctc ttgctatcaa tctctttata
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2161 gatagggtag ggttggagct gttatggagg ccacatctgt aaaagcaggt atgcaaccgg
2221 cttctgagga cgcccaccat catctatcca ccccattaag caagataatt ctcgtagcat
2281 ccatagctgc gggtgttcaa ttcggatggg ctcttcagct ttccctcttg accccatatg
2341 ttcagctcct cggcgtccct cacacatggg cttcgttcat ttggctttgt ggtcccatct
2401 ctggcatgct catccagccc acggttggat actatagcga ccactgcaac tcccaatggg
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2581 ttcgagcggn tgttgtgttt gtcctagggt tttgggtcct tgacgttgcc aataacatga
2641 tgcagggccc ttgccgagct ttattagctg atatgtcagg gcataaccac aagaaaacaa
2701 agaaaacaag gacngccaaa ttgtataatt gttttttcat ggcgttcggg aatttcctgg
2761 gtnatgcaag tggttnttat actgaccttt ataaggtntt cccattcaca aagacaaagg
2821 cttgtgatgt gtactgngcg aaccttaaaa cttgcttcat tttcgctatt attctccttc
2881 tggtcttaac cactgcggct atgactttag taaaagaaag gccacttgtt ttaactcatc
2941 aatacaacgc agaccaggat gaagaggacg aagaggaggt ttcaatgcca tttttcgggc
3001 agatgttgtc tgcattaggg aacttatccc ggtcaatgtg gatgctaatt gttgttacat
3061 ccttgaactg gcttgcctgg tttggtttcc tattgtttga catcgactgg atggggaaag
3121 aagtctacgg agggacggtc aaaggtaaag aatcaaagct gtatgatagg ggngtacacg
3181 caggttcgct agggttgatg agaaattcat tgntgntagg gttaangtca ntggcaatcg
3241 agccagcagc tcgtttgatg ggtggtgtga agcgggtatg ggtattgggg aacttcatac
3301 tagccatttg cttgggactt actgttgcgg tcacaaagat gcaatcttcc agacatgaag
3361 ctgctgctgc tgaagggcga agcttgatgc ttccagccaa cgttaagatt tttgccctta
3421 cgatcttcgc cttgttgggc atacctcaag cggttagtcc ctcattctcc cctgttcgtc
3481 aaaggaaatt aaaatttata tacatttggt cagttactta acaacttata tatacgagga
3541 gtcctaatta aaagggttcg tacagcctga ttatctagtt gattgggtat attctgtgtt
3601 agagtgaaag cccaataagt tcaatataca ttaattgtgg tgttaaggct aagacataga
3661 taataagatt gatatgcatt gtttgtcaca ctgtctaaaa cttaagttng aggtaatagg
3721 taggttagca tccaatccaa tccaagagtg tagtgtaata aactattaac ttattttgtg
3781 acatagttca aaggagtccg ttaactgtat attttccttt tgtgcagatc acatacagta
3841 tccccttcgc cctagcatcc atattttcca atgcctctgg tgctggccaa ggtaaatgat
3901 taatgttttt cccgaaggtt tnccttgaaa agttttgttc caagaaacag tttcacaaat
3961 ctgatatttc tctgagacta attttgggat tatatacgca tatcaggcat ccttngacat
4021 tctctggatg tttcaatctt acaggccttt ctctaggagt tttaaacatg gcaatagtgc
4081 taccacaggt tcggtcccac tgcaacattg ttactttata taagctaaaa ttttaaaatc
```

```
     4141 aactattaaa ttttgtttta tataatctta attcgtatca acaaagtaat tttcatttaa
     4201 ngaattatta atgttttata gcgaacactg gcctttntagg ttaaagaaga aaaaattgag
     4261 ctaattaatt catgataagt aagaatatac atatcattat ttatggaaga aaaatgatga
     4321 gaaggttttt gaactatttc caaaagcata gggacatcat tttcattaca aaattaactg
     4381 tatttgtacc attaataagc tggtcgttgg ttgaatgctt aaacaggata ctagtttctg
     4441 cggtcagcgg actgttggat gatttatttg gtggtggtaa cttaccagtc tttgttgcgg
     4501 gagccatcgc tgctgcagca agtggggtat ttgcactcac cattctacca tctccaccgg
     4561 cgcaaccttc taggctgtga atcgaagagt tggagtcaat caagggtaaa attgccctca
     4621 cctgatgatt gatcct
//
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Remark; the underlined sequences are the ERELEE4 box (awttcaaa).

BIBLIOGRAPHY

Miss Tira Kuapunyakoon was born on May 15th, 1976 in Nakhon Ratchasima, Thailand. She graduated with the Bachelor Degree of Animal Production Technology, Suranaree University of Technology in 1998. During her Master Degree enrollment in the School of Biotechnology, Institute of Agricultural Technology, Suranaree University of Technology (2001-2004), she went to Toulouse, France for five months (December 2003-May 2004) for her laboratory training, which was part of her master thesis, at the laboratory of INP-ENSAT. Besides, she presented research work in the 4th National Symposium on Graduate Research in 2004 at Lotus Hotel Pang Suan Kaew, Chiang Mai, Thailand.