SEQUENCING AND ANALYSIS OF GENES EXPRESSED IN THE CAMBIAL TISSUE OF *QUERCUS RUBRA* USING A NORMALIZED, LARGE-INSERT cDNA LIBRARY

By

Jesse Joseph Walsh
A Thesis
Submitted to the
Faculty of the Graduate School
of
Western Carolina University
in Partial Fulfillment of
the Requirements for the Degree
of
Master of Science

Committee:

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A thesis presented to the faculty of the Graduate School of
Western Carolina University in partial fulfillment of the
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By

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ABSTRACT

SEQUENCING AND ANALYSIS OF GENES EXPRESSED IN THE CAMBIAL TISSUE OF *QUERCUS RUBRA* USING A NORMALIZED, LARGE-INSERT cDNA LIBRARY.

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Western Carolina University (August 2008)
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The logistical issues associated with completely sequencing a very large genome greatly limit the number organisms that can have such a project devoted to them. One of the methods developed to circumvent this impasse is the sequencing of expressed sequence tags (ESTs), that is, partial cDNAs. The technique is often used as an introduction to completely unsequenced genomes as well as a more detailed analysis of previously characterized genomes. In the case of poorly characterized genomes, EST sequencing provides a quick, efficient profile of the nucleotide sequences of messenger RNA. Furthermore, many plant ESTs have been quickly annotated via regions of sequence similarity comparisons with genes of model organisms such as the mustard, *Arabidopsis thaliana* Heynh, and the hardwood, *Populus trichocarpa* Torr. & A.Gray.

This project focused on rapidly dividing cambial tissue from a *Quercus rubra* L. individual with a partially characterized ancestry. That individual was recovered from one of the few oak nurseries in the world, namely the Watauga Genetic Research Orchard near Elizabethton, TN. The cambial transcriptome provided 984 cDNA clones resulting in 870 unique sequences. After appropriate filtering the unique sequences were submitted for homology comparison against the gene databases of *Arabidopsis*, *Populus*, as well as the generalized UniProt database. Putative function was assigned to more than 90% of the unique sequences; however forty sequences have no significant homology to any known protein.

The nucleotide sequences produced in this study will be submitted to the GenBank database where they will become the foundation for a *Q. rubra* sequence resource. Since the sequences were recovered from cambial tissue of spring wood, they will assist in better understanding wood formation within this species. Such studies should lead to increases in both the quality and quantity of this valuable hardwood found in western North Carolina.

INTRODUCTION

Throughout history, trees have been an essential part of mankind's existence. Since the dawn of civilization they have provided material for buildings, furnishings, paper production, and an energy source for heating and cooking. On a global scale, trees are a valued economic commodity and a fundamental component of the biosphere.

Presently plants are divided into two main taxa, the gymnosperms and the angiosperms. These groups diverged during the Carboniferous period (300 Mya) and each has evolved into many different species (Bowe et al., 2000). The gymnosperms form a monophyletic clade that is widespread across temperate ecosystems but includes only 700-1000 species, all of which are woody plants (Kirst et al., 2003). The angiosperms are vastly dominant in numbers and diversity, comprising approximately 250,000 species and including many woody plants as well as all of the staple food crops (Wikstrom et al., 2001). The model organisms *Arabidopsis thaliana* Heynh (Brassicales order, Brassicaceae family) and *Populus trichocarpa* Torr. & A.Gray (Malpighiales order, Salicaceae family) are angiosperms which are related at the Rosids subclass level. The focus of this study, *Quercus rubra* L. (Fagales order, Fagaceae family), shares the Eurosid I group with *Populus* and is closely related to the common forest hardwoods beech and chestnut (Taxbrowser 2008). As shall be discussed, it is this shared ancestry which forms the basis for genetic comparison between individual plant species.

Quercus rubra

Of the myriad of different tree genera, the oaks (*Quercus*) are a noteworthy group within the angiosperms. They are hardwoods indigenous to temperate regions of the northern hemisphere and are rarely found below the equator. *Quercus* is a very diverse genus which is estimated to contain more than 500 species spread across the globe (Manos et al., 1999). Oaks are acknowledged as having poor barriers to hybridization, even between species that are very different morphologically and physiologically, leading to large populations of infertile hybrids (Whittemore and Schaal, 1991). Even within a species, individuals can display a wide variety of phenotypes, making identification by visual inspection very difficult at times (Aldrich et al., 2003b). *Quercus rubra* (northern red oak, NRO) is a significant species within the genus since it occurs as the dominant tree species in many forest communities and is one of the more valuable timber species (Tirmenstein 1991). In North America, NRO is native to the northeast and midwest regions of the continent ranging from 32° to 47° N latitude and 60° to 96° W longitude (Burns and Honkala, 1990). Samples for this study were gathered on the eastern Tennessee border, a location that is near the southern and western tip of the range.

Wood from northern red oak is valued for being hard, heavy, strong, coarse-grained, and moderately durable (Tirmenstein 1991). *Q. rubra* trees are self-pruning which results in wood with fewer knots, a characteristic that is especially important to the timber industry. Logging of NRO produces timber for many applications such as lumber, railroad ties, fence posts, veneer, pulpwood, and fuel wood. The lumber of *Q. rubra* is further refined into many items including flooring, furniture, boxes, pallets, crates, caskets, and wooden ware (Miller 1999).

Quercus rubra is the tallest and fastest growing of the oak species, average adults rise to heights ranging from 19.8 to 29.9 meters with diameters of 0.6 to 0.9 meters. Superior individuals that receive optimal growing conditions may reach heights over 48.8 meters and attain diameters up to 2.4 meters (Tirmenstein 1991). Trees of this species have life spans which can exceed 200 years in the absence of disease and disturbances, but their growth rate slows considerably after the age of 100 (Hicks 1998). *Q. rubra* trees mature sexually and begin to produce acorns at approximately 25 years of age, but will generally not produce large crop yields until around the age of 50 (Hicks 1998).

NRO is a key habitat for an assortment of animals ranging from birds to small mammals (Tirmenstein 1991). Many of these animals are acorn predators whose foraging habits also provide the primary mode of *Q. rubra* seed dispersal. *Q. rubra* individuals usually spawn large acorn crops every 2-5 years, with exact numbers of acorn production being dependent upon the individual, as well as site and climactic factors (Sander 1990). In forests where oak is the dominant species, bumper crops of acorns can reach production levels greater than 96,500 per square kilometer (Hicks 1998). As much as 35% of these acorns may be eaten by insects (Beck 1977) and another 40% by deer and small rodents (Steiner 1995). Due to heavy acorn predation, seedlings are not usually generated except in years of high yield where production exceeds consumption (Hicks 1998).

Northern red oaks are moderately vulnerable to insect and disease infestations and will usually survive an attack unless more than one pathogen is present. For example, Liebhold et al. (2005) states that if an insect, such as the gypsy moth (*Lymantria dispar* L.), looper (*Phigalia titea)*, or cankerworm (*Alsophila pometaria*) defoliates a tree, the tree will be weakened. When this occurs in concurrence with a drought or an infestation by another organism such as the two-lined chestnut borer (*Agrilus bilineatus)* or the shoestring fungus (*Armillaria mellea)* there can be high mortality rates. A recent development in forest pathology is sudden oak death syndrome, which has begun to affect forests in North America and Europe. The disease is caused by the Oomycete *Phytophthora ramorum* and was first observed during the mid 1990s in California forests (Withgott 2004). While more than forty genera or plants are known hosts to the pathogen, widespread mortality is usually limited to members of the Fagaceae family (Rizzo et al., 2005). Other hosts tend to be only moderately affected by the disease and are thought to act as vectors by which the disease is spread (*Rhododendron indicum* (L.) Sweet, for example, which is widely disseminated as an ornamental plant). Fears are escalating that the disease will come to the oak forests of Eastern North America, which would be a serious problem since red oaks are known to be susceptible to infestation (Withgott 2004). Federal regulations are in place to curb the spread of the disease but there have already been lapses. In 2005, nurseries in 23 states around the country received infected plants from California and distributed locally before realizing what was transpiring (Associated Press 2005). The real threat that sudden oak death presents is an example of the need for active management of resources.

While oak are presently one of the dominant species found in eastern United States landscapes, concern has been mounting for some time that oaks are not regenerating at an adequate rate to sustain the population and diversity of individuals that is currently observed (Clark 1992). There is no single explanation as to why this is happening but it is believed that there are several factors, which together, are responsible for declining oak regeneration. These problems include introduction of new insect species, changes in animal communities due to decline of predators, reduction of forest fires, and changes in the demographics of forest communities (Lorimer 1992).

The increasing demand for oak lumber in concurrence with the escalating problem of oak regeneration and infestation by parasites poses a serious problem to the present prevelance of oaks. Significant decline of oaks in North American forests would be a disastrous event on par with the chestnut blight (*Cryphonectria parasitica* (Murrill) M.E. Barr) epidemic of the early twentieth century. Loss of oaks from forests would allow for less desirable tree species to enter an area, causing severe stress to the presently observed community of plants and animals inhabiting the ecosystem. For example, research has correlated increased damage to livestock and crops caused by black bears to years of poor acorn production (Rogers 1976). Decline of the oak population would also seriously affect the hardwood timber economy, of which oak is a staple product. The encumbrance to developing management techniques has been exacerbated by the slow growth rate of trees and the fact that traits cannot properly be assessed until a tree reaches adulthood (Boerjan 2005).

Xylogenesis

The strong and rigid nature of hardwood trees is due the structural characteristics of the secondary xylem cell wall. This integrity of the secondary cell wall is a result of a dense network of cellulose and lignin fibers. Cellulose is a polymer composed of β-1, 4 linked glucosyl residues, which assemble to form microfibrils measuring 2-10 nm in diameter and hundreds of nanometers in length (Brown 1996). Cellulose microfibrils are stabilized by hydrophobic and van der Waals interactions which make them insoluble in water, chemically resistant to degredation, and mechanically strong (Williamson and Hocart 2002). Lignin is a highly heterogeneous class of phenolic polymers involved in mechanical support, water transportation and disease resistance (Lapierre et al., 1999). Lignin is vital to the mechanical properties of wood but is detrimental to the pulping process because toxic chemicals are required to separate lignin from cellulose (Lapierre et al., 1999). Together, cellulose and lignin compose the majority of the dry weight of wood.

Samuels et al. (2006) states that “xylogenesis can be defined as the series of common developmental steps found in differentiation of both primary xylem (produced via procambium by apical meristems) and secondary xylem (produced by the vascular cambium).” In hardwoods, it is xylogenesis initiated in the vascular cambium cells of the lateral meristem which is of most importance economically in the timber industry since it results in the formation of the substance that is commonly referred to as “wood”. In the lateral meristem, vascular cambium is located between the bark and the heartwood of the tree. The process of xylogenesis directs these cells through division, expansion, secondary cell wall formation, lignification, and finally programmed cell death (Hertzberg et al. 2001). The cells that will eventually become the dead secondary xylem begin as progeny of undifferentiated mother cells and are guided to their fate by a complex interaction of genetic regulation and environmental stimuli.

Highly analogous genes coding for xylogenesis proteins have been found in very divergent plants. It is has been proffered that “secondary growth is a measure of degree, rather than a trait that is present or absent or a trait that has arisen uniquely within a single lineage" (Groover 2005). While the underlying process is conserved it is believed that there are also genes which are rarely expressed or not present at all in herbaceous plants which account for the phenotypic difference between woody and herbaceous plants (Allona et al., 1998).

Expressed Sequence Tags

It has been determined that *Quercus rubra* has a chromosome compliment of 2n = 24 plus a B chromosome of uncertain function (Ohri and Ahuja, 1990). The size of the genome has been determined to be 761 Mbp / 1C (Carlson 2007). Aside from this information, relatively little is known about the genome of northern red oak. While large scale EST sequencing projects are currently underway (Fagaceae.org 2007) there are only 9991 *Quercus* ESTs in GenBank and these are primarily from *Quercus petraea* (Mattuschka) Liebl (2300), *Quercus mongolica* subsp. *crispula (3385)* and *Quercus robur* (3499) (NCBI 2008). There are presently 118 CoreNucleotide sequences and no EST sequences for *Quercus rubra* in GenBank (NCBI 2008).

Sequencing the entire *Quercus rubra* genome would undeniably be the best method for comprehending the exact genetic compliment of the species, but that is a very costly and time intensive process. A practical alternative is the analysis of expressed sequence tags (ESTs), which is a proven quick and inexpensive means to identify the nucleotide sequence of active genes in a given tissue (Sterky et al., 1998). Information garnered from EST sequencing provides valuable insight in gene discovery as well as a first step in functional genomics studies.

The first step in creation of an EST library is the acquisition and purification of mRNA from a tissue. Working with mRNA is a very delicate and exacting process. Thankfully, groundwork for the application of existing isolation techniques to processing NRO cambial tissue was laid by Mathews et al. (2003). The mRNAs were used as templates to generate complimentary DNA (cDNA) molecules which are inserted into plasmid vectors. The vector is then introduced into a bacterial cell for purposes of replication and storage. EST sequences are usually generated as part of large scale high throughput projects and are generally single read passes of the gene insert (Bouck and Vision, 2007).

Once an EST has been sequenced there is a considerable amount of bioinformatics that must be done in order to elucidate useful information about the gene. With any sequencing run the quality of the electropherogram is poor at the beginning and the end of the read. Usually there is a subset of EST sequences that either completely lack gene inserts or are contaminated with vector/primer sequence stretches to some degree. With the aid of computer programs, these tracts of contamination and poor quality reads are located and excised. There are also inevitably a number of duplicate copies of highly expressed genes which must be identified and assembled into consensus sequences. Once a set of unique genes has been created, the task becomes identification of the peptide coding region and the function of the translated protein. These tasks are also accomplished with the use of computer programs that search for sequence homology to proteins of known function.

A major problem associated with EST sequencing arises from the large dynamic range of transcripts (1:10,000). Consequently, there is a good chance that rare transcripts will not be sequenced and abundant transcripts will be sequenced many times. One way to circumvent this dilemma is normalization of the library, which consists of reducing the concentration of highly expressed transcripts (Soares et al., 1994). ESTs also do not provide any information about intron sequences, gene order, gene placement or regulatory motifs (Bouck and Vision, 2007). They do, however, provide sequence information from which primers could be developed for use in further projects that could address these issues. ESTs can also be valuable to the development of genetic markers such as single nucleotide polymorphisms (SNPs), exon-primed intron-crossing markers (EPIC), and simple sequence repeats (SSRs).

Plant genetics and the study of plant derived ESTs are intrinsically linked to the model organism *Arabidopsis thaliana*, which is one of the most characterized and comprehensively studied organisms on Earth. In 2000, an international consortium known as the *Arabidopsis* Genome Initiative released an annotated genome sequence (115.4 Mb of estimated 125 Mb) that identified 25,498 genes on five haploid chromosomes. In 2003 Zhu et al. released a study that mapped more than 96% of the available *Arabidopsis* ESTs (176,915 at the time) to a specific genomic locus. Placement of the ESTs within the genome facilitated a better understanding of gene regulatory elements as well as providing splicing and intron information that ESTs lack. Consequent to the wealth of information available on *Arabidopsis*, it has become the basis for plant EST sequence comparison and *in vivo* studies of plant gene expression.

In 2006, Tuskan et al. released the draft genomic sequence of *Populus trichocarpa*, making it the first hardwood organism to have a sequenced genome and solidifying its spot as the model organism for deciduous trees. The study purports that there are more than 45,000 putative protein-coding genes at work in *Populus*. Aside from having more putative protein-coding genes than *Arabidopsis*, it was found that there are specifically more genes that function in lignocellulosic wall biosynthesis, meristem development, disease resistance and metabolite transport. These genes represent the difference in lifestyle habit between the two organisms and are especially important to genetic research conducted on other forest hardwoods.

Published oak genetic studies to date have primarily dealt with phylogeny studies (Aldrich et al., 2003a, Casasoli et al., 2006, Grivet et al., 2006, Muir and Schlotterer 2006, Romero-Severson et al., 2003) using chloroplast DNA or genetic markers of some kind (SNP, SSR, RFLP). There have also been several gene expression studies (Derory et al., 2006, Soler et al., 2007), but the issue of xylogenesis genetics in *Quercus* has not been addressed. ESTs in GenBank from papers with published results include those submitted by Derory et al. (2006), who published a paper on the bud burst transcriptome in *Quercus petraea.* This paper was supported by 801 ESTs (233 unique genes) which used suppression subtractive hybridization (SSH) to focus on the genetic control of bud formation. Soler et al. (2007) reported 236 ESTs from a study that focused on elucidating the genetic component of suberin production in cork oak (*Quercus suber* L.).

Several projects related to xylogenesis and cambial tissue ESTs of hardwood trees have been published and are an excellent guide to applying proven techniques to studying *Quercus rubra*. Studies of ESTs from poplar (Sterky et al., 1998), pine (*Pinus taeda* L.) (Allona et al., 1998, Pavy et al., 2005), eucalyptus (*Eucalyptus globules* Labill) (Paux et al., 2004), and white spruce *Picea glauca* (Moench) Vossa (Pavy et al., 2005b) have produced results on ESTs from cambial tissue and will serve as a basis for the work done in this project.

The focus of this study is gene discovery in cambial cells from a NRO with partially defined phenotype. This tissue was chosen because it is the site of xylogenesis and it is believed to provide the most useful information in identification of genes involved in production of xylem and phloem (Sterky et al., 1998). This makes cambial tissue the best target for strategies to improve the quality and quantity of secondary wall production. The genes identified in this study will hopefully give an introduction into the genetic machinery of NRO and establish a base for comparison to other plants. This comparison should help establish how NRO is similar and how it is different, both in the sequence differences of conserved genes and the plausible identification of unknown genes specific to *Quercus rubra*. ESTs from this project could also be used to produce various kinds of genetic markers (SSR, SNP, EPIC) (Bouck and Vision, 2007).

MATERIALS AND METHODS

Sample Collection

Samples were collected from the Watauga Northern Red Oak Seed Orchard near Elizabethton, Tennessee on May 6, 2005. The Watauga Orchard was planted in 1973 with open pollinated progeny from mother trees found in the Tennessee River Valley that were deemed of generally good phenotype (Schlarbaum et al., 1994). Cambial tissue samples for this study were collected exclusively from NRO Family 555, whose mother was located in Morgan County, TN. The sample tree was sited at Latitude: 36° 08', Longitude: 84° 28' at an elevation of 609.6 meters.

The tree was felled at a height of 0.3 meters by a technician employed at the Department of Forestry, University of Tennessee-Knoxville. The following steps were performed with utmost haste to minimize mRNA degradation in the cambial layer. Limbs and canopy were quickly removed to minimize desiccation. Next, 4.5 meters of trunk was cut into 1 meter long sections. To facilitate rapid bark separation a chainsaw was used to cut 0.15 meter wide longitudinal strips into the upper heartwood layer. A hammer and chisel was used to pry away strips of bark. Then a razor was used to scrape the cambial tissue from the inner side of the bark and the surface of the sapwood. The scraped cambial tissue was quickly deposited onto labeled sheets of aluminum foil which were folded tightly and flash-frozen in liquid nitrogen. The time interval between cell disruption and freezing the scraped samples was 3-5 minutes. The frozen sample packets were sandwiched between dry ice slabs in an ice chest for transportation to the lab. Samples were stored at -80ºC in a Revco low temperature freezer until processing. The chisels and paint scrapers were sterilized by autoclaving prior to collection and gloves were worn at all times while samples were handled.

Total RNA isolation

Isolation of RNA from the cambial cells was based on a protocol first described by Chang et al. (1993) and is rooted on the properties of the cationic surfactant cetyltrimethylammonium bromide (CTAB). The extraction buffer contained final concentrations of 2% (w/v) CTAB, 2% (w/v) polyvinylpyrrolidone (PVP), 100mM Tris-Cl (pH 8), 2M NaCl, 0.5g/l spermidine, and 2% (v/v) β-mercaptoethanol (BME). All ingredients except the BME were mixed and autoclaved; BME was added just before use. Aliquots of CTAB extraction buffer (20 ml) were dispensed into eight autoclaved 50 ml conical polycarbonate centrifuge (Oak Ridge) tubes and were equilibrated to 65ºC in a water bath. Approximately 2 g of cambial tissue (16 g total) was added to each tube and shaken vigorously before ten minutes of incubation in a 65ºC water bath. Chloroform (15 ml) was added to the solution and mixed by shaking. Centrifuge tubes were balanced using chloroform and then spun for 10 min at 10,000 RPM in Beckman JA-20 rotor using a Sorvall RC-5 centrifuge. The aqueous (top) phase was removed and transferred to a fresh centrifuge tube being careful to avoid contamination from the interphase and the organic phase. Chloroform (15 ml) was added to the supernatant and shaken vigorously before again being balanced with chloroform and centrifuged for 10 min at 10,000 RPM in a Beckman JA-20 rotor. The supernatant was carefully removed and transferred to a third centrifuge tube to which an equal volume of 7.5 M $LiCl_2$ / 50 mM EDTA (ethylenediaminetetraacetic acid) was added. This solution was precipitated at -20ºC for four hours, at which time a set of tubes were balanced with 7.5 M $LiCl_2$ and centrifuged at 10,000 RPM in a Beckman JA-20 rotor for 20 min. The supernatant was removed from the centrifuge tube leaving a pellet of total RNA. RNA pellets were dissolved in SSTE solution (1000 µl) [1 M NaCl, 0.5% (w/v) SDS (sodium dodecyl sulfate), 10 mM Tris-Cl, and 1 mM EDTA] and incubated in a 65ºC water bath for 10 min. The solutions were consolidated into two Oak Ridge tubes and extracted with chloroform (12ml), vortexed, and then centrifuged at 10,000 in a Beckman JA-20 rotor for 10 min. The aqueous phase was transferred to a fresh tube where two volumes of 95% (v/v) ethanol were added to the sample and precipitated at -80ºC overnight. The Oak Ridge tubes were spun at 10,000 RPM in a Beckman JA-20 rotor for 20 min, after which the supernatant was removed leaving a pellet of total RNA. The pellets were washed with ice cold 70% (v/v) ethanol (1 ml) and centrifuged at 10,000 RPM for 5 min. and the supernatant discarded. The pellet was air dried and dissolved in sterile deionized water (300 µl). The contents of each Oak Ridge tube were aliquotted into three 1.5 ml tubes (100 µl each) and stored at -80ºC.

The RNA extraction procedure was repeated twice more on crude samples and the product of each was consolidated. A total of 3 mg was collected for transport to Open Biosystems in Huntsville, AL for cDNA synthesis and normalization.

Total RNA Quality Control

The purity of the total RNA was checked by formaldehyde/agarose gel electrophoresis using a protocol described by Sambrook and Russel (2001). Gels were cast in a 16 cm electrophoresis box (Fisher Model FB-SB-710) using a 3 mm, 10 tooth comb. The gel consisted 5X MOPS buffer (20 ml) [0.1 M 3-(N-mopholino) propanesulfonic acid (pH 7), 40 mM sodium acetate, 5 mM EDTA (pH 8)], 37% formaldehyde (18 ml), DEPC (diethylpyrocarbonate) treated water (62 ml), 1μg/ml ethidium bromide (3 μl), and agarose (1 g). To create the gel, the agarose was dissolved in nearly boiling water which was then cooled to 60ºC before addition of the formaldehyde, ethidium bromide, and MOPS. The gel was allowed to solidify at room temperature in a hood for at least 30 min. The electrophoresis box, gel tray and comb were all washed with nearly boiling water and approximately 5 ml of 20% (w/v) SDS and rinsed repeatedly with deionized water.

Total RNA samples were prepared by mixing 5X MOPS buffer (2.0 μl), formaldehyde (3.5 μl), formamide (10 μl), and total RNA (4.5 μl) in autoclaved microfuge tubes. The tubes were incubated for 15 min at 65ºC and then chilled on ice. Samples were centrifuged to collect the solution on the bottom of the tube. Formaldehyde gel-loading buffer (2 μl) [50% (v/v) glycerol, 1 mM EDTA (pH 8), 0.25% (w/v) bromophenol blue, and 0.25% (w/v) xylene cyanol FF] was added to each sample and mixed by pipette. The gel tray was placed in the electrophoresis box and a solution of 1X MOPS buffer (diluted with water) was used to fill the box to a level that was a few millimeters higher than the gel. The gel was run for 5 min before addition of the samples. Invitrogen 0.24-9.5 Kb RNA Standard (1 μl) was mixed with formaldehyde gel-loading buffer (2 μl) and loaded into to the outer lanes of the gel. Then gel was run at 4 V/cm until the dye had migrated to nearly the end of the gel (approximately 3 hours), the running buffer was recirculated every 45 min.

Visualization of RNA gels was performed using an International Biotechnologies Inc. (IBI) UVT 400-M ultraviolet transilluminator. Images of the gel were captured using a Kodak QuickShooter QSP Gel Electrophoresis Photosystem using an IBI QSP #14 hood. Quantification of the total RNA samples was performed using a Nanodrop ND-1000 spectrophotometer. The calibration of the ND-1000 was checked by running serial dilutions of Invitrogen 0.24-9.5 Kb RNA ladder as a standard and comparing them to the values given by the Nanodrop machine. For sample measurements, aliquots (2 µl) of total RNA solution were used.

mRNA Isolation and cDNA Synthesis

Our collaborative partner, Open Biosystems of Huntsville, Alabama, was responsible for mRNA isolation and cDNA synthesis from the total RNA samples. The exact protocols that they used are proprietary, but an outline of the procedures was made available by Stephanie Sieja of Open Biosystems (Sieja 2006).

The process summarized by Sieja (2006) began with isolation of poly(A) RNA. Total RNA (750 µg), was purified by two rounds of affinity chromatography using oligo(dT) coated magnetic particles from Seradyn, Inc. A quantity of 3.6 µg of poly(A) mRNA was recovered. First strand cDNA synthesis was accomplished using an oligo (dT) primer that contained a *Not* I restriction site and Moloney Murine Leukemia Virus Reverse Transcriptase (M-MLV RT). Open Biosystems would not release their methods for second strand synthesis.

The ds-cDNA was digested with *Not* I and then size-fractionated to select for pieces larger than 1.4 kb. The cDNA was directionally cloned in one bulk step using *Not*

I-*Eco* RV cut pExpress1 vector (300 ng), and *Not* I digested cDNA (120 ng) per 120 µl of ligation. The entire sequence of pExpress1 is found in Appendix A and the multiple cloning site and restriction map is shown in Figure 1. Plasmid vectors were inserted into DH10-B T1 phage resistant *E. coli* cells by electroporation. Approximately 9 x 10^6 primary clones (i.e., not *unique* clones) were produced from about 1 mg of total RNA starting material. Next, 24 inserts were randomly selected and sized after digestion with *Eco* RV and *Not* I. Electrophoresis revealed an average library insert length of 1.5 kb.

The primary cDNA library was normalized based on the principles of re-association kinetics (Soares et al., 1994). This was done by producing biotinylated driver RNA from the T7 RNA polymerase promoter and single-stranded target DNA produced from the F1 Ori. The RNA and the DNA were hybridized together at a low Cot (concentration of driver times the time of hybridization) value. The RNA:DNA hybrids were removed using phenol extraction and the remaining ssDNA target was converted into dsDNA with a “repair oligo” and Taq DNA polymerase. These plasmids were again electroporated into *E. coli* and sampled for sizing. Electrophoresis of the normalized library revealed an average insert length of 1.4 kb, slightly less than the 1.5 kb average of the unnormalized library.

Library Titer and Colony Picking

The library titer was determined as per directions from Wes Bonds (2005) which consisted of creating serial dilution with LB broth [20 g LB, 750 µg ampicillin, q.s. to 1 liter with autoclaved water]. Colonies from these dilutions were grown on LB/AMP agar plates [20 g LB, 15 g Bacto-agar, and 750 µg of ampicillin, q.s. to 1 liter with autoclaved water] overnight at 37°C. The titer revealed that a 25,000X dilution was optimal for generating well spread colonies for picking. The typical plate contained about 300 separated colonies.

Plasmid Isolation, Amplification and Storage

A team of nine undergraduate students assisted in the isolation, amplification and storage. Cells from each colony were picked using a flame-sterilized inoculating loop or an autoclaved toothpick and used to inoculate liquid LB/AMP medium (5 ml) in a 50 ml Falcon tube. Each sample was assigned a four digit (0001-1305) number at this point which it kept for the duration of the study. The samples were incubated at 37ºC over night with constant agitation. The following day, 400 µl of culture was transferred to an autoclaved 0.6 ml microfuge tube bearing the sample number, and mixed with autoclaved glycerol (100 µl). This solution was stored at -80ºC as a backup.

The remaining culture was processed by an alkaline lysis protocol taken from Sambrook and Russel (2001) which is described hereafter. A 50 ml Falcon tube containing the remaining culture was spun in a Beckman JA-20 rotor using a Sorvall RC-5 centrifuge for 10 min at 4°C and 1000 RPM to collect the cells. The supernatant was removed and the cells were resuspended in STE buffer (1 ml) [10 mM Tris-Cl pH 8.0, 0.1 M NaCl, 1 mM EDTA pH 8.0]. The cells were collected by spinning at 1000 rpm for 5 min. The supernatant was removed and the cells were mixed with ice cold alkaline lysis solution I (200 µl) [50 mM glucose, 25 mM Tris-Cl pH 8.0, 10 mM EDTA] and lysozyme buffer (40 µl) [10 mM Tris-Cl, 10 mg/ml lysozyme] and transferred to a correspondingly labeled 1.5 ml microfuge tube. Alkaline lysis solution II (400 µl) [0.2 N

NaOH, 1% (w/v) SDS] was added to the tube and the contents was mixed manually by shaking. Next, alkaline lysis solution III (300 μl) [5 M potassium acetate, 11.5 % (v/v) glacial acetic acid] was mixed into solution and the tubes were stored on ice for 5 min. The tubes were then spun at maximum speed in a microfuge for 5 min at 4ºC. The supernatant (600 μl) was transferred to a fresh tube and 10 mg/ml RNase A solution (3 μl) was added before a 15 min incubation in a 37ºC water bath. Next, 20mg/ml proteinase K solution (3 μl) and 20% (w/v) SDS (1 μl) was added and the samples were incubated for 30 min at 50ºC in a water bath. The samples were then extracted using an equal volume of phenol:chloroform [25 parts phenol, 24 parts chloroform, and 1 part isoamyl alcohol]. The phases were then separated by centrifugation for 2 min at maximum speed (18,000 g) at 4ºC in a microfuge. The aqueous phase was removed to a fresh 1.5 ml microfuge tube and was extracted again in the same manner as above except that chloroform was used instead of phenol:chloroform to remove any remaining phenol, which is detrimental to following chemical reactions. The aqueous layer was again removed and transferred to a fresh 1.5 ml tube; nucleic acids were precipitated by addition of two volumes of 2-propanol with a two minute of incubation at room temperature. The nucleic acids were then collected by centrifugation at max speed in a microfuge for 10 min at 4ºC. The supernatant was removed by pipette and the pellet was washed in 70% (v/v) ethanol (1 ml) and collected by spinning at maximum speed in a microfuge for 2 min at 4ºC. The supernatant was again removed and the pellet was allowed to air dry. Once dry, the pellet was dissolved in pH 8.0 TE (50 μl) [Tris-Cl, EDTA pH 8] and stored at -80 ºC. After plasmid isolation all samples were quantified using the ND-1000 spectrophotometer.

Polymerase Chain Reaction

The polymerase chain reaction (PCR) was used to measure the size of the cDNA insert and as a way to screen for non-recombinants. The PCR method used a combination hot start/touchdown technique and utilized a betaine-modified reaction mixture developed by Baskaran et al. (1996). The primers used were #011893 [TAA TAC GAC TCA CTA TAG GGA CCA CTC CTC G] (primer 93) and #011894 [TAT TTA GGT GAC ACT ATA GAA CAA GTT TCG GTC CGG] (primer 94).

PCR amplification was performed on an Applied Biosystems 2720 Thermal Cycler using autoclaved 0.2 ml PCR tubes. The hot start conditions were 1 min of denaturation at 93ºC followed by a 7 min hold at 80°C at which time the deoxyribonucleotide triphosphates (dNTPs) were added. The touchdown effect was achieved by lowering the annealing temperature by 2ºC on each of the first five cycles. The complete cycling parameters used are found in Table 1.

PCR was performed in reaction buffer that contained final concentrations of [20 mM Tris-Cl pH 9.0, 5% (v/v) DMSO (dimethyl sulfoxide), 3 mM $MgCl_2$, 16 mM $(NH_4)_2SO_4$, 75 ug/ml bovine serum albumin (BSA), 1.3 M betaine, 0.046 Units Klentaq polymerase, 50 ng of each primer, and approximately 200 ng DNA template]. Reaction buffer (49 µl) was added to the tubes and hot started, then a dNTP solution mix (1 µl) [100 mM dATP, 100 mM dCTP, 100 mM dGTP, and 100 mM dTTP] was added.

All PCR products were examined by agarose gel electrophoresis to determine the presence of product, its purity and insert size. Gels were visualized by ethidium bromide/UV fluorescence/Polaroid photography as with the RNA gels. Insert length was determined by creating a regression equation using the distances traveled by the 1 kb DNA ladder standard and interpolating their size from the distance migrated.

Sequencing Reaction

Thermal cycling for the sequencing reaction was performed on an Applied Biosystems 2720 Thermal Cycler with a schedule of 1 min at 95ºC, and 25 cycles of 10 sec at 95ºC, 10 sec at 53ºC, and 4 min at 60ºC. Applied Biosystems BigDye v3.1 dye terminators were used at ¼X manufacturer's suggested concentration [BigDye v3(2 μl).1, ABI 5X buffer (3μl), 5 ρM/μl primer (1 μl), DI H_2O (13 μl), and 2 ug/ul template (1 μl)]. Clones 0001-0093 were sequenced in both directions, however, the balance of the clones were only sequenced from the 5' end to avoid slippage over the 3' polyA tail. Reactions were performed in a 96 well plate and executed as per the directions from the BigDye v3.1 Applied Biosystems.

Sequencing products were separated using an Applied Biosystems 3130xl Genetic Analyzer and analyzed with Applied Biosystems 3130xl Genetic Analyzer Data Collection Software v3.0. A 16-capillary array (Applied Biosystems 3130xl and 3100 50cm Capillary Array) and Pop-7 polymer was used as the separation medium.

Bioinformatics

Project data was generated from 184 sequencing runs each containing 16 capillaries per cycle. Initially, runs were visually screened to remove poor quality data. Base calling of raw electropherograms was performed with the ContigExpress module of Vector NTI software (Invitrogen 2007). This module also trimmed and assembled raw sequences. Terminal sequence regions were strictly trimmed in the following way. Poor quality base calls were removed according to the criterion that a maximum of 1 base out of 25 on both the 5’ and 3’ ends had a Quality Value of less than 20. Vector contamination was removed by screening the sequences against a database of vector sequences and the known primer sequences. ContigExpress used the CAP3 sequence assembly program (Huang and Madan 1999) to create the unique consensus sequences. The Sequin program was used to label the sequences in correct GenBank format before submission to the NCBI EST database.

Vector NTI was used to generate a concatenated text file of the unique sequences in FASTA format. This file was used as the query set for sequence annotation and comparison searching, which was performed using PERL modules on a Unix based XML web server located at the UNC Chapel Hill Bioinformatics Institute. The *Arabidopsis*, *Populus* and UniProt protein databases were downloaded on Chapel Hill’s server and BlastX (Altschul et al., 1997) (word size=3, E value cutoff=5) was used to search for protein sequence comparison using the Blast prescript (Fargo 2007). The TAIR7 (Swarbreck et al., 2007) annotation of the *Arabidopsis* protein database was obtained from the *Arabidopsis* information resource (TAIR) website, www.arabidopsis.org. The *Populus* protein database was downloaded from the *Populus trichocarpa* sequencing project website, www.jgi.doe.gov/poplar (Tuskan et al., 2006). The UniRef protein database (UniProt Consortium 2006) was downloaded from the UniProt website (www.UniProt.org). BLASTN (Altschul et al., 1997) of nucleotide sequences were performed against the NCBI non-redundant (NR) database using NCBI’s web based blast platform. Results for all were parsed by the readblastdesc PERL module into a format that reported the top hit, E value, ID, and description for the match to each query (Fargo 2007). The BLASTN search criteria were as follows: searched against Nucleotide Collection (NR) database, somewhat similar sequences (blastn), 10 results, expect threshold .1, word size 11, match/mismatch scores =2,-3, gap cost: existence=5, extension=2.

Clones that produced a significant match to an *Arabidopsis* protein were assigned into Gene Ontology functional categories (Gene Ontology Consortium 2004) on the basis of that match by using the TAIR locus identifier. This was accomplished by using Gene Ontology search function located on the TAIR webpage. Functional categories were grouped into three main domains which include Biological Processes, Molecular Function, and Cellular Components.

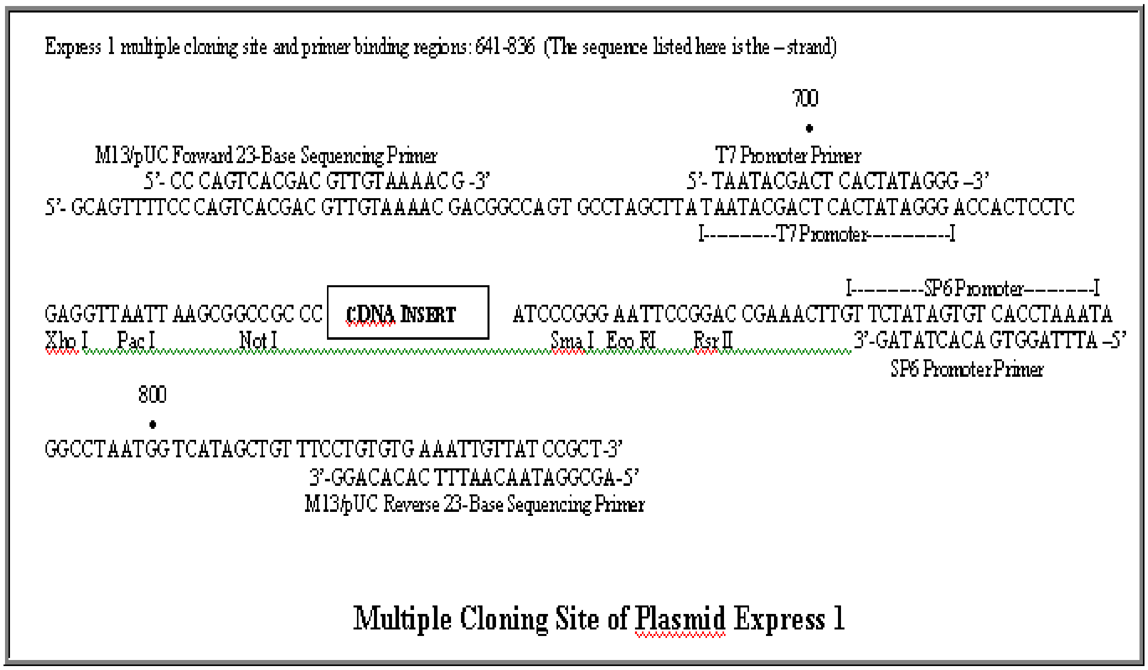
A reverse BLASTN search was done using cell wall biosynthesis proteins from *Arabidopsis* as a query against the NRO data as a way to ascertain the clones involved in lignocellulosic pathways. The search was accomplished by creating a dataset of *Arabidopsis* genes garnered from the TAIR database that had keywords tags associated with cell wall biosynthesis (lignin, cellulose, cell wall). This data set was then compared to the NRO unique sequence dataset as a way to identify possible xylogenesis genes by sequence homology.

A centralized Excel spreadsheet was created that contained all results information. The spreadsheet includes information on trim lengths, clustering, top BLAST hits, Gene Ontology summary, putative xylogenesis genes, contig and singlet lengths and totals of each. BLAST results included the E value, match description, and the identification tag for the top hit against each database. The *Arabidopsis* results also included locus id, chromosome number, chromosome position and strand origin.

Table 1. PCR cycling conditions for cDNA insert amplification (Bonds 2005)

Cycle Number	Denaturation	Annealing	Extension
Hot Start	1 min at 93°C	7 min hold at 80°C for hot start	
1	45 sec at 93°C	4 min at 68°C as first in touchdown cycles	
2	45 sec at 93°C	45 sec at 66°C	4 min at 68°C
3	45 sec at 93°C	45 sec at 64°C	4 min at 68°C
4	45 sec at 93°C	45 sec at 62°C	4 min at 68°C
5-27	45 sec at 93°C	45 sec at 60°C	4 min at 68°C

Figure 1. Multiple cloning site nucleotide sequence of Plasmid Express1 (Sieja 2005)



Express 1 multiple cloning site and primer binding regions: 641-836 (The sequence listed here is the – strand)

5'- CC CAGTCACGAC GTTGTAAAAC G -3'

5'- TAATACGACT CACTATAGGG –3'

5'- GCAGTTTTCC CAGTCACGAC GTTGTAAAAC GACGGCCAGT GCCTAGCTTA TAATACGACT CACTATAGGG ACCACTCCTC

GAGGTTAATT AAGCGGCCGC CC **CDNA INSERT** ATCCCGGG AATTCCGGAC CGAAACTTGT TCTATAGTGT CACCTAAATA

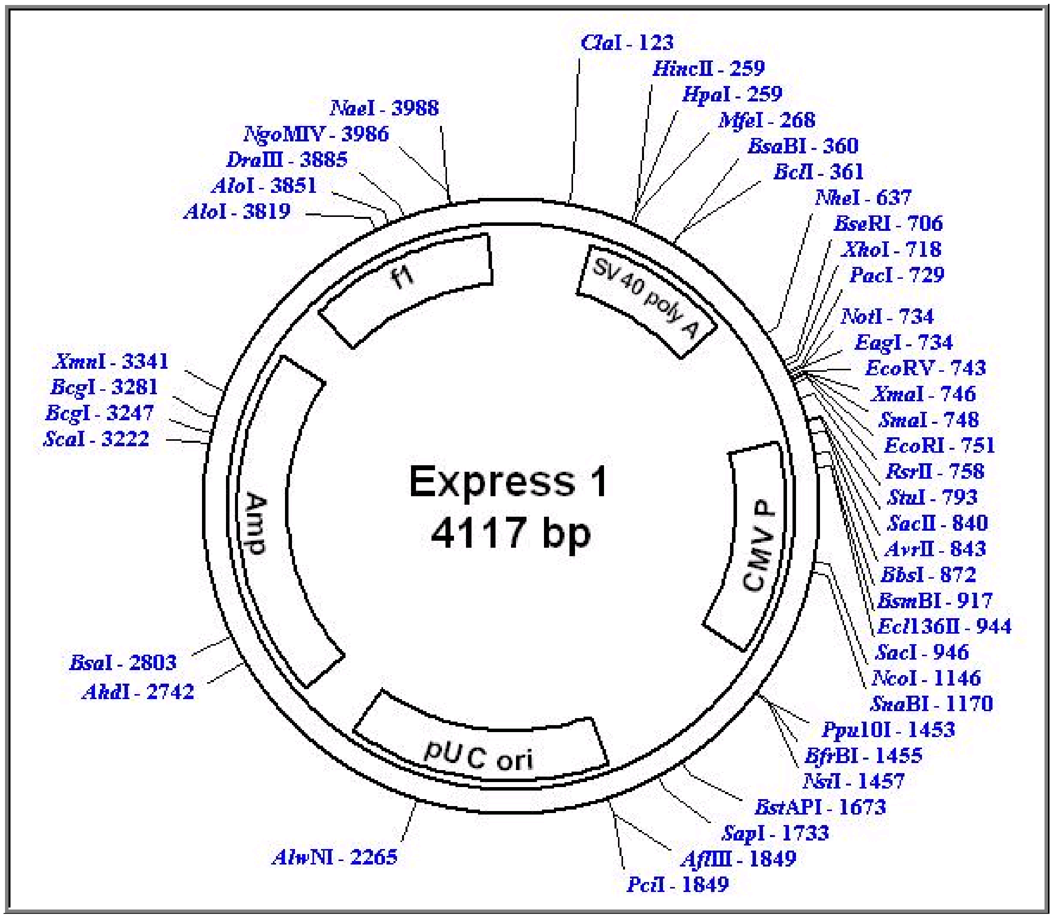
3'-GATATCACA GTGGATTTA –5'

GGCCTAATGG TCATAGCTGT TTCCTGTGTG AAATTGTTAT CCGCT-3'

3'-GGACACAC TTTAACAATAGGCGA-5'

Multiple Cloning Site of Plasmid Express 1

Figure 2. Restriction enzyme cleavage sites and gene/promoter map of plasmid Express1 (Sieja 2005)



RESULTS

Total RNA isolation yielded a quantity of 3 mg. Formaldehyde/agarose gel electrophoresis of the total RNA suggested the presence of substantial concentrations of long RNA fragments since distinct 18S and 28S ribosomal RNA bands were visible (Figure 3). Analysis of the primary NRO cDNA library (unnormalized) as stated by Open Biosystems yielded an average insert length of 1.5kb, a titer of 9.0×10^5 CFU/ml, and a recombinant percentage of 98%. The normalized library produced an average length of 1.4 kb, a titer of 7.4×10^6 CFU/ml, and a recombinant percentage of 87% in a total volume of 6.0 ml. A replicate titer performed in lab on the normalized NRO cDNA library resulted in the observation of 4.8×10^6 CFU/ml.

UV spectroscopy performed on each of 594 plasmid preparations resulted in an average plasmid DNA concentration of 1813 ng/μl and a very wide range of observed values (0-6286.8 ng/μl) and a large standard deviation (±1159.53 ng/μl). Analysis of PCR amplification for 331 clones resulted in average insert size of 1356.2 bases and revealed 4 clones without an insert. Images of electrophoresis separated PCR products can be viewed in Appendix B. Appendix C contains information used to interpolate insert lengths including standard migration distances, insert migration distances, regression equations calculations and graphs. PCR amplification gels generally displayed distinct insert bands and faint or nonexistent bands for extraneous reaction products.

A total of 984 cDNA clones from the normalized NRO library were sequenced resulting in 1,190 reads of appropriate quality and sequence lengths greater than 50 bp. A typical electropherogram (Clone # 0943) can be found in Appendix D and a graphical representation of quality trimming can be seen in Figure 4. After quality trimming, only one clone did not produce a sequence that met the quality trimming cutoff criteria. Another 14 clones were eliminated due to lack of insert sequence resulting in 1,166 sequences from 969 clones. Assembly of redundant sequences resulted in 870 unique sequences including 668 singlet sequences and 202 contiged sequences. A concatenated list of all unique NRO sequences in FASTA format can be seen in Appendix E. A summary of fragment lengths and their assigned contigs is compiled in Appendix F while information on the unassembled sequences is listed in Appendix G. Unique sequences identified during this study were submitted to the NCBI EST database.

The length of singlet sequences averaged 668 nucleotides while the length of contig sequences averaged 941 nucleotides. Contig sequences included clones which had been sequenced more than once as well as clones which had insert sequences that were redundant within the library. The library contained a total of 193 clones whose sequence was redundant to another clone which is a rate of 19.9% redundancy. A total of 69 gene inserts were found to be doubly redundant accounting for a total of 138 clones while 12 were found to be triply redundant (36 clones). Finally, two were quadruply redundant (8 clones) and one each exhibited 5X and 6X redundancy.

BLASTX of the NRO query set against the *Arabidopsis* protein database resulted in significant matches for 819 of 870 (94.1%) unique sequences. Comparison to the *Populus* protein database generated the highest number of significant matches with a total of 824/870 (94.7%). The UniProt database yielded the lowest number of significant hits with 608/870 (69.8%). Appendices H, I and J contain the BLASTX results for *Arabidopsis*, *Populus*, and UniProt respectively and report the description of the top hit and E value for each clone. A total of 40 genes did not produce a significant hit in any of the analyses, a result which translates to a total of 830/870 (95.4%) sequences that could be identified by sequence similarity (Table 2). Table 3 gives general information about the assembly and redundancy of the library

In addition, 45 putative xylogenesis genes (Table 4) were identified from the reverse BLASTN computation, a result that translates to 5% of the unique sequences from this study. To accomplish this test a database of *Arabidopsis* genes containing cell wall biosynthesis keywords was created using the TAIR gene database. This reverse BLASTN search was performed using cell wall biosynthesis proteins from *Arabidopsis* as the query against the NRO data as a way to ascertain the clones involved in lignocellulosic pathways. In a separate BLASTN analysis employing the unique sequence dataset as the query and the GenBank NR database as the target, a total of six matches were found to have non-plant similarities while 38 were without a significant match to any known sequence (Appendix K).

Arabidopsis BLASTX results were used to classify the genes into Gene Ontology categories based on their function and location in the cell. There are three main Gene Ontology categories; cellular components, biological process and molecular function. Tables 5-7 list the results for each category. There are more total hits across the three categories than number of unique sequences because many genes can be classified by more than one keyword and functional category.

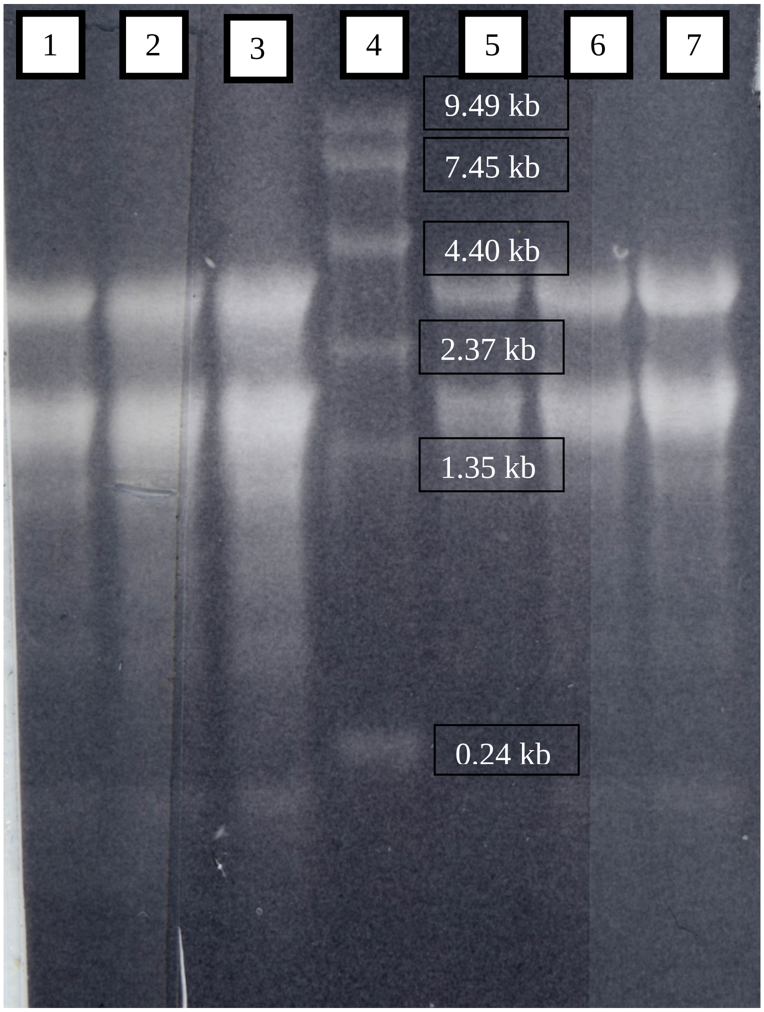
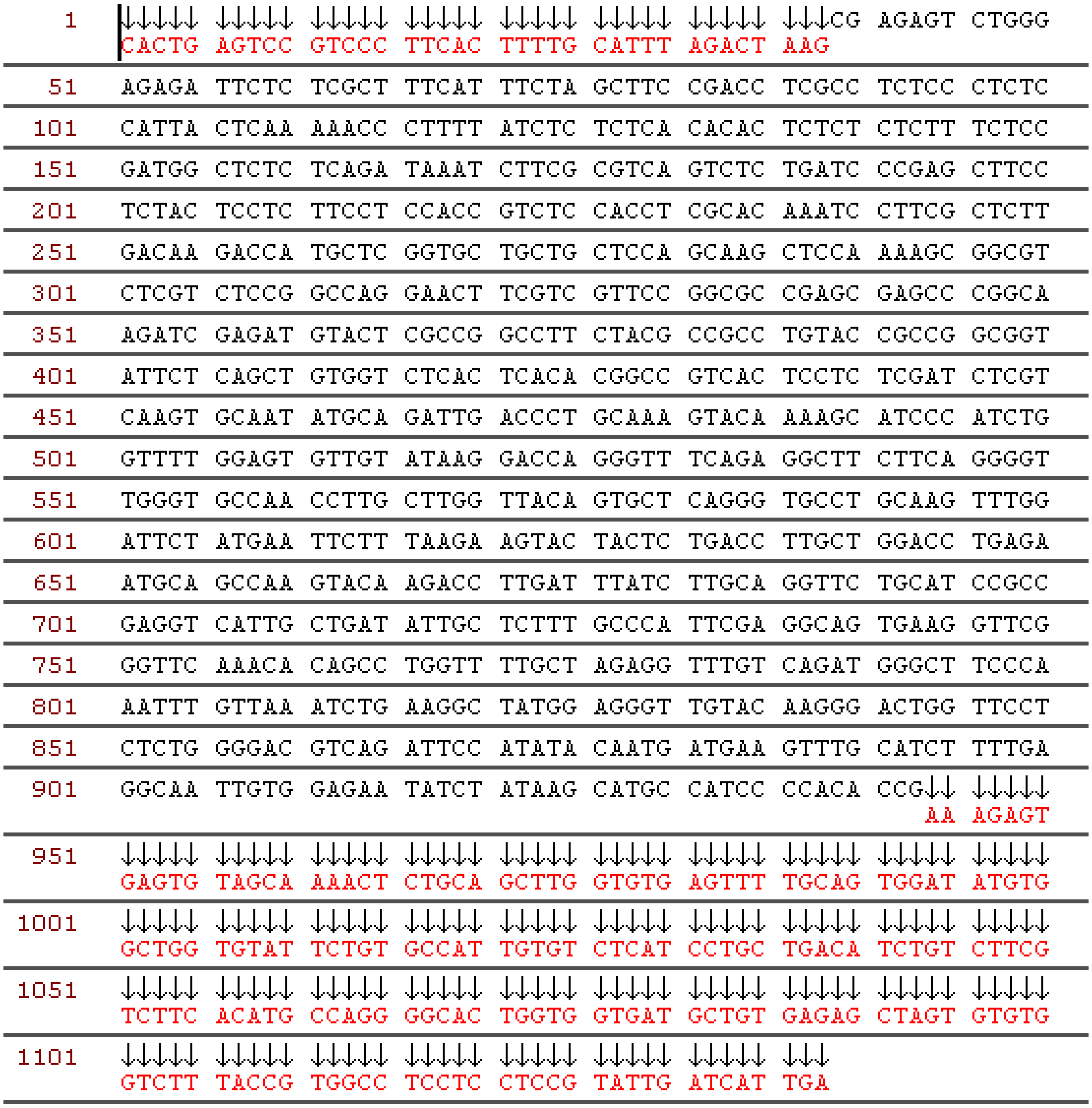


Figure 3. Denaturing gel electrophoresis of NRO total RNA. Lane 1: 1 μl NRO prep 9-7-05, lane 2: 2 μl of NRO prep 9-7-05, lane 3: 3 μl of NRO prep 9-7-05, lane 4: 3 μl of Invitrogen 0.24-9.5 kb RNA ladder, lane 5: 1 μl NRO prep 9-16-05, lane 6: 2 μl of NRO prep 9-16-05 and lane 7: 3 μl of NRO prep 9-16-05.



```
   1    ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓CG AGAGT CTGGG
        CACTG AGTCC GTCCC TTCAC TTTTG CATTT AGACT AAG
  51    AGAGA TTCTC TCGCT TTCAT TTCTA GCTTC CGACC TCGCC TCTCC CTCTC
 101    CATTA CTCAA AAACC CTTTT ATCTC TCTCA CACAC TCTCT CTCTT TCTCC
 151    GATGG CTCTC TCAGA TAAAT CTTCG CGTCA GTCTC TGATC CCGAG CTTCC
 201    TCTAC TCCTC TTCCT CCACC GTCTC CACCT CGCAC AAATC CTTCG CTCTT
 251    GACAA GACCA TGCTC GGTGC TGCTG CTCCA GCAAG CTCCA AAAGC GGCGT
 301    CTCGT CTCCG GCCAG GAACT TCGTC GTTCC GGCGC CGAGC GAGCC CGGCA
 351    AGATC GAGAT GTACT CGCCG GCCTT CTACG CCGCC TGTAC CGCCG GCGGT
 401    ATTCT CAGCT GTGGT CTCAC TCACA CGGCC GTCAC TCCTC TCGAT CTCGT
 451    CAAGT GCAAT ATGCA GATTG ACCCT GCAAA GTACA AAAGC ATCCC ATCTG
 501    GTTTT GGAGT GTTGT ATAAG GACCA GGGTT TCAGA GGCTT CTTCA GGGGT
 551    TGGGT GCCAA CCTTG CTTGG TTACA GTGCT CAGGG TGCCT GCAAG TTTGG
 601    ATTCT ATGAA TTCTT TAAGA AGTAC TACTC TGACC TTGCT GGACC TGAGA
 651    ATGCA GCCAA GTACA AGACC TTGAT TTATC TTGCA GGTTC TGCAT CCGCC
 701    GAGGT CATTG CTGAT ATTGC TCTTT GCCCA TTCGA GGCAG TGAAG GTTCG
 751    GGTTC AAACA CAGCC TGGTT TTGCT AGAGG TTTGT CAGAT GGGCT TCCCA
 801    AATTT GTTAA ATCTG AAGGC TATGG AGGGT TGTAC AAGGG ACTGG TTCCT
 851    CTCTG GGGAC GTCAG ATTCC ATATA CAATG ATGAA GTTTG CATCT TTTGA
 901    GGCAA TTGTG GAGAA TATCT ATAAG CATGC CATCC CCACA CCG↓↓ ↓↓↓↓↓
                                                           AA AGAGT
 951    ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓
        GAGTG TAGCA AAACT CTGCA GCTTG GTGTG AGTTT TGCAG TGGAT ATGTG
1001    ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓
        GCTGG TGTAT TCTGT GCCAT TGTGT CTCAT CCTGC TGACA TCTGT CTTCG
1051    ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓
        TCTTC ACATG CCAGG GGCAC TGGTG GTGAT GCTGT GAGAG CTAGT GTGTG
1101    ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓↓↓ ↓↓↓
        GTCTT TACCG TGGCC TCCTC CTCCG TATTG ATCAT TGA
```

Figure 4. Quality trimming information for clone 0943 (arrows indicate base calls which were removed due to low quality scores).

Table 2. Sequences that lack a significant match within the *Arabidopsis*, *Populus*, or Uniprot databases.

concensus no hit	concensus no hit
0023-94_016(5-31-06)	0718-94-(6-7-06)_B03
0037-94-D02(4-28-06)	0730-94-(6-7-06)_F04
0047-94-F03(4-28-06)	0760-94-(6-7-06)_D08
0052-94-C04(4-28-06)	0776-94-(6-7-06)_A10
0136-94(5-31-06)_011	0791-94-(6-7-06)_G11
0161-94-A07(5-5-06)	0889-94-(6-5-06)_A12
0229-94-F10(5-10-06)	0894-94-(6-5-06)_F12
0241-94-B12(5-10-06)	0927-94-(6-15-06)_F01
0270-94(5-31-06)_002	0938-94-(6-15-06)_A03
0292-94(5-31-06)_014	1027-94-(6-2-06)_B04
0367-94-(6-12-06)_D08	1069-94-(6-2-06)_C09
0382-94-(6-12-06)_A10	Contig\107
0452-94-(6-16-06)_B04	Contig\11
0503-94-(6-8-06)_C01	Contig\110
0521-94-(6-8-06)_E03	Contig\134
0543-94-(6-8-06)_C06	Contig\175
0604-94-(6-6-06)_D01	Contig\178
0634-94-(6-6-06)_B05	Contig\45
0638-94-(6-6-06)_F05	Contig\47
0659-94-(6-6-06)_C08	Contig\87

Table 3. Bioinformatics results summary

Total Clones	984
Electropherograms	1190
Vector Sequences	14
Poor Quality	4
Unique sequences	870
Singlets	668
Average Singlets Lengths	827
Contigs	202
Average Contig Lengths	941
redundanct clones	193
2 redundancies	69
3 redundancies	12
4 redundancies	2
5 redundancies	1
6 redundancies	1
Significant Matches to *Arabidopsis* Protein DB	819
No Significant Match to Arabidopsis Protein DB	51
Significant Matches to *Populus* Protein DB	824
No Significant Matches to *Populus* Protein DB	46
Significant Matches to UniProt Protein DB	608
No Significant Matches to UniProt Protein DB	262
Putative Xylogenesis Proteins	45

Table 4. Putative xylogenesis proteins based on *Arabidopsis* homology

Unique Hit	
0030-94-E01(4-28-06)	1105-94-(6-9-06)_E07
0097-94-H09(4-28-06)	1111-94-(6-9-06)_C08
0143-94(5-31-06)_013	1116-94-(6-9-06)_H08
0303-94(5-31-06)_002	1182-94-(6-15-06)_H06
0400-94-(6-8-06)_H12	Contig\102
0523-94-(6-8-06)_G03	Contig\115
0545-94-(6-8-06)_E06	Contig\116
0548-94-(6-8-06)_H06	Contig\12
0576-94-(6-12-06)_E11	Contig\138
0581-94-(6-8-06)_E09	Contig\140
0665-94-(6-6-06)_A09	Contig\155
0714-94-(6-7-06)_F02	Contig\159
0766-94-(6-7-06)_A09	Contig\18
0801-94-(6-5-06)_A01	Contig\196
0808-94-(6-5-06)_H01	Contig\21
0825-94-(6-5-06)_A04	Contig\35
0839-94-(6-14-06)_C06	Contig\37
0856-94-(6-5-06)_H07	Contig\41
0860-94-(6-5-06)_D08	Contig\81
0898-94-(6-14-06)_H07	Contig\83
0904-94-(6-14-06)_G10	Contig\92
0940-94-(6-15-06)_C03	Contig\96
1004-94(6-2-06Truncated)_D01	

Table 5. Distribution of Gene Ontology: Cellular Components

Functional Category	Annotation Count	Gene Count
other membranes	204	190
other intracellular components	174	143
unknown cellular components	172	172
other cytoplasmic components	130	111
chloroplast	90	79
nucleus	90	84
mitochondria	48	42
plastid	39	31
Golgi apparatus	28	27
ER	27	27
plasma membrane	26	25
cytosol	21	19
cell wall	20	20
ribosome	16	10
extracellular	10	10
other cellular components	8	8

Table 6. Distribution of Gene Ontology: Molecular Function

Functional Category	Annotation Count	Gene Count
unknown molecular functions	160	160
other enzyme activity	144	129
hydrolase activity	119	101
protein binding	99	86
other binding	93	85
transferase activity	90	68
DNA or RNA binding	60	54
transporter activity	57	44
transcription factor activity	54	54
nucleotide binding	48	46
kinase activity	47	35
nucleic acid binding	29	29
other molecular functions	23	22
structural molecule activity	13	13
receptor binding or activity	7	7

Table 7. Distribution of Gene Ontology: Biological Process

Functional Category	Annotation Count	Gene Count
other metabolic processes	443	338
other cellular processes	424	320
unknown biological processes	187	187
protein metabolism	132	121
cell organization and biogenesis	102	77
response to abiotic or biotic stimulus	96	63
transport	90	73
response to stress	82	52
developmental processes	70	50
other biological processes	62	42
transcription	55	52
signal transduction	26	23
electron transport or energy pathways	23	16
DNA or RNA metabolism	20	14

DISCUSSION

Maximizing mRNA Quality

Full length cDNA libraries necessitate high quality, undegraded mRNA. This project employed a number of strategies to accomplish that goal. Among those strategies are: (1) minimizing contamination in field-collected material; (2) haste in recovery of raw cambial tissue; (3) RNase free handling conditions; and (4) use of the CTAB total RNA isolation procedure.

The project required collection of total RNA under field conditions. The Watauga oak orchard is located in a rural Tennessee mountain environment about 12 miles east of Elizabethton, TN at an altitude of 2,000 feet. No laboratory space, electricity or other utilities were available at the collection site. Previously, Mathews et al. (2003) employed the same CTAB based mRNA isolation protocol on cambial samples collected by peeling away 3 inch squares of NRO bark at Watauga. However, their small sample sizes and lack of significant EST sequence data prevented validation of the approach as a legitimate means for obtaining EST sequence data from NRO trees.

Sample handling was performed with extreme care to avoid RNase degradation and DNA contamination. Reagents and buffers were treated with DEPC and autoclaved for at least 1 hour at 220°C. Gel boxes, gel combs and labware were autoclaved or treated with boiling water/SDS then stored in covered plastic containers. The intense 28S ribosomal band present on gels of total RNA samples attest to the high quality of this project’s total RNA. Furthermore, average insert sizes in excess of 1 kb support these observations and validate both the lab and field protocols employed.

Samples were collected from a tree that was grown in a modestly controlled environment (i.e., a grassy field surrounded by other half-sib NRO family members). Because these are field samples, capture of other organisms in the cambial scrapings is possible. Among those could be fungi, bacteria, algae and small insects. Total RNA isolation techniques cannot separate messages from different organisms. The obvious problem is the potential of carrying foreign messages further into the EST sequencing program.

Several measures performed in the course of this study serve as steps to refute the possibility of genetic contamination. PolyA affinity chromatography serves as the first filter by removing bacterial messages. Since bacterial cells do not attach polyA tails to their transcripts, these mRNAs are rejected by the oligo(dT) column. Unfortunately, fungae and insects messages remain as the most likely sources of contamination. Short, genomic DNA fragments which persisted after the CTAB and DNase treatments represent another type of potential contamination. Should any of these fragments contain sufficient polyA stretches they might be collected by the oligo(dT) column and cloned into the library. The bioinformatics analysis discussed below serve as means of eliminating these sequences due to their lack of an open reading frame or homology to a known plant gene.

A second filter against EST contamination is the obvious bioinformatics test of sequence homology comparison with regard to message origin. The two primary models used for sequence homology comparison were BLASTX against the *Populus trichocarpa* and *Arabidopsis thalania* gene databases. Based on similar EST studies done on hardwoods (Sterky et al., 1998, Pavy et al., 2005b) it was assumed in this study that most

NRO ESTs would have a significant match to one of these or a related plant genome. As another means of ensuring quality, all sequences were submitted to a BLASTN nucleotide search against the GenBank non-redundant (NR) nucleotide database at the National Center for Biotechnology Information of the NIH. This strategy performs a similarity search against all ESTs against all sequences in the GenBank database, regardless of origin. If a clone displayed significant similarity to a sequence of non-plant origin, then contamination would be suspected. A more detailed presentation of this analysis will be presented in the following pages.

Bioinformatics Analysis

Similarity analysis yielded a small percentage of ESTs that did not produce a significant match to any nucleotide database. Further study will be required to assign these sequences to the *Quercus rubra* gene set. This result is commonplace in studies of this type (Sterky et al., 1998, Pavy et al., 2005b). Trees are genetically complex organisms with genomes in excess of 3 Gb and complex biochemistries containing many unusual genes not found elsewhere. Unfortunately, relatively few hardwood genomes have been thoroughly scrutinized. Consequently, EST sequencing on a species such as NRO may reveal a number of novel transcripts. These potential novel transcripts hold great promise in regard to elucidating the genetic structure and interactions responsible for physiological processes and structural components unique to NRO. Due to the wealth of information about highly conserved genes that has been garnered from studying *Arabidopsis* especially, unknown transcripts from gene rich organisms such as hardwood trees could be expected to have a larger chance of being involved in gene regulation and the synthesis of organic compounds (Sterky et al., 1998).

Using the NRO EST dataset as a query, a BLASTX comparison (operating in all six reading frames) against the UniProt database revealed a large number of sequences whose best match were to non-plant organisms. This is because UniProt is a condensed database which reduces groups of functionally similar proteins from different organisms into a single example to speed up the searching process. Consequently genes that do not have a plant as the top match cannot be assumed to stem from contamination and are likely to be functionally conserved across many different organisms (Uniprot Consortium 2006).

Electrophoresis performed on the PCR products of clones 0001-0300 and 0501-0536 provided the added benefit of corroborating the results obtained by computer-based analysis techniques, specifically the presence or absence of a gene insert. PCR failed to produce products for clones 0014, 0027, 0050, 0122 and 0241. Of this set, bioinformatic analysis supported the argument that clones 0014, 0027 and 0122 did not have an insert. Clone 0050 did not produce a usable sequencing electropherogram in four sequencing reactions and, thereby, it cannot be determined if an insert is present. Bioinformatic analysis performed on clone 0241 revealed no BLASTX matches for all three databases as well as a no significant match against the NCBI NR nucleotide database. This information points to a flaw in the PCR reaction such as pipetting error since even if a vector sequence had made it past VectorNTI's trimming function it would surely have been identified by a significant match to a vector sequence in the NR database by BLASTN searching. Since electrophoresis of PCR products was only performed on a subset of the total number of sequenced clones, only three of fourteen vector sequences identified by bioinformatics could be supported by this technique.

Library Normalization

The normalization step was used to increase the percentage of unique clones in the dataset. A total of 19.6 % of the clones sequenced in this study were found to be redundant in the library. This low result contrasts with other EST experiments. Pavy et al. (2005b) reported a 39% redundancy rate in a study of white spruce ESTs and Sterky et al. (1998) reported 53% redundancy in a poplar EST study. By improving the quality of the input EST library through normalization, a genuine cost savings was realized by minimizing the number of sequencing reactions/runs that had to be performed. Had this study operated with a 53% clone redundancy rate, almost 1,500 clones, not 984 clones would have been required to gather the same number of unique sequences. Consequently, this strategy permits programs with limited resources to make the most of their available assets.

Theoretically sequences that displayed high redundancy should come from genes with elevated expression profiles within the transcriptome. The most highly redundant sequence within this library was that of Contig 157 and was found to be six-fold redundant. The sequence had a highly significant match ($2E^{-98}$) to the *Arabidopsis* xyloglucan endoglucotransferase. This protein functions in xyloglucan biosynthesis, a molecular process expected to be highly active during spring wood formation. The sequence with the next highest frequency was that of Contig 153 (five duplicates), which has a close match ($5E^{-95}$) to an *Arabidopsis* protein of unknown function containing a

LIM-type zinc binding domain. The sequence of Contig 78 was identified four times and has a highly significant match (E^{-107}) to the *Arabidopsis* triosephosphate isomerase protein, an enzyme in the glycolytic pathway. This pathway should be highly active in a growing tree. Contig 7 is also a quadruple redundant sequence which is almost identical (E^{-101}) to an EIF2 transcription initiation factor (TAIR 2008).

BLASTN of the library against NCBI's NR nucleotide database revealed eleven sequences which had top matches that were non-plant organisms. Upon further inspection, 5 of these sequences were determined to be insert-less clones that were not properly removed by the Vector NTI screening algorithm, a common occurrence in complex libraries such as this (Fargo 2007). Of the remaining six, two (0016-93-A12(4-21-06) and 1147-94-(6-9-06Truncated)_G12) had significant BLASTX matches to the *Arabidopsis* and *Populus* databases and could be dismissed as potential contamination due to this homology. Three of the remaining four; (0521-94-(6-8-06)_E03, 0927-94-(6-15-06)_F01 and 0938-94-(6-15-06)_A03) yielded no significant hits to any gene in BLASTX comparisons done against the *Arabidopsis*, *Populus*, Uniprot and NCBI databases and remain ambiguous since their nucleotide similarity could not be corroborated by translational querying. The matches to these clones all came from whole genome sequencing projects as uncharacterized hypothetical proteins. The final clone; 0806-94-(6-5-06)_F01 displayed a significant UNIPROT BLASTX match to human Ras related GTP binding protein ($E = 8^{-33}$). A manual BLASTX search using the NCBI website server (NCBI 2008) corroborated this match by returning an E-value of 1^{-31} in regard to a chimpanzee RAS related GTP binding protein. The BLASTN comparison also supported this result by revealing a hit to the same type of gene again in humans with an E value equal to zero. Upon visual inspection the high correlation between these two proteins is due to the Ras domain which they share. While this result is very odd, it must be noted that the Ras protein superfamily are examples of small GTPases, which are a fundamental cell signaling process in that is found Eukaryotes (Vernoud et al., 2003).

Nucleotide similarity comparison is a much less rigorous test of genetic correlation than peptide sequence evaluation (Bonds 2005). Since an mRNA can be read in six possible orientations, chances of false similarity are greatly increased by not limiting the query to a single translated sequence. There is also the issue of codon bias between organisms and frame shift mutations which result in large disparities in translation products between two highly similar sequences. In an ideal situation, a polypeptide would be sequenced and used as the basis for genetic comparison and correlated to mRNA and genomic DNA sequences. A much more practical employment of resources was undertaken in this study where mRNA transcripts served as the basis for computer aided translation and searching.

Annotation

There are three principle Gene Ontology (GO) classifications into which sequences were binned: cellular components, biological processes and molecular functions (Gene Ontology 2004). Cellular components are defined as subunits of anatomical structures (e.g., rough endoplasmic reticulum or nucleus) or gene product groups (e.g., ribosome, proteasome, or a protein dimer). Molecular function describes activities such as catalysis or binding that occurs at the molecular level. Functions are usually performed by single gene products but can be performed by complexes of gene products. Biological processes are categorized as assemblies of molecular functions and as a rule require more than one step, a broad example being signal transduction pathways.

Since GO Biological Processes are by definition groups of individual molecular functions that have a concerted goal, they cannot be assigned a single gene as an example. Molecular functions however, can be specific to a gene. Contig_25 has a match of E-value=0 to the *Arabidopsis* gene locus AT5G56030.1, which codes for an ATP binding protein (a molecular function). This gene functions in several biological processes including defense response, protein folding, flower development, protein stabilization, leaf development and heat acclimation (Gene Ontology website 2008).

Clone 1308-94-(6-16-06)_B07 is an example of nuclear cellular component in the Gene Ontology diction and likely encodes for actin, a cytoskeleton structural protein. The *Arabidopsis* locus associated with this clone is AT5G6180 and is described as encoding a protein whose sequence is similar to actin-related proteins (ARPs) in other organism and as being a member of the nuclear ARP family of genes (Gene Ontology website 2008).

Clone 0097-94-H09(4-28-06) is an example of a gene that has a primary role in the physical process of cell wall production. Similarity comparison identifies the gene as a putative cinnamyl-alcohol dehydrogenase, which catalyzes the reaction of cinnamyl alcohol to cinnamaldehyde (cinnamyl alcohol + NADP$^+$ $\rightleftharpoons$ cinnamaldehyde + NADPH + H$^+$) as a step in the lignin biosynthesis pathway (Gene Ontology website 2008). Clones 0576-94-(6-12-06)_E11 and 0714-94-(6-7-06)_F02 are two genes that putatively function in gene regulation. They are two of the four poorest matches among the xylogenesis dataset and their matches are to poorly understood genes in *Arabidopsis.* Inspection of the putative xylogenesis genes reveals that the majority of the descriptions are for genes that are structural in nature, as opposed to regulatory elements. A result could be expected since one of the proposed differences in xylogenesis between woody and herbaceous plants is not the machinery for this process but its regulation (Groover 2005).

Due to the nature of how the *Arabidopsis* xylogenesis reference dataset was populated, the NRO sequences identified do not exclusively encode proteins that are obvious members of the xylogenesis schema. Genes that function in the concerted process that is required for the end goal of cell wall synthesis were also identified as xylogenesis genes due to their ancillary support of that process. The NRO clone that had the highest degree of similarity to an *Arabidopsis* xylogenesis protein was Contig_81, which had an E-value match of $1E^{-166}$ to the protein calnexin. Calnexin is a chaperone protein that functions in the endoplasmic reticulum and is responsible for directing the folding of glycoproteins (Gene Ontology website 2008).

Data generated in this study lays the groundwork for further projects involved with NRO genetics. The in-depth annotation of these sequences is a large undertaking in itself; each clone could have an entire research project devoted to it. In regard to the sequences that displayed significant similarity, much exploration could be done as to exactly how they are different from the homologous sequences in other organisms. More interesting might be the characterization of sequences that did not display a match to any known sequence. Plausible targets of research for these novel clones would be to determine their presence or absence in related hardwoods. This objective could be accomplished by generating primers from the novel clones and performing PCR on genomic samples from related species to identify species that produce products. Their bioinformatic analysis could also be taken to new levels of scrutiny by implementing more complex protein motif searching to elucidate if there are any characterized domains coded by their sequence.

The most practical evolution of this research would be the development of genetic markers from the data set. This process would necessitate the collection of DNA from other NRO individuals in order to compare any sequence variation that might be present. There are several kinds of markers that could be employed in such a study but the most widely employed is SNP detection. Identification of such sequence variation could aid in the development of marker assisted breeding techniques and possibly increase NRO production.

The experimental method employed in this project has proven to be very successful as a means of developing EST sequence information from NRO trees. Throughout the entire process results confirm the validity of the approach. The CTAB method of RNA isolation produced more than enough quality total RNA to produce a quantity of mRNA that was needed to develop a large and complex library such as this one. Long sequencing reads also validate the process by testifying to the quality of the cDNA clones and the sequencing protocol. While the sequencing method employed in this study was certainly effective and reliable, future studies could make use of next generation sequencing platforms such a 454 and Illumina to more efficiently handle that aspect of the project since they are quickly becoming the standard for DNA sequencing applications. The bioinformatic analysis performed on the data set was standard to these sorts of studies (Fargo 2007) and while it is currently cutting edge technology, any future studies of this kind or if this study was to be repeated, would surely make use of new technologies which are being developed at a very quick rate.

Data presented here will be of great value especially to ongoing NRO sequencing projects by expanding the basis for comparison of new sequences. Of special interest among the sequences disseminated with this thesis are the unknown genes. While it is possible that they are contamination or code for genes that are of no use to humans, it is also possible that they hold the keys to understanding what makes a northern red oak tree different from all the other organisms in the world or encode a protein that is great value to mankind.

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APPENDIX A: pExpress1 in FASTA Format

```
>pExpress1 o4117 bp
CCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCT
ATTACGCCAGCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAG
GATCGATCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCA
GTGAAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTAT
AAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGG
GGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGCTGATTA
TGATCATGAACAGACTGTGAGGACTGAGGGGCCTGAAATGAGCCTTGGGACTGTGAATCT
AAAATACACAAACAATTAGAATCACTAGCTCCTGTGTATAATATTTTCATAAATCATACT
CAGTAAGCAAAACTCTCAAGCAGCAAGCATATGCAGCTAGTTTAACACATTATACACTTA
AAAATTTTATATTTACCTTAGAGCTTTAAATCTCTGTAGGTAGTTTGTCCAATTATGTCA
CACCACAGAAGTAAGGTTCCTTCACAAAGATCCCAAGCTAGCAGTTTTCCCAGTCACGAC
GTTGTAAAACGACGGCCAGTGCCTAGCTTATAATACGACTCACTATAGGGACCACTCCTC
GAGGTTAATTAAGCGGCCGCGATATCCCGGGAATTCCGGACCGAAACTTGTTCTATAGTG
TCACCTAAATAGGCCTAATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCCGC
GGCCTAGGCTAGAGTCCGGAGGCTGGATCGGTCCCGGTGTCTTCTATGGAGGTCAAAACA
GCGTGGATGGCGTCTCCAGGCGATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGAC
CTCCCACCGTACACGCCTACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTT
TGGAAAGTCCCGTTGATTTTGGTGCCAAAACAAACTCCCATTGACGTCAATGGGGTGGAG
ACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCCATTGATGTACTGCCAAAACCG
CATCACCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCA
TAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGG
GGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATA
CTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAT
TATTGACGTCAATGGGCGGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAG
TTATGTAACGACATGCATCTAATGAGTGAAAGGGCCTCGTACTACGCCTATTTTTATAGG
TTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGC
GCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGAC
AATAACCCTGATAAATGCTTCAATAATATTGAAAAACGCGCGAATTGCAAGCTCTGCATT
AATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCT
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AGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAA
AAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGC
TCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGA
CAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTC
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GTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTG
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GAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTA
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AATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCC
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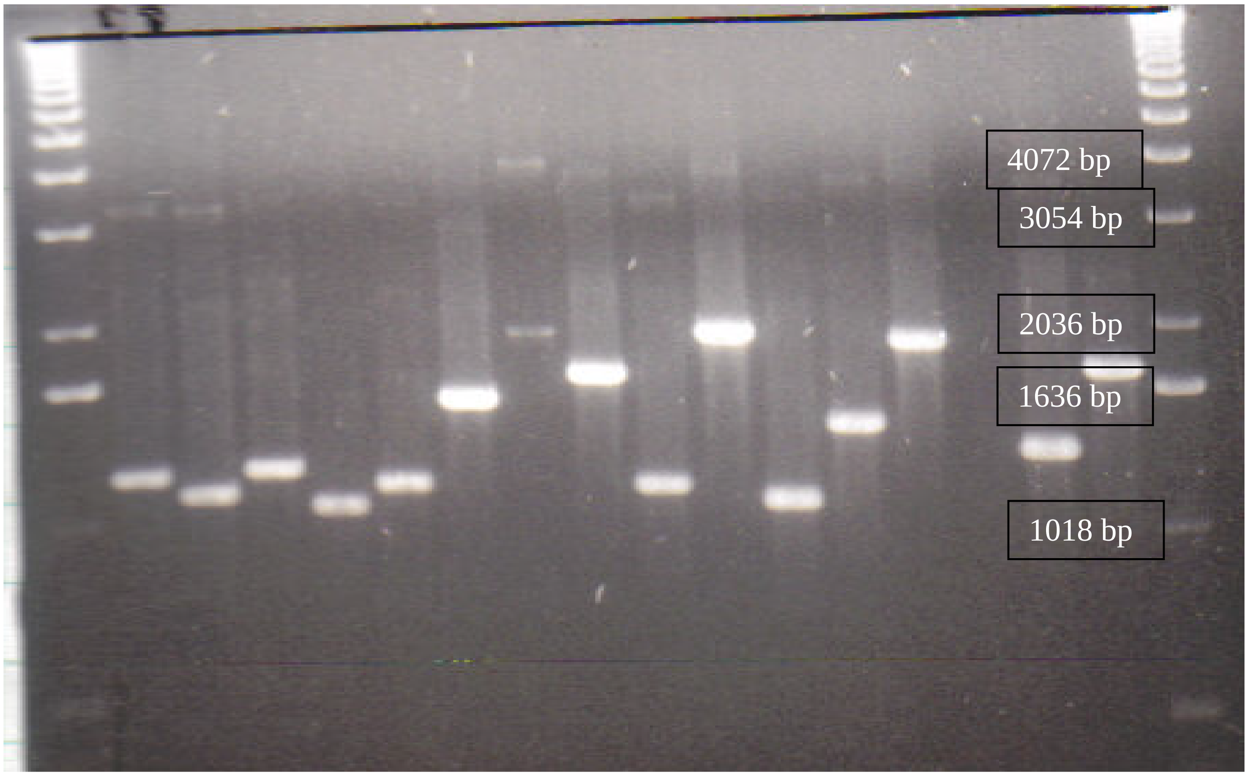
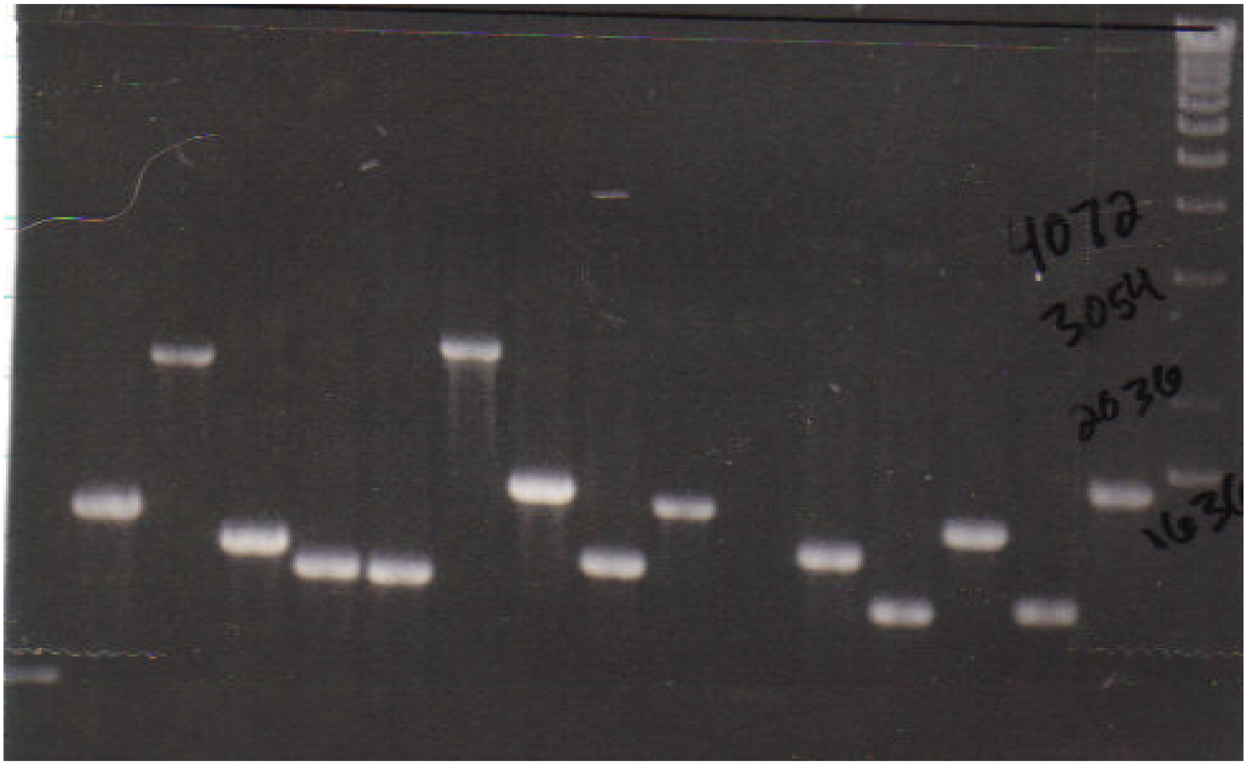
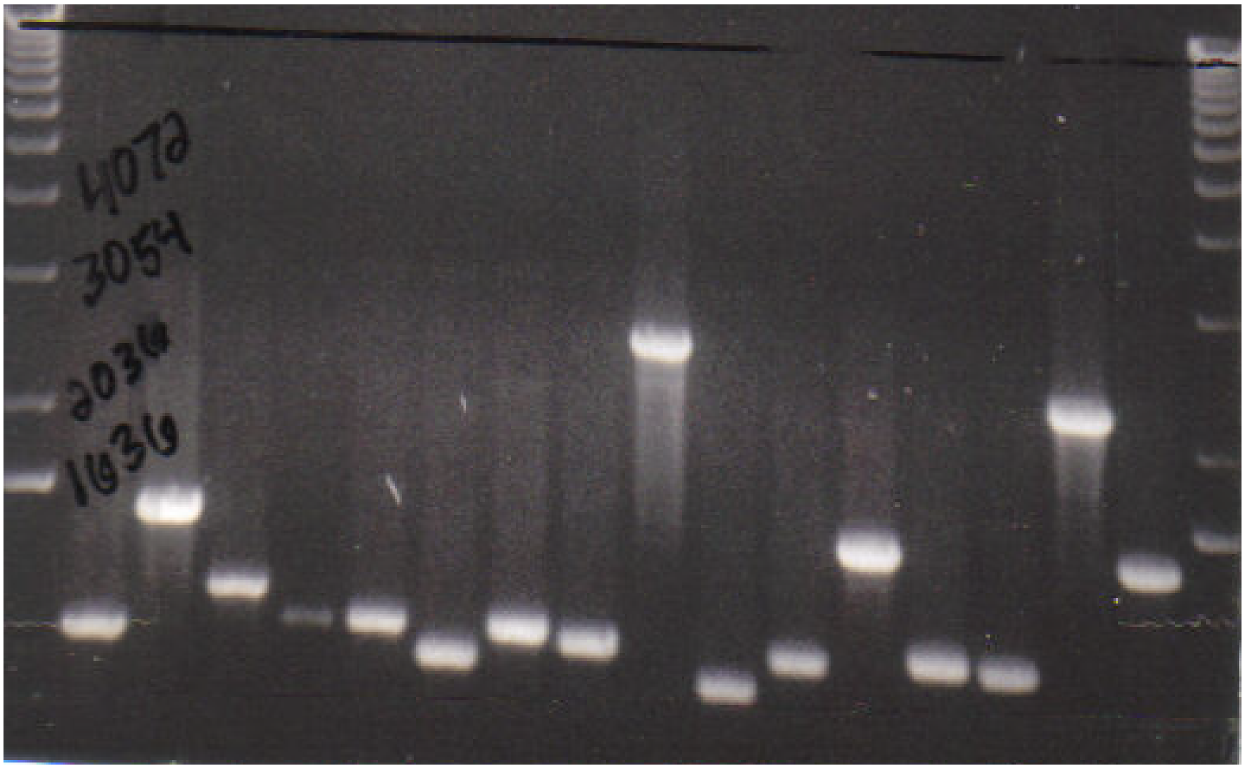
Appendix B: PCR Product Electrophoresis Images



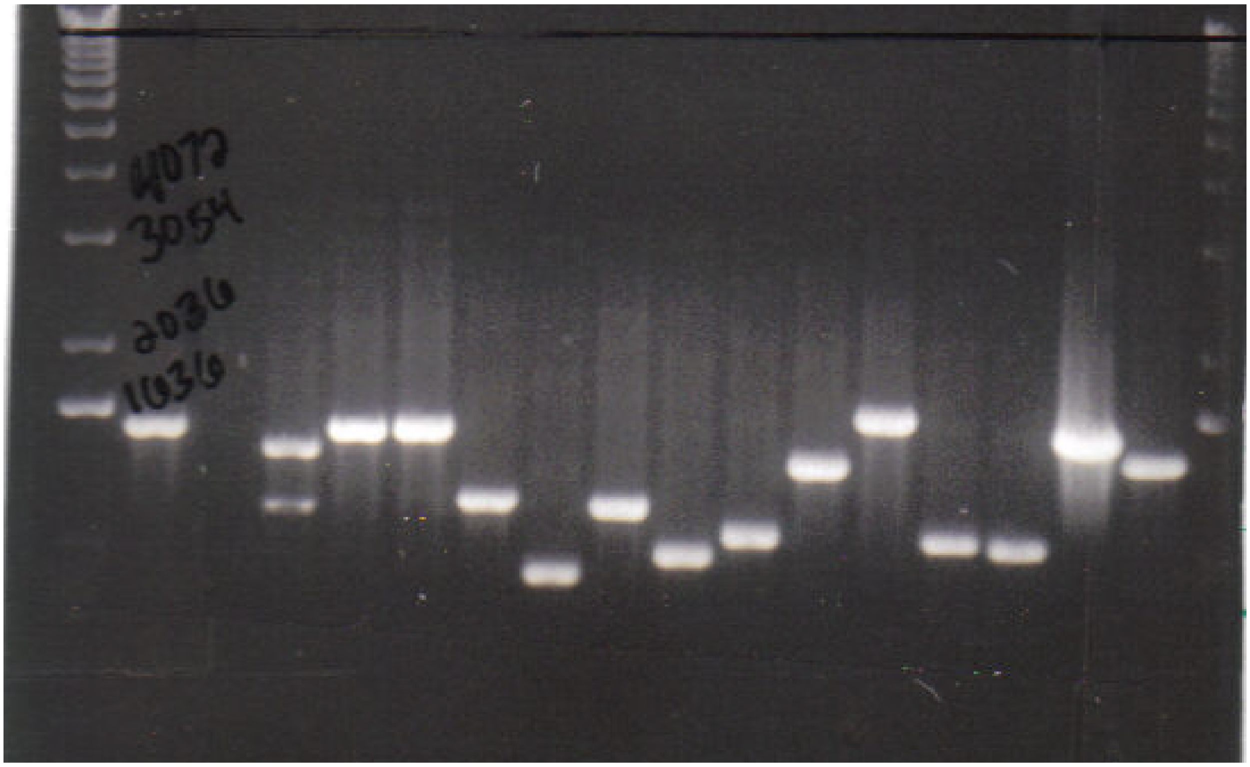
Gel Electrophoresis of PCR Products for Clones 0001-0016 (left to right), DNA standard is Invitrogen 1 Kb ladder



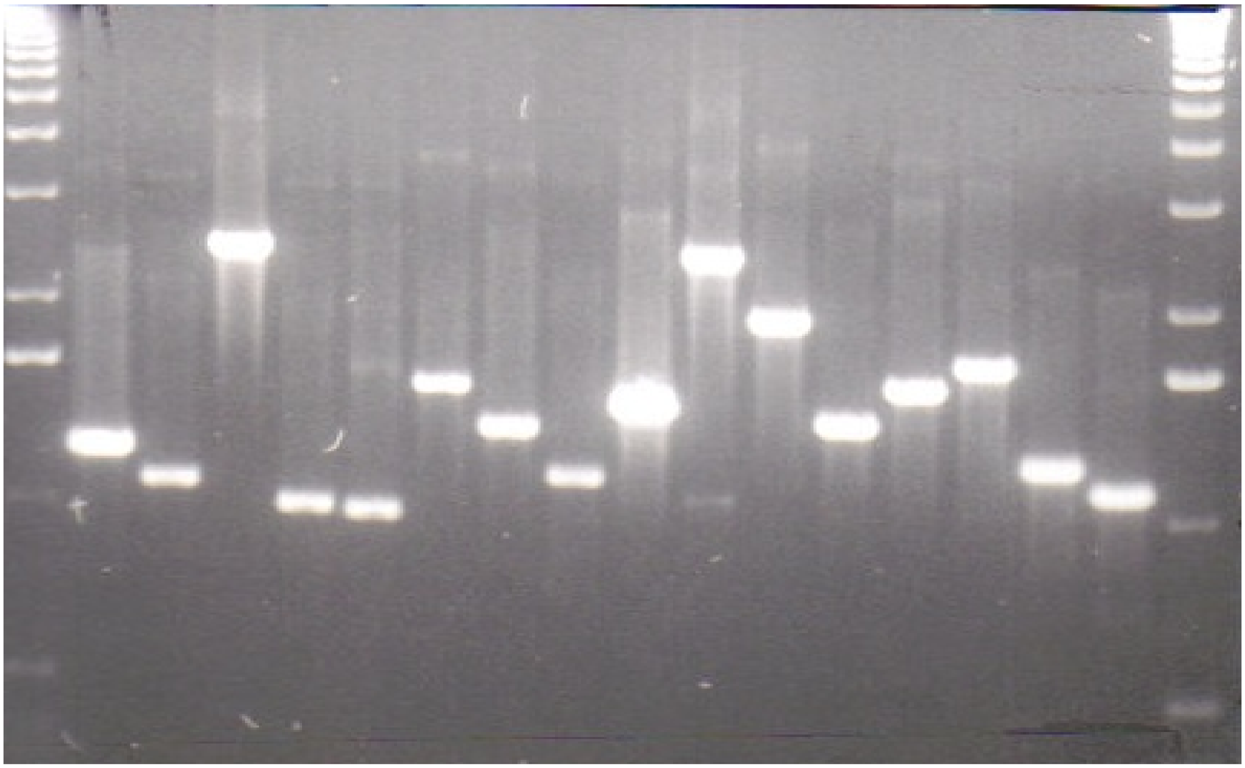
Gel Electrophoresis of PCR Products for Clones 0017-0032



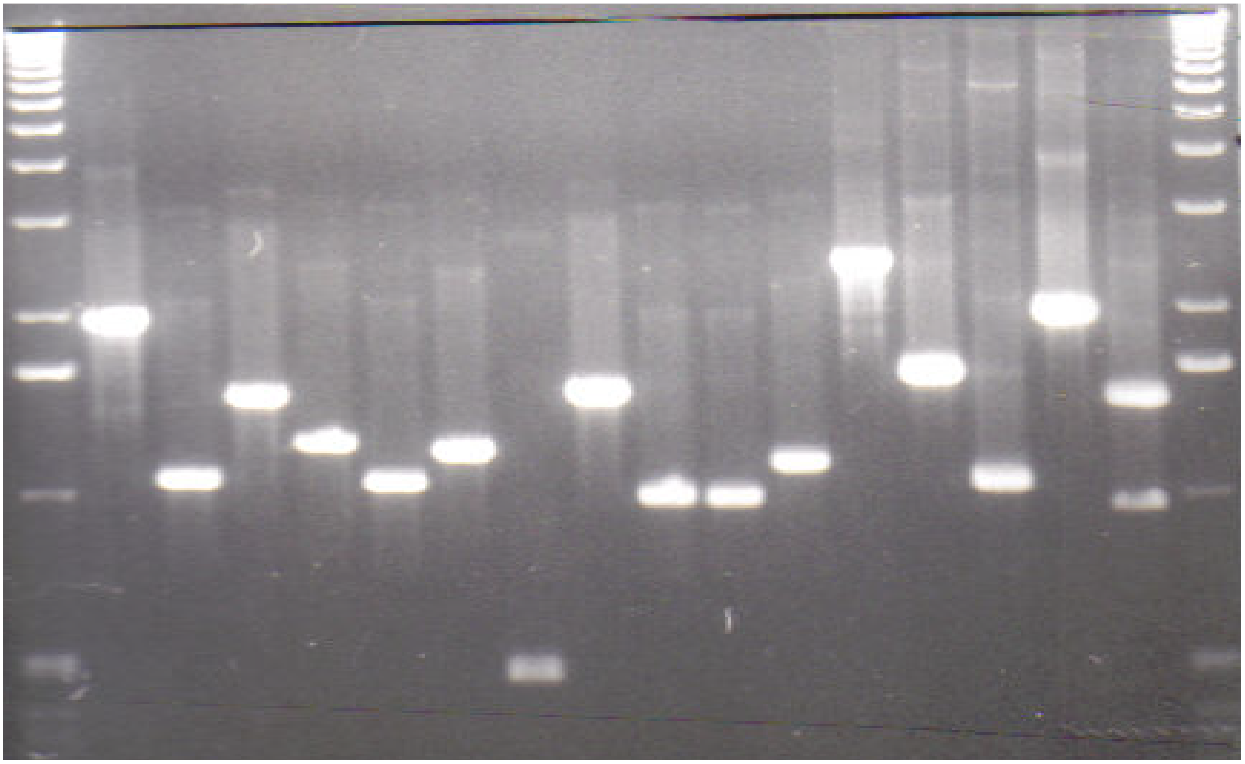
Gel Electrophoresis of PCR Products for Clones 0033-0048



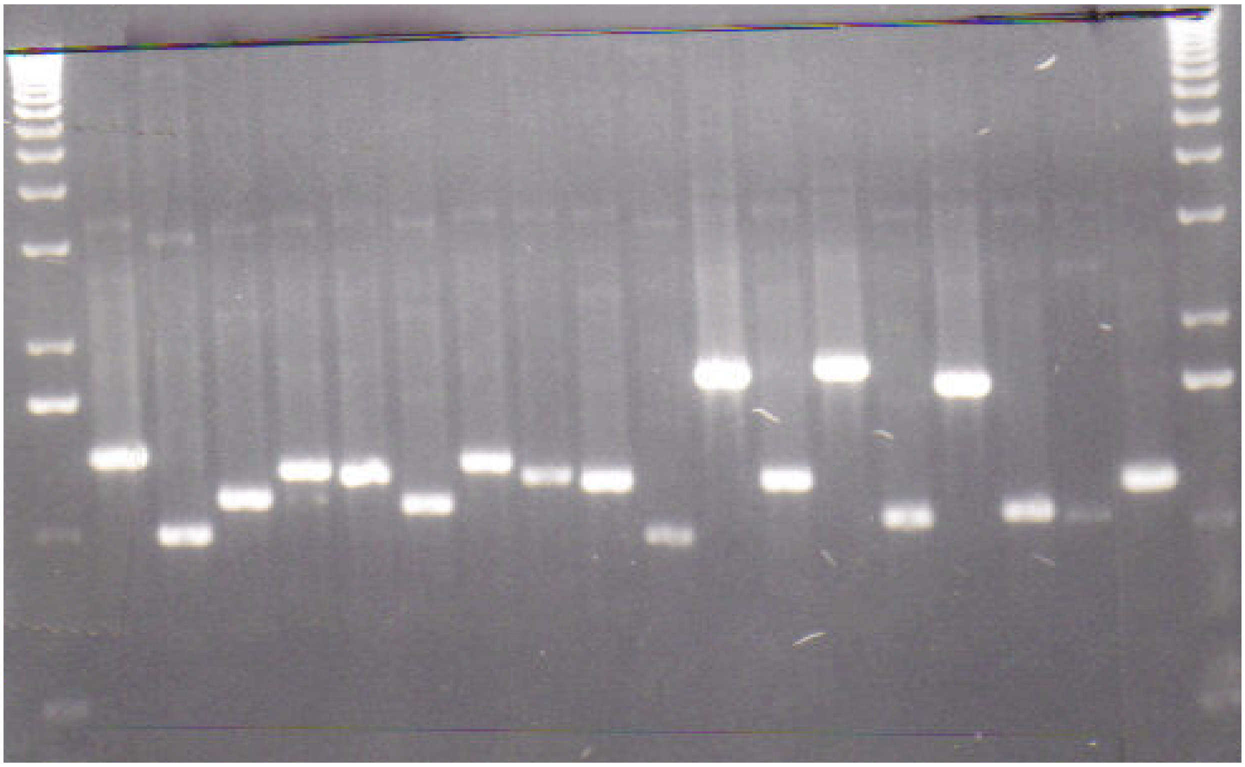
Gel Electrophoresis of PCR Products for Clones 0049-50, 55-68



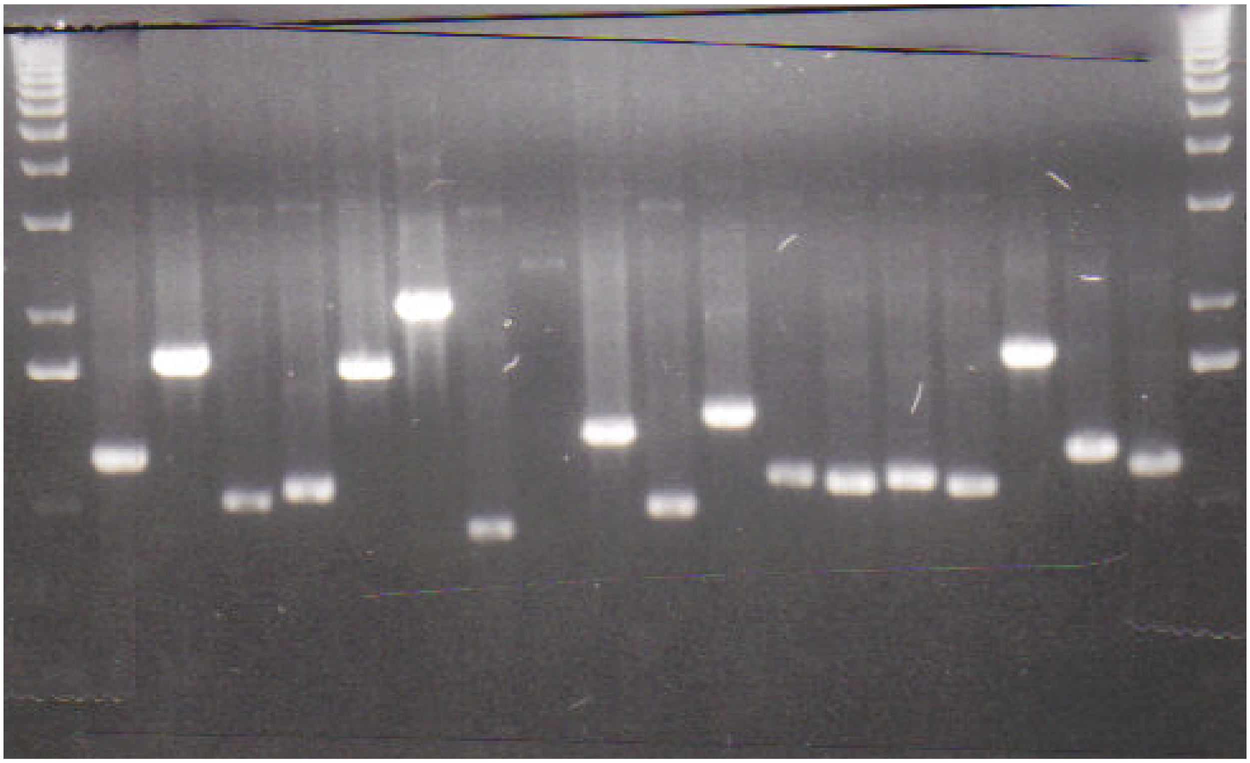
Gel Electrophoresis of PCR Products for Clones 0069-0084



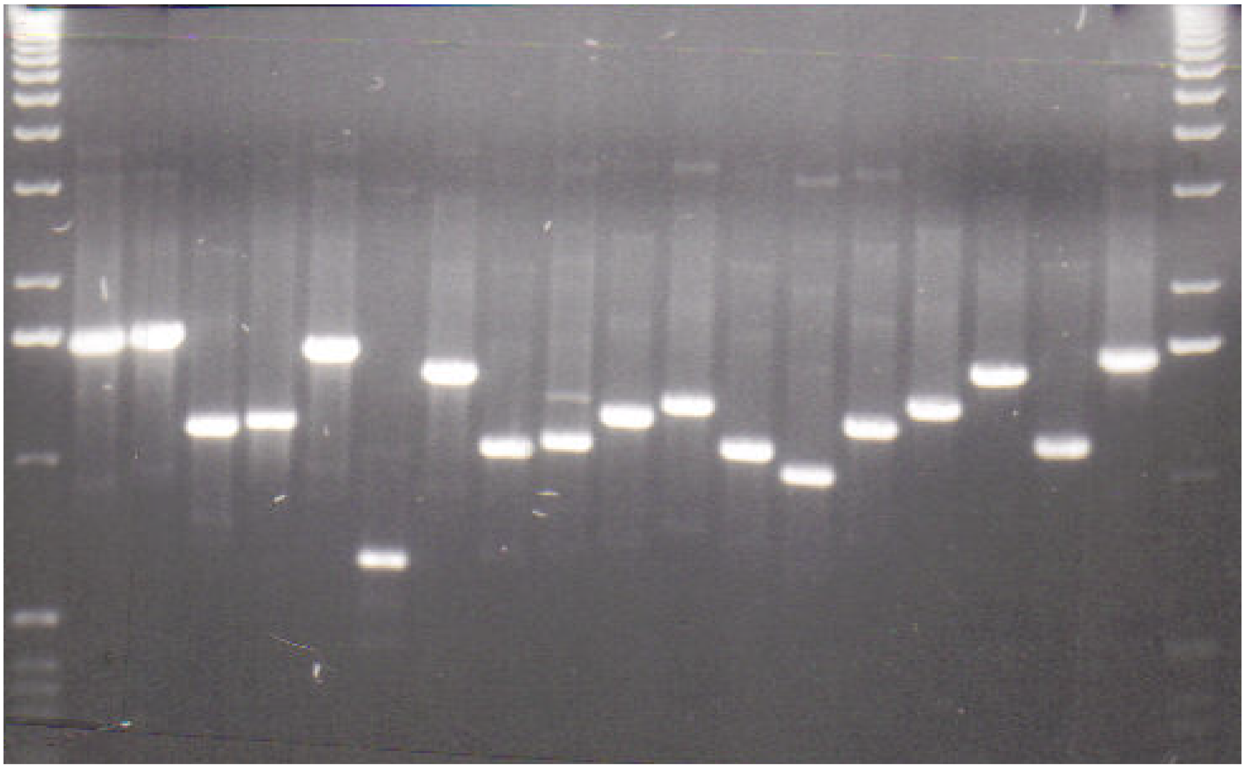
Gel Electrophoresis of PCR Products for Clones 0085-0100



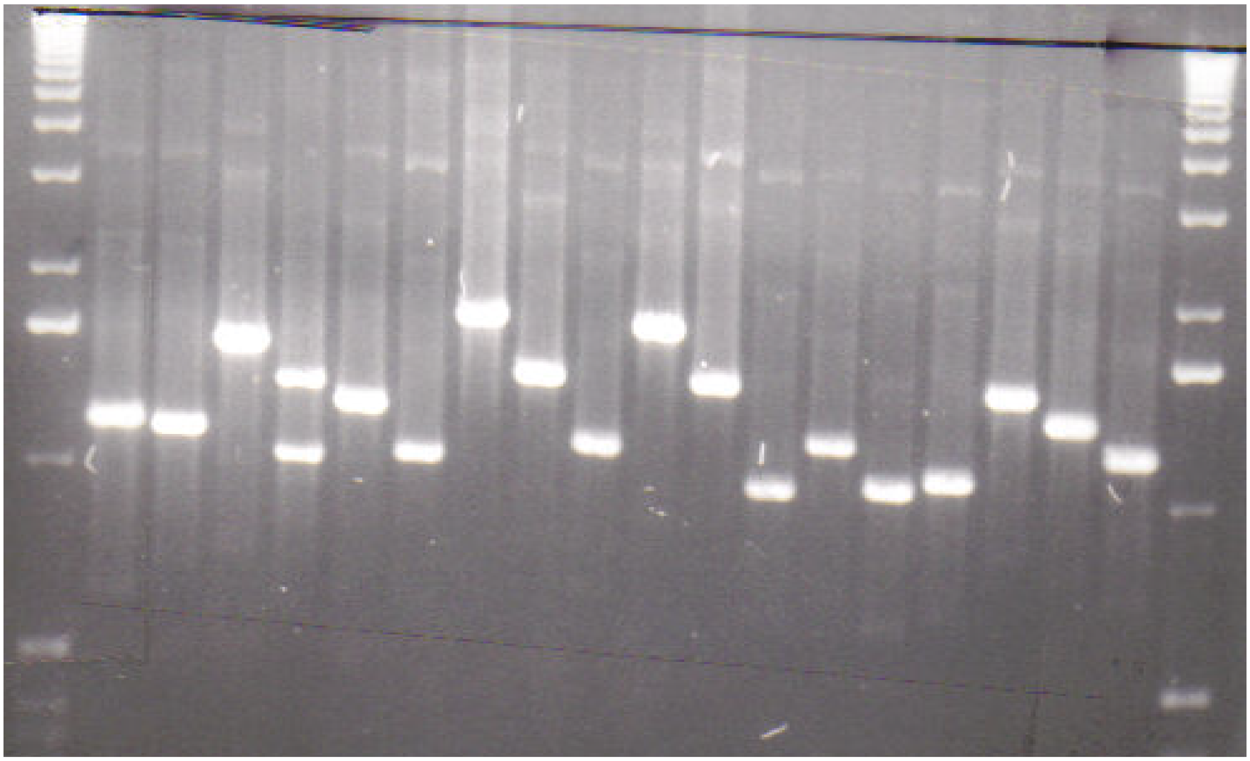
Gel Electrophoresis of PCR Products for Clones 0051-0054, 0101-0114



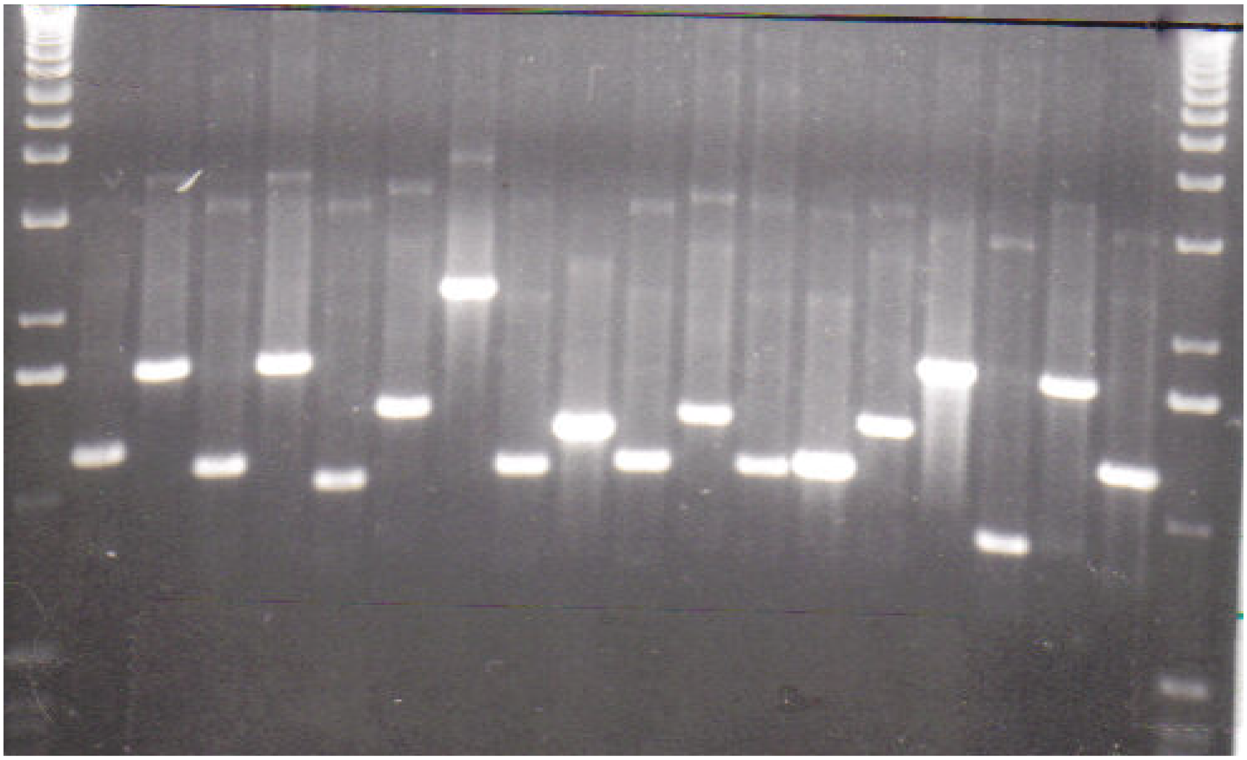
Gel Electrophoresis of PCR Products for Clones 0115-0132



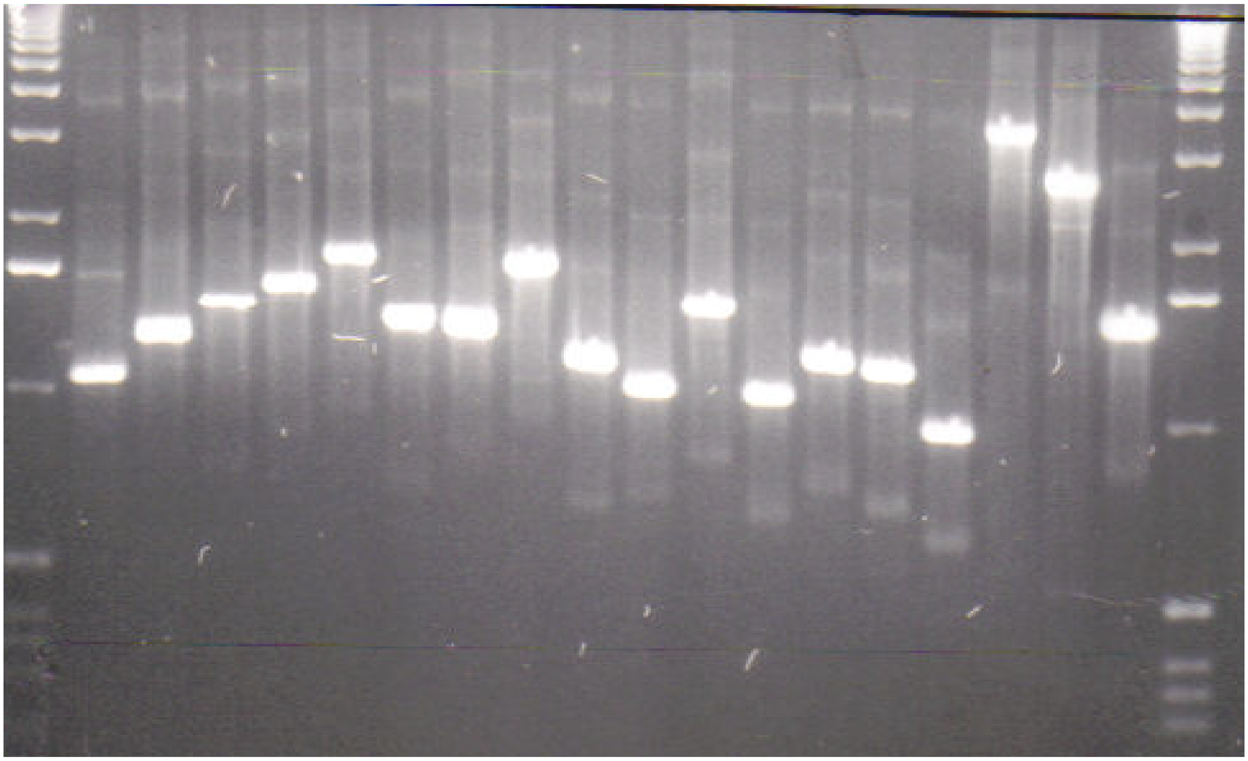
Gel Electrophoresis of PCR Products for Clones 0133-0150



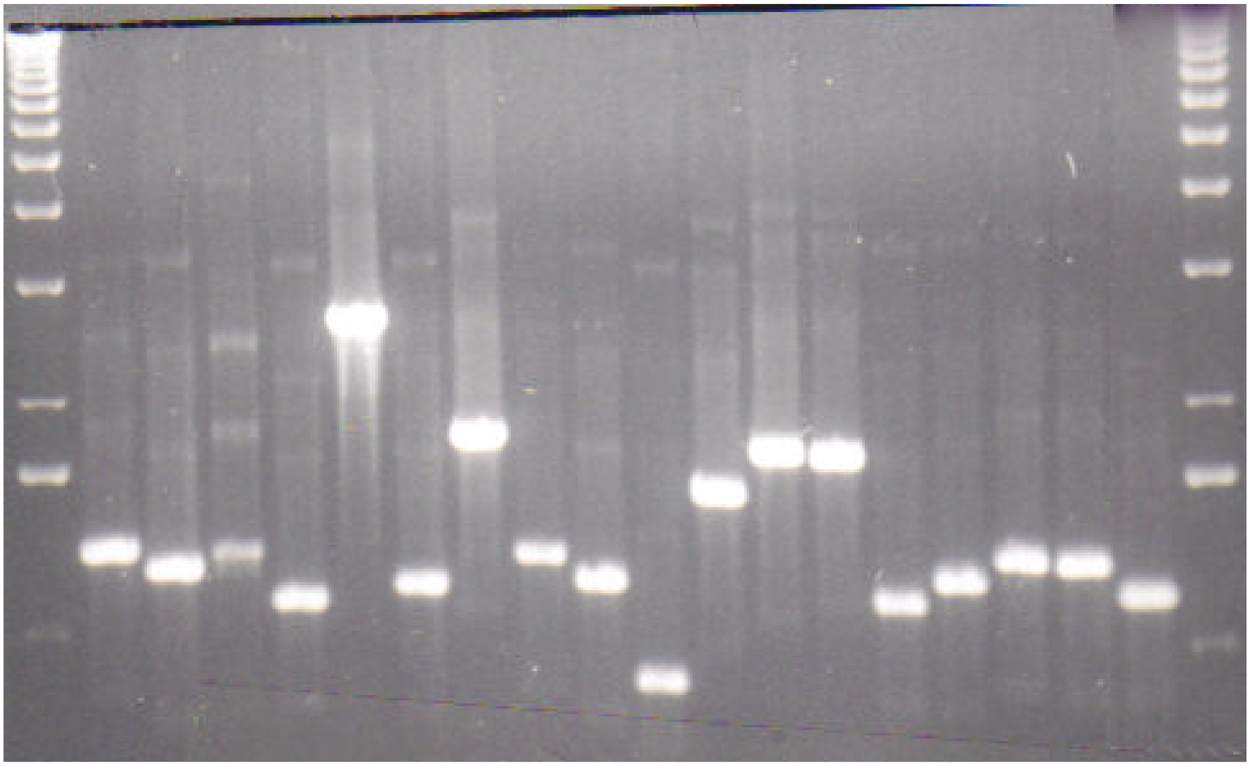
Gel Electrophoresis of PCR Products for Clones 0151-0168



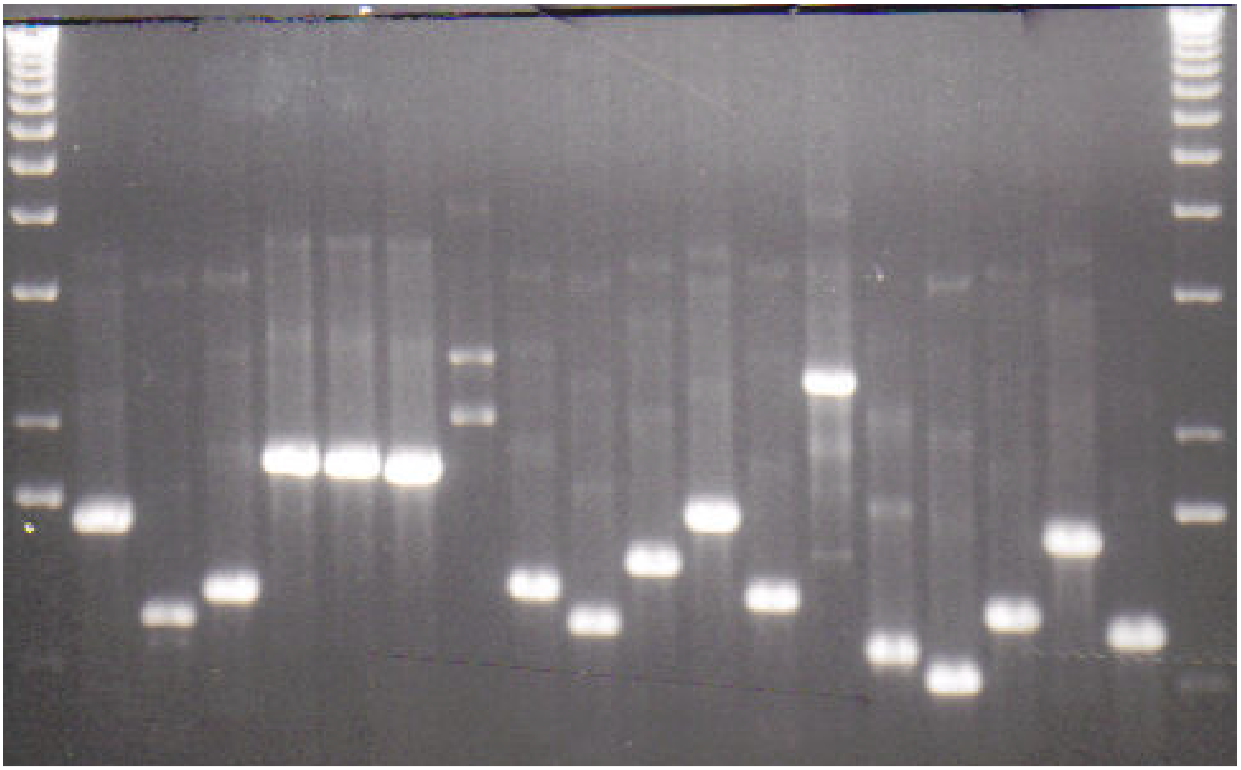
Gel Electrophoresis of PCR Products for Clones 0169-0186



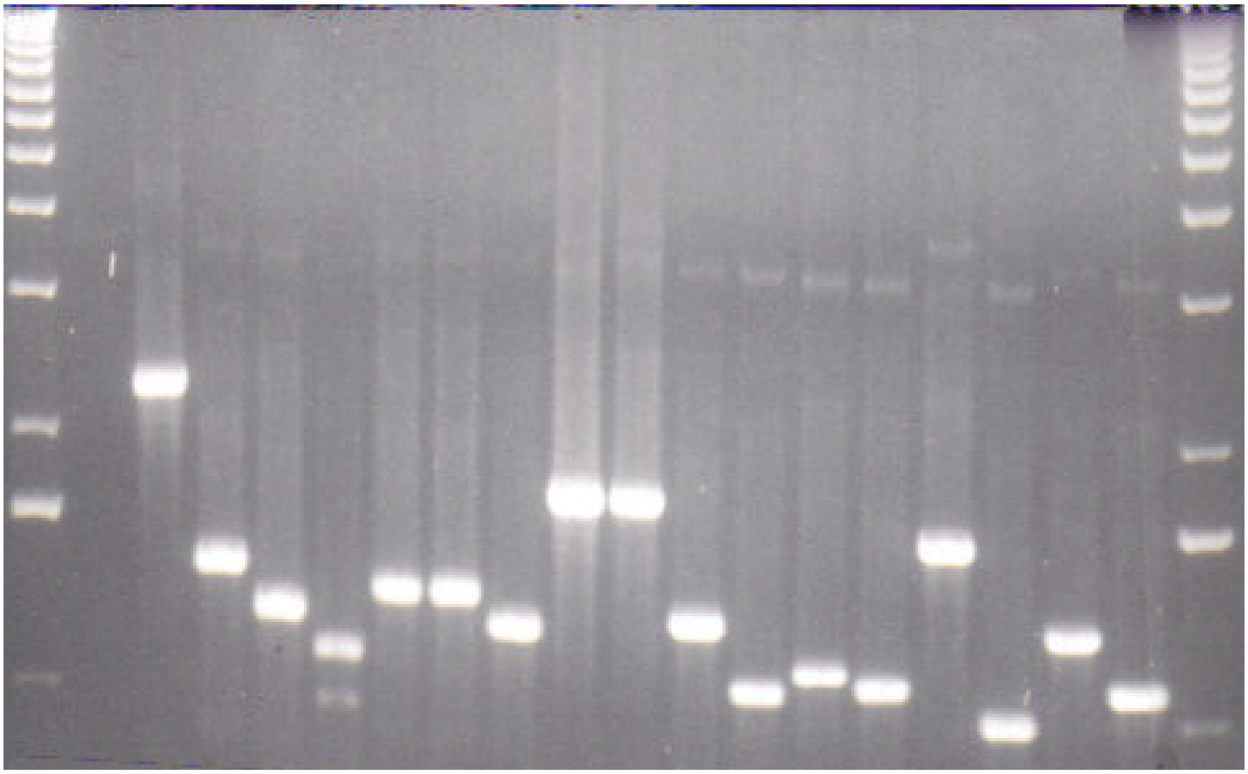
Gel Electrophoresis of PCR Products for Clones 0187-0204



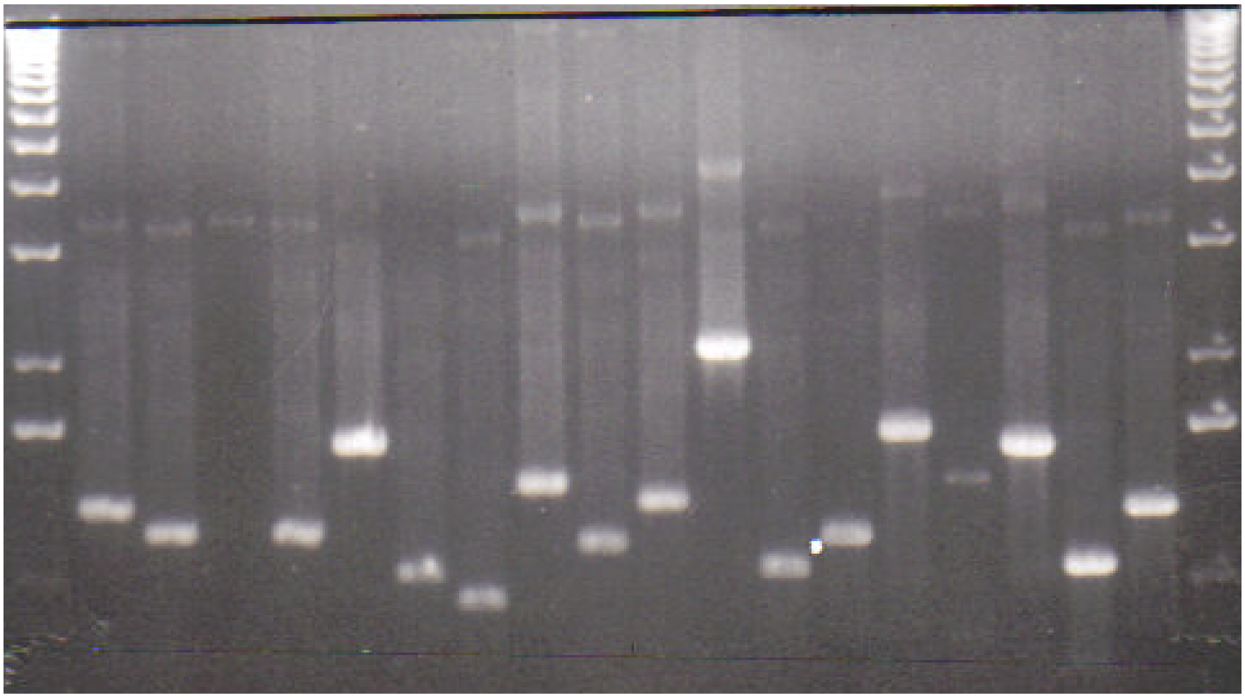
Gel Electrophoresis of PCR Products for Clones 0205-0222



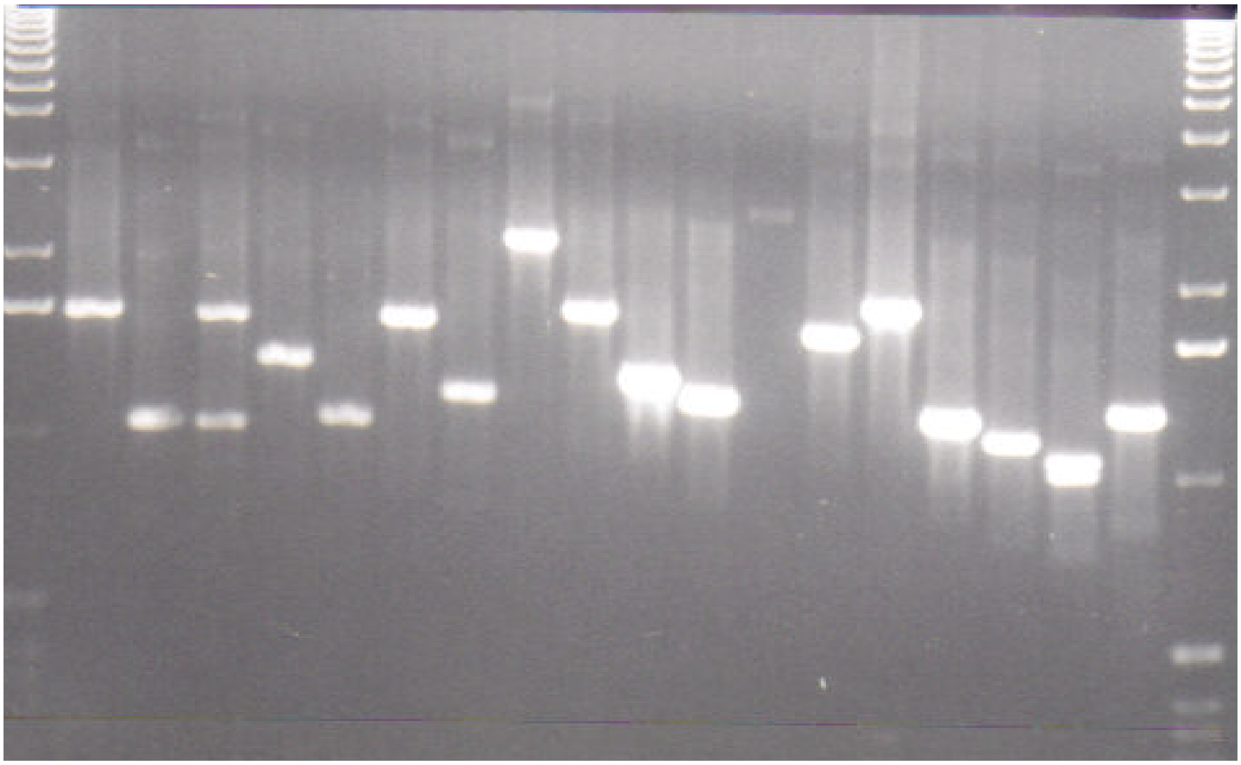
Gel Electrophoresis of PCR Products for Clones 0223-0240



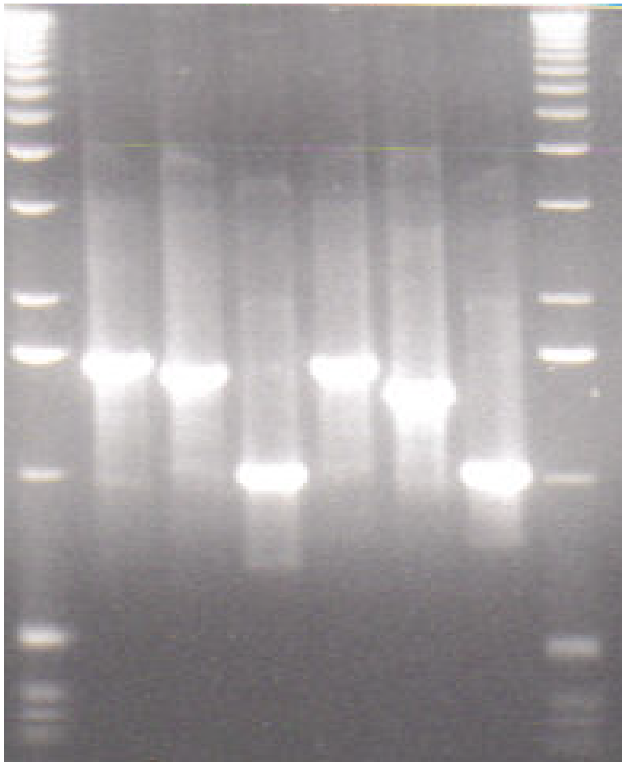
Gel Electrophoresis of PCR Products for Clones 0241-0258



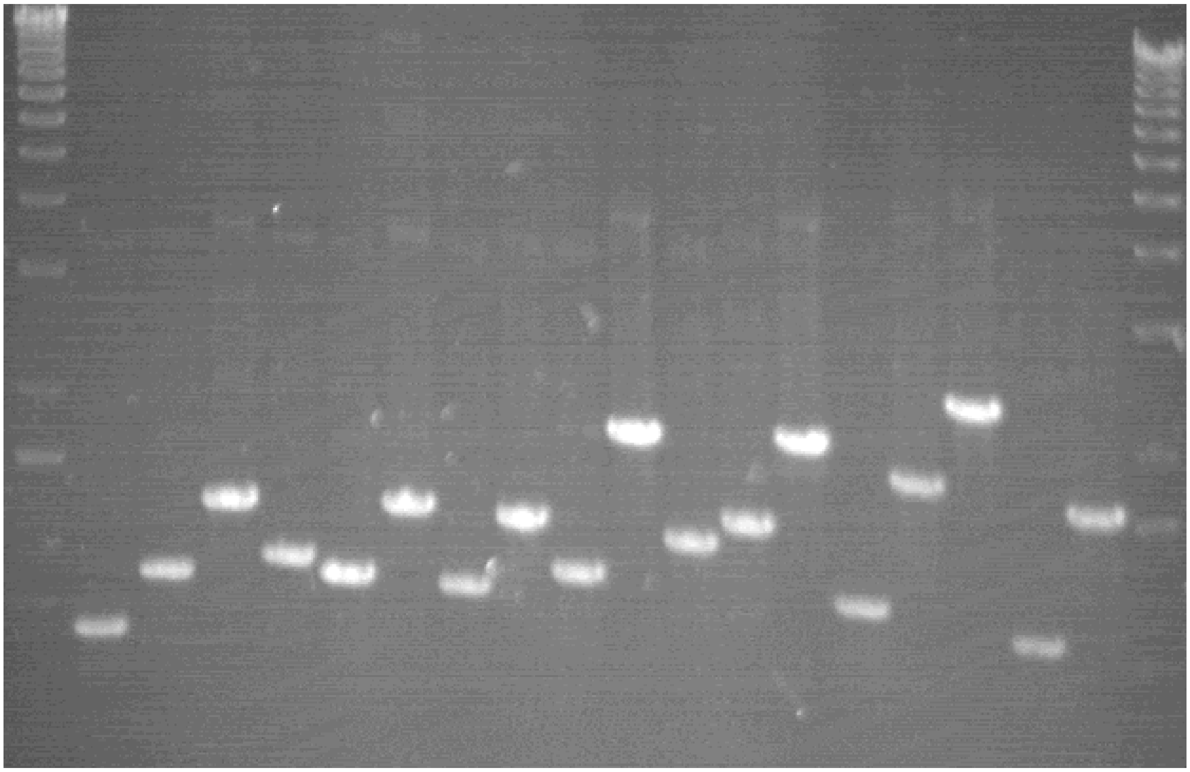
Gel Electrophoresis of PCR Products for Clones 0259-0276



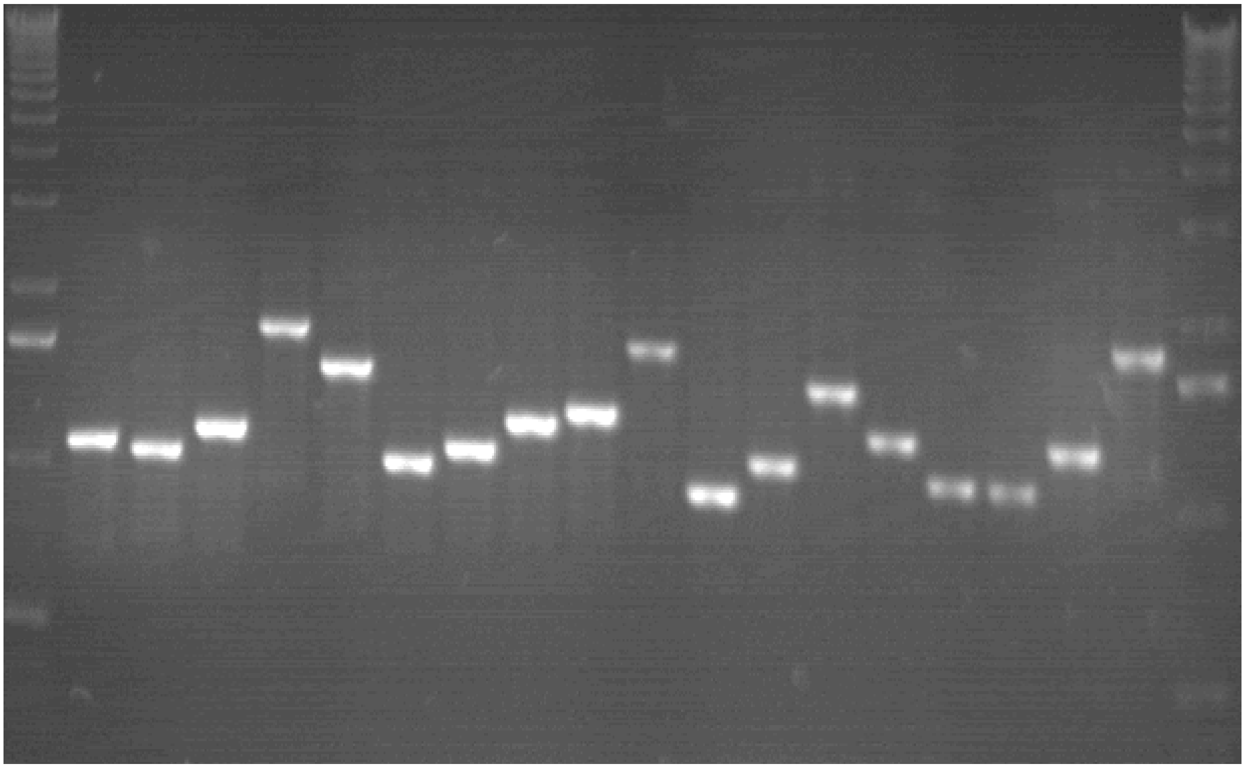
Gel Electrophoresis of PCR Products for Clones 02777-0294



Gel Electrophoresis of PCR Products for Clones 0295-0300



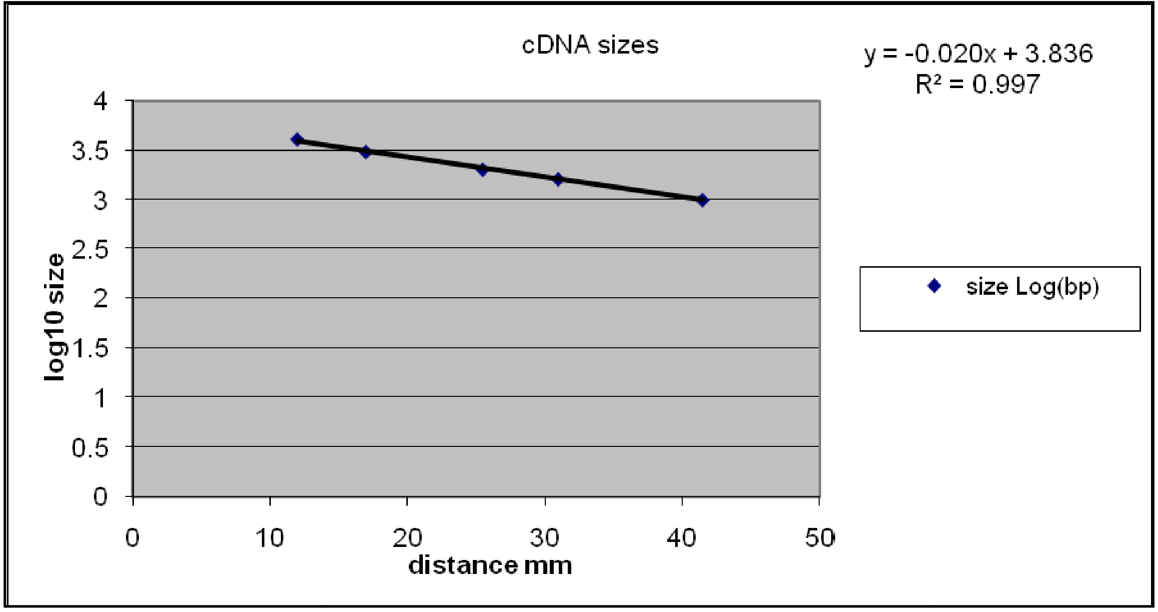
Gel Electrophoresis of PCR Products of Clones 0501-0518



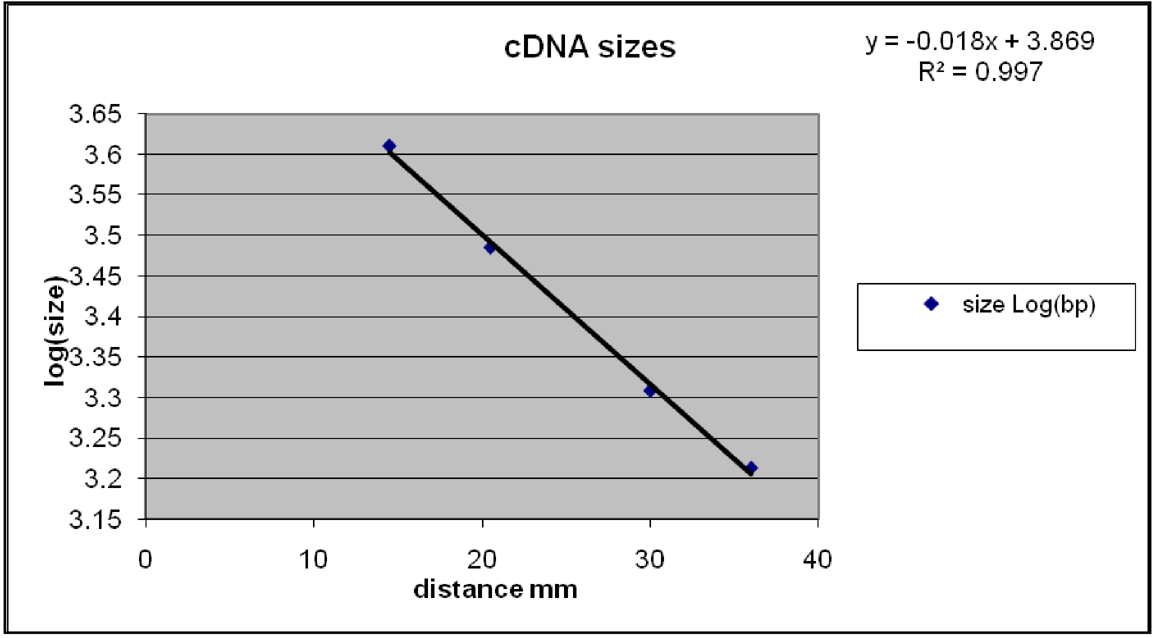
Gel Electrohporesis of PCR Products for Clones 0519-0536

Appendix C: cDNA Size Calculations

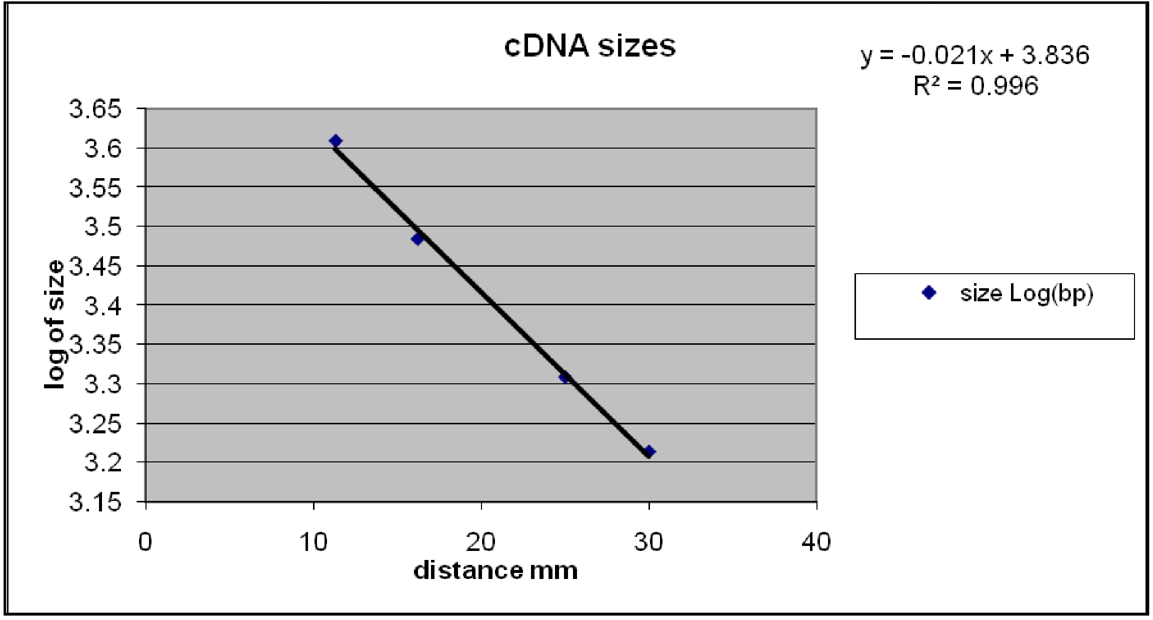
Standards:					Log adjustment	Sample size bp
distance mm	size Log(bp)	size bp	sample #	distance mm	"=-0.0201*(x)+3.8366	"=10eX
12	3.6098078	4072	1	36	3.113	1297.18
17	3.484869	3054	2	38	3.0728	1182.50
25.5	3.3087778	2036	3	35.5	3.12305	1327.55
31	3.2137833	1636	4	39	3.0527	1129.02
41.5	3.0077478	1018	5	37	3.0929	1238.51
			6	30.7	3.21953	1657.79
			7	25	3.3341	2158.24
			8	29	3.2537	1793.49
			9	38	3.0728	1182.50
			10	26	3.314	2060.63
			11	39.5	3.04265	1103.19
			12	33.3	3.16727	1469.84
			13	27	3.2939	1967.43
			14	no product		
			15	36	3.113	1297.18
			16	29.5	3.24365	1752.47



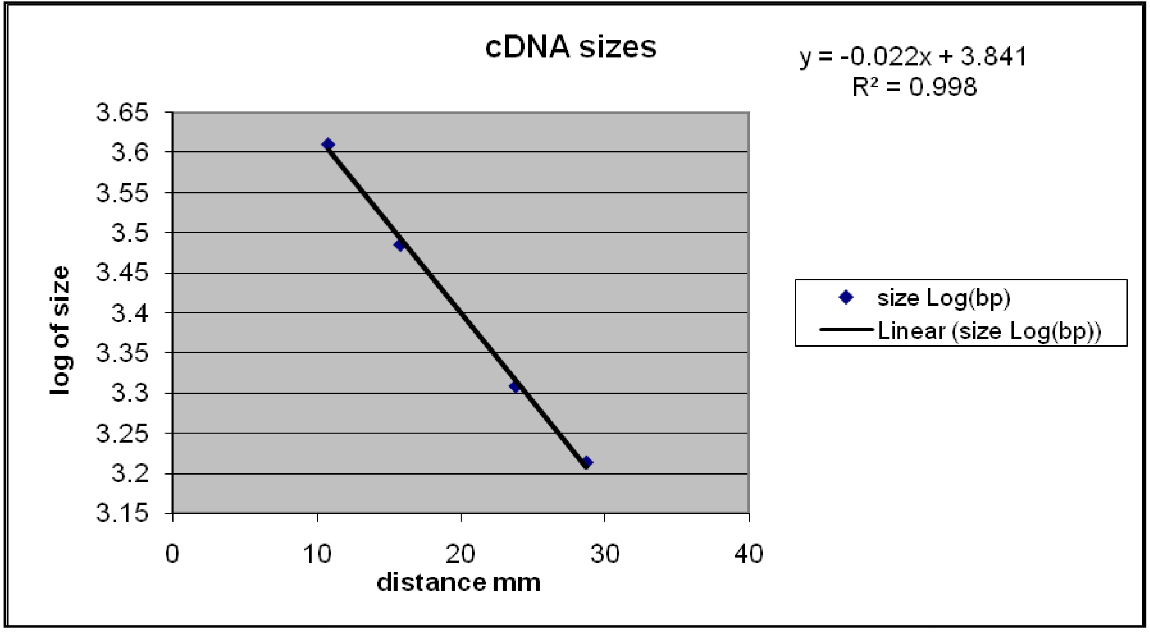
Standards:					Log adjustment	Sample size bp
distance mm	size Log(bp)	size bp	sample #	distance mm	y = -0.0184x + 3.8699	"=10eX
14.5	3.6098078	4072	17	55	2.8579	720.94
20.5	3.484869	3054	18	41	3.1155	1304.67
30	3.3087778	2036	19	28.5	3.3455	2215.64
36	3.2137833	1636	20	43.5	3.0695	1173.55
			21	45.5	3.0327	1078.20
			22	46	3.0235	1055.60
			23	27.8	3.35838	2282.34
			24	39	3.1523	1420.04
			25	45	3.0419	1101.29
			26	40	3.1339	1361.13
			27	no data		
			28	43.7	3.06582	1163.64
			29	48	2.9867	969.84
			30	42	3.0971	1250.55
			31	47.5	2.9959	990.60
			32	38.2	3.16702	1468.99



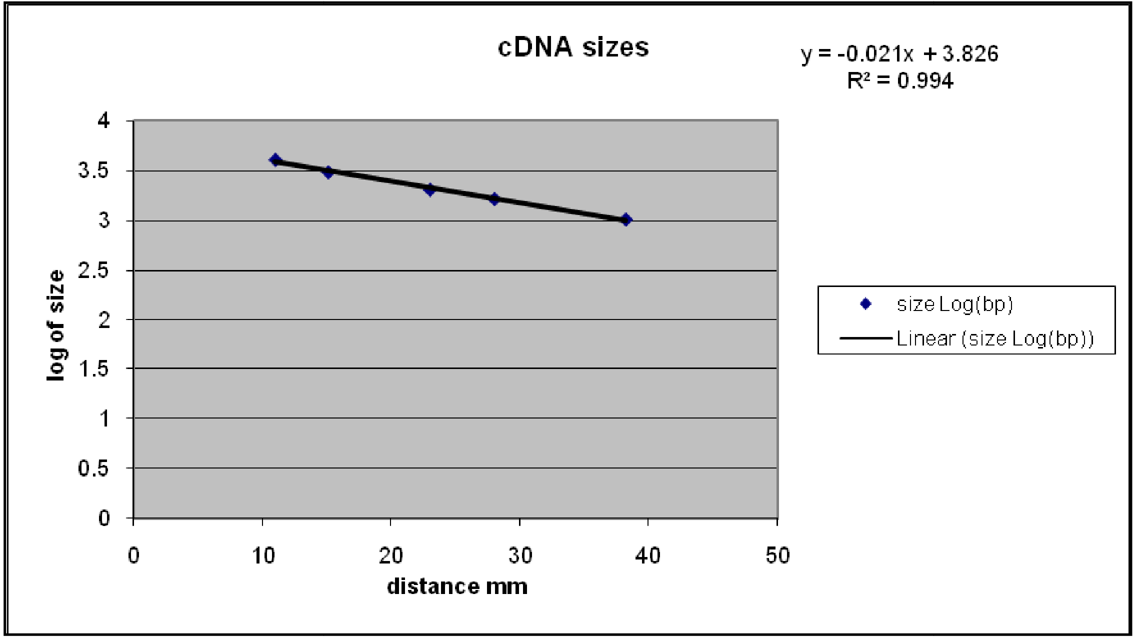
Standards:					Log adjustment	Sample size bp
distance mm	size Log(bp)	size bp	sample #	distance mm	y = -0.021x + 3.8367	"=10eX
11.3	3.6098078	4072	33	39.5	3.0072	1016.72
16.2	3.484869	3054	34	32	3.1647	1461.17
25	3.3087778	2036	35	37	3.0597	1147.36
30	3.2137833	1636	36	38	3.0387	1093.20
			37	38.5	3.0282	1067.09
			38	40.7	2.982	959.40
			39	39	3.0177	1041.60
			40	40	2.9967	992.43
			41	20.4	3.4083	2560.35
			42	42.5	2.9442	879.43
			43	40.7	2.982	959.40
			44	33.8	3.1269	1339.37
			45	40.3	2.9904	978.14
			46	41	2.9757	945.58
			47	24.2	3.3285	2130.59
			48	34	3.1227	1326.48



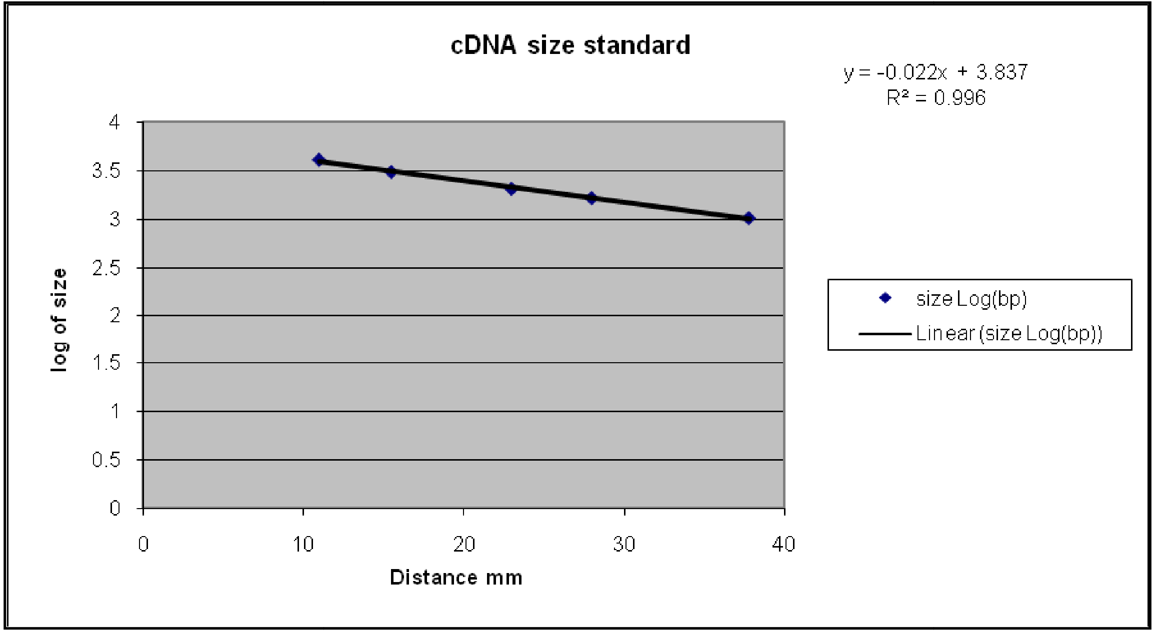
Standards:					Log adjustment	Sample size bp
distance mm	size Log(bp)	size bp	sample #	distance mm	y = -0.0221x + 3.8415	"=10eX
10.8	3.6098078	4072	49	30	3.1785	1508.34
15.8	3.484869	3054	50			
23.8	3.3087778	2036	55	32	3.1343	1362.39
28.7	3.2137833	1636	56	31	3.1564	1433.51
			57	31	3.1564	1433.51
			58	36	3.0459	1111.48
			59	41.8	2.91772	827.41
			60	36.9	3.02601	1061.72
			61	40.5	2.94645	884.00
			62	38.8	2.98402	963.87
			63	33.3	3.10557	1275.18
			64	30	3.1785	1508.34
			65	39	2.9796	954.11
			66	39.7	2.96413	920.73
			67	32	3.1343	1362.39
			68	33.2	3.10778	1281.68



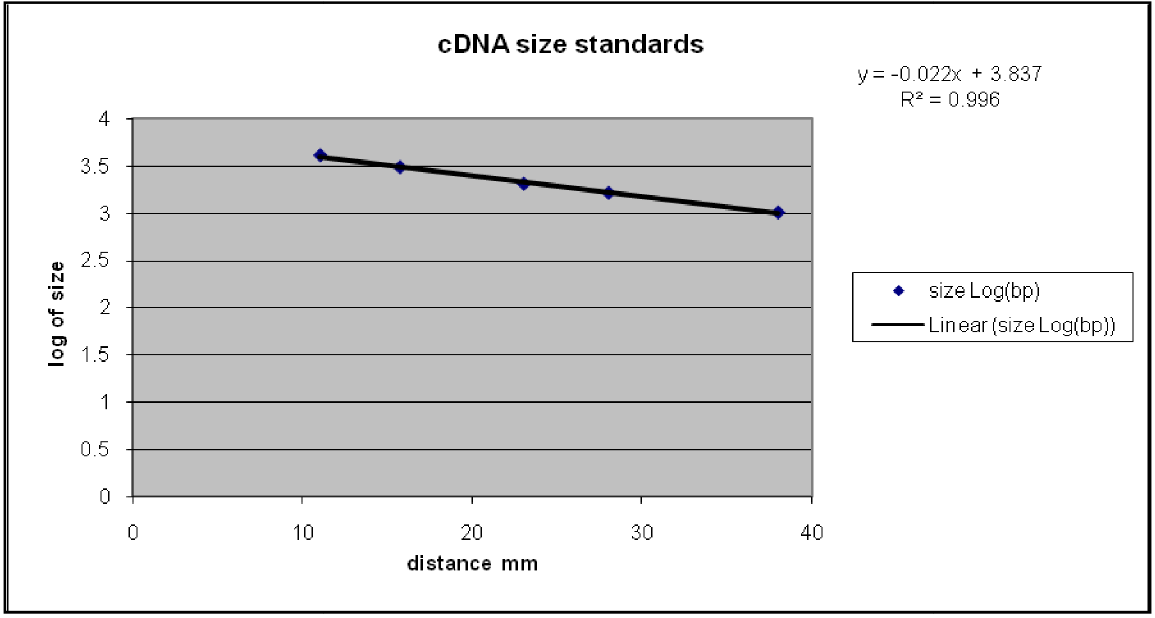
Standards:					Log adjustment	Sample size bp
distance mm	size Log(bp)	size bp	sample #	distance mm	y = -0.0218x + 3.8266	"=10eX
11	3.6098078	4072	69	33.3	3.10066	1260.84
15.1	3.484869	3054	70	36	3.0418	
23	3.3087778	2036	71	19	3.4124	2584.64
28	3.2137833	1636	72	37.7	3.00474	1010.97
38.2	3.0077478	1018	73	38	2.9982	995.86
			74	28.5	3.2053	1604.35
			75	32	3.129	1345.86
			76	35.5	3.0527	1129.02
			77	31	3.1508	1415.14
			78	19.8	3.39496	2482.90
			79	24.1	3.30122	2000.88
			80	32	3.129	1345.86
			81	29	3.1944	1564.59
			82	27.2	3.23364	1712.54
			83	35	3.0636	1157.71
			84	33.2	3.10284	1267.18



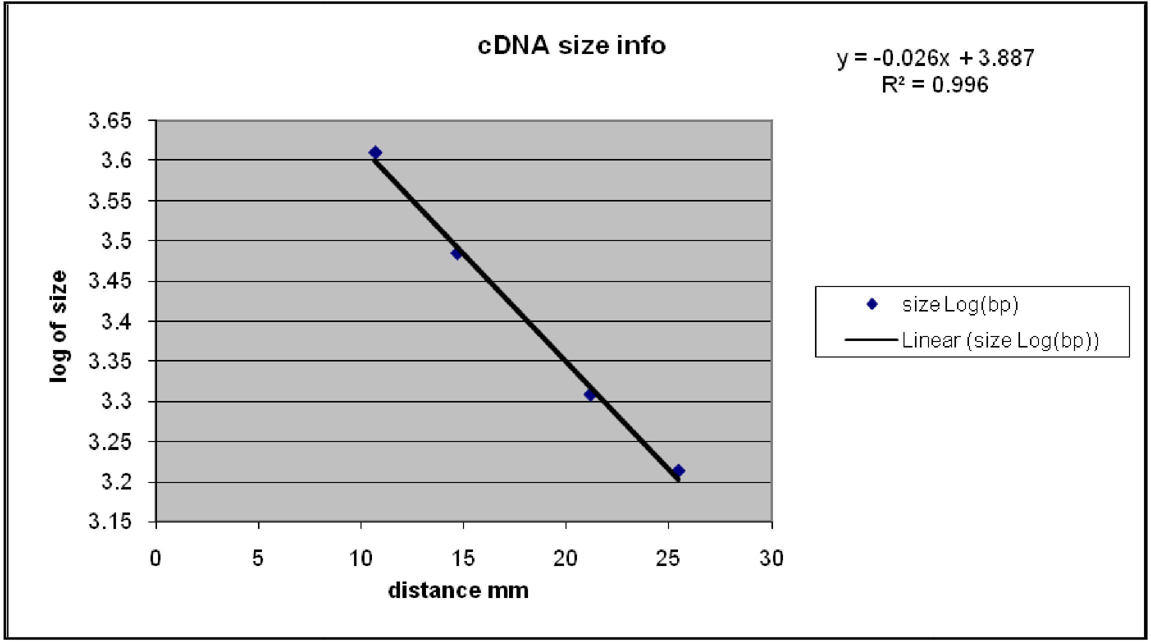
Standards:					Log adjustment	Sample size bp
distance mm	size Log(bp)	size bp	sample #	distance mm	y = -0.0222x + 3.8372	"=10eX
11	3.6098078	4072	85	23.5	3.3155	2067.76
15.5	3.484869	3054	86	36	3.038	1091.44
23	3.3087778	2036	87	29.8	3.17564	1498.44
28	3.2137833	1636	88	33.2	3.10016	1259.39
37.8	3.0077478	1018	89	36.3	3.03134	1074.83
			90	34	3.0824	1208.93
			91	50.4	2.71832	522.78
			92	30	3.1712	1483.20
			93	37.8	2.99804	995.50
			94	38	2.9936	985.37
			95	35.2	3.05576	1137.00
			96	20	3.3932	2472.86
			97	28.5	3.2045	1601.40
			98	37	3.0158	1037.05
			99	24	3.3044	2015.58
			100	30.5	3.1601	1445.77



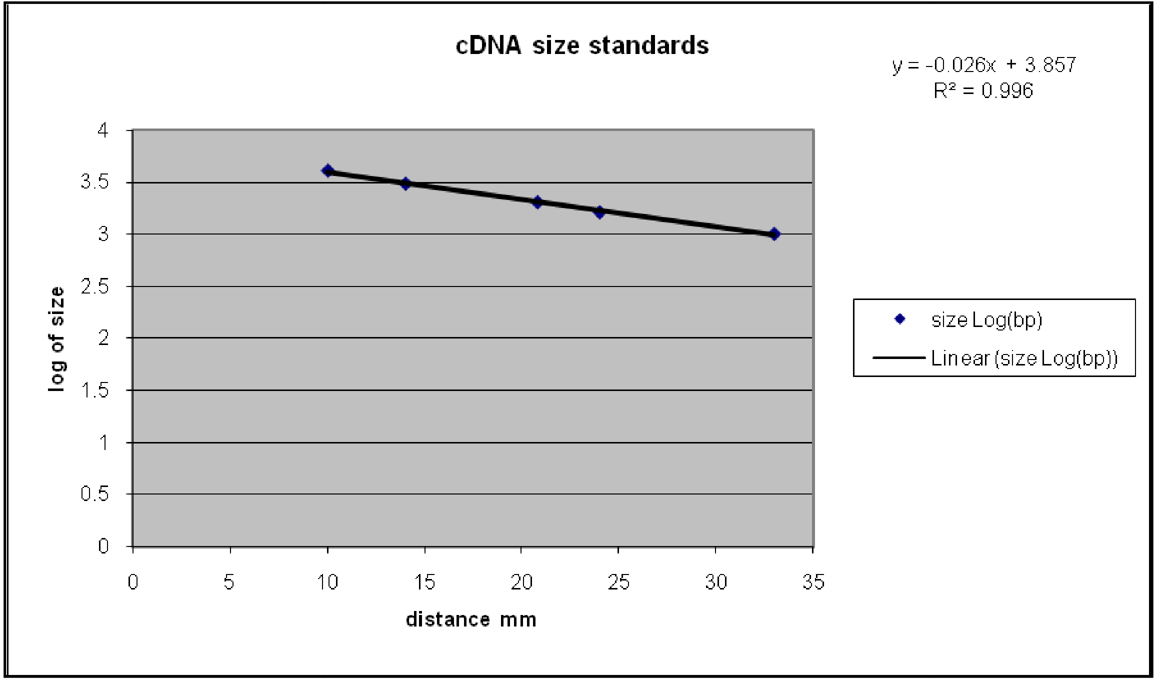
Standards:					Log adjustment	Sample size bp
distance mm	size Log(bp)	size bp	sample #	distance mm	y = -0.0221x + 3.8373	"=10eX
11	3.6098078	4072	51	31	3.1522	1419.71
15.7	3.484869	3054	52	37	3.0196	1046.16
23	3.3087778	2036	53	34.2	3.08148	1206.37
28	3.2137833	1636	54	32.4	3.12126	1322.09
38	3.0077478	1018	101	33	3.108	1282.33
			102	35.2	3.05938	1146.52
			103	32.3	3.12347	1328.83
			104	33.1	3.10579	1275.82
			105	34	3.0859	1218.71
			106	38	2.9975	994.26
			107	36.5	3.03065	1073.12
			108	34.2	3.08148	1206.37
			109	26	3.2627	1831.05
			110	37	3.0196	1046.16
			111	27.4	3.23176	1705.14
			112	37	3.0196	1046.16
			113	36.8	3.02402	1056.87
			114	35	3.0638	1158.24



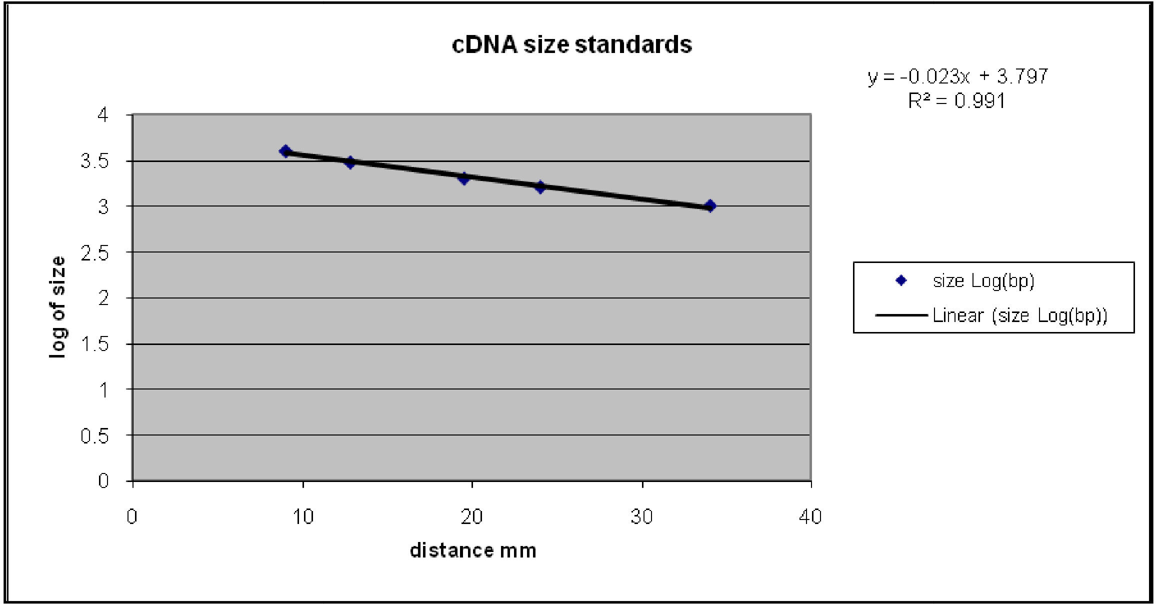
Standards:					Log adjustment	Sample size bp
distance mm	size Log(bp)	size bp	sample #	distance mm	y = -0.0268x + 3.8872	"=10eX
10.7	3.6098078	4072	115	32	3.0296	1070.53
14.7	3.484869	3054	116	25.3	3.20916	1618.68
21.2	3.3087778	2036	117	35	2.9492	889.61
25.5	3.2137833	1636	118	34.4	2.96528	923.17
	3.0077478	1018	119	26.2	3.18504	1531.23
			120	22	3.2976	1984.27
			121	37.8	2.87416	748.45
			122	no product		
			123	31.3	3.04836	1117.79
			124	36.1	2.91972	831.23
			125	30	3.0832	1211.16
			126	34.5	2.9626	917.49
			127	35.2	2.94384	878.70
			128	35	2.9492	889.61
			129	35.8	2.92776	846.76
			130	26.2	3.18504	1531.23
			131	33.5	2.9894	975.89
			132	34.8	2.95456	900.66



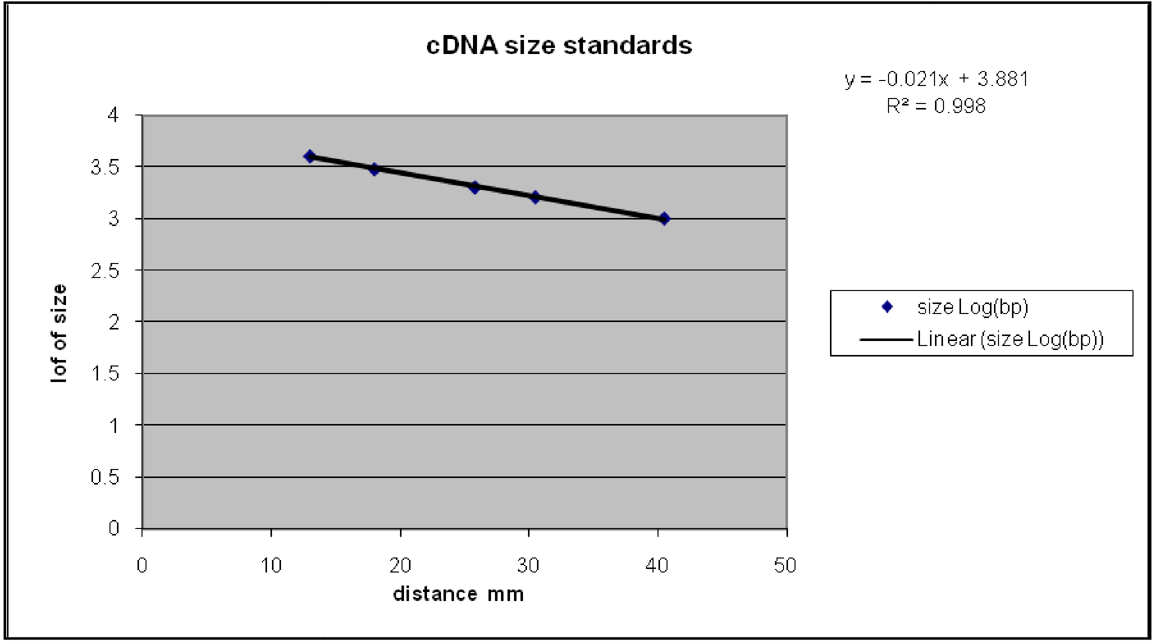
Standards:					Log adjustment	Sample size bp
distance mm	size Log(bp)	size bp	sample #	distance mm	y = -0.0261x + 3.8571	"=10eX
10	3.6098078	4072	133	26	3.1785	1508.34
14	3.484869	3054	134	25.4	3.19416	1563.72
20.8	3.3087778	2036	135	32	3.0219	1051.72
24	3.2137833	1636	136	31.3	3.04017	1096.91
33	3.0077478	1018	137	26.4	3.16806	1472.52
			138	42	2.7609	576.63
			139	28	3.1263	1337.52
			140	34	2.9697	932.61
			141	33.2	2.99058	978.54
			142	31.6	3.03234	1077.31
			143	30.8	3.05322	1130.37
			144	34.1	2.96709	927.02
			145	36	2.9175	826.99
			146	32.5	3.00885	1020.59
			147	31.1	3.04539	1110.17
			148	29	3.1002	1259.51
			149	34	2.9697	932.61
			150	27.8	3.13152	1353.69



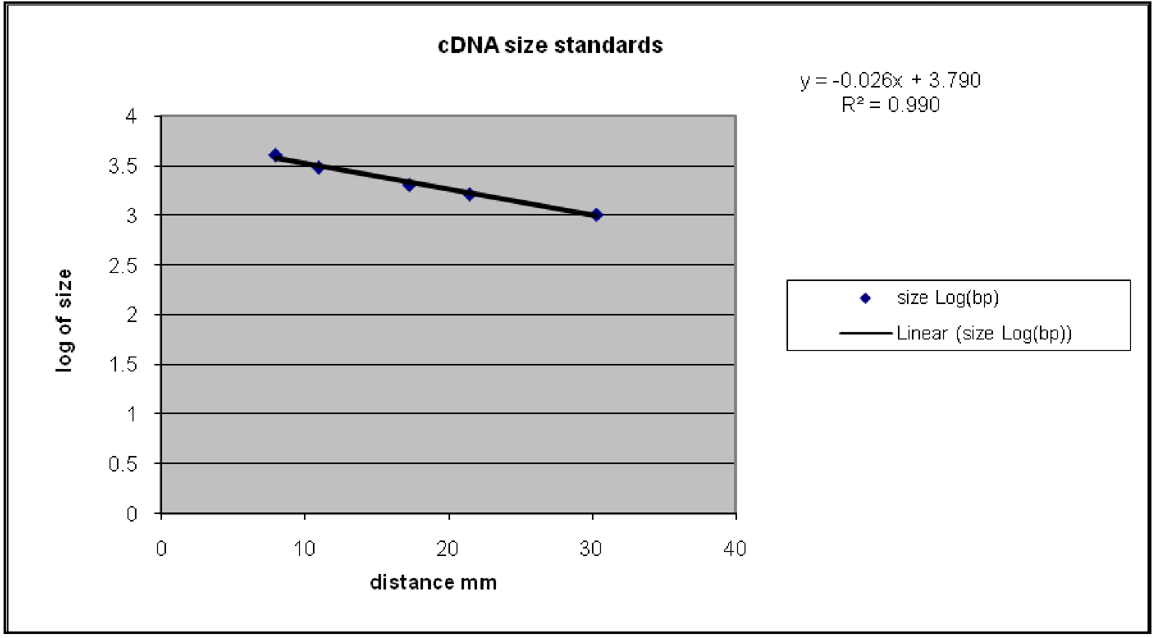
Standards:					Log adjustment	Sample size bp
distance mm	size Log(bp)	size bp	sample #	distance mm	y = -0.0238x + 3.7976	"=10eX
9	3.6098078	4072	151	31	3.0598	1147.62
12.8	3.484869	3054	152	31.1	3.05742	1141.35
19.5	3.3087778	2036	153	25	3.2026	1594.41
24	3.2137833	1636	154	27.2	3.15024	1413.32
34	3.0077478	1018	155	29.2	3.10264	1266.60
			156	33	3.0122	1028.49
			157	22.3	3.26686	1848.67
			158	26.8	3.15976	1444.64
			159	32	3.036	1086.43
			160	23.2	3.24544	1759.71
			161	27	3.155	1428.89
			162	34.7	2.97174	937.00
			163	31	3.0598	1147.62
			164	35	2.9646	921.72
			165	34	2.9884	973.64
			166	27.2	3.15024	1413.32
			167	29.3	3.10026	1259.68
			168	32	3.036	1086.43



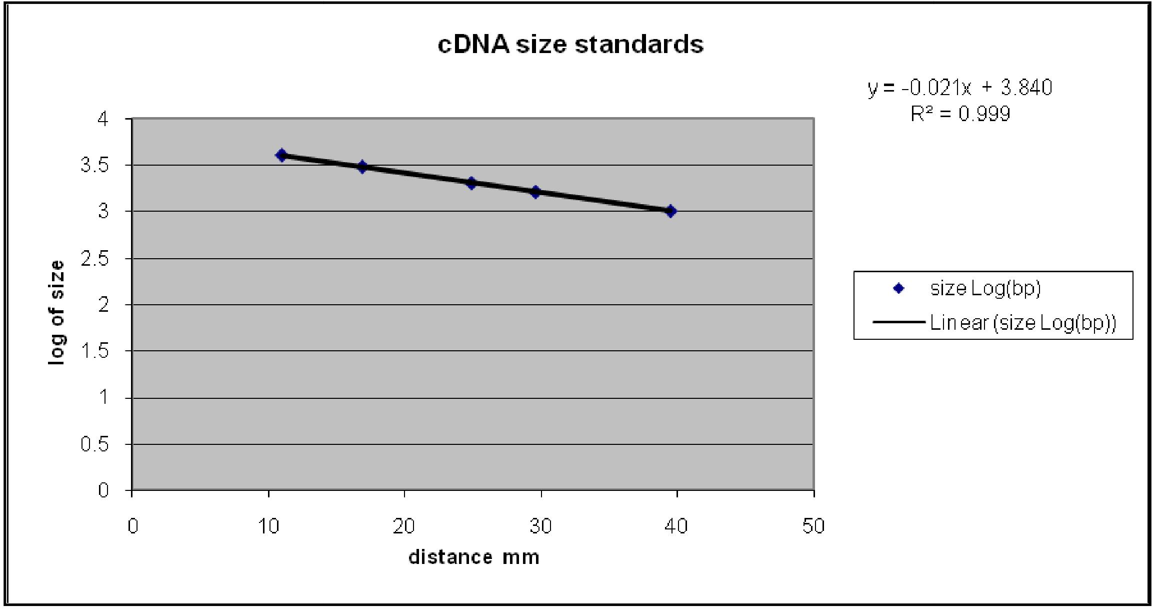
Standards:					Log adjustment	Sample size bp
distance mm	size Log(bp)	size bp	sample #	distance mm	y = -0.0218x + 3.8819	"=10eX
13	3.6098078	4072	169	36.8	3.07966	1201.32
18	3.484869	3054	170	30	3.2279	1690.05
25.8	3.3087778	2036	171	37.6	3.06222	1154.04
30.5	3.2137833	1636	172	29	3.2497	1777.05
40.5	3.0077478	1018	173	38.3	3.04696	1114.19
			174	32.2	3.17994	1513.35
			175	22.8	3.38486	2425.83
			176	37	3.0753	1189.32
			177	34	3.1407	1382.61
			178	36.3	3.09056	1231.86
			179	32.2	3.17994	1513.35
			180	36.4	3.08838	1225.69
			181	37	3.0753	1189.32
			182	33.1	3.16032	1446.51
			183	29	3.2497	1777.05
			184	42.8	2.94886	888.91
			185	30	3.2279	1690.05
			186	37	3.0753	1189.32



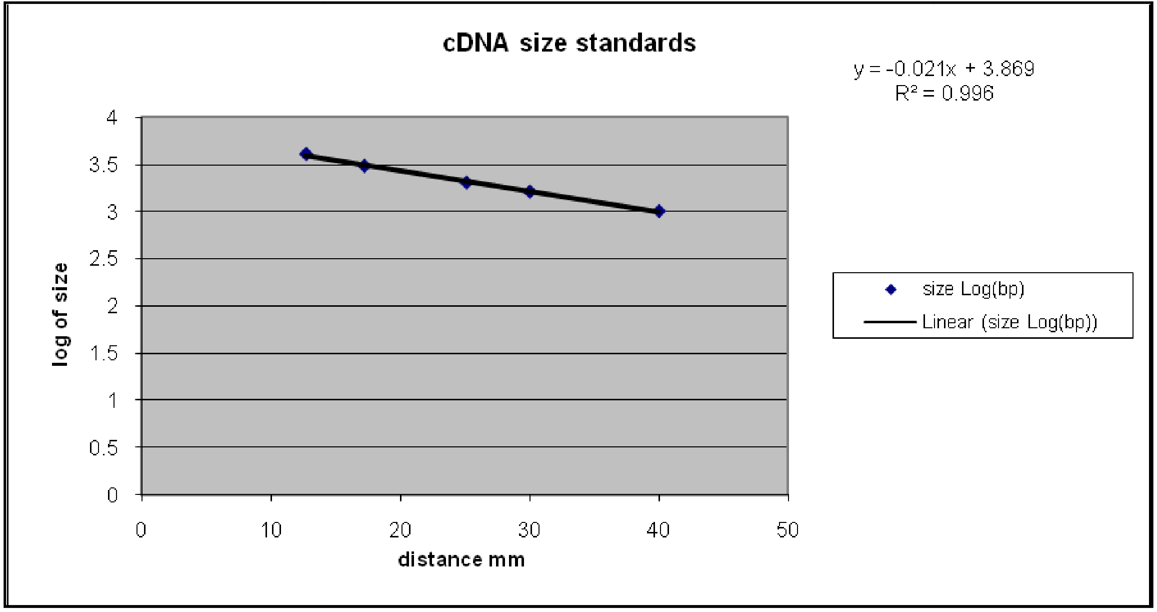
Standards:					Log adjustment	Sample size bp
distance mm	size Log(bp)	size bp	sample #	distance mm	y = -0.0264x + 3.7903	"=10eX
8	3.6098078	4072	187	29.5	3.0115	1026.83
11	3.484869	3054	188	26.8	3.08278	1209.99
17.3	3.3087778	2036	189	24.1	3.15406	1425.80
21.5	3.2137833	1636	190	22.2	3.20422	1600.37
30.3	3.0077478	1018	191	20	3.2623	1829.36
			192	25.2	3.12502	1333.58
			193	25.8	3.10918	1285.82
			194	20.7	3.24382	1753.15
			195	27.9	3.05374	1131.72
			196	30	2.9983	996.09
			197	24	3.1567	1434.50
			198	30.2	2.99302	984.06
			199	27.3	3.06958	1173.76
			200	28	3.0511	1124.86
			201	33	2.9191	830.04
			202	10	3.5263	3359.70
			203	13.7	3.42862	2683.00
			204	25	3.1303	1349.90



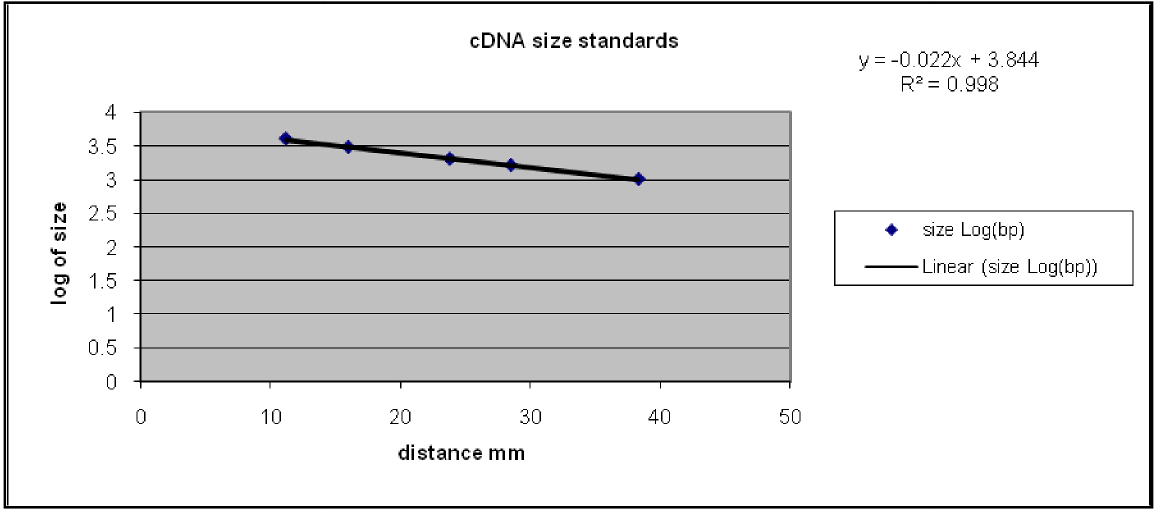
Standards:					Log adjustment	Sample size bp
distance mm	size Log(bp)	size bp	sample #	distance mm	y = -0.0212x + 3.8409	"=10eX
11	3.6098078	4072	205	34.8	3.10314	1268.06
16.9	3.484869	3054	206	36	3.0777	1195.91
24.9	3.3087778	2036	207	34.5	3.1095	1286.77
29.6	3.2137833	1636	208	38	3.0353	1084.68
39.5	3.0077478	1018	209	19.8	3.42114	2637.18
			210	37	3.0565	1138.94
			211	27.8	3.25154	1784.60
			212	35.1	3.09678	1249.63
			213	37.1	3.05438	1133.39
			214	43.3	2.92294	837.41
			215	32	3.1625	1453.78
			216	29.3	3.21974	1658.59
			217	29.8	3.20914	1618.60
			218	39	3.0141	1033.00
			219	37.8	3.03954	1095.32
			220	36.5	3.0671	1167.08
			221	37	3.0565	1138.94
			222	39	3.0141	1033.00



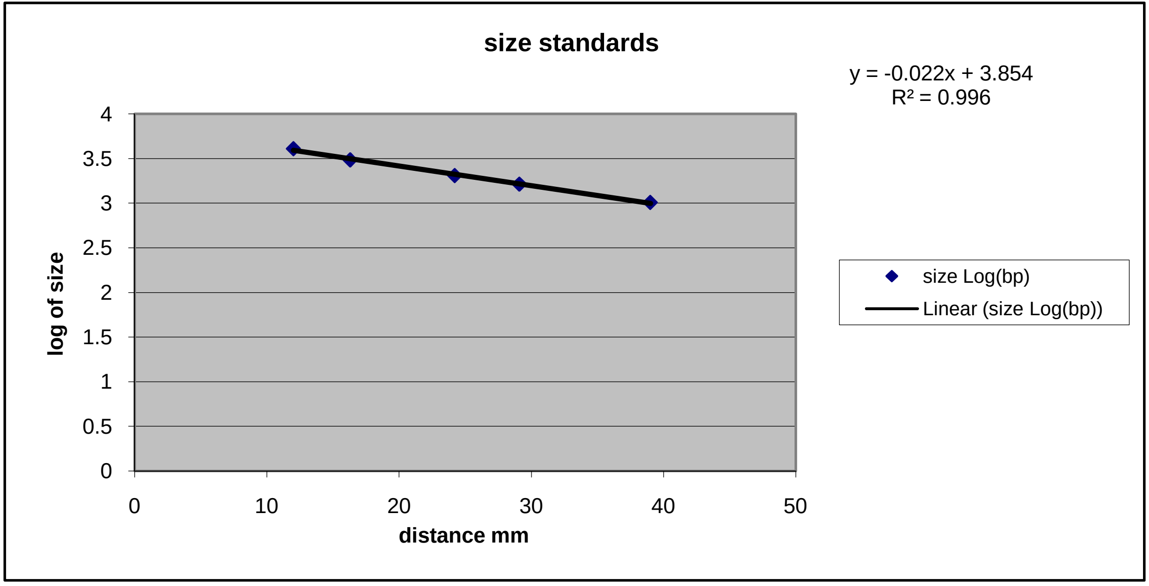
Standards:					Log adjustment	Sample size bp
distance mm	size Log(bp)	size bp	sample #	distance mm	y = -0.0218x + 3.8696	"=10eX
12.7	3.6098078	4072	223	31.5	3.1829	1523.70
17.2	3.484869	3054	224	38	3.0412	1099.51
25.1	3.3087778	2036	225	36.4	3.07608	1191.46
30	3.2137833	1636	226	28.5	3.2483	1771.33
40	3.0077478	1018	227	28.8	3.24176	1744.86
			228	29.1	3.23522	1718.78
			229	25.5	3.3137	2059.21
			230	36.6	3.07172	1179.56
			231	39	3.0194	1045.68
			232	35.2	3.10224	1265.44
			233	32.5	3.1611	1449.11
			234	37.5	3.0521	1127.46
			235	24	3.3464	2220.24
			236	41.2	2.97144	936.35
			237	43	2.9322	855.46
			238	39	3.0194	1045.68
			239	34.4	3.11968	1317.29
			240	40.5	2.9867	969.84



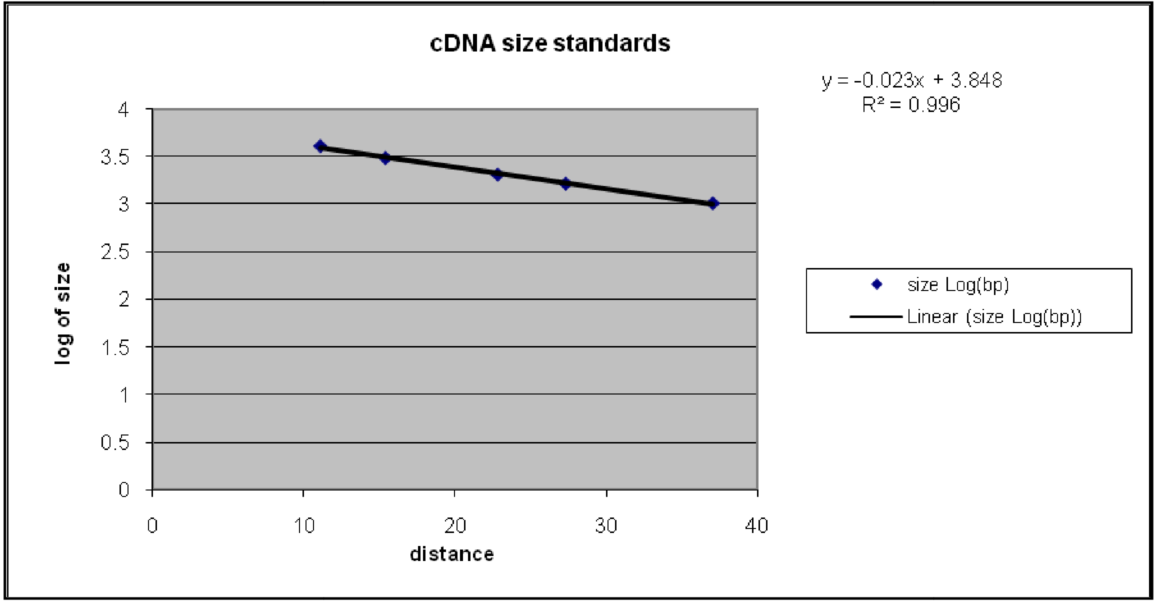
Standards:					Log adjustment	Sample size bp
distance mm	size Log(bp)	size bp	sample #	distance mm	y = -0.022x + 3.8445	"=10eX
11.2	3.6098078	4072	241	no product		
16	3.484869	3054	242	21.9	3.3627	2305.15
23.8	3.3087778	2036	243	32	3.1405	1381.97
28.5	3.2137833	1636	244	34.2	3.0921	1236.23
38.3	3.0077478	1018	245	37	3.0305	1072.75
			246	33.5	3.1075	1280.86
			247	34	3.0965	1248.82
			248	36	3.0525	1128.50
			249	28.3	3.2219	1666.86
			250	28.3	3.2219	1666.86
			251	36	3.0525	1128.50
			252	40	2.9645	921.51
			253	39	2.9865	969.39
			254	39.5	2.9755	945.15
			255	31.8	3.1449	1396.05
			256	42	2.9205	832.72
			257	36.9	3.0327	1078.20
			258	40.2	2.9601	912.22



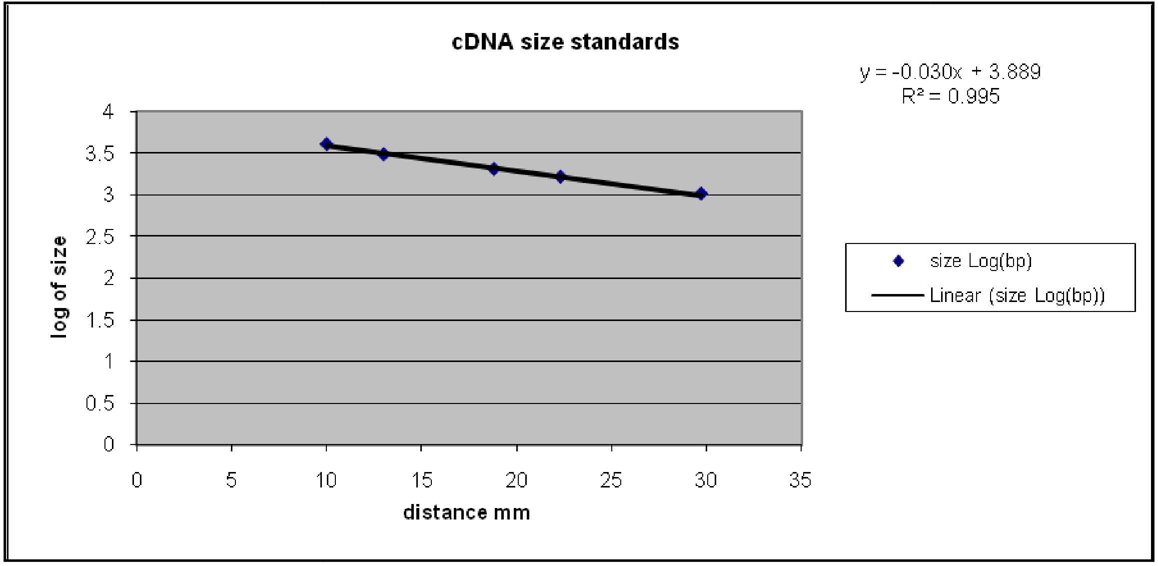
Standards:					Log adjustment	Sample size bp
distance mm	size Log(bp)	size bp	sample #	distance mm	y = -0.0222x + 3.8548	"=10eX
12	3.6098078	4072	259	34	3.1	1258.93
16.3	3.484869	3054	260	36.8	3.03784	1091.04
24.2	3.3087778	2036	261	0	3.8548	7158.14
29.1	3.2137833	1636	262	36	3.0556	1136.58
39	3.0077478	1018	263	30	3.1888	1544.54
			264	37.8	3.01564	1036.67
			265	40.5	2.9557	903.03
			266	32.8	3.12664	1338.57
			267	36.8	3.03784	1091.04
			268	34	3.1	1258.93
			269	24	3.322	2098.94
			270	38.5	3.0001	1000.23
			271	36.2	3.05116	1125.02
			272	29.3	3.20434	1600.81
			273	32.2	3.13996	1380.26
			274	30.4	3.17992	1513.28
			275	39	2.989	974.99
			276	35	3.0778	1196.19



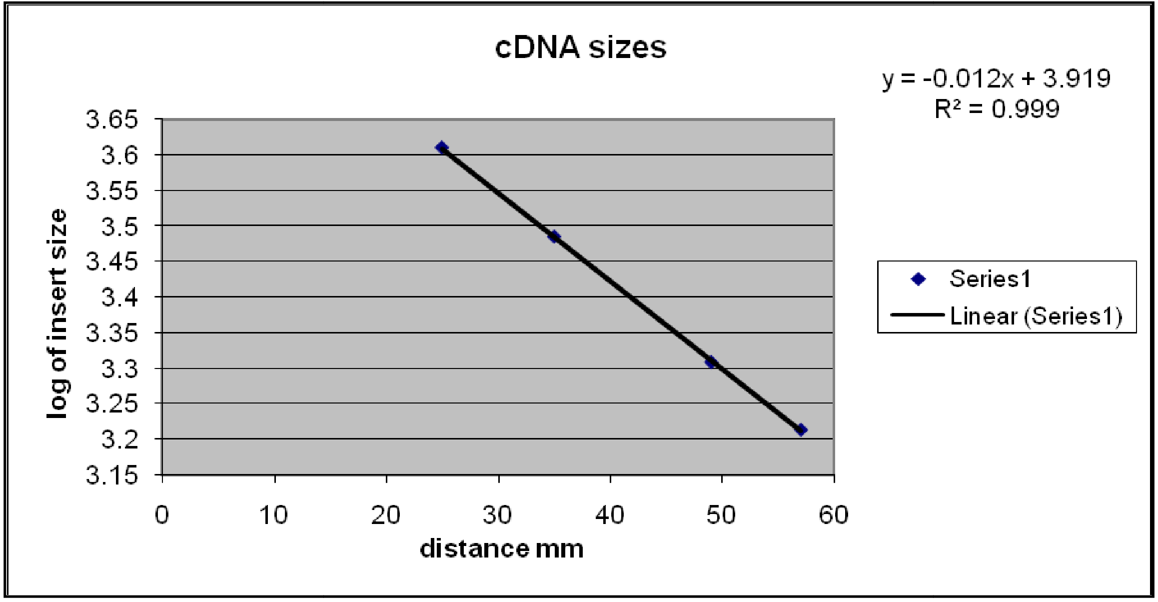
Standards:					Log adjustment	Sample size bp
distance mm	size Log(bp)	size bp	sample #	distance mm	y = -0.023x + 3.8481	"=10eX
11.1	3.6098078	4072	277	27	3.2271	1686.94
15.4	3.484869	3054	278	35	3.0431	1104.33
22.8	3.3087778	2036	279	26	3.2501	1778.69
27.3	3.2137833	1636	280	30	3.1581	1439.13
37	3.0077478	1018	281	34	3.0661	1164.39
			282	26	3.2501	1778.69
			283	32	3.1121	1294.49
			284	20.3	3.3812	2405.47
			285	26	3.2501	1778.69
			286	31	3.1351	1364.90
			287	33	3.0891	1227.72
			288	0	3.8481	7048.55
			289	27.5	3.2156	1642.86
			290	26	3.2501	1778.69
			291	33.5	3.0776	1195.64
			292	35	3.0431	1104.33
			293	37	2.9971	993.34
			294	33.3	3.0822	1208.37



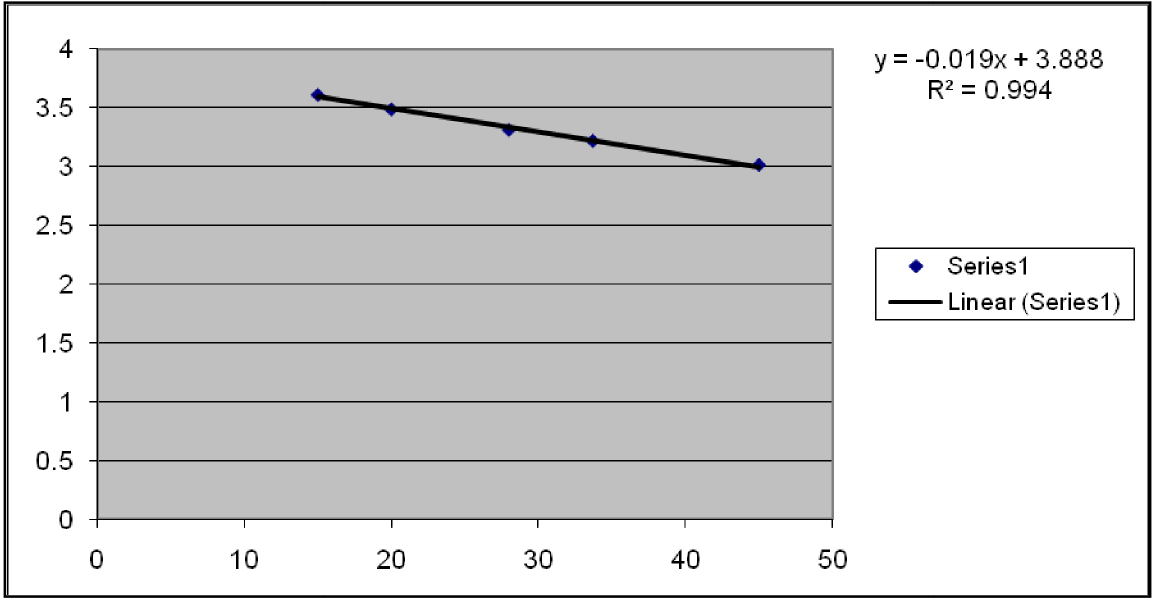
Standards:					Log adjustment	Sample size bp
distance mm	size Log(bp)	size bp	sample #	distance mm	y = -0.0301x + 3.8891	"=10eX
10	3.6098078	4072	295	23.5	3.18175	1519.67
13	3.484869	3054	296	24	3.1667	1467.91
18.8	3.3087778	2036	297	30	2.9861	968.50
22.3	3.2137833	1636	298	23.5	3.18175	1519.67
29.7	3.0077478	1018	299	25.2	3.13058	1350.77
			300	30.2	2.98008	955.17



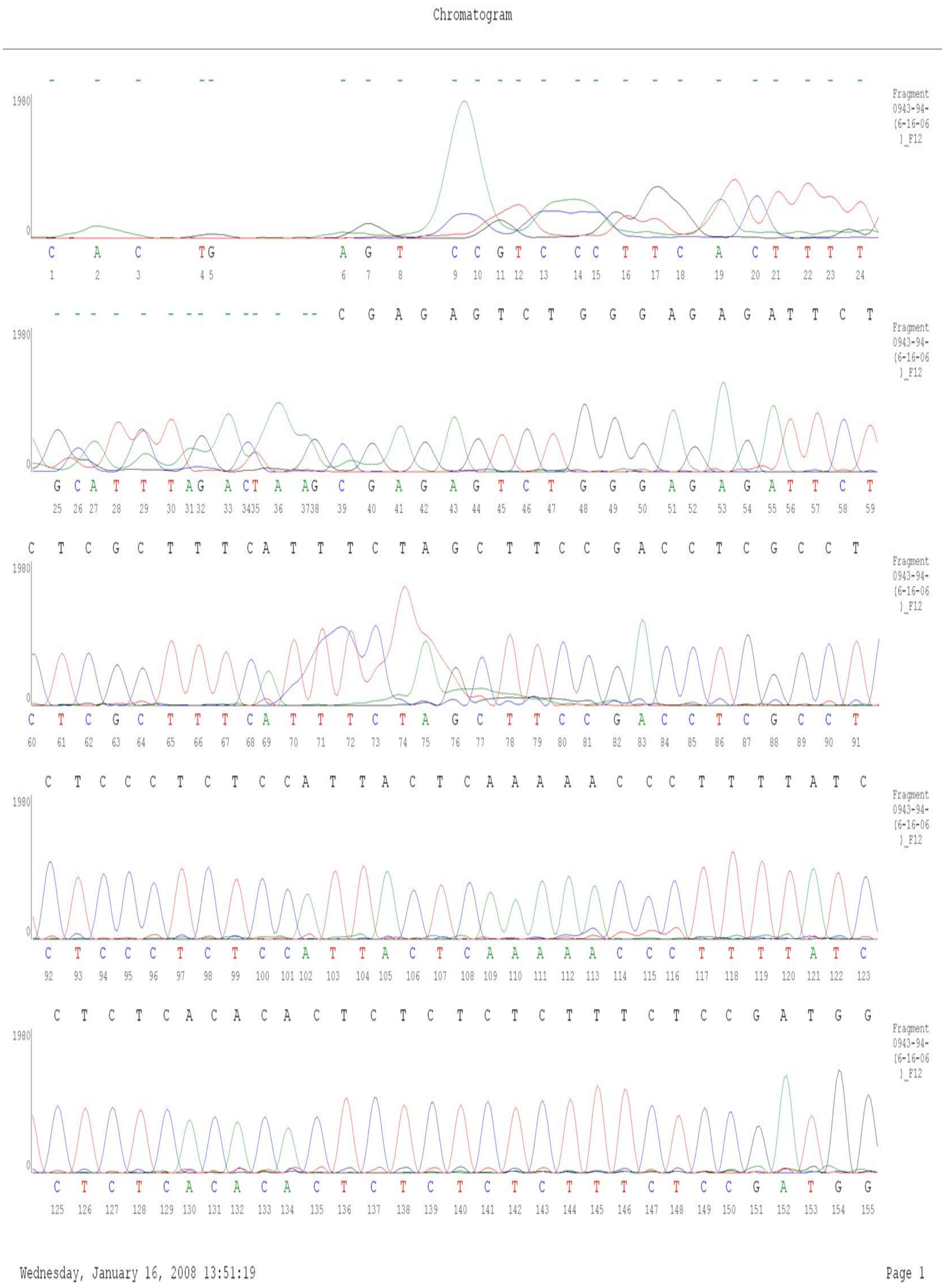
Standards:					Log adjustment	Sample size bp
distance mm	size Log(bp)	size bp	sample #	distance mm	"=-0.0124*(x)+3.9194	"=10eX
25	3.6098078	4072	501	56.5	3.2188	1655.01
35	3.484869	3054	502	72	3.0266	1063.16
49	3.3087778	2036	503	45	3.3614	2298.26
57	3.2137833	1636	504	53.5	3.256	1803.02
0	3.0077478	1018	505	67.5	3.0824	1208.93
			506	49	3.3118	2050.22
			507	58	3.2002	1585.62
			508	60.5	3.1692	1476.39
			509	48	3.3242	2109.60
			510	64.5	3.1196	1317.04
			511	58.5	3.194	1563.15
			512	66	3.101	1261.83
			513	56	3.225	1678.80
			514	65	3.1134	1298.37
			515	63	3.1382	1374.67
			516	56.5	3.2188	1655.01
			517	65	3.1134	1298.37
			518	71.5	3.0328	1078.45



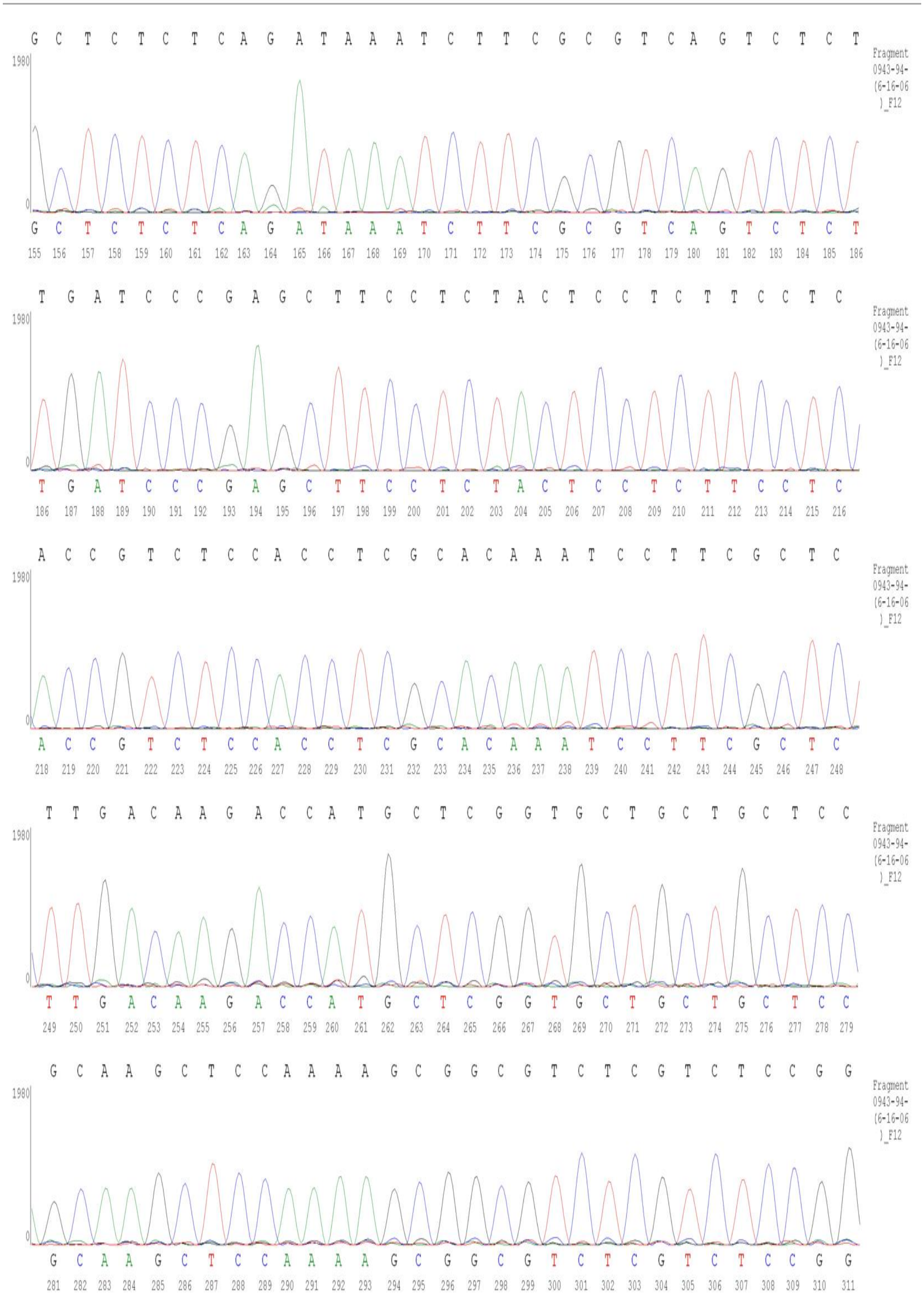
Standards:					Log adjustment	Sample size bp
distance mm	size Log(bp)	size bp	sample #	distance mm	"=-0.0199*(x)+3.8882	"=10eX
15	3.6098078	4072	519	35	3.1917	1554.89
20	3.484869	3054	520	45	2.9927	983.33
28	3.3087778	2036	521	48	2.933	857.04
33.7	3.2137833	1636	522	47.5	2.94295	876.90
45	3.0077478	1018	523	44	3.0126	1029.44
			524	39	3.1121	1294.49
			525	46	2.9728	939.29
			526	49	2.9131	818.65
			527	34.5	3.20165	1590.93
			528	41	3.0723	1181.14
			529	42	3.0524	1128.24
			530	44.5	3.00265	1006.12
			531	46	2.9728	939.29
			532	36	3.1718	1485.25
			533	32	3.2514	1784.02
			534	43	3.0325	1077.71
			535	44.5	3.00265	1006.12
			536	43.2	3.02852	1067.87



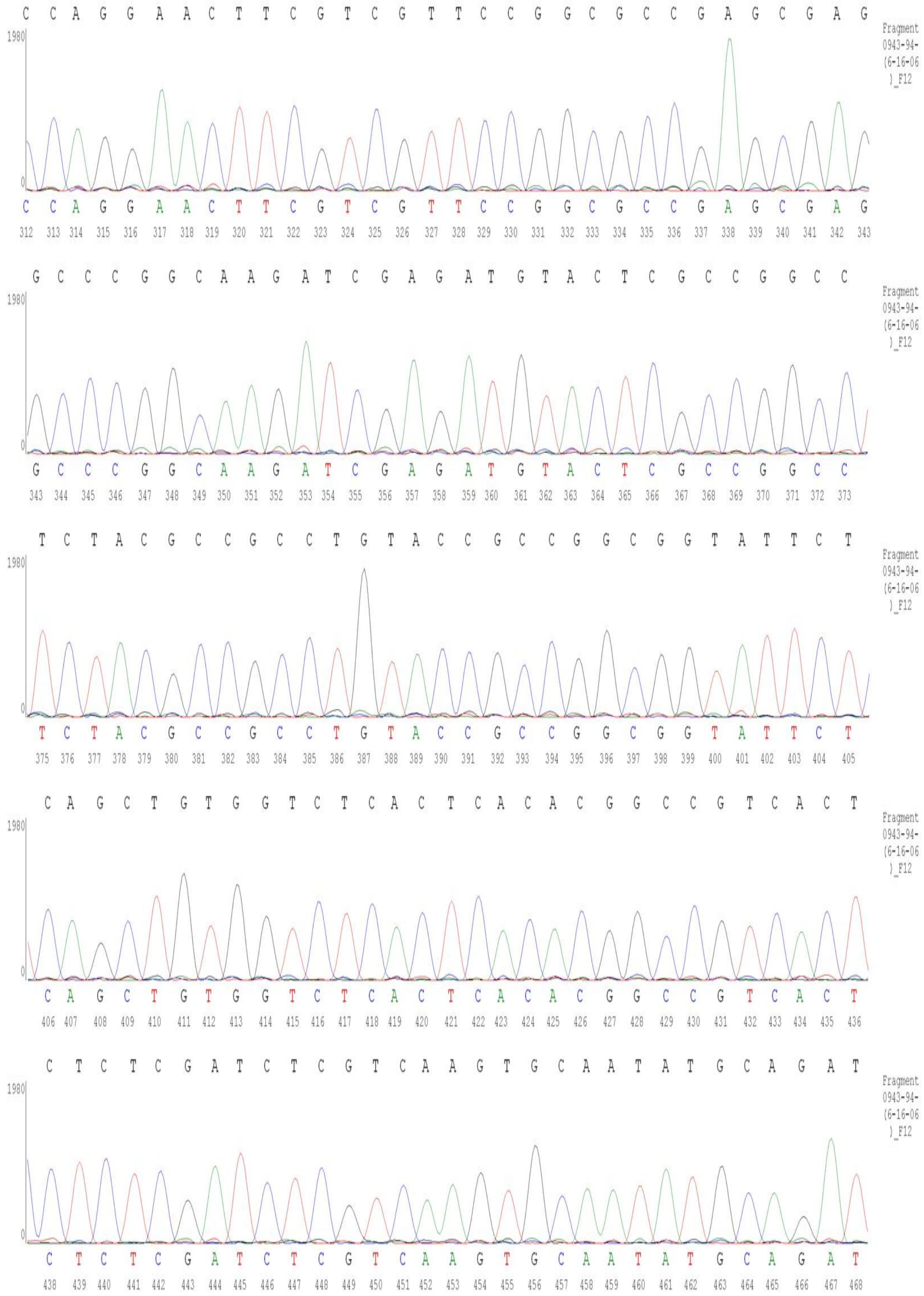
APPENDIX D: Chromatogram of Clone 0943

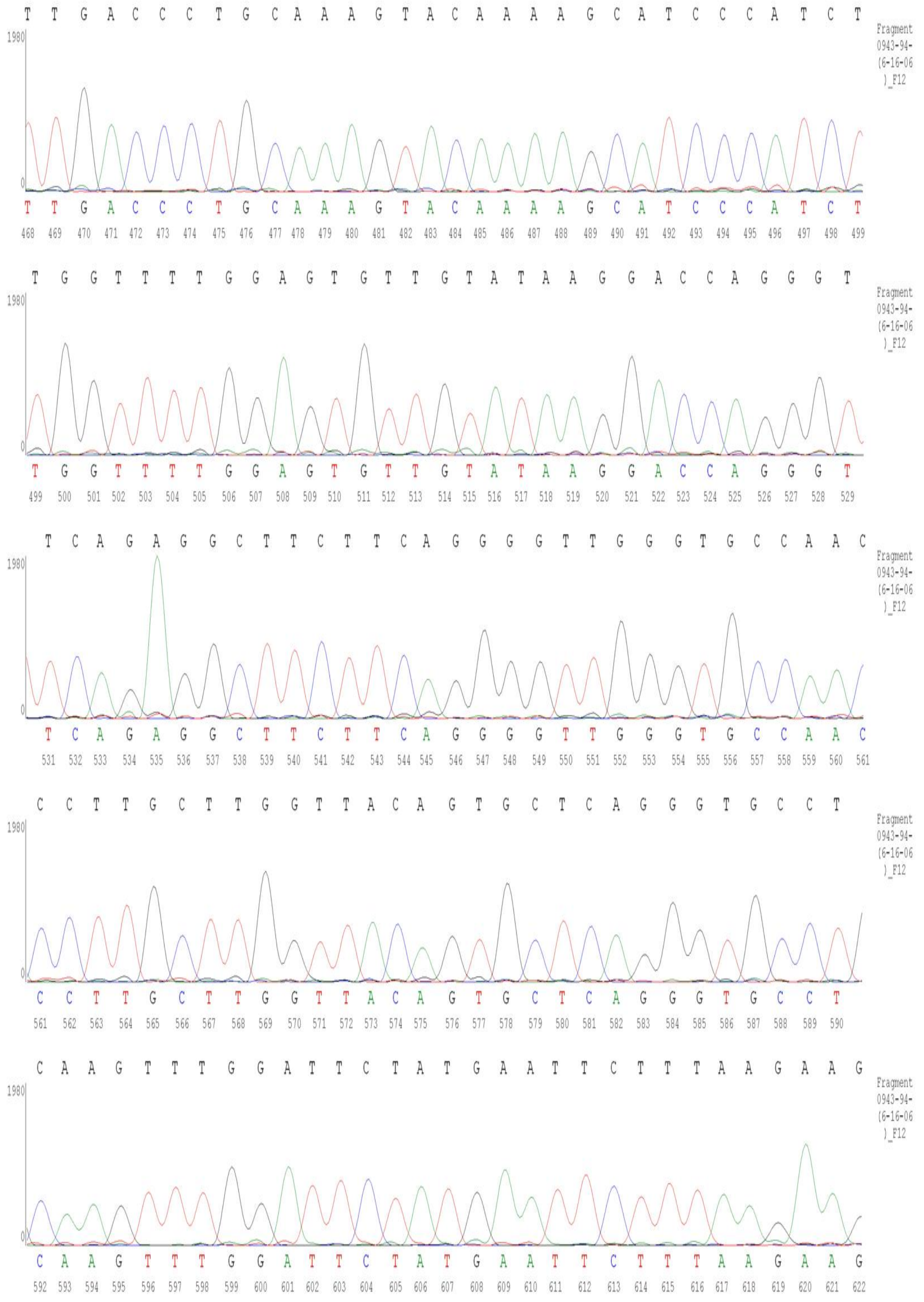


Chromatogram



Chromatogram

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1980
0
Fragment 0943-94-(6-16-06)_F12
499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529
T C A G A G G C T T C T T C A G G G G T T G G G T G C C A A C
1980
0
Fragment 0943-94-(6-16-06)_F12
531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561
C C T T G C T T G G T T A C A G T G C T C A G G G T G C C T
1980
0
Fragment 0943-94-(6-16-06)_F12
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C A A G T T T G G A T T C T A T G A A T T C T T T A A G A A G
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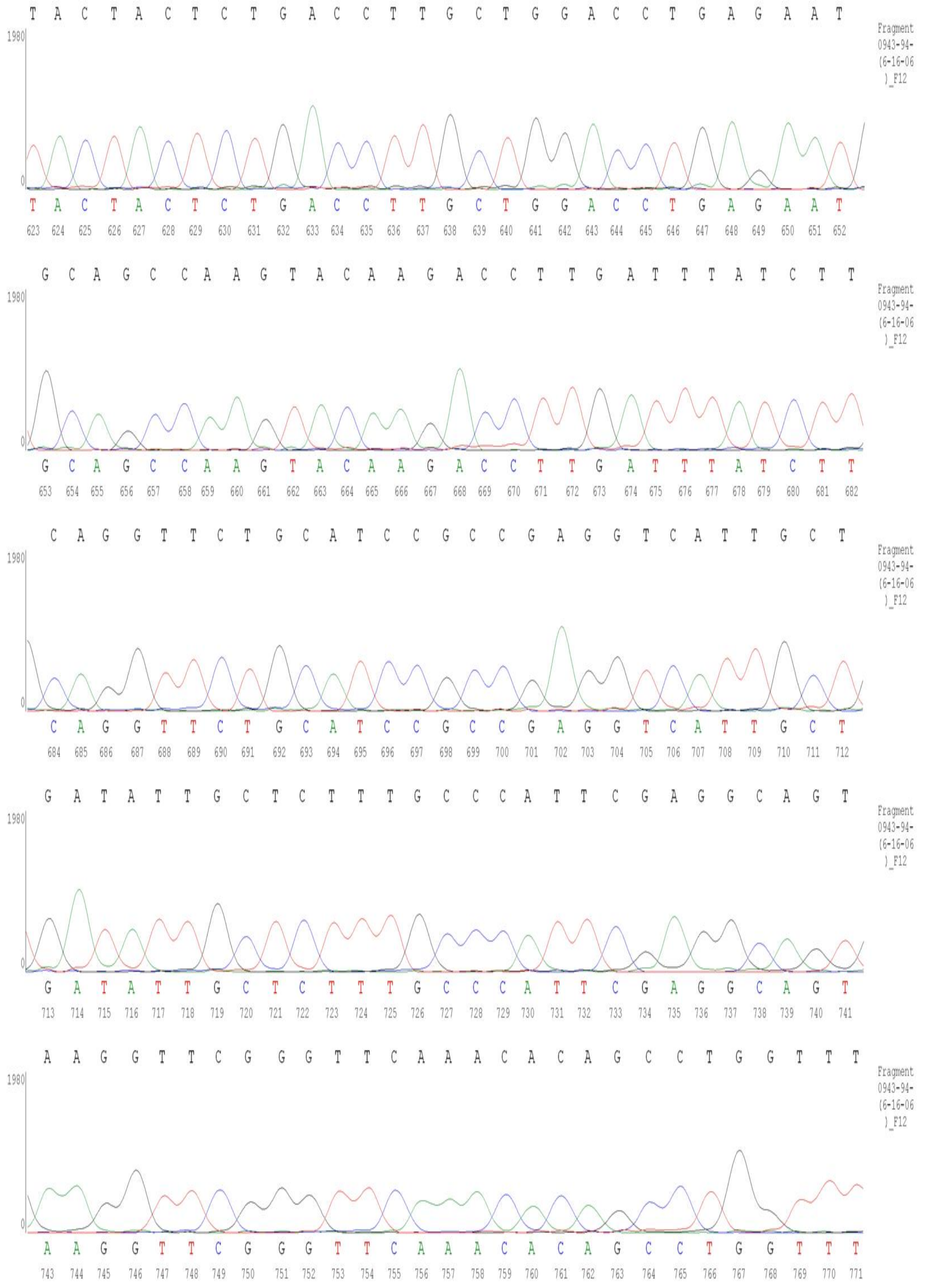
Chromatogram



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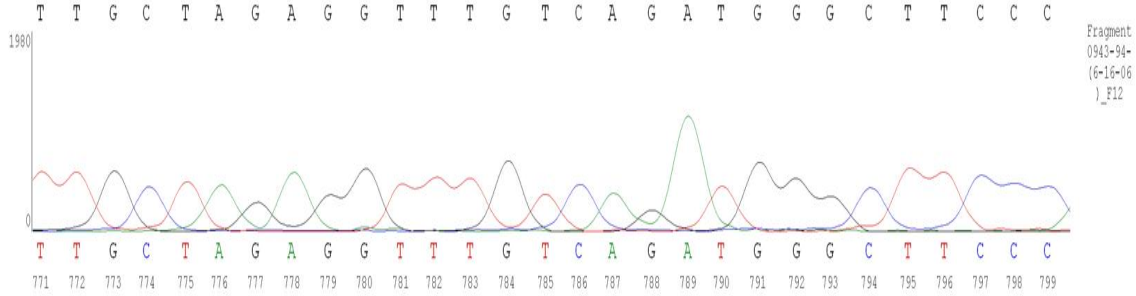
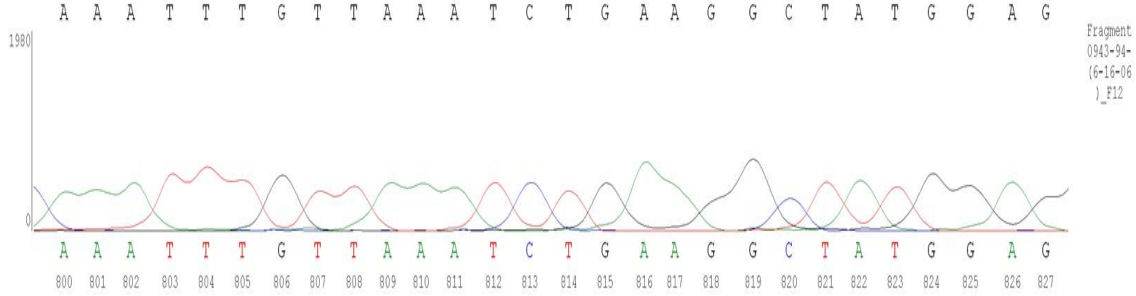
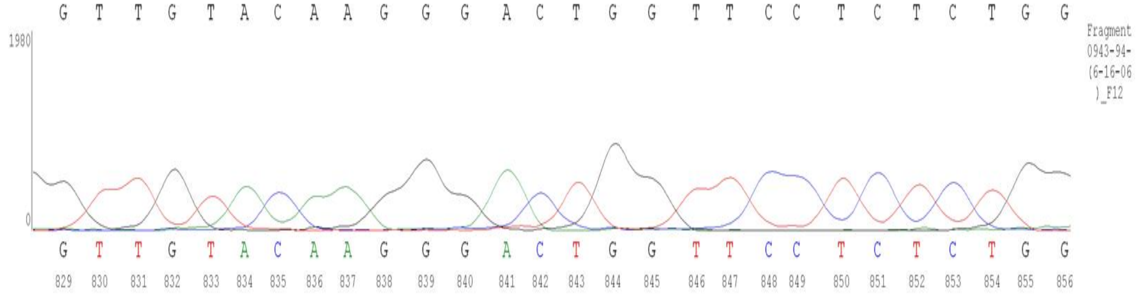
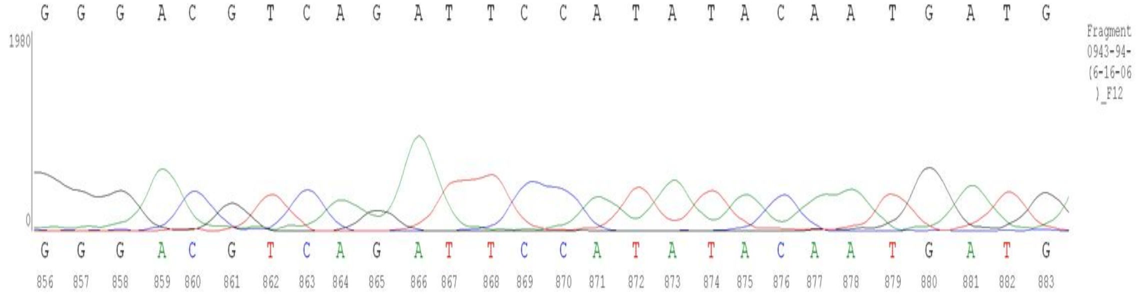
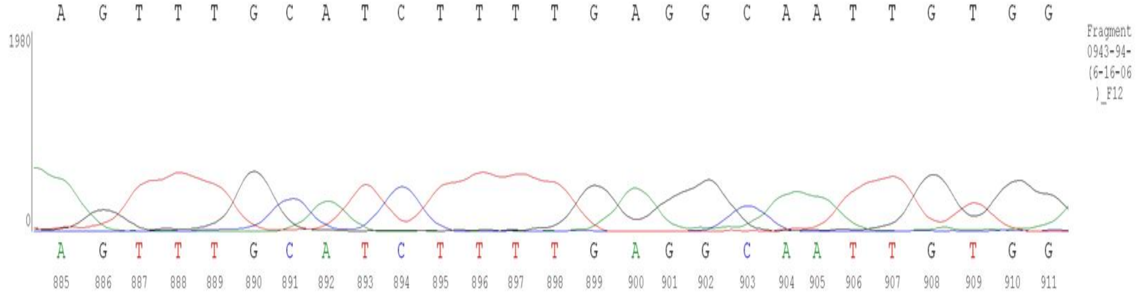


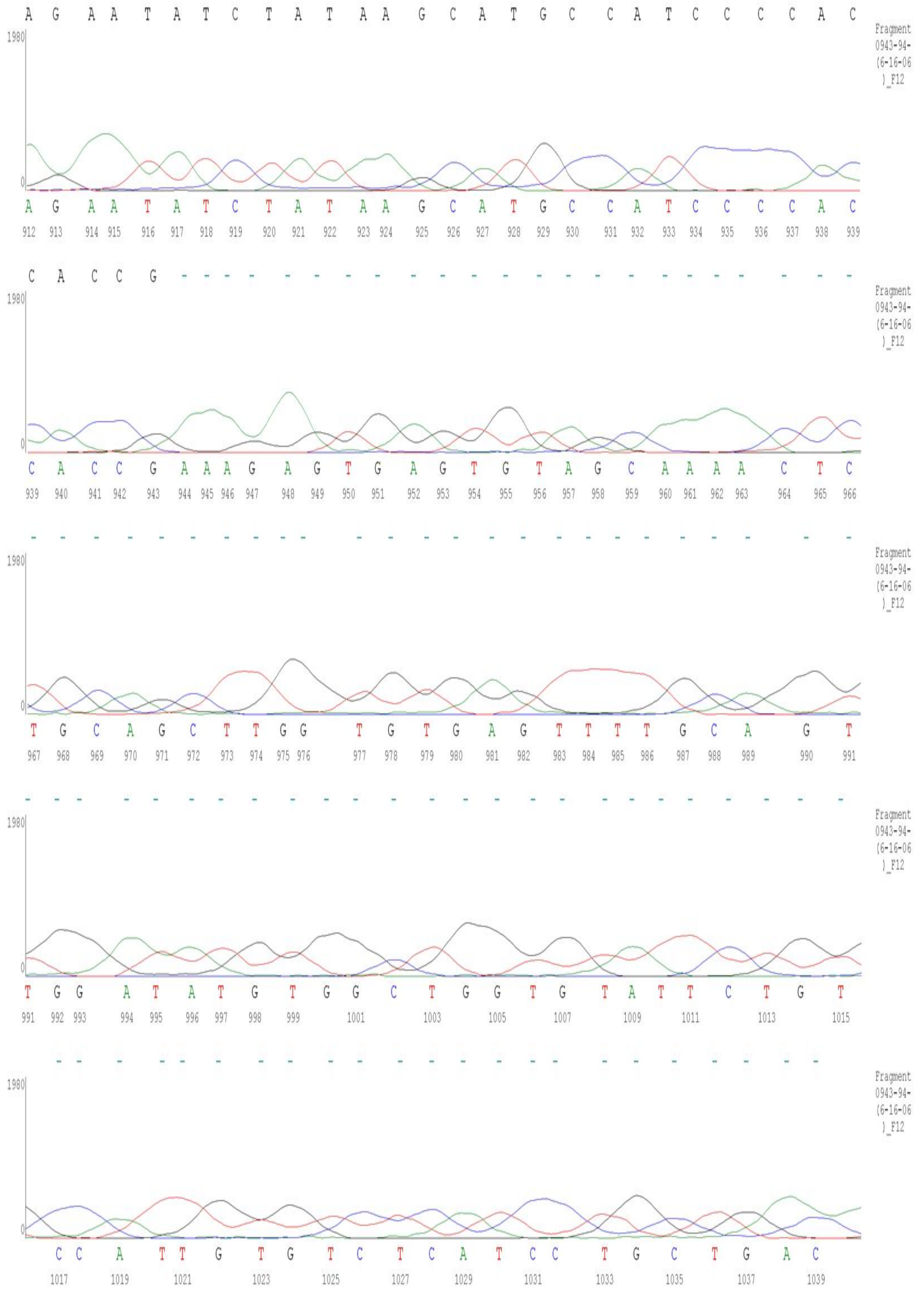




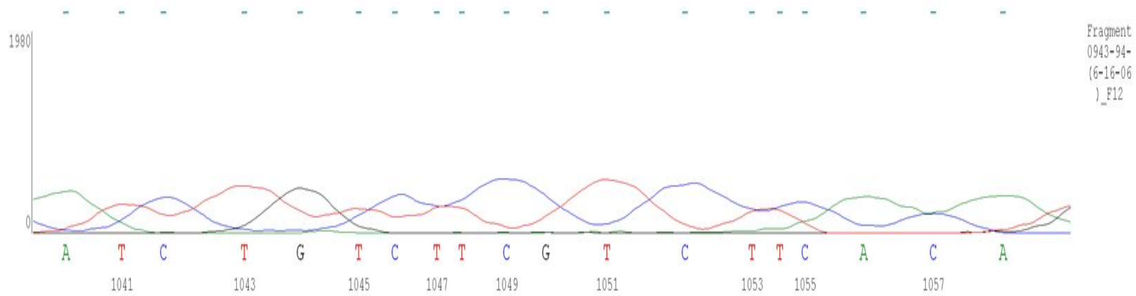


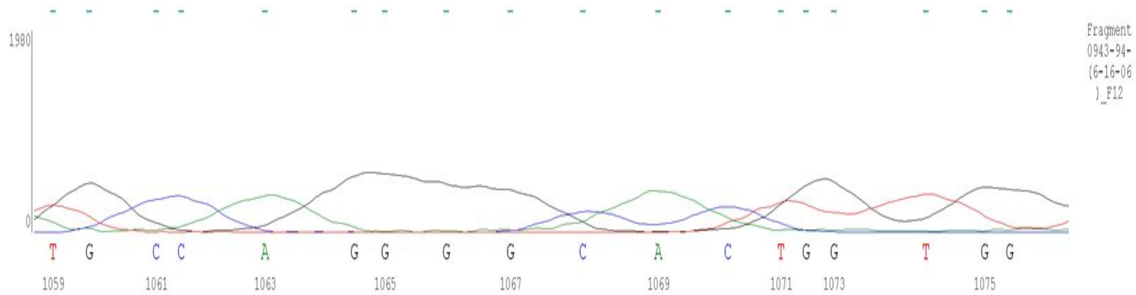


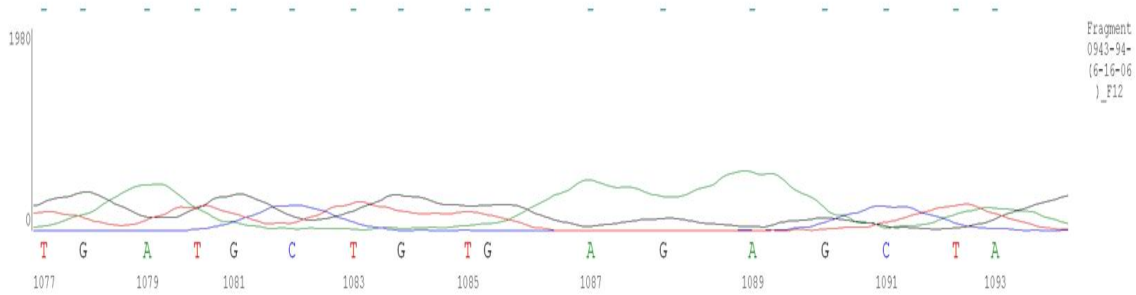
Chromatogram

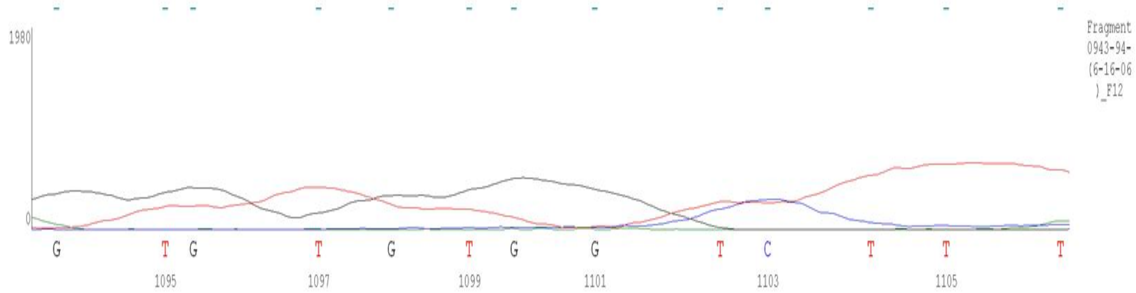


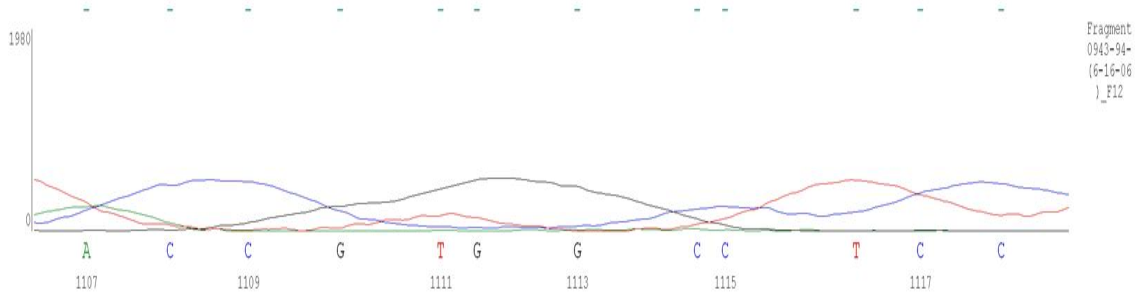
Chromatogram

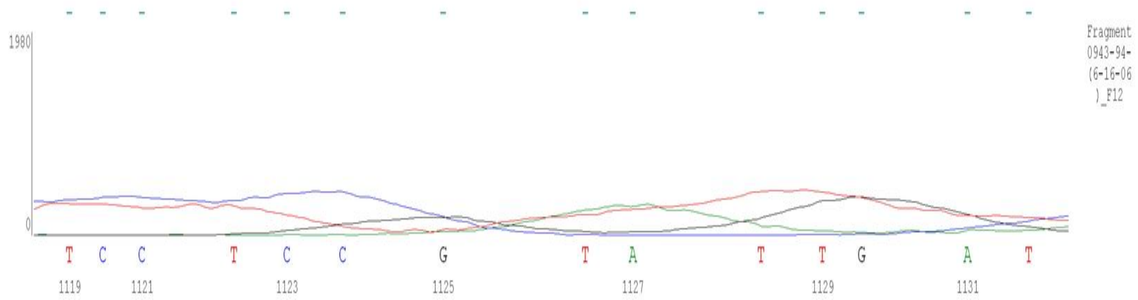








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1125
1127
1129
1131
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0943-94-
(6-16-06
)_F12


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Appendix E: Unique NRO cDNA Sequences in FASTA Format

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>1301-94-(6-16-06)_C06
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>0019-94_008(5-31-06)
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>0027-94-C01(4-28-06)
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>0119-94-F12(4-28-06)
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>0120-94-A02(5-9-06)
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>0121-94-H12(4-28-06)
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>0122-94-B02(5-9-06)

>0123-94-C02(5-9-06)
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>0124-94-D02(5-9-06)
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>0127-94(5-31-06)_007
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>0128-94(5-31-06)_009
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>0129-94-A03(5-9-06)
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>0130-94-B03(5-9-06)
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>0131-94-C03(5-9-06)
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>0133-94-E03(5-9-06)
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>0134-94-F03(5-9-06)
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>0136-94(5-31-06)_011
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>0137-94-A04(5-9-06)
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>0139-94-C04(5-9-06)
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>0140-94-D04(5-9-06)
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>0141-94-E04(5-9-06)
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>0143-94(5-31-06)_013
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>0147-94-C05(5-9-06)
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>0148-94-D05(5-9-06)
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>0149-94-E05(5-9-06)
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>0159-94(5-31-06)_004
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>0161-94-A07(5-5-06)
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>0162-94-B07(5-5-06)
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>0163-94-C07(5-5-06)
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>0164-94-D07(5-5-06)
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>0172-94-E03(5-10-06)
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>0175-94-H03(5-10-06)
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>0177-94-B04(5-10-06)
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>0179-94-D04(5-10-06)
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>0180-94-E04(5-10-06)
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>0185-94-B05(5-10-06)
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>0199-94(5-31-06)_008
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>0214-94(5-31-06)_010
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>0215-94(5-31-06)_012
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>0217-94-(6-16-06)_B09
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>0223-94-H09(5-10-06)
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>0227-94-D10(5-10-06)
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>0230-94(5-31-06)_014
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>0244-94-E12(5-10-06)
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>0247-94(5-31-06)_003
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>0391-94-(6-27-06)_E05
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>0393-94-(6-8-06)_B12
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>1021-94-(6-2-06)_D03
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>1025-94-(6-2-06)_H03
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>1029-94-(6-2-06)_D04
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>1032-94-(6-2-06)_G04
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>1033-94-(6-2-06)_H04
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>1034-94-(6-14-06)_F08
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>1039-94-(6-2-06)_F05
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>1042-94-(6-15-06)_E12
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>1046-94-(6-2-06)_E06
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>1047-94-(6-2-06)_F06
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>1078-94-(6-2-06)_D10
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>1138-94-(6-9-06)_F11
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>1139-94-(6-9-06)_G11
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>1141-94-(6-9-06)_A12
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>1142-94-(6-9-06)_B12
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>1143-94-(6-9-06)_C12
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>1144-94-(6-9-06)_D12
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>1145-94-(6-9-06TRUNCATED)_E12
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>1146-94-(6-9-06)_F12
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>1147-94-(6-9-06TRUNCATED)_G12
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>1148-94-(6-9-06)_H12
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>1151-94-(6-15-06)_C04
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>1152-94-(6-15-06)_D04
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>1159-94-(6-15-06)_A05
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>1160-94-(6-15-06)_B05
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>1163-94-(6-15-06)_C05
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>1166-94-(6-15-06)_E05
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>1167-94-(6-15-06)_F05
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>1169-94-(6-15-06)_G05
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>1170-94-(6-15-06)_H05
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>1171-94-(6-15-06)_A06
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>1172-94-(6-15-06)_B06
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>1174-94-(6-15-06)_D06
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TCTCATTGTG

>1178-94-(6-15-06)_E06
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>1179-94-(6-15-06)_F06
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APPENDIX F: Contig Information

Name	Length	Status	Frag	Non-ambiguous bases	Type
Contig 1	836	'Assembly 1'	3	99.64%	Contig
0181-94-E09(5-5-06)	594	In contig 'Contig 1'			Frag
0181-94-F04(5-10-06)	721	In contig 'Contig 1'			Frag
1195-94-(6-15-06)_G07	835	In contig 'Contig 1'			Frag
Contig 2	912	'Assembly 1'	3	99.45%	Contig
1199-94-(6-15-06)_H07	835	In contig 'Contig 2'			Frag
0441-94-(6-16-06)_A03	817	In contig 'Contig 2'			Frag
0441-94-(6-27-06)_F06	910	In contig 'Contig 2'			Frag
Contig 3	878	'Assembly 1'	2	100.00%	Contig
1303p_C05	617	In contig 'Contig 3'			Frag
1303-94-(6-16-06)_E06	841	In contig 'Contig 3'			Frag
Contig 4	829	'Assembly 1'	2	100.00%	Contig
1304_E03	523	In contig 'Contig 4'			Frag
1304-94-(6-16-06truncated)_F06	452	In contig 'Contig 4'			Frag
Contig 5	891	'Assembly 1'	2	99.89%	Contig
1309p_A06	671	In contig 'Contig 5'			Frag
1309-94-(6-16-06)_C07	890	In contig 'Contig 5'			Frag
Contig 6	797	'Assembly 1'	4	99.37%	Contig
0013_C03	762	In contig 'Contig 6'			Frag
0001_A01	710	In contig 'Contig 6'			Frag
0014_D03	752	In contig 'Contig 6'			Frag
0002_B01	794	In contig 'Contig 6'			Frag
Contig 7	973	'Assembly 1'	4	99.90%	Contig
2_D02	557	In contig 'Contig 7'			Frag
0002_E04	474	In contig 'Contig 7'			Frag
0002for_B04(4-20-06)	705	In contig 'Contig 7'			Frag
0002rev_C04(4-20-06)	779	In contig 'Contig 7'			Frag
Contig 8	928	'Assembly 1'	4	99.68%	Contig
0004_G04	476	In contig 'Contig 8'			Frag
0004for(4-20-06)_F04	695	In contig 'Contig 8'			Frag
0004p_F06	636	In contig 'Contig 8'			Frag
0004-94-G04(4-20-06)	734	In contig 'Contig 8'			Frag
Contig 9	1036	'Assembly 1'	3	99.90%	Contig
0005-94-A05(4-20-06)	706	In contig 'Contig 9'			Frag
0005p_G06	673	In contig 'Contig 9'			Frag
0005for_H04'	696	In contig 'Contig 9'			Frag

Contig 10	1095	'Assembly 1'	19	97.90%	Contig
0005_E01	519	In contig 'Contig 10'			Frag
0001-93_C06(4-10-06)	663	In contig 'Contig 10'			Frag
0001-94-(4-6-06)_C02	630	In contig 'Contig 10'			Frag
0006_F01	547	In contig 'Contig 10'			Frag
0006_D02	716	In contig 'Contig 10'			Frag
0009_G02	712	In contig 'Contig 10'			Frag
0002_H01	702	In contig 'Contig 10'			Frag
0003_C01	624	In contig 'Contig 10'			Frag
0004_D01	606	In contig 'Contig 10'			Frag
0011_A03	606	In contig 'Contig 10'			Frag
0003_A02	658	In contig 'Contig 10'			Frag
0007_E02	671	In contig 'Contig 10'			Frag
0010_H02	671	In contig 'Contig 10'			Frag
0004_B02	689	In contig 'Contig 10'			Frag
0005_C02	684	In contig 'Contig 10'			Frag
0008_F02	685	In contig 'Contig 10'			Frag
0001-93_G01	667	In contig 'Contig 10'			Frag
0012_B03	681	In contig 'Contig 10'			Frag
0001-94_A04(4-20-06)	757	In contig 'Contig 10'			Frag
Contig 11	1035	'Assembly 1'	3	99.13%	Contig
0009-94_003(5-31-06)	821	In contig 'Contig 11'			Frag
0009-94-(6-27-06best)_B01	999	In contig 'Contig 11'			Frag
0009_93-H12(4-21-06)	589	In contig 'Contig 11'			Frag
Contig 12	940	'Assembly 1'	2	100.00%	Contig
0025_A01(For4-28-06)	556	In contig 'Contig 12'			Frag
0025-94-(6-27-06)_C01	940	In contig 'Contig 12'			Frag
Contig 13	762	'Assembly 1'	2	100.00%	Contig
0027-93-F10(4-21-06)	727	In contig 'Contig 13'			Frag
0014-93-C12(4-21-06)	705	In contig 'Contig 13'			Frag
Contig 14	1035	'Assembly 1'	2	99.71%	Contig
0034-94-A02(4-28-06)	476	In contig 'Contig 14'			Frag
0034-94-(6-27-06)_D01	1035	In contig 'Contig 14'			Frag
Contig 15	1076	'Assembly 1'	4	99.35%	Contig
0035-94-B02(4-28-06)	723	In contig 'Contig 15'			Frag
1091-94-(6-14-06)_A10	788	In contig 'Contig 15'			Frag
1091-94-(6-2-06)_A12	868	In contig 'Contig 15'			Frag
0035-93-F09(4-21-06)	682	In contig 'Contig 15'			Frag
Contig 16	834	'Assembly 1'	7	99.88%	Contig
0201-94-A12(5-5-06)	667	In contig 'Contig 16'			Frag
0066-94-A06(4-28-06)	704	In contig 'Contig 16'			Frag
0038-94-(6-12-06)_B01	735	In contig 'Contig 16'			Frag

0093-94-D09(4-28-06)	656	In contig 'Contig 16'			Frag
0038-94-E02(4-28-06)	725	In contig 'Contig 16'			Frag
0201-94-B07(5-10-06)	766	In contig 'Contig 16'			Frag
0066-94-(6-12-06)_C02	833	In contig 'Contig 16'			Frag
Contig 17	840	'Assembly 1'	2	99.76%	Contig
0039-94-F02(4-28-06)	717	In contig 'Contig 17'			Frag
0039-94-(6-12-06)_C01	840	In contig 'Contig 17'			Frag
Contig 18	995	'Assembly 1'	3	100.00%	Contig
0040-94-B01(5-9-06best)	711	In contig 'Contig 18'			Frag
0040-94(5-31-06)_003	877	In contig 'Contig 18'			Frag
0040-93-A09(4-21-06)	724	In contig 'Contig 18'			Frag
Contig 19	1002	'Assembly 1'	2	100.00%	Contig
0041-94-H02(4-28-06)	691	In contig 'Contig 19'			Frag
0041-94-(6-27-06)_F01	1002	In contig 'Contig 19'			Frag
Contig 20	879	'Assembly 1'	2	100.00%	Contig
0043-94-B03(4-28-06)	725	In contig 'Contig 20'			Frag
0043-93-F08(4-21-06)	638	In contig 'Contig 20'			Frag
Contig 21	1030	'Assembly 1'	3	100.00%	Contig
0044-94-C01(5-9-06)	729	In contig 'Contig 21'			Frag
0044-94(5-31-06)_005	902	In contig 'Contig 21'			Frag
0044-94-(6-27-06best)_G01	1029	In contig 'Contig 21'			Frag
Contig 22	1407	'Assembly 1'	3	100.00%	Contig
0049-94-H03(4-28-06)	714	In contig 'Contig 22'			Frag
0049-94-(6-12-06)_D01	839	In contig 'Contig 22'			Frag
0049-93-H07(4-21-06)	692	In contig 'Contig 22'			Frag
Contig 23	1040	'Assembly 1'	2	100.00%	Contig
0050-94-(6-12-06)_E01	898	In contig 'Contig 23'			Frag
0050-94-(6-27-06)_H01	1040	In contig 'Contig 23'			Frag
Contig 24	1170	'Assembly 1'	2	100.00%	Contig
0051-94-B04(4-28-06)	663	In contig 'Contig 24'			Frag
0051-93-F07(4-21-06)	644	In contig 'Contig 24'			Frag
Contig 25	1375	'Assembly 1'	3	100.00%	Contig
0057-94-H04(4-28-06)	610	In contig 'Contig 25'			Frag
0057-94-(6-12-06)_G01	769	In contig 'Contig 25'			Frag
0057-93-H06(4-21-06)	659	In contig 'Contig 25'			Frag
Contig 26	1037	'Assembly 1'	2	99.90%	Contig
0058-94-(6-12-06Poor intensity)_H01	729	In contig 'Contig 26'			Frag
0058-93-G06(4-21-06)	572	In contig 'Contig 26'			Frag
Contig 27	908	'Assembly 1'	3	98.46%	Contig
0059-94-(6-12-06)_A02	820	In contig 'Contig 27'			Frag
0059-93-F06(4-21-06)	761	In contig 'Contig 27'			Frag

0059-94-(6-15-06)_B08	908	In contig 'Contig 27'			Frag
Contig 28	875	'Assembly 1'	2	98.97%	Contig
0061-94-D05(4-28-06)	751	In contig 'Contig 28'			Frag
0061-93-D06(4-21-06)	662	In contig 'Contig 28'			Frag
Contig 29	825	'Assembly 1'	2	99.88%	Contig
0064-94-G05(4-28-06)	717	In contig 'Contig 29'			Frag
0064-94-(6-12-06)_B02	825	In contig 'Contig 29'			Frag
Contig 30	1358	'Assembly 1'	3	100.00%	Contig
0067-94-B06(4-28-06)	673	In contig 'Contig 30'			Frag
0067-94-(6-12-06)_D02	862	In contig 'Contig 30'			Frag
0067-93-F05(4-21-06)	663	In contig 'Contig 30'			Frag
Contig 31	1296	'Assembly 1'	3	100.00%	Contig
0068-94-E01(5-5-06)	224	In contig 'Contig 31'			Frag
0068-94-E01(5-9-06best)	725	In contig 'Contig 31'			Frag
0068-93-E05(4-21-06)	726	In contig 'Contig 31'			Frag
Contig 32	862	'Assembly 1'	2	100.00%	Contig
0073-94-H06(4-28-06)	575	In contig 'Contig 32'			Frag
0073-93-H04(4-21-06)	677	In contig 'Contig 32'			Frag
Contig 33	944	'Assembly 1'	2	99.89%	Contig
0076-94-C07(4-28-06)	735	In contig 'Contig 33'			Frag
0076-93-E04(4-21-06)	588	In contig 'Contig 33'			Frag
Contig 34	1299	'Assembly 1'	2	100.00%	Contig
0077_D04(Rev4-21-06)	685	In contig 'Contig 34'			Frag
0077-94-D07(4-28-06)	693	In contig 'Contig 34'			Frag
Contig 35	869	'Assembly 1'	2	100.00%	Contig
0078-94-E07(4-28-06)	700	In contig 'Contig 35'			Frag
0078-94-(6-27-06)_A02	869	In contig 'Contig 35'			Frag
Contig 36	863	'Assembly 1'	2	100.00%	Contig
0079-94-F07(4-28-06)	702	In contig 'Contig 36'			Frag
0079-94-(6-12-06)_E02	863	In contig 'Contig 36'			Frag
Contig 37	808	'Assembly 1'	2	100.00%	Contig
0080-94-G07(4-28-06)	488	In contig 'Contig 37'			Frag
0080-94-(6-12-06)_F02	808	In contig 'Contig 37'			Frag
Contig 38	1384	'Assembly 1'	3	99.86%	Contig
0081-94-H07(4-28-06)	677	In contig 'Contig 38'			Frag
0081-94-(6-12-06)_G02	829	In contig 'Contig 38'			Frag
0081-93-H03(4-21-06)	690	In contig 'Contig 38'			Frag
Contig 39	830	'Assembly 1'	2	100.00%	Contig
0082-94-A08(4-28-06)	672	In contig 'Contig 39'			Frag
0082-94-(6-12-06)_H02	830	In contig 'Contig 39'			Frag
Contig 40	924	'Assembly 1'	2	99.89%	Contig
0083-94-B08(4-28-06)	711	In contig 'Contig 40'			Frag

0083-94-(6-12-06)_A03	924	In contig 'Contig 40'			Frag
Contig 41	768	'Assembly 1'	2	99.87%	Contig
0033-94-H01(4-28-06)	659	In contig 'Contig 41'			Frag
0084-94-C08(4-28-06)	768	In contig 'Contig 41'			Frag
Contig 42	1037	'Assembly 1'	4	99.90%	Contig
0088-94-G01(5-5-06)	524	In contig 'Contig 42'			Frag
0088-94-G01(5-9-06best)	704	In contig 'Contig 42'			Frag
1053-94-(6-2-06)_D07	805	In contig 'Contig 42'			Frag
0088-93-A03(4-21-06)	705	In contig 'Contig 42'			Frag
Contig 43	947	'Assembly 1'	2	99.79%	Contig
0089-94-H08(4-28-06)	676	In contig 'Contig 43'			Frag
0089-93-H02(4-21-06)	687	In contig 'Contig 43'			Frag
Contig 44	1091	'Assembly 1'	2	99.91%	Contig
0090-94-(6-12-06)_B03	865	In contig 'Contig 44'			Frag
0090-93-G02(4-21-06)	551	In contig 'Contig 44'			Frag
Contig 45	821	'Assembly 1'	2	100.00%	Contig
0092-94-C09(4-28-06)	582	In contig 'Contig 45'			Frag
0092-94-(6-12-06)_C03	821	In contig 'Contig 45'			Frag
Contig 46	881	'Assembly 1'	3	100.00%	Contig
0094-94-E09(4-28-06)	701	In contig 'Contig 46'			Frag
0094-94-(6-12-06)_D03	849	In contig 'Contig 46'			Frag
0094-93-C02(4-21-06)	678	In contig 'Contig 46'			Frag
Contig 47	884	'Assembly 1'	2	100.00%	Contig
0096-94-G09(4-28-06)	739	In contig 'Contig 47'			Frag
0096-94-(6-12-06)_E03	884	In contig 'Contig 47'			Frag
Contig 48	946	'Assembly 1'	5	99.47%	Contig
0236-94-E11(5-10-06)	530	In contig 'Contig 48'			Frag
0098-94-(6-12-06)_F03	869	In contig 'Contig 48'			Frag
0742-94-(6-7-06)_B06	842	In contig 'Contig 48'			Frag
0236-94-(6-16-06)_D09	809	In contig 'Contig 48'			Frag
0098-93-(4-21-06)_G01	365	In contig 'Contig 48'			Frag
Contig 49	1061	'Assembly 1'	2	100.00%	Contig
0101-94-D10(4-28-06)	621	In contig 'Contig 49'			Frag
0101-93-D01(4-21-06)	614	In contig 'Contig 49'			Frag
Contig 50	961	'Assembly 1'	2	99.69%	Contig
0102-94-E10(4-28-06)	712	In contig 'Contig 50'			Frag
0102-93-C01(4-21-06)	693	In contig 'Contig 50'			Frag
Contig 51	1137	'Assembly 1'	2	100.00%	Contig
0103-94-F10(4-28-06)	700	In contig 'Contig 51'			Frag
0103-93-B01(4-21-06)	637	In contig 'Contig 51'			Frag
Contig 52	866	'Assembly 1'	2	99.77%	Contig
0104-94-H01(5-9-06)	674	In contig 'Contig 52'			Frag

0104-94-(6-12-06)_H03	866	In contig 'Contig 52'			Frag
Contig 53	924	'Assembly 1'	3	99.89%	Contig
0108-94-(6-12-06Truncated)_B04	661	In contig 'Contig 53'			Frag
0108-94-C11(4-28-06)	629	In contig 'Contig 53'			Frag
0108-94-(6-14-06)_D01	923	In contig 'Contig 53'			Frag
Contig 54	860	'Assembly 1'	2	99.53%	Contig
0109-94-D11(4-28-06)	679	In contig 'Contig 54'			Frag
0109-94-(6-12-06)_C04	858	In contig 'Contig 54'			Frag
Contig 55	864	'Assembly 1'	2	99.88%	Contig
0114-94-A12(4-28-06)	711	In contig 'Contig 55'			Frag
0114-94-(6-12-06)_F04	864	In contig 'Contig 55'			Frag
Contig 56	743	'Assembly 1'	2	100.00%	Contig
0116-94-C12(4-28-06)	677	In contig 'Contig 56'			Frag
0116-94-(6-12-06)_G04	743	In contig 'Contig 56'			Frag
Contig 57	876	'Assembly 1'	2	100.00%	Contig
0125-94-E02(5-9-06)	706	In contig 'Contig 57'			Frag
0125-94-(6-12-06)_H04	876	In contig 'Contig 57'			Frag
Contig 58	696	'Assembly 1'	2	100.00%	Contig
0126-94-F02(5-9-06)	646	In contig 'Contig 58'			Frag
0070_E06(For4-28-06)	546	In contig 'Contig 58'			Frag
Contig 59	768	'Assembly 1'	3	100.00%	Contig
0145-94-A05(5-9-06best)	670	In contig 'Contig 59'			Frag
0031-94-F01(4-28-06)	732	In contig 'Contig 59'			Frag
0145-94-A05(5-5-06redo)	598	In contig 'Contig 59'			Frag
Contig 60	681	'Assembly 1'	2	100.00%	Contig
0150-94-F05(5-9-06best)	671	In contig 'Contig 60'			Frag
0150-94-F05(5-5-06)	663	In contig 'Contig 60'			Frag
Contig 61	785	'Assembly 1'	3	97.71%	Contig
0151-94-G05(5-9-06)	677	In contig 'Contig 61'			Frag
0142-94-F04(5-9-06)	544	In contig 'Contig 61'			Frag
0069-94-D06(4-28-06)	652	In contig 'Contig 61'			Frag
Contig 62	749	'Assembly 1'	2	100.00%	Contig
0153-94-A06(5-9-06best)	749	In contig 'Contig 62'			Frag
0153-94-A06(5-5-06)	697	In contig 'Contig 62'			Frag
Contig 63	708	'Assembly 1'	2	100.00%	Contig
0155-94-C06(5-9-06best)	708	In contig 'Contig 63'			Frag
0155-94-C06(5-5-06)	604	In contig 'Contig 63'			Frag
Contig 64	761	'Assembly 1'	2	100.00%	Contig
0157-94-E06(5-9-06best)	733	In contig 'Contig 64'			Frag
0157-94-E06(5-5-06)	724	In contig 'Contig 64'			Frag
Contig 65	1299	'Assembly 1'	4	99.62%	Contig
0158-94-F06(5-5-06)	655	In contig 'Contig 65'			Frag

0158-94-F06(5-9-06best)	754	In contig 'Contig 65'			Frag
1001-94-(6-2-06)_A01	945	In contig 'Contig 65'			Frag
0715-94-(6-7-06)_G02	851	In contig 'Contig 65'			Frag
Contig 66	870	'Assembly 1'	2	99.77%	Contig
0160_H06(5-5-06)	769	In contig 'Contig 66'			Frag
0160-94-(6-16-06)_G07	870	In contig 'Contig 66'			Frag
Contig 67	955	'Assembly 1'	3	100.00%	Contig
0165-94-E07(5-5-06)	573	In contig 'Contig 67'			Frag
0165-94-(6-16-06)_H07	897	In contig 'Contig 67'			Frag
1048-94-(6-2-06)_G06	903	In contig 'Contig 67'			Frag
Contig 68	848	'Assembly 1'	2	99.76%	Contig
0166-94-F07(5-5-06)	577	In contig 'Contig 68'			Frag
0166-94-(6-16-06)_A08	848	In contig 'Contig 68'			Frag
Contig 69	912	'Assembly 1'	2	99.34%	Contig
0167-94-G07(5-5-06)	551	In contig 'Contig 69'			Frag
0167-94-(6-16-06)_B08	910	In contig 'Contig 69'			Frag
Contig 70	769	'Assembly 1'	2	99.87%	Contig
0168-94-A03(5-10-06best)	769	In contig 'Contig 70'			Frag
0168-94-H07(5-5-06)	685	In contig 'Contig 70'			Frag
Contig 71	731	'Assembly 1'	2	100.00%	Contig
0170-94-C03(5-10-06)	731	In contig 'Contig 71'			Frag
0170-94-B08(5-5-06)	722	In contig 'Contig 71'			Frag
Contig 72	741	'Assembly 1'	2	100.00%	Contig
0171-94-D03(5-10-06)	711	In contig 'Contig 72'			Frag
0171-94-C08(5-5-06)	739	In contig 'Contig 72'			Frag
Contig 73	896	'Assembly 1'	3	99.89%	Contig
0173-94-E08(5-5-06)	600	In contig 'Contig 73'			Frag
0173-94-F03(5-10-06)	698	In contig 'Contig 73'			Frag
0173-94-(6-16-06)_C08	895	In contig 'Contig 73'			Frag
Contig 74	852	'Assembly 1'	2	100.00%	Contig
0174-94-G03(5-10-06)	735	In contig 'Contig 74'			Frag
0758-94-(6-7-06)_B08	850	In contig 'Contig 74'			Frag
Contig 75	708	'Assembly 1'	2	100.00%	Contig
0176-94-H08(5-5-06)	637	In contig 'Contig 75'			Frag
0176-94-A04(5-10-06)	708	In contig 'Contig 75'			Frag
Contig 76	859	'Assembly 1'	2	100.00%	Contig
0183-94-G09(5-5-06)	674	In contig 'Contig 76'			Frag
0183-94-(6-16-06)_F08	859	In contig 'Contig 76'			Frag
Contig 77	749	'Assembly 1'	2	100.00%	Contig
0184-94-A05(5-10-06)	749	In contig 'Contig 77'			Frag
0184-94-H09(5-5-06)	728	In contig 'Contig 77'			Frag
Contig 78	999	'Assembly 1'	6	99.80%	Contig

0135-94-G03(5-9-06)	599	In contig 'Contig 78'			Frag
0135-94-G03(5-5-06best)	643	In contig 'Contig 78'			Frag
0186-94-C05(5-10-06)	726	In contig 'Contig 78'			Frag
0941-94-(6-15-06)_D03	771	In contig 'Contig 78'			Frag
0333-94-(6-9-06)_B03	821	In contig 'Contig 78'			Frag
0333-94-(6-27-06)_B04	985	In contig 'Contig 78'			Frag
Contig 79	696	'Assembly 1'	2	100.00%	Contig
0189-94-F05(5-10-06)	696	In contig 'Contig 79'			Frag
0189-94-E10(5-5-06)	579	In contig 'Contig 79'			Frag
Contig 80	699	'Assembly 1'	2	99.86%	Contig
0190-94-F10(5-5-06)	569	In contig 'Contig 80'			Frag
0190-94-G05(5-10-06)	698	In contig 'Contig 80'			Frag
Contig 81	1276	'Assembly 1'	2	100.00%	Contig
0191-94-H05(5-10-06)	685	In contig 'Contig 81'			Frag
0152-94-H05(5-9-06best)	671	In contig 'Contig 81'			Frag
Contig 82	709	'Assembly 1'	2	100.00%	Contig
0193-94-B06(5-10-06)	709	In contig 'Contig 82'			Frag
0193-94-A11(5-5-06)	664	In contig 'Contig 82'			Frag
Contig 83	872	'Assembly 1'	2	100.00%	Contig
0194-94-C06(5-10-06)	672	In contig 'Contig 83'			Frag
0194-94-(6-16-06)_G08	872	In contig 'Contig 83'			Frag
Contig 84	703	'Assembly 1'	2	100.00%	Contig
0196-94-D11(5-5-06)	703	In contig 'Contig 84'			Frag
0196-94-E06(5-10-06)	680	In contig 'Contig 84'			Frag
Contig 85	728	'Assembly 1'	2	100.00%	Contig
0197-94-F06(5-10-06)	726	In contig 'Contig 85'			Frag
0197-94-E11(5-5-06)	714	In contig 'Contig 85'			Frag
Contig 86	774	'Assembly 1'	2	100.00%	Contig
0202-94-C07(5-10-06)	774	In contig 'Contig 86'			Frag
0202-94-C12(5-5-06)	683	In contig 'Contig 86'			Frag
Contig 87	747	'Assembly 1'	2	100.00%	Contig
0203-94-D07(5-10-06)	713	In contig 'Contig 87'			Frag
0203-94-D12(5-5-06)	747	In contig 'Contig 87'			Frag
Contig 88	725	'Assembly 1'	2	100.00%	Contig
0204-94-E07(5-10-06)	725	In contig 'Contig 88'			Frag
0204-94-E12(5-5-06)	635	In contig 'Contig 88'			Frag
Contig 89	1059	'Assembly 1'	3	99.81%	Contig
0205-94-F12(5-5-06)	479	In contig 'Contig 89'			Frag
0205-94-F07(5-10-06)	766	In contig 'Contig 89'			Frag
0670-94-(6-6-06)_F09	864	In contig 'Contig 89'			Frag
Contig 90	1001	'Assembly 1'	3	94.21%	Contig
0343-94-(6-12-06Truncated)_E06	368	In contig 'Contig 90'			Frag

0207-94-H07(5-10-06)	544	In contig 'Contig 90'			Frag
0882-94-(6-5-06)_B11	857	In contig 'Contig 90'			Frag
Contig 91	1012	'Assembly 1'	3	100.00%	Contig
0212-94-E08(5-10-06)	764	In contig 'Contig 91'			Frag
0212-94-(6-16-06poor)_A09	893	In contig 'Contig 91'			Frag
0212-94-(6-27-06)_D02	1010	In contig 'Contig 91'			Frag
Contig 92	878	'Assembly 1'	2	100.00%	Contig
0216-94-A09(5-10-06)	756	In contig 'Contig 92'			Frag
0386-94-(6-12-06)_C10	857	In contig 'Contig 92'			Frag
Contig 93	890	'Assembly 1'	2	100.00%	Contig
0243-94-D12(5-10-06)	720	In contig 'Contig 93'			Frag
0243-94-(6-16-06)_F09	854	In contig 'Contig 93'			Frag
Contig 94	1138	'Assembly 1'	3	99.38%	Contig
0246-94-(6-16-06)_G09	886	In contig 'Contig 94'			Frag
0246-94(5-31-06)_001	908	In contig 'Contig 94'			Frag
0913-94-(6-14-06)_H11	822	In contig 'Contig 94'			Frag
Contig 95	890	'Assembly 1'	3	99.66%	Contig
0248-94(5-31-06)_005	647	In contig 'Contig 95'			Frag
0248-94-(6-12-06)_C05	855	In contig 'Contig 95'			Frag
0248-94-(6-16-06)_H09	888	In contig 'Contig 95'			Frag
Contig 96	899	'Assembly 1'	2	99.78%	Contig
0251-94(5-31-06)_011	826	In contig 'Contig 96'			Frag
0251-94-(6-16-06)_A10	898	In contig 'Contig 96'			Frag
Contig 97	1021	'Assembly 1'	2	99.71%	Contig
0253-94(5-31-06)_015	867	In contig 'Contig 97'			Frag
0253-94-(6-27-06)_E02	1018	In contig 'Contig 97'			Frag
Contig 98	903	'Assembly 1'	2	99.89%	Contig
0512-94-(6-8-06)_D02	806	In contig 'Contig 98'			Frag
0258-94(5-31-06)_010	902	In contig 'Contig 98'			Frag
Contig 99	906	'Assembly 1'	2	100.00%	Contig
0267-94(5-31-06)_011	334	In contig 'Contig 99'			Frag
0267-94-(6-16-06)_C10	906	In contig 'Contig 99'			Frag
Contig 100	836	'Assembly 1'	2	100.00%	Contig
0268-94-(6-16-06)_D10	836	In contig 'Contig 100'			Frag
0268-94(5-31-06)_013	801	In contig 'Contig 100'			Frag
Contig 101	920	'Assembly 1'	2	99.89%	Contig
0273-94(5-31-06)_008	811	In contig 'Contig 101'			Frag
0273-94-(6-16-06)_E10	920	In contig 'Contig 101'			Frag
Contig 102	898	'Assembly 1'	2	100.00%	Contig
0274-94-(6-16-06)_F10	857	In contig 'Contig 102'			Frag
0274-94(5-31-06)_010	887	In contig 'Contig 102'			Frag
Contig 103	882	'Assembly 1'	2	100.00%	Contig

0277-94-(6-16-06)_G10	882	In contig 'Contig 103'			Frag
0277-94(5-31-06)_016	865	In contig 'Contig 103'			Frag
Contig 104	1002	'Assembly 1'	3	99.60%	Contig
0053-94-D04(4-28-06)	731	In contig 'Contig 104'			Frag
0281-94(5-31-06)_007	901	In contig 'Contig 104'			Frag
0053-93-D07(4-21-06)	669	In contig 'Contig 104'			Frag
Contig 105	1010	'Assembly 1'	2	99.70%	Contig
0287-94(5-31-06)_004	880	In contig 'Contig 105'			Frag
0287-94-(6-27-06)_G02	1007	In contig 'Contig 105'			Frag
Contig 106	1001	'Assembly 1'	2	100.00%	Contig
0289-94(5-31-06)_008	834	In contig 'Contig 106'			Frag
0289-94-(6-27-06)_H02	1001	In contig 'Contig 106'			Frag
Contig 107	494	'Assembly 1'	2	100.00%	Contig
0290-94(5-31-06)_010	493	In contig 'Contig 107'			Frag
0290-94-(6-16-06truncated)_A11	494	In contig 'Contig 107'			Frag
Contig 108	899	'Assembly 1'	2	99.67%	Contig
0291-94(5-31-06)_012	899	In contig 'Contig 108'			Frag
0575-94-(6-8-06)_H08	845	In contig 'Contig 108'			Frag
Contig 109	886	'Assembly 1'	2	100.00%	Contig
0299-94(5-31-06)_011	404	In contig 'Contig 109'			Frag
0299-94-(6-16-06)_B11	886	In contig 'Contig 109'			Frag
Contig 110	1019	'Assembly 1'	2	99.90%	Contig
0308-94(5-31-06)_010	832	In contig 'Contig 110'			Frag
0308-94-(6-27-06)_E03	1018	In contig 'Contig 110'			Frag
Contig 111	1065	'Assembly 1'	3	99.81%	Contig
0314-94-(6-9-06)_C01	756	In contig 'Contig 111'			Frag
0314-94-(6-27-06)_F03	843	In contig 'Contig 111'			Frag
0264-94(5-31-06)_005	887	In contig 'Contig 111'			Frag
Contig 112	883	'Assembly 1'	2	99.89%	Contig
0320-94-(6-9-06)_H01	751	In contig 'Contig 112'			Frag
0560-94-(6-12-06)_C11	857	In contig 'Contig 112'			Frag
Contig 113	963	'Assembly 1'	2	100.00%	Contig
0321-94-(6-9-06)_A02	666	In contig 'Contig 113'			Frag
0321-94-(6-27-06)_G03	963	In contig 'Contig 113'			Frag
Contig 114	894	'Assembly 1'	2	100.00%	Contig
0322-94-(6-12-06)_A06	800	In contig 'Contig 114'			Frag
0322-94-(6-14-06)_C02	894	In contig 'Contig 114'			Frag
Contig 115	854	'Assembly 1'	2	100.00%	Contig
0324-94-(6-12-06)_B06	851	In contig 'Contig 115'			Frag
0324-94-(6-14-06)_D02	854	In contig 'Contig 115'			Frag
Contig 116	956	'Assembly 1'	3	99.37%	Contig
0327-94-(6-9-06)_F02	446	In contig 'Contig 116'			Frag

0327-94-(6-14-06)_G02	748	In contig 'Contig 116'			Frag
0705-94-(6-14-06)_G04	857	In contig 'Contig 116'			Frag
Contig 117	968	'Assembly 1'	2	99.38%	Contig
0330-94-(6-9-06)_H02	842	In contig 'Contig 117'			Frag
0330-94-(6-27-06)_A04	940	In contig 'Contig 117'			Frag
Contig 118	880	'Assembly 1'	2	100.00%	Contig
0334-94-(6-12-06)_D06	880	In contig 'Contig 118'			Frag
0334-94-(6-14-06)_H02	850	In contig 'Contig 118'			Frag
Contig 119	890	'Assembly 1'	2	100.00%	Contig
0337-94-(6-9-06bad)_E03	788	In contig 'Contig 119'			Frag
0337-94-(6-14-06)_A03	890	In contig 'Contig 119'			Frag
Contig 120	943	'Assembly 1'	2	100.00%	Contig
0338-94-(6-27-06)_C04	943	In contig 'Contig 120'			Frag
0338-94-(6-9-06)_F03	862	In contig 'Contig 120'			Frag
Contig 121	640	'Assembly 1'	3	99.84%	Contig
0340-94-(6-9-06Truncated)_H03	306	In contig 'Contig 121'			Frag
0340-94-(6-14-06Truncated)_B03	640	In contig 'Contig 121'			Frag
0340-94-(6-15-06)_B09	640	In contig 'Contig 121'			Frag
Contig 122	1014	'Assembly 1'	3	99.70%	Contig
0344-94-(6-9-06)_B04	798	In contig 'Contig 122'			Frag
0542-94-(6-8-06)_B06	856	In contig 'Contig 122'			Frag
0344-94-(6-27-06)_D04	968	In contig 'Contig 122'			Frag
Contig 123	911	'Assembly 1'	2	99.12%	Contig
0345-94-(6-9-06bad)_C04	909	In contig 'Contig 123'			Frag
0345-94-(6-14-06)_D03	908	In contig 'Contig 123'			Frag
Contig 124	956	'Assembly 1'	2	99.90%	Contig
0351-94-(6-9-06)_H04	804	In contig 'Contig 124'			Frag
0351-94-(6-27-06)_G04	955	In contig 'Contig 124'			Frag
Contig 125	1243	'Assembly 1'	2	100.00%	Contig
0353-94-(6-12-06)_G06	814	In contig 'Contig 125'			Frag
0266-94(5-31-06)_009	847	In contig 'Contig 125'			Frag
Contig 126	943	'Assembly 1'	2	100.00%	Contig
0355-94-(6-12-06)_H06	816	In contig 'Contig 126'			Frag
0256-94(5-31-06)_006	875	In contig 'Contig 126'			Frag
Contig 127	883	'Assembly 1'	2	99.89%	Contig
0357-94-(6-12-06)_B07	808	In contig 'Contig 127'			Frag
0555-94-(6-12-06)_G10	852	In contig 'Contig 127'			Frag
Contig 128	945	'Assembly 1'	2	100.00%	Contig
0370-94-(6-12-06)_G08	838	In contig 'Contig 128'			Frag
0370-94-(6-27-06)_A05	945	In contig 'Contig 128'			Frag
Contig 129	998	'Assembly 1'	3	100.00%	Contig
0374-94-(6-12-06)_B09	759	In contig 'Contig 129'			Frag

1185-94-(6-15-06)_A07	874	In contig 'Contig 129'			Frag
0374-94-(6-27-06)_B05	998	In contig 'Contig 129'			Frag
Contig 130	936	'Assembly 1'	2	99.89%	Contig
0392-94-(6-8-06)_A12	873	In contig 'Contig 130'			Frag
0392-94-(6-27-06)_F05	935	In contig 'Contig 130'			Frag
Contig 131	921	'Assembly 1'	2	100.00%	Contig
0504-94-(6-8-06)_D01	889	In contig 'Contig 131'			Frag
0397-94-(6-8-06)_E12	921	In contig 'Contig 131'			Frag
Contig 132	943	'Assembly 1'	2	100.00%	Contig
0399-94-(6-8-06)_G12	762	In contig 'Contig 132'			Frag
0399-94-(6-27-06)_G05	943	In contig 'Contig 132'			Frag
Contig 133	963	'Assembly 1'	2	99.79%	Contig
0425-94-(6-16-06)_A01	895	In contig 'Contig 133'			Frag
0425-94-(6-27-06)_H05	960	In contig 'Contig 133'			Frag
Contig 134	905	'Assembly 1'	2	100.00%	Contig
0428-94-(6-27-06)_A06	862	In contig 'Contig 134'			Frag
0428-94-(6-16-06)_D01	867	In contig 'Contig 134'			Frag
Contig 135	941	'Assembly 1'	2	99.89%	Contig
0435-94-(6-16-06)_C02	420	In contig 'Contig 135'			Frag
0435-94-(6-27-06)_E06	941	In contig 'Contig 135'			Frag
Contig 136	946	'Assembly 1'	2	100.00%	Contig
0456-94-(6-16-06)_F04	888	In contig 'Contig 136'			Frag
0456-94-(6-27-06)_H06	945	In contig 'Contig 136'			Frag
Contig 137	1461	'Assembly 1'	3	99.86%	Contig
0466-94-(6-16-06)_H05	932	In contig 'Contig 137'			Frag
0182-94-F09(5-5-06poor)	563	In contig 'Contig 137'			Frag
0182-94-(6-16-06)_E08	850	In contig 'Contig 137'			Frag
Contig 138	985	'Assembly 1'	5	99.19%	Contig
0502-94-(6-8-06)_B01	793	In contig 'Contig 138'			Frag
0156-94-D06(5-9-06best)	779	In contig 'Contig 138'			Frag
0022-94-(6-16-06)_F07	872	In contig 'Contig 138'			Frag
0022-94_014(5-31-06)	921	In contig 'Contig 138'			Frag
0022-93-C11(4-21-06)	649	In contig 'Contig 138'			Frag
Contig 139	723	'Assembly 1'	3	100.00%	Contig
0505-94-(6-8-06)_E01	597	In contig 'Contig 139'			Frag
0222-94-G09(5-10-06)	706	In contig 'Contig 139'			Frag
0169-94-B03(5-10-06)	717	In contig 'Contig 139'			Frag
Contig 140	682	'Assembly 1'	2	100.00%	Contig
0508-94-(6-8-06)_H01	682	In contig 'Contig 140'			Frag
0508-94-(6-8-06bad)_H01	682	In contig 'Contig 140'			Frag
Contig 141	802	'Assembly 1'	2	99.63%	Contig
0510-94-(6-8-06)_B02	713	In contig 'Contig 141'			Frag

0697-94-(6-12-06)_F12	796	In contig 'Contig 141'			Frag
Contig 142	1153	'Assembly 1'	2	99.91%	Contig
0557-94-(6-12-06)_A11	847	In contig 'Contig 142'			Frag
1121-94-(6-9-06)_E09	896	In contig 'Contig 142'			Frag
Contig 143	920	'Assembly 1'	3	99.89%	Contig
0224-94-A10(5-10-06)	735	In contig 'Contig 143'			Frag
0848-94-(6-5-06)_H06	807	In contig 'Contig 143'			Frag
0569-94-(6-8-06)_D08	920	In contig 'Contig 143'			Frag
Contig 144	946	'Assembly 1'	2	99.79%	Contig
0585-94-(6-8-06)_H09	898	In contig 'Contig 144'			Frag
0018-94_006(5-31-06)	843	In contig 'Contig 144'			Frag
Contig 145	898	'Assembly 1'	3	85.08%	Contig
0601-94-(6-6-06)_A01	644	In contig 'Contig 145'			Frag
1165-94-(6-15-06)_D05	768	In contig 'Contig 145'			Frag
0590-94-(6-8-06)_E10	895	In contig 'Contig 145'			Frag
Contig 146	798	'Assembly 1'	2	100.00%	Contig
0602-94-(6-12-06)_F11	717	In contig 'Contig 146'			Frag
0602-94-(6-14-06)_H03	798	In contig 'Contig 146'			Frag
Contig 147	867	'Assembly 1'	2	99.88%	Contig
0187-94-D05(5-10-06)	645	In contig 'Contig 147'			Frag
0623-94-(6-6-06)_G03	867	In contig 'Contig 147'			Frag
Contig 148	928	'Assembly 1'	3	99.35%	Contig
0188-94-E05(5-10-06)	712	In contig 'Contig 148'			Frag
0188-94-D10(5-5-06)	614	In contig 'Contig 148'			Frag
0629-94-(6-6-06)_E04	923	In contig 'Contig 148'			Frag
Contig 149	956	'Assembly 1'	2	100.00%	Contig
0631-94-(6-6-06)_G04	880	In contig 'Contig 149'			Frag
0339-94-(6-9-06)_G03	905	In contig 'Contig 149'			Frag
Contig 150	1236	'Assembly 1'	2	100.00%	Contig
0662-94-(6-6-06)_F08	844	In contig 'Contig 150'			Frag
0675-94-(6-6-06)_C10	896	In contig 'Contig 150'			Frag
Contig 151	1188	'Assembly 1'	2	99.75%	Contig
0673-94-(6-12-06)_D12	874	In contig 'Contig 151'			Frag
0620-94-(6-6-06)_D03	838	In contig 'Contig 151'			Frag
Contig 152	1227	'Assembly 1'	3	99.59%	Contig
0682-94-(6-6-06)_B11	856	In contig 'Contig 152'			Frag
0015-94_015(5-31-06)	843	In contig 'Contig 152'			Frag
0015-94-B12(4-21-06)	712	In contig 'Contig 152'			Frag
Contig 153	964	'Assembly 1'	5	99.79%	Contig
0213-94-F08(5-10-06)	671	In contig 'Contig 153'			Frag
0685-94-(6-6-06)_E11	908	In contig 'Contig 153'			Frag
1122-94-(6-9-06)_F09	894	In contig 'Contig 153'			Frag

0231-94(5-31-06)_016	855	In contig 'Contig 153'			Frag
0011-94_007(5-31-06)	865	In contig 'Contig 153'			Frag
Contig 154	950	'Assembly 1'	2	99.89%	Contig
0689-94-(6-6-06)_A12	744	In contig 'Contig 154'			Frag
0947-94-(6-15-06)_B04	912	In contig 'Contig 154'			Frag
Contig 155	866	'Assembly 1'	2	99.08%	Contig
0703-94-(6-7-06)_C01	843	In contig 'Contig 155'			Frag
0593-94-(6-8-06)_H10	856	In contig 'Contig 155'			Frag
Contig 156	886	'Assembly 1'	3	100.00%	Contig
0706-94-(6-7-06)_F01	808	In contig 'Contig 156'			Frag
0712-94-(6-7-06)_D02	878	In contig 'Contig 156'			Frag
0677-94-(6-6-06)_E10	834	In contig 'Contig 156'			Frag
Contig 157	999	'Assembly 1'	7	99.60%	Contig
0206-94-B12(5-5-06)	621	In contig 'Contig 157'			Frag
0206-94-G07(5-10-06)	711	In contig 'Contig 157'			Frag
1062-94-(6-2-06)_D08	737	In contig 'Contig 157'			Frag
0722-94-(6-7-06)_F03	882	In contig 'Contig 157'			Frag
0939-94-(6-15-06)_B03	828	In contig 'Contig 157'			Frag
0845-94-(6-5-06)_E06	861	In contig 'Contig 157'			Frag
0751-94-(6-7-06)_C07	759	In contig 'Contig 157'			Frag
Contig 158	1152	'Assembly 1'	2	100.00%	Contig
0723-94-(6-7-06)_G03	828	In contig 'Contig 158'			Frag
0589-94-(6-8-06)_D10	873	In contig 'Contig 158'			Frag
Contig 159	881	'Assembly 1'	2	98.98%	Contig
0741-94-(6-7-06)_A06	881	In contig 'Contig 159'			Frag
1070-94-(6-14-06)_H09	838	In contig 'Contig 159'			Frag
Contig 160	950	'Assembly 1'	2	99.58%	Contig
0761-94-(6-7-06)_E08	864	In contig 'Contig 160'			Frag
1013-94-(6-2-06)_D02	719	In contig 'Contig 160'			Frag
Contig 161	1365	'Assembly 1'	2	100.00%	Contig
0764-94-(6-7-06)_H08	796	In contig 'Contig 161'			Frag
0132-94-D03(5-9-06)	747	In contig 'Contig 161'			Frag
Contig 162	947	'Assembly 1'	3	99.47%	Contig
0610-94-(6-6-06)_B02	810	In contig 'Contig 162'			Frag
0769-94-(6-7-06)_D09	896	In contig 'Contig 162'			Frag
0561-94-(6-12-06)_D11	883	In contig 'Contig 162'			Frag
Contig 163	1050	'Assembly 1'	2	97.05%	Contig
0772-94-(6-7-06)_F09	595	In contig 'Contig 163'			Frag
0912-94-(6-14-06)_G11	868	In contig 'Contig 163'			Frag
Contig 164	922	'Assembly 1'	2	100.00%	Contig
0783-94-(6-7-06)_H10	922	In contig 'Contig 164'			Frag
0368-94-(6-12-06)_E08	887	In contig 'Contig 164'			Frag

Contig 165	948	'Assembly 1'	2	99.68%	Contig
0240-94-A12(5-10-06)	755	In contig 'Contig 165'			Frag
0784-94-(6-7-06)_A11	947	In contig 'Contig 165'			Frag
Contig 166	1401	'Assembly 1'	3	100.00%	Contig
0586-94-(6-8-06Truncated)_A10	195	In contig 'Contig 166'			Frag
0787-94-(6-7-06)_C11	831	In contig 'Contig 166'			Frag
0924-94-(6-15-06)_C01	872	In contig 'Contig 166'			Frag
Contig 167	919	'Assembly 1'	3	99.78%	Contig
1044-94-(6-2-06)_C06	615	In contig 'Contig 167'			Frag
0812-94-(6-5-06)_D02	882	In contig 'Contig 167'			Frag
1044-94-(6-14-06)_B09	899	In contig 'Contig 167'			Frag
Contig 168	864	'Assembly 1'	2	100.00%	Contig
0832-94-(6-5-06)_H04	845	In contig 'Contig 168'			Frag
0832-94-(6-14-06)_H05	836	In contig 'Contig 168'			Frag
Contig 169	812	'Assembly 1'	3	100.00%	Contig
0837-94-(6-15-06)_A11	428	In contig 'Contig 169'			Frag
0837-94-(6-5-06)_E05	491	In contig 'Contig 169'			Frag
0837-94-(6-14-06)_B06	806	In contig 'Contig 169'			Frag
Contig 170	814	'Assembly 1'	2	100.00%	Contig
0840-94-(6-5-06)_H05	434	In contig 'Contig 170'			Frag
0809-94-(6-15-06)_E10	800	In contig 'Contig 170'			Frag
Contig 171	934	'Assembly 1'	2	100.00%	Contig
0516-94-(6-8-06)_H02	854	In contig 'Contig 171'			Frag
0850-94-(6-5-06)_B07	934	In contig 'Contig 171'			Frag
Contig 172	837	'Assembly 1'	2	98.45%	Contig
0852-94-(6-5-06)_D07	649	In contig 'Contig 172'			Frag
0099-93-F01(4-21-06)	667	In contig 'Contig 172'			Frag
Contig 173	894	'Assembly 1'	2	100.00%	Contig
0862-94-(6-5-06)_F08	879	In contig 'Contig 173'			Frag
1065-94-(6-2-06)_G08	891	In contig 'Contig 173'			Frag
Contig 174	1183	'Assembly 1'	2	99.49%	Contig
0868-94-(6-5-06)_D09	878	In contig 'Contig 174'			Frag
1119-94-(6-9-06)_C09	881	In contig 'Contig 174'			Frag
Contig 175	1185	'Assembly 1'	4	94.60%	Contig
0869-94-(6-5-06)_E09	791	In contig 'Contig 175'			Frag
0003-94-E04(4-20-06redo)	632	In contig 'Contig 175'			Frag
0003p_E06	655	In contig 'Contig 175'			Frag
0003-94_001(5-31-06)	826	In contig 'Contig 175'			Frag
Contig 176	881	'Assembly 1'	2	100.00%	Contig
0615-94-(6-6-06)_G02	788	In contig 'Contig 176'			Frag
0879-94-(6-5-06)_G10	881	In contig 'Contig 176'			Frag
Contig 177	939	'Assembly 1'	2	99.79%	Contig

0650-94-(6-6-06)_B07	856	In contig 'Contig 177'			Frag
0880-94-(6-5-06)_H10	938	In contig 'Contig 177'			Frag
Contig 178	804	'Assembly 1'	2	100.00%	Contig
0893-94-(6-14-06)_F07	804	In contig 'Contig 178'			Frag
0893-94-(6-5-06)_E12	762	In contig 'Contig 178'			Frag
Contig 179	893	'Assembly 1'	2	98.99%	Contig
0711-94-(6-7-06)_C02	752	In contig 'Contig 179'			Frag
0900-94-(6-14-06)_B08	888	In contig 'Contig 179'			Frag
Contig 180	964	'Assembly 1'	2	99.48%	Contig
0909-94-(6-14-06)_D11	835	In contig 'Contig 180'			Frag
1109-94-(6-9-06)_A08	876	In contig 'Contig 180'			Frag
Contig 181	670	'Assembly 1'	2	100.00%	Contig
0928-94-(6-15-06)_G01	285	In contig 'Contig 181'			Frag
0928-94-(6-16-06)_E11	670	In contig 'Contig 181'			Frag
Contig 182	871	'Assembly 1'	2	100.00%	Contig
0932-94-(6-15-06)_C02	324	In contig 'Contig 182'			Frag
0932-94-(6-16-06)_H11	871	In contig 'Contig 182'			Frag
Contig 183	871	'Assembly 1'	2	100.00%	Contig
0934-94-(6-15-06)_E02	293	In contig 'Contig 183'			Frag
0934-94-(6-16-06)_B12	871	In contig 'Contig 183'			Frag
Contig 184	876	'Assembly 1'	2	100.00%	Contig
0935-94-(6-15-06)_F02	632	In contig 'Contig 184'			Frag
0935-94-(6-16-06)_C12	828	In contig 'Contig 184'			Frag
Contig 185	936	'Assembly 1'	2	99.89%	Contig
0937-94-(6-15-06)_H02	625	In contig 'Contig 185'			Frag
0937-94-(6-16-06)_E12	936	In contig 'Contig 185'			Frag
Contig 186	915	'Assembly 1'	2	100.00%	Contig
1012-94-(6-2-06)_C02	798	In contig 'Contig 186'			Frag
0903-94-(6-14-06)_F10	906	In contig 'Contig 186'			Frag
Contig 187	1256	'Assembly 1'	2	99.76%	Contig
1022-94-(6-2-06)_E03	893	In contig 'Contig 187'			Frag
0692-94-(6-6-06)_D12	904	In contig 'Contig 187'			Frag
Contig 188	846	'Assembly 1'	2	100.00%	Contig
1024-94-(6-2-06)_G03	237	In contig 'Contig 188'			Frag
1024-94-(6-14-06)_E08	846	In contig 'Contig 188'			Frag
Contig 189	852	'Assembly 1'	2	100.00%	Contig
1038-94-(6-2-06)_E05	686	In contig 'Contig 189'			Frag
0467-94-(6-16-06)_A06	847	In contig 'Contig 189'			Frag
Contig 190	1263	'Assembly 1'	2	99.76%	Contig
1043-94-(6-2-06)_B06	823	In contig 'Contig 190'			Frag
0138-94-B04(5-9-06)	731	In contig 'Contig 190'			Frag
Contig 191	847	'Assembly 1'	3	100.00%	Contig

1045-94-(6-2-06)_D06	414	In contig 'Contig 191'			Frag
1045-94-(6-15-06)_F12	819	In contig 'Contig 191'			Frag
1045-94-(6-14-06)_C09	816	In contig 'Contig 191'			Frag
Contig 192	990	'Assembly 1'	2	100.00%	Contig
1049-94-(6-2-06)_H06	872	In contig 'Contig 192'			Frag
0754-94-(6-7-06)_F07	833	In contig 'Contig 192'			Frag
Contig 193	933	'Assembly 1'	2	98.29%	Contig
1051-94-(6-2-06)_B07	859	In contig 'Contig 193'			Frag
0781-94-(6-7-06)_F10	861	In contig 'Contig 193'			Frag
Contig 194	842	'Assembly 1'	2	99.29%	Contig
1055-94-(6-2-06)_F07	539	In contig 'Contig 194'			Frag
1055-94-(6-14-06)_D09	838	In contig 'Contig 194'			Frag
Contig 195	901	'Assembly 1'	2	84.46%	Contig
0146-94-B05(5-9-06)	412	In contig 'Contig 195'			Frag
1059-94-(6-2-06)_A08	901	In contig 'Contig 195'			Frag
Contig 196	881	'Assembly 1'	2	99.77%	Contig
1066-94-(6-14-06)_F09	879	In contig 'Contig 196'			Frag
1066-94-(6-2-06)_H08	837	In contig 'Contig 196'			Frag
Contig 197	880	'Assembly 1'	2	98.98%	Contig
1074-94-(6-2-06)_H09	880	In contig 'Contig 197'			Frag
0376-94-(6-12-06)_C09	835	In contig 'Contig 197'			Frag
Contig 198	986	'Assembly 1'	3	98.78%	Contig
1093-94-(6-2-06)_C12	852	In contig 'Contig 198'			Frag
0632-94-(6-6-06)_H04	825	In contig 'Contig 198'			Frag
0820-94-(6-5-06)_D03	781	In contig 'Contig 198'			Frag
Contig 199	763	'Assembly 1'	2	99.48%	Contig
1095-94-(6-2-06)_E12	692	In contig 'Contig 199'			Frag
1095-94-(6-14-06)_C10	763	In contig 'Contig 199'			Frag
Contig 200	1590	'Assembly 1'	2	100.00%	Contig
1098-94-(6-2-06)_H12	898	In contig 'Contig 200'			Frag
0757-94-(6-7-06)_A08	915	In contig 'Contig 200'			Frag
Contig 201	1262	'Assembly 1'	2	99.92%	Contig
1103-94-(6-9-06)_C07	859	In contig 'Contig 201'			Frag
0827-94-(6-5-06)_C04	911	In contig 'Contig 201'			Frag
Contig 202	1032	'Assembly 1'	2	97.77%	Contig
1117-94-(6-9-06)_A09	806	In contig 'Contig 202'			Frag
0794-94-(6-7-06)_B12	847	In contig 'Contig 202'			Frag
Contig 203	876	'Assembly 1'	2	99.77%	Contig
1129-94-(6-9-06)_E10	875	In contig 'Contig 203'			Frag
0680-94-(6-6-06)_H10	865	In contig 'Contig 203'			Frag
Contig 204	896	'Assembly 1'	2	99.55%	Contig
1132-94-(6-9-06)_H10	895	In contig 'Contig 204'			Frag

0816-94-(6-5-06)_H02	843	In contig 'Contig 204'			Frag
Contig 205	985	'Assembly 1'	2	100.00%	Contig
1157-94-(6-15-06)_G04	837	In contig 'Contig 205'			Frag
0364-94-(6-12-06)_A08	855	In contig 'Contig 205'			Frag
Contig 206	974	'Assembly 1'	2	99.90%	Contig
1173-94-(6-15-06)_C06	947	In contig 'Contig 206'			Frag
1020-94-(6-2-06)_C03	906	In contig 'Contig 206'			Frag
Singlets					
1180-94-(6-15-06)_G06	881	Not assembled			Frag
1182-94-(6-15-06)_H06	847	Not assembled			Frag
1187-94-(6-15-06)_B07	938	Not assembled			Frag
1188-94-(6-15-06)_C07	895	Not assembled			Frag
1192-94-(6-15-06)_D07	871	Not assembled			Frag
1193-94-(6-15-06)_E07	830	Not assembled			Frag
1194-94-(6-15-06)_F07	882	Not assembled			Frag
1301-94-(6-16-06)_C06	808	Not assembled			Frag
1305-94-(6-16-06)_G06	719	Not assembled			Frag
1307-94-(6-16-06)_A07	901	Not assembled			Frag
1308-94-(6-16-06)_B07	865	Not assembled			Frag
1310-94-(6-16-06)_D07	923	Not assembled			Frag
0006-93-B05(4-20-06)	628	Not assembled			Frag
0006-94-C05(4-20-06)	683	Not assembled			Frag
006-94-E05(4-28-06)	650	Not assembled			Frag
0007for_D05'	687	Not assembled			Frag
0008-94-G05(4-20-06)	701	Not assembled			Frag
0010-93-G12(4-21-06)	346	Not assembled			Frag
0010-94_005(5-31-06)	882	Not assembled			Frag
0012-94_009(5-31-06)	840	Not assembled			Frag
0013-94_011(5-31-06)	857	Not assembled			Frag
0014-94_013(5-31-06)	0	Not assembled			Frag
0016-93-A12(4-21-06)	756	Not assembled			Frag
0016-94_002(5-31-06)	845	Not assembled			Frag
0017-94_004(5-31-06)	895	Not assembled			Frag
0019-94_008(5-31-06)	792	Not assembled			Frag
0020-94_010(5-31-06)	895	Not assembled			Frag
0021-94_012(5-31-06)	885	Not assembled			Frag
0023-94_016(5-31-06)	845	Not assembled			Frag
0024-94(5-31-06)_001	933	Not assembled			Frag
0026-94-(6-12-06)_A01	707	Not assembled			Frag
0027-94-C01(4-28-06)	1	Not assembled			Frag
0029-94-D01(4-28-06)	674	Not assembled			Frag
0030-94-E01(4-28-06)	706	Not assembled			Frag

0032-93-A10(4-21-06)	643	Not assembled			Frag
0032-94-G01(4-28-06)	729	Not assembled			Frag
0037-94-D02(4-28-06)	471	Not assembled			Frag
0042-93-G08(4-21-06)	675	Not assembled			Frag
0045-94-D03(4-28-06)	708	Not assembled			Frag
0046-94-E03(4-28-06)	659	Not assembled			Frag
0047-93-B08(4-21-06)	675	Not assembled			Frag
0047-94-F03(4-28-06)	718	Not assembled			Frag
0048-94-G03(4-28-06)	670	Not assembled			Frag
0052-94-C04(4-28-06)	697	Not assembled			Frag
0054-94-E04(4-28-06)	729	Not assembled			Frag
0060-94-C05(4-28-06)	758	Not assembled			Frag
0063-94-F05(4-28-06)	711	Not assembled			Frag
0065-94-H05(4-28-06)	697	Not assembled			Frag
0071_B05(Rev4-21-06)	675	Not assembled			Frag
0071_F06(For4-28-06)	705	Not assembled			Frag
0072-94-F01(5-9-06)	684	Not assembled			Frag
0074-93-G04(4-21-06)	682	Not assembled			Frag
0074-94-A07(4-28-06)	719	Not assembled			Frag
0075-94-B07(4-28-06)	768	Not assembled			Frag
0079-93-B04(4-21-06)	726	Not assembled			Frag
0085-94-D08(4-28-06)	788	Not assembled			Frag
0086-94-E08(4-28-06)	709	Not assembled			Frag
0087-93-B03(4-21-06)	665	Not assembled			Frag
0087-94-F08(4-28-06)	698	Not assembled			Frag
0091-94-B09(4-28-06)	640	Not assembled			Frag
0095-93-B02(4-21-06)	719	Not assembled			Frag
0097-94-H09(4-28-06)	680	Not assembled			Frag
0099-94-B10(4-28-06)	786	Not assembled			Frag
0105-94-H10(4-28-06)	705	Not assembled			Frag
0106-94-A11(4-28-06)	696	Not assembled			Frag
0107-94-(6-12-06)_A04	861	Not assembled			Frag
0110-94-E11(4-28-06)	734	Not assembled			Frag
0111-94-F11(4-28-06)	717	Not assembled			Frag
0112-94-(6-12-06)_D04	807	Not assembled			Frag
0115-94-B12(4-28-06)	753	Not assembled			Frag
0117-94-D12(4-28-06)	675	Not assembled			Frag
0118-94-E12(4-28-06)	721	Not assembled			Frag
0119-94-F12(4-28-06)	664	Not assembled			Frag
0120-94-A02(5-9-06)	709	Not assembled			Frag
0121-94-H12(4-28-06)	706	Not assembled			Frag
0122-94-B02(5-9-06)	0	Not assembled			Frag

0123-94-C02(5-9-06)	728	Not assembled			Frag
0124-94-D02(5-9-06)	794	Not assembled			Frag
0127-94(5-31-06)_007	819	Not assembled			Frag
0128-94(5-31-06)_009	850	Not assembled			Frag
0129-94-A03(5-9-06)	748	Not assembled			Frag
0130-94-B03(5-9-06)	605	Not assembled			Frag
0131-94-C03(5-9-06)	684	Not assembled			Frag
0133-94-E03(5-9-06)	712	Not assembled			Frag
0134-94-F03(5-9-06)	728	Not assembled			Frag
0136-94(5-31-06)_011	759	Not assembled			Frag
0137-94-A04(5-9-06)	710	Not assembled			Frag
0139-94-C04(5-9-06)	726	Not assembled			Frag
0140-94-D04(5-9-06)	714	Not assembled			Frag
0141-94-E04(5-9-06)	675	Not assembled			Frag
0143-94(5-31-06)_013	828	Not assembled			Frag
0144-94(5-31-06)_015	865	Not assembled			Frag
0147-94-C05(5-9-06)	718	Not assembled			Frag
0148-94-D05(5-9-06)	740	Not assembled			Frag
0149-94-E05(5-9-06)	654	Not assembled			Frag
0159-94(5-31-06)_004	822	Not assembled			Frag
0161-94-A07(5-5-06)	471	Not assembled			Frag
0162-94-B07(5-5-06)	697	Not assembled			Frag
0163-94-C07(5-5-06)	756	Not assembled			Frag
0164-94-D07(5-5-06)	644	Not assembled			Frag
0172-94-E03(5-10-06)	702	Not assembled			Frag
0175-94-H03(5-10-06)	766	Not assembled			Frag
0177-94-B04(5-10-06)	746	Not assembled			Frag
0179-94-D04(5-10-06)	737	Not assembled			Frag
0180-94-E04(5-10-06)	708	Not assembled			Frag
0185-94-B05(5-10-06)	733	Not assembled			Frag
0192-94-A06(5-10-06)	698	Not assembled			Frag
0195-94-D06(5-10-06)	722	Not assembled			Frag
0198-94-(6-16-06)_H08	863	Not assembled			Frag
0199-94(5-31-06)_008	945	Not assembled			Frag
0200-94-A07(5-10-06)	756	Not assembled			Frag
0208-94-A08(5-10-06)	744	Not assembled			Frag
0209-94-B08(5-10-06)	711	Not assembled			Frag
0210-94-C08(5-10-06)	752	Not assembled			Frag
0211-94-D08(5-10-06)	756	Not assembled			Frag
0214-94(5-31-06)_010	757	Not assembled			Frag
0215-94(5-31-06)_012	870	Not assembled			Frag
0217-94-(6-16-06)_B09	929	Not assembled			Frag

0219-94-D09(5-10-06)	768	Not assembled			Frag
0220-94E09(5-10-06)	700	Not assembled			Frag
0221-94-F09(5-10-06)	713	Not assembled			Frag
0223-94-H09(5-10-06)	784	Not assembled			Frag
0225-94-B10(5-10-06)	736	Not assembled			Frag
0226-94-C10(5-10-06)	759	Not assembled			Frag
0227-94-D10(5-10-06)	730	Not assembled			Frag
0228-94-E10(5-10-06)	738	Not assembled			Frag
0229-94-F10(5-10-06)	689	Not assembled			Frag
0230-94(5-31-06)_014	930	Not assembled			Frag
0232-94-A11(5-10-06)	830	Not assembled			Frag
0233-94-B11(5-10-06)	674	Not assembled			Frag
0234-94-C11(5-10-06)	748	Not assembled			Frag
0235-94-D11(5-10-06)	720	Not assembled			Frag
0237-94-F11(5-10-06)	712	Not assembled			Frag
0238-94-G11(5-10-06)	714	Not assembled			Frag
0239-94-H11(5-10-06)	669	Not assembled			Frag
0241-94-B12(5-10-06)	748	Not assembled			Frag
0242-94-C12(5-10-06)	720	Not assembled			Frag
0244-94-E12(5-10-06)	663	Not assembled			Frag
0245-94-F12(5-10-06)	725	Not assembled			Frag
0247-94(5-31-06)_003	874	Not assembled			Frag
0249-94(5-31-06)_007	890	Not assembled			Frag
0250-94(5-31-06)_009	784	Not assembled			Frag
0252-94(5-31-06)_013	837	Not assembled			Frag
0254-94-(6-16-06)_B10	904	Not assembled			Frag
0255-94(5-31-06)_004	907	Not assembled			Frag
0257-94(5-31-06)_008	805	Not assembled			Frag
0259-94(5-31-06)_012	932	Not assembled			Frag
0260-94(5-31-06)_014	852	Not assembled			Frag
0261-94(5-31-06)_016	857	Not assembled			Frag
0262-94(5-31-06)_001	941	Not assembled			Frag
0263-94(5-31-06)_003	886	Not assembled			Frag
0265-94(5-31-06)_007	843	Not assembled			Frag
0269-94(5-31-06)_015	851	Not assembled			Frag
0270-94(5-31-06)_002	892	Not assembled			Frag
0271-94(5-31-06)_004	870	Not assembled			Frag
0272-94(5-31-06)_006	882	Not assembled			Frag
0275-94(5-31-06)_012	893	Not assembled			Frag
0276-94(5-31-06)_014	860	Not assembled			Frag
0278-94(5-31-06)_001	810	Not assembled			Frag
0280-94(5-31-06)_005	915	Not assembled			Frag

0282-94(5-31-06)_009	940	Not assembled			Frag
0283-94(5-31-06)_011	773	Not assembled			Frag
0284-94(5-31-06)_013	874	Not assembled			Frag
0285-94(5-31-06)_015	852	Not assembled			Frag
0286-94(5-31-06)_002	817	Not assembled			Frag
0288-94(5-31-06)_006	0	Not assembled			Frag
0292-94(5-31-06)_014	893	Not assembled			Frag
0294-94(5-31-06)_001	944	Not assembled			Frag
0295-94(5-31-06)_003	882	Not assembled			Frag
0296-94(5-31-06)_005	920	Not assembled			Frag
0297-94(5-31-06)_007	883	Not assembled			Frag
0298-94(5-31-06)_009	869	Not assembled			Frag
0300-94(5-31-06)_013	820	Not assembled			Frag
0303-94(5-31-06)_002	947	Not assembled			Frag
0305-94(5-31-06)_004	883	Not assembled			Frag
0306-94(5-31-06)_006	858	Not assembled			Frag
0307-94-(6-12-06)_F05	855	Not assembled			Frag
0309-94(5-31-06)_012	802	Not assembled			Frag
0311-94(5-31-06)_016	813	Not assembled			Frag
0312-94-(6-9-06)_A01	868	Not assembled			Frag
0313-94-(6-9-06)_B01	776	Not assembled			Frag
0315-94-(6-9-06)_D01	814	Not assembled			Frag
0316-94-(6-9-06)_E01	868	Not assembled			Frag
0319-94-(6-9-06)_G01	811	Not assembled			Frag
0323-94-(6-9-06)_C02	788	Not assembled			Frag
0325-94-(6-14-06)_E02	879	Not assembled			Frag
0326-94-(6-14-06)_F02	874	Not assembled			Frag
0328-94-(6-9-06)_G02	823	Not assembled			Frag
0329-94-(6-27-06)_H03	458	Not assembled			Frag
0332-94-(6-9-06)_A03	849	Not assembled			Frag
0336-94-(6-9-06)_D03	897	Not assembled			Frag
0346-94-(6-9-06)_D04	892	Not assembled			Frag
0347-94-(6-12-06)_F06	762	Not assembled			Frag
0349-94-(6-9-06)_F04	777	Not assembled			Frag
0350-94-(6-9-06)_G04	757	Not assembled			Frag
0352-94-(6-27-06)_H04	657	Not assembled			Frag
0356-94-(6-12-06)_A07	862	Not assembled			Frag
0358-94-(6-12-06)_C07	818	Not assembled			Frag
0359-94-(6-12-06)_D07	861	Not assembled			Frag
0360-94-(6-12-06)_E07	824	Not assembled			Frag
0361-94-(6-12-06)_F07	841	Not assembled			Frag
0362-94-(6-12-06)_G07	862	Not assembled			Frag

0363-94-(6-12-06)_H07	881	Not assembled			Frag
0365-94-(6-12-06)_B08	831	Not assembled			Frag
0367-94-(6-12-06)_D08	868	Not assembled			Frag
0369-94-(6-12-06)_F08	855	Not assembled			Frag
0372-94-(6-12-06)_H08	851	Not assembled			Frag
0373-94-(6-12-06)_A09	859	Not assembled			Frag
0377-94-(6-12-06)_D09	865	Not assembled			Frag
0378-94-(6-12-06)_E09	857	Not assembled			Frag
0379-94-(6-12-06)_F09	859	Not assembled			Frag
0380-94-(6-12-06)_G09	804	Not assembled			Frag
0381-94-(6-12-06)_H09	893	Not assembled			Frag
0382-94-(6-12-06)_A10	892	Not assembled			Frag
0385-94-(6-12-06)_B10	863	Not assembled			Frag
0387-94-(6-12-06)_D10	873	Not assembled			Frag
0388-94-(6-12-06)_E10	888	Not assembled			Frag
0390-94-(6-8-06)_G11	828	Not assembled			Frag
0391-94-(6-8-06)_H11	37	Not assembled			Frag
0391-94-(6-27-06)_E05	28	Not assembled			Frag
0393-94-(6-8-06)_B12	963	Not assembled			Frag
0394-94-(6-8-06)_C12	897	Not assembled			Frag
0398-94-(6-8-06)_F12	762	Not assembled			Frag
0400-94-(6-8-06)_H12	922	Not assembled			Frag
0426-94-(6-16-06)_B01	857	Not assembled			Frag
0427-94-(6-16-06)_C01	935	Not assembled			Frag
0429-94-(6-27-06)_B06	991	Not assembled			Frag
0430-94-(6-16-06)_F01	720	Not assembled			Frag
0431-94-(6-16-06)_G01	600	Not assembled			Frag
0433-94-(6-27-06)_D06	1014	Not assembled			Frag
0434-94-(6-16-06)_B02	915	Not assembled			Frag
0436-94-(6-16-06)_D02	876	Not assembled			Frag
0437-94-(6-16-06)_E02	893	Not assembled			Frag
0438-94-(6-16-06)_F02	906	Not assembled			Frag
0439-94-(6-16-06)_G02	857	Not assembled			Frag
0440-94-(6-16-06)_H02	888	Not assembled			Frag
0442-94-(6-16-06)_B03	0	Not assembled			Frag
0444-94-(6-16-06)_C03	937	Not assembled			Frag
0445-94-(6-16-06)_D03	895	Not assembled			Frag
0446-94-(6-16-06)_E03	750	Not assembled			Frag
0447-94-(6-16-06)_F03	866	Not assembled			Frag
0449-94-(6-27-06)_G06	976	Not assembled			Frag
0450-94-(6-16-06)_H03	709	Not assembled			Frag
0451-94-(6-16-06)_A04	933	Not assembled			Frag

0452-94-(6-16-06)_B04	881	Not assembled			Frag
0453-94-(6-16-06)_C04	866	Not assembled			Frag
0454-94-(6-16-06)_D04	860	Not assembled			Frag
0455-94-(6-16-06)_E04	922	Not assembled			Frag
0457-94-(6-16-06)_G04	699	Not assembled			Frag
0459-94-(6-16-06)_A05	855	Not assembled			Frag
0460-94-(6-16-06)_B05	822	Not assembled			Frag
0462-94-(6-16-06)_D05	872	Not assembled			Frag
0463-94-(6-16-06)_E05	631	Not assembled			Frag
0464-94-(6-16-06)_F05	881	Not assembled			Frag
0465-94-(6-16-06)_G05	776	Not assembled			Frag
0468-94-(6-16-06)_B06	782	Not assembled			Frag
0503-94-(6-8-06)_C01	840	Not assembled			Frag
0506-94-(6-8-06)_F01	794	Not assembled			Frag
0507-94-(6-8-06)_G01	852	Not assembled			Frag
0509-94-(6-8-06)_A02	607	Not assembled			Frag
0511-94-(6-8-06)_C02	823	Not assembled			Frag
0513-94-(6-8-06)_E02	786	Not assembled			Frag
0514-94-(6-8-06)_F02	741	Not assembled			Frag
0515-94-(6-8-06)_G02	826	Not assembled			Frag
0517-94-(6-8-06)_A03	860	Not assembled			Frag
0518-94-(6-8-06)_B03	748	Not assembled			Frag
0519-94-(6-8-06)_C03	918	Not assembled			Frag
0520-94-(6-8-06)_D03	856	Not assembled			Frag
0521-94-(6-8-06)_E03	863	Not assembled			Frag
0522-94-(6-8-06)_F03	912	Not assembled			Frag
0523-94-(6-8-06)_G03	837	Not assembled			Frag
0524-94-(6-8-06)_H03	921	Not assembled			Frag
0525-94-(6-8-06)_A04	927	Not assembled			Frag
0526-94-(6-8-06)_B04	887	Not assembled			Frag
0527-94-(6-8-06)_C04	885	Not assembled			Frag
0528-94-(6-8-06)_D04	837	Not assembled			Frag
0529-94-(6-8-06)_E04	831	Not assembled			Frag
0530-94-(6-8-06)_F04	930	Not assembled			Frag
0531-94-(6-8-06)_G04	838	Not assembled			Frag
0532-94-(6-8-06)_H04	856	Not assembled			Frag
0533-94-(6-8-06)_A05	794	Not assembled			Frag
0534-94-(6-8-06)_B05	865	Not assembled			Frag
0535-94-(6-8-06)_C05	808	Not assembled			Frag
0536-94-(6-8-06)_D05	871	Not assembled			Frag
0537-94-(6-8-06)_E05	878	Not assembled			Frag
0538-94-(6-8-06)_F05	866	Not assembled			Frag

0539-94-(6-8-06)_G05	890	Not assembled			Frag
0540-94-(6-8-06)_H05	832	Not assembled			Frag
0541-94-(6-8-06)_A06	854	Not assembled			Frag
0543-94-(6-8-06)_C06	880	Not assembled			Frag
0544-94-(6-8-06)_D06	822	Not assembled			Frag
0545-94-(6-8-06)_E06	856	Not assembled			Frag
0546-94-(6-8-06)_F06	859	Not assembled			Frag
0547-94-(6-8-06)_G06	891	Not assembled			Frag
0548-94-(6-8-06)_H06	858	Not assembled			Frag
0549-94-(6-12-06)_F10	812	Not assembled			Frag
0556-94-(6-12-06)_H10	800	Not assembled			Frag
0562-94-(6-8-06)_H07	724	Not assembled			Frag
0566-94-(6-8-06)_A08	863	Not assembled			Frag
0567-94-(6-8-06)_B08	848	Not assembled			Frag
0568-94-(6-8-06)_C08	888	Not assembled			Frag
0570-94-(6-8-06)_E08	892	Not assembled			Frag
0571-94-(6-8-06)_F08	830	Not assembled			Frag
0572-94-(6-8-06)_G08	755	Not assembled			Frag
0576-94-(6-12-06)_E11	650	Not assembled			Frag
0577-94-(6-8-06)_B09	875	Not assembled			Frag
0578-94-(6-8-06)_C09	912	Not assembled			Frag
0580-94-(6-8-06)_D09	837	Not assembled			Frag
0581-94-(6-8-06)_E09	931	Not assembled			Frag
0583-94-(6-8-06)_F09	881	Not assembled			Frag
0584-94-(6-8-06)_G09	791	Not assembled			Frag
0587-94-(6-8-06)_B10	831	Not assembled			Frag
0588-94-(6-8-06)_C10	894	Not assembled			Frag
0591-94-(6-8-06)_F10	788	Not assembled			Frag
0592-94-(6-8-06)_G10	856	Not assembled			Frag
0594-94-(6-8-06)_A11	882	Not assembled			Frag
0595-94-(6-8-06)_B11	857	Not assembled			Frag
0596-94-(6-8-06)_C11	894	Not assembled			Frag
0597-94-(6-8-06)_D11	846	Not assembled			Frag
0598-94-(6-8-06)_E11	766	Not assembled			Frag
0599-94-(6-8-06)_F11	882	Not assembled			Frag
0603-94-(6-6-06)_C01	742	Not assembled			Frag
0604-94-(6-6-06)_D01	819	Not assembled			Frag
0605-94-(6-6-06)_E01	830	Not assembled			Frag
0606-94-(6-6-06)_F01	834	Not assembled			Frag
0607-94-(6-6-06)_G01	744	Not assembled			Frag
0609-94-(6-6-06)_A02	808	Not assembled			Frag
0611-94-(6-6-06)_C02	903	Not assembled			Frag

0612-94-(6-6-06)_D02	848	Not assembled			Frag
0613-94-(6-6-06)_E02	819	Not assembled			Frag
0614-94-(6-6-06)_F02	855	Not assembled			Frag
0616-94-(6-6-06)_H02	833	Not assembled			Frag
0617-94-(6-6-06)_A03	823	Not assembled			Frag
0619-94-(6-6-06)_C03	900	Not assembled			Frag
0621-94-(6-6-06)_E03	876	Not assembled			Frag
0624-94-(6-6-06)_H03	905	Not assembled			Frag
0625-94-(6-6-06)_A04	698	Not assembled			Frag
0626-94-(6-6-06)_B04	779	Not assembled			Frag
0627-94-(6-6-06)_C04	887	Not assembled			Frag
0628-94-(6-6-06)_D04	865	Not assembled			Frag
0630-94-(6-6-06)_F04	902	Not assembled			Frag
0633-94-(6-6-06)_A05	830	Not assembled			Frag
0634-94-(6-6-06)_B05	885	Not assembled			Frag
0635-94-(6-6-06)_C05	923	Not assembled			Frag
0636-94-(6-6-06)_D05	900	Not assembled			Frag
0638-94-(6-6-06)_F05	891	Not assembled			Frag
0639-94-(6-6-06)_G05	886	Not assembled			Frag
0640-94-(6-6-06)_H05	862	Not assembled			Frag
0641-94-(6-6-06)_A06	902	Not assembled			Frag
0642-94-(6-6-06)_B06	832	Not assembled			Frag
0643-94-(6-6-06)_C06	776	Not assembled			Frag
0644-94-(6-6-06)_D06	820	Not assembled			Frag
0645-94-(6-6-06)_E06	818	Not assembled			Frag
0647-94-(6-6-06)_G06	832	Not assembled			Frag
0648-94(6-6-06)_H06	780	Not assembled			Frag
0649-94-(6-6-06)_A07	754	Not assembled			Frag
0652-94-(6-6-06)_D07	856	Not assembled			Frag
0653-94-(6-6-06)_E07	818	Not assembled			Frag
0654-94-(6-6-06)_F07	881	Not assembled			Frag
0655-94-(6-6-06)_G07	817	Not assembled			Frag
0656-94-(6-6-06)_H07	875	Not assembled			Frag
0657-94-(6-6-06)_A08	836	Not assembled			Frag
0658-94-(6-6-06)_B08	870	Not assembled			Frag
0659-94-(6-6-06)_C08	860	Not assembled			Frag
0660-94-(6-6-06)_D08	753	Not assembled			Frag
0661-94-(6-6-06)_E08	863	Not assembled			Frag
0663-94-(6-6-06)_G08	857	Not assembled			Frag
0664-94-(6-6-06)_H08	856	Not assembled			Frag
0665-94-(6-6-06)_A09	887	Not assembled			Frag
0666-94-(6-6-06)_B09	840	Not assembled			Frag

0667-94-(6-6-06)_C09	832	Not assembled			Frag
0668-94-(6-6-06)_D09	865	Not assembled			Frag
0671-94-(6-6-06)_G09	861	Not assembled			Frag
0672-94-(6-6-06)_H09	833	Not assembled			Frag
0676-94-(6-6-06)_D10	854	Not assembled			Frag
0678-94-(6-6-06)_F10	878	Not assembled			Frag
0679-94-(6-6-06)_G10	828	Not assembled			Frag
0681-94-(6-6-06)_A11	898	Not assembled			Frag
0683-94-(6-6-06)_C11	898	Not assembled			Frag
0684-94-(6-6-06)_D11	820	Not assembled			Frag
0686-94-(6-6-06)_F11	885	Not assembled			Frag
0687-94-(6-6-06)_G11	861	Not assembled			Frag
0688-94-(6-6-06)_H11	829	Not assembled			Frag
0690-94-(6-6-06)_B12	899	Not assembled			Frag
0691-94-(6-6-06)_C12	842	Not assembled			Frag
0693-94-(6-6-06)_E12	901	Not assembled			Frag
0694-94-(6-6-06)_F12	870	Not assembled			Frag
0695-94-(6-6-06)_G12	915	Not assembled			Frag
0696-94-(6-6-06)_H12	861	Not assembled			Frag
0698-94-(6-12-06)_G12	828	Not assembled			Frag
0699-94-(6-12-06)_H12	906	Not assembled			Frag
0701-94-(6-7-06)_A01	894	Not assembled			Frag
0702-94-(6-7-06)_B01	838	Not assembled			Frag
0704-94-(6-7-06)_D01	806	Not assembled			Frag
0707-94-(6-7-06)_G01	876	Not assembled			Frag
0708-94-(6-7-06)_H01	786	Not assembled			Frag
0709-94-(6-7-06)_A02	812	Not assembled			Frag
0710-94-(6-7-06)_B02	848	Not assembled			Frag
0713-94-(6-7-06)_E02	902	Not assembled			Frag
0714-94-(6-7-06)_F02	891	Not assembled			Frag
0716-94-(6-14-06)_H04	848	Not assembled			Frag
0717-94-(6-7-06)_A03	851	Not assembled			Frag
0718-94-(6-7-06)_B03	873	Not assembled			Frag
0719-94-(6-7-06)_C03	798	Not assembled			Frag
0720-94-(6-7-06)_D03	917	Not assembled			Frag
0721-94-(6-7-06)_E03	862	Not assembled			Frag
0724-94-(6-7-06)_H03	835	Not assembled			Frag
0725-94-(6-7-06)_A04	866	Not assembled			Frag
0726-94-(6-7-06)_B04	865	Not assembled			Frag
0727-94-(6-7-06)_C04	881	Not assembled			Frag
0728-94-(6-7-06)_D04	427	Not assembled			Frag
0729-94-(6-7-06)_E04	861	Not assembled			Frag

0730-94-(6-7-06)_F04	882	Not assembled			Frag
0731-94-(6-7-06)_G04	0	Not assembled			Frag
0732-94-(6-14-06)_A05	906	Not assembled			Frag
0733-94-(6-7-06)_A05	858	Not assembled			Frag
0734-94-(6-7-06)_B05	849	Not assembled			Frag
0735-94-(6-7-06)_C05	813	Not assembled			Frag
0736-94-(6-7-06)_D05	806	Not assembled			Frag
0737-94-(6-7-06)_E05	864	Not assembled			Frag
0738-94-(6-7-06)_F05	831	Not assembled			Frag
0739-94-(6-7-06)_G05	802	Not assembled			Frag
0740-94-(6-7-06)_H05	815	Not assembled			Frag
0743-94-(6-7-06)_C06	910	Not assembled			Frag
0744-94-(6-7-06)_D06	838	Not assembled			Frag
0745-94-(6-7-06)_E06	917	Not assembled			Frag
0746-94-(6-7-06)_F06	852	Not assembled			Frag
0747-94-(6-7-06)_G06	876	Not assembled			Frag
0748-94-(6-7-06)_H06	845	Not assembled			Frag
0749-94-(6-7-06)_A07	866	Not assembled			Frag
0750-94-(6-7-06)_B07	853	Not assembled			Frag
0752-94-(6-7-06)_D07	831	Not assembled			Frag
0753-94-(6-7-06)_E07	880	Not assembled			Frag
0755-94-(6-7-06)_G07	830	Not assembled			Frag
0756-94-(6-7-06)_H07	802	Not assembled			Frag
0759-94-(6-7-06)_C08	775	Not assembled			Frag
0760-94-(6-7-06)_D08	918	Not assembled			Frag
0762-94-(6-7-06)_F08	872	Not assembled			Frag
0763-94-(6-7-06)_G08	820	Not assembled			Frag
0766-94-(6-7-06)_A09	885	Not assembled			Frag
0767-94-(6-7-06)_B09	885	Not assembled			Frag
0768-94-(6-7-06)_C09	872	Not assembled			Frag
0770-94-(6-14-06)_B05'	826	Not assembled			Frag
0773-94-(6-7-06)_G09	894	Not assembled			Frag
0774-94-(6-7-06)_H09	829	Not assembled			Frag
0776-94-(6-7-06)_A10	880	Not assembled			Frag
0777-94-(6-7-06)_B10	850	Not assembled			Frag
0778-94-(6-7-06)_C10	818	Not assembled			Frag
0779-94-(6-7-06)_D10	867	Not assembled			Frag
0780-94-(6-7-06)_E10	851	Not assembled			Frag
0782-94-(6-7-06)_G10	843	Not assembled			Frag
0785-94-(6-7-06)_B11	853	Not assembled			Frag
0788-94-(6-7-06)_D11	818	Not assembled			Frag
0789-94-(6-7-06)_E11	871	Not assembled			Frag

0790-94-(6-7-06)_F11	884	Not assembled			Frag
0791-94-(6-7-06)_G11	854	Not assembled			Frag
0792-94-(6-7-06)_H11	781	Not assembled			Frag
0793-94-(6-14-06)_C05	838	Not assembled			Frag
0795-94-(6-7-06)_C12	856	Not assembled			Frag
0796-94-(6-7-06)_D12	873	Not assembled			Frag
0797-94-(6-7-06)_E12	849	Not assembled			Frag
0799-94-(6-7-06)_F12	831	Not assembled			Frag
0800-94-(6-7-06)_G12	861	Not assembled			Frag
0801-94-(6-5-06)_A01	948	Not assembled			Frag
0802-94-(6-5-06)_B01	831	Not assembled			Frag
0803-94-(6-5-06)_C01	943	Not assembled			Frag
0804-94-(6-5-06)_D01	907	Not assembled			Frag
0805-94-(6-5-06)_E01	908	Not assembled			Frag
0806-94-(6-5-06)_F01	777	Not assembled			Frag
0807-94-(6-5-06)_G01	728	Not assembled			Frag
0808-94-(6-5-06)_H01	924	Not assembled			Frag
0810-94-(6-5-06)_B02	910	Not assembled			Frag
0811-94-(6-5-06)_C02	941	Not assembled			Frag
0813-94-(6-5-06)_E02	896	Not assembled			Frag
0814-94-(6-5-06)_F02	923	Not assembled			Frag
0815-94-(6-14-06)_E05	873	Not assembled			Frag
0817-94-(6-5-06)_A03	860	Not assembled			Frag
0818-94-(6-5-06)_B03	435	Not assembled			Frag
0821-94-(6-5-06)_E03	870	Not assembled			Frag
0822-94-(6-5-06)_F03	769	Not assembled			Frag
0823-94-(6-5-06)_G03	547	Not assembled			Frag
0824-94-(6-5-06)_H03	901	Not assembled			Frag
0825-94-(6-5-06)_A04	842	Not assembled			Frag
0826-94-(6-5-06)_B04	822	Not assembled			Frag
0829-94-(6-5-06)_E04	909	Not assembled			Frag
0830-94-(6-5-06)_F04	879	Not assembled			Frag
0831-94-(6-5-06)_G04	816	Not assembled			Frag
0833-94-(6-5-06)_A05	865	Not assembled			Frag
0834-94-(6-15-06bad)_H10	617	Not assembled			Frag
0835-94-(6-5-06)_C05	837	Not assembled			Frag
0836-94-(6-5-06)_D05	888	Not assembled			Frag
0838-94-(6-5-06)_F05	926	Not assembled			Frag
0839-94-(6-14-06)_C06	959	Not assembled			Frag
0841-94-(6-5-06)_A06	923	Not assembled			Frag
0842-94-(6-5-06)_B06	938	Not assembled			Frag
0843-94-(6-5-06)_C06	929	Not assembled			Frag

0844-94-(6-5-06)_D06	875	Not assembled			Frag
0846-94-(6-5-06)_F06	825	Not assembled			Frag
0847-94-(6-5-06)_G06	634	Not assembled			Frag
0849-94-(6-5-06)_A07	858	Not assembled			Frag
0851-94-(6-5-06)_C07	944	Not assembled			Frag
0854-94-(6-5-06)_F07	810	Not assembled			Frag
0855-94-(6-5-06)_G07	915	Not assembled			Frag
0856-94-(6-5-06)_H07	836	Not assembled			Frag
0857-94-(6-5-06)_A08	952	Not assembled			Frag
0858-94-(6-5-06)_B08	897	Not assembled			Frag
0859-94-(6-5-06)_C08	890	Not assembled			Frag
0860-94-(6-5-06)_D08	892	Not assembled			Frag
0861-94-(6-5-06)_E08	748	Not assembled			Frag
0863-94-(6-5-06)_G08	941	Not assembled			Frag
0866-94-(6-5-06)_B09	850	Not assembled			Frag
0867-94-(6-5-06)_C09	0	Not assembled			Frag
0870-94-(6-5-06)_F09	747	Not assembled			Frag
0871-94-(6-14-06)_G06	874	Not assembled			Frag
0872-94-(6-5-06)_H09	861	Not assembled			Frag
0881-94-(6-5-06)_A11	881	Not assembled			Frag
0883-94-(6-5-06)_C11	864	Not assembled			Frag
0884-94-(6-5-06)_D11	933	Not assembled			Frag
0885-94-(6-5-06)_E11	925	Not assembled			Frag
0886-94-(6-5-06)_F11	862	Not assembled			Frag
0887-94-(6-5-06)_G11	804	Not assembled			Frag
0888-94-(6-5-06)_H11	911	Not assembled			Frag
0889-94-(6-5-06)_A12	882	Not assembled			Frag
0890-94-(6-14-06)_E07	904	Not assembled			Frag
0891-94-(6-5-06)_C12	921	Not assembled			Frag
0892-94-(6-5-06)_D12	820	Not assembled			Frag
0894-94-(6-5-06)_F12	830	Not assembled			Frag
0895-94-(6-5-06)_G12	699	Not assembled			Frag
0896-94-(6-5-06)_H12	865	Not assembled			Frag
0897-94-(6-14-06)_G07	881	Not assembled			Frag
0898-94-(6-14-06)_H07	840	Not assembled			Frag
0901-94-(6-14-06)_D10	872	Not assembled			Frag
0902-94-(6-14-06)_E10	801	Not assembled			Frag
0904-94-(6-14-06)_G10	841	Not assembled			Frag
0905-94-(6-14-06)_H10	895	Not assembled			Frag
0907-94-(6-14-06)_B11	953	Not assembled			Frag
0908-94-(6-14-06)_C11	845	Not assembled			Frag
0910-94-(6-14-06)_E11	880	Not assembled			Frag

0911-94-(6-14-06)_F11	925	Not assembled			Frag
0914-94-(6-14-06)_A12	871	Not assembled			Frag
0915-94-(6-14-06)_B12	889	Not assembled			Frag
0916-94-(6-14-06)_C12	933	Not assembled			Frag
0917-94-(6-14-06)_D12	815	Not assembled			Frag
0918-94-(6-14-06)_E12	877	Not assembled			Frag
0919-94-(6-14-06)_F12	879	Not assembled			Frag
0920-94-(6-14-06)_G12	870	Not assembled			Frag
0921-94-(6-14-06)_H12	851	Not assembled			Frag
0922-94-(6-15-06)_A01	928	Not assembled			Frag
0923-94-(6-15-06)_B01	833	Not assembled			Frag
0925-94-(6-16-06)_C11	905	Not assembled			Frag
0926-94-(6-15-06)_E01	25	Not assembled			Frag
0926-94-(6-16-06)_D11	904	Not assembled			Frag
0927-94-(6-15-06)_F01	739	Not assembled			Frag
0929-94-(6-15-06)_H01	702	Not assembled			Frag
0930-94-(6-16-06)_F11	706	Not assembled			Frag
0931-94-(6-16-06)_G11	899	Not assembled			Frag
0933-94-(6-16-06)_A12	0	Not assembled			Frag
0936-94-(6-16-06)_D12	917	Not assembled			Frag
0938-94-(6-15-06)_A03	823	Not assembled			Frag
0940-94-(6-15-06)_C03	851	Not assembled			Frag
0942-94-(6-15-06)_E03	818	Not assembled			Frag
0943-94-(6-16-06)_F12	905	Not assembled			Frag
0944-94-(6-15-06)_G03	878	Not assembled			Frag
0945-94-(6-15-06)_H03	870	Not assembled			Frag
0946-94-(6-15-06)_A04	612	Not assembled			Frag
1002-94-(6-2-06)_B01	924	Not assembled			Frag
1003-94-(6-2-06)_C01	881	Not assembled			Frag
1004-94(6-2-06Truncated)_D01	376	Not assembled			Frag
1005-94-(6-2-06)_E01	903	Not assembled			Frag
1006-94-(6-2-06)_F01	742	Not assembled			Frag
1007-94-(6-2-06)_G01	920	Not assembled			Frag
1008-94-(6-2-06)_H01	822	Not assembled			Frag
1009-94-(6-2-06)_A02	849	Not assembled			Frag
1010-94-(6-2-06)_B02	860	Not assembled			Frag
1014-94-(6-2-06)_E02	880	Not assembled			Frag
1015-94-(6-2-06)_F02	895	Not assembled			Frag
1016-94-(6-2-06)_G02	936	Not assembled			Frag
1017-94-(6-2-06)_H02	878	Not assembled			Frag
1018-94-(6-2-06)_A03	896	Not assembled			Frag
1019-94-(6-2-06)_B03	883	Not assembled			Frag

1021-94-(6-2-06)_D03	831	Not assembled			Frag
1025-94-(6-2-06)_H03	822	Not assembled			Frag
1026-94-(6-2-06)_A04	809	Not assembled			Frag
1027-94-(6-2-06)_B04	957	Not assembled			Frag
1028-94-(6-2-06)_C04	944	Not assembled			Frag
1029-94-(6-2-06)_D04	699	Not assembled			Frag
1030-94-(6-2-06)_E04	917	Not assembled			Frag
1031-94-(6-2-06)_F04	770	Not assembled			Frag
1032-94-(6-2-06)_G04	883	Not assembled			Frag
1032-94-(6-16-06)_D06	756	Not assembled			Frag
1033-94-(6-2-06)_H04	1	Not assembled			Frag
1034-94-(6-14-06)_F08	887	Not assembled			Frag
1035-94-(6-14-06)_G08	903	Not assembled			Frag
1036-94-(6-2-06)_C05	766	Not assembled			Frag
1037-94-(6-14-06)_H08	0	Not assembled			Frag
1039-94-(6-2-06)_F05	850	Not assembled			Frag
1040-94-(6-2-06)_G05	917	Not assembled			Frag
1041-94-(6-2-06)_H05	870	Not assembled			Frag
1042-94-(6-15-06)_E12	886	Not assembled			Frag
1046-94-(6-2-06)_E06	886	Not assembled			Frag
1047-94-(6-2-06)_F06	821	Not assembled			Frag
1050-94-(6-2-06)_A07	856	Not assembled			Frag
1052-94-(6-2-06)_C07	870	Not assembled			Frag
1054-94-(6-2-06)_E07	863	Not assembled			Frag
1058-94-(6-2-06)_H07	794	Not assembled			Frag
1060-94-(6-2-06)_B08	871	Not assembled			Frag
1061-94-(6-2-06)_C08	877	Not assembled			Frag
1063-94-(6-2-06)_E08	660	Not assembled			Frag
1064-94-(6-2-06)_F08	882	Not assembled			Frag
1067-94-(6-2-06)_A09	908	Not assembled			Frag
1069-94-(6-2-06)_C09	820	Not assembled			Frag
1071-94-(6-2-06)_E09	916	Not assembled			Frag
1072-94-(6-2-06)_F09	919	Not assembled			Frag
1073-94-(6-2-06)_G09	911	Not assembled			Frag
1075-94-(6-2-06)_A10	832	Not assembled			Frag
1076-94-(6-2-06)_B10	923	Not assembled			Frag
1077-94-(6-2-06)_C10	913	Not assembled			Frag
1078-94-(6-2-06)_D10	665	Not assembled			Frag
1079-94-(6-2-06)_E10	850	Not assembled			Frag
1080-94-(6-2-06)_F10	910	Not assembled			Frag
1081-94-(6-2-06)_G10	896	Not assembled			Frag
1082-94-(6-2-06)_H10	872	Not assembled			Frag

1083-94-(6-2-06)_A11	871	Not assembled			Frag
1084-94-(6-2-06)_B11	866	Not assembled			Frag
1085-94-(6-2-06)_C11	827	Not assembled			Frag
1086-94-(6-2-06)_D11	915	Not assembled			Frag
1087-94-(6-2-06)_E11	853	Not assembled			Frag
1088-94-(6-2-06)_F11	871	Not assembled			Frag
1089-94-(6-2-06)_G11	831	Not assembled			Frag
1090-94-(6-2-06)_H11	877	Not assembled			Frag
1092-94-(6-2-06)_B12	177	Not assembled			Frag
1094-94-(6-2-06)_D12	733	Not assembled			Frag
1096-94-(6-2-06)_F12	871	Not assembled			Frag
1097-94-(6-2-06)_G12	864	Not assembled			Frag
1101-94-(6-9-06)_A07	926	Not assembled			Frag
1102-94-(6-9-06)_B07	894	Not assembled			Frag
1104-94-(6-9-06)_D07	902	Not assembled			Frag
1105-94-(6-9-06)_E07	848	Not assembled			Frag
1107-94-(6-9-06)_G07	940	Not assembled			Frag
1108-94-(6-9-06)_H07	798	Not assembled			Frag
1110-94-(6-9-06)_B08	868	Not assembled			Frag
1111-94-(6-9-06)_C08	661	Not assembled			Frag
1113-94-(6-9-06)_E08	872	Not assembled			Frag
1115-94-(6-9-06)_G08	897	Not assembled			Frag
1116-94-(6-9-06)_H08	870	Not assembled			Frag
1118-94-(6-9-06)_B09	833	Not assembled			Frag
1120-94-(6-9-06)_D09	929	Not assembled			Frag
1123-94-(6-9-06)_G09	852	Not assembled			Frag
1124-94-(6-9-06)_H09	759	Not assembled			Frag
1125-94-(6-9-06)_A10	920	Not assembled			Frag
1126-94-(6-9-06)_B10	792	Not assembled			Frag
1127-94-(6-9-06Truncated)_C10	789	Not assembled			Frag
1128-94-(6-9-06Truncated)_D10	713	Not assembled			Frag
1130-94-(6-9-06)_F10	888	Not assembled			Frag
1133-94-(6-9-06)_A11	901	Not assembled			Frag
1134-94-(6-9-06)_B11	829	Not assembled			Frag
1135-94-(6-9-06)_C11	854	Not assembled			Frag
1137-94-(6-9-06)_E11	900	Not assembled			Frag
1138-94-(6-9-06)_F11	846	Not assembled			Frag
1139-94-(6-9-06)_G11	800	Not assembled			Frag
1141-94-(6-9-06)_A12	921	Not assembled			Frag
1142-94-(6-9-06)_B12	926	Not assembled			Frag
1143-94-(6-9-06)_C12	863	Not assembled			Frag
1144-94-(6-9-06)_D12	914	Not assembled			Frag

1145-94-(6-9-06Truncated)_E12	355	Not assembled			Frag
1146-94-(6-9-06)_F12	883	Not assembled			Frag
1147-94-(6-9-06Truncated)_G12	258	Not assembled			Frag
1148-94-(6-9-06)_H12	864	Not assembled			Frag
1151-94-(6-15-06)_C04	920	Not assembled			Frag
1152-94-(6-15-06)_D04	870	Not assembled			Frag
1159-94-(6-15-06)_A05	887	Not assembled			Frag
1160-94-(6-15-06)_B05	795	Not assembled			Frag
1163-94-(6-15-06)_C05	927	Not assembled			Frag
1166-94-(6-15-06)_E05	874	Not assembled			Frag
1167-94-(6-15-06)_F05	900	Not assembled			Frag
1169-94-(6-15-06)_G05	803	Not assembled			Frag
1170-94-(6-15-06)_H05	861	Not assembled			Frag
1171-94-(6-15-06)_A06	933	Not assembled			Frag
1172-94-(6-15-06)_B06	899	Not assembled			Frag
1174-94-(6-15-06)_D06	920	Not assembled			Frag
1178-94-(6-15-06)_E06	864	Not assembled			Frag
1179-94-(6-15-06)_F06	905	Not assembled			Frag

APPENDIX G: SINGLET INFORMATION

Name	Length	Original length	5'Trimmed bases	3'Trimmed bases
1092-94-(6-2-06)_B12	177	1230	74	979
1147-94-(6-9-06Truncated)_G12	258	398	63	77
0010-93-G12(4-21-06)	346	557	44	167
1145-94-(6-9-06Truncated)_E12	355	1186	62	769
1004-94(6-2-06Truncated)_D01	376	598	29	193
0728-94-(6-7-06)_D04	427	799	70	302
0818-94-(6-5-06)_B03	435	640	72	133
0329-94-(6-27-06)_H03	458	639	29	152
0037-94-D02(4-28-06)	471	1017	33	513
0161-94-A07(5-5-06)	471	640	36	133
0823-94-(6-5-06)_G03	547	1112	73	492
0431-94-(6-16-06)_G01	600	1071	73	398
0130-94-B03(5-9-06)	605	1019	67	347
0509-94-(6-8-06)_A02	607	1213	69	537
0946-94-(6-15-06)_A04	612	1071	51	408
0834-94-(6-15-06bad)_H10	617	1225	147	461
0006-93-B05(4-20-06)	628	1017	91	298
0463-94-(6-16-06)_E05	631	1038	64	343
0847-94-(6-5-06)_G06	634	1099	84	381
0032-93-A10(4-21-06)	643	1004	45	316
0164-94-D07(5-5-06)	644	1007	88	275
006-94-E05(4-28-06)	650	1015	73	292
0576-94-(6-12-06)_E11	650	925	28	247
0149-94-E05(5-9-06)	654	995	29	312
0352-94-(6-27-06)_H04	657	1125	14	454
0046-94-E03(4-28-06)	659	992	115	218
1063-94-(6-2-06)_E08	660	1135	32	443
1111-94-(6-9-06)_C08	661	695	14	20
0244-94-E12(5-10-06)	663	857	68	126
0119-94-F12(4-28-06)	664	996	31	301
0087-93-B03(4-21-06)	665	1011	42	304
1078-94-(6-2-06)_D10	665	1129	67	397
0239-94-H11(5-10-06)	669	892	73	150
0048-94-G03(4-28-06)	670	1019	73	276
0029-94-D01(4-28-06)	674	1004	73	257
0233-94-B11(5-10-06)	674	873	68	131
0042-93-G08(4-21-06)	675	882	16	191

0047-93-B08(4-21-06)	675	1000	43	282
0071_B05(Rev4-21-06)	675	998	41	282
0117-94-D12(4-28-06)	675	985	110	200
0141-94-E04(5-9-06)	675	1002	37	290
0097-94-H09(4-28-06)	680	1015	74	261
0074-93-G04(4-21-06)	682	995	45	268
0006-94-C05(4-20-06)	683	1025	69	273
0072-94-F01(5-9-06)	684	1010	81	245
0131-94-C03(5-9-06)	684	1025	81	260
0007for_D05'	687	996	39	270
0229-94-F10(5-10-06)	689	1013	42	282
0106-94-A11(4-28-06)	696	992	72	224
0052-94-C04(4-28-06)	697	999	92	210
0065-94-H05(4-28-06)	697	998	33	268
0162-94-B07(5-5-06)	697	1039	76	266
0087-94-F08(4-28-06)	698	1025	35	292
0192-94-A06(5-10-06)	698	1017	77	242
0625-94-(6-6-06)_A04	698	1069	21	350
0457-94-(6-16-06)_G04	699	1065	61	305
0895-94-(6-5-06)_G12	699	1193	80	414
1029-94-(6-2-06)_D04	699	1128	38	391
0220-94E09(5-10-06)	700	1012	61	251
0008-94-G05(4-20-06)	701	1022	37	284
0172-94-E03(5-10-06)	702	1005	44	259
0929-94-(6-15-06)_H01	702	1165	79	384
0071_F06(For4-28-06)	705	1020	72	243
0105-94-H10(4-28-06)	705	1021	73	243
0030-94-E01(4-28-06)	706	984	69	209
0121-94-H12(4-28-06)	706	1028	75	247
0930-94-(6-16-06)_F11	706	1084	44	334
0026-94-(6-12-06)_A01	707	871	30	134
0045-94-D03(4-28-06)	708	1020	76	236
0180-94-E04(5-10-06)	708	1010	30	272
0086-94-E08(4-28-06)	709	1013	77	227
0120-94-A02(5-9-06)	709	1004	88	207
0450-94-(6-16-06)_H03	709	1086	34	343
0137-94-A04(5-9-06)	710	991	35	246
0063-94-F05(4-28-06)	711	1012	69	232
0209-94-B08(5-10-06)	711	1026	29	286
0133-94-E03(5-9-06)	712	1006	71	223
0237-94-F11(5-10-06)	712	893	48	133
0221-94-F09(5-10-06)	713	1008	53	242

1128-94-(6-9-06Truncated)_D10	713	837	27	97
0140-94-D04(5-9-06)	714	1014	75	225
0238-94-G11(5-10-06)	714	889	21	154
0111-94-F11(4-28-06)	717	1012	36	259
0047-94-F03(4-28-06)	718	1024	27	279
0147-94-C05(5-9-06)	718	998	33	247
1305-94-(6-16-06)_G06	719	1152	123	310
0074-94-A07(4-28-06)	719	1022	88	215
0095-93-B02(4-21-06)	719	1024	28	277
0235-94-D11(5-10-06)	720	871	55	96
0242-94-C12(5-10-06)	720	852	70	62
0430-94-(6-16-06)_F01	720	1042	38	284
0118-94-E12(4-28-06)	721	997	72	204
0195-94-D06(5-10-06)	722	1009	31	256
0562-94-(6-8-06)_H07	724	1130	69	337
0245-94-F12(5-10-06)	725	886	44	117
0079-93-B04(4-21-06)	726	1036	17	293
0139-94-C04(5-9-06)	726	999	70	203
0123-94-C02(5-9-06)	728	1004	76	200
0134-94-F03(5-9-06)	728	1000	33	239
0807-94-(6-5-06)_G01	728	1128	26	374
0032-94-G01(4-28-06)	729	1014	72	213
0054-94-E04(4-28-06)	729	1046	75	242
0227-94-D10(5-10-06)	730	1037	45	262
0185-94-B05(5-10-06)	733	1013	45	235
1094-94-(6-2-06)_D12	733	1085	40	312
0110-94-E11(4-28-06)	734	1025	75	216
0225-94-B10(5-10-06)	736	1020	76	208
0179-94-D04(5-10-06)	737	995	73	185
0228-94-E10(5-10-06)	738	1020	30	252
0927-94-(6-15-06)_F01	739	1171	72	360
0148-94-D05(5-9-06)	740	1015	65	210
0514-94-(6-8-06)_F02	741	944	20	183
0603-94-(6-6-06)_C01	742	1216	75	399
1006-94-(6-2-06)_F01	742	1103	36	325
0208-94-A08(5-10-06)	744	1014	65	205
0607-94-(6-6-06)_G01	744	938	48	146
0177-94-B04(5-10-06)	746	988	36	206
0870-94-(6-5-06)_F09	747	1161	78	336
0129-94-A03(5-9-06)	748	1003	69	186
0234-94-C11(5-10-06)	748	877	37	92
0241-94-B12(5-10-06)	748	851	42	61

0518-94-(6-8-06)_B03	748	1127	27	352
0861-94-(6-5-06)_E08	748	949	30	171
0446-94-(6-16-06)_E03	750	1079	34	295
0210-94-C08(5-10-06)	752	1023	31	240
0115-94-B12(4-28-06)	753	988	46	189
0660-94-(6-6-06)_D08	753	1148	46	349
0649-94-(6-6-06)_A07	754	1194	82	358
0572-94-(6-8-06)_G08	755	1132	62	315
0016-93-A12(4-21-06)	756	991	15	220
0163-94-C07(5-5-06)	756	1017	66	195
0200-94-A07(5-10-06)	756	1010	32	222
0211-94-D08(5-10-06)	756	1017	44	217
1032-94-(6-16-06)_D06	756	1167	122	289
0214-94(5-31-06)_010	757	1140	36	347
0350-94-(6-9-06)_G04	757	1135	26	352
0060-94-C05(4-28-06)	758	1016	35	223
0136-94(5-31-06)_011	759	1182	79	344
0226-94-C10(5-10-06)	759	1026	45	222
1124-94-(6-9-06)_H09	759	1135	72	304
0347-94-(6-12-06)_F06	762	1206	79	365
0398-94-(6-8-06)_F12	762	1135	47	326
0175-94-H03(5-10-06)	766	976	34	176
0598-94-(6-8-06)_E11	766	1177	36	375
1036-94-(6-2-06)_C05	766	1191	77	348
0075-94-B07(4-28-06)	768	998	36	194
0219-94-D09(5-10-06)	768	1049	34	247
0822-94-(6-5-06)_F03	769	1192	23	400
1031-94-(6-2-06)_F04	770	1128	172	186
0283-94(5-31-06)_011	773	1092	33	286
0759-94-(6-7-06)_C08	775	1094	71	248
0313-94-(6-9-06)_B01	776	1165	33	356
0465-94-(6-16-06)_G05	776	1107	69	262
0643-94-(6-6-06)_C06	776	1192	41	375
0349-94-(6-9-06)_F04	777	1183	71	335
0806-94-(6-5-06)_F01	777	1101	24	300
0626-94-(6-6-06)_B04	779	1115	71	265
0648-94(6-6-06)_H06	780	1131	79	272
0792-94-(6-7-06)_H11	781	1135	70	284
0468-94-(6-16-06)_B06	782	1170	121	267
0223-94-H09(5-10-06)	784	1012	37	191
0250-94(5-31-06)_009	784	1182	46	352
0099-94-B10(4-28-06)	786	1007	36	185

0513-94-(6-8-06)_E02	786	1219	30	403
0708-94-(6-7-06)_H01	786	1089	26	277
0085-94-D08(4-28-06)	788	1010	37	185
0323-94-(6-9-06)_C02	788	1174	70	316
0591-94-(6-8-06)_F10	788	1153	31	334
1127-94-(6-9-06Truncated)_C10	789	889	17	83
0584-94-(6-8-06)_G09	791	1146	40	315
0019-94_008(5-31-06)	792	1137	80	265
1126-94-(6-9-06)_B10	792	1185	34	359
0124-94-D02(5-9-06)	794	992	32	166
0506-94-(6-8-06)_F01	794	1148	52	302
0533-94-(6-8-06)_A05	794	1162	39	329
1058-94-(6-2-06)_H07	794	1149	41	314
1160-94-(6-15-06)_B05	795	1183	31	357
0719-94-(6-7-06)_C03	798	1113	73	242
1108-94-(6-9-06)_H07	798	1142	73	271
0556-94-(6-12-06)_H10	800	1127	69	258
1139-94-(6-9-06)_G11	800	1151	22	329
0902-94-(6-14-06)_E10	801	1010	27	182
0309-94(5-31-06)_012	802	1132	85	245
0739-94-(6-7-06)_G05	802	1173	121	250
0756-94-(6-7-06)_H07	802	1135	71	262
1169-94-(6-15-06)_G05	803	1114	45	266
0380-94-(6-12-06)_G09	804	1143	64	275
0887-94-(6-5-06)_G11	804	1188	31	353
0257-94(5-31-06)_008	805	1135	75	255
0704-94-(6-7-06)_D01	806	1141	33	302
0736-94-(6-7-06)_D05	806	1174	72	296
0112-94-(6-12-06)_D04	807	1144	41	296
1301-94-(6-16-06)_C06	808	1152	122	222
0535-94-(6-8-06)_C05	808	1166	77	281
0609-94-(6-6-06)_A02	808	1173	71	294
1026-94-(6-2-06)_A04	809	1171	78	284
0278-94(5-31-06)_001	810	1122	72	240
0854-94-(6-5-06)_F07	810	1114	31	273
0319-94-(6-9-06)_G01	811	1151	65	275
0549-94-(6-12-06)_F10	812	1155	79	264
0709-94-(6-7-06)_A02	812	1174	40	322
0311-94(5-31-06)_016	813	1147	70	264
0735-94-(6-7-06)_C05	813	1116	67	236
0315-94-(6-9-06)_D01	814	1198	40	344
0740-94-(6-7-06)_H05	815	1116	68	233

0917-94-(6-14-06)_D12	815	1085	30	240
0831-94-(6-5-06)_G04	816	1150	32	302
0286-94(5-31-06)_002	817	1151	80	254
0655-94-(6-6-06)_G07	817	1141	69	255
0358-94-(6-12-06)_C07	818	1141	76	247
0645-94-(6-6-06)_E06	818	1138	75	245
0653-94-(6-6-06)_E07	818	1137	71	248
0778-94-(6-7-06)_C10	818	1138	31	289
0788-94-(6-7-06)_D11	818	1155	66	271
0942-94-(6-15-06)_E03	818	1132	40	274
0127-94(5-31-06)_007	819	1113	73	221
0604-94-(6-6-06)_D01	819	1167	81	267
0613-94-(6-6-06)_E02	819	1144	26	299
0300-94(5-31-06)_013	820	1148	68	260
0644-94-(6-6-06)_D06	820	1187	42	325
0684-94-(6-6-06)_D11	820	1119	68	231
0763-94-(6-7-06)_G08	820	1148	72	256
0892-94-(6-5-06)_D12	820	1173	71	282
1069-94-(6-2-06)_C09	820	1134	29	285
1047-94-(6-2-06)_F06	821	1158	68	269
0159-94(5-31-06)_004	822	1108	61	225
0460-94-(6-16-06)_B05	822	1135	70	243
0544-94-(6-8-06)_D06	822	1150	79	249
0826-94-(6-5-06)_B04	822	1166	19	325
1008-94-(6-2-06)_H01	822	1157	70	265
1025-94-(6-2-06)_H03	822	1159	78	259
0328-94-(6-9-06)_G02	823	1190	36	331
0511-94-(6-8-06)_C02	823	1192	30	339
0617-94-(6-6-06)_A03	823	1146	32	291
0938-94-(6-15-06)_A03	823	1184	83	278
0360-94-(6-12-06)_E07	824	1139	34	281
0846-94-(6-5-06)_F06	825	1150	36	289
0515-94-(6-8-06)_G02	826	1159	44	289
0770-94-(6-14-06)_B05'	826	1146	66	254
1085-94-(6-2-06)_C11	827	1151	81	243
0143-94(5-31-06)_013	828	1188	73	287
0390-94-(6-8-06)_G11	828	1131	83	220
0679-94-(6-6-06)_G10	828	1156	38	290
0698-94-(6-12-06)_G12	828	1178	72	278
0688-94-(6-6-06)_H11	829	1127	22	276
0774-94-(6-7-06)_H09	829	1128	67	232
1134-94-(6-9-06)_B11	829	1175	78	268

1193-94-(6-15-06)_E07	830	1139	23	286
0232-94-A11(5-10-06)	830	881	34	17
0571-94-(6-8-06)_F08	830	1137	62	245
0605-94-(6-6-06)_E01	830	1148	31	287
0633-94-(6-6-06)_A05	830	1080	25	225
0755-94-(6-7-06)_G07	830	1154	55	269
0894-94-(6-5-06)_F12	830	1010	76	104
0365-94-(6-12-06)_B08	831	1165	32	302
0529-94-(6-8-06)_E04	831	1153	46	276
0587-94-(6-8-06)_B10	831	1121	11	279
0738-94-(6-7-06)_F05	831	1126	43	252
0752-94-(6-7-06)_D07	831	1140	72	237
0799-94-(6-7-06)_F12	831	1162	60	271
0802-94-(6-5-06)_B01	831	1163	74	258
1021-94-(6-2-06)_D03	831	1139	68	240
1089-94-(6-2-06)_G11	831	1158	34	293
0540-94-(6-8-06)_H05	832	1143	45	266
0642-94-(6-6-06)_B06	832	1088	77	179
0647-94-(6-6-06)_G06	832	1159	42	285
0667-94-(6-6-06)_C09	832	1137	65	240
1075-94-(6-2-06)_A10	832	1174	74	268
0616-94-(6-6-06)_H02	833	1139	52	254
0672-94-(6-6-06)_H09	833	1152	21	298
0923-94-(6-15-06)_B01	833	1153	29	291
1118-94-(6-9-06)_B09	833	1146	34	279
0606-94-(6-6-06)_F01	834	1172	43	295
0724-94-(6-7-06)_H03	835	1140	28	277
0657-94-(6-6-06)_A08	836	1184	84	264
0856-94-(6-5-06)_H07	836	1116	66	214
0252-94(5-31-06)_013	837	1129	68	224
0523-94-(6-8-06)_G03	837	1138	72	229
0528-94-(6-8-06)_D04	837	1150	44	269
0580-94-(6-8-06)_D09	837	1149	34	278
0835-94-(6-5-06)_C05	837	1177	79	261
0531-94-(6-8-06)_G04	838	1134	74	222
0702-94-(6-7-06)_B01	838	1181	35	308
0744-94-(6-7-06)_D06	838	1139	72	229
0793-94-(6-14-06)_C05	838	1129	64	227
0012-94_009(5-31-06)	840	1141	73	228
0503-94-(6-8-06)_C01	840	1175	38	297
0666-94-(6-6-06)_B09	840	1151	70	241
0898-94-(6-14-06)_H07	840	1130	26	264

0361-94-(6-12-06)_F07	841	1163	22	300
0904-94-(6-14-06)_G10	841	1159	34	284
0691-94-(6-6-06)_C12	842	1131	63	226
0825-94-(6-5-06)_A04	842	1179	80	257
0265-94(5-31-06)_007	843	1124	22	259
0782-94-(6-7-06)_G10	843	1148	30	275
0016-94_002(5-31-06)	845	1133	30	258
0023-94_016(5-31-06)	845	1118	33	240
0748-94-(6-7-06)_H06	845	1109	28	236
0908-94-(6-14-06)_C11	845	1153	27	281
0597-94-(6-8-06)_D11	846	1136	50	240
1138-94-(6-9-06)_F11	846	1155	63	246
1182-94-(6-15-06)_H06	847	1145	74	224
0567-94-(6-8-06)_B08	848	1168	77	243
0612-94-(6-6-06)_D02	848	1169	51	270
0710-94-(6-7-06)_B02	848	1173	25	300
0716-94-(6-14-06)_H04	848	1150	37	265
1105-94-(6-9-06)_E07	848	1156	64	244
0332-94-(6-9-06)_A03	849	1166	40	277
0734-94-(6-7-06)_B05	849	1161	37	275
0797-94-(6-7-06)_E12	849	1165	42	274
1009-94-(6-2-06)_A02	849	1148	67	232
0128-94(5-31-06)_009	850	1145	80	215
0777-94-(6-7-06)_B10	850	1125	29	246
0866-94-(6-5-06)_B09	850	1143	23	270
1039-94-(6-2-06)_F05	850	1140	14	276
1079-94-(6-2-06)_E10	850	1131	35	246
0269-94(5-31-06)_015	851	1135	41	243
0372-94-(6-12-06)_H08	851	1111	50	210
0717-94-(6-7-06)_A03	851	1123	35	237
0780-94-(6-7-06)_E10	851	1138	38	249
0921-94-(6-14-06)_H12	851	1165	39	275
0940-94-(6-15-06)_C03	851	1151	43	257
0260-94(5-31-06)_014	852	1141	71	218
0285-94(5-31-06)_015	852	1155	65	238
0507-94-(6-8-06)_G01	852	1178	70	256
0746-94-(6-7-06)_F06	852	1168	72	244
1123-94-(6-9-06)_G09	852	1154	35	267
0750-94-(6-7-06)_B07	853	1152	38	261
0785-94-(6-7-06)_B11	853	1164	28	283
1087-94-(6-2-06)_E11	853	1121	34	234
0541-94-(6-8-06)_A06	854	1158	41	263

0676-94-(6-6-06)_D10	854	1133	30	249
0791-94-(6-7-06)_G11	854	1135	43	238
1135-94-(6-9-06)_C11	854	903	33	16
0307-94-(6-12-06)_F05	855	1152	35	262
0369-94-(6-12-06)_F08	855	1128	64	209
0459-94-(6-16-06)_A05	855	1151	47	249
0614-94-(6-6-06)_F02	855	1139	31	253
0520-94-(6-8-06)_D03	856	1144	38	250
0532-94-(6-8-06)_H04	856	1160	45	259
0545-94-(6-8-06)_E06	856	1161	36	269
0592-94-(6-8-06)_G10	856	1162	63	243
0652-94-(6-6-06)_D07	856	1153	83	214
0664-94-(6-6-06)_H08	856	1112	34	222
0795-94-(6-7-06)_C12	856	1161	31	274
1050-94-(6-2-06)_A07	856	1165	76	233
0013-94_011(5-31-06)	857	1143	41	245
0261-94(5-31-06)_016	857	1131	39	235
0378-94-(6-12-06)_E09	857	1151	20	274
0426-94-(6-16-06)_B01	857	1162	47	258
0439-94-(6-16-06)_G02	857	1147	29	261
0595-94-(6-8-06)_B11	857	1156	51	248
0663-94-(6-6-06)_G08	857	1154	28	269
0306-94(5-31-06)_006	858	1149	80	211
0548-94-(6-8-06)_H06	858	1152	44	250
0733-94-(6-7-06)_A05	858	1174	44	272
0849-94-(6-5-06)_A07	858	1173	39	276
0373-94-(6-12-06)_A09	859	1108	39	210
0379-94-(6-12-06)_F09	859	1157	75	223
0546-94-(6-8-06)_F06	859	1153	53	241
0276-94(5-31-06)_014	860	1147	45	242
0454-94-(6-16-06)_D04	860	1131	78	193
0517-94-(6-8-06)_A03	860	1143	46	237
0659-94-(6-6-06)_C08	860	1167	27	280
0817-94-(6-5-06)_A03	860	1196	82	254
1010-94-(6-2-06)_B02	860	1150	69	221
0107-94-(6-12-06)_A04	861	1141	24	256
0359-94-(6-12-06)_D07	861	1150	44	245
0671-94-(6-6-06)_G09	861	1149	84	204
0687-94-(6-6-06)_G11	861	1136	32	243
0696-94-(6-6-06)_H12	861	1155	31	263
0729-94-(6-7-06)_E04	861	1139	38	240
0800-94-(6-7-06)_G12	861	1142	21	260

0872-94-(6-5-06)_H09	861	1165	33	271
1170-94-(6-15-06)_H05	861	1181	110	210
0356-94-(6-12-06)_A07	862	1140	37	241
0362-94-(6-12-06)_G07	862	1138	68	208
0640-94-(6-6-06)_H05	862	1147	41	244
0721-94-(6-7-06)_E03	862	1131	29	240
0886-94-(6-5-06)_F11	862	1141	32	247
0198-94-(6-16-06)_H08	863	1090	36	191
0385-94-(6-12-06)_B10	863	1142	30	249
0521-94-(6-8-06)_E03	863	1133	45	225
0566-94-(6-8-06)_A08	863	1153	76	214
0661-94-(6-6-06)_E08	863	1185	82	240
1054-94-(6-2-06)_E07	863	1166	41	262
1143-94-(6-9-06)_C12	863	1196	75	258
0737-94-(6-7-06)_E05	864	1167	46	257
0883-94-(6-5-06)_C11	864	1136	70	202
1097-94-(6-2-06)_G12	864	1148	60	224
1148-94-(6-9-06)_H12	864	1164	31	269
1178-94-(6-15-06)_E06	864	1151	20	267
1308-94-(6-16-06)_B07	865	1161	15	281
0144-94(5-31-06)_015	865	1143	34	244
0377-94-(6-12-06)_D09	865	1133	35	233
0534-94-(6-8-06)_B05	865	1148	43	240
0628-94-(6-6-06)_D04	865	1165	32	268
0668-94-(6-6-06)_D09	865	1146	32	249
0726-94-(6-7-06)_B04	865	1150	31	254
0833-94-(6-5-06)_A05	865	1133	64	204
0896-94-(6-5-06)_H12	865	1146	32	249
0447-94-(6-16-06)_F03	866	1170	58	246
0453-94-(6-16-06)_C04	866	1135	57	212
0538-94-(6-8-06)_F05	866	1159	45	248
0725-94-(6-7-06)_A04	866	1142	33	243
0749-94-(6-7-06)_A07	866	1161	33	262
1084-94-(6-2-06)_B11	866	1153	35	252
0779-94-(6-7-06)_D10	867	1139	26	246
0312-94-(6-9-06)_A01	868	1162	79	215
0316-94-(6-9-06)_E01	868	922	45	9
0367-94-(6-12-06)_D08	868	1147	40	239
1110-94-(6-9-06)_B08	868	1163	40	255
0298-94(5-31-06)_009	869	1146	41	236
0215-94(5-31-06)_012	870	1150	33	247
0271-94(5-31-06)_004	870	1111	70	171

0658-94-(6-6-06)_B08	870	1176	44	262
0694-94-(6-6-06)_F12	870	1142	67	205
0821-94-(6-5-06)_E03	870	1158	70	218
0920-94-(6-14-06)_G12	870	1134	36	228
0945-94-(6-15-06)_H03	870	1143	40	233
1041-94-(6-2-06)_H05	870	1116	36	210
1052-94-(6-2-06)_C07	870	1145	68	207
1116-94-(6-9-06)_H08	870	1142	31	241
1152-94-(6-15-06)_D04	870	1146	110	166
1192-94-(6-15-06)_D07	871	1154	30	253
0536-94-(6-8-06)_D05	871	1118	39	208
0789-94-(6-7-06)_E11	871	1134	32	231
0914-94-(6-14-06)_A12	871	1142	24	247
1060-94-(6-2-06)_B08	871	1186	71	244
1083-94-(6-2-06)_A11	871	1146	75	200
1088-94-(6-2-06)_F11	871	1146	34	241
1096-94-(6-2-06)_F12	871	1140	36	233
0462-94-(6-16-06)_D05	872	1138	74	192
0762-94-(6-7-06)_F08	872	1146	28	246
0768-94-(6-7-06)_C09	872	1151	64	215
0901-94-(6-14-06)_D10	872	1156	47	237
1082-94-(6-2-06)_H10	872	1180	85	223
1113-94-(6-9-06)_E08	872	1151	32	247
0387-94-(6-12-06)_D10	873	1141	34	234
0718-94-(6-7-06)_B03	873	1175	26	276
0796-94-(6-7-06)_D12	873	1166	38	255
0815-94-(6-14-06)_E05	873	1126	36	217
0247-94(5-31-06)_003	874	1132	62	196
0284-94(5-31-06)_013	874	1145	72	199
0326-94-(6-14-06)_F02	874	1153	35	244
0871-94-(6-14-06)_G06	874	1134	76	184
1166-94-(6-15-06)_E05	874	1162	30	258
0577-94-(6-8-06)_B09	875	1130	25	230
0656-94-(6-6-06)_H07	875	1155	47	233
0844-94-(6-5-06)_D06	875	1167	78	214
0436-94-(6-16-06)_D02	876	1137	38	223
0621-94-(6-6-06)_E03	876	1155	41	238
0707-94-(6-7-06)_G01	876	1137	29	232
0747-94-(6-7-06)_G06	876	1138	33	229
0918-94-(6-14-06)_E12	877	1117	30	210
1061-94-(6-2-06)_C08	877	1155	40	238
1090-94-(6-2-06)_H11	877	1162	37	248

0537-94-(6-8-06)_E05	878	1151	45	228
0678-94-(6-6-06)_F10	878	1157	29	250
0944-94-(6-15-06)_G03	878	1177	42	257
1017-94-(6-2-06)_H02	878	1113	32	203
0325-94-(6-14-06)_E02	879	1153	29	245
0830-94-(6-5-06)_F04	879	1149	45	225
0919-94-(6-14-06)_F12	879	1173	36	258
0543-94-(6-8-06)_C06	880	1172	43	249
0753-94-(6-7-06)_E07	880	1151	26	245
0776-94-(6-7-06)_A10	880	1188	43	265
0910-94-(6-14-06)_E11	880	1159	29	250
1014-94-(6-2-06)_E02	880	1115	34	201
1180-94-(6-15-06)_G06	881	1165	44	240
0363-94-(6-12-06)_H07	881	1181	43	257
0452-94-(6-16-06)_B04	881	1145	35	229
0464-94-(6-16-06)_F05	881	1155	31	243
0583-94-(6-8-06)_F09	881	1141	33	227
0654-94-(6-6-06)_F07	881	1184	42	261
0727-94-(6-7-06)_C04	881	1139	37	221
0881-94-(6-5-06)_A11	881	1178	49	248
0897-94-(6-14-06)_G07	881	1155	42	232
1003-94-(6-2-06)_C01	881	1239	71	287
1194-94-(6-15-06)_F07	882	1164	64	218
0010-94_005(5-31-06)	882	1142	32	228
0272-94(5-31-06)_006	882	1132	28	222
0295-94(5-31-06)_003	882	1131	45	204
0594-94-(6-8-06)_A11	882	1152	48	222
0599-94-(6-8-06)_F11	882	1168	31	255
0730-94-(6-7-06)_F04	882	1178	40	256
0889-94-(6-5-06)_A12	882	1164	66	216
1064-94-(6-2-06)_F08	882	1128	40	206
0297-94(5-31-06)_007	883	1167	43	241
0305-94(5-31-06)_004	883	1115	41	191
1019-94-(6-2-06)_B03	883	1154	27	244
1032-94-(6-2-06)_G04	883	1156	36	237
1146-94-(6-9-06)_F12	883	1192	31	278
0790-94-(6-7-06)_F11	884	1154	41	229
0021-94_012(5-31-06)	885	1136	30	221
0527-94-(6-8-06)_C04	885	1152	44	223
0634-94-(6-6-06)_B05	885	1147	23	239
0686-94-(6-6-06)_F11	885	1140	21	234
0766-94-(6-7-06)_A09	885	1151	32	234

0767-94-(6-7-06)_B09	885	1158	31	242
0263-94(5-31-06)_003	886	1165	34	245
0639-94-(6-6-06)_G05	886	1138	21	231
1042-94-(6-15-06)_E12	886	1157	25	246
1046-94-(6-2-06)_E06	886	1167	28	253
0526-94-(6-8-06)_B04	887	1166	44	235
0627-94-(6-6-06)_C04	887	1156	38	231
0665-94-(6-6-06)_A09	887	1166	46	233
1034-94-(6-14-06)_F08	887	1144	41	216
1159-94-(6-15-06)_A05	887	1160	46	227
0388-94-(6-12-06)_E10	888	1134	34	212
0440-94-(6-16-06)_H02	888	1135	29	218
0568-94-(6-8-06)_C08	888	1151	69	194
0836-94-(6-5-06)_D05	888	1129	45	196
1130-94-(6-9-06)_F10	888	1137	22	227
0915-94-(6-14-06)_B12	889	1140	38	213
0249-94(5-31-06)_007	890	1155	35	230
0539-94-(6-8-06)_G05	890	1153	44	219
0859-94-(6-5-06)_C08	890	1178	79	209
0547-94-(6-8-06)_G06	891	1150	46	213
0638-94-(6-6-06)_F05	891	1136	27	218
0714-94-(6-7-06)_F02	891	1151	25	235
0270-94(5-31-06)_002	892	1107	33	182
0346-94-(6-9-06)_D04	892	1167	69	206
0382-94-(6-12-06)_A10	892	1162	38	232
0570-94-(6-8-06)_E08	892	1176	40	244
0860-94-(6-5-06)_D08	892	1156	34	230
0275-94(5-31-06)_012	893	1155	74	188
0292-94(5-31-06)_014	893	1137	67	177
0381-94-(6-12-06)_H09	893	1152	26	233
0437-94-(6-16-06)_E02	893	1132	29	210
0588-94-(6-8-06)_C10	894	1150	45	211
0596-94-(6-8-06)_C11	894	1160	34	232
0701-94-(6-7-06)_A01	894	1159	28	237
0773-94-(6-7-06)_G09	894	1137	35	208
1102-94-(6-9-06)_B07	894	1157	49	214
1188-94-(6-15-06)_C07	895	1142	40	207
0017-94_004(5-31-06)	895	1126	37	194
0020-94_010(5-31-06)	895	1123	72	156
0445-94-(6-16-06)_D03	895	1148	47	206
0905-94-(6-14-06)_H10	895	1176	28	253
1015-94-(6-2-06)_F02	895	1144	35	214

0813-94-(6-5-06)_E02	896	1163	26	241
1018-94-(6-2-06)_A03	896	1136	27	213
1081-94-(6-2-06)_G10	896	1161	40	225
0336-94-(6-9-06)_D03	897	1160	34	229
0394-94-(6-8-06)_C12	897	1144	42	205
0858-94-(6-5-06)_B08	897	1175	46	232
1115-94-(6-9-06)_G08	897	1175	40	238
0681-94-(6-6-06)_A11	898	1153	28	227
0683-94-(6-6-06)_C11	898	1170	22	250
0690-94-(6-6-06)_B12	899	1153	27	227
0931-94-(6-16-06)_G11	899	1178	81	198
1172-94-(6-15-06)_B06	899	1142	68	175
0619-94-(6-6-06)_C03	900	1127	33	194
0636-94-(6-6-06)_D05	900	1136	22	214
1137-94-(6-9-06)_E11	900	1166	29	237
1167-94-(6-15-06)_F05	900	1123	31	192
1307-94-(6-16-06)_A07	901	1137	23	213
0693-94-(6-6-06)_E12	901	1200	75	224
0824-94-(6-5-06)_H03	901	1157	30	226
1133-94-(6-9-06)_A11	901	1172	30	241
0630-94-(6-6-06)_F04	902	1166	29	235
0641-94-(6-6-06)_A06	902	1163	23	238
0713-94-(6-7-06)_E02	902	1159	23	234
1104-94-(6-9-06)_D07	902	1168	32	234
0611-94-(6-6-06)_C02	903	1155	42	210
1005-94-(6-2-06)_E01	903	1130	22	205
1035-94-(6-14-06)_G08	903	1170	40	227
0254-94-(6-16-06)_B10	904	1172	36	232
0890-94-(6-14-06)_E07	904	1154	38	212
0926-94-(6-16-06)_D11	904	1165	48	213
0624-94-(6-6-06)_H03	905	1135	32	198
0925-94-(6-16-06)_C11	905	1177	37	235
0943-94-(6-16-06)_F12	905	1138	38	195
1179-94-(6-15-06)_F06	905	1144	29	210
0438-94-(6-16-06)_F02	906	1158	42	210
0699-94-(6-12-06)_H12	906	1139	69	164
0732-94-(6-14-06)_A05	906	1173	70	197
0255-94(5-31-06)_004	907	1145	34	204
0804-94-(6-5-06)_D01	907	1136	20	209
0805-94-(6-5-06)_E01	908	1143	31	204
1067-94-(6-2-06)_A09	908	1160	36	216
0829-94-(6-5-06)_E04	909	1155	34	212

0743-94-(6-7-06)_C06	910	1161	32	219
0810-94-(6-5-06)_B02	910	1187	80	197
1080-94-(6-2-06)_F10	910	1142	40	192
0888-94-(6-5-06)_H11	911	1159	32	216
1073-94-(6-2-06)_G09	911	1166	41	214
0522-94-(6-8-06)_F03	912	1145	30	203
0578-94-(6-8-06)_C09	912	1164	71	181
1077-94-(6-2-06)_C10	913	1167	29	225
1144-94-(6-9-06)_D12	914	1144	27	203
0280-94(5-31-06)_005	915	1149	39	195
0434-94-(6-16-06)_B02	915	1141	34	192
0695-94-(6-6-06)_G12	915	1159	32	212
0855-94-(6-5-06)_G07	915	1152	29	208
1086-94-(6-2-06)_D11	915	1150	38	197
1071-94-(6-2-06)_E09	916	1167	43	208
0720-94-(6-7-06)_D03	917	1129	25	187
0745-94-(6-7-06)_E06	917	1172	30	225
0936-94-(6-16-06)_D12	917	1149	33	199
1030-94-(6-2-06)_E04	917	1148	32	199
1040-94-(6-2-06)_G05	917	1166	27	222
0519-94-(6-8-06)_C03	918	1142	36	188
0760-94-(6-7-06)_D08	918	1137	30	189
1072-94-(6-2-06)_F09	919	1167	39	209
0296-94(5-31-06)_005	920	1148	79	149
1007-94-(6-2-06)_G01	920	1147	27	200
1125-94-(6-9-06)_A10	920	1164	31	213
1151-94-(6-15-06)_C04	920	1153	76	157
1174-94-(6-15-06)_D06	920	1150	26	204
0524-94-(6-8-06)_H03	921	1136	28	187
0891-94-(6-5-06)_C12	921	1182	40	221
1141-94-(6-9-06)_A12	921	1175	26	228
0400-94-(6-8-06)_H12	922	1175	45	208
0455-94-(6-16-06)_E04	922	1172	40	210
1310-94-(6-16-06)_D07	923	1168	30	215
0635-94-(6-6-06)_C05	923	1142	35	184
0814-94-(6-5-06)_F02	923	1169	28	218
0841-94-(6-5-06)_A06	923	1167	43	201
1076-94-(6-2-06)_B10	923	1171	34	214
0808-94-(6-5-06)_H01	924	1159	29	206
1002-94-(6-2-06)_B01	924	1137	23	190
0885-94-(6-5-06)_E11	925	1146	34	187
0911-94-(6-14-06)_F11	925	1168	27	216

0838-94-(6-5-06)_F05	926	1137	52	159
1101-94-(6-9-06)_A07	926	1192	44	222
1142-94-(6-9-06)_B12	926	1155	28	201
0525-94-(6-8-06)_A04	927	1160	45	188
1163-94-(6-15-06)_C05	927	1142	32	183
0922-94-(6-15-06)_A01	928	1168	40	200
0217-94-(6-16-06)_B09	929	1160	25	206
0843-94-(6-5-06)_C06	929	1176	39	208
1120-94-(6-9-06)_D09	929	1172	28	215
0230-94(5-31-06)_014	930	1157	41	186
0530-94-(6-8-06)_F04	930	1139	45	164
0581-94-(6-8-06)_E09	931	1156	31	194
0259-94(5-31-06)_012	932	1129	38	159
0024-94(5-31-06)_001	933	1144	38	173
0451-94-(6-16-06)_A04	933	1158	41	184
0884-94-(6-5-06)_D11	933	1131	29	169
0916-94-(6-14-06)_C12	933	1169	27	209
1171-94-(6-15-06)_A06	933	1168	43	192
0427-94-(6-16-06)_C01	935	1151	34	182
1016-94-(6-2-06)_G02	936	1145	34	175
0444-94-(6-16-06)_C03	937	1147	32	178
1187-94-(6-15-06)_B07	938	1165	35	192
0842-94-(6-5-06)_B06	938	1154	38	178
0282-94(5-31-06)_009	940	1125	41	144
1107-94-(6-9-06)_G07	940	1117	34	143
0262-94(5-31-06)_001	941	1113	34	138
0811-94-(6-5-06)_C02	941	1155	31	183
0863-94-(6-5-06)_G08	941	1153	48	164
0803-94-(6-5-06)_C01	943	1164	29	192
0294-94(5-31-06)_001	944	1139	41	154
0851-94-(6-5-06)_C07	944	1160	31	185
1028-94-(6-2-06)_C04	944	1155	42	169
0199-94(5-31-06)_008	945	1132	35	152
0303-94(5-31-06)_002	947	1135	35	153
0801-94-(6-5-06)_A01	948	1198	33	217
0857-94-(6-5-06)_A08	952	1160	48	160
0907-94-(6-14-06)_B11	953	1143	40	150
1027-94-(6-2-06)_B04	957	1194	36	201
0839-94-(6-14-06)_C06	959	1157	38	160
0393-94-(6-8-06)_B12	963	1169	31	175
0449-94-(6-27-06)_G06	976	1203	35	192
0429-94-(6-27-06)_B06	991	1191	32	168

0433-94-(6-27-06)_D06	1014	1212	48	150
Average Length	827.058			
Total	668			

APPENDIX H: *Arabidopsis* BLASTX

Query	**E-value**	**Description**
Contig_161	0	LOX2 (LIPOXYGENASE 2)
Contig_200	0	pepsin A
Contig_25	0	HSP81-2 (EARLY-RESPONSIVE TO DEHYDRATION 8); ATP binding
0275-94(5-31-06)_012	1.00E-99	SLT1 (SODIUM- AND LITHIUM-TOLERANT 1)
0356-94-(6-12-06)_A07	1.00E-99	C2 domain-containing protein
Contig_16	1.00E-99	ATARFA1E (ADP-ribosylation factor A1E); GTP binding / phospholipase activator/ protein binding
0943-94-(6-16-06)_F12	2.00E-99	mitochondrial phosphate transporter
1193-94-(6-15-06)_E07	2.00E-99	magnesium transporter CorA-like family protein (MRS2-2)
Contig_27	3.00E-99	PIP1;5/PIP1D (plasma membrane intrinsic protein 1;5); water channel
1169-94-(6-15-06)_G05	4.00E-99	HSP81-1 (HEAT SHOCK PROTEIN 81-1); ATP binding / unfolded protein binding
0684-94-(6-6-06)_D11	5.00E-99	ATEXLA1 (ARABIDOPSIS THALIANA EXPANSIN-LIKE A1)
0726-94-(6-7-06)_B04	9.00E-99	AtTLP7 (TUBBY LIKE PROTEIN 7); phosphoric diester hydrolase/ transcription factor
1188-94-(6-15-06)_C07	9.00E-99	GER2; catalytic
0710-94-(6-7-06)_B02	1.00E-98	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G23080.1); similar to putative membrane related protein CP5 [Oryza sativa (japonica cultivar-group)] (GB:BAC83004.1); contains InterPro domain Lipid-binding START; (InterPro:IPR002913)
Contig_198	1.00E-98	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G25170.1); similar to expressed protein [Oryza sativa (japonica cultivar-group)] (GB:ABB47783.1); similar to unknown protein [Oryza sativa] (GB:AAG16855.1); similar to Os02g0814000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001048488.1); contains InterPro domain Protein of unknown function DUF862, eukaryotic; (InterPro:IPR008580)
0400-94-(6-8-06)_H12	2.00E-98	leucine-rich repeat protein, putative
Contig_157	2.00E-98	XTR3 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 3); hydrolase, acting on glycosyl bonds
1152-94-(6-15-06)_D04	3.00E-98	ATPPC1 (PHOSPHOENOLPYRUVATE CARBOXYLASE 1); phosphoenolpyruvate carboxylase
0759-94-(6-7-06)_C08	5.00E-98	peptide methionine sulfoxide reductase family protein
Contig_40	6.00E-98	TAP46 (2A PHOSPHATASE ASSOCIATED PROTEIN OF 46 KD)
Contig_5	6.00E-98	IAR3 (IAA-ALANINE RESISTANT 3); metallopeptidase
0661-94-(6-6-06)_E08	2.00E-97	ATMAP70-3 (microtubule-associated proteins 70-3); microtubule binding
Contig_61	2.00E-97	XTR6 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 6); hydrolase, acting on glycosyl bonds

0546-94-(6-8-06)_F06	6.00E-97	phototropic-responsive NPH3 family protein
0789-94-(6-7-06)_E11	6.00E-97	transducin family protein / WD-40 repeat family protein
0119-94-F12(4-28-06)	7.00E-97	ATBCAT-5; branched-chain-amino-acid transaminase/catalytic
0230-94(5-31-06)_014	7.00E-97	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G50290.1); similar to Os05g0409100 [Oryza sativa (japonica cultivar-group)] (GB:NP_001055526.1); similar to Os06g0364500 [Oryza sativa (japonica cultivar-group)] (GB:NP_001057608.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAB84591.1)
Contig_182	8.00E-97	SOS1 (SALT OVERLY SENSITIVE 1); sodium:hydrogen antiporter
Contig_111	1.00E-96	GDSL-motif lipase/hydrolase family protein
Contig_15	1.00E-96	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G40000.1); similar to putative Hs1pro-1-like receptor [Glycine max] (GB:AAG44839.1); contains InterPro domain Hs1pro-1, C-terminal; (InterPro:IPR009743); contains InterPro domain Hs1pro-1, N-terminal; (InterPro:IPR009869)
Contig_100	3.00E-96	PAB8 (POLY(A) BINDING PROTEIN 8); RNA binding / translation initiation factor
0606-94-(6-6-06)_F01	7.00E-96	inorganic pyrophosphatase, putative (soluble) / pyrophosphate phospho-hydrolase, putative / PPase, putative
0525-94-(6-8-06)_A04	8.00E-96	AtTLP3 (TUBBY LIKE PROTEIN 3); phosphoric diester hydrolase/ transcription factor
1105-94-(6-9-06)_E07	9.00E-96	pectinesterase family protein
0451-94-(6-16-06)_A04	2.00E-95	zinc finger (C2H2 type) family protein
Contig_146	3.00E-95	CPN20 (CHAPERONIN 20); calmodulin binding
Contig_165	4.00E-95	transcription factor LIM, putative
1018-94-(6-2-06)_A03	5.00E-95	phosphofructokinase family protein
Contig_153	5.00E-95	zinc ion binding
Contig_132	9.00E-95	CCR4-NOT transcription complex protein, putative
0808-94-(6-5-06)_H01	1.00E-94	RLK902 (receptor-like kinase 902); ATP binding / kinase/ protein serine/threonine kinase
1179-94-(6-15-06)_F06	1.00E-94	EMB2024 (EMBRYO DEFECTIVE 2024); catalytic
0312-94-(6-9-06)_A01	2.00E-94	SAR1 (SYNAPTOBREVIN-RELATED PROTEIN 1)
0440-94-(6-16-06)_H02	2.00E-94	ATTIC110/TIC110 (TRANSLOCON AT THE INNER ENVELOPE MEMBRANE OF CHLOROPLASTS 110)
1050-94-(6-2-06)_A07	5.00E-94	zinc finger (C2H2 type) protein (WIP3)
1082-94-(6-2-06)_H10	5.00E-94	aspartate/glutamate/uridylate kinase family protein
Contig_114	7.00E-94	GA5 (GA REQUIRING 5); gibberellin 20-oxidase/ gibberellin 3-beta-dioxygenase

Contig_91	8.00E-94	BGAL1 (BETA GALACTOSIDASE 1); beta-galactosidase
1126-94-(6-9-06)_B10	1.00E-93	TMT2 (TONOPLAST MONOSACCHARIDE TRANSPORTER2); carbohydrate transporter/ sugar porter
1137-94-(6-9-06)_E11	3.00E-93	IBR5 (INDOLE-3-BUTYRIC ACID RESPONSE 5); protein tyrosine/serine/threonine phosphatase
0072-94-F01(5-9-06)	1.00E-92	MA3 domain-containing protein
0347-94-(6-12-06)_F06	1.00E-92	ATRBP45B; RNA binding
0192-94-A06(5-10-06)	2.00E-92	PSBO-2/PSBO2 (PHOTOSYSTEM II SUBUNIT O-2); oxygen evolving
0817-94-(6-5-06)_A03	2.00E-92	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G58010.1); similar to Os04g0665800 [Oryza sativa (japonica cultivar-group)] (GB:NP_001054180.1); similar to unknown [Vitis pseudoreticulata] (GB:ABC69760.1)
Contig_116	2.00E-92	ATPHB1 (PROHIBITIN 1)
Contig_44	3.00E-92	40S ribosomal protein S9 (RPS9C)
Contig_93	3.00E-92	CLC-E (CHLORIDE CHANNEL E); voltage-gated chloride channel
1047-94-(6-2-06)_F06	4.00E-92	transducin family protein / WD-40 repeat family protein
0185-94-B05(5-10-06)	5.00E-92	homeotic gene regulator, putative
Contig_147	5.00E-92	60S ribosomal protein L10A (RPL10aA)
Contig_173	5.00E-92	AT1G75840.1/ATGP3/ATROP4 (RHO-LIKE GTP BINDING PROTEIN 4); GTP binding / GTPase
0307-94-(6-12-06)_F05	8.00E-92	COP13 (CONSTITUTIVE PHOTOMORPHOGENIC 13)
0536-94-(6-8-06)_D05	8.00E-92	ASAR1 (Arabidopsis thaliana secretion-associated RAS super family 2); GTP binding
0598-94-(6-8-06)_E11	1.00E-91	short-chain dehydrogenase/reductase (SDR) family protein
1054-94-(6-2-06)_E07	1.00E-91	AFB5 (AUXIN F-BOX PROTEIN 5); ubiquitin-protein ligase
0349-94-(6-9-06)_F04	2.00E-91	fringe-related protein
0607-94-(6-6-06)_G01	2.00E-91	pectate lyase family protein
0854-94-(6-5-06)_F07	2.00E-91	similar to conserved hypothetical protein [Medicago truncatula] (GB:ABE78854.1)
0359-94-(6-12-06)_D07	3.00E-91	haloacid dehalogenase-like hydrolase family protein
0591-94-(6-8-06)_F10	3.00E-91	catalytic
0713-94-(6-7-06)_E02	4.00E-91	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G22270.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD52714.1); contains domain SUBFAMILY NOT NAMED (PTHR21551:SF13); contains domain FAMILY NOT NAMED (PTHR21551)
1171-94-(6-15-06)_A06	4.00E-91	replication protein, putative

0030-94-E01(4-28-06)	5.00E-91	leucine-rich repeat family protein / protein kinase family protein
1125-94-(6-9-06)_A10	7.00E-91	VTI12 (VESICAL TRANSPORT V-SNARE 12, vesical transport v-SNARE 12); SNARE binding / receptor
0431-94-(6-16-06)_G01	8.00E-91	KNAT7 (Knotted-like Arabidopsis thaliana); DNA binding / transcription factor
0325-94-(6-14-06)_E02	9.00E-91	transcription factor LIM, putative
0656-94-(6-6-06)_H07	9.00E-91	SNF4 (Sucrose NonFermenting 4)
0326-94-(6-14-06)_F02	1.00E-90	mannitol transporter, putative
0755-94-(6-7-06)_G07	2.00E-90	CM1 (chorismate mutase 1); chorismate mutase
0788-94-(6-7-06)_D11	2.00E-90	glycosyl hydrolase family 17 protein
0583-94-(6-8-06)_F09	3.00E-90	leucine-rich repeat family protein / protein kinase family protein
0642-94-(6-6-06)_B06	3.00E-90	Identical to Probable ATP synthase 24 kDa subunit, mitochondrial precursor (EC 3.6.3.14) [Arabidopsis Thaliana] (GB:Q9SJ12;GB:Q8LBN3); similar to hypothetical protein MtrDRAFT_AC155898g5v1 [Medicago truncatula] (GB:ABE87707.1)
0541-94-(6-8-06)_A06	4.00E-90	AR401
Contig_95	5.00E-90	patched family protein
1178-94-(6-15-06)_E06	6.00E-90	beta-galactosidase
0159-94(5-31-06)_004	7.00E-90	RHA1
0896-94-(6-5-06)_H12	7.00E-90	zinc finger (C2H2 type, AN1-like) family protein
0748-94-(6-7-06)_H06	9.00E-90	leucine-rich repeat family protein
0210-94-C08(5-10-06)	3.00E-89	synbindin, putative
0657-94-(6-6-06)_A08	4.00E-89	60S ribosomal protein L18 (RPL18C)
0107-94-(6-12-06)_A04	1.00E-88	UVH1 (ULTRAVIOLET HYPERSENSITIVE 1)
Contig_122	2.00E-88	60S ribosomal protein L6 (RPL6A)
Contig_126	2.00E-88	Ras-related GTP-binding family protein
Contig_166	3.00E-88	translation elongation factor
0447-94-(6-16-06)_F03	5.00E-88	MIR domain-containing protein
0514-94-(6-8-06)_F02	6.00E-88	TIC20; protein translocase
0572-94-(6-8-06)_G08	1.00E-87	RHL2 (ROOT HAIRLESS 2); ATP binding / DNA binding / DNA topoisomerase (ATP-hydrolyzing)
0666-94-(6-6-06)_B09	1.00E-87	catalytic

0908-94-(6-14-06)_C11	2.00E-87	methyladenine glycosylase family protein
0599-94-(6-8-06)_F11	3.00E-87	GHMP kinase-related
0923-94-(6-15-06)_B01	3.00E-87	EMB2386 (EMBRYO DEFECTIVE 2386); structural constituent of ribosome
1077-94-(6-2-06)_C10	8.00E-87	similar to conserved hypothetical protein [Medicago truncatula] (GB:ABE83236.1)
0276-94(5-31-06)_014	1.00E-86	zinc finger (ZPR1-type) family protein
0570-94-(6-8-06)_E08	1.00E-86	HEMB1
Contig_190	1.00E-86	glutamate decarboxylase, putative
0861-94-(6-5-06)_E08	2.00E-86	In2-1 protein, putative
Contig_70	2.00E-86	ADK1 (ADENYLATE KINASE 1); adenylate kinase
1064-94-(6-2-06)_F08	9.00E-86	ATRSP41 (Arabidopsis thaliana arginine/serine-rich splicing factor 41); RNA binding
0144-94(5-31-06)_015	1.00E-85	transcription factor S-II (TFIIS) domain-containing protein
0112-94-(6-12-06)_D04	2.00E-85	SNF7 family protein
0530-94-(6-8-06)_F04	2.00E-85	VTI11 (VESICLE TRANSPORT V-SNARE 11, vesicle transport v-SNARE 11); receptor
0739-94-(6-7-06)_G05	2.00E-85	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G45750.1); similar to Os01g0846500 [Oryza sativa (japonica cultivar-group)] (GB:NP_001044790.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD81827.1); contains InterPro domain PAP/25A-associated; (InterPro:IPR002058); contains InterPro domain PAP/25A core; (InterPro:IPR001201)
0942-94-(6-15-06)_E03	2.00E-85	DNAJ heat shock family protein
Contig_63	2.00E-85	similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD81183.1); contains InterPro domain Breast carcinoma amplified sequence 2; (InterPro:IPR008409)
0305-94(5-31-06)_004	3.00E-85	peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative
1096-94-(6-2-06)_F12	3.00E-85	similar to NERD [Medicago truncatula] (GB:ABE94711.1); contains InterPro domain NERD; (InterPro:IPR011528)
0749-94-(6-7-06)_A07	4.00E-85	similar to Os01g0184800 [Oryza sativa (japonica cultivar-group)] (GB:NP_001042236.1); similar to phosducin-like 3 [Homo sapiens] (GB:NP_076970.1); contains InterPro domain Thioredoxin-like fold; (InterPro:IPR012336); contains InterPro domain Phosducin; (InterPro:IPR001200); contains InterPro domain Thioredoxin fold; (InterPro:IPR012335)
0886-94-(6-5-06)_F11	4.00E-85	CYCD3;2 (CYCLIN D3;2); cyclin-dependent protein kinase
0946-94-(6-15-06)_A04	5.00E-85	PBG1 (20S proteasome beta subunit G1); peptidase
0227-94-D10(5-10-06)	6.00E-85	PECT1 (PHOSPHORYLETHANOLAMINE CYTIDYLYLTRANSFERASE 1); ethanolamine-phosphate cytidylyltransferase

0785-94-(6-7-06)_B11	9.00E-85	GPT (UDP-GLCNAC%3ADOLICHOL+PHOSPHATE+GLCNAC-1-P+TRANSFERASE); UDP-N-acetylglucosamine-dolichyl-phosphate N-acetylglucosaminephosphotransferase
0284-94(5-31-06)_013	1.00E-84	QUA1 (QUASIMODO1); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups
0450-94-(6-16-06)_H03	1.00E-84	short-chain dehydrogenase/reductase (SDR) family protein
0708-94-(6-7-06)_H01	1.00E-84	similar to Os03g0849600 [Oryza sativa (japonica cultivar-group)] (GB:NP_001051898.1); similar to Low density lipoprotein receptor (ISS) [Ostreococcus tauri] (GB:CAL52868.1); contains InterPro domain COG complex component, COG2; (InterPro:IPR009316)
0740-94-(6-7-06)_H05	2.00E-84	GLP10 (GERMIN-LIKE PROTEIN 10); manganese ion binding / metal ion binding / nutrient reservoir
0929-94-(6-15-06)_H01	2.00E-84	lysine decarboxylase family protein
Contig_172	2.00E-84	ATGDI2 (RAB GDP DISSOCIATION INHIBITOR 2); RAB GDP-dissociation inhibitor
0008-94-G05(4-20-06)	3.00E-84	coatomer protein complex, subunit alpha, putative
0509-94-(6-8-06)_A02	3.00E-84	enolase, putative
1087-94-(6-2-06)_E11	4.00E-84	zinc finger (C2H2 type) family protein
Contig_17	6.00E-84	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G01360.1); similar to CAPIP1 [Capsicum annuum] (GB:AAT35532.1); similar to CAPIP1-like [Solanum tuberosum] (GB:ABB29920.1); contains domain Bet v1-like (SSF55961); contains domain no description (G3D.3.30.530.20)
Contig_35	8.00E-84	NIK1 (NSP-INTERACTING KINASE 1); kinase
0738-94-(6-7-06)_F05	1.00E-83	similar to unnamed protein product [Ostreococcus tauri] (GB:CAL57827.1); similar to Os01g0271000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001042705.1)
0824-94-(6-5-06)_H03	1.00E-83	UBC35; ubiquitin-protein ligase
0917-94-(6-14-06)_D12	1.00E-83	NIK3 (NSP-INTERACTING KINASE 3); kinase
1130-94-(6-9-06)_F10	1.00E-83	glucosamine/galactosamine-6-phosphate isomerase family protein
Contig_54	1.00E-83	HUB1 (HISTONE MONO-UBIQUITINATION 1); protein binding / zinc ion binding
0295-94(5-31-06)_003	2.00E-83	U-box domain-containing protein
Contig_48	2.00E-83	UBC28; ubiquitin-protein ligase
0099-94-B10(4-28-06)	3.00E-83	ATGDI1 (Arabidopsis thaliana guanosine diphosphate dissociation inhibitor 1)
0198-94-(6-16-06)_H08	3.00E-83	lipocalin, putative
0529-94-(6-8-06)_E04	1.00E-82	PIMT1 (PROTEIN-L-ISOASPARTATE METHYLTRANSFERASE 1); protein-L-isoaspartate (D-aspartate) O-methyltransferase
Contig_79	2.00E-82	2-oxoacid dehydrogenase family protein
0297-94(5-31-	3.00E-	ORMDL family protein

06)_007	82	
0686-94-(6-6-06)_F11	8.00E-82	transferase family protein
1073-94-(6-2-06)_G09	8.00E-82	similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:AT5G38560.1); similar to Os01g0653800 [Oryza sativa (japonica cultivar-group)] (GB:NP_001043744.1); similar to WD-40 repeat family protein [Medicago sativa] (GB:AAZ31064.1); similar to Peptidase S8 and S53, subtilisin, kexin, sedolisin; WD40-like [Medicago truncatula] (GB:ABD32844.1); contains InterPro domain WD-40 repeat; (InterPro:IPR001680); contains InterPro domain WD40-like; (InterPro:IPR011046)
0782-94-(6-7-06)_G10	9.00E-82	COI1 (CORONATINE INSENSITIVE 1); ubiquitin-protein ligase
1015-94-(6-2-06)_F02	1.00E-81	UBC20 (ubiquitin-conjugating enzyme 20); ubiquitin-protein ligase
0524-94-(6-8-06)_H03	2.00E-81	zinc finger (B-box type) family protein
0780-94-(6-7-06)_E10	2.00E-81	UBC13 (ubiquitin-conjugating enzyme 13); ubiquitin-protein ligase
1025-94-(6-2-06)_H03	2.00E-81	ABI1L1 (ABI-1-LIKE 1)
0527-94-(6-8-06)_C04	4.00E-81	binding
1036-94-(6-2-06)_C05	7.00E-81	bZIP transcription factor family protein
Contig_171	7.00E-81	AT-HSFB4 (Arabidopsis thaliana heat shock transcription factor B4); DNA binding / transcription factor
0012-94_009(5-31-06)	1.00E-80	similar to EDA30 (embryo sac development arrest 30) [Arabidopsis thaliana] (TAIR:AT3G03810.1); similar to putative auxin-independent growth promoter protein [Oryza sativa (japonica cultivar-group)] (GB:AAT85168.1); similar to Os05g0132500 [Oryza sativa (japonica cultivar-group)] (GB:NP_001054559.1); contains InterPro domain Protein of unknown function DUF246, plant; (InterPro:IPR004348)
0446-94-(6-16-06)_E03	2.00E-80	ATBETAFRUCT4/VAC-INV (VACUOLAR INVERTASE); beta-fructofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds
0752-94-(6-7-06)_D07	2.00E-80	VAMP7C (VESICLE-ASSOCIATED MEMBRANE PROTEIN 7C)
Contig_32	2.00E-80	GCN5-related N-acetyltransferase, putative
Contig_83	4.00E-80	hydrolase, hydrolyzing O-glycosyl compounds
Contig_67	5.00E-80	zinc finger (C3HC4-type RING finger) family protein
0905-94-(6-14-06)_H10	6.00E-80	CNGC1 (CYCLIC NUCLEOTIDE GATED CHANNEL 1); calmodulin binding / cation channel/ cyclic nucleotide binding / inward rectifier potassium channel
1061-94-(6-2-06)_C08	7.00E-80	peptidyl-prolyl cis-trans isomerase, putative / FK506-binding protein, putative
0462-94-(6-16-06)_D05	9.00E-80	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G34215.2); similar to Os03g0857500 [Oryza sativa (japonica cultivar-group)] (GB:NP_001051956.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAP21393.1); contains InterPro domain Protein of unknown function DUF303, acetylesterase putative; (InterPro:IPR005181)

0074-93-G04(4-21-06)	1.00E-79	PLDALPHA2 (PHOSPHLIPASE D ALPHA 2); phospholipase D
0278-94(5-31-06)_001	1.00E-79	cysteine proteinase (RD21A) / thiol protease
0208-94-A08(5-10-06)	2.00E-78	protein phosphatase 2C-related / PP2C-related
Contig_31	3.00E-78	peptidoglycan-binding LysM domain-containing protein
0603-94-(6-6-06)_C01	4.00E-78	ALPHA-SNAP2 (ALPHA-SOLUBLE NSF ATTACHMENT PROTEIN); soluble NSF attachment protein
0597-94-(6-8-06)_D11	5.00E-78	ATRSP31 (ARGININE/SERINE-RICH SPLICING FACTOR 31); RNA binding
Contig_123	5.00E-78	DNAJ heat shock N-terminal domain-containing protein
0430-94-(6-16-06)_F01	6.00E-78	PQ-loop repeat family protein / transmembrane family protein
0679-94-(6-6-06)_G10	6.00E-78	EMB3004/MEE32 (EMBRYO DEFECTIVE 3004, maternal effect embryo arrest 32); 3-dehydroquinate dehydratase/ NADP binding / shikimate 5-dehydrogenase
Contig_191	1.00E-77	PEX22 (PEROXIN 22); protein binding
0457-94-(6-16-06)_G04	4.00E-77	4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein
0857-94-(6-5-06)_A08	6.00E-77	LIL3:1; transcription factor
1128-94-(6-9-06Truncated)_D10	1.00E-76	DNAJ heat shock protein, putative
0522-94-(6-8-06)_F03	2.00E-76	RTH (RTE1-HOMOLOG)
0387-94-(6-12-06)_D10	3.00E-76	nucleolar protein Nop56, putative
0223-94-H09(5-10-06)	4.00E-76	zinc finger (C3HC4-type RING finger) family protein
0792-94-(6-7-06)_H11	4.00E-76	similar to unnamed protein product; contains similarity to unknown protein gb
0095-93-B02(4-21-06)	4.00E-75	vesicle tethering family protein
0460-94-(6-16-06)_B05	6.00E-75	ARL1 (ARG1-LIKE1); heat shock protein binding / unfolded protein binding
1029-94-(6-2-06)_D04	6.00E-75	microtubule associated protein (MAP65/ASE1) family protein
Contig_195	6.00E-75	oxidoreductase, 2OG-Fe(II) oxygenase family protein
0360-94-(6-12-06)_E07	8.00E-75	RNA binding / tRNA methyltransferase
0567-94-(6-8-06)_B08	1.00E-74	aconitase C-terminal domain-containing protein
1111-94-(6-9-06)_C08	1.00E-74	phosphate-responsive 1 family protein
0702-94-(6-7-06)_B01	2.00E-74	similar to Os01g0112100 [Oryza sativa (japonica cultivar-group)] (GB:NP_001041811.1)
Contig_104	4.00E-74	similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAL86463.1); contains InterPro domain Sigma factor, regions 3 and 4; (InterPro:IPR013324)

0444-94-(6-16-06)_C03	5.00E-74	similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAO38479.1)
Contig_73	5.00E-74	EMB1467 (EMBRYO DEFECTIVE 1467); NADH dehydrogenase
0285-94(5-31-06)_015	7.00E-74	RNA recognition motif (RRM)-containing protein
0257-94(5-31-06)_008	9.00E-74	mitochondrial substrate carrier family protein
0221-94-F09(5-10-06)	1.00E-73	similar to VIP2 (VIRE2 INTERACTING PROTEIN2), transcription regulator [Arabidopsis thaliana] (TAIR:AT5G59710.1); similar to NOT2/NOT3/NOT5 [Medicago truncatula] (GB:ABE93791.1); similar to NOT2/NOT3/NOT5 family protein, expressed [Oryza sativa (japonica cultivar-group)] (GB:ABF98742.1); similar to VIP2 [Nicotiana benthamiana] (GB:AAY15746.1); contains InterPro domain NOT2/NOT3/NOT5; (InterPro:IPR007282)
0533-94-(6-8-06)_A05	1.00E-73	DNAJ heat shock N-terminal domain-containing protein
1108-94-(6-9-06)_H07	2.00E-73	eukaryotic translation initiation factor SUI1 family protein
0141-94-E04(5-9-06)	3.00E-73	zinc knuckle (CCHC-type) family protein
Contig_205	3.00E-73	ATAUX2-11 (indoleacetic acid-induced protein 4); transcription factor
0901-94-(6-14-06)_D10	1.00E-72	phosphoglycerate/bisphosphoglycerate mutase family protein
0921-94-(6-14-06)_H12	1.00E-72	TOM2A (TOBAMOVIRUS MULTIPLICATION 2A)
1144-94-(6-9-06)_D12	2.00E-72	MEMB11 (Golgi SNARE protein membrin 11); v-SNARE
Contig_180	2.00E-72	mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein
0811-94-(6-5-06)_C02	3.00E-72	PDE135 (PIGMENT DEFECTIVE EMBRYO 135); permease
Contig_155	3.00E-72	NHL1 (NDR1/HIN1-like 1)
0513-94-(6-8-06)_E02	6.00E-72	PDC2 (PYRUVATE DECARBOXYLASE-2); pyruvate decarboxylase
0162-94-B07(5-5-06)	1.00E-71	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G74440.1); similar to YGL010w-like protein [Picea mariana] (GB:AAC32136.1); contains InterPro domain Protein of unknown function DUF962; (InterPro:IPR009305)
1017-94-(6-2-06)_H02	1.00E-71	glycosyl hydrolase family 5 protein / cellulase family protein
1067-94-(6-2-06)_A09	2.00E-71	RHL1 (ROOT HAIRLESS 1)
0239-94-H11(5-10-06)	4.00E-71	PQ-loop repeat family protein / transmembrane family protein
0687-94-(6-6-06)_G11	6.00E-71	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G45060.1); similar to conserved hypothetical protein [Medicago truncatula] (GB:ABE90926.1)
Contig_69	6.00E-71	protein phosphatase 2C, putative / PP2C, putative
0866-94-(6-5-06)_B09	1.00E-70	HAT22 (homeobox-leucine zipper protein 22); transcription factor
0006-94-C05(4-20-	2.00E-	similar to AMP-dependent synthetase and ligase [Medicago

06)	70	truncatula] (GB:ABE91856.1)
0595-94-(6-8-06)_B11	2.00E-70	ATWHY2 (A. THALIANA WHIRLY 2); DNA binding
0313-94-(6-9-06)_B01	4.00E-70	RPS6 (RIBOSOMAL PROTEIN S6); structural constituent of ribosome
0079-93-B04(4-21-06)	5.00E-70	lysyl-tRNA synthetase, putative / lysine--tRNA ligase, putative
Contig_68	6.00E-70	MYB88 (myb domain protein 88); DNA binding / transcription factor
0653-94-(6-6-06)_E07	8.00E-70	isochorismatase hydrolase family protein
0255-94(5-31-06)_004	9.00E-70	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G42860.1); similar to H0814G11.12 [Oryza sativa (indica cultivar-group)] (GB:CAJ86345.1); similar to CAA30379.1 protein [Oryza sativa] (GB:CAB53482.1)
0847-94-(6-5-06)_G06	3.00E-69	ATP binding / protein kinase/ protein serine/threonine kinase
0920-94-(6-14-06)_G12	3.00E-69	enoyl-CoA hydratase/isomerase family protein
Contig_62	3.00E-69	THI1 (THIAZOLE REQUIRING)
0654-94-(6-6-06)_F07	4.00E-69	FATB (FATTY ACYL-ACP THIOESTERASES B); acyl carrier/ acyl-ACP thioesterase
0803-94-(6-5-06)_C01	4.00E-69	F-box family protein
1308-94-(6-16-06)_B07	6.00E-69	ATARP8 (ACTIN-RELATED PROTEIN 8); structural constituent of cytoskeleton
0123-94-C02(5-9-06)	7.00E-69	EMB1067 (EMBRYO DEFECTIVE 1067); tRNA 2'-phosphotransferase
Contig_72	2.00E-68	chalcone-flavanone isomerase family protein
0833-94-(6-5-06)_A05	5.00E-68	ACX4 (ACYL-COA OXIDASE 4); oxidoreductase
0897-94-(6-14-06)_G07	2.00E-67	transcription factor IIA large subunit / TFIIA large subunit (TFIIA-L)
Contig_124	2.00E-67	NADH:ubiquinone oxidoreductase family protein
0017-94_004(5-31-06)	3.00E-67	WRKY17 (WRKY DNA-binding protein 17); transcription factor
Contig_24	3.00E-67	calmodulin-binding protein
0846-94-(6-5-06)_F06	4.00E-67	late embryogenesis abundant family protein / LEA family protein
Contig_71	4.00E-67	PEX10 (peroxin 10); protein binding / zinc ion binding
0691-94-(6-6-06)_C12	7.00E-67	GCN5-related N-acetyltransferase (GNAT) family protein
0105-94-H10(4-28-06)	9.00E-67	PAB8 (POLY(A) BINDING PROTEIN 8); RNA binding / translation initiation factor
1182-94-(6-15-06)_H06	1.00E-66	33 kDa secretory protein-related
0537-94-(6-8-06)_E05	2.00E-66	OTU-like cysteine protease family protein
0907-94-(6-14-	3.00E-	calcium ion binding

06)_B11	66	
Contig_181	7.00E-66	26S proteasome regulatory subunit, putative
0821-94-(6-5-06)_E03	8.00E-66	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G12030.1); similar to fiber protein Fb27 [Gossypium barbadense] (GB:AAQ84318.1); contains InterPro domain Protein of unknown function DUF841, eukaryotic; (InterPro:IPR008559)
Contig_37	9.00E-66	UDP-glucoronosyl/UDP-glucosyl transferase family protein
0032-93-A10(4-21-06)	1.00E-65	H+-transporting two-sector ATPase, putative
0639-94-(6-6-06)_G05	1.00E-65	lectin protein kinase, putative
1192-94-(6-15-06)_D07	1.00E-65	lipase class 3 family protein
0640-94-(6-6-06)_H05	2.00E-65	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G21460.1); similar to Os08g0513300 [Oryza sativa (japonica cultivar-group)] (GB:NP_001062225.1); similar to Protein involved in high osmolarity signaling pathway (ISS) [Ostreococcus tauri] (GB:CAL57599.1); contains domain SUBFAMILY NOT NAMED (PTHR13490:SF4); contains domain FAMILY NOT NAMED (PTHR13490)
0130-94-B03(5-9-06)	8.00E-65	ATR1 (ARABIDOPSIS CYTOCHROME REDUCTASE)
1194-94-(6-15-06)_F07	9.00E-65	basic helix-loop-helix (bHLH) family protein
Contig_120	9.00E-65	glutamate binding
0835-94-(6-5-06)_C05	1.00E-64	SEC10 (EXOCYST COMPLEX COMPONENT SEC10)
1058-94-(6-2-06)_H07	1.00E-64	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27435.1); similar to Os09g0281300 [Oryza sativa (japonica cultivar-group)] (GB:NP_001062767.1); similar to fiber protein Fb34 [Gossypium barbadense] (GB:AAR07596.1); contains InterPro domain Protein of unknown function DUF1218; (InterPro:IPR009606)
0658-94-(6-6-06)_B08	2.00E-64	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G11560.4); similar to Os08g0482100 [Oryza sativa (japonica cultivar-group)] (GB:NP_001062067.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD09288.1); contains InterPro domain LETM1-like; (InterPro:IPR011685)
Contig_131	6.00E-64	transporter-related
1076-94-(6-2-06)_B10	8.00E-64	NDP1 (RANDOM POTATO CDNA CLONE); binding
0120-94-A02(5-9-06)	9.00E-64	alpha-mannosidase
0177-94-B04(5-10-06)	1.00E-63	AGL20 (AGAMOUS-LIKE 20); transcription factor
0696-94-(6-6-06)_H12	1.00E-63	myb family transcription factor
0736-94-(6-7-06)_D05	1.00E-63	NPL4 family protein
Contig_186	2.00E-63	translocon-associated protein beta (TRAPB) family protein

1041-94-(6-2-06)_H05	3.00E-63	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G21140.1); similar to Os01g0511200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001043171.1)
0922-94-(6-15-06)_A01	5.00E-63	ATFP3 (Arabidopsis thaliana farnesylated protein 3)
1080-94-(6-2-06)_F10	5.00E-63	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G07090.1); similar to Protein of unknown function DUF640 [Medicago truncatula] (GB:ABE92798.1); contains InterPro domain Protein of unknown function DUF640; (InterPro:IPR006936)
0545-94-(6-8-06)_E06	8.00E-63	ATOMT1 (O-METHYLTRANSFERASE 1)
Contig_59	9.00E-63	universal stress protein (USP) family protein
0147-94-C05(5-9-06)	2.00E-62	IQD13 (IQ-domain 13); calmodulin binding
0810-94-(6-5-06)_B02	2.00E-62	FIP1 (FH INTERACTING PROTEIN 1)
1086-94-(6-2-06)_D11	3.00E-62	CRY2 (CRYPTOCHROME 2)
0436-94-(6-16-06)_D02	4.00E-62	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G24805.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAC75560.1); contains InterPro domain Methyltransferase FkbM; (InterPro:IPR006342)
0625-94-(6-6-06)_A04	6.00E-62	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G65810.1); similar to Os01g0144000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001042001.1); similar to conserved hypothetical protein [Medicago truncatula] (GB:ABE78370.1); contains domain S-adenosyl-L-methionine-dependent methyltransferases (SSF53335)
Contig_188	6.00E-62	F-box family protein (FBX13)
0118-94-E12(4-28-06)	7.00E-62	GLP7 (GERMIN-LIKE PROTEIN 7); manganese ion binding / metal ion binding / nutrient reservoir
0129-94-A03(5-9-06)	7.00E-62	NADP-dependent oxidoreductase, putative
0531-94-(6-8-06)_G04	8.00E-62	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G48660.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD69146.1); similar to Os02g0321800 [Oryza sativa (japonica cultivar-group)] (GB:NP_001046689.1); similar to Os05g0272900 [Oryza sativa (japonica cultivar-group)] (GB:NP_001055067.1); contains InterPro domain B-cell receptor-associated 31-like; (InterPro:IPR008417)
0121-94-H12(4-28-06)	1.00E-61	GAE4 (UDP-D-GLUCURONATE 4-EPIMERASE 4); catalytic
0329-94-(6-27-06)_H03	1.00E-61	aspartyl protease family protein
Contig_34	1.00E-61	(1-4)-beta-mannan endohydrolase, putative
0717-94-(6-7-06)_A03	2.00E-61	MSBP1 (ARABIDOPSIS THALIANA MEMBRANE-ASSOCIATED PROGESTERONE BINDING PROTEIN 5)
Contig_88	7.00E-61	nucleoside-triphosphatase/ nucleotide binding
0843-94-(6-5-06)_C06	8.00E-61	ATRPAC43 (Arabidopsis thaliana RNA polymerase I subunit 43); DNA binding / DNA-directed RNA polymerase
0856-94-(6-5-	9.00E-	ankyrin repeat family protein

06)_H07	61	
0029-94-D01(4-28-06)	1.00E-60	copine-related
0704-94-(6-7-06)_D01	1.00E-60	Clp amino terminal domain-containing protein
0729-94-(6-7-06)_E04	1.00E-60	RNA recognition motif (RRM)-containing protein
0010-94_005(5-31-06)	2.00E-60	arginine biosynthesis protein ArgJ family
1079-94-(6-2-06)_E10	2.00E-60	zinc finger (C3HC4-type RING finger) family protein
1003-94-(6-2-06)_C01	4.00E-60	cupin family protein
Contig_86	9.00E-60	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G05830.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD86886.1); similar to Os05g0135900 [Oryza sativa (japonica cultivar-group)] (GB:NP_001054577.1); contains InterPro domain tRNA-binding arm; (InterPro:IPR010978)
0252-94(5-31-06)_013	1.00E-59	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G24610.1); similar to expressed protein [Oryza sativa (japonica cultivar-group)] (GB:ABB47870.1)
0260-94(5-31-06)_014	1.00E-59	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G10385.1); similar to expressed protein (with alternative splicing) [Oryza sativa (japonica cultivar-group)] (GB:AAS07222.1); similar to AT5g49830/K21G20_4 [Medicago truncatula] (GB:ABE86338.1); similar to Os07g0200000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001059127.1); contains domain FAMILY NOT NAMED (PTHR21426); contains domain gb def: Gb
0830-94-(6-5-06)_F04	1.00E-59	dentin sialophosphoprotein-related
0895-94-(6-5-06)_G12	1.00E-59	similar to Os01g0166800 [Oryza sativa (japonica cultivar-group)] (GB:NP_001042118.1); similar to P0028E10.3 [Oryza sativa (japonica cultivar-group)] (GB:BAB39900.1); contains domain gb def: Hypothetical protein At2g40550 (PTHR13489:SF2); contains domain FAMILY NOT NAMED (PTHR13489)
0914-94-(6-14-06)_A12	2.00E-59	RCD1 (RADICAL-INDUCED CELL DEATH1)
0540-94-(6-8-06)_H05	3.00E-59	aldo/keto reductase, putative
1104-94-(6-9-06)_D07	7.00E-59	SPL1 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 1); DNA binding / transcription factor
0128-94(5-31-06)_009	9.00E-59	AOC4 (ALLENE OXIDE CYCLASE 4)
Contig_9	1.00E-58	delta-OAT (ornithine- delta-aminotransferase); ornithine-oxo-acid transaminase
0688-94-(6-6-06)_H11	2.00E-58	U-box domain-containing protein
Contig_23	2.00E-58	ACD32.1 (ALPHA-CRYSTALLIN DOMAIN 31.2)
0636-94-(6-6-06)_D05	6.00E-58	AKRP/EMB2036 (EMBRYO DEFECTIVE 2036); protein binding
0655-94-(6-6-06)_G07	7.00E-58	PPI1 (PROTON PUMP INTERACTOR 1)

0179-94-D04(5-10-06)	1.00E-57	similar to Cupin, RmlC-type [Medicago truncatula] (GB:ABD28667.1); similar to Os01g0810200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001044582.1); contains InterPro domain Cupin, RmlC-type; (InterPro:IPR011051)
0373-94-(6-12-06)_A09	1.00E-57	SNF7 family protein
0892-94-(6-5-06)_D12	1.00E-57	F-box family protein
0426-94-(6-16-06)_B01	2.00E-57	ALF4 (ABERRANT LATERAL ROOT FORMATION 4)
0663-94-(6-6-06)_G08	2.00E-57	LIM domain-containing protein
1085-94-(6-2-06)_C11	2.00E-57	armadillo/beta-catenin repeat family protein
Contig_3	3.00E-57	polcalcin, putative / calcium-binding pollen allergen, putative
1307-94-(6-16-06)_A07	5.00E-57	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G57280.1); similar to non-green plastid inner envelope membrane protein precursor (GB:AAA84891.1); contains InterPro domain Protein of unknown function UPF0136, Transmembrane; (InterPro:IPR005349)
1026-94-(6-2-06)_A04	6.00E-57	kinesin motor protein-related
0584-94-(6-8-06)_G09	1.00E-56	similar to BSD domain-containing protein [Arabidopsis thaliana] (TAIR:AT1G26300.1); similar to Os04g0662000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001054153.1); similar to Os02g0726400 [Oryza sativa (japonica cultivar-group)] (GB:NP_001047990.1); contains InterPro domain BSD; (InterPro:IPR005607)
0770-94-(6-14-06)_B05'	1.00E-56	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G52330.1); similar to Os03g0696000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001050978.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:AAO19373.1)
0300-94(5-31-06)_013	2.00E-56	ATKINESIN-13A/KINESIN-13A; microtubule motor
Contig_176	6.00E-56	DNA-binding protein-related
0048-94-G03(4-28-06)	1.00E-55	mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein
0562-94-(6-8-06)_H07	2.00E-55	CDR1 (CONSTITUTIVE DISEASE RESISTANCE 1); aspartic-type endopeptidase/ pepsin A
Contig_194	2.00E-55	reticulon family protein (RTNLB3)
Contig_99	2.00E-55	carbon-sulfur lyase
0454-94-(6-16-06)_D04	3.00E-55	similar to hypothetical protein [Prunus persica] (GB:AAO14625.1)
Contig_199	3.00E-55	SVP (SHORT VEGETATIVE PHASE); transcription factor
0578-94-(6-8-06)_C09	6.00E-55	protein binding / zinc ion binding
0086-94-E08(4-28-06)	1.00E-54	heme binding / transition metal ion binding
Contig_187	6.00E-	octicosapeptide/Phox/Bem1p (PB1) domain-containing protein

	54	
0773-94-(6-7-06)_G09	7.00E-54	similar to nuclear matrix constituent protein-related [Arabidopsis thaliana] (TAIR:AT1G13220.2); similar to Alpha-taxilin, putative, expressed [Oryza sativa (japonica cultivar-group)] (GB:ABF95380.1); contains InterPro domain Prefoldin; (InterPro:IPR009053)
1305-94-(6-16-06)_G06	7.00E-54	ADL6 (DYNAMIN-LIKE PROTEIN 6)
0180-94-E04(5-10-06)	8.00E-54	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G12400.1); similar to H0306F03.12 [Oryza sativa (indica cultivar-group)] (GB:CAH68245.1); similar to Os01g0121300 [Oryza sativa (japonica cultivar-group)] (GB:NP_001041875.1); similar to Os02g0799300 [Oryza sativa (japonica cultivar-group)] (GB:NP_001048408.1); contains InterPro domain Acid phosphatase/vanadium-dependent haloperoxidase; (InterPro:IPR008934)
0517-94-(6-8-06)_A03	1.00E-53	ADL2 (ARABIDOPSIS DYNAMIN-LIKE 2); GTP binding / GTPase
1102-94-(6-9-06)_B07	1.00E-53	similar to intracellular protein transport protein USO1-related [Arabidopsis thaliana] (TAIR:AT1G64180.1); similar to unnamed protein product; gb
Contig_204	1.00E-53	glutaredoxin family protein
Contig_46	1.00E-53	ATHB54 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 54); nucleic acid binding / transcription factor
0306-94(5-31-06)_006	2.00E-53	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G64780.1); similar to conserved hypothetical protein [Medicago truncatula] (GB:ABE81201.1); contains InterPro domain Tetraspanin; (InterPro:IPR008952)
0887-94-(6-5-06)_G11	2.00E-53	lanthionine synthetase C-like family protein
0690-94-(6-6-06)_B12	6.00E-53	AtMYB82 (myb domain protein 82); DNA binding / transcription factor
0581-94-(6-8-06)_E09	8.00E-53	glycosyl hydrolase family 17 protein
0647-94-(6-6-06)_G06	9.00E-53	5'-AMP-activated protein kinase beta-1 subunit-related
0214-94(5-31-06)_010	1.00E-52	homeobox-leucine zipper transcription factor family protein
1134-94-(6-9-06)_B11	3.00E-52	ERD7 (EARLY-RESPONSIVE TO DEHYDRATION 7)
0026-94-(6-12-06)_A01	6.00E-52	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G48700.1); similar to Esterase/lipase/thioesterase [Medicago truncatula] (GB:ABE83378.1); contains InterPro domain Esterase/lipase/thioesterase; (InterPro:IPR000379); contains InterPro domain Alpha/beta hydrolase fold-3; (InterPro:IPR013094)
0841-94-(6-5-06)_A06	7.00E-52	Identical to Protein At2g40430 [Arabidopsis Thaliana] (GB:O22892;GB:Q93XZ8); similar to Os05g0144200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001054623.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAU90201.1); contains InterPro domain P60-like; (InterPro:IPR011687)
0683-94-(6-6-06)_C11	9.00E-52	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G03610.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:AAO39871.1); similar to Os10g0494000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001064942.1); similar to hypothetical protein [Oryza sativa

		(japonica cultivar-group)] (GB:AAP46235.1); contains InterPro domain Protein of unknown function DUF789; (InterPro:IPR008507)
0316-94-(6-9-06)_E01	1.00E-51	similar to hypothetical protein MtrDRAFT_AC150207g26v1 [Medicago truncatula] (GB:ABD32636.1)
0372-94-(6-12-06)_H08	2.00E-51	mitochondrial glycoprotein family protein / MAM33 family protein
0649-94-(6-6-06)_A07	3.00E-51	AML5 (ARABIDOPSIS MEI2-LIKE PROTEIN 5); RNA binding
1060-94-(6-2-06)_B08	4.00E-51	zinc finger protein-related
0576-94-(6-12-06)_E11	1.00E-50	nucleic acid binding
0802-94-(6-5-06)_B01	1.00E-50	ribulose bisphosphate carboxylase small chain 3B / RuBisCO small subunit 3B (RBCS-3B) (ATS3B)
1004-94(6-2-06Truncated)_D01	1.00E-50	DFR (DIHYDROFLAVONOL 4-REDUCTASE); dihydrokaempferol 4-reductase
1021-94-(6-2-06)_D03	1.00E-50	DNA binding / zinc ion binding
Contig_148	6.00E-50	IAA16 (indoleacetic acid-induced protein 16); transcription factor
Contig_142	9.00E-50	basic helix-loop-helix (bHLH) family protein
0219-94-D09(5-10-06)	2.00E-49	YGGT family protein
0535-94-(6-8-06)_C05	3.00E-49	pleckstrin homology (PH) domain-containing protein
0075-94-B07(4-28-06)	4.00E-49	WNK1 (WITH NO LYSINE (K) 1); kinase
0859-94-(6-5-06)_C08	5.00E-49	ARID/BRIGHT DNA-binding domain-containing protein / ELM2 domain-containing protein / Myb-like DNA-binding domain-containing protein
0779-94-(6-7-06)_D10	6.00E-49	selenoprotein-related
Contig_203	7.00E-49	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G52910.1); similar to fiber protein Fb34 [Gossypium barbadense] (GB:AAR07596.1); contains InterPro domain Protein of unknown function DUF1218; (InterPro:IPR009606)
Contig_20	1.00E-48	similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:AT4G22760.1); similar to hypothetical protein [Catharanthus roseus] (GB:CAC09928.1)
0807-94-(6-5-06)_G01	2.00E-48	MLO10 (MILDEW RESISTANCE LOCUS O 10); calmodulin binding
0831-94-(6-5-06)_G04	2.00E-48	hydrolase
Contig_179	3.00E-48	plastocyanin-like domain-containing protein
0111-94-F11(4-28-06)	5.00E-48	UNE1 (unfertilized embryo sac 1)
0220-94E09(5-10-06)	5.00E-48	zinc finger (C3HC4-type RING finger) family protein
0352-94-(6-27-06)_H04	6.00E-48	transporter
0925-94-(6-16-06)_C11	8.00E-48	Identical to Golgin-84 [Arabidopsis Thaliana] (GB:Q8S8N9;GB:Q6NMI2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G18190.1); similar to Gol (GB:Q6GNT7); similar

		to Os01g0744400 [Oryza sativa (japonica cultivar-group)] (GB:NP_001044225.1); contains domain SUBFAMILY NOT NAMED (PTHR13815:SF1); contains domain FAMILY NOT NAMED (PTHR13815)
0211-94-D08(5-10-06)	2.00E-47	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G18720.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G18740.1); similar to heat shock protein DnaJ N-terminal domain-containing protein [Musa acuminata] (GB:ABF69988.1); similar to Os01g0375100 [Oryza sativa (japonica cultivar-group)] (GB:NP_001043077.1); contains domain DNAJ/HSP40 (PTHR11821); contains domain gb def: T12H1.7 protein (PTHR11821:SF3)
0358-94-(6-12-06)_C07	2.00E-47	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G00355.2); similar to conserved hypothetical protein [Medicago truncatula] (GB:ABE80179.1)
1116-94-(6-9-06)_H08	2.00E-47	leucine-rich repeat family protein / protein kinase family protein
1301-94-(6-16-06)_C06	2.00E-47	RNA recognition motif (RRM)-containing protein
Contig_2	2.00E-47	adenylate cyclase
0369-94-(6-12-06)_F08	3.00E-47	FTSZ2-1 (FtsZ homolog 2-1); structural molecule
0915-94-(6-14-06)_B12	3.00E-47	copine-related
0804-94-(6-5-06)_D01	6.00E-47	nucleic acid binding / zinc ion binding
0881-94-(6-5-06)_A11	8.00E-47	transcription factor
0438-94-(6-16-06)_F02	1.00E-46	pentatricopeptide (PPR) repeat-containing protein
0863-94-(6-5-06)_G08	3.00E-46	fructose-bisphosphate aldolase, putative
Contig_141	8.00E-46	myb family transcription factor
Contig_98	1.00E-45	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G02555.1); similar to hypothetical protein [Cleome spinosa] (GB:ABD96917.1)
0164-94-D07(5-5-06)	2.00E-45	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G04040.1); similar to Os01g0264500 [Oryza sativa (japonica cultivar-group)] (GB:NP_001042664.1); similar to gb protein [Sorghum bicolor] (GB:AAL68853.1)
1035-94-(6-14-06)_G08	3.00E-45	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G40060.1); similar to conserved hypothetical protein [Medicago truncatula] (GB:ABE83515.1); contains InterPro domain Clathrin light chain; (InterPro:IPR000996)
0021-94_012(5-31-06)	6.00E-45	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G74950.1); similar to PnFL-2 [Ipomoea nil] (GB:AAG49896.1); contains InterPro domain ZIM; (InterPro:IPR010399)
0228-94-E10(5-10-06)	1.00E-44	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G08460.2); similar to Pm27 [Prunus mume] (GB:BAE48661.1); contains InterPro domain Protein of unknown function DUF1644; (InterPro:IPR012866)
0269-94(5-31-	2.00E-	transferase family protein

06)_015	44	
Contig_168	2.00E-44	ATPU1 (PULLULANASE 1); alpha-amylase/ limit dextrinase
0790-94-(6-7-06)_F11	3.00E-44	transducin family protein / WD-40 repeat family protein
0823-94-(6-5-06)_G03	7.00E-44	pyruvate kinase, putative
1075-94-(6-2-06)_A10	8.00E-44	zinc finger (Ran-binding) family protein
0265-94(5-31-06)_007	7.00E-43	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G51890.1); similar to conserved hypothetical protein [Medicago truncatula] (GB:ABE83515.1); contains InterPro domain Clathrin light chain; (InterPro:IPR000996)
0643-94-(6-6-06)_C06	1.00E-42	armadillo/beta-catenin repeat family protein
Contig_169	1.00E-42	integral membrane protein, putative
0388-94-(6-12-06)_E10	2.00E-42	epsin N-terminal homology (ENTH) domain-containing protein
1107-94-(6-9-06)_G07	3.00E-42	AtMYB73/MYB73 (myb domain protein 73); DNA binding / transcription factor
0667-94-(6-6-06)_C09	4.00E-42	SPL7 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 7); DNA binding / transcription factor
1127-94-(6-9-06Truncated)_C10	1.00E-41	similar to expressed protein [Oryza sativa (japonica cultivar-group)] (GB:ABA99446.2); contains domain Winged helix DNA-binding domain (SSF46785)
0315-94-(6-9-06)_D01	2.00E-41	transporter-related
1006-94-(6-2-06)_F01	9.00E-41	RNA recognition motif (RRM)-containing protein
1170-94-(6-15-06)_H05	1.00E-40	ubiquitin-specific protease 8, putative (UBP8)
Contig_1	1.00E-40	ATERF-2/ATERF2/ERF2 (ETHYLENE RESPONSE FACTOR 2); DNA binding / transcription factor/ transcriptional activator
Contig_84	1.00E-40	AT-IMP (Arabidopsis thaliana importin alpha); protein transporter
0725-94-(6-7-06)_A04	2.00E-40	similar to WDL1 (WVD2-LIKE 1) [Arabidopsis thaliana] (TAIR:AT3G04630.3); similar to Targeting protein for Xklp2 containing protein, expressed [Oryza sativa (japonica cultivar-group)] (GB:ABF99369.1); similar to Os03g0799100 [Oryza sativa (japonica cultivar-group)] (GB:NP_001051574.1); contains InterPro domain Targeting for Xklp2; (InterPro:IPR009675)
1040-94-(6-2-06)_G05	3.00E-40	protein kinase family protein
0106-94-A11(4-28-06)	7.00E-40	similar to PREDICTED: similar to CG15168-PA [Apis mellifera] (GB:XP_001121144.1); similar to Os12g0566400 [Oryza sativa (japonica cultivar-group)] (GB:NP_001067053.1); contains domain FAMILY NOT NAMED (PTHR21181); contains domain gb def: Hypothetical protein (PTHR21181:SF6)
0829-94-(6-5-06)_E04	8.00E-40	zinc finger protein (PRAF1) / regulator of chromosome condensation (RCC1) family protein
0046-94-E03(4-28-06)	2.00E-39	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G50040.1); similar to IMP dehydrogenase/GMP reductase [Medicago truncatula] (GB:ABE93135.1); contains InterPro domain Protein of unknown function DUF1005; (InterPro:IPR010410)

Contig_130	3.00E-39	J20 (DNAJ-LIKE 20); heat shock protein binding
Contig_33	4.00E-39	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G11220.1); similar to cotton fiber expressed protein 1 [Gossypium hirsutum] (GB:AAC33276.1); contains InterPro domain Protein of unknown function DUF761, plant; (InterPro:IPR008480)
0681-94-(6-6-06)_A11	2.00E-38	bZIP transcription factor family protein
0746-94-(6-7-06)_F06	2.00E-38	seven in absentia (SINA) family protein
0883-94-(6-5-06)_C11	2.00E-38	tRNA pseudouridine synthase family protein
1172-94-(6-15-06)_B06	2.00E-38	NADH-ubiquinone oxidoreductase-related
0309-94(5-31-06)_012	2.00E-37	protein kinase family protein
1094-94-(6-2-06)_D12	2.00E-37	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G25640.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD07762.1); contains InterPro domain Protein of unknown function DUF617, plant; (InterPro:IPR006460)
Contig_10	2.00E-37	KH domain-containing protein
0263-94(5-31-06)_003	3.00E-37	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G19330.2); similar to unknown [Vitis pseudoreticulata] (GB:ABC69763.1)
0694-94-(6-6-06)_F12	7.00E-37	CIC7E11; protein binding / zinc ion binding
0328-94-(6-9-06)_G02	9.00E-37	squamosa promoter-binding protein, putative
0890-94-(6-14-06)_E07	1.00E-36	IAA11 (indoleacetic acid-induced protein 11)
0720-94-(6-7-06)_D03	1.00E-35	similar to EMB2170 (EMBRYO DEFECTIVE 2170) [Arabidopsis thaliana] (TAIR:AT1G21390.1)
0087-93-B03(4-21-06)	2.00E-35	ATRAD21.3 (Arabidopsis homolog of RAD21 3)
Contig_58	3.00E-35	XTR3 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 3); hydrolase, acting on glycosyl bonds
0047-93-B08(4-21-06)	4.00E-35	WD-40 repeat family protein
0131-94-C03(5-9-06)	4.00E-35	Dof-type zinc finger domain-containing protein
0140-94-D04(5-9-06)	4.00E-35	bZIP transcription factor family protein
0796-94-(6-7-06)_D12	7.00E-35	BPC2 (BASIC PENTACYSTEINE 2)
Contig_121	7.00E-35	RNA and export factor-binding protein, putative
0296-94(5-31-06)_005	2.00E-34	kinase interacting family protein
0870-94-(6-5-06)_F09	2.00E-34	ARF2 (AUXIN RESPONSE FACTOR 2)
0577-94-(6-8-06)_B09	3.00E-34	glycine-rich protein

0834-94-(6-15-06bad)_H10	3.00E-34	zinc finger (C3HC4-type RING finger) family protein
1160-94-(6-15-06)_B05	5.00E-34	similar to YLS7 (yellow-leaf-specific gene 7) [Arabidopsis thaliana] (TAIR:AT5G51640.1); similar to unknown [Gymnadenia conopsea] (GB:ABD66519.1); similar to Os01g0914800 [Oryza sativa (japonica cultivar-group)] (GB:NP_001045183.1); contains InterPro domain Protein of unknown function DUF231, plant; (InterPro:IPR004253)
0633-94-(6-6-06)_A05	6.00E-34	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G20900.1); similar to P0482D04.10 [Oryza sativa (japonica cultivar-group)] (GB:BAB89663.1); similar to Os04g0395800 [Oryza sativa (japonica cultivar-group)] (GB:NP_001052661.1); similar to Os10g0392400 [Oryza sativa (japonica cultivar-group)] (GB:NP_001064513.1); contains InterPro domain ZIM; (InterPro:IPR010399)
0007for_D05'	2.00E-33	AAA-type ATPase family protein
0280-94(5-31-06)_005	2.00E-33	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G70420.1); similar to Os01g0639600 [Oryza sativa (japonica cultivar-group)] (GB:NP_001043675.1); similar to Protein of unknown function DUF1645 [Medicago truncatula] (GB:ABE93113.1); contains InterPro domain Protein of unknown function DUF1645; (InterPro:IPR012442)
Contig_82	2.00E-33	VIM1 (VARIANT IN METHYLATION 1); DNA binding
Contig_26	8.00E-33	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G02430.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD08943.1); contains InterPro domain Protein of unknown function DUF679; (InterPro:IPR007770)
0124-94-D02(5-9-06)	3.00E-32	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G41980.1); similar to Os06g0226000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001057201.1); similar to Transposase, IS4 [Medicago truncatula] (GB:ABE82048.1); contains domain FAMILY NOT NAMED (PTHR22930)
0588-94-(6-8-06)_C10	6.00E-32	nodulin MtN21 family protein
1083-94-(6-2-06)_A11	4.00E-31	AP2 domain-containing transcription factor, putative
0261-94(5-31-06)_016	5.00E-31	UBC11 (ubiquitin-conjugating enzyme 11); ubiquitin-protein ligase
0777-94-(6-7-06)_B10	8.00E-31	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G32330.1); similar to putative BRI1-KD interacting protein [Oryza sativa (japonica cultivar-group)] (GB:BAD15848.1); similar to Os02g0200800 [Oryza sativa (japonica cultivar-group)] (GB:NP_001046221.1); similar to Os11g0571900 [Oryza sativa (japonica cultivar-group)] (GB:NP_001068122.1); contains InterPro domain Targeting for Xklp2; (InterPro:IPR009675)
0800-94-(6-7-06)_G12	2.00E-30	ANAC053 (Arabidopsis NAC domain containing protein 53); transcription factor
Contig_57	3.00E-30	RNA recognition motif (RRM)-containing protein
0693-94-(6-6-06)_E12	5.00E-30	GLA1 (GLOBULAR ARREST1); tetrahydrofolylpolyglutamate synthase
0930-94-(6-16-06)_F11	2.00E-29	transporter
0795-94-(6-7-	3.00E-	SCL1 (SCARECROW-LIKE 1); transcription factor

06)_C12	29	
0902-94-(6-14-06)_E10	3.00E-29	IAA29 (indoleacetic acid-induced protein 29); transcription factor
Contig_189	3.00E-29	senescence-associated protein-related
0756-94-(6-7-06)_H07	4.00E-29	D111/G-patch domain-containing protein
1101-94-(6-9-06)_A07	1.00E-28	HDA15 (histone deacetylase 15); histone deacetylase
0635-94-(6-6-06)_C05	4.00E-28	zinc finger (C3HC4-type RING finger) family protein
0526-94-(6-8-06)_B04	6.00E-28	zinc finger protein-related
0071_F06(For4-28-06)	8.00E-28	MBD8 (methyl-CpG-binding domain 8)
0511-94-(6-8-06)_C02	1.00E-27	protein binding / zinc ion binding
1145-94-(6-9-06Truncated)_E12	1.00E-27	TTN8 (TITAN8); ATP binding
0199-94(5-31-06)_008	2.00E-27	formin homology 2 domain-containing protein / FH2 domain-containing protein
0753-94-(6-7-06)_E07	2.00E-27	kinesin light chain-related
0645-94-(6-6-06)_E06	4.00E-27	VQ motif-containing protein
Contig_53	4.00E-27	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G26110.1); similar to hypothetical protein [Glycine max] (GB:BAB41197.1); contains domain gb def: Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K9E15 (Hypothetical pr (PTHR13586:SF4); contains domain UNCHARACTERIZED (PTHR13586)
0904-94-(6-14-06)_G10	5.00E-27	no apical meristem (NAM) family protein
0149-94-E05(5-9-06)	2.00E-26	C2 domain-containing protein
0885-94-(6-5-06)_E11	2.00E-26	similar to CIL [Arabidopsis thaliana] (TAIR:AT4G25990.1); similar to CCT [Medicago truncatula] (GB:ABE93500.1); contains InterPro domain CCT; (InterPro:IPR010402)
0931-94-(6-16-06)_G11	3.00E-26	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G25870.1); similar to Os01g0131300 [Oryza sativa (japonica cultivar-group)] (GB:NP_001041925.1)
1014-94-(6-2-06)_E02	3.00E-26	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G25170.1); similar to expressed protein [Oryza sativa (japonica cultivar-group)] (GB:ABB47783.1); similar to unknown protein [Oryza sativa] (GB:AAG16855.1); similar to Os02g0814000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001048488.1); contains InterPro domain Protein of unknown function DUF862, eukaryotic; (InterPro:IPR008580)
0127-94(5-31-06)_007	4.00E-26	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G17300.1); similar to Os02g0715300 [Oryza sativa (japonica cultivar-group)] (GB:NP_001047925.1); similar to Os08g0511400 [Oryza sativa (japonica cultivar-group)] (GB:NP_001062213.1); contains domain N-terminal domain of cbl (N-cbl) (SSF47668)

0380-94-(6-12-06)_G09	5.00E-26	unknown protein
0379-94-(6-12-06)_F09	8.00E-26	translocon-associated protein alpha (TRAP alpha) family protein
0013-94_011(5-31-06)	4.00E-25	protein phosphatase 2C, putative / PP2C, putative
0818-94-(6-5-06)_B03	4.00E-25	similar to Os03g0747100 [Oryza sativa (japonica cultivar-group)] (GB:NP_001051255.1)
0872-94-(6-5-06)_H09	6.00E-25	OST1 (OPEN STOMATA 1); kinase/ protein kinase
0630-94-(6-6-06)_F04	7.00E-25	ATSC35 (Arabidopsis thaliana arginine/serine-rich splicing factor 35, 35 kDa protein); RNA binding
1032-94-(6-2-06)_G04	7.00E-25	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G10440.1); similar to Globin-like [Medicago truncatula] (GB:ABE79971.1); similar to Os08g0564800 [Oryza sativa (japonica cultivar-group)] (GB:NP_001062533.1); similar to CTV.22 [Poncirus trifoliata] (GB:AAN62354.1); contains domain no description (G3D.1.10.246.20); contains domain Kix domain of CBP (creb binding protein) (SSF47040)
Contig_43	7.00E-25	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G01240.3); similar to Os09g0363500 [Oryza sativa (japonica cultivar-group)] (GB:NP_001062992.1); similar to Os08g0400300 [Oryza sativa (japonica cultivar-group)] (GB:NP_001061754.1); similar to hypothetical protein MtrDRAFT_AC145165g14v1 [Medicago truncatula] (GB:ABE91800.1)
0254-94-(6-16-06)_B10	9.00E-25	3-phosphoinositide-dependent protein kinase-1, putative
0936-94-(6-16-06)_D12	1.00E-24	PRR7 (PSEUDO-RESPONSE REGULATOR 7); transcription regulator
Contig_156	3.00E-24	similar to Os03g0110300 [Oryza sativa (japonica cultivar-group)] (GB:NP_001048714.1); similar to Unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAN61478.1)
0891-94-(6-5-06)_C12	4.00E-24	ankyrin repeat family protein
0750-94-(6-7-06)_B07	7.00E-24	HSF1 (ARABIDOPSIS HEAT SHOCK FACTOR 1); DNA binding / transcription factor
0175-94-H03(5-10-06)	8.00E-24	zinc finger (CCCH-type) family protein
0271-94(5-31-06)_004	4.00E-23	AAA-type ATPase family protein
0644-94-(6-6-06)_D06	6.00E-23	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G13420.1); similar to hypothetical protein MtrDRAFT_AC146567g1v1 [Medicago truncatula] (GB:ABE90925.1)
0619-94-(6-6-06)_C03	4.00E-22	BPC2 (BASIC PENTACYSTEINE 2)
Contig_162	1.00E-21	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G26240.1); similar to Os04g0653100 [Oryza sativa (japonica cultivar-group)] (GB:NP_001054104.1); similar to transmembrane protein 14C [Argas monolakensis] (GB:ABI52790.1); similar to Os03g0568500 [Oryza sativa (japonica cultivar-group)] (GB:NP_001050510.1); contains InterPro domain Protein of unknown function UPF0136, Transmembrane; (InterPro:IPR005349)
0664-94-(6-6-	2.00E-	zinc finger (C3HC4-type RING finger) family protein

06)_H08	21	
1167-94-(6-15-06)_F05	3.00E-21	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G55210.1); similar to conserved hypothetical protein [Medicago truncatula] (GB:ABD28485.1)
Contig_117	4.00E-21	similar to cation exchanger, putative (CAX10) [Arabidopsis thaliana] (TAIR:AT1G54110.1); similar to Os09g0272500 [Oryza sativa (japonica cultivar-group)] (GB:NP_001062740.1); similar to Os08g0533700 [Oryza sativa (japonica cultivar-group)] (GB:NP_001062347.1); similar to cation exchanger-like protein [Oryza sativa (japonica cultivar-group)] (GB:BAD13159.1); contains domain no description (G3D.1.20.5.110)
0010-93-G12(4-21-06)	6.00E-21	arginine biosynthesis protein ArgJ family
0518-94-(6-8-06)_B03	1.00E-20	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G04690.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G04680.1); similar to Ankyrin [Medicago truncatula] (GB:ABE89653.1); contains InterPro domain Ankyrin; (InterPro:IPR002110)
1147-94-(6-9-06Truncated)_G12	1.00E-20	SET domain-containing protein (ASHH1)
1180-94-(6-15-06)_G06	1.00E-20	ATERF-9/ATERF9/ERF9 (ERF domain protein 9); DNA binding / transcription factor/ transcriptional repressor
1110-94-(6-9-06)_B08	6.00E-20	F-box family protein
Contig_113	7.00E-20	ATERF3/ERF3 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 3); DNA binding / protein binding / transcription factor/ transcriptional repressor
0244-94-E12(5-10-06)	9.00E-20	ATUPF3/UPF3; nucleotide binding
0045-94-D03(4-28-06)	2.00E-19	similar to cupin family protein [Arabidopsis thaliana] (TAIR:AT2G18540.1); similar to Os06g0352900 [Oryza sativa (japonica cultivar-group)] (GB:NP_001057589.1); similar to PREDICTED: hypothetical protein, partial [Strongylocentrotus purpuratus] (GB:XP_001185087.1)
0627-94-(6-6-06)_C04	2.00E-19	F-box family protein
0714-94-(6-7-06)_F02	2.00E-19	GASA4 (GAST1 PROTEIN HOMOLOG 4)
1071-94-(6-2-06)_E09	4.00E-19	zinc finger protein-related
1148-94-(6-9-06)_H12	7.00E-19	CID3 (CTC-Interacting Domain 3)
0617-94-(6-6-06)_A03	8.00E-19	F-box family protein
0134-94-F03(5-9-06)	1.00E-18	reticulon family protein
0054-94-E04(4-28-06)	6.00E-18	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to unnamed protein product; gene_id:K19B1.16 unknown protein-related [Medicago truncatula] (GB:ABE84483.1)
1120-94-(6-9-06)_D09	8.00E-18	TRFL7 (TRF-LIKE 7); DNA binding / transcription factor
1063-94-(6-2-06)_E08	9.00E-18	YDA (YODA); kinase

0628-94-(6-6-06)_D04	3.00E-17	proteophosphoglycan-related
0676-94-(6-6-06)_D10	1.00E-16	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G17510.1); similar to expressed protein [Oryza sativa (japonica cultivar-group)] (GB:ABG22017.1)
1166-94-(6-15-06)_E05	4.00E-16	disease resistance protein (NBS-LRR class), putative
1092-94-(6-2-06)_B12	5.00E-16	COI1 (CORONATINE INSENSITIVE 1); ubiquitin-protein ligase
0735-94-(6-7-06)_C05	7.00E-16	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G17540.1); similar to Os06g0728500 [Oryza sativa (japonica cultivar-group)] (GB:NP_001058643.1)
0695-94-(6-6-06)_G12	1.00E-15	pseudouridine synthase family protein
0085-94-D08(4-28-06)	2.00E-15	senescence/dehydration-associated protein-related
0836-94-(6-5-06)_D05	2.00E-15	ATBAG5 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 5); protein binding
0381-94-(6-12-06)_H09	5.00E-15	hydroxyproline-rich glycoprotein family protein
0945-94-(6-15-06)_H03	5.00E-15	transmembrane protein, putative
0668-94-(6-6-06)_D09	3.00E-14	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G56210.1); similar to OSJNBa0084A10.5 [Oryza sativa (japonica cultivar-group)] (GB:CAE03030.1); similar to dentin sialophosphoprotein preproprotein [Homo sapiens] (GB:NP_055023.2); contains domain no description (G3D.4.10.900.10)
0737-94-(6-7-06)_E05	3.00E-14	nodulin MtN21 family protein
0016-94_002(5-31-06)	7.00E-14	hydroxyproline-rich glycoprotein family protein
Contig_163	1.00E-13	similar to Os03g0412200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001050353.1); similar to expressed protein [Oryza sativa (japonica cultivar-group)] (GB:AAO37502.2); similar to Os03g0595200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001050595.1)
0226-94-C10(5-10-06)	3.00E-13	DNA-binding family protein
0024-94(5-31-06)_001	6.00E-13	VHS domain-containing protein / GAT domain-containing protein
0365-94-(6-12-06)_B08	7.00E-13	UBC13 (ubiquitin-conjugating enzyme 13); ubiquitin-protein ligase
0019-94_008(5-31-06)	8.00E-13	disease resistance protein (TIR-NBS class), putative
1115-94-(6-9-06)_G08	3.00E-12	histone H1.2
0728-94-(6-7-06)_D04	7.00E-12	PHR1 (PHOSPHATE STARVATION RESPONSE 1); transcription factor
0580-94-(6-8-06)_D09	1.00E-11	SWAP (Suppressor-of-White-APricot)/surp domain-containing protein
0822-94-(6-5-06)_F03	1.00E-11	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G10080.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD82228.1)
0016-93-A12(4-21-	2.00E-	hydroxyproline-rich glycoprotein family protein

06)	11	
0139-94-C04(5-9-06)	2.00E-11	F-box family protein
0721-94-(6-7-06)_E03	2.00E-11	AR791; actin binding
Contig_119	2.00E-11	WAVE1 (WASP (Wiskott-Aldrich syndrome protein)-family verprolin homologous protein 1)
0286-94(5-31-06)_002	4.00E-11	RNase H domain-containing protein
0235-94-D11(5-10-06)	5.00E-11	amidase family protein
0826-94-(6-5-06)_B04	9.00E-10	nucleic acid binding / nucleotide binding / zinc ion binding
1084-94-(6-2-06)_B11	1.00E-09	PEL1 (PELOTA); translation release factor
0195-94-D06(5-10-06)	2.00E-09	zinc finger (C3HC4-type RING finger) family protein / ankyrin repeat family protein
1146-94-(6-9-06)_F12	2.00E-09	armadillo/beta-catenin repeat family protein
Contig_28	2.00E-09	TOPII (TOPOISOMERASE II); ATP binding / DNA binding / DNA topoisomerase (ATP-hydrolyzing)
Contig_184	3.00E-09	octicosapeptide/Phox/Bem1p (PB1) domain-containing protein
0433-94-(6-27-06)_D06	5.00E-09	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G31300.2); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD53332.1); similar to Os05g0511000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001056013.1); similar to Os03g0666700 [Oryza sativa (japonica cultivar-group)] (GB:NP_001050848.1); contains InterPro domain TRAM, LAG1 and CLN8 homology; (InterPro:IPR006634); contains InterPro domain Protein of unknown function DUF887, TLC-like; (InterPro:IPR010283)
0594-94-(6-8-06)_A11	1.00E-08	EMB2654 (EMBRYO DEFECTIVE 2654); binding
Contig_50	1.00E-08	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G06980.1); similar to ACI112 [Lycopersicon esculentum] (GB:AAY97870.1)
Contig_4	5.00E-08	F-box family protein
0262-94(5-31-06)_001	6.00E-08	PHD finger family protein
Contig_164	1.00E-07	3'-5' exonuclease domain-containing protein
Contig_30	1.00E-07	NFD1 (NUCLEAR FUSION DEFECTIVE 1); structural constituent of ribosome
0571-94-(6-8-06)_F08	2.00E-07	NPSN11 (NOVEL PLANT SNARE 11); protein transporter
Contig_80	6.00E-07	UBP25 (UBIQUITIN-SPECIFIC PROTEASE 25); ubiquitin-specific protease
Contig_177	9.00E-07	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G33850.1); similar to arabinogalactan-protein; AGP [Pyrus communis] (GB:AAB35283.1)
0592-94-(6-8-06)_G10	2.00E-06	DNA binding / ligand-dependent nuclear receptor

0849-94-(6-5-06)_A07	2.00E-06	zinc finger (GATA type) family protein
0916-94-(6-14-06)_C12	3.00E-06	similar to unnamed protein product [Ostreococcus tauri] (GB:CAL54919.1); similar to Os05g0148300 [Oryza sativa (japonica cultivar-group)] (GB:NP_001054647.1); contains InterPro domain Ribosomal protein S27, mitochondrial; (InterPro:IPR013219)
1124-94-(6-9-06)_H09	9.00E-06	protein kinase, putative
0225-94-B10(5-10-06)	e-100	SAR1 (SYNAPTOBREVIN-RELATED PROTEIN 1)
0233-94-B11(5-10-06)	e-100	SERK1 (SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE 1); kinase
0363-94-(6-12-06)_H07	e-100	VCS (VARICOSE); nucleotide binding
0394-94-(6-8-06)_C12	e-100	ATARFA1E (ADP-ribosylation factor A1E); GTP binding / phospholipase activator/ protein binding
0626-94-(6-6-06)_B04	e-100	exostosin family protein
0660-94-(6-6-06)_D08	e-100	pfkB-type carbohydrate kinase family protein
Contig_85	e-100	band 7 family protein
0137-94-A04(5-9-06)	e-101	LPAT4; acyltransferase
0250-94(5-31-06)_009	e-101	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G34220.2); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD46466.1); similar to Os09g0547200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001063848.1); contains InterPro domain Protein of unknown function DUF292, eukaryotic; (InterPro:IPR005061)
0465-94-(6-16-06)_G05	e-101	NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial (TYKY)
0519-94-(6-8-06)_C03	e-101	F-box family protein (FBL3)
0605-94-(6-6-06)_E01	e-101	palmitoyl protein thioesterase family protein
0724-94-(6-7-06)_H03	e-101	indigoidine synthase A family protein
0733-94-(6-7-06)_A05	e-101	(1-4)-beta-mannan endohydrolase, putative
1042-94-(6-15-06)_E12	e-101	FUS6 (FUSCA 6)
1078-94-(6-2-06)_D10	e-101	protein kinase
1135-94-(6-9-06)_C11	e-101	PBD1 (PROTEASOME SUBUNIT PRGB); peptidase
Contig_152	e-101	microtubule motor
Contig_52	e-101	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G01100.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G54100.1); similar to Os05g0451900 [Oryza sativa (japonica cultivar-group)] (GB:NP_001055708.1); similar to putative axi 1 [Oryza sativa (japonica cultivar-group)] (GB:BAD82651.1); contains InterPro domain Protein of unknown function DUF246, plant; (InterPro:IPR004348)
Contig_55	e-101	GAMMA CAL2 (GAMMA CARBONIC ANHYDRASE-LIKE 2);

		acyltransferase
Contig_7	e-101	EIF2 BETA (EMBRYO DEFECTIVE 1401)
Contig_74	e-101	CCR4-NOT transcription complex protein, putative
0110-94-E11(4-28-06)	e-102	mannose 6-phosphate reductase (NADPH-dependent), putative
0200-94-A07(5-10-06)	e-102	chaperone protein dnaJ-related
0507-94-(6-8-06)_G01	e-102	binding
0534-94-(6-8-06)_B05	e-102	similar to Rho-GTPase-activating protein-related [Arabidopsis thaliana] (TAIR:AT4G35750.1); similar to Cellular retinaldehyde-binding/triple function, C-terminal [Medicago truncatula] (GB:ABD28324.1); contains InterPro domain Cellular retinaldehyde-binding/triple function, C-terminal; (InterPro:IPR001251)
0774-94-(6-7-06)_H09	e-102	heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative
0910-94-(6-14-06)_E11	e-102	similar to Unknown (protein for IMAGE:6863324) [Xenopus laevis] (GB:AAH84304.1); similar to Unknown (protein for IMAGE:8320811) [Xenopus laevis] (GB:AAI24845.1); similar to Os11g0264600 [Oryza sativa (japonica cultivar-group)] (GB:NP_001067654.1)
0918-94-(6-14-06)_E12	e-102	VHS domain-containing protein / GAT domain-containing protein
Contig_66	e-102	beta-adaptin, putative
Contig_8	e-102	CA2 (BETA CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding
0115-94-B12(4-28-06)	e-103	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G22850.1); similar to aluminum-induced protein-like protein [Thellun (GB:AAM19711.1); contains domain no description (G3D.3.60.20.10); contains domain N-terminal nucleophile aminohydrolases (Ntn hydrolases) (SSF56235)
0385-94-(6-12-06)_B10	e-103	similar to BPS1 (BYPASS 1) [Arabidopsis thaliana] (TAIR:AT1G01550.2); similar to unknown [Solanum tuberosum] (GB:ABB16971.1); contains InterPro domain Glutathione S-transferase, C-terminal-like; (InterPro:IPR010987)
0463-94-(6-16-06)_E05	e-103	ATMLO1/MLO1 (MILDEW RESISTANCE LOCUS O 1); calmodulin binding
0613-94-(6-6-06)_E02	e-103	AXS1 (UDP-D-APIOSE/UDP-D-XYLOSE SYNTHASE 1)
0652-94-(6-6-06)_D07	e-103	CLPP3 (Clp protease proteolytic subunit 3); endopeptidase Clp
0911-94-(6-14-06)_F11	e-103	AtRABD2b/AtRab1A (Arabidopsis Rab GTPase homolog D2b); GTP binding
Contig_197	e-103	BMY3 (beta-amylase 3); beta-amylase
Contig_60	e-103	CYP707A1 (cytochrome P450, family 707, subfamily A, polypeptide 1); oxygen binding
0060-94-C05(4-28-06)	e-104	ATG2 (G2p-related protein); metalloexopeptidase
0209-94-B08(5-10-06)	e-104	importin beta-2 subunit family protein
0245-94-F12(5-10-06)	e-104	HSA32 (HEAT-STRESS-ASSOCIATED 32)
0362-94-(6-12-	e-104	transcription-coupled DNA repair protein-related

06)_G07		
0523-94-(6-8-06)_G03	e-104	peroxidase 64 (PER64) (P64) (PRXR4)
0744-94-(6-7-06)_D06	e-104	thiF family protein
Contig_160	e-104	MVD1 (mevalonate diphosphate decarboxylase 1)
0766-94-(6-7-06)_A09	e-105	GRF9 (General regulatory factor 9); protein phosphorylated amino acid binding
0919-94-(6-14-06)_F12	e-105	ATFATA (ARABIDOPSIS FATA ACYL-ACP THIOESTERASE); acyl carrier/ acyl-ACP thioesterase
1072-94-(6-2-06)_F09	e-105	CLIP-associating protein (CLASP) -related
1159-94-(6-15-06)_A05	e-105	zinc finger (C2H2 type) protein (WIP2)
Contig_144	e-105	DNAJ heat shock N-terminal domain-containing protein
Contig_149	e-105	2-cys peroxiredoxin, chloroplast, putative
Contig_29	e-105	CARA (CARBAMOYL PHOSPHATE SYNTHETASE A); carbamoyl-phosphate synthase (glutamine-hydrolyzing)
Contig_41	e-105	thaumatin-like protein, putative / pathogenesis-related protein, putative
006-94-E05(4-28-06)	e-106	SHM2 (SERINE HYDROXYMETHYLTRANSFERASE 2); glycine hydroxymethyltransferase
0172-94-E03(5-10-06)	e-106	ATISA2/BE2/DBE1/ISA2 (DEBRANCHING ENZYME 1); 1,4-alpha-glucan branching enzyme/ alpha-amylase/ isoamylase
0238-94-G11(5-10-06)	e-106	acetylornithine aminotransferase, mitochondrial, putative / acetylornithine transaminase, putative / AOTA, putative / ACOAT, putative
0249-94(5-31-06)_007	e-106	ECR1 (E1 C-TERMINAL RELATED 1); small protein activating enzyme
0283-94(5-31-06)_011	e-106	porin, putative
0445-94-(6-16-06)_D03	e-106	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G78150.2); similar to TPA: TPA_inf: HN1-like protein isoform 1 [Oryza sativa (japonica cultivar-group)] (GB:DAA01822.1); similar to Os04g0455600 [Oryza sativa (japonica cultivar-group)] (GB:NP_001052962.1); similar to Os02g0574600 [Oryza sativa (japonica cultivar-group)] (GB:NP_001047207.1)
0539-94-(6-8-06)_G05	e-106	glucose-6-phosphate/phosphate translocator-related
0548-94-(6-8-06)_H06	e-106	glycosyl hydrolase family 17 protein
0762-94-(6-7-06)_F08	e-106	NADP-dependent oxidoreductase, putative
0871-94-(6-14-06)_G06	e-106	ATEXPA1 (ARABIDOPSIS THALIANA EXPANSIN A1)
0944-94-(6-15-06)_G03	e-106	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G31110.2); similar to unknown [Pisum sativum] (GB:ABA29158.1); contains InterPro domain Protein of unknown function DUF231, plant; (InterPro:IPR004253)
1032-94-(6-16-06)_D06	e-106	PAF1 (proteasome alpha subunit F1); peptidase
0163-94-C07(5-5-06)	e-107	6-phosphogluconate dehydrogenase NAD-binding domain-containing protein

0378-94-(6-12-06)_E09	e-107	cholinephosphate cytidylyltransferase, putative / phosphorylcholine transferase, putative / CTP:phosphocholine cytidylyltransferase, putative
0459-94-(6-16-06)_A05	e-107	transducin family protein / WD-40 repeat family protein
0747-94-(6-7-06)_G06	e-107	similar to Hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:AAN52749.1); contains InterPro domain Conserved oligomeric complex COG6; (InterPro:IPR010490)
1039-94-(6-2-06)_F05	e-107	APX3 (ASCORBATE PEROXIDASE 3); L-ascorbate peroxidase
Contig_108	e-107	thaumatin-like protein, putative
Contig_78	e-107	ATCTIMC (CYTOSOLIC TRIOSE PHOSPHATE ISOMERASE); triose-phosphate isomerase
0097-94-H09(4-28-06)	e-108	cinnamyl-alcohol dehydrogenase, putative
0707-94-(6-7-06)_G01	e-108	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G18180.1); similar to B0616E02-H0507E05.2 [Oryza sativa (indica cultivar-group)] (GB:CAH67826.1); contains InterPro domain Protein of unknown function DUF1295; (InterPro:IPR010721); contains InterPro domain 3-oxo-5-alpha-steroid 4-dehydrogenase, C-terminal; (InterPro:IPR001104)
0716-94-(6-14-06)_H04	e-108	guanine nucleotide exchange family protein
0801-94-(6-5-06)_A01	e-108	dehydration-responsive protein-related
1002-94-(6-2-06)_B01	e-108	ATGOLS2 (ARABIDOPSIS THALIANA GALACTINOL SYNTHASE 2); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups
1118-94-(6-9-06)_B09	e-108	TPR3 (TOPLESS-RELATED 3)
1139-94-(6-9-06)_G11	e-108	BFN1 (BIFUNCTIONAL NUCLEASE I); nucleic acid binding
0350-94-(6-9-06)_G04	e-109	RD19 (RESPONSIVE TO DEHYDRATION 19); cysteine-type peptidase
Contig_101	e-109	SH3 domain-containing protein 3 (SH3P3)
Contig_138	e-109	DELTA-TIP (delta tonoplast integral protein); water channel
Contig_14	e-109	HPT1 (HOMOGENTISATE PHYTYLTRANSFERASE 1); prenyltransferase
Contig_75	e-109	tRNA synthetase class II (G, H, P and S) family protein
0133-94-E03(5-9-06)	e-110	AVP2 (ARABIDOPSIS VACUOLAR H+-PYROPHOSPHATASE 2)
0815-94-(6-14-06)_E05	e-110	band 7 family protein
0844-94-(6-5-06)_D06	e-110	dihydrodipicolinate reductase family protein
Contig_106	e-110	ACX4 (ACYL-COA OXIDASE 4); oxidoreductase
0566-94-(6-8-06)_A08	e-111	ketose-bisphosphate aldolase class-II family protein
0616-94-(6-6-06)_H02	e-111	TET6 (TETRASPANIN6)
0671-94-(6-6-06)_G09	e-111	40S ribosomal protein S2 (RPS2D)
Contig_135	e-111	malate dehydrogenase, cytosolic, putative

Contig_167	e-111	LHCB2.1 (Photosystem II light harvesting complex gene 2.1); chlorophyll binding
Contig_96	e-111	endomembrane protein 70, putative
0390-94-(6-8-06)_G11	e-112	oxidoreductase, 2OG-Fe(II) oxygenase family protein
0528-94-(6-8-06)_D04	e-112	TRN1 (LOPPED 1, TORNADO 1)
0532-94-(6-8-06)_H04	e-112	ATATP-PRT2 (ATP PHOSPHORIBOSYL TRANSFERASE 2); ATP phosphoribosyltransferase
1005-94-(6-2-06)_E01	e-112	RDR1 (RNA-DEPENDENT RNA POLYMERASE 1); RNA-directed RNA polymerase/ nucleic acid binding
1007-94-(6-2-06)_G01	e-112	proton-dependent oligopeptide transport (POT) family protein
1010-94-(6-2-06)_B02	e-112	pentatricopeptide (PPR) repeat-containing protein
1031-94-(6-2-06)_F04	e-112	NADP-dependent oxidoreductase, putative
1090-94-(6-2-06)_H11	e-112	importin beta-2 subunit family protein
1123-94-(6-9-06)_G09	e-112	aspartyl aminopeptidase, putative
1151-94-(6-15-06)_C04	e-112	F-actin capping protein beta subunit family protein
Contig_196	e-112	SKS5 (SKU5 Similar 5); copper ion binding / oxidoreductase
Contig_76	e-112	proteasome family protein
0323-94-(6-9-06)_C02	e-113	GPT2 (glucose-6-phosphate/phosphate translocator 2); antiporter/ glucose-6-phosphate transporter
0332-94-(6-9-06)_A03	e-113	ANNAT1 (ANNEXIN ARABIDOPSIS 1); calcium ion binding / calcium-dependent phospholipid binding
0538-94-(6-8-06)_F05	e-113	EOL1 (ETO1-LIKE 1); binding
0587-94-(6-8-06)_B10	e-113	UREG (urease accessory protein G); metal ion binding / nucleotide binding
0611-94-(6-6-06)_C02	e-113	ATCYSD1 (Arabidopsis thaliana cysteine synthase D1); cysteine synthase
0793-94-(6-14-06)_C05	e-113	peroxidase 72 (PER72) (P72) (PRXR8)
1009-94-(6-2-06)_A02	e-113	amino acid transporter family protein
Contig_159	e-113	aspartyl protease family protein
Contig_39	e-113	formin homology 2 domain-containing protein / FH2 domain-containing protein
0678-94-(6-6-06)_F10	e-114	FLA10 (fasciclin-like arabinogalactan-protein 10)
0745-94-(6-7-06)_E06	e-114	5'-AMP-activated protein kinase beta-2 subunit, putative
0763-94-(6-7-06)_G08	e-114	kinesin motor protein-related
0767-94-(6-7-06)_B09	e-114	SHM7 (serine hydroxymethyltransferase 7); glycine hydroxymethyltransferase
1138-94-(6-9-06)_F11	e-114	AFH1 (FORMIN HOMOLOGY 1); actin binding
Contig_139	e-114	ATGLX1 (GLYOXALASE I HOMOLOG); lactoylglutathione lyase

0549-94-(6-12-06)_F10	e-115	similar to conserved hypothetical protein [Medicago truncatula] (GB:ABE83163.1); contains domain SPHINGOMYELIN SYNTHETASE (PTHR21290)
0556-94-(6-12-06)_H10	e-115	PAG1 (20S proteasome alpha subunit G1); peptidase
1187-94-(6-15-06)_B07	e-115	protein kinase family protein
Contig_97	e-115	40S ribosomal protein S3A (RPS3aB)
0242-94-C12(5-10-06)	e-116	endomembrane protein 70, putative
0439-94-(6-16-06)_G02	e-116	cyclase family protein
0851-94-(6-5-06)_C07	e-116	ATARP7 (ACTIN-RELATED PROTEIN 7); structural constituent of cytoskeleton
Contig_136	e-116	ATTOC34/OEP34 (Translocase of chloroplast 34)
0074-94-A07(4-28-06)	e-117	PLDALPHA1 (PHOSPHOLIPASE D ALPHA 1); phospholipase D
0427-94-(6-16-06)_C01	e-117	MAP3KA (Mitogen-activated protein kinase kinase kinase 3); kinase
0449-94-(6-27-06)_G06	e-117	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G42050.1); similar to hypothetical protein [Citrus x paradisi] (GB:CAA04664.1); contains domain KELCH-RELATED PROTEINS (PTHR23230); contains domain no description (SM00767); contains domain SUBFAMILY NOT NAMED (PTHR23230:SF15)
0701-94-(6-7-06)_A01	e-117	HTH (HOTHEAD); aldehyde-lyase
1008-94-(6-2-06)_H01	e-117	AMY2/ATAMY2 (ALPHA-AMYLASE-LIKE 2); alpha-amylase
1034-94-(6-14-06)_F08	e-117	APM1 (Aberrant peroxisome morphology 1)
1052-94-(6-2-06)_C07	e-117	histidyl-tRNA synthetase, putative / histidine--tRNA ligase, putative
1143-94-(6-9-06)_C12	e-117	translocation protein-related
Contig_143	e-117	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative
0838-94-(6-5-06)_F05	e-118	flavin-containing monooxygenase family protein / FMO family protein
1089-94-(6-2-06)_G11	e-118	26S proteasome regulatory subunit, putative (RPN12)
Contig_112	e-118	GAMMA-TIP3/TIP1;3 (tonoplast intrinsic protein 1;3); water channel
0672-94-(6-6-06)_H09	e-119	VTC4; 3'(2'),5'-bisphosphate nucleotidase/ inositol or phosphatidylinositol phosphatase
0858-94-(6-5-06)_B08	e-119	OPR3 (OPDA-REDUCTASE 3)
Contig_127	e-119	RAN3; GTP binding
Contig_140	e-119	endomembrane protein 70, putative
Contig_18	e-119	peroxidase, putative
Contig_183	e-119	ABC1 family protein
Contig_90	e-119	XTR6 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 6); hydrolase, acting on glycosyl bonds

0298-94(5-31-06)_009	e-120	XCP1 (XYLEM CYSTEINE PEPTIDASE 1); cysteine-type peptidase
0311-94(5-31-06)_016	e-120	autophagy 3 (APG3)
0778-94-(6-7-06)_C10	e-120	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G01690.1); similar to Esterase/lipase/thioesterase [Medicago truncatula] (GB:ABD32255.1); contains InterPro domain Esterase/lipase/thioesterase; (InterPro:IPR000379); contains InterPro domain Alpha/beta hydrolase fold-1; (InterPro:IPR000073)
0813-94-(6-5-06)_E02	e-120	lectin protein kinase, putative
1142-94-(6-9-06)_B12	e-120	arginase
0148-94-D05(5-9-06)	e-121	MFP2 (MULTIFUNCTIONAL PROTEIN); enoyl-CoA hydratase
0303-94(5-31-06)_002	e-121	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G11420.1); similar to unknown [Ricinus communis] (GB:CAB02653.1); contains InterPro domain Galactose-binding like; (InterPro:IPR008979); contains InterPro domain Protein of unknown function DUF642; (InterPro:IPR006946)
0319-94-(6-9-06)_G01	e-121	calmodulin binding
0377-94-(6-12-06)_D09	e-121	protein phosphatase 2C, putative / PP2C, putative
0398-94-(6-8-06)_F12	e-121	galactosyltransferase family protein
0665-94-(6-6-06)_A09	e-121	GDSL-motif lipase/hydrolase family protein
0065-94-H05(4-28-06)	e-122	UXS4 (UDP-XYLOSE SYNTHASE 4); catalytic
0648-94(6-6-06)_H06	e-122	PDX1 (PYRIDOXINE BIOSYNTHESIS 1.3); protein heterodimerization/ protein homodimerization
1046-94-(6-2-06)_E06	e-122	ATJ3 (Arabidopsis thaliana DnaJ homologue 3)
Contig_206	e-122	ATEXPA13 (ARABIDOPSIS THALIANA EXPANSIN A13)
0232-94-A11(5-10-06)	e-123	tetratricopeptide repeat (TPR)-containing protein
0547-94-(6-8-06)_G06	e-123	aldose 1-epimerase family protein
0709-94-(6-7-06)_A02	e-123	luminal binding protein 1 (BiP-1) (BP1)
0719-94-(6-7-06)_C03	e-123	aspartyl protease family protein
0768-94-(6-7-06)_C09	e-123	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G10020.1); similar to putative stress-induced protein [Solanum commersonii] (GB:CAJ19269.1); contains InterPro domain Protein of unknown function DUF1005; (InterPro:IPR010410)
Contig_154	e-123	glycosyl hydrolase family 79 N-terminal domain-containing protein
Contig_185	e-123	carbon-nitrogen hydrolase family protein
Contig_193	e-123	STM (SHOOT MERISTEMLESS); transcription factor
0247-94(5-31-06)_003	e-124	ATCUL1 (CULLIN 1)
0464-94-(6-16-06)_F05	e-124	protein kinase family protein

Contig_128	e-124	GLX2-4 (GLYOXALASE 2-4); hydroxyacylglutathione hydrolase
Contig_174	e-124	ATCES1 (ATCES1); catalytic
0032-94-G01(4-28-06)	e-125	H+-transporting two-sector ATPase, putative
0259-94(5-31-06)_012	e-125	merozoite surface protein-related
0346-94-(6-9-06)_D04	e-125	glycosyl hydrolase family 20 protein
0468-94-(6-16-06)_B06	e-125	ATGCN1 (Arabidopsis thaliana general control non-repressible 1)
1141-94-(6-9-06)_A12	e-125	galactosyltransferase family protein
Contig_65	e-125	regulator of chromosome condensation (RCC1) family protein
1163-94-(6-15-06)_C05	e-127	UDP-glucose 6-dehydrogenase, putative
Contig_192	e-127	ATEXPA6 (ARABIDOPSIS THALIANA EXPANSIN A6)
Contig_36	e-127	lysyl-tRNA synthetase, putative / lysine--tRNA ligase, putative
0805-94-(6-5-06)_E01	e-128	AFC1 (ARABIDOPSIS FUS3-COMPLEMENTING GENE 1); kinase
Contig_151	e-128	glycosyl hydrolase family 5 protein / cellulase family protein
0612-94-(6-6-06)_D02	e-129	signal recognition particle-related / SRP-related
0621-94-(6-6-06)_E03	e-129	AtRPN1a/RPN1A (26S proteasome regulatory subunit S2 1A); binding
0698-94-(6-12-06)_G12	e-129	ACLA-3 (ATP-citrate lyase A-3)
0799-94-(6-7-06)_F12	e-129	band 7 family protein
0839-94-(6-14-06)_C06	e-129	ATCBR (NADH:CYTOCHROME B5 REDUCTASE 1)
1016-94-(6-2-06)_G02	e-129	UBP1B (OLIGOURIDYLATE BINDING PROTEIN 1B); mRNA 3'-UTR binding
Contig_12	e-129	caffeoyl-CoA 3-O-methyltransferase, putative
0020-94_010(5-31-06)	e-130	aspartyl protease family protein
0641-94-(6-6-06)_A06	e-130	XF1; oxidoreductase
0884-94-(6-5-06)_D11	e-130	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G64650.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G49310.1); similar to expressed protein [Oryza sativa (japonica cultivar-group)] (GB:ABF93637.1); similar to Os10g0519600 [Oryza sativa (japonica cultivar-group)] (GB:NP_001065080.1); similar to Major Facilitator Superfamily protein, expressed [Oryza sativa (japonica cultivar-group)] (GB:ABB47893.2); contains InterPro domain Protein of unknown function DUF791; (InterPro:IPR008509)
1088-94-(6-2-06)_F11	e-130	nucleotide-binding family protein
Contig_103	e-131	PAT1 (PHYTOCHROME A SIGNAL TRANSDUCTION 1); transcription factor
Contig_145	e-131	40S ribosomal protein S4 (RPS4D)
0614-94-(6-6-	e-132	EMB1507 (EMBRYO DEFECTIVE 1507); ATP-dependent helicase

06)_F02		
0624-94-(6-6-06)_H03	e-132	endomembrane protein 70, putative
0743-94-(6-7-06)_C06	e-132	leucine-rich repeat transmembrane protein kinase, putative
0797-94-(6-7-06)_E12	e-132	AJH2 (COP9-signalosome 5B); protein binding
1174-94-(6-15-06)_D06	e-132	3-dehydroquinate synthase, putative
Contig_109	e-132	kelch repeat-containing serine/threonine phosphoesterase family protein
0568-94-(6-8-06)_C08	e-133	STP1 (SUGAR TRANSPORTER 1); carbohydrate transporter/ sugar porter
0898-94-(6-14-06)_H07	e-133	COB (COBRA)
1081-94-(6-2-06)_G10	e-133	RNA binding
Contig_92	e-133	DEAD/DEAH box helicase, putative (RH15)
0727-94-(6-7-06)_C04	e-134	chaperone protein dnaJ-related
0361-94-(6-12-06)_F07	e-135	URE (UREASE); urease
0234-94-C11(5-10-06)	e-136	AUX1 (AUXIN RESISTANT 1); amino acid permease/ transporter
Contig_42	e-136	esterase, putative
0215-94(5-31-06)_012	e-137	SFR2 (SENSITIVE TO FREEZING 2); hydrolase, hydrolyzing O-glycosyl compounds
0393-94-(6-8-06)_B12	e-137	translational activator family protein
0544-94-(6-8-06)_D06	e-137	TSO2 (TSO2); ribonucleoside-diphosphate reductase
0609-94-(6-6-06)_A02	e-137	GAUT10/LGT4 (Galacturonosyltransferase 10); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups
0860-94-(6-5-06)_D08	e-137	ATPAP27/PAP27 (purple acid phosphatase 27); acid phosphatase/ protein serine/threonine phosphatase
1133-94-(6-9-06)_A11	e-137	BOR1 (REQUIRES HIGH BORON 1)
Contig_89	e-137	dehydration-responsive protein-related
0282-94(5-31-06)_009	e-138	pectate lyase family protein
0455-94-(6-16-06)_E04	e-138	ceramidase family protein
0515-94-(6-8-06)_G02	e-139	STT3B (STAUROSPORIN AND TEMPERATURE SENSITIVE 3-LIKE B); oligosaccharyl transferase
0520-94-(6-8-06)_D03	e-139	FTSH3 (FtsH protease 3); ATP-dependent peptidase/ ATPase
1028-94-(6-2-06)_C04	e-139	aconitase family protein / aconitate hydratase family protein
1113-94-(6-9-06)_E08	e-139	glycine dehydrogenase (decarboxylating), putative / glycine decarboxylase, putative / glycine cleavage system P-protein, putative
0506-94-(6-8-06)_F01	e-140	glycine-rich protein

0825-94-(6-5-06)_A04	e-140	leucine-rich repeat transmembrane protein kinase, putative
0888-94-(6-5-06)_H11	e-140	PYRD (PYRIMIDINE D); dihydroorotate dehydrogenase
1310-94-(6-16-06)_D07	e-140	ATNADP-ME4 (NADP-MALIC ENZYME 4); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)/ malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor
0272-94(5-31-06)_006	e-141	PIP (proline iminopeptidase); prolyl aminopeptidase
Contig_115	e-141	MSP1 protein, putative / intramitochondrial sorting protein, putative
0143-94(5-31-06)_013	e-142	EXGT-A4 (ENDOXYLOGLUCAN TRANSFERASE A4); hydrolase, acting on glycosyl bonds
0217-94-(6-16-06)_B09	e-142	CGL1 (COMPLEX GLYCAN LESS)
0940-94-(6-15-06)_C03	e-142	alpha-galactosidase, putative / melibiase, putative / alpha-D-galactoside galactohydrolase, putative
Contig_201	e-142	dicarboxylate/tricarboxylate carrier (DTC)
1030-94-(6-2-06)_E04	e-143	long-chain-fatty-acid--CoA ligase, putative / long-chain acyl-CoA synthetase, putative
Contig_51	e-144	aspartyl-tRNA synthetase, putative / aspartate--tRNA ligase, putative
Contig_133	e-145	PGI1 (CHLOROPLASTIC PHOSPHOGLUCOSE ISOMERASE)
0437-94-(6-16-06)_E02	e-146	signal recognition particle 54 kDa protein 3 / SRP54 (SRP-54C)
0734-94-(6-7-06)_B05	e-146	elongation factor family protein
Contig_137	e-147	CIPK25 (CBL-INTERACTING PROTEIN KINASE 25); kinase
Contig_49	e-147	SOX (SULFITE OXIDASE); sulfite oxidase
1097-94-(6-2-06)_G12	e-148	CHR11 (CHROMATIN-REMODELING PROTEIN 11); DNA-dependent ATPase
0294-94(5-31-06)_001	e-149	glucose-6-phosphate isomerase, cytosolic (PGIC)
Contig_202	e-149	NADP-dependent oxidoreductase, putative
0453-94-(6-16-06)_C04	e-150	GUT2; catalytic
0596-94-(6-8-06)_C11	e-150	DNAJ heat shock family protein
0814-94-(6-5-06)_F02	e-150	pyruvate kinase, putative
Contig_102	e-150	leucine-rich repeat transmembrane protein kinase, putative
0429-94-(6-27-06)_B06	e-151	PDH-E1 ALPHA (PYRUVATE DEHYDROGENASE E1 ALPHA); pyruvate dehydrogenase (acetyl-transferring)
0699-94-(6-12-06)_H12	e-151	CNGC1 (CYCLIC NUCLEOTIDE GATED CHANNEL 1); calmodulin binding / cation channel/ cyclic nucleotide binding / inward rectifier potassium channel
1019-94-(6-2-06)_B03	e-152	LPD1 (LIPOAMIDE DEHYDROGENASE 1)
0926-94-(6-16-06)_D11	e-153	POP2 (POLLEN-PISTIL INCOMPATIBILITY 2); 4-aminobutyrate transaminase
Contig_118	e-154	similar to ankyrin repeat family protein [Arabidopsis thaliana] (TAIR:AT1G04780.1); similar to Os02g0810100 [Oryza sativa (japonica cultivar-group)] (GB:NP_001048467.1); similar to

		hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAC80109.1); contains InterPro domain Ankyrin; (InterPro:IPR002110)
Contig_22	e-154	ATGOLS4 (ARABIDOPSIS THALIANA GALACTINOL SYNTHASE 4); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups
0336-94-(6-9-06)_D03	e-155	MUR4 (MURUS 4)
Contig_21	e-155	dehydration-responsive protein-related
Contig_94	e-155	phenylalanyl-tRNA synthetase, putative / phenylalanine--tRNA ligase, putative
0842-94-(6-5-06)_B06	e-156	MTO1 (METHIONINE OVERACCUMULATION 1)
0855-94-(6-5-06)_G07	e-158	SUS3; UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups
Contig_150	e-158	malate dehydrogenase, cytosolic, putative
0732-94-(6-14-06)_A05	e-160	DEAD box RNA helicase, putative
Contig_129	e-160	ACLA-1 (ATP-citrate lyase A-1)
0434-94-(6-16-06)_B02	e-162	SHM4 (SERINE HYDROXYMETHYLTRANSFERASE 4); glycine hydroxymethyltransferase
Contig_105	e-166	DWF1 (DIMINUTO 1); catalytic
Contig_158	e-166	GAUT12/IRX8/LGT6 (GALACTURONOSYLTRANSFERASE 12); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups
Contig_81	e-166	calnexin 1 (CNX1)
Contig_125	e-169	protein kinase family protein
Contig_38	e-174	protein kinase family protein
0006-93-B05(4-20-06)	No Hit	
0023-94_016(5-31-06)	No Hit	
0037-94-D02(4-28-06)	No Hit	
0042-93-G08(4-21-06)	No Hit	
0047-94-F03(4-28-06)	No Hit	
0052-94-C04(4-28-06)	No Hit	
0063-94-F05(4-28-06)	No Hit	
0071_B05(Rev4-21-06)	No Hit	
0087-94-F08(4-28-06)	No Hit	
0117-94-D12(4-28-06)	No Hit	
0136-94(5-31-06)_011	No Hit	
0161-94-A07(5-5-06)	No Hit	

0229-94-F10(5-10-06)	No Hit	
0237-94-F11(5-10-06)	No Hit	
0241-94-B12(5-10-06)	No Hit	
0270-94(5-31-06)_002	No Hit	
0292-94(5-31-06)_014	No Hit	
0367-94-(6-12-06)_D08	No Hit	
0382-94-(6-12-06)_A10	No Hit	
0452-94-(6-16-06)_B04	No Hit	
0503-94-(6-8-06)_C01	No Hit	
0521-94-(6-8-06)_E03	No Hit	
0543-94-(6-8-06)_C06	No Hit	
0604-94-(6-6-06)_D01	No Hit	
0634-94-(6-6-06)_B05	No Hit	
0638-94-(6-6-06)_F05	No Hit	
0659-94-(6-6-06)_C08	No Hit	
0718-94-(6-7-06)_B03	No Hit	
0730-94-(6-7-06)_F04	No Hit	
0760-94-(6-7-06)_D08	No Hit	
0776-94-(6-7-06)_A10	No Hit	
0791-94-(6-7-06)_G11	No Hit	
0806-94-(6-5-06)_F01	No Hit	
0889-94-(6-5-06)_A12	No Hit	
0894-94-(6-5-06)_F12	No Hit	
0927-94-(6-15-06)_F01	No Hit	
0938-94-(6-15-06)_A03	No Hit	
1027-94-(6-2-06)_B04	No Hit	
1069-94-(6-2-06)_C09	No Hit	

Contig_107	No Hit	
Contig_11	No Hit	
Contig_110	No Hit	
Contig_134	No Hit	
Contig_175	No Hit	
Contig_178	No Hit	
Contig_45	No Hit	
Contig_47	No Hit	
Contig_56	No Hit	
Contig_64	No Hit	
Contig_77	No Hit	
Contig_87	No Hit	

APPENDIX I: *Populus* BLASTX

Query	**E-value**	**Contig**	**ID**	**Description**
Contig\38	0	685	649807	grail3.0001078401
Contig\25	0	677	550613	eugene3.00013054
Contig\200	0	756	828515	estExt_fgenesh4_pg.C_1660009
Contig\161	0	776	835648	estExt_fgenesh4_pm.C_LG_XVII0021
0724-94-(6-7-06)_H03	2.00E-99	358	172207	gw1.I.807.1
0208-94-A08(5-10-06)	3.00E-99	357	784817	fgenesh4_pg.C_scaffold_133000078
1025-94-(6-2-06)_H03	4.00E-99	357	664050	grail3.0035024401
0276-94(5-31-06)_014	5.00E-99	357	759183	fgenesh4_pg.C_LG_IV000811
0431-94-(6-16-06)_G01	7.00E-99	356	180608	gw1.I.9208.1
1125-94-(6-9-06)_A10	2.00E-98	355	833700	estExt_fgenesh4_pm.C_LG_X0632
0607-94-(6-6-06)_G01	4.00E-98	354	228166	gw1.X.2863.1
Contig\123	6.00E-98	353	209205	gw1.V.4606.1
0095-93-B02(4-21-06)	6.00E-98	353	797875	fgenesh4_pm.C_LG_I000878
Contig\27	8.00E-98	353	711735	estExt_Genewise1_v1.C_LG_III0271
0349-94-(6-9-06)_F04	9.00E-98	353	554403	eugene3.00031036
0917-94-(6-14-06)_D12	1.00E-97	353	230613	gw1.X.5310.1
Contig\54	2.00E-97	352	826706	estExt_fgenesh4_pg.C_400053
1301-94-(6-16-06)_C06	2.00E-97	352	729008	estExt_Genewise1_v1.C_LG_XII1492
0656-94-(6-6-06)_H07	2.00E-97	352	833401	estExt_fgenesh4_pm.C_LG_X0108
0185-94-B05(5-10-06)	5.00E-97	350	419389	gw1.VIII.817.1
Contig\52	7.00E-97	350	257510	gw1.XVI.3449.1
0739-94-(6-7-06)_G05	1.00E-96	349	227358	gw1.X.2055.1
0524-94-(6-8-06)_H03	1.00E-96	349	837482	estExt_fgenesh4_pm.C_1710004
0159-94(5-31-06)_004	3.00E-96	348	837541	estExt_fgenesh4_pm.C_2000003
0591-94-(6-8-06)_F10	6.00E-96	347	799426	fgenesh4_pm.C_LG_II001115
Contig\173	8.00E-96	347	745080	estExt_Genewise1_v1.C_1420243
Contig\116	1.00E-95	346	594617	eugene3.00640205
0598-94-(6-8-06)_E11	1.00E-95	345	770239	fgenesh4_pg.C_LG_X001729
1018-94-(6-2-06)_A03	2.00E-95	345	269600	gw1.137.65.1
0541-94-(6-8-06)_A06	4.00E-95	344	744153	estExt_Genewise1_v1.C_1290084
0817-94-(6-5-06)_A03	5.00E-95	344	777108	fgenesh4_pg.C_LG_XVI000350
0012-94_009(5-31-06)	6.00E-95	343	837444	estExt_fgenesh4_pm.C_1650007
0914-94-(6-14-06)_A12	8.00E-95	343	554061	eugene3.00030694
0570-94-(6-8-06)_E08	9.00E-95	343	551443	eugene3.00020758
Contig\44	1.00E-94	343	735328	estExt_Genewise1_v1.C_LG_XVI2405
0447-94-(6-16-06)_F03	1.00E-94	342	835832	estExt_fgenesh4_pm.C_LG_XVIII0163
0446-94-(6-16-06)_E03	1.00E-94	342	817289	estExt_fgenesh4_pg.C_LG_III0902

0008-94-G05(4-20-06)	1.00E-94	342	575095	eugene3.00150490
1087-94-(6-2-06)_E11	2.00E-94	342	256847	gw1.XVI.2786.1
0929-94-(6-15-06)_H01	2.00E-94	342	419160	gw1.VIII.588.1
0861-94-(6-5-06)_E08	2.00E-94	342	256678	gw1.XVI.2617.1
0657-94-(6-6-06)_A08	3.00E-94	341	572675	eugene3.00140720
1082-94-(6-2-06)_H10	7.00E-94	340	271681	gw1.147.249.1
1085-94-(6-2-06)_C11	8.00E-94	340	831763	estExt_fgenesh4_pm.C_LG_VI0046
0854-94-(6-5-06)_F07	1.00E-93	339	198372	gw1.IV.3461.1
1171-94-(6-15-06)_A06	2.00E-93	339	783062	fgenesh4_pg.C_scaffold_82000017
1064-94-(6-2-06)_F08	2.00E-93	339	411608	gw1.II.2943.1
0529-94-(6-8-06)_E04	2.00E-93	338	733451	estExt_Genewise1_v1.C_LG_XV1823
Contig\24	3.00E-93	338	825902	estExt_fgenesh4_pg.C_LG_XVIII0821
1102-94-(6-9-06)_B07	5.00E-93	337	180122	gw1.I.8722.1
0462-94-(6-16-06)_D05	5.00E-93	337	287193	gw1.40.953.1
0514-94-(6-8-06)_F02	6.00E-93	337	816050	estExt_fgenesh4_pg.C_LG_II0292
Contig\70	8.00E-93	336	823409	estExt_fgenesh4_pg.C_LG_XII0928
Contig\188	1.00E-92	336	802283	fgenesh4_pm.C_LG_VI000630
0530-94-(6-8-06)_F04	1.00E-92	336	825574	estExt_fgenesh4_pg.C_LG_XVII0427
0198-94-(6-16-06)_H08	1.00E-92	336	738040	estExt_Genewise1_v1.C_LG_XVIII3287
0210-94-C08(5-10-06)	2.00E-92	335	741129	estExt_Genewise1_v1.C_440677
0642-94-(6-6-06)_B06	3.00E-92	335	832292	estExt_fgenesh4_pm.C_LG_VII0233
0144-94(5-31-06)_015	4.00E-92	334	560996	eugene3.00060955
0099-94-B10(4-28-06)	6.00E-92	333	832169	estExt_fgenesh4_pm.C_LG_VII0004
0789-94-(6-7-06)_E11	1.00E-91	332	251915	gw1.XV.1351.1
0740-94-(6-7-06)_H05	2.00E-91	332	644713	grail3.0039027801
0457-94-(6-16-06)_G04	3.00E-91	331	827131	estExt_fgenesh4_pg.C_640066
0597-94-(6-8-06)_D11	4.00E-91	331	552308	eugene3.00021623
0450-94-(6-16-06)_H03	4.00E-91	330	727523	estExt_Genewise1_v1.C_LG_XI1696
1073-94-(6-2-06)_G09	6.00E-91	330	819144	estExt_fgenesh4_pg.C_LG_VI0631
Contig\63	7.00E-91	330	574967	eugene3.00150362
0536-94-(6-8-06)_D05	7.00E-91	330	659048	grail3.0006046301
Contig\147	9.00E-91	330	741795	estExt_Genewise1_v1.C_660484
0749-94-(6-7-06)_A07	1.00E-90	329	549662	eugene3.00012103
0572-94-(6-8-06)_G08	2.00E-90	328	675953	grail3.0028011201
0227-94-D10(5-10-06)	4.00E-90	327	254612	gw1.XVI.551.1
0866-94-(6-5-06)_B09	5.00E-90	327	718007	estExt_Genewise1_v1.C_LG_VII0041
0107-94-(6-12-06)_A04	8.00E-90	327	589928	eugene3.00290111
Contig\126	9.00E-90	327	822499	estExt_fgenesh4_pg.C_LG_X1876
Contig\83	1.00E-89	326	226761	gw1.X.1458.1
0655-94-(6-6-06)_G07	3.00E-89	325	834106	estExt_fgenesh4_pm.C_LG_XI0297
1077-94-(6-2-06)_C10	4.00E-89	324	550738	eugene3.00020053
0358-94-(6-12-06)_C07	4.00E-89	324	834748	estExt_fgenesh4_pm.C_LG_XIV0126

0522-94-(6-8-06)_F03	7.00E-89	323	655385	grail3.0019025401
Contig\17	2.00E-88	322	824546	estExt_fgenesh4_pg.C_LG_XV0194
0112-94-(6-12-06)_D04	2.00E-88	322	559722	eugene3.00051337
0923-94-(6-15-06)_B01	3.00E-88	321	728694	estExt_Genewise1_v1.C_LG_XII0631
0942-94-(6-15-06)_E03	4.00E-88	321	216305	gw1.VII.610.1
1026-94-(6-2-06)_A04	5.00E-88	320	831996	estExt_fgenesh4_pm.C_LG_VI0481
0857-94-(6-5-06)_A08	6.00E-88	320	740033	estExt_Genewise1_v1.C_290436
0752-94-(6-7-06)_D07	7.00E-88	320	737243	estExt_Genewise1_v1.C_LG_XVIII1645
0527-94-(6-8-06)_C04	1.00E-87	320	726951	estExt_Genewise1_v1.C_LG_XI0012
0278-94(5-31-06)_001	1.00E-87	319	781583	fgenesh4_pg.C_scaffold_40000333
0257-94(5-31-06)_008	1.00E-87	319	831456	estExt_fgenesh4_pm.C_LG_V0273
0755-94-(6-7-06)_G07	3.00E-87	318	259284	gw1.XVII.1275.1
Contig\79	4.00E-87	317	727965	estExt_Genewise1_v1.C_LG_XI2803
1029-94-(6-2-06)_D04	8.00E-87	316	179069	gw1.I.7669.1
Contig\205	1.00E-86	317	726443	estExt_Genewise1_v1.C_LG_X5603
Contig\172	1.00E-86	316	828557	estExt_fgenesh4_pg.C_1700012
Contig\190	2.00E-86	316	569405	eugene3.00120058
Contig\122	2.00E-86	316	821385	estExt_fgenesh4_pg.C_LG_IX0938
0105-94-H10(4-28-06)	4.00E-86	314	287102	gw1.40.862.1
0305-94(5-31-06)_004	5.00E-86	314	821105	estExt_fgenesh4_pg.C_LG_IX0343
0897-94-(6-14-06)_G07	2.00E-85	312	706098	estExt_Genewise1_v1.C_LG_I1143
0223-94-H09(5-10-06)	2.00E-85	311	654056	grail3.0013032202
0831-94-(6-5-06)_G04	4.00E-85	311	201569	gw1.IX.2034.1
1015-94-(6-2-06)_F02	6.00E-85	310	815294	estExt_fgenesh4_pg.C_LG_I1595
0785-94-(6-7-06)_B11	6.00E-85	310	255482	gw1.XVI.1421.1
Contig\37	7.00E-85	310	290393	gw1.494.4.1
0708-94-(6-7-06)_H01	7.00E-85	310	806538	fgenesh4_pm.C_LG_XII000358
Contig\72	8.00E-85	310	836090	estExt_fgenesh4_pm.C_LG_XIX0169
0581-94-(6-8-06)_E09	8.00E-85	310	559973	eugene3.00051588
Contig\69	1.00E-84	309	245453	gw1.XIV.2196.1
Contig\191	1.00E-84	310	679507	grail3.0064002001
0738-94-(6-7-06)_F05	2.00E-84	309	575181	eugene3.00150576
0533-94-(6-8-06)_A05	2.00E-84	309	647622	grail3.0111007201
Contig\48	3.00E-84	308	561006	eugene3.00060965
0824-94-(6-5-06)_H03	5.00E-84	307	672515	grail3.0146000902
0578-94-(6-8-06)_C09	5.00E-84	307	580140	eugene3.01180075
1076-94-(6-2-06)_B10	9.00E-84	306	710908	estExt_Genewise1_v1.C_LG_II2559
0773-94-(6-7-06)_G09	9.00E-84	306	567576	eugene3.00102134
0444-94-(6-16-06)_C03	9.00E-84	306	816442	estExt_fgenesh4_pg.C_LG_II1049
0537-94-(6-8-06)_E05	1.00E-83	306	824199	estExt_fgenesh4_pg.C_LG_XIV0731
0792-94-(6-7-06)_H11	2.00E-83	305	837355	estExt_fgenesh4_pm.C_1520013
0830-94-(6-5-06)_F04	3.00E-83	305	827419	estExt_fgenesh4_pg.C_820030

0782-94-(6-7-06)_G10	4.00E-83	304	659564	grail3.0022016401
0074-93-G04(4-21-06)	4.00E-83	304	810176	fgenesh4_pm.C_scaffold_44000016
Contig\32	5.00E-83	304	650021	grail3.0001096401
Contig\73	1.00E-82	303	552885	eugene3.00002200
0921-94-(6-14-06)_H12	2.00E-82	302	739998	estExt_Genewise1_v1.C_290374
0901-94-(6-14-06)_D10	2.00E-82	302	655170	grail3.0019008001
0946-94-(6-15-06)_A04	3.00E-82	301	737038	estExt_Genewise1_v1.C_LG_XVIII1299
0702-94-(6-7-06)_B01	3.00E-82	301	581352	eugene3.01290009
0603-94-(6-6-06)_C01	4.00E-82	301	832606	estExt_fgenesh4_pm.C_LG_VIII0297
1036-94-(6-2-06)_C05	7.00E-82	300	242954	gw1.XIII.3203.1
1111-94-(6-9-06)_C08	2.00E-81	298	836707	estExt_fgenesh4_pm.C_660087
0920-94-(6-14-06)_G12	2.00E-81	299	770389	fgenesh4_pg.C_LG_X001879
0811-94-(6-5-06)_C02	3.00E-81	298	411672	gw1.II.3007.1
0430-94-(6-16-06)_F01	3.00E-81	298	740479	estExt_Genewise1_v1.C_400905
0780-94-(6-7-06)_E10	5.00E-81	297	227541	gw1.X.2238.1
0509-94-(6-8-06)_A02	7.00E-81	296	834280	estExt_fgenesh4_pm.C_LG_XII0191
1192-94-(6-15-06)_D07	1.00E-80	296	817045	estExt_fgenesh4_pg.C_LG_III0255
0300-94(5-31-06)_013	1.00E-80	296	833382	estExt_fgenesh4_pm.C_LG_X0062
0284-94(5-31-06)_013	1.00E-80	296	799474	fgenesh4_pm.C_LG_II001163
0297-94(5-31-06)_007	2.00E-80	295	731385	estExt_Genewise1_v1.C_LG_XIV1781
0239-94-H11(5-10-06)	3.00E-80	294	219003	gw1.VII.3308.1
0172-94-E03(5-10-06)	4.00E-80	294	246129	gw1.XIV.2872.1
0856-94-(6-5-06)_H07	9.00E-80	293	757271	fgenesh4_pg.C_LG_III000813
Contig\35	1.00E-79	293	199158	gw1.IV.4247.1
0653-94-(6-6-06)_E07	1.00E-79	293	583484	eugene3.01500033
0387-94-(6-12-06)_D10	1.00E-79	293	252605	gw1.XV.2041.1
0460-94-(6-16-06)_B05	2.00E-79	292	657565	grail3.0009041102
0360-94-(6-12-06)_E07	4.00E-79	291	560099	eugene3.00060058
Contig\34	5.00E-79	291	559750	eugene3.00051365
0908-94-(6-14-06)_C11	8.00E-79	290	421498	gw1.VIII.2926.1
0847-94-(6-5-06)_G06	9.00E-79	289	205531	gw1.V.932.1
0255-94(5-31-06)_004	9.00E-79	290	644105	grail3.0033011202
0214-94(5-31-06)_010	1.00E-78	289	836454	estExt_fgenesh4_pm.C_400124
0306-94(5-31-06)_006	3.00E-78	288	651611	grail3.0002029801
Contig\31	4.00E-78	288	240724	gw1.XIII.973.1
Contig\155	5.00E-78	287	835469	estExt_fgenesh4_pm.C_LG_XVI0242
0905-94-(6-14-06)_H10	7.00E-78	287	569505	eugene3.00120158
0162-94-B07(5-5-06)	7.00E-78	286	720740	estExt_Genewise1_v1.C_LG_VIII1964
0513-94-(6-8-06)_E02	2.00E-77	285	235411	gw1.XI.3391.1
0141-94-E04(5-9-06)	2.00E-77	285	195673	gw1.IV.762.1
0006-94-C05(4-20-06)	3.00E-77	284	272274	gw1.150.89.1
0654-94-(6-6-06)_F07	5.00E-77	284	831973	estExt_fgenesh4_pm.C_LG_VI0445

0802-94-(6-5-06)_B01	1.00E-76	283	578586	eugene3.00180810
0221-94-F09(5-10-06)	1.00E-76	282	173806	gw1.I.2406.1
0687-94-(6-6-06)_G11	3.00E-76	281	639592	grail3.0116001202
0296-94(5-31-06)_005	3.00E-76	281	657188	grail3.0009010801
1108-94-(6-9-06)_H07	4.00E-76	281	561654	eugene3.00061613
0118-94-E12(4-28-06)	5.00E-76	280	421537	gw1.VIII.2965.1
0567-94-(6-8-06)_B08	6.00E-76	280	415236	gw1.III.2339.1
0021-94_012(5-31-06)	7.00E-76	280	739192	estExt_Genewise1_v1.C_280165
Contig\104	2.00E-75	279	197007	gw1.IV.2096.1
0717-94-(6-7-06)_A03	2.00E-75	279	662371	grail3.0079006701
0688-94-(6-6-06)_H11	2.00E-75	278	803799	fgenesh4_pm.C_LG_VIII000754
0595-94-(6-8-06)_B11	2.00E-75	278	414440	gw1.III.1543.1
0079-93-B04(4-21-06)	2.00E-75	278	743405	estExt_Genewise1_v1.C_1210133
Contig\71	3.00E-75	278	717083	estExt_Genewise1_v1.C_LG_VI0901
0846-94-(6-5-06)_F06	3.00E-75	278	819645	estExt_fgenesh4_pg.C_LG_VII0010
1128-94-(6-9-06Truncated)_D10	4.00E-75	277	594630	eugene3.00640218
0071_F06(For4-28-06)	4.00E-75	277	549842	eugene3.00012283
1080-94-(6-2-06)_F10	6.00E-75	277	585775	eugene3.01820038
0859-94-(6-5-06)_C08	6.00E-75	277	644482	grail3.0039007801
Contig\181	8.00E-75	276	653576	grail3.0030018001
0128-94(5-31-06)_009	1.00E-74	276	198984	gw1.IV.4073.1
0640-94-(6-6-06)_H05	2.00E-74	276	251374	gw1.XV.810.1
0535-94-(6-8-06)_C05	2.00E-74	275	643362	grail3.0003048701
0313-94-(6-9-06)_B01	2.00E-74	275	718718	estExt_Genewise1_v1.C_LG_VII1719
Contig\68	3.00E-74	275	769367	fgenesh4_pg.C_LG_X000857
0810-94-(6-5-06)_B02	3.00E-74	275	559032	eugene3.00050647
1144-94-(6-9-06)_D12	1.00E-73	273	730037	estExt_Genewise1_v1.C_LG_XIII2126
1067-94-(6-2-06)_A09	1.00E-73	273	197320	gw1.IV.2409.1
0649-94-(6-6-06)_A07	2.00E-73	271	714870	estExt_Genewise1_v1.C_LG_V0611
Contig\179	3.00E-73	271	259282	gw1.XVII.1273.1
Contig\62	4.00E-73	271	817727	estExt_fgenesh4_pg.C_LG_IV0080
Contig\120	2.00E-72	269	710099	estExt_Genewise1_v1.C_LG_II0822
0029-94-D01(4-28-06)	2.00E-72	268	662072	grail3.0015020301
Contig\59	3.00E-72	268	833661	estExt_fgenesh4_pm.C_LG_X0562
1308-94-(6-16-06)_B07	3.00E-72	268	798305	fgenesh4_pm.C_LG_I001308
1003-94-(6-2-06)_C01	4.00E-72	268	253095	gw1.XV.2531.1
1058-94-(6-2-06)_H07	1.00E-71	266	723751	estExt_Genewise1_v1.C_LG_X0207
0835-94-(6-5-06)_C05	2.00E-71	266	816613	estExt_fgenesh4_pg.C_LG_II1494
0329-94-(6-27-06)_H03	2.00E-71	264	552931	eugene3.00002246
0086-94-E08(4-28-06)	5.00E-71	264	641332	grail3.0053005601
0691-94-(6-6-06)_C12	8.00E-71	263	564771	eugene3.00081366

1104-94-(6-9-06)_D07	1.00E-70	263	644912	grail3.0050015101
0683-94-(6-6-06)_C11	1.00E-70	263	580373	eugene3.01200058
0388-94-(6-12-06)_E10	1.00E-70	263	801848	fgenesh4_pm.C_LG_VI000195
0211-94-D08(5-10-06)	1.00E-70	263	768859	fgenesh4_pg.C_LG_X000349
0130-94-B03(5-9-06)	3.00E-70	261	818445	estExt_fgenesh4_pg.C_LG_V0696
1307-94-(6-16-06)_A07	2.00E-69	259	653209	grail3.0023037001
1182-94-(6-15-06)_H06	3.00E-69	258	566455	eugene3.00101013
0829-94-(6-5-06)_E04	3.00E-69	258	710838	estExt_Genewise1_v1.C_LG_II2421
Contig\86	4.00E-69	258	570664	eugene3.00130028
0010-94_005(5-31-06)	4.00E-69	258	746969	estExt_Genewise1_v1.C_2320006
0177-94-B04(5-10-06)	6.00E-69	257	644373	grail3.0033033502
Contig\124	1.00E-68	256	828781	estExt_fgenesh4_pg.C_2580005
0639-94-(6-6-06)_G05	1.00E-68	256	227389	gw1.X.2086.1
Contig\204	2.00E-68	255	549440	eugene3.00011881
0736-94-(6-7-06)_D05	2.00E-68	255	552641	eugene3.00001956
0887-94-(6-5-06)_G11	3.00E-68	254	718708	estExt_Genewise1_v1.C_LG_VII1709
Contig\186	5.00E-68	254	815610	estExt_fgenesh4_pg.C_LG_I2376
0895-94-(6-5-06)_G12	5.00E-68	254	249166	gw1.XIX.1566.1
0770-94-(6-14-06)_B05'	6.00E-68	254	837384	estExt_fgenesh4_pm.C_1570006
0636-94-(6-6-06)_D05	7.00E-68	254	276101	gw1.181.10.1
0048-94-G03(4-28-06)	8.00E-68	253	790520	fgenesh4_pg.C_scaffold_1291000001
0804-94-(6-5-06)_D01	1.00E-67	253	561030	eugene3.00060989
0179-94-D04(5-10-06)	4.00E-67	251	761918	fgenesh4_pg.C_LG_VI000228
0907-94-(6-14-06)_B11	6.00E-67	251	734872	estExt_Genewise1_v1.C_LG_XVI1451
0833-94-(6-5-06)_A05	7.00E-67	250	735866	estExt_Genewise1_v1.C_LG_XVI3692
0658-94-(6-6-06)_B08	9.00E-67	250	256434	gw1.XVI.2373.1
0545-94-(6-8-06)_E06	9.00E-67	250	834247	estExt_fgenesh4_pm.C_LG_XII0129
0120-94-A02(5-9-06)	9.00E-67	249	572859	eugene3.00140904
0032-93-A10(4-21-06)	1.00E-66	249	825536	estExt_fgenesh4_pg.C_LG_XVII0338
0584-94-(6-8-06)_G09	2.00E-66	249	564448	eugene3.00081043
Contig\199	1.00E-65	246	643871	grail3.0003092401
Contig\194	1.00E-65	246	829457	estExt_fgenesh4_pm.C_LG_I0339
0750-94-(6-7-06)_B07	1.00E-65	246	813327	fgenesh4_pm.C_scaffold_29000103
0017-94_004(5-31-06)	1.00E-65	246	261634	gw1.XVIII.2175.1
0252-94(5-31-06)_013	2.00E-65	246	732714	estExt_Genewise1_v1.C_LG_XV0025
0841-94-(6-5-06)_A06	3.00E-65	245	820440	estExt_fgenesh4_pg.C_LG_VIII0650
0843-94-(6-5-06)_C06	4.00E-65	244	550226	eugene3.00012667
0795-94-(6-7-06)_C12	7.00E-65	244	551373	eugene3.00020688
0372-94-(6-12-06)_H08	2.00E-64	242	567369	eugene3.00101927
0369-94-(6-12-06)_F08	2.00E-64	242	679935	grail3.0066013202
0260-94(5-31-06)_014	6.00E-64	241	765056	fgenesh4_pg.C_LG_VIII000070
1079-94-(6-2-06)_E10	7.00E-64	240	769953	fgenesh4_pg.C_LG_X001443

Contig\99	8.00E-64	240	645201	grail3.0021004701
Contig\131	8.00E-64	240	826313	estExt_fgenesh4_pg.C_LG_XIX0951
Contig\88	2.00E-63	238	826161	estExt_fgenesh4_pg.C_LG_XIX0457
Contig\203	3.00E-63	238	834110	estExt_fgenesh4_pm.C_LG_XI0311
0870-94-(6-5-06)_F09	3.00E-63	238	834367	estExt_fgenesh4_pm.C_LG_XII0386
0180-94-E04(5-10-06)	8.00E-63	236	566526	eugene3.00101084
1035-94-(6-14-06)_G08	9.00E-63	237	555555	eugene3.00040268
Contig\176	1.00E-62	236	833483	estExt_fgenesh4_pm.C_LG_X0247
0821-94-(6-5-06)_E03	2.00E-62	236	814433	estExt_fgenesh4_kg.C_LG_XVI0013
Contig\187	3.00E-62	236	550077	eugene3.00012518
1021-94-(6-2-06)_D03	3.00E-62	235	639885	grail3.0161001401
0540-94-(6-8-06)_H05	3.00E-62	235	766719	fgenesh4_pg.C_LG_VIII001733
0352-94-(6-27-06)_H04	5.00E-62	234	721963	estExt_Genewise1_v1.C_LG_IX1678
1041-94-(6-2-06)_H05	7.00E-62	234	805919	fgenesh4_pm.C_LG_XI000194
0373-94-(6-12-06)_A09	7.00E-62	234	561117	eugene3.00061076
0129-94-A03(5-9-06)	7.00E-62	233	275272	gw1.170.184.1
Contig\9	2.00E-61	233	234520	gw1.XI.2500.1
0696-94-(6-6-06)_H12	2.00E-61	233	705907	estExt_Genewise1_v1.C_LG_I0681
0254-94-(6-16-06)_B10	2.00E-61	232	560697	eugene3.00060656
0576-94-(6-12-06)_E11	3.00E-61	231	411875	gw1.II.3210.1
Contig\189	8.00E-61	230	589316	eugene3.00280052
0925-94-(6-16-06)_C11	8.00E-61	230	669377	grail3.0020010802
0454-94-(6-16-06)_D04	1.00E-60	229	823440	estExt_fgenesh4_pg.C_LG_XII1036
0026-94-(6-12-06)_A01	1.00E-60	229	596314	eugene3.08120001
0121-94-H12(4-28-06)	2.00E-60	228	646482	grail3.0018019001
0123-94-C02(5-9-06)	3.00E-60	228	412800	gw1.II.4135.1
Contig\3	7.00E-60	227	231748	gw1.X.6445.1
0436-94-(6-16-06)_D02	9.00E-60	227	577091	eugene3.00161226
1305-94-(6-16-06)_G06	1.00E-59	226	743875	estExt_Genewise1_v1.C_1250046
Contig\98	2.00E-59	226	670909	grail3.0123008202
1148-94-(6-9-06)_H12	3.00E-59	225	640624	grail3.0084001702
0922-94-(6-15-06)_A01	3.00E-59	225	252781	gw1.XV.2217.1
0228-94-E10(5-10-06)	6.00E-59	224	410491	gw1.II.1826.1
0892-94-(6-5-06)_D12	7.00E-59	224	663890	grail3.0035010801
0779-94-(6-7-06)_D10	2.00E-58	222	723032	estExt_Genewise1_v1.C_LG_IX3715
1006-94-(6-2-06)_F01	3.00E-58	221	201180	gw1.IX.1645.1
0063-94-F05(4-28-06)	3.00E-58	221	420955	gw1.VIII.2383.1
0517-94-(6-8-06)_A03	4.00E-58	221	292354	gw1.64.6.1
0262-94(5-31-06)_001	5.00E-58	221	663278	grail3.0055005501
0438-94-(6-16-06)_F02	6.00E-58	221	231518	gw1.X.6215.1
0663-94-(6-6-06)_G08	2.00E-57	219	218990	gw1.VII.3295.1
0511-94-(6-8-06)_C02	2.00E-57	219	829912	estExt_fgenesh4_pm.C_LG_I1184

0316-94-(6-9-06)_E01	2.00E-57	219	826819	estExt_fgenesh4_pg.C_400327
Contig\142	3.00E-57	219	410027	gw1.II.1362.1
1127-94-(6-9-06Truncated)_C10	3.00E-57	218	744470	estExt_Genewise1_v1.C_1320075
0667-94-(6-6-06)_C09	3.00E-57	218	832886	estExt_fgenesh4_pm.C_LG_VIII0830
1134-94-(6-9-06)_B11	4.00E-57	218	818188	estExt_fgenesh4_pg.C_LG_IV1449
0625-94-(6-6-06)_A04	8.00E-57	216	821310	estExt_fgenesh4_pg.C_LG_IX0791
1060-94-(6-2-06)_B08	1.00E-56	216	822354	estExt_fgenesh4_pg.C_LG_X1609
1116-94-(6-9-06)_H08	3.00E-56	215	800968	fgenesh4_pm.C_LG_V000060
0800-94-(6-7-06)_G12	7.00E-56	214	228193	gw1.X.2890.1
0562-94-(6-8-06)_H07	7.00E-56	213	245415	gw1.XIV.2158.1
0531-94-(6-8-06)_G04	7.00E-56	214	732253	estExt_Genewise1_v1.C_LG_XIV3351
Contig\148	8.00E-56	214	294718	gw1.70.171.1
0704-94-(6-7-06)_D01	1.00E-55	213	776603	fgenesh4_pg.C_LG_XV001031
0111-94-F11(4-28-06)	1.00E-55	213	555635	eugene3.00040348
0690-94-(6-6-06)_B12	3.00E-55	212	259595	gw1.XVIII.136.1
Contig\10	4.00E-55	212	574729	eugene3.00150124
0263-94(5-31-06)_003	9.00E-55	210	709311	estExt_Genewise1_v1.C_LG_I8875
Contig\168	1.00E-54	209	833878	estExt_fgenesh4_pm.C_LG_X0918
Contig\141	1.00E-54	209	286841	gw1.40.601.1
0902-94-(6-14-06)_E10	3.00E-54	208	561907	eugene3.00061866
1004-94(6-2-06Truncated)_D01	5.00E-54	205	710083	estExt_Genewise1_v1.C_LG_II0799
0796-94-(6-7-06)_D12	5.00E-54	207	597452	eugene3.09440001
Contig\2	1.00E-53	207	647295	grail3.0074007501
Contig\1	1.00E-53	206	286208	gw1.399.10.1
Contig\46	2.00E-53	206	565424	eugene3.00082019
0725-94-(6-7-06)_A04	3.00E-53	205	595399	eugene3.00700040
Contig\23	6.00E-53	204	572838	eugene3.00140883
0140-94-D04(5-9-06)	8.00E-53	203	774123	fgenesh4_pg.C_LG_XIV000033
0807-94-(6-5-06)_G01	1.00E-51	199	412008	gw1.II.3343.1
0244-94-E12(5-10-06)	2.00E-51	198	827452	estExt_fgenesh4_pg.C_860046
0164-94-D07(5-5-06)	2.00E-51	199	750703	fgenesh4_pg.C_LG_I000306
0863-94-(6-5-06)_G08	5.00E-51	198	822107	estExt_fgenesh4_pg.C_LG_X1062
0219-94-D09(5-10-06)	3.00E-50	195	553241	eugene3.00002556
0380-94-(6-12-06)_G09	6.00E-50	194	644143	grail3.0033014101
0915-94-(6-14-06)_B12	2.00E-49	192	226626	gw1.X.1323.1
0220-94E09(5-10-06)	5.00E-49	191	837174	estExt_fgenesh4_pm.C_1330018
Contig\33	6.00E-49	191	811252	fgenesh4_pm.C_scaffold_134000015
0127-94(5-31-06)_007	8.00E-49	190	595021	eugene3.00660215
0883-94-(6-5-06)_C11	9.00E-49	190	786197	fgenesh4_pg.C_scaffold_164000053
0777-94-(6-7-06)_B10	1.00E-48	189	667581	grail3.0004025702
0328-94-(6-9-06)_G02	2.00E-48	189	733659	estExt_Genewise1_v1.C_LG_XV2187

Contig\53	6.00E-48	187	783288	fgenesh4_pg.C_scaffold_86000148
0746-94-(6-7-06)_F06	1.00E-47	186	592924	eugene3.00440259
Contig\130	3.00E-47	185	742765	estExt_Genewise1_v1.C_880038
0881-94-(6-5-06)_A11	5.00E-47	184	271641	gw1.147.209.1
0720-94-(6-7-06)_D03	5.00E-47	184	559307	eugene3.00050922
0285-94(5-31-06)_015	5.00E-47	184	286469	gw1.40.229.1
0681-94-(6-6-06)_A11	1.00E-46	183	651568	grail3.0002026401
0753-94-(6-7-06)_E07	2.00E-46	182	423063	gw1.XII.1523.1
0729-94-(6-7-06)_E04	2.00E-46	182	412711	gw1.II.4046.1
1075-94-(6-2-06)_A10	4.00E-46	181	554787	eugene3.00031420
0834-94-(6-15-06bad)_H10	9.00E-46	179	761292	fgenesh4_pg.C_LG_V001344
1107-94-(6-9-06)_G07	1.00E-45	180	644073	grail3.0033008701
0890-94-(6-14-06)_E07	1.00E-45	180	710452	estExt_Genewise1_v1.C_LG_II1635
Contig\43	2.00E-45	179	245011	gw1.XIV.1754.1
0599-94-(6-8-06)_F11	2.00E-45	179	664148	grail3.0035032201
0823-94-(6-5-06)_G03	5.00E-45	177	589553	eugene3.00280289
0149-94-E05(5-9-06)	5.00E-45	177	656208	grail3.0049029701
0006-93-B05(4-20-06)	1.00E-44	176	272274	gw1.150.89.1
1170-94-(6-15-06)_H05	2.00E-44	176	171961	gw1.I.561.1
0265-94(5-31-06)_007	2.00E-44	176	567287	eugene3.00101845
0075-94-B07(4-28-06)	2.00E-44	176	241122	gw1.XIII.1371.1
1040-94-(6-2-06)_G05	5.00E-44	174	225829	gw1.X.526.1
0643-94-(6-6-06)_C06	1.00E-43	173	832159	estExt_fgenesh4_pm.C_LG_VI0817
Contig\84	2.00E-43	172	742293	estExt_Genewise1_v1.C_770044
0526-94-(6-8-06)_B04	2.00E-43	172	564550	eugene3.00081145
1094-94-(6-2-06)_D12	3.00E-43	172	416906	gw1.VI.1279.1
1063-94-(6-2-06)_E08	5.00E-43	171	709331	estExt_Genewise1_v1.C_LG_I8903
Contig\20	1.00E-42	170	649081	grail3.0001016801
0694-94-(6-6-06)_F12	1.00E-42	170	815182	estExt_fgenesh4_pg.C_LG_I1200
0269-94(5-31-06)_015	2.00E-42	169	810871	fgenesh4_pm.C_scaffold_121000022
0087-93-B03(4-21-06)	2.00E-42	168	820452	estExt_fgenesh4_pg.C_LG_VIII0671
0106-94-A11(4-28-06)	1.00E-41	166	589466	eugene3.00280202
0931-94-(6-16-06)_G11	2.00E-41	166	596467	eugene3.00820056
0054-94-E04(4-28-06)	2.00E-41	165	827918	estExt_fgenesh4_pg.C_1290017
0735-94-(6-7-06)_C05	5.00E-41	164	674261	grail3.0186000501
Contig\169	1.00E-40	163	834328	estExt_fgenesh4_pm.C_LG_XII0282
Contig\57	3.00E-40	162	259036	gw1.XVII.1027.1
0131-94-C03(5-9-06)	4.00E-40	161	563045	eugene3.00070983
Contig\58	5.00E-40	160	570685	eugene3.00130049
0315-94-(6-9-06)_D01	2.00E-39	159	215882	gw1.VII.187.1
0007for_D05'	6.00E-39	157	572434	eugene3.00140479

0645-94-(6-6-06)_E06	8.00E-39	157	810775	fgenesh4_pm.C_scaffold_118000005
0619-94-(6-6-06)_C03	3.00E-38	155	564713	eugene3.00081308
0633-94-(6-6-06)_A05	4.00E-38	155	712551	estExt_Genewise1_v1.C_LG_III2193
Contig\119	6.00E-38	154	555677	eugene3.00040390
0046-94-E03(4-28-06)	6.00E-38	154	551729	eugene3.00021044
0047-93-B08(4-21-06)	2.00E-37	152	651301	grail3.0002003502
0016-94_002(5-31-06)	3.00E-37	152	558991	eugene3.00050606
0756-94-(6-7-06)_H07	4.00E-37	151	416472	gw1.VI.845.1
1167-94-(6-15-06)_F05	5.00E-37	151	815733	estExt_fgenesh4_pg.C_LG_I2759
0199-94(5-31-06)_008	1.00E-36	150	744173	estExt_Genewise1_v1.C_1290136
1172-94-(6-15-06)_B06	7.00E-36	147	731841	estExt_Genewise1_v1.C_LG_XIV2544
Contig\121	1.00E-35	146	815363	estExt_fgenesh4_pg.C_LG_I1776
0818-94-(6-5-06)_B03	2.00E-35	144	564856	eugene3.00081451
0635-94-(6-6-06)_C05	2.00E-35	146	595585	eugene3.00700226
0628-94-(6-6-06)_D04	9.00E-35	144	571342	eugene3.00130706
1166-94-(6-15-06)_E05	1.00E-34	144	594919	eugene3.00660113
1083-94-(6-2-06)_A11	2.00E-34	143	739204	estExt_Genewise1_v1.C_280192
0664-94-(6-6-06)_H08	4.00E-34	142	418717	gw1.VIII.145.1
0588-94-(6-8-06)_C10	8.00E-34	140	251990	gw1.XV.1426.1
0379-94-(6-12-06)_F09	8.00E-34	140	556593	eugene3.00041306
1160-94-(6-15-06)_B05	1.00E-33	140	773472	fgenesh4_pg.C_LG_XII001247
Contig\26	2.00E-32	136	297162	gw1.86.53.1
0175-94-H03(5-10-06)	5.00E-32	134	561711	eugene3.00061670
Contig\82	1.00E-31	133	179353	gw1.I.7953.1
0836-94-(6-5-06)_D05	3.00E-31	132	554739	eugene3.00031372
0045-94-D03(4-28-06)	4.00E-31	131	771542	fgenesh4_pg.C_LG_XI000695
0261-94(5-31-06)_016	6.00E-31	131	738992	estExt_Genewise1_v1.C_LG_XIX2586
1014-94-(6-2-06)_E02	1.00E-30	130	816898	estExt_fgenesh4_pg.C_LG_II2402
0936-94-(6-16-06)_D12	2.00E-30	129	832516	estExt_fgenesh4_pm.C_LG_VIII0151
1145-94-(6-9-06Truncated)_E12	4.00E-30	126	559701	eugene3.00051316
0872-94-(6-5-06)_H09	5.00E-30	128	827940	estExt_fgenesh4_pg.C_1300020
Contig\80	9.00E-30	127	568834	eugene3.00110848
0013-94_011(5-31-06)	9.00E-30	127	762321	fgenesh4_pg.C_LG_VI000631
Contig\77	2.00E-29	126	554422	eugene3.00031055
1180-94-(6-15-06)_G06	2.00E-29	126	817844	estExt_fgenesh4_pg.C_LG_IV0491
0577-94-(6-8-06)_B09	4.00E-29	125	205136	gw1.V.537.1
0930-94-(6-16-06)_F11	6.00E-29	124	177316	gw1.I.5916.1
1032-94-(6-2-06)_G04	8.00E-29	124	640823	grail3.0069007901
0381-94-(6-12-06)_H09	8.00E-29	124	759956	fgenesh4_pg.C_LG_V000008
0693-94-(6-6-06)_E12	1.00E-28	124	277470	gw1.197.19.1
0195-94-D06(5-10-06)	3.00E-28	122	559706	eugene3.00051321

0822-94-(6-5-06)_F03	4.00E-28	121	738728	estExt_Genewise1_v1.C_LG_XIX1752
0668-94-(6-6-06)_D09	7.00E-28	121	582529	eugene3.01400010
0728-94-(6-7-06)_D04	3.00E-27	117	711538	estExt_Genewise1_v1.C_LG_II4005
0309-94(5-31-06)_012	5.00E-27	118	418713	gw1.VIII.141.1
0271-94(5-31-06)_004	6.00E-27	118	219367	gw1.VII.3672.1
1101-94-(6-9-06)_A07	2.00E-26	116	421550	gw1.XII.10.1
Contig\50	3.00E-26	115	547790	eugene3.00010231
Contig\162	2.00E-25	113	416447	gw1.VI.820.1
Contig\156	2.00E-25	112	592848	eugene3.00440183
Contig\117	2.00E-25	113	826036	estExt_fgenesh4_pg.C_LG_XVIII1135
0630-94-(6-6-06)_F04	3.00E-25	112	709848	estExt_Genewise1_v1.C_LG_II0296
0891-94-(6-5-06)_C12	1.00E-24	110	294622	gw1.70.75.1
0071_B05(Rev4-21-06)	1.00E-24	110	549842	eugene3.00012283
1110-94-(6-9-06)_B08	2.00E-24	110	568920	eugene3.00110934
0904-94-(6-14-06)_G10	2.00E-24	109	421750	gw1.XII.210.1
0617-94-(6-6-06)_A03	4.00E-24	108	783326	fgenesh4_pg.C_scaffold_88000019
Contig\113	5.00E-24	108	707534	estExt_Genewise1_v1.C_LG_I4397
Contig\28	8.00E-24	107	557797	eugene3.00091057
0010-93-G12(4-21-06)	9.00E-24	105	746969	estExt_Genewise1_v1.C_2320006
0885-94-(6-5-06)_E11	4.00E-23	105	752629	fgenesh4_pg.C_LG_I002232
0721-94-(6-7-06)_E03	4.00E-23	105	273904	gw1.162.1.1
0714-94-(6-7-06)_F02	5.00E-23	105	825556	estExt_fgenesh4_pg.C_LG_XVII0378
0280-94(5-31-06)_005	9.00E-23	104	230669	gw1.X.5366.1
Contig\184	1.00E-22	103	649767	grail3.0001075101
0644-94-(6-6-06)_D06	4.00E-22	102	758269	fgenesh4_pg.C_LG_III001811
0518-94-(6-8-06)_B03	4.00E-22	101	563608	eugene3.00080203
1147-94-(6-9-06Truncated)_G12	2.00E-21	97	801345	fgenesh4_pm.C_LG_V000437
0024-94(5-31-06)_001	4.00E-21	99	416572	gw1.VI.945.1
0134-94-F03(5-9-06)	1.00E-20	97	665630	grail3.0095006401
0580-94-(6-8-06)_D09	3.00E-20	96	642208	grail3.0032001401
1092-94-(6-2-06)_B12	5.00E-20	93	659564	grail3.0022016401
0087-94-F08(4-28-06)	5.00E-20	95	820452	estExt_fgenesh4_pg.C_LG_VIII0671
0016-93-A12(4-21-06)	4.00E-18	89	816422	estExt_fgenesh4_pg.C_LG_II1017
0085-94-D08(4-28-06)	5.00E-18	88	262067	gw1.XVIII.2608.1
Contig\163	3.00E-17	86	176152	gw1.I.4752.1
0139-94-C04(5-9-06)	3.00E-17	86	770387	fgenesh4_pg.C_LG_X001877
0676-94-(6-6-06)_D10	1.00E-16	84	571396	eugene3.00130760
0945-94-(6-15-06)_H03	2.00E-16	83	667058	grail3.0005062601
0019-94_008(5-31-06)	9.00E-16	81	596129	eugene3.00770103
1120-94-(6-9-06)_D09	1.00E-15	81	571876	eugene3.00131240
0226-94-C10(5-10-06)	2.00E-15	79	644342	grail3.0033030801

Contig\4	1.00E-14	77	200562	gw1.IX.1027.1
0737-94-(6-7-06)_E05	1.00E-14	77	177037	gw1.I.5637.1
Contig\177	4.00E-14	76	562170	eugene3.00070108
0286-94(5-31-06)_002	9.00E-14	74	762402	fgenesh4_pg.C_LG_VI000712
0647-94-(6-6-06)_G06	1.00E-13	74	573846	eugene3.00190320
0365-94-(6-12-06)_B08	1.00E-13	74	227541	gw1.X.2238.1
1115-94-(6-9-06)_G08	2.00E-13	73	559654	eugene3.00051269
0695-94-(6-6-06)_G12	1.00E-12	71	783210	fgenesh4_pg.C_scaffold_86000070
0235-94-D11(5-10-06)	2.00E-11	66	829866	estExt_fgenesh4_pm.C_LG_I1097
Contig\64	3.00E-11	66	570710	eugene3.00130074
0627-94-(6-6-06)_C04	4.00E-11	65	568923	eugene3.00110937
0803-94-(6-5-06)_C01	1.00E-10	64	230616	gw1.X.5313.1
0042-93-G08(4-21-06)	1.00E-10	64	647368	grail3.0074013501
0237-94-F11(5-10-06)	2.00E-10	63	820472	estExt_fgenesh4_pg.C_LG_VIII0722
0571-94-(6-8-06)_F08	6.00E-10	62	264725	gw1.118.213.1
0826-94-(6-5-06)_B04	2.00E-09	60	423773	gw1.29.285.1
0594-94-(6-8-06)_A11	2.00E-09	60	418033	gw1.VI.2406.1
0433-94-(6-27-06)_D06	2.00E-09	60	575532	eugene3.00150927
1084-94-(6-2-06)_B11	3.00E-09	59	205284	gw1.V.685.1
1146-94-(6-9-06)_F12	4.00E-09	59	751593	fgenesh4_pg.C_LG_I001196
0790-94-(6-7-06)_F11	5.00E-09	59	551164	eugene3.00020479
0592-94-(6-8-06)_G10	2.00E-08	57	642306	grail3.0032009701
1124-94-(6-9-06)_H09	1.00E-07	54	829985	estExt_fgenesh4_pm.C_LG_II0021
Contig\56	1.00E-06	50	552310	eugene3.00021625
0117-94-D12(4-28-06)	1.00E-06	50	550250	eugene3.00012691
Contig\67	e-100	363	719424	estExt_Genewise1_v1.C_LG_VII3310
Contig\166	e-100	363	827456	estExt_fgenesh4_pg.C_860050
1169-94-(6-15-06)_G05	e-100	362	592912	eugene3.00440247
1126-94-(6-9-06)_B10	e-100	362	293950	gw1.66.623.1
0943-94-(6-16-06)_F12	e-100	363	815615	estExt_fgenesh4_pg.C_LG_I2387
0910-94-(6-14-06)_E11	e-100	361	814508	estExt_fgenesh4_kg.C_LG_XIX0006
0844-94-(6-5-06)_D06	e-100	360	746317	estExt_Genewise1_v1.C_1700073
0759-94-(6-7-06)_C08	e-100	362	655450	grail3.0019030401
0583-94-(6-8-06)_F09	e-100	360	766588	fgenesh4_pg.C_LG_VIII001602
0347-94-(6-12-06)_F06	e-100	361	713522	estExt_Genewise1_v1.C_LG_IV1715
Contig\16	e-101	363	671531	grail3.0131005102
1054-94-(6-2-06)_E07	e-101	364	651225	grail3.0083002901
0660-94-(6-6-06)_D08	e-101	363	570537	eugene3.00121190
0394-94-(6-8-06)_C12	e-101	366	671531	grail3.0131005102
Contig\180	e-102	367	661644	grail3.0031027502
Contig\146	e-102	367	736748	estExt_Genewise1_v1.C_LG_XVIII0619
Contig\111	e-102	369	659520	grail3.0022013602

1178-94-(6-15-06)_E06	e-102	369	289054	gw1.44.267.1
1152-94-(6-15-06)_D04	e-102	366	745223	estExt_Genewise1_v1.C_1460016
1135-94-(6-9-06)_C11	e-102	367	814139	estExt_fgenesh4_kg.C_LG_X0022
1130-94-(6-9-06)_F10	e-102	366	659198	grail3.0006058601
1096-94-(6-2-06)_F12	e-102	368	663292	grail3.0055006901
1047-94-(6-2-06)_F06	e-102	366	215931	gw1.VII.236.1
0919-94-(6-14-06)_F12	e-102	368	412325	gw1.II.3660.1
0613-94-(6-6-06)_E02	e-102	367	836675	estExt_fgenesh4_pm.C_660024
0440-94-(6-16-06)_H02	e-102	367	571873	eugene3.00131237
0363-94-(6-12-06)_H07	e-102	367	560059	eugene3.00060018
0325-94-(6-14-06)_E02	e-102	368	649691	grail3.0001068602
0312-94-(6-9-06)_A01	e-102	368	746680	estExt_Genewise1_v1.C_2000046
0295-94(5-31-06)_003	e-102	369	561154	eugene3.00061113
0192-94-A06(5-10-06)	e-102	366	716206	estExt_Genewise1_v1.C_LG_V3745
0119-94-F12(4-28-06)	e-102	367	215747	gw1.VII.52.1
0110-94-E11(4-28-06)	e-102	366	833028	estExt_fgenesh4_pm.C_LG_IX0206
Contig\93	e-103	370	595045	eugene3.00660239
Contig\5	e-103	372	711792	estExt_Genewise1_v1.C_LG_III0403
1188-94-(6-15-06)_C07	e-103	370	561376	eugene3.00061335
0133-94-E03(5-9-06)	e-103	372	725225	estExt_Genewise1_v1.C_LG_X3050
Contig\55	e-104	375	662171	grail3.0015028601
0666-94-(6-6-06)_B09	e-104	375	833728	estExt_fgenesh4_pm.C_LG_X0673
0465-94-(6-16-06)_G05	e-104	375	833062	estExt_fgenesh4_pm.C_LG_IX0254
0451-94-(6-16-06)_A04	e-104	375	174243	gw1.I.2843.1
0400-94-(6-8-06)_H12	e-104	375	650389	grail3.0001126601
0233-94-B11(5-10-06)	e-104	374	249816	gw1.XIX.2216.1
0147-94-C05(5-9-06)	e-104	373	582750	eugene3.01420057
Contig\85	e-105	377	226137	gw1.X.834.1
Contig\195	e-105	377	830724	estExt_fgenesh4_pm.C_LG_III0184
Contig\153	e-105	377	814181	estExt_fgenesh4_kg.C_LG_X0064
0896-94-(6-5-06)_H12	e-105	379	819064	estExt_fgenesh4_pg.C_LG_VI0432
0686-94-(6-6-06)_F11	e-105	379	572536	eugene3.00140581
0275-94(5-31-06)_012	e-105	378	656079	grail3.0049019501
0225-94-B10(5-10-06)	e-105	377	830952	estExt_fgenesh4_pm.C_LG_III0602
0163-94-C07(5-5-06)	e-105	377	262082	gw1.XVIII.2623.1
0072-94-F01(5-9-06)	e-105	376	666576	grail3.0005020301
Contig\95	e-106	380	550764	eugene3.00020079
Contig\165	e-106	380	663729	grail3.0126006201
0886-94-(6-5-06)_F11	e-106	382	558898	eugene3.00050513
0710-94-(6-7-06)_B02	e-106	382	564926	eugene3.00081521
0525-94-(6-8-06)_A04	e-106	381	820895	estExt_fgenesh4_pg.C_LG_VIII1741
Contig\198	e-107	383	816898	estExt_fgenesh4_pg.C_LG_II2402

Contig\157	e-107	385	570685	eugene3.00130049
Contig\136	e-107	385	834816	estExt_fgenesh4_pm.C_LG_XIV0229
1061-94-(6-2-06)_C08	e-107	385	412805	gw1.II.4140.1
1042-94-(6-15-06)_E12	e-107	385	823927	estExt_fgenesh4_pg.C_LG_XIV0200
0733-94-(6-7-06)_A05	e-107	385	577200	eugene3.00161335
0626-94-(6-6-06)_B04	e-107	384	773462	fgenesh4_pg.C_LG_XII001237
0539-94-(6-8-06)_G05	e-107	385	551463	eugene3.00020778
0426-94-(6-16-06)_B01	e-107	385	415786	gw1.VI.159.1
0385-94-(6-12-06)_B10	e-107	384	409839	gw1.II.1174.1
0245-94-F12(5-10-06)	e-107	385	660497	grail3.0091010302
Contig\66	e-108	389	709305	estExt_Genewise1_v1.C_LG_I8866
Contig\61	e-108	389	570685	eugene3.00130049
Contig\40	e-108	387	823215	estExt_fgenesh4_pg.C_LG_XII0215
1078-94-(6-2-06)_D10	e-108	388	410678	gw1.II.2013.1
1032-94-(6-16-06)_D06	e-108	389	410548	gw1.II.1883.1
0815-94-(6-14-06)_E05	e-108	389	772921	fgenesh4_pg.C_LG_XII000696
0652-94-(6-6-06)_D07	e-108	387	198370	gw1.IV.3459.1
0606-94-(6-6-06)_F01	e-108	386	764756	fgenesh4_pg.C_LG_VII001101
0532-94-(6-8-06)_H04	e-108	389	249204	gw1.XIX.1604.1
0326-94-(6-14-06)_F02	e-108	388	800401	fgenesh4_pm.C_LG_IV000088
006-94-E05(4-28-06)	e-108	387	643921	grail3.0003095602
Contig\100	e-109	392	815675	estExt_fgenesh4_pg.C_LG_I2562
1179-94-(6-15-06)_F06	e-109	390	574687	eugene3.00150082
1086-94-(6-2-06)_D11	e-109	391	281234	gw1.273.26.1
0911-94-(6-14-06)_F11	e-109	390	830731	estExt_fgenesh4_pm.C_LG_III0194
0548-94-(6-8-06)_H06	e-109	392	592408	eugene3.04210001
0137-94-A04(5-9-06)	e-109	390	816499	estExt_fgenesh4_pg.C_LG_II1199
Contig\96	e-110	394	592879	eugene3.00440214
1193-94-(6-15-06)_E07	e-110	394	766426	fgenesh4_pg.C_LG_VIII001440
1017-94-(6-2-06)_H02	e-110	395	804902	fgenesh4_pm.C_LG_X000208
0918-94-(6-14-06)_E12	e-110	396	573860	eugene3.00190334
0546-94-(6-8-06)_F06	e-110	394	245919	gw1.XIV.2662.1
0463-94-(6-16-06)_E05	e-110	395	594744	eugene3.06600002
Contig\160	e-111	399	660167	grail3.0106013901
Contig\149	e-111	399	576525	eugene3.00160660
Contig\108	e-111	397	416620	gw1.VI.993.1
0200-94-A07(5-10-06)	e-111	398	416267	gw1.VI.640.1
Contig\7	e-112	402	834674	estExt_fgenesh4_pm.C_LG_XIII0470
Contig\60	e-112	402	783291	fgenesh4_pg.C_scaffold_86000151
Contig\39	e-112	400	415875	gw1.VI.248.1
Contig\106	e-112	402	735866	estExt_Genewise1_v1.C_LG_XVI3692
1159-94-(6-15-06)_A05	e-112	400	777162	fgenesh4_pg.C_LG_XVI000404

1137-94-(6-9-06)_E11	e-112	400	732365	estExt_Genewise1_v1.C_LG_XIV3568
1050-94-(6-2-06)_A07	e-112	402	196418	gw1.IV.1507.1
1002-94-(6-2-06)_B01	e-112	402	834449	estExt_fgenesh4_pm.C_LG_XIII0025
0726-94-(6-7-06)_B04	e-112	402	811813	fgenesh4_pm.C_scaffold_182000007
Contig\91	e-113	405	802053	fgenesh4_pm.C_LG_VI000400
Contig\114	e-113	404	824891	estExt_fgenesh4_pg.C_LG_XV1053
1194-94-(6-15-06)_F07	e-113	404	755405	fgenesh4_pg.C_LG_II001585
1105-94-(6-9-06)_E07	e-113	406	567840	eugene3.00102398
0713-94-(6-7-06)_E02	e-113	404	254922	gw1.XVI.861.1
0459-94-(6-16-06)_A05	e-113	405	287651	gw1.41.136.1
0115-94-B12(4-28-06)	e-113	403	658469	grail3.0175001701
Contig\171	e-114	407	287051	gw1.40.811.1
Contig\132	e-114	408	654220	grail3.0013046101
1039-94-(6-2-06)_F05	e-114	407	831312	estExt_fgenesh4_pm.C_LG_IV0530
1034-94-(6-14-06)_F08	e-114	407	417380	gw1.VI.1753.1
0766-94-(6-7-06)_A09	e-114	406	672511	grail3.0146000801
0445-94-(6-16-06)_D03	e-114	408	562605	eugene3.00070543
0439-94-(6-16-06)_G02	e-114	408	175303	gw1.I.3903.1
0242-94-C12(5-10-06)	e-114	407	592879	eugene3.00440214
Contig\112	e-115	412	822504	estExt_fgenesh4_pg.C_LG_X1886
1139-94-(6-9-06)_G11	e-115	410	771158	fgenesh4_pg.C_LG_XI000311
0871-94-(6-14-06)_G06	e-115	410	659295	grail3.0154002001
0762-94-(6-7-06)_F08	e-115	409	836840	estExt_fgenesh4_pm.C_860049
0661-94-(6-6-06)_E08	e-115	410	416714	gw1.VI.1087.1
0587-94-(6-8-06)_B10	e-115	411	645427	grail3.0021023901
0359-94-(6-12-06)_D07	e-115	411	658536	grail3.0006002201
0350-94-(6-9-06)_G04	e-115	412	816035	estExt_fgenesh4_pg.C_LG_II0263
0209-94-B08(5-10-06)	e-115	411	832631	estExt_fgenesh4_pm.C_LG_VIII0340
0097-94-H09(4-28-06)	e-115	410	232836	gw1.XI.816.1
Contig\167	e-116	414	830495	estExt_fgenesh4_pm.C_LG_II0962
Contig\135	e-116	413	551994	eugene3.00021309
1118-94-(6-9-06)_B09	e-116	414	773603	fgenesh4_pg.C_LG_XIII000057
0944-94-(6-15-06)_G03	e-116	414	592181	eugene3.00410024
0611-94-(6-6-06)_C02	e-116	414	673917	grail3.1757000202
0323-94-(6-9-06)_C02	e-116	414	196703	gw1.IV.1792.1
0307-94-(6-12-06)_F05	e-116	415	752684	fgenesh4_pg.C_LG_I002287
0030-94-E01(4-28-06)	e-116	414	804616	fgenesh4_pm.C_LG_IX000663
Contig\97	e-117	418	231096	gw1.X.5793.1
Contig\78	e-117	419	724697	estExt_Genewise1_v1.C_LG_X2172
Contig\206	e-117	418	198725	gw1.IV.3814.1
Contig\154	e-117	417	775808	fgenesh4_pg.C_LG_XV000236
Contig\138	e-117	419	548890	eugene3.00011331

Contig\101	e-117	417	828703	estExt_fgenesh4_pg.C_2040024
0788-94-(6-7-06)_D11	e-117	417	172693	gw1.I.1293.1
0671-94-(6-6-06)_G09	e-117	416	549239	eugene3.00011680
0605-94-(6-6-06)_E01	e-117	417	423789	gw1.29.301.1
0250-94(5-31-06)_009	e-117	418	554016	eugene3.00030649
Contig\75	e-118	421	552617	eugene3.00021932
Contig\139	e-118	419	713477	estExt_Genewise1_v1.C_LG_IV1582
Contig\127	e-118	422	717966	estExt_Genewise1_v1.C_LG_VI2910
1151-94-(6-15-06)_C04	e-118	420	831563	estExt_fgenesh4_pm.C_LG_V0447
1089-94-(6-2-06)_G11	e-118	419	712298	estExt_Genewise1_v1.C_LG_III1640
1031-94-(6-2-06)_F04	e-118	421	673777	grail3.0170002101
0851-94-(6-5-06)_C07	e-118	420	706403	estExt_Genewise1_v1.C_LG_I1765
0748-94-(6-7-06)_H06	e-118	420	583604	eugene3.01520008
0747-94-(6-7-06)_G06	e-118	422	783302	fgenesh4_pg.C_scaffold_86000162
0744-94-(6-7-06)_D06	e-118	422	733616	estExt_Genewise1_v1.C_LG_XV2116
0378-94-(6-12-06)_E09	e-118	421	254849	gw1.XVI.788.1
0249-94(5-31-06)_007	e-118	422	803920	fgenesh4_pm.C_LG_VIII000875
0238-94-G11(5-10-06)	e-118	422	760304	fgenesh4_pg.C_LG_V000356
Contig\8	e-119	423	814132	estExt_fgenesh4_kg.C_LG_X0015
Contig\29	e-119	425	553916	eugene3.00030549
1123-94-(6-9-06)_G09	e-119	423	835204	estExt_fgenesh4_pm.C_LG_XV0274
0763-94-(6-7-06)_G08	e-119	425	256525	gw1.XVI.2464.1
0707-94-(6-7-06)_G01	e-119	424	834815	estExt_fgenesh4_pm.C_LG_XIV0228
0679-94-(6-6-06)_G10	e-119	424	742170	estExt_Genewise1_v1.C_700420
0534-94-(6-8-06)_B05	e-119	423	560425	eugene3.00060384
0507-94-(6-8-06)_G01	e-119	424	241081	gw1.XIII.1330.1
0356-94-(6-12-06)_A07	e-119	424	727951	estExt_Genewise1_v1.C_LG_XI2776
Contig\74	e-120	428	679906	grail3.0066011001
Contig\182	e-120	427	420499	gw1.VIII.1927.1
1052-94-(6-2-06)_C07	e-120	427	249362	gw1.XIX.1762.1
0745-94-(6-7-06)_E06	e-120	429	652366	grail3.0024005201
0684-94-(6-6-06)_D11	e-120	426	832983	estExt_fgenesh4_pm.C_LG_IX0135
0672-94-(6-6-06)_H09	e-120	428	716898	estExt_Genewise1_v1.C_LG_VI0423
0556-94-(6-12-06)_H10	e-120	427	548687	eugene3.00011128
Contig\185	e-121	432	819468	estExt_fgenesh4_pg.C_LG_VI1497
1163-94-(6-15-06)_C05	e-121	432	835719	estExt_fgenesh4_pm.C_LG_XVII0156
1142-94-(6-9-06)_B12	e-121	431	552033	eugene3.00021348
0774-94-(6-7-06)_H09	e-121	430	172927	gw1.I.1527.1
0060-94-C05(4-28-06)	e-121	430	819223	estExt_fgenesh4_pg.C_LG_VI0826
Contig\15	e-122	433	833774	estExt_fgenesh4_pm.C_LG_X0749
Contig\140	e-122	434	561994	eugene3.00061953
1187-94-(6-15-06)_B07	e-122	433	820414	estExt_fgenesh4_pg.C_LG_VIII0583

0767-94-(6-7-06)_B09	e-122	434	181230	gw1.I.9830.1
0648-94(6-6-06)_H06	e-122	434	560912	eugene3.00060871
0549-94-(6-12-06)_F10	e-122	433	816211	estExt_fgenesh4_pg.C_LG_II0615
0390-94-(6-8-06)_G11	e-122	434	418724	gw1.VIII.152.1
1010-94-(6-2-06)_B02	e-123	436	775989	fgenesh4_pg.C_LG_XV000417
1009-94-(6-2-06)_A02	e-123	437	836427	estExt_fgenesh4_pm.C_400084
1008-94-(6-2-06)_H01	e-123	436	798380	fgenesh4_pm.C_LG_II000069
0065-94-H05(4-28-06)	e-123	438	799184	fgenesh4_pm.C_LG_II000873
Contig\159	e-124	441	409495	gw1.II.830.1
Contig\14	e-124	440	578578	eugene3.00180802
0801-94-(6-5-06)_A01	e-124	442	174072	gw1.I.2672.1
0719-94-(6-7-06)_C03	e-124	442	218470	gw1.VII.2775.1
0709-94-(6-7-06)_A02	e-124	441	829431	estExt_fgenesh4_pm.C_LG_I0291
0523-94-(6-8-06)_G03	e-124	442	827034	estExt_fgenesh4_pg.C_570040
0230-94(5-31-06)_014	e-124	441	564336	eugene3.00080931
0032-94-G01(4-28-06)	e-124	441	825536	estExt_fgenesh4_pg.C_LG_XVII0338
Contig\196	e-125	443	556695	eugene3.00041408
1005-94-(6-2-06)_E01	e-125	446	820696	estExt_fgenesh4_pg.C_LG_VIII1203
0793-94-(6-14-06)_C05	e-125	442	827081	estExt_fgenesh4_pg.C_570132
0778-94-(6-7-06)_C10	e-125	446	752623	fgenesh4_pg.C_LG_I002226
0519-94-(6-8-06)_C03	e-125	446	780863	fgenesh4_pg.C_LG_XIX001002
0398-94-(6-8-06)_F12	e-125	442	727295	estExt_Genewise1_v1.C_LG_XI0896
0311-94(5-31-06)_016	e-125	442	836380	estExt_fgenesh4_pm.C_290161
0303-94(5-31-06)_002	e-125	444	832139	estExt_fgenesh4_pm.C_LG_VI0765
Contig\41	e-126	447	729141	estExt_Genewise1_v1.C_LG_XII1843
Contig\197	e-126	446	420524	gw1.VIII.1952.1
0808-94-(6-5-06)_H01	e-126	447	824615	estExt_fgenesh4_pg.C_LG_XV0398
1007-94-(6-2-06)_G01	e-127	451	804521	fgenesh4_pm.C_LG_IX000568
0716-94-(6-14-06)_H04	e-127	451	572117	eugene3.00140162
0678-94-(6-6-06)_F10	e-127	450	730906	estExt_Genewise1_v1.C_LG_XIV0850
0528-94-(6-8-06)_D04	e-127	450	753234	fgenesh4_pg.C_LG_I002837
Contig\76	e-128	455	736462	estExt_Genewise1_v1.C_LG_XVII1414
Contig\65	e-128	454	816029	estExt_fgenesh4_pg.C_LG_II0244
Contig\18	e-128	453	737716	estExt_Genewise1_v1.C_LG_XVIII2665
Contig\144	e-128	454	552515	eugene3.00021830
Contig\143	e-128	456	711461	estExt_Genewise1_v1.C_LG_II3807
1138-94-(6-9-06)_F11	e-128	454	664956	grail3.0012038601
1090-94-(6-2-06)_H11	e-128	455	822312	estExt_fgenesh4_pg.C_LG_X1515
0838-94-(6-5-06)_F05	e-128	453	834297	estExt_fgenesh4_pm.C_LG_XII0228
0799-94-(6-7-06)_F12	e-128	454	835283	estExt_fgenesh4_pm.C_LG_XV0396
0377-94-(6-12-06)_D09	e-128	455	761626	fgenesh4_pg.C_LG_V001678
0148-94-D05(5-9-06)	e-128	452	725677	estExt_Genewise1_v1.C_LG_X3923

0074-94-A07(4-28-06)	e-128	455	829577	estExt_fgenesh4_pm.C_LG_I0571
Contig\174	e-129	457	837466	estExt_fgenesh4_pm.C_1660029
0884-94-(6-5-06)_D11	e-129	459	824511	estExt_fgenesh4_pg.C_LG_XV0082
0464-94-(6-16-06)_F05	e-129	459	288212	gw1.41.697.1
0346-94-(6-9-06)_D04	e-129	457	720563	estExt_Genewise1_v1.C_LG_VIII1629
0332-94-(6-9-06)_A03	e-129	459	643752	grail3.0003082501
Contig\192	e-130	461	652979	grail3.0023018201
Contig\145	e-130	461	837007	estExt_fgenesh4_pm.C_1220043
1143-94-(6-9-06)_C12	e-130	460	821451	estExt_fgenesh4_pg.C_LG_IX1052
1072-94-(6-2-06)_F09	e-130	461	816957	estExt_fgenesh4_pg.C_LG_II2510
0839-94-(6-14-06)_C06	e-130	462	571289	eugene3.00130653
0566-94-(6-8-06)_A08	e-130	461	733116	estExt_Genewise1_v1.C_LG_XV1100
0538-94-(6-8-06)_F05	e-130	459	715033	estExt_Genewise1_v1.C_LG_V0974
0298-94(5-31-06)_009	e-130	460	810417	fgenesh4_pm.C_scaffold_66000095
0283-94(5-31-06)_011	e-130	461	565435	eugene3.00082030
Contig\90	e-131	465	570685	eugene3.00130049
0624-94-(6-6-06)_H03	e-131	466	592757	eugene3.00440092
0547-94-(6-8-06)_G06	e-131	465	719543	estExt_Genewise1_v1.C_LG_VII3592
0449-94-(6-27-06)_G06	e-131	466	742855	estExt_Genewise1_v1.C_880303
0362-94-(6-12-06)_G07	e-131	463	713683	estExt_Genewise1_v1.C_LG_IV2251
Contig\36	e-132	466	828898	estExt_fgenesh4_pg.C_6580001
Contig\12	e-132	467	649581	grail3.0001059501
0468-94-(6-16-06)_B06	e-132	468	584435	eugene3.01630004
0319-94-(6-9-06)_G01	e-132	466	285870	gw1.3811.3.1
0282-94(5-31-06)_009	e-132	466	282224	gw1.28.798.1
1174-94-(6-15-06)_D06	e-133	470	796681	fgenesh4_pg.C_scaffold_57000060
0805-94-(6-5-06)_E01	e-133	470	576599	eugene3.00160734
0621-94-(6-6-06)_E03	e-133	470	827164	estExt_fgenesh4_pg.C_640219
0361-94-(6-12-06)_F07	e-133	471	420355	gw1.VIII.1783.1
0259-94(5-31-06)_012	e-133	472	563449	eugene3.00080044
0232-94-A11(5-10-06)	e-133	472	658487	grail3.0175003001
Contig\183	e-134	474	277221	gw1.193.71.1
1088-94-(6-2-06)_F11	e-134	474	174225	gw1.I.2825.1
0698-94-(6-12-06)_G12	e-134	475	827990	estExt_fgenesh4_pg.C_1310041
Contig\109	e-135	476	572775	eugene3.00140820
Contig\103	e-135	479	176020	gw1.I.4620.1
1081-94-(6-2-06)_G10	e-135	476	245147	gw1.XIV.1890.1
0858-94-(6-5-06)_B08	e-135	477	780930	fgenesh4_pg.C_scaffold_28000012
0612-94-(6-6-06)_D02	e-135	478	835242	estExt_fgenesh4_pm.C_LG_XV0330
0898-94-(6-14-06)_H07	e-136	479	827930	estExt_fgenesh4_pg.C_1290056
0797-94-(6-7-06)_E12	e-136	481	828262	estExt_fgenesh4_pg.C_1470039
0768-94-(6-7-06)_C09	e-136	479	807002	fgenesh4_pm.C_LG_XIII000302

1046-94-(6-2-06)_E06	e-137	483	709907	estExt_Genewise1_v1.C_LG_II0445
Contig\92	e-138	486	819597	estExt_fgenesh4_pg.C_LG_VI1784
Contig\193	e-138	488	233519	gw1.XI.1499.1
Contig\128	e-138	486	741505	estExt_Genewise1_v1.C_640417
0813-94-(6-5-06)_E02	e-138	488	227389	gw1.X.2086.1
0614-94-(6-6-06)_F02	e-138	488	776276	fgenesh4_pg.C_LG_XV000704
0427-94-(6-16-06)_C01	e-138	488	764015	fgenesh4_pg.C_LG_VII000360
1133-94-(6-9-06)_A11	e-139	490	774660	fgenesh4_pg.C_LG_XIV000570
1016-94-(6-2-06)_G02	e-139	492	673211	grail3.0158002202
0234-94-C11(5-10-06)	e-139	490	653103	grail3.0023028402
Contig\151	e-140	496	418949	gw1.VIII.377.1
0701-94-(6-7-06)_A01	e-140	494	781965	fgenesh4_pg.C_scaffold_44000095
0641-94-(6-6-06)_A06	e-141	497	831444	estExt_fgenesh4_pm.C_LG_V0246
0616-94-(6-6-06)_H02	e-141	496	720187	estExt_Genewise1_v1.C_LG_VIII0790
0568-94-(6-8-06)_C08	e-141	497	831066	estExt_fgenesh4_pm.C_LG_IV0065
0247-94(5-31-06)_003	e-141	498	725818	estExt_Genewise1_v1.C_LG_X4345
0020-94_010(5-31-06)	e-141	497	642209	grail3.0032001501
0665-94-(6-6-06)_A09	e-142	499	827359	estExt_fgenesh4_pg.C_700188
0609-94-(6-6-06)_A02	e-142	500	783905	fgenesh4_pg.C_scaffold_120000045
0520-94-(6-8-06)_D03	e-142	500	804555	fgenesh4_pm.C_LG_IX000602
0455-94-(6-16-06)_E04	e-142	502	576910	eugene3.00161045
0860-94-(6-5-06)_D08	e-143	503	423272	gw1.XII.1732.1
1141-94-(6-9-06)_A12	e-144	507	226026	gw1.X.723.1
0393-94-(6-8-06)_B12	e-144	508	573768	eugene3.00190242
1310-94-(6-16-06)_D07	e-145	510	737670	estExt_Genewise1_v1.C_LG_XVIII2568
0743-94-(6-7-06)_C06	e-145	512	646071	grail3.0096005001
0727-94-(6-7-06)_C04	e-145	509	416488	gw1.VI.861.1
0515-94-(6-8-06)_G02	e-145	512	743464	estExt_Genewise1_v1.C_1220082
0217-94-(6-16-06)_B09	e-145	512	199716	gw1.IX.181.1
Contig\94	e-146	513	195427	gw1.IV.516.1
Contig\115	e-146	514	835057	estExt_fgenesh4_pm.C_LG_XV0031
0506-94-(6-8-06)_F01	e-146	513	264686	gw1.118.174.1
Contig\89	e-147	517	718612	estExt_Genewise1_v1.C_LG_VII1503
Contig\42	e-147	517	652670	grail3.0024031501
Contig\152	e-147	517	816703	estExt_fgenesh4_pg.C_LG_II1760
1113-94-(6-9-06)_E08	e-147	516	832093	estExt_fgenesh4_pm.C_LG_VI0678
1019-94-(6-2-06)_B03	e-147	518	225877	gw1.X.574.1
0888-94-(6-5-06)_H11	e-147	516	818330	estExt_fgenesh4_pg.C_LG_V0296
0734-94-(6-7-06)_B05	e-147	519	819068	estExt_fgenesh4_pg.C_LG_VI0439
0940-94-(6-15-06)_C03	e-148	520	249183	gw1.XIX.1583.1
0825-94-(6-5-06)_A04	e-149	524	589556	eugene3.00280292
1028-94-(6-2-06)_C04	e-150	529	821804	estExt_fgenesh4_pg.C_LG_X0404

Contig\133	e-151	530	411695	gw1.II.3030.1
Contig\102	e-151	532	676675	grail3.0029028801
1071-94-(6-2-06)_E09	e-151	531	268089	gw1.131.91.1
0699-94-(6-12-06)_H12	e-151	532	807853	fgenesh4_pm.C_LG_XV000064
0544-94-(6-8-06)_D06	e-152	533	752731	fgenesh4_pg.C_LG_I002334
0453-94-(6-16-06)_C04	e-152	535	640119	grail3.0008017001
1030-94-(6-2-06)_E04	e-153	536	709180	estExt_Genewise1_v1.C_LG_I8598
0842-94-(6-5-06)_B06	e-153	539	835709	estExt_fgenesh4_pm.C_LG_XVII0132
0814-94-(6-5-06)_F02	e-153	538	589553	eugene3.00280289
0437-94-(6-16-06)_E02	e-153	536	257619	gw1.XVI.3558.1
0336-94-(6-9-06)_D03	e-153	539	823130	estExt_fgenesh4_pg.C_LG_XI1340
0272-94(5-31-06)_006	e-153	537	175641	gw1.I.4241.1
Contig\21	e-154	542	724641	estExt_Genewise1_v1.C_LG_X2034
Contig\202	e-154	540	673777	grail3.0170002101
0596-94-(6-8-06)_C11	e-154	541	217453	gw1.VII.1758.1
0215-94(5-31-06)_012	e-154	542	225986	gw1.X.683.1
Contig\49	e-155	545	829778	estExt_fgenesh4_pm.C_LG_I0927
1097-94-(6-2-06)_G12	e-155	545	229734	gw1.X.4431.1
0294-94(5-31-06)_001	e-155	545	421146	gw1.VIII.2574.1
Contig\201	e-156	548	817666	estExt_fgenesh4_pg.C_LG_III1822
0855-94-(6-5-06)_G07	e-156	546	830445	estExt_fgenesh4_pm.C_LG_II0867
0143-94(5-31-06)_013	e-156	547	708892	estExt_Genewise1_v1.C_LG_I8040
Contig\51	e-159	559	652970	grail3.0023017401
Contig\137	e-159	559	717895	estExt_Genewise1_v1.C_LG_VI2708
Contig\118	e-159	557	729899	estExt_Genewise1_v1.C_LG_XIII1701
0429-94-(6-27-06)_B06	e-159	559	755473	fgenesh4_pg.C_LG_II001653
Contig\129	e-160	561	832869	estExt_fgenesh4_pm.C_LG_VIII0801
Contig\81	e-162	569	733819	estExt_Genewise1_v1.C_LG_XV2501
0926-94-(6-16-06)_D11	e-162	568	652454	grail3.0024013201
0732-94-(6-14-06)_A05	e-162	566	296528	gw1.82.68.1
Contig\150	e-163	572	747123	estExt_Genewise1_v1.C_2730019
0434-94-(6-16-06)_B02	e-167	583	829808	estExt_fgenesh4_pm.C_LG_I0969
Contig\22	e-168	587	657524	grail3.0009037801
Contig\158	e-171	598	834622	estExt_fgenesh4_pm.C_LG_XIII0357
Contig\125	e-173	603	741188	estExt_Genewise1_v1.C_570107
Contig\105	e-177	619	765722	fgenesh4_pg.C_LG_VIII000736
Contig\87	No Hit			
Contig\47	No Hit			
Contig\45	No Hit			
Contig\30	No Hit			
Contig\178	No Hit			
Contig\175	No Hit			

Contig\164	No Hit			
Contig\134	No Hit			
Contig\110	No Hit			
Contig\11	No Hit			
Contig\107	No Hit			
1069-94-(6-2-06)_C09	No Hit			
1027-94-(6-2-06)_B04	No Hit			
0938-94-(6-15-06)_A03	No Hit			
0927-94-(6-15-06)_F01	No Hit			
0916-94-(6-14-06)_C12	No Hit			
0894-94-(6-5-06)_F12	No Hit			
0889-94-(6-5-06)_A12	No Hit			
0849-94-(6-5-06)_A07	No Hit			
0806-94-(6-5-06)_F01	No Hit			
0791-94-(6-7-06)_G11	No Hit			
0776-94-(6-7-06)_A10	No Hit			
0760-94-(6-7-06)_D08	No Hit			
0730-94-(6-7-06)_F04	No Hit			
0718-94-(6-7-06)_B03	No Hit			
0659-94-(6-6-06)_C08	No Hit			
0638-94-(6-6-06)_F05	No Hit			
0634-94-(6-6-06)_B05	No Hit			
0604-94-(6-6-06)_D01	No Hit			
0543-94-(6-8-06)_C06	No Hit			
0521-94-(6-8-06)_E03	No Hit			
0503-94-(6-8-06)_C01	No Hit			
0452-94-(6-16-06)_B04	No Hit			
0382-94-(6-12-06)_A10	No Hit			
0367-94-(6-12-06)_D08	No Hit			
0292-94(5-31-06)_014	No Hit			
0270-94(5-31-06)_002	No Hit			
0241-94-B12(5-10-06)	No Hit			
0229-94-F10(5-10-06)	No Hit			
0161-94-A07(5-5-06)	No Hit			
0136-94(5-31-06)_011	No Hit			
0124-94-D02(5-9-06)	No Hit			
0052-94-C04(4-28-06)	No Hit			
0047-94-F03(4-28-06)	No Hit			
0037-94-D02(4-28-06)	No Hit			
0023-94_016(5-31-06)	No Hit			

APPENDIX J: UNIPROT BLASTX

Query	**E-value**	**Description**
Contig\161	0	LOXC_ARATH Lipoxygenase, chloroplast precursor
Contig\200	0	ASPR_CUCPE Aspartic proteinase precursor
Contig\25	0	HSP80_SOLLC Heat shock cognate protein 80
1169-94-(6-15-06)_G05	2.00E-99	HSP82_TOBAC Heat shock protein 82
1179-94-(6-15-06)_F06	2.00E-99	6PGL4_ORYSJ Probable 6-phosphogluconolactonase 4, chloroplast precursor
Contig\27	2.00E-98	PIP15_ARATH Probable aquaporin PIP1-5
0684-94-(6-6-06)_D11	3.00E-98	EXLA1_ARATH Expansin-like A1 precursor
0726-94-(6-7-06)_B04	6.00E-98	TLP7_ARATH Tubby-like F-box protein 7
1188-94-(6-15-06)_C07	6.00E-98	FCL2_ARATH Putative GDP-L-fucose synthase 2
Contig\157	1.00E-97	XTH25_ARATH Probable xyloglucan endotransglucosylase/hydrolase protein 25 precursor
0606-94-(6-6-06)_F01	2.00E-97	IPYR_ORYSJ Soluble inorganic pyrophosphatase
Contig\173	4.00E-97	RAC2_LOTJA Rac-like GTP-binding protein RAC2 precursor
Contig\40	4.00E-97	TAP46_ARATH PP2A regulatory subunit TAP46
Contig\5	4.00E-97	ILL4_ARATH IAA-amino acid hydrolase ILR1-like 4 precursor
Contig\137	6.00E-97	CPK15_ARATH CBL-interacting serine/threonine-protein kinase 15
Contig\61	1.00E-96	XTH23_ARATH Probable xyloglucan endotransglucosylase/hydrolase protein 23 precursor
Contig\91	1.00E-96	BGAL_SOLLC Beta-galactosidase precursor
0429-94-(6-27-06)_B06	4.00E-96	ODPA_PORYE Pyruvate dehydrogenase E1 component subunit alpha
0119-94-F12(4-28-06)	5.00E-96	BCAT5_ARATH Branched-chain-amino-acid aminotransferase 5, chloroplast precursor
0233-94-B11(5-10-06)	5.00E-96	BAK1_ARATH BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor
0515-94-(6-8-06)_G02	5.00E-96	STT3A_MOUSE Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A
Contig\182	6.00E-96	NHX7_ARATH Sodium/hydrogen exchanger 7
0525-94-(6-8-06)_A04	5.00E-95	TLP3_ARATH Tubby-like F-box protein 3
1019-94-(6-2-06)_B03	2.00E-94	DLDH_SYNY3 Dihydrolipoyl dehydrogenase
Contig\146	2.00E-94	CH10C_ARATH 20 kDa chaperonin, chloroplast precursor
0312-94-(6-9-06)_A01	2.00E-93	VA722_ARATH Vesicle-associated membrane protein 722
Contig\114	5.00E-93	GAOX1_ARATH Gibberellin 20 oxidase 1
1126-94-(6-9-06)_B10	9.00E-93	MSSP2_ARATH Monosaccharide-sensing protein 2

1078-94-(6-2-06)_D10	5.00E-92	PBS1_ARATH Serine/threonine-protein kinase PBS1
Contig\70	5.00E-92	KAD2_ORYSJ Adenylate kinase B
0446-94-(6-16-06)_E03	9.00E-92	INVA_PHAAU Acid beta-fructofuranosidase precursor
0817-94-(6-5-06)_A03	1.00E-91	PAP13_ARATH Probable plastid-lipid-associated protein 13, chloroplast precursor
Contig\44	2.00E-91	RS92_ARATH 40S ribosomal protein S9-2
Contig\93	2.00E-91	CLCE_ARATH Chloride channel protein CLC-e
0431-94-(6-16-06)_G01	3.00E-91	HD1_BRANA Homeobox protein HD1
Contig\147	3.00E-91	R10A1_ARATH 60S ribosomal protein L10a-1
0307-94-(6-12-06)_F05	5.00E-91	CSN3_ARATH COP9 signalosome complex subunit 3
0536-94-(6-8-06)_D05	6.00E-91	SAR1A_ARATH GTP-binding protein SAR1A
1054-94-(6-2-06)_E07	9.00E-91	FBL92_ARATH F-box/LRR-repeat protein At5g49980
0607-94-(6-6-06)_G01	2.00E-90	PEL13_ARATH Probable pectate lyase 13 precursor
1125-94-(6-9-06)_A10	5.00E-90	VTI12_ARATH Vesicle transport v-SNARE 12
0326-94-(6-14-06)_F02	8.00E-90	PLT4_ARATH Probable polyol transporter 4
0755-94-(6-7-06)_G07	1.00E-89	CHMU_ARATH Chorismate mutase, chloroplast precursor
0030-94-E01(4-28-06)	2.00E-89	TMK1_ARATH Putative receptor protein kinase TMK1 precursor
0642-94-(6-6-06)_B06	2.00E-89	ATP7_ARATH Probable ATP synthase 24 kDa subunit, mitochondrial precursor
1088-94-(6-2-06)_F11	2.00E-89	NBP35_YARLI Cytosolic Fe-S cluster assembling factor NBP35
1178-94-(6-15-06)_E06	4.00E-89	BGL17_ARATH Beta-galactosidase 17 precursor
0159-94(5-31-06)_004	5.00E-89	RHA1_ARATH Ras-related protein RHA1
0896-94-(6-5-06)_H12	5.00E-89	SAP11_ARATH Zinc finger AN1 and C2H2 domain-containing stress-associated protein 11
Contig\122	7.00E-89	RL6_MESCR 60S ribosomal protein L6
0434-94-(6-16-06)_B02	1.00E-88	GLYM_PEA Serine hydroxymethyltransferase, mitochondrial precursor
1105-94-(6-9-06)_E07	1.00E-88	PME3_PHAVU Pectinesterase-3 precursor
0657-94-(6-6-06)_A08	2.00E-88	RL183_ARATH 60S ribosomal protein L18-3
0107-94-(6-12-06)_A04	7.00E-88	UVH1_ARATH DNA repair endonuclease UVH1
0468-94-(6-16-06)_B06	8.00E-88	ABCF2_MOUSE ATP-binding cassette sub-family F member 2
1174-94-(6-15-06)_D06	2.00E-87	AROB_THICR 3-dehydroquinate synthase
Contig\108	2.00E-87	TLPH_ORYSJ Thaumatin-like protein precursor

0447-94-(6-16-06)_F03	4.00E-87	SDF2_ARATH Stromal cell-derived factor 2-like protein precursor
Contig\126	4.00E-87	ARA3_ARATH Ras-related protein ARA-3
0923-94-(6-15-06)_B01	2.00E-86	RL191_ARATH 60S ribosomal protein L19-1
1007-94-(6-2-06)_G01	3.00E-86	PTR2_ARATH Peptide transporter PTR2
0570-94-(6-8-06)_E08	7.00E-86	HEM2_ARATH Delta-aminolevulinic acid dehydratase, chloroplast precursor
Contig\100	7.00E-86	PABP2_ARATH Polyadenylate-binding protein 2
0530-94-(6-8-06)_F04	1.00E-85	VTI13_ARATH Vesicle transport v-SNARE 13
1064-94-(6-2-06)_F08	6.00E-85	RSP41_ARATH Arginine/serine-rich-splicing factor RSP41
0614-94-(6-6-06)_F02	1.00E-84	U520_HUMAN U5 small nuclear ribonucleoprotein 200 kDa helicase
0609-94-(6-6-06)_A02	3.00E-84	GLTR_ARATH Uncharacterized glycosyltransferase At3g02350
0886-94-(6-5-06)_F11	3.00E-84	CCD32_ARATH Cyclin-D3-2
0946-94-(6-15-06)_A04	4.00E-84	PSB4_ARATH Proteasome subunit beta type-4 precursor
0008-94-G05(4-20-06)	6.00E-84	COPA3_ORYSJ Coatomer subunit alpha-3
0284-94(5-31-06)_013	9.00E-84	QUA1_ARATH Glycosyltransferase QUASIMODO1
0740-94-(6-7-06)_H05	1.00E-83	GL24_ARATH Germin-like protein subfamily 2 member 4 precursor
0825-94-(6-5-06)_A04	1.00E-83	Y2267_ARATH Putative inactive receptor kinase At2g26730 precursor
1130-94-(6-9-06)_F10	3.00E-83	6PGL2_ORYSJ Probable 6-phosphogluconolactonase 2
Contig\48	6.00E-83	UBC4_SOLLC Ubiquitin-conjugating enzyme E2-17 kDa
Contig\54	9.00E-83	BRE1A_ARATH E3 ubiquitin-protein ligase BRE1-like 1
Contig\190	4.00E-82	DCE_SOLLC Glutamate decarboxylase
0529-94-(6-8-06)_E04	7.00E-82	PIMT_ARATH Protein-L-isoaspartate O-methyltransferase
0110-94-E11(4-28-06)	1.00E-81	S6PD_MALDO NADP-dependent D-sorbitol-6-phosphate dehydrogenase
0782-94-(6-7-06)_G10	6.00E-81	COI1_ARATH Coronatine-insensitive protein 1
0520-94-(6-8-06)_D03	1.00E-80	AFG32_HUMAN AFG3-like protein 2
0524-94-(6-8-06)_H03	1.00E-80	COL5_ARATH Zinc finger protein CONSTANS-LIKE 5
0780-94-(6-7-06)_E10	1.00E-80	UBC13_ARATH Ubiquitin-conjugating enzyme E2 13
1025-94-(6-2-06)_H03	1.00E-80	ABIL1_ARATH Protein ABIL1
0074-93-G04(4-21-	4.00E-80	PLDA1_RICCO Phospholipase D alpha 1 precursor

06)		
Contig\171	5.00E-80	HSFB4_ARATH Heat stress transcription factor B-4
0752-94-(6-7-06)_D07	2.00E-79	VA711_ARATH Vesicle-associated membrane protein 711
0596-94-(6-8-06)_C11	3.00E-79	DNAJ_SYNPX Chaperone protein dnaJ
1050-94-(6-2-06)_A07	3.00E-79	TT1_ARATH Protein TRANSPARENT TESTA 1
0905-94-(6-14-06)_H10	4.00E-79	CNGC1_ARATH Cyclic nucleotide-gated ion channel 1
1061-94-(6-2-06)_C08	4.00E-79	FKB70_WHEAT 70 kDa peptidyl-prolyl isomerase
0278-94(5-31-06)_001	7.00E-79	ORYA_ORYSJ Oryzain alpha chain precursor
Contig\62	7.00E-79	THI4_ALNGL Thiazole biosynthetic enzyme, chloroplast precursor
1159-94-(6-15-06)_A05	9.00E-79	TT1_ARATH Protein TRANSPARENT TESTA 1
Contig\73	9.00E-79	NDUS1_SOLTU NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor
Contig\158	1.00E-78	GLTR_ARATH Uncharacterized glycosyltransferase At3g02350
0660-94-(6-6-06)_D08	3.00E-78	SCRK4_ARATH Probable fructokinase-4
0808-94-(6-5-06)_H01	3.00E-78	Y2267_ARATH Putative inactive receptor kinase At2g26730 precursor
Contig\165	6.00E-78	SF3_HELAN Pollen-specific protein SF3
Contig\31	2.00E-77	FB60_ARATH F-box protein At1g55000
0597-94-(6-8-06)_D11	3.00E-77	RSP31_ARATH Arginine/serine-rich-splicing factor RSP31
0603-94-(6-6-06)_C01	3.00E-77	SNAA2_ARATH Alpha-soluble NSF attachment protein 2
0679-94-(6-6-06)_G10	4.00E-77	DHQSD_ARATH Bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase, chloroplast precursor
Contig\140	1.00E-76	TM9S2_RAT Transmembrane 9 superfamily protein member 2 precursor
0325-94-(6-14-06)_E02	3.00E-76	SF3_HELAN Pollen-specific protein SF3
0457-94-(6-16-06)_G04	3.00E-76	4CLL9_ARATH 4-coumarate--CoA ligase-like 9
0734-94-(6-7-06)_B05	6.00E-76	TYPA_SYNY3 GTP-binding protein TypA/BipA homolog
0460-94-(6-16-06)_B05	4.00E-74	DNJ16_ARATH Chaperone protein dnaJ 16
1036-94-(6-2-06)_C05	1.00E-73	RF2B_ORYSJ Transcription factor RF2b
Contig\205	3.00E-73	AX22B_PHAAU Auxin-induced protein 22B
0767-94-(6-7-06)_B09	4.00E-73	GLYC_RABIT Serine hydroxymethyltransferase, cytosolic
0065-94-H05(4-28-06)	5.00E-73	UXS1_RAT UDP-glucuronic acid decarboxylase 1
0621-94-(6-6-06)_E03	5.00E-73	PSMD2_PONPY 26S proteasome non-ATPase regulatory subunit 2
1082-94-(6-	5.00E-73	ARGB_ANASP Acetylglutamate kinase

2-06)_H10		
0513-94-(6-8-06)_E02	6.00E-73	PDC1_PEA Pyruvate decarboxylase isozyme 1
0079-93-B04(4-21-06)	7.00E-73	SYK_ORYSJ Lysyl-tRNA synthetase
0744-94-(6-7-06)_D06	2.00E-72	UE1D1_RAT Ubiquitin-activating enzyme E1 domain-containing protein 1
1144-94-(6-9-06)_D12	1.00E-71	MEM11_ARATH Membrin-11
0799-94-(6-7-06)_F12	2.00E-71	PLZ12_LUPPO Protein PPLZ12
0811-94-(6-5-06)_C02	2.00E-71	NAT3_ARATH Nucleobase-ascorbate transporter 3
0097-94-H09(4-28-06)	4.00E-71	MTDH_MEDSA Probable mannitol dehydrogenase
0926-94-(6-16-06)_D11	1.00E-70	Y4UB_RHISN Uncharacterized aminotransferase y4uB
Contig\115	1.00E-70	ATD1A_DANRE ATPase family AAA domain-containing protein 1-A
Contig\196	1.00E-70	ASOL_BRANA L-ascorbate oxidase homolog precursor
0654-94-(6-6-06)_F07	3.00E-70	FATB_GOSHI Myristoyl-acyl carrier protein thioesterase, chloroplast precursor
1008-94-(6-2-06)_H01	3.00E-70	AMY3E_ORYSJ Alpha-amylase isozyme 3E precursor
0130-94-B03(5-9-06)	4.00E-70	NCPR_PHAAU NADPH--cytochrome P450 reductase
0866-94-(6-5-06)_B09	7.00E-70	HAT22_ARATH Homeobox-leucine zipper protein HAT22
0788-94-(6-7-06)_D11	2.00E-69	E13B_WHEAT Glucan endo-1,3-beta-glucosidase precursor
0313-94-(6-9-06)_B01	3.00E-69	RS61_ARATH 40S ribosomal protein S6-1
0426-94-(6-16-06)_B01	3.00E-69	ALF4_ARATH Aberrant root formation protein 4
0545-94-(6-8-06)_E06	3.00E-69	COMT1_CATRO Caffeic acid 3-O-methyltransferase
0861-94-(6-5-06)_E08	8.00E-69	IN21_MAIZE IN2-1 protein
Contig\129	1.00E-68	ACLY_MOUSE ATP-citrate synthase
Contig\75	1.00E-68	SYEP_DROME Bifunctional aminoacyl-tRNA synthetase [Includes: Glutamyl-tRNA synthetase
0449-94-(6-27-06)_G06	2.00E-68	B2_DAUCA B2 protein
0814-94-(6-5-06)_F02	2.00E-68	KPYC_SOYBN Pyruvate kinase, cytosolic isozyme
Contig\152	2.00E-68	ATK4_ARATH Kinesin-4
0803-94-(6-5-06)_C01	3.00E-68	FBK69_ARATH F-box/Kelch-repeat protein At3g24760
Contig\201	3.00E-68	M2OM_NEUCR Putative mitochondrial 2-oxoglutarate/malate carrier protein
1308-94-(6-16-06)_B07	4.00E-68	ARP8_ARATH Actin-related protein 8

1123-94-(6-9-06)_G09	5.00E-68	DNPEP_BOVIN Aspartyl aminopeptidase
0430-94-(6-16-06)_F01	6.00E-68	MPU1_ARATH Mannose-P-dolichol utilization defect 1 protein homolog
0824-94-(6-5-06)_H03	2.00E-67	UBE2N_PONPY Ubiquitin-conjugating enzyme E2 N
0833-94-(6-5-06)_A05	3.00E-67	ACOX4_ARATH Acyl-coenzyme A oxidase 4, peroxisomal
0665-94-(6-6-06)_A09	4.00E-67	FUCO3_ARATH Alpha-L-fucosidase 3 precursor
0462-94-(6-16-06)_D05	1.00E-66	CAES_ARATH Probable carbohydrate esterase At4g34215
Contig\124	1.00E-66	NDUAC_ARATH Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12
0017-94_004(5-31-06)	2.00E-66	WRK17_ARATH Probable WRKY transcription factor 17
0835-94-(6-5-06)_C05	3.00E-66	EXOC5_ORYSJ Exocyst complex component 5
Contig\116	3.00E-66	PHB2_YEAST Prohibitin-2
Contig\185	3.00E-66	YAUB_SCHPO UPF0012 hydrolase C26A3.11
Contig\71	3.00E-66	PEX10_ARATH Peroxisome assembly protein 10
Contig\102	4.00E-66	Y1154_ARATH Putative serine/threonine-protein kinase At1g01540
1182-94-(6-15-06)_H06	1.00E-65	CRR12_ARATH Cysteine-rich repeat secretory protein 12 precursor
Contig\37	2.00E-65	ANGLT_ROSHC Anthocyanidin 5,3-O-glucosyltransferase
0032-93-A10(4-21-06)	3.00E-65	VA0D_ORYSJ Probable vacuolar ATP synthase subunit d
1030-94-(6-2-06)_E04	2.00E-64	ACSL5_RAT Long-chain-fatty-acid--CoA ligase 5
Contig\85	6.00E-64	ERLN1_MOUSE Erlin-1 precursor
Contig\131	4.00E-63	Y1689_ARATH Uncharacterized membrane protein At1g06890
0378-94-(6-12-06)_E09	5.00E-63	PCY1B_HUMAN Choline-phosphate cytidylyltransferase B
0736-94-(6-7-06)_D05	7.00E-63	NPL42_ARATH NPL4-like protein 2
0177-94-B04(5-10-06)	8.00E-63	SOC1_ARATH MADS-box protein SOC1
0305-94(5-31-06)_004	8.00E-63	CP19D_ARATH Peptidyl-prolyl cis-trans isomerase CYP19-4 precursor
0387-94-(6-12-06)_D10	1.00E-62	NOL5A_MOUSE Nucleolar protein 5A
0943-94-(6-16-06)_F12	2.00E-62	MPCP_BOVIN Phosphate carrier protein, mitochondrial precursor
0698-94-(6-12-06)_G12	3.00E-62	ACLY_MOUSE ATP-citrate synthase
Contig\132	4.00E-62	CNOT7_MOUSE CCR4-NOT transcription complex subunit 7
0548-94-(6-8-06)_H06	9.00E-62	E1311_ARATH Putative glucan endo-1,3-beta-glucosidase 11 precursor
0509-94-(6-	1.00E-61	ENO_DROME Enolase

8-06)_A02		
1086-94-(6-2-06)_D11	2.00E-61	CRY2_ARATH Cryptochrome-2
0118-94-E12(4-28-06)	4.00E-61	GL11_ARATH Germin-like protein subfamily 1 member 1 precursor
0625-94-(6-6-06)_A04	4.00E-61	Y3972_ARATH Uncharacterized protein At3g49720
Contig\188	4.00E-61	FBX13_ARATH F-box only protein 13
0121-94-H12(4-28-06)	7.00E-61	GAE4_ARATH UDP-glucuronate 4-epimerase 4
0217-94-(6-16-06)_B09	7.00E-61	MGAT1_RABIT Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase
0717-94-(6-7-06)_A03	1.00E-60	MSBP1_ARATH Membrane steroid-binding protein 1
Contig\34	1.00E-60	MAN7_ARATH Mannan endo-1,4-beta-mannosidase 7 precursor
0060-94-C05(4-28-06)	5.00E-60	PA2G4_MOUSE Proliferation-associated protein 2G4
0105-94-H10(4-28-06)	5.00E-60	PABP2_ARATH Polyadenylate-binding protein 2
0129-94-A03(5-9-06)	2.00E-59	P1_ARATH Probable NADP-dependent oxidoreductase P1
0813-94-(6-5-06)_E02	3.00E-59	CRK6_ARATH Cysteine-rich receptor-like protein kinase 6 precursor
1003-94-(6-2-06)_C01	3.00E-59	GL34_ARATH Germin-like protein subfamily 3 member 4 precursor
0743-94-(6-7-06)_C06	5.00E-59	PBS1_ARATH Serine/threonine-protein kinase PBS1
0400-94-(6-8-06)_H12	6.00E-59	BAK1_ARATH BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor
1028-94-(6-2-06)_C04	2.00E-58	LEU21_METMA 3-isopropylmalate dehydratase large subunit 1
1104-94-(6-9-06)_D07	5.00E-58	SPL1_ARATH Squamosa promoter-binding-like protein 1
0128-94(5-31-06)_009	6.00E-58	AOC4_ARATH Allene oxide cyclase 4, chloroplast precursor
0724-94-(6-7-06)_H03	6.00E-58	YEIN_ECOLI Uncharacterized protein yeiN
0917-94-(6-14-06)_D12	6.00E-58	BAK1_ARATH BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor
0587-94-(6-8-06)_B10	1.00E-57	UREG_PSEAE Urease accessory protein ureG
Contig\153	2.00E-57	SF3_HELAN Pollen-specific protein SF3
0636-94-(6-6-06)_D05	4.00E-57	AKR_ARATH Ankyrin repeat domain-containing protein, chloroplast precursor
Contig\29	8.00E-57	CARA_ANASP Carbamoyl-phosphate synthase small chain
0540-94-(6-8-06)_H05	1.00E-56	6DCS_SOYBN NAD(P)H-dependent 6'-deoxychalcone synthase
0385-94-(6-12-06)_B10	2.00E-56	U496D_ORYSI UPF0496 protein 4

0652-94-(6-6-06)_D07	3.00E-56	CLPP1_ANASP ATP-dependent Clp protease proteolytic subunit 1
0762-94-(6-7-06)_F08	3.00E-56	QOR_PSEAE Quinone oxidoreductase
0099-94-B10(4-28-06)	4.00E-56	GDIA_MOUSE Rab GDP dissociation inhibitor alpha
Contig\74	7.00E-56	CNOT7_MOUSE CCR4-NOT transcription complex subunit 7
Contig\160	1.00E-55	ERG19_MOUSE Diphosphomevalonate decarboxylase
0427-94-(6-16-06)_C01	2.00E-55	M3K2_ARATH Mitogen-activated protein kinase kinase kinase 2
0839-94-(6-14-06)_C06	3.00E-55	NB5R1_RAT NADH-cytochrome b5 reductase 1
1021-94-(6-2-06)_D03	8.00E-55	SAP8_ORYSJ Zinc finger A20 and AN1 domain-containing stress-associated protein 8
Contig\96	1.00E-54	TM9S1_MOUSE Transmembrane 9 superfamily protein member 1 precursor
Contig\199	2.00E-54	SVP_ARATH MADS-box protein SVP
0048-94-G03(4-28-06)	3.00E-54	Y1861_ARATH Uncharacterized mscS family protein At1g78610
0624-94-(6-6-06)_H03	4.00E-54	TM9S4_HUMAN Transmembrane 9 superfamily protein member 4
Contig\32	1.00E-53	ARD1B_MOUSE N-terminal acetyltransferase complex ARD1 subunit homolog B
Contig\79	1.00E-53	ODO2_RICFE Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex
1305-94-(6-16-06)_G06	4.00E-53	DRP2A_ARATH Dynamin-2A
0517-94-(6-8-06)_A03	8.00E-53	DRP3A_ARATH Dynamin-related protein 3A
1004-94(6-2-06Truncated)_D01	8.00E-53	DFRA_VITVI Dihydroflavonol-4-reductase
Contig\46	8.00E-53	ATB54_ARATH Homeobox-leucine zipper protein ATHB-54
0546-94-(6-8-06)_F06	4.00E-52	RPT2_ARATH Root phototropism protein 2
0581-94-(6-8-06)_E09	6.00E-52	E1312_ARATH Putative glucan endo-1,3-beta-glucosidase 12 precursor
0214-94(5-31-06)_010	9.00E-52	WOX4_ARATH WUSCHEL-related homeobox 4
0802-94-(6-5-06)_B01	1.00E-51	RBS_PINTH Ribulose bisphosphate carboxylase small chain, chloroplast precursor
Contig\1	1.00E-51	EF100_ARATH Ethylene-responsive transcription factor 1A
0778-94-(6-7-06)_C10	2.00E-51	F108C_DANRE Abhydrolase domain-containing protein FAM108C1
1015-94-(6-2-06)_F02	3.00E-51	UBE2C_BOVIN Ubiquitin-conjugating enzyme E2 C
0841-94-(6-5-06)_A06	5.00E-51	GSR2_ARATH Uncharacterized protein At2g40430
0831-94-(6-5-06)_G04	7.00E-51	PNAE_RAUSE Polyneuridine-aldehyde esterase precursor
0459-94-(6-	9.00E-51	AAMP_BOVIN Angio-associated migratory cell protein

16-06)_A05		
Contig\95	2.00E-50	NPC1_MOUSE Niemann-Pick C1 protein precursor
Contig\125	5.00E-50	HT1_ARATH Serine/threonine-protein kinase HT1
0163-94-C07(5-5-06)	1.00E-49	YKWC_BACSU Uncharacterized oxidoreductase ykwC
0626-94-(6-6-06)_B04	2.00E-49	KATAM_ARATH Xyloglucan galactosyltransferase KATAMARI1
Contig\148	4.00E-49	IAA16_ARATH Auxin-responsive protein IAA16
0748-94-(6-7-06)_H06	7.00E-49	RCH2_ARATH Receptor-like protein kinase 2 precursor
0242-94-C12(5-10-06)	1.00E-47	TM9S1_RAT Transmembrane 9 superfamily protein member 1 precursor
0807-94-(6-5-06)_G01	2.00E-47	MLO10_ARATH MLO-like protein 10
Contig\179	2.00E-47	LAML_ARATH Lamin-like protein precursor
0925-94-(6-16-06)_C11	5.00E-47	GOGA5_ARATH Golgin-84
0362-94-(6-12-06)_G07	6.00E-47	SYF1_EMENI Pre-mRNA-splicing factor syf1
Contig\172	3.00E-46	GDIA_RAT Rab GDP dissociation inhibitor alpha
0612-94-(6-6-06)_D02	4.00E-46	SRP68_CANFA Signal recognition particle 68 kDa protein
0372-94-(6-12-06)_H08	5.00E-46	YB95_ARATH Uncharacterized protein At2g39795, mitochondrial precursor
0185-94-B05(5-10-06)	7.00E-46	SMCA2_HUMAN Probable global transcription activator SNF2L2
0779-94-(6-7-06)_D10	7.00E-46	SELT_ARATH SelT-like protein precursor
Contig\9	9.00E-46	OAT_DROME Ornithine aminotransferase, mitochondrial precursor
0393-94-(6-8-06)_B12	1.00E-45	GCN1L_HUMAN GCN1-like protein 1
0863-94-(6-5-06)_G08	2.00E-45	ALFC3_ARATH Probable fructose-bisphosphate aldolase 3, chloroplast precursor
1081-94-(6-2-06)_G10	3.00E-45	HNRPQ_HUMAN Heterogeneous nuclear ribonucleoprotein Q
Contig\83	2.00E-44	BGLT_TRIRP Cyanogenic beta-glucosidase precursor
0021-94_012(5-31-06)	4.00E-44	TI10A_ARATH Protein TIFY 10A
0450-94-(6-16-06)_H03	4.00E-44	DHRS4_PIG Dehydrogenase/reductase SDR family member 4
0346-94-(6-9-06)_D04	9.00E-44	HEXA_DICDI Beta-hexosaminidase A precursor
0347-94-(6-12-06)_F06	3.00E-43	CSX1_SCHPO RNA-binding post-transcriptional regulator csx1
0719-94-(6-7-06)_C03	3.00E-43	ASPL1_ARATH Aspartic proteinase-like protein 1 precursor
1075-94-(6-2-06)_A10	5.00E-43	YZR3_ARATH RanBP2-type zinc finger protein At1g67325
0747-94-(6-	7.00E-43	COG6_HUMAN Conserved oligomeric Golgi complex component 6

7-06)_G06		
1034-94-(6-14-06)_F08	1.00E-42	PSA_MOUSE Puromycin-sensitive aminopeptidase
Contig\159	6.00E-42	NEP1_NEPGR Aspartic proteinase nepenthesin-1 precursor
Contig\169	7.00E-42	U49A7_ARATH UPF0497 membrane protein At5g40300
0666-94-(6-6-06)_B09	8.00E-42	Y283_BACHD Uncharacterized isomerase BH0283
0388-94-(6-12-06)_E10	1.00E-41	CAP10_ARATH Putative clathrin assembly protein At5g35200
1089-94-(6-2-06)_G11	2.00E-41	PSMD8_DICDI Probable 26S proteasome non-ATPase regulatory subunit 8
0227-94-D10(5-10-06)	3.00E-41	PCY2_BOVIN Ethanolamine-phosphate cytidylyltransferase
0667-94-(6-6-06)_C09	3.00E-41	SPL7_ARATH Squamosa promoter-binding-like protein 7
Contig\66	9.00E-41	AP1B1_RAT AP-1 complex subunit beta-1
1016-94-(6-2-06)_G02	1.00E-40	TIAR_MOUSE Nucleolysin TIAR
0598-94-(6-8-06)_E11	2.00E-40	FVT1_HUMAN 3-ketodihydrosphingosine reductase precursor
1194-94-(6-15-06)_F07	2.00E-40	RAP1_ARATH Transcription factor AtMYC2
0690-94-(6-6-06)_B12	3.00E-40	MYB23_ARATH Transcription factor MYB23
1187-94-(6-15-06)_B07	4.00E-40	DYRK4_MOUSE Dual specificity tyrosine-phosphorylation-regulated kinase 4
Contig\84	7.00E-40	IMA1_ARATH Importin subunit alpha-1
0851-94-(6-5-06)_C07	9.00E-40	ACT1_PEA Actin-1
Contig\176	5.00E-39	Y4844_ARATH Uncharacterized protein At4g28440
1085-94-(6-2-06)_C11	2.00E-38	PUB14_ARATH E3 ubiquitin-protein ligase PUB14
Contig\130	2.00E-38	DNJ20_ARATH Chaperone protein dnaJ 20, chloroplast precursor
0328-94-(6-9-06)_G02	4.00E-38	SPL18_ORYSJ Squamosa promoter-binding-like protein 18
0746-94-(6-7-06)_F06	2.00E-37	SIL10_ARATH E3 ubiquitin-protein ligase SINA-like 10
1128-94-(6-9-06Truncated)_D10	2.00E-37	DNJB1_HUMAN DnaJ homolog subfamily B member 1
Contig\65	2.00E-37	RCC2_MOUSE Protein RCC2
0750-94-(6-7-06)_B07	3.00E-37	HSF8_SOLPE Heat shock factor protein HSF8
Contig\197	3.00E-37	AMYB_ARATH Beta-amylase
1005-94-(6-2-06)_E01	8.00E-37	RDR1_SCHPO RNA-dependent RNA polymerase 1
0890-94-(6-14-06)_E07	7.00E-36	IAA11_ARATH Auxin-responsive protein IAA11
0681-94-(6-6-06)_A11	2.00E-35	GBF4_ARATH G-box-binding factor 4

0908-94-(6-14-06)_C11	2.00E-35	GUAA_HELHP Probable GMP synthase [glutamine-hydrolyzing]
1170-94-(6-15-06)_H05	2.00E-35	UBP5_ARATH Ubiquitin carboxyl-terminal hydrolase 5
0605-94-(6-6-06)_E01	4.00E-35	PPT1_CAEEL Palmitoyl-protein thioesterase 1 precursor
Contig\141	8.00E-35	MYBA_CHICK Myb-related protein A
0131-94-C03(5-9-06)	2.00E-34	DOF58_ARATH Dof zinc finger protein DOF5.8
0172-94-E03(5-10-06)	2.00E-34	GLGX_MYCTU Glycogen operon protein glgX homolog
0547-94-(6-8-06)_G06	2.00E-34	AAPC_CENCI Putative apospory-associated protein C
Contig\3	2.00E-34	POLC2_JUNOX Polcalcin Jun o 2
Contig\58	2.00E-34	XTH25_ARATH Probable xyloglucan endotransglucosylase/hydrolase protein 25 precursor
0759-94-(6-7-06)_C08	3.00E-34	MSRA_DROME Peptide methionine sulfoxide reductase
0522-94-(6-8-06)_F03	5.00E-34	CA160_HUMAN Uncharacterized protein C1orf160
0821-94-(6-5-06)_E03	1.00E-33	TMCO1_RAT Transmembrane and coiled-coil domains protein 1
0870-94-(6-5-06)_F09	1.00E-33	ARFB_ARATH Auxin response factor 2
Contig\174	2.00E-33	APHC_MOUSE Alkaline phytoceramidase
0199-94(5-31-06)_008	4.00E-33	FH20_ARATH Formin-like protein 20
0633-94-(6-6-06)_A05	4.00E-33	TIF9_ARATH Protein TIFY 9
0806-94-(6-5-06)_F01	8.00E-33	RRAGB_HUMAN Ras-related GTP-binding protein B
0843-94-(6-5-06)_C06	1.00E-32	RPAC1_BOVIN DNA-directed RNA polymerases I and III subunit RPAC1
0112-94-(6-12-06)_D04	2.00E-32	CHM2B_DANRE Charged multivesicular body protein 2b
Contig\99	2.00E-32	PRR6_MOUSE Proline-rich protein 6
Contig\120	3.00E-32	FBL4_ARATH Protein FBL4
0010-94_005(5-31-06)	5.00E-32	ARGJ_SYNEL Arginine biosynthesis bifunctional protein argJ [Includes: Glutamate N-acetyltransferase
0815-94-(6-14-06)_E05	5.00E-32	PLZ12_LUPPO Protein PPLZ12
0942-94-(6-15-06)_E03	9.00E-32	DNJB1_HUMAN DnaJ homolog subfamily B member 1
0613-94-(6-6-06)_E02	2.00E-31	ARNA_ERWCT Bifunctional polymyxin resistance protein arnA [Includes: UDP-4-amino-4-deoxy-L-arabinose formyltransferase
Contig\118	2.00E-31	AN13B_HUMAN Ankyrin repeat domain-containing protein 13B
0223-94-H09(5-10-06)	7.00E-31	ZN363_HUMAN RING finger and CHY zinc finger domain-containing protein 1
0847-94-(6-5-06)_G06	8.00E-31	PRPK_HUMAN TP53-regulating kinase

0377-94-(6-12-06)_D09	2.00E-30	PPM1G_BOVIN Protein phosphatase 1G
1083-94-(6-2-06)_A11	2.00E-30	ERF17_ARATH Ethylene-responsive transcription factor ERF017
0261-94(5-31-06)_016	3.00E-30	UBC11_ARATH Ubiquitin-conjugating enzyme E2-17 kDa 11
0464-94-(6-16-06)_F05	3.00E-30	SCYL2_MOUSE SCY1-like protein 2
0639-94-(6-6-06)_G05	3.00E-30	CRK41_ARATH Cysteine-rich receptor-like protein kinase 41 precursor
Contig\67	4.00E-30	RNF5_CAEEL RING finger protein 5
0785-94-(6-7-06)_B11	5.00E-30	GPT_HUMAN UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase
0115-94-B12(4-28-06)	6.00E-30	TSJT1_TOBAC Stem-specific protein TSJT1
0144-94(5-31-06)_015	7.00E-30	TFS2_SCHPO Transcription elongation factor S-II
0209-94-B08(5-10-06)	9.00E-30	IPO4_MOUSE Importin-4
0360-94-(6-12-06)_E07	1.00E-29	TRM10_SCHPO tRNA
0749-94-(6-7-06)_A07	2.00E-29	PDCL3_HUMAN Phosducin-like protein 3
0276-94(5-31-06)_014	8.00E-29	ZPR1_YEAST Zinc finger protein ZPR1
0297-94(5-31-06)_007	2.00E-28	YBA9_SCHPO Uncharacterized protein C119.09c
0902-94-(6-14-06)_E10	2.00E-28	IAA29_ARATH Auxin-responsive protein IAA29
0930-94-(6-16-06)_F11	2.00E-28	PATL4_ARATH Patellin-4
0269-94(5-31-06)_015	3.00E-28	HCBT1_DIACA Anthranilate N-benzoyltransferase protein 1
0257-94(5-31-06)_008	6.00E-28	DIC_HUMAN Mitochondrial dicarboxylate carrier
1101-94-(6-9-06)_A07	1.00E-27	HDA15_ARATH Histone deacetylase 15
0215-94(5-31-06)_012	2.00E-27	BGAL_SULSH Beta-galactosidase
0390-94-(6-8-06)_G11	2.00E-27	P4HA1_RAT Prolyl 4-hydroxylase subunit alpha-1 precursor
0774-94-(6-7-06)_H09	2.00E-27	HNRPF_MACFA Heterogeneous nuclear ribonucleoprotein F
Contig\88	2.00E-27	RFC5_SCHPO Replication factor C subunit 5
1107-94-(6-9-06)_G07	5.00E-27	MYB_MOUSE Myb proto-oncogene protein
0210-94-C08(5-10-06)	8.00E-27	TPPC1_MOUSE Trafficking protein particle complex subunit 1
1108-94-(6-9-06)_H07	2.00E-26	DENR_SCHPO Density-regulated protein homolog
1040-94-(6-	3.00E-26	NAK_ARATH Probable serine/threonine-protein kinase NAK

2-06)_G05		
0729-94-(6-7-06)_E04	4.00E-26	RBM38_HUMAN RNA-binding protein 38
Contig\63	4.00E-26	BCAS2_DANRE BCAS2 protein homolog
Contig\35	1.00E-25	BAK1_ARATH BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor
0141-94-E04(5-9-06)	2.00E-25	GIS2_YEAST Zinc finger protein GIS2
0800-94-(6-7-06)_G12	2.00E-25	NAC78_ARATH NAC domain-containing protein 78
0686-94-(6-6-06)_F11	3.00E-25	DBNBT_TAXCA 3'-N-debenzoyl-2'-deoxytaxol N-benzoyltransferase
1171-94-(6-15-06)_A06	3.00E-25	RFA1_XENLA Replication protein A 70 kDa DNA-binding subunit
0379-94-(6-12-06)_F09	5.00E-25	SSRA_ARATH Translocon-associated protein subunit alpha precursor
0295-94(5-31-06)_003	7.00E-25	SL11_ORYSJ Protein spotted leaf 11
0532-94-(6-8-06)_H04	7.00E-25	HIS1_CAMJR ATP phosphoribosyltransferase
Contig\52	7.00E-25	Y1491_ARATH DUF246 domain-containing protein At1g04910
0533-94-(6-8-06)_A05	1.00E-24	DNJ2_CAEEL DnaJ homolog dnj-2 precursor
Contig\69	3.00E-24	PPM1G_MOUSE Protein phosphatase 1G
1141-94-(6-9-06)_A12	4.00E-24	B3GT5_HUMAN Beta-1,3-galactosyltransferase 5
0936-94-(6-16-06)_D12	8.00E-24	APRR7_ARATH Two-component response regulator-like APRR7
1180-94-(6-15-06)_G06	8.00E-24	ERF4_TOBAC Ethylene-responsive transcription factor 4
Contig\113	9.00E-24	ERF3_TOBAC Ethylene-responsive transcription factor 3
0727-94-(6-7-06)_C04	2.00E-23	CC032_HUMAN Uncharacterized protein C3orf32
1090-94-(6-2-06)_H11	2.00E-23	IPO4_HUMAN Importin-4
Contig\38	2.00E-23	HT1_ARATH Serine/threonine-protein kinase HT1
Contig\28	6.00E-23	TOP2_PEA DNA topoisomerase 2
0884-94-(6-5-06)_D11	7.00E-23	MFSD5_PONPY Major facilitator superfamily domain-containing protein 5
0026-94-(6-12-06)_A01	1.00E-22	GID1_ORYSJ Gibberellin receptor GID1
0790-94-(6-7-06)_F11	1.00E-22	CSTF1_PONPY Cleavage stimulation factor 50 kDa subunit
0872-94-(6-5-06)_H09	1.00E-22	SAPKA_ORYSJ Serine/threonine-protein kinase SAPK10
0250-94(5-31-06)_009	3.00E-22	K0174_HUMAN Uncharacterized protein KIAA0174
0086-94-E08(4-28-06)	7.00E-22	NB5R4_MOUSE Cytochrome b5 reductase 4
0562-94-(6-8-06)_H07	1.00E-21	NEP1_NEPGR Aspartic proteinase nepenthesin-1 precursor

0838-94-(6-5-06)_F05	1.00E-21	FMO4_MOUSE Dimethylaniline monooxygenase [N-oxide-forming] 4
0539-94-(6-8-06)_G05	4.00E-21	S35E3_BOVIN Solute carrier family 35 member E3
1139-94-(6-9-06)_G11	5.00E-21	NUP3_PENSQ Nuclease PA3
0198-94-(6-16-06)_H08	6.00E-21	BLC_CITFR Outer membrane lipoprotein blc precursor
0369-94-(6-12-06)_F08	6.00E-21	FTSZ_ANASP Cell division protein ftsZ
Contig\121	6.00E-21	THOC4_MOUSE THO complex subunit 4
0887-94-(6-5-06)_G11	9.00E-21	LANC1_DANRE LanC-like protein 1
0904-94-(6-14-06)_G10	1.00E-20	NAC74_ORYSJ NAC domain-containing protein 74
Contig\111	3.00E-20	IAH1_YEAST Isoamyl acetate-hydrolyzing esterase
0856-94-(6-5-06)_H07	5.00E-20	Y381_RICFE Putative ankyrin repeat protein RF_0381
Contig\181	6.00E-20	PSMD9_RAT 26S proteasome non-ATPase regulatory subunit 9
0577-94-(6-8-06)_B09	7.00E-20	Y3377_ARATH Uncharacterized protein At3g03773
0162-94-B07(5-5-06)	8.00E-20	YGB0_YEAST Uncharacterized endoplasmic reticulum membrane protein YGL010W
0653-94-(6-6-06)_E07	1.00E-19	DHBB_BACSU Isochorismatase
1137-94-(6-9-06)_E11	1.00E-19	DUS1_HUMAN Dual specificity protein phosphatase 1
1147-94-(6-9-06Truncated)_G12	1.00E-19	ASHH1_ARATH Histone-lysine N-methyltransferase ASHH1
0572-94-(6-8-06)_G08	2.00E-19	SPO11_HUMAN Meiotic recombination protein SPO11
0907-94-(6-14-06)_B11	2.00E-19	PEF1_XENLA Peflin
Contig\183	3.00E-19	YS81_CAEEL Uncharacterized protein ZK945.1
0537-94-(6-8-06)_E05	4.00E-19	OTU6B_DANRE OTU domain-containing protein 6B
1110-94-(6-9-06)_B08	4.00E-19	FBK50_ARATH F-box/Kelch-repeat protein At3g06240
0901-94-(6-14-06)_D10	7.00E-19	GPMB_PHOLL Probable phosphoglycerate mutase gpmB
1116-94-(6-9-06)_H08	7.00E-19	BAK1_ARATH BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor
0714-94-(6-7-06)_F02	1.00E-18	GASA4_ARATH Gibberellin-regulated protein 4 precursor
0072-94-F01(5-9-06)	2.00E-18	PDCD4_MOUSE Programmed cell death protein 4
0232-94-A11(5-10-06)	2.00E-18	STIP_SOYBN Heat shock protein STI
0627-94-(6-6-06)_C04	2.00E-18	FDL41_ARATH Putative F-box/FBD/LRR-repeat protein At5g62970

0823-94-(6-5-06)_G03	4.00E-18	KPYK_ASPNG Pyruvate kinase
Contig\195	5.00E-18	FLS_MALDO Flavonol synthase/flavanone 3-hydroxylase
0617-94-(6-6-06)_A03	6.00E-18	FBK67_ARATH F-box/Kelch-repeat protein At3g23880
1047-94-(6-2-06)_F06	7.00E-18	THOC6_HUMAN THO complex subunit 6 homolog
0567-94-(6-8-06)_B08	8.00E-18	LEUD2_THEMA 3-isopropylmalate dehydratase small subunit 2
0398-94-(6-8-06)_F12	1.00E-17	SQV2_CAEEL Beta-1,3-galactosyltransferase sqv-2
0541-94-(6-8-06)_A06	1.00E-17	YHRE_SCHPO Uncharacterized protein C839.14c
0526-94-(6-8-06)_B04	3.00E-17	ZFP6_ARATH Zinc finger protein 6
0123-94-C02(5-9-06)	7.00E-17	TRPT1_MOUSE tRNA 2'-phosphotransferase 1
Contig\162	3.00E-16	U136_ARATH UPF0136 membrane protein At2g26240
0010-93-G12(4-21-06)	5.00E-16	ARGJ1_ANASP Arginine biosynthesis bifunctional protein argJ 1 [Includes: Glutamate N-acetyltransferase
0739-94-(6-7-06)_G05	5.00E-16	ZCH11_HUMAN Zinc finger CCHC domain-containing protein 11
0792-94-(6-7-06)_H11	5.00E-16	CD029_MOUSE Uncharacterized protein C4orf29 homolog precursor
0789-94-(6-7-06)_E11	8.00E-16	YY46_ANASP Uncharacterized WD repeat-containing protein alr3466
0507-94-(6-8-06)_G01	2.00E-15	MON2_XENLA Protein MON2 homolog
0239-94-H11(5-10-06)	3.00E-15	YBZ7_YEAST Uncharacterized membrane protein YBR147W
0588-94-(6-8-06)_C10	3.00E-15	5NG4_PINTA Auxin-induced protein 5NG4
1166-94-(6-15-06)_E05	3.00E-15	DRL21_ARATH Putative disease resistance protein At3g14460
1092-94-(6-2-06)_B12	4.00E-15	COI1_ARATH Coronatine-insensitive protein 1
Contig\119	4.00E-15	SCRL2_ORYSJ SCAR-like protein 2
Contig\72	5.00E-15	CFI_ALLCE Chalcone--flavonone isomerase
0029-94-D01(4-28-06)	7.00E-15	TG308_CAEEL Putative protein tag-308
0915-94-(6-14-06)_B12	7.00E-15	TG308_CAEEL Putative protein tag-308
0359-94-(6-12-06)_D07	2.00E-14	PHM8_YEAST Phosphate metabolism protein 8
0773-94-(6-7-06)_G09	3.00E-14	TXLNB_MOUSE Beta-taxilin
0656-94-(6-6-06)_H07	7.00E-14	AAKG2_MOUSE 5'-AMP-activated protein kinase subunit gamma-2
0895-94-(6-5-06)_G12	7.00E-14	CJ119_MOUSE Uncharacterized protein C10orf119 homolog

0373-94-(6-12-06)_A09	9.00E-14	CHM4B_DANRE Charged multivesicular body protein 4b
0221-94-F09(5-10-06)	2.00E-13	CNOT2_MOUSE CCR4-NOT transcription complex subunit 2
0315-94-(6-9-06)_D01	2.00E-13	SVOP_XENLA Synaptic vesicle 2-related protein
0438-94-(6-16-06)_F02	2.00E-13	RF1_ORYSI Protein Rf1, mitochondrial precursor
Contig\23	5.00E-13	HSPC2_RICFE Small heat shock protein C2
1087-94-(6-2-06)_E11	6.00E-13	TT1_ARATH Protein TRANSPARENT TESTA 1
Contig\76	6.00E-13	EIF3M_CHICK Eukaryotic translation initiation factor 3 subunit M
0120-94-A02(5-9-06)	7.00E-13	MA2B1_MOUSE Lysosomal alpha-mannosidase precursor
Contig\151	9.00E-13	GUN1_ACIC1 Endoglucanase E1 precursor
0710-94-(6-7-06)_B02	1.00E-12	STAR7_MOUSE StAR-related lipid transfer protein 7
0704-94-(6-7-06)_D01	3.00E-12	CLPC_CYACA ATP-dependent Clp protease ATP-binding subunit clpA homolog
Contig\22	3.00E-12	MU136_SCHPO Meiotically up-regulated gene 136 protein precursor
0219-94-D09(5-10-06)	4.00E-12	YCF19_GUITH Uncharacterized protein ycf19
Contig\123	4.00E-12	HLJ1_YEAST Protein HLJ1
0365-94-(6-12-06)_B08	5.00E-12	UBC7_ARATH Ubiquitin-conjugating enzyme E2 7
0599-94-(6-8-06)_F11	5.00E-12	FUK_HUMAN L-fucose kinase
0708-94-(6-7-06)_H01	1.00E-11	COG2_DROME Conserved oligomeric Golgi complex component 2
0140-94-D04(5-9-06)	2.00E-11	CPRF2_PETCR Light-inducible protein CPRF-2
0576-94-(6-12-06)_E11	2.00E-11	RPP25_HUMAN Ribonuclease P protein subunit p25
1115-94-(6-9-06)_G08	2.00E-11	H12_ARATH Histone H1.2
0918-94-(6-14-06)_E12	4.00E-11	TM1L2_MOUSE TOM1-like protein 2
0693-94-(6-6-06)_E12	6.00E-11	FOLC_HUMAN Folylpolyglutamate synthase, mitochondrial precursor
1002-94-(6-2-06)_B01	6.00E-11	GLYG_MOUSE Glycogenin-1
0583-94-(6-8-06)_F09	1.00E-10	NORK_PEA Nodulation receptor kinase precursor
0139-94-C04(5-9-06)	2.00E-10	FBK50_ARATH F-box/Kelch-repeat protein At3g06240
0286-94(5-31-06)_002	4.00E-10	RNHX1_ARATH Putative ribonuclease H protein At1g65750
0087-93-B03(4-21-06)	7.00E-10	SCC12_ARATH Sister chromatid cohesion 1 protein 2
0271-94(5-	8.00E-10	BCS1_SCHPO Probable mitochondrial chaperone BCS1

31-06)_004		
0363-94-(6-12-06)_H07	8.00E-10	EDC4_HUMAN Enhancer of mRNA-decapping protein 4
0012-94_009(5-31-06)	1.00E-09	Y1491_ARATH DUF246 domain-containing protein At1g04910
0635-94-(6-6-06)_C05	1.00E-09	TOPRS_MOUSE E3 ubiquitin-protein ligase Topors
0019-94_008(5-31-06)	2.00E-09	TMVRN_NICGU TMV resistance protein N
0309-94(5-31-06)_012	2.00E-09	PBS1_ARATH Serine/threonine-protein kinase PBS1
Contig\198	2.00E-09	U326_ARATH UPF0326 protein At4g17486
0716-94-(6-14-06)_H04	3.00E-09	BIG2_HUMAN Brefeldin A-inhibited guanine nucleotide-exchange protein 2
0453-94-(6-16-06)_C04	5.00E-09	EXT1_DROME Exostosin-1
0688-94-(6-6-06)_H11	6.00E-09	PUB14_ARATH E3 ubiquitin-protein ligase PUB14
1006-94-(6-2-06)_F01	9.00E-09	RBM28_HUMAN RNA-binding protein 28
0534-94-(6-8-06)_B05	1.00E-08	RHG01_HUMAN Rho GTPase-activating protein 1
1120-94-(6-9-06)_D09	1.00E-08	TERF1_HUMAN Telomeric repeat-binding factor 1
Contig\142	1.00E-08	ICE1_ARATH Transcription factor ICE1
0329-94-(6-27-06)_H03	2.00E-08	NEP1_NEPGR Aspartic proteinase nepenthesin-1 precursor
0630-94-(6-6-06)_F04	2.00E-08	SFRS2_RAT Splicing factor, arginine/serine-rich 2
0296-94(5-31-06)_005	5.00E-08	MYH9_HUMAN Myosin-9
0920-94-(6-14-06)_G12	6.00E-08	ECHH_RHOCA Probable enoyl-CoA hydratase
0106-94-A11(4-28-06)	9.00E-08	TMM32_DANRE Transmembrane protein 32 precursor
0737-94-(6-7-06)_E05	2.00E-07	5NG4_PINTA Auxin-induced protein 5NG4
0897-94-(6-14-06)_G07	2.00E-07	TOA1_YEAST Transcription initiation factor IIA large subunit
1026-94-(6-2-06)_A04	2.00E-07	NU211_SCHPO Nucleoporin nup211
1301-94-(6-16-06)_C06	2.00E-07	RBPS2_HUMAN RNA-binding protein with multiple splicing 2
0591-94-(6-8-06)_F10	3.00E-07	CL005_HUMAN Uncharacterized protein C12orf5
0592-94-(6-8-06)_G10	3.00E-07	RPB1_CAEBR DNA-directed RNA polymerase II subunit RPB1
0643-94-(6-6-06)_C06	3.00E-07	PUB14_ARATH E3 ubiquitin-protein ligase PUB14
1073-94-(6-2-06)_G09	3.00E-07	MUC2_HUMAN Mucin-2 precursor

Contig\163	3.00E-07	ST_SV40 Small t antigen
Contig\4	4.00E-07	FB109_ARATH F-box protein At2g17030
0245-94-F12(5-10-06)	5.00E-07	COMA_METTH Phosphosulfolactate synthase
Contig\186	5.00E-07	SSRB_CANFA Translocon-associated protein subunit beta precursor
Contig\30	9.00E-07	RM21_ARATH 50S ribosomal protein L21, mitochondrial precursor
0571-94-(6-8-06)_F08	1.00E-06	NPS13_ARATH Novel plant SNARE 13
0658-94-(6-6-06)_B08	1.00E-06	YLH47_YEAST Protein YLH47, mitochondrial precursor
Contig\177	1.00E-06	E6_GOSHI Protein E6
Contig\59	1.00E-06	USPAL_ARATH Universal stress protein A-like protein
0124-94-D02(5-9-06)	2.00E-06	CK077_HUMAN Uncharacterized protein C11orf77
0696-94-(6-6-06)_H12	2.00E-06	DNJC2_MACFA DnaJ homolog subfamily C member 2
1193-94-(6-15-06)_E07	2.00E-06	MRS2L_MOUSE Magnesium transporter MRS2L, mitochondrial precursor
Contig\86	2.00E-06	SMC4_MOUSE Structural maintenance of chromosomes protein 4
0095-93-B02(4-21-06)	4.00E-06	USO1_HUMAN General vesicular transport factor p115
0225-94-B10(5-10-06)	e-100	VA722_ARATH Vesicle-associated membrane protein 722
0394-94-(6-8-06)_C12	e-100	ARF2_ORYSJ ADP-ribosylation factor 2
0519-94-(6-8-06)_C03	e-100	FBL3_ARATH F-box/LRR-repeat protein 3
0733-94-(6-7-06)_A05	e-100	MAN6_ARATH Mannan endo-1,4-beta-mannosidase 6 precursor
1042-94-(6-15-06)_E12	e-100	CSN1_ARATH COP9 signalosome complex subunit 1
1135-94-(6-9-06)_C11	e-100	PSB2A_ARATH Proteasome subunit beta type-2-A
Contig\16	e-100	ARF2_ORYSJ ADP-ribosylation factor 2
Contig\55	e-100	UMP8_ARATH Uncharacterized mitochondrial protein At3g48680
0137-94-A04(5-9-06)	e-101	LPAT4_ARATH Probable 1-acyl-sn-glycerol-3-phosphate acyltransferase 4
0465-94-(6-16-06)_G05	e-101	NDUS8_ARATH NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial precursor
1152-94-(6-15-06)_D04	e-101	CAPP1_SOYBN Phosphoenolpyruvate carboxylase, housekeeping isozyme
0192-94-A06(5-10-06)	e-102	PSBO_SOLTU Oxygen-evolving enhancer protein 1, chloroplast precursor
0463-94-(6-16-06)_E05	e-102	MLO1_ARATH MLO-like protein 1
0919-94-(6-14-06)_F12	e-102	FATA_CORSA Oleoyl-acyl carrier protein thioesterase, chloroplast precursor
Contig\60	e-102	ABAH1_ARATH Abscisic acid 8'-hydroxylase 1

0523-94-(6-8-06)_G03	e-103	PER64_ARATH Peroxidase 64 precursor
0911-94-(6-14-06)_F11	e-103	ARA5_ARATH Ras-related protein ARA-5
Contig\51	e-103	SYDC_RAT Aspartyl-tRNA synthetase, cytoplasmic
006-94-E05(4-28-06)	e-104	GLYM_SOLTU Serine hydroxymethyltransferase, mitochondrial precursor
Contig\149	e-104	BAS1B_ARATH 2-Cys peroxiredoxin BAS1-like, chloroplast precursor
Contig\41	e-104	TLPH_ARATH Thaumatin-like protein precursor
0249-94(5-31-06)_007	e-105	UBA3_ARATH NEDD8-activating enzyme E1 catalytic subunit
0871-94-(6-14-06)_G06	e-105	EXPA1_ARATH Expansin-A1 precursor
Contig\133	e-105	G6PI_ANASP Glucose-6-phosphate isomerase
1032-94-(6-16-06)_D06	e-106	PSA1A_ARATH Proteasome subunit alpha type-1-A
1039-94-(6-2-06)_F05	e-106	APX3_ARATH L-ascorbate peroxidase 3, peroxisomal precursor
Contig\8	e-106	CAHC_TOBAC Carbonic anhydrase, chloroplast precursor
Contig\7	e-107	IF2B_MALDO Eukaryotic translation initiation factor 2 subunit beta
0350-94-(6-9-06)_G04	e-108	RD19A_ARATH Cysteine proteinase RD19a precursor
0940-94-(6-15-06)_C03	e-108	AGAL_COFAR Alpha-galactosidase precursor
Contig\138	e-108	TIP21_ARATH Aquaporin TIP2-1
0133-94-E03(5-9-06)	e-109	AVP2_ARATH Pyrophosphate-energized membrane proton pump 2
0844-94-(6-5-06)_D06	e-109	DAPB1_ARATH Dihydrodipicolinate reductase 1, chloroplast precursor
Contig\106	e-109	ACOX4_ARATH Acyl-coenzyme A oxidase 4, peroxisomal
Contig\78	e-109	TPIS_COPJA Triosephosphate isomerase, cytosolic
0238-94-G11(5-10-06)	e-110	ARGD_ALNGL Acetylornithine aminotransferase, mitochondrial precursor
0671-94-(6-6-06)_G09	e-110	RS24_ARATH 40S ribosomal protein S2-4
1031-94-(6-2-06)_F04	e-110	P2_ARATH Probable NADP-dependent oxidoreductase P2
0323-94-(6-9-06)_C02	e-111	GPT2_ARATH Glucose-6-phosphate/phosphate translocator 2, chloroplast precursor
0672-94-(6-6-06)_H09	e-111	IMP3_SOLLC Inositol monophosphatase 3
1151-94-(6-15-06)_C04	e-111	CAPZB_ARATH Probable F-actin-capping protein subunit beta
0332-94-(6-9-06)_A03	e-112	ANXD1_ARATH Annexin D1
0538-94-(6-8-06)_F05	e-112	ETOL1_ARATH ETO1-like protein 1
0793-94-(6-14-06)_C05	e-112	PER72_ARATH Peroxidase 72 precursor
Contig\135	e-112	MDHC_MEDSA Malate dehydrogenase, cytoplasmic

Contig\167	e-112	CB26_PETSP Chlorophyll a-b binding protein 37, chloroplast precursor
0678-94-(6-6-06)_F10	e-113	FLA10_ARATH Fasciclin-like arabinogalactan protein 10 precursor
1138-94-(6-9-06)_F11	e-113	FH1_ARATH Formin-like protein 1 precursor
Contig\139	e-113	LGUL_BRAOG Putative lactoylglutathione lyase
Contig\39	e-113	FH13_ARATH Formin-like protein 13
0745-94-(6-7-06)_E06	e-114	KINB2_ARATH SNF1-related protein kinase regulatory subunit beta-2
0611-94-(6-6-06)_C02	e-115	CYSK_CITLA Cysteine synthase
1052-94-(6-2-06)_C07	e-115	SYH_ORYSJ Histidyl-tRNA synthetase
0701-94-(6-7-06)_A01	e-116	HTH_ARATH Protein HOTHEAD precursor
0763-94-(6-7-06)_G08	e-116	K125_TOBAC 125 kDa kinesin-related protein
0766-94-(6-7-06)_A09	e-116	1433D_SOYBN 14-3-3-like protein D
Contig\97	e-116	RS3A_CATRO 40S ribosomal protein S3a
0556-94-(6-12-06)_H10	e-117	PSA3_SPIOL Proteasome subunit alpha type-3
0732-94-(6-14-06)_A05	e-117	HELC1_HUMAN Activating signal cointegrator 1 complex subunit 3
Contig\112	e-118	TIP13_ARATH Aquaporin TIP1-3
Contig\127	e-118	RAN3_ARATH GTP-binding nuclear protein Ran-3
Contig\18	e-118	PER16_ARATH Peroxidase 16 precursor
Contig\90	e-118	XTH23_ARATH Probable xyloglucan endotransglucosylase/hydrolase protein 23 precursor
0148-94-D05(5-9-06)	e-119	MFPA_BRANA Glyoxysomal fatty acid beta-oxidation multifunctional protein MFP-a [Includes: Enoyl-CoA hydratase/3-2-trans-enoyl-CoA isomerase/3-hydroxybutyryl-CoA epimerase
0298-94(5-31-06)_009	e-119	XCP1_ARATH Xylem cysteine proteinase 1 precursor
1142-94-(6-9-06)_B12	e-119	ARGI1_ARATH Arginase
0311-94(5-31-06)_016	e-120	ATG3_ARATH Autophagy-related protein 3
Contig\128	e-120	GLO2N_ARATH Putative hydroxyacylglutathione hydrolase 2, mitochondrial precursor
0074-94-A07(4-28-06)	e-121	PLDA1_VIGUN Phospholipase D alpha 1
Contig\206	e-121	EXP13_ARATH Expansin-A13 precursor
0648-94(6-6-06)_H06	e-122	PDX1_HEVBR Probable pyridoxal biosynthesis protein PDX1
Contig\103	e-122	CIGR2_ORYSJ Chitin-inducible gibberellin-responsive protein 2
Contig\154	e-122	HPSE1_ARATH Heparanase-like protein 1 precursor
0247-94(5-31-06)_003	e-123	CUL1_ARATH Cullin-1
0283-94(5-31-06)_011	e-123	VDAC2_SOLTU 36 kDa outer mitochondrial membrane protein porin

0032-94-G01(4-28-06)	e-124	VA0D1_ARATH Probable vacuolar ATP synthase subunit d 1
0259-94(5-31-06)_012	e-124	Y1686_ARATH Uncharacterized membrane protein At1g16860
1046-94-(6-2-06)_E06	e-125	DNJH2_ALLPO DnaJ protein homolog 2
Contig\193	e-125	HSBH1_SOYBN Homeobox protein SBH1
0709-94-(6-7-06)_A02	e-126	BIP_SOLLC Luminal-binding protein precursor
Contig\192	e-126	EXPA6_ARATH Expansin-A6 precursor
Contig\136	e-127	TOC34_PEA Translocase of chloroplast 34
Contig\36	e-127	SYK_ARATH Lysyl-tRNA synthetase
0805-94-(6-5-06)_E01	e-128	AFC1_ARATH Serine/threonine-protein kinase AFC1
1163-94-(6-15-06)_C05	e-128	UGDH_SOYBN UDP-glucose 6-dehydrogenase
0860-94-(6-5-06)_D08	e-129	NPP_HORVU Nucleotide pyrophosphatase/phosphodiesterase
0020-94_010(5-31-06)	e-130	ASPR_CUCPE Aspartic proteinase precursor
Contig\109	e-130	BSL1_ARATH Serine/threonine-protein phosphatase BSL1
Contig\145	e-130	RS43_ARATH 40S ribosomal protein S4-3
0797-94-(6-7-06)_E12	e-131	CSN5A_ARATH COP9 signalosome complex subunit 5a
Contig\12	e-131	CAMT_POPTM Caffeoyl-CoA O-methyltransferase
0641-94-(6-6-06)_A06	e-132	ERG1_PANGI Squalene monooxygenase
0858-94-(6-5-06)_B08	e-132	OPR3_SOLLC 12-oxophytodienoate reductase 3
Contig\143	e-132	BRU1_SOYBN Brassinosteroid-regulated protein BRU1 precursor
Contig\92	e-132	RH56_ARATH DEAD-box ATP-dependent RNA helicase 56
0361-94-(6-12-06)_F07	e-133	UREA_CANEN Urease
0898-94-(6-14-06)_H07	e-133	COBRA_ARATH Protein COBRA precursor
0455-94-(6-16-06)_E04	e-135	NCASE_ARATH Neutral ceramidase precursor
Contig\42	e-135	SFGH_ARATH S-formylglutathione hydrolase
0234-94-C11(5-10-06)	e-136	AUX1_ARATH Auxin transporter protein 1
1133-94-(6-9-06)_A11	e-136	BOR1_ARATH Boron transporter 1
0282-94(5-31-06)_009	e-137	PEL12_ARATH Probable pectate lyase 12 precursor
0568-94-(6-8-06)_C08	e-137	STC_RICCO Sugar carrier protein C
0888-94-(6-5-06)_H11	e-139	PYRD_ARATH Dihydroorotate dehydrogenase, mitochondrial precursor

0272-94(5-31-06)_006	e-140	PIP_ARATH Proline iminopeptidase
0544-94-(6-8-06)_D06	e-142	RIR2_TOBAC Ribonucleoside-diphosphate reductase small chain
0143-94(5-31-06)_013	e-145	XTH_SOYBN Probable xyloglucan endotransglucosylase/hydrolase precursor
1113-94-(6-9-06)_E08	e-145	GCSP_PEA Glycine dehydrogenase [decarboxylating], mitochondrial precursor
1310-94-(6-16-06)_D07	e-146	MAOX_VITVI NADP-dependent malic enzyme
Contig\49	e-146	SUOX_ARATH Sulfite oxidase
1097-94-(6-2-06)_G12	e-147	ISW2_ARATH Putative chromatin-remodeling complex ATPase chain
Contig\202	e-148	P2_ARATH Probable NADP-dependent oxidoreductase P2
0699-94-(6-12-06)_H12	e-151	CNGC1_ARATH Cyclic nucleotide-gated ion channel 1
0437-94-(6-16-06)_E02	e-152	SR542_SOLLC Signal recognition particle 54 kDa protein 2
0336-94-(6-9-06)_D03	e-154	ARAE1_ARATH UDP-arabinose 4-epimerase 1
Contig\94	e-154	SYFA_ARATH Probable phenylalanyl-tRNA synthetase alpha chain
0842-94-(6-5-06)_B06	e-155	METB_ARATH Cystathionine gamma-synthase, chloroplast precursor
0855-94-(6-5-06)_G07	e-156	SUS2_PEA Sucrose synthase 2
0294-94(5-31-06)_001	e-157	G6PI1_CLAWI Glucose-6-phosphate isomerase, cytosolic 1
Contig\150	e-160	MDHC_MEDSA Malate dehydrogenase, cytoplasmic
Contig\81	e-169	CALX_SOYBN Calnexin homolog precursor
Contig\166	e-170	EF1G_PRUAV Elongation factor 1-gamma
Contig\105	e-175	DIM_PEA Cell elongation protein diminuto
0006-93-B05(4-20-06)	No Hit	
0006-94-C05(4-20-06)	No Hit	
0007for_D05'	No Hit	
0013-94_011(5-31-06)	No Hit	
0016-93-A12(4-21-06)	No Hit	
0016-94_002(5-31-06)	No Hit	
0023-94_016(5-31-06)	No Hit	

0024-94(5-31-06)_001	No Hit	
0037-94-D02(4-28-06)	No Hit	
0042-93-G08(4-21-06)	No Hit	
0045-94-D03(4-28-06)	No Hit	
0046-94-E03(4-28-06)	No Hit	
0047-93-B08(4-21-06)	No Hit	
0047-94-F03(4-28-06)	No Hit	
0052-94-C04(4-28-06)	No Hit	
0054-94-E04(4-28-06)	No Hit	
0063-94-F05(4-28-06)	No Hit	
0071_B05(Rev4-21-06)	No Hit	
0071_F06(For4-28-06)	No Hit	
0075-94-B07(4-28-06)	No Hit	
0085-94-D08(4-28-06)	No Hit	
0087-94-F08(4-28-06)	No Hit	
0111-94-F11(4-28-06)	No Hit	
0117-94-D12(4-28-06)	No Hit	
0127-94(5-31-06)_007	No Hit	
0134-94-F03(5-9-06)	No Hit	
0136-94(5-	No Hit	

31-06)_011		
0147-94-C05(5-9-06)	No Hit	
0149-94-E05(5-9-06)	No Hit	
0161-94-A07(5-5-06)	No Hit	
0164-94-D07(5-5-06)	No Hit	
0175-94-H03(5-10-06)	No Hit	
0179-94-D04(5-10-06)	No Hit	
0180-94-E04(5-10-06)	No Hit	
0195-94-D06(5-10-06)	No Hit	
0200-94-A07(5-10-06)	No Hit	
0208-94-A08(5-10-06)	No Hit	
0211-94-D08(5-10-06)	No Hit	
0220-94E09(5-10-06)	No Hit	
0226-94-C10(5-10-06)	No Hit	
0228-94-E10(5-10-06)	No Hit	
0229-94-F10(5-10-06)	No Hit	
0230-94(5-31-06)_014	No Hit	
0235-94-D11(5-10-06)	No Hit	
0237-94-F11(5-10-06)	No Hit	
0241-94-B12(5-10-06)	No Hit	
0244-94-E12(5-10-	No Hit	

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0252-94(5-31-06)_013	No Hit	
0254-94-(6-16-06)_B10	No Hit	
0255-94(5-31-06)_004	No Hit	
0260-94(5-31-06)_014	No Hit	
0262-94(5-31-06)_001	No Hit	
0263-94(5-31-06)_003	No Hit	
0265-94(5-31-06)_007	No Hit	
0270-94(5-31-06)_002	No Hit	
0275-94(5-31-06)_012	No Hit	
0280-94(5-31-06)_005	No Hit	
0285-94(5-31-06)_015	No Hit	
0292-94(5-31-06)_014	No Hit	
0300-94(5-31-06)_013	No Hit	
0303-94(5-31-06)_002	No Hit	
0306-94(5-31-06)_006	No Hit	
0316-94-(6-9-06)_E01	No Hit	
0319-94-(6-9-06)_G01	No Hit	
0349-94-(6-9-06)_F04	No Hit	
0352-94-(6-27-06)_H04	No Hit	
0356-94-(6-12-06)_A07	No Hit	
0358-94-(6-12-06)_C07	No Hit	
0367-94-(6-12-06)_D08	No Hit	
0380-94-(6-12-06)_G09	No Hit	
0381-94-(6-12-06)_H09	No Hit	
0382-94-(6-12-06)_A10	No Hit	
0433-94-(6-27-06)_D06	No Hit	
0436-94-(6-	No Hit	

16-06)_D02		
0439-94-(6-16-06)_G02	No Hit	
0440-94-(6-16-06)_H02	No Hit	
0444-94-(6-16-06)_C03	No Hit	
0445-94-(6-16-06)_D03	No Hit	
0451-94-(6-16-06)_A04	No Hit	
0452-94-(6-16-06)_B04	No Hit	
0454-94-(6-16-06)_D04	No Hit	
0503-94-(6-8-06)_C01	No Hit	
0506-94-(6-8-06)_F01	No Hit	
0511-94-(6-8-06)_C02	No Hit	
0514-94-(6-8-06)_F02	No Hit	
0518-94-(6-8-06)_B03	No Hit	
0521-94-(6-8-06)_E03	No Hit	
0527-94-(6-8-06)_C04	No Hit	
0528-94-(6-8-06)_D04	No Hit	
0531-94-(6-8-06)_G04	No Hit	
0535-94-(6-8-06)_C05	No Hit	
0543-94-(6-8-06)_C06	No Hit	
0549-94-(6-12-06)_F10	No Hit	
0566-94-(6-8-06)_A08	No Hit	
0578-94-(6-8-06)_C09	No Hit	
0580-94-(6-8-06)_D09	No Hit	
0584-94-(6-8-06)_G09	No Hit	
0594-94-(6-8-06)_A11	No Hit	
0595-94-(6-8-06)_B11	No Hit	
0604-94-(6-6-06)_D01	No Hit	
0616-94-(6-	No Hit	

6-06)_H02		
0619-94-(6-6-06)_C03	No Hit	
0628-94-(6-6-06)_D04	No Hit	
0634-94-(6-6-06)_B05	No Hit	
0638-94-(6-6-06)_F05	No Hit	
0640-94-(6-6-06)_H05	No Hit	
0644-94-(6-6-06)_D06	No Hit	
0645-94-(6-6-06)_E06	No Hit	
0647-94-(6-6-06)_G06	No Hit	
0649-94-(6-6-06)_A07	No Hit	
0655-94-(6-6-06)_G07	No Hit	
0659-94-(6-6-06)_C08	No Hit	
0661-94-(6-6-06)_E08	No Hit	
0663-94-(6-6-06)_G08	No Hit	
0664-94-(6-6-06)_H08	No Hit	
0668-94-(6-6-06)_D09	No Hit	
0676-94-(6-6-06)_D10	No Hit	
0683-94-(6-6-06)_C11	No Hit	
0687-94-(6-6-06)_G11	No Hit	
0691-94-(6-6-06)_C12	No Hit	
0694-94-(6-6-06)_F12	No Hit	
0695-94-(6-6-06)_G12	No Hit	
0702-94-(6-7-06)_B01	No Hit	
0707-94-(6-7-06)_G01	No Hit	
0713-94-(6-7-06)_E02	No Hit	
0718-94-(6-7-06)_B03	No Hit	
0720-94-(6-7-06)_D03	No Hit	
0721-94-(6-	No Hit	

7-06)_E03		
0725-94-(6-7-06)_A04	No Hit	
0728-94-(6-7-06)_D04	No Hit	
0730-94-(6-7-06)_F04	No Hit	
0735-94-(6-7-06)_C05	No Hit	
0738-94-(6-7-06)_F05	No Hit	
0753-94-(6-7-06)_E07	No Hit	
0756-94-(6-7-06)_H07	No Hit	
0760-94-(6-7-06)_D08	No Hit	
0768-94-(6-7-06)_C09	No Hit	
0770-94-(6-14-06)_B05'	No Hit	
0776-94-(6-7-06)_A10	No Hit	
0777-94-(6-7-06)_B10	No Hit	
0791-94-(6-7-06)_G11	No Hit	
0795-94-(6-7-06)_C12	No Hit	
0796-94-(6-7-06)_D12	No Hit	
0801-94-(6-5-06)_A01	No Hit	
0804-94-(6-5-06)_D01	No Hit	
0810-94-(6-5-06)_B02	No Hit	
0818-94-(6-5-06)_B03	No Hit	
0822-94-(6-5-06)_F03	No Hit	
0826-94-(6-5-06)_B04	No Hit	
0829-94-(6-5-06)_E04	No Hit	
0830-94-(6-5-06)_F04	No Hit	
0834-94-(6-15-06bad)_H10	No Hit	
0836-94-(6-5-06)_D05	No Hit	
0846-94-(6-5-06)_F06	No Hit	

0849-94-(6-5-06)_A07	No Hit	
0854-94-(6-5-06)_F07	No Hit	
0857-94-(6-5-06)_A08	No Hit	
0859-94-(6-5-06)_C08	No Hit	
0881-94-(6-5-06)_A11	No Hit	
0883-94-(6-5-06)_C11	No Hit	
0885-94-(6-5-06)_E11	No Hit	
0889-94-(6-5-06)_A12	No Hit	
0891-94-(6-5-06)_C12	No Hit	
0892-94-(6-5-06)_D12	No Hit	
0894-94-(6-5-06)_F12	No Hit	
0910-94-(6-14-06)_E11	No Hit	
0914-94-(6-14-06)_A12	No Hit	
0916-94-(6-14-06)_C12	No Hit	
0921-94-(6-14-06)_H12	No Hit	
0922-94-(6-15-06)_A01	No Hit	
0927-94-(6-15-06)_F01	No Hit	
0929-94-(6-15-06)_H01	No Hit	
0931-94-(6-16-06)_G11	No Hit	
0938-94-(6-15-06)_A03	No Hit	
0944-94-(6-15-06)_G03	No Hit	
0945-94-(6-15-06)_H03	No Hit	
1009-94-(6-2-06)_A02	No Hit	
1010-94-(6-2-06)_B02	No Hit	
1014-94-(6-2-06)_E02	No Hit	
1017-94-(6-2-06)_H02	No Hit	
1018-94-(6-2-06)_A03	No Hit	

1027-94-(6-2-06)_B04	No Hit	
1029-94-(6-2-06)_D04	No Hit	
1032-94-(6-2-06)_G04	No Hit	
1035-94-(6-14-06)_G08	No Hit	
1041-94-(6-2-06)_H05	No Hit	
1058-94-(6-2-06)_H07	No Hit	
1060-94-(6-2-06)_B08	No Hit	
1063-94-(6-2-06)_E08	No Hit	
1067-94-(6-2-06)_A09	No Hit	
1069-94-(6-2-06)_C09	No Hit	
1071-94-(6-2-06)_E09	No Hit	
1072-94-(6-2-06)_F09	No Hit	
1076-94-(6-2-06)_B10	No Hit	
1077-94-(6-2-06)_C10	No Hit	
1079-94-(6-2-06)_E10	No Hit	
1080-94-(6-2-06)_F10	No Hit	
1084-94-(6-2-06)_B11	No Hit	
1094-94-(6-2-06)_D12	No Hit	
1096-94-(6-2-06)_F12	No Hit	
1102-94-(6-9-06)_B07	No Hit	
1111-94-(6-9-06)_C08	No Hit	
1118-94-(6-9-06)_B09	No Hit	
1124-94-(6-9-06)_H09	No Hit	
1127-94-(6-9-06Truncated)_C10	No Hit	
1134-94-(6-9-06)_B11	No Hit	
1143-94-(6-9-06)_C12	No Hit	

1145-94-(6-9-06Truncated)_E12	No Hit	
1146-94-(6-9-06)_F12	No Hit	
1148-94-(6-9-06)_H12	No Hit	
1160-94-(6-15-06)_B05	No Hit	
1167-94-(6-15-06)_F05	No Hit	
1172-94-(6-15-06)_B06	No Hit	
1192-94-(6-15-06)_D07	No Hit	
1307-94-(6-16-06)_A07	No Hit	
Contig\10	No Hit	
Contig\101	No Hit	
Contig\104	No Hit	
Contig\107	No Hit	
Contig\11	No Hit	
Contig\110	No Hit	
Contig\117	No Hit	
Contig\134	No Hit	
Contig\14	No Hit	
Contig\144	No Hit	
Contig\15	No Hit	
Contig\155	No Hit	
Contig\156	No Hit	
Contig\164	No Hit	
Contig\168	No Hit	
Contig\17	No Hit	
Contig\175	No Hit	
Contig\178	No Hit	
Contig\180	No Hit	
Contig\184	No Hit	
Contig\187	No Hit	
Contig\189	No Hit	
Contig\191	No Hit	
Contig\194	No Hit	
Contig\2	No Hit	
Contig\20	No Hit	
Contig\203	No Hit	
Contig\204	No Hit	

Contig\21	No Hit	
Contig\24	No Hit	
Contig\26	No Hit	
Contig\33	No Hit	
Contig\43	No Hit	
Contig\45	No Hit	
Contig\47	No Hit	
Contig\50	No Hit	
Contig\53	No Hit	
Contig\56	No Hit	
Contig\57	No Hit	
Contig\64	No Hit	
Contig\68	No Hit	
Contig\77	No Hit	
Contig\80	No Hit	
Contig\82	No Hit	
Contig\87	No Hit	
Contig\89	No Hit	
Contig\98	No Hit	

APPENDIX K: Putative Xylogenesis Genes

ID	E-value	TAIR Locus	Descriptions
Contig_81	e-166	AT5G61790.1	calnexin 1 (CNX1)
Contig_21	e-155	AT5G06050.1	dehydration-responsive protein-related
Contig_102	e-150	AT2G35620.1	leucine-rich repeat transmembrane protein kinase, putative
0143-94(5-31-06)_013	e-142	AT5G13870.1	EXGT-A4 (ENDOXYLOGLUCAN TRANSFERASE A4); hydrolase, acting on glycosyl bonds
0940-94-(6-15-06)_C03	e-142	AT3G56310.1	alpha-galactosidase, putative / melibiase, putative / alpha-D-galactoside galactohydrolase, putative
Contig_115	e-141	AT4G27680.1	MSP1 protein, putative / intramitochondrial sorting protein, putative
0825-94-(6-5-06)_A04	e-140	AT2G36570.1	leucine-rich repeat transmembrane protein kinase, putative
0860-94-(6-5-06)_D08	e-137	AT5G50400.1	ATPAP27/PAP27 (purple acid phosphatase 27); acid phosphatase/ protein serine/threonine phosphatase
0898-94-(6-14-06)_H07	e-133	AT5G60920.1	COB (COBRA)
Contig_92	e-133	AT5G11170.1	DEAD/DEAH box helicase, putative (RH15)
0839-94-(6-14-06)_C06	e-129	AT5G17770.1	ATCBR (NADH:CYTOCHROME B5 REDUCTASE 1)
Contig_12	e-129	AT4G34050.1	caffeoyl-CoA 3-O-methyltransferase, putative
0665-94-(6-6-06)_A09	e-121	AT1G54790.1	GDSL-motif lipase/hydrolase family protein
0303-94(5-31-06)_002	e-121	AT5G25460.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G11420.1);
Contig_140	e-119	AT5G25100.1	endomembrane protein 70, putative
Contig_18	e-119	AT2G18980.1	peroxidase, putative
Contig_159	e-113	AT1G01300.1	aspartyl protease family protein
Contig_196	e-112	AT1G76160.1	SKS5 (SKU5 Similar 5); copper ion binding / oxidoreductase
Contig_96	e-111	AT1G14670.1	endomembrane protein 70, putative
Contig_138	e-109	AT3G16240.1	DELTA-TIP (delta tonoplast integral protein); water channel
0801-94-(6-5-06)_A01	e-108	AT5G14430.2	dehydration-responsive protein-related
0097-94-H09(4-28-06)	e-108	AT1G72680.1	cinnamyl-alcohol dehydrogenase, putative
0548-94-(6-8-06)_H06	e-106	AT5G55180.1	glycosyl hydrolase family 17 protein
Contig_41	e-105	AT1G73620.1	thaumatin-like protein, putative / pathogenesis-related protein, putative
0766-94-(6-7-06)_A09	e-105	AT2G42590.2	GF14 MU, GENERAL REGULATORY FACTOR 9, GRF9

0523-94-(6-8-06)_G03	e-104	AT5G42180.1	peroxidase 64 (PER64) (P64) (PRXR4)
0400-94-(6-8-06)_H12	2.00E-98	AT5G21090.1	leucine-rich repeat protein, putative
1105-94-(6-9-06)_E07	9.00E-96	AT3G10710.1	pectinesterase family protein
0808-94-(6-5-06)_H01	1.00E-94	AT3G17840.1	RLK902 (receptor-like kinase 902); ATP binding / kinase/ protein serine/threonine kinase
Contig_116	2.00E-92	AT4G28510.1	ATPHB1 (PROHIBITIN 1)
0030-94-E01(4-28-06)	5.00E-91	AT3G23750.1	leucine-rich repeat family protein / protein kinase family protein
Contig_35	8.00E-84	AT5G16000.1	NIK1 (NSP-INTERACTING KINASE 1); kinase
Contig_83	4.00E-80	AT5G36890.2	hydrolase, hydrolyzing O-glycosyl compounds
1111-94-(6-9-06)_C08	1.00E-74	AT2G17230.1	phosphate-responsive 1 family protein
Contig_155	3.00E-72	AT3G11660.1	NHL1 (NDR1/HIN1-like 1)
1182-94-(6-15-06)_H06	1.00E-66	AT2G01660.1	33 kDa secretory protein-related
Contig_37	9.00E-66	AT3G16520.2	UDP-glucoronosyl/UDP-glucosyl transferase family protein
0545-94-(6-8-06)_E06	8.00E-63	AT5G54160.1	ATOMT1 (O-METHYLTRANSFERASE 1)
0856-94-(6-5-06)_H07	9.00E-61	AT4G19150.1	ankyrin repeat family protein
0581-94-(6-8-06)_E09	8.00E-53	AT4G29360.1	glycosyl hydrolase family 17 protein
1004-94(6-2-06Truncated)_D01	1.00E-50	AT5G42800.1	DFR (DIHYDROFLAVONOL 4-REDUCTASE); dihydrokaempferol 4-reductase
0576-94-(6-12-06)_E11	1.00E-50	AT1G76010.1	nucleic acid binding
1116-94-(6-9-06)_H08	2.00E-47	AT5G10290.1	leucine-rich repeat family protein / protein kinase family protein
0904-94-(6-14-06)_G10	5.00E-27	AT4G35580.1	no apical meristem (NAM) family protein
0714-94-(6-7-06)_F02	2.00E-19	AT5G15230.2	GASA4 (GAST1 PROTEIN HOMOLOG 4)

APPENDIX L: NR BLASTN

Query	E-value	Hit 1
0238-94-G11(5-10-06)	6.00E-157	emb|Y08680.1|AGAG118 A.glutinosa mRNA for acetylornithine transaminase
0897-94-(6-14-06)_G07	9.00E-57	emb|X98861.1|ATTFIIAL A.thaliana mRNA for large subunit of TFIIA
0532-94-(6-8-06)_H04	3.00E-177	gb|AY570536.1| Alyssum montanum chloroplast ATP phosphoribosyl transferase (ATP-PRT1) mRNA, complete cds; nuclear gene for chloroplast product
0060-94-C05(4-28-06)	0	gb|DQ519359.2| Ammopiptanthus mongolicus EBP1 mRNA, complete cds
Contig\34	2.00E-45	ref|NM_126044.3| Arabidopsis thaliana (1-4)-beta-mannan endohydrolase, putative (AT5G66460) mRNA, complete cds
0946-94-(6-15-06)_A04	2.00E-147	gb|AF043538.1|AF043538 Arabidopsis thaliana 20S proteasome beta subunit PBG1 (PBG1) mRNA, complete cds
Contig\181	4.00E-55	ref|NM_125180.2| Arabidopsis thaliana 26S proteasome regulatory subunit, putative (AT5G57950) mRNA, complete cds
Contig\79	1.00E-149	ref|NM_179121.2| Arabidopsis thaliana 2-oxoacid dehydrogenase family protein (AT4G26910) mRNA, complete cds
0647-94-(6-6-06)_G06	4.00E-99	ref|NM_111017.2| Arabidopsis thaliana 5'-AMP-activated protein kinase beta-1 subunit-related (AT3G01510) mRNA, complete cds
Contig\122	1.00E-169	ref|NM_106064.3| Arabidopsis thaliana 60S ribosomal protein L6 (RPL6C) (AT1G74050) mRNA, complete cds
Contig\183	1.00E-162	ref|NM_122390.3| Arabidopsis thaliana ABC1 family protein (AT5G24810) mRNA, complete cds
1025-94-(6-2-06)_H03	8.00E-89	ref|NM_130185.3| Arabidopsis thaliana ABI1L1 (ABI-1-LIKE 1) (ABI1L1) mRNA, complete cds
Contig\23	5.00E-22	ref|NM_100526.4| Arabidopsis thaliana ACD32.1 (ALPHA-CRYSTALLIN DOMAIN 31.2) (ACD32.1) mRNA, complete cds
Contig\106	0	ref|NM_115043.2| Arabidopsis thaliana ACX4 (ACYL-COA OXIDASE 4); oxidoreductase (ACX4) mRNA, complete cds
0517-94-(6-8-06)_A03	3.00E-81	ref|NM_119521.3| Arabidopsis thaliana ADL2 (ARABIDOPSIS DYNAMIN-LIKE 2); GTP binding / GTPase (ADL2) mRNA, complete cds
0805-94-(6-5-06)_E01	0	ref|NM_202696.2| Arabidopsis thaliana AFC1 (ARABIDOPSIS FUS3-COMPLEMENTING GENE 1); kinase (AFC1) mRNA, complete cds
0940-94-(6-15-06)_C03	0	ref|NM_202718.2| Arabidopsis thaliana alpha-galactosidase, putative / melibiase, putative / alpha-D-galactoside galactohydrolase, putative (AT3G56310) mRNA, complete cds
1009-94-(6-2-06)_A02	5.00E-161	ref|NM_103660.5| Arabidopsis thaliana amino acid transporter family protein (AT1G47670) mRNA, complete cds
1133-94-(6-9-06)_A11	0	ref|NM_116092.3| Arabidopsis thaliana anion exchange family protein (AT3G62270) mRNA, complete cds
1034-94-(6-14-06)_F08	7.00E-178	ref|NM_119463.4| Arabidopsis thaliana APM1 (Aminopeptidase M1) mRNA, complete cds
0460-94-(6-16-06)_B05	8.00E-127	ref|NM_102258.4| Arabidopsis thaliana ARL1 (ARG1-LIKE1); heat shock protein binding / unfolded protein binding (ARL1) mRNA, complete cds
1146-94-(6-9-06)_F12	3.00E-18	ref|NM_123088.3| Arabidopsis thaliana armadillo/beta-catenin repeat family protein (AT5G37290) mRNA, complete cds
1123-94-(6-9-06)_G09	3.00E-144	ref|NM_125409.4| Arabidopsis thaliana aspartyl aminopeptidase, putative (AT5G60160) mRNA, complete cds

Contig\159	8.00E-140	ref|NM_100012.2| Arabidopsis thaliana aspartyl protease family protein (AT1G01300) mRNA, complete cds
0719-94-(6-7-06)_C03	2.00E-171	ref|NM_119754.3| Arabidopsis thaliana aspartyl protease family protein (AT4G35880) mRNA, complete cds
Contig\51	0	ref|NM_179227.2| Arabidopsis thaliana aspartyl-tRNA synthetase, putative / aspartate--tRNA ligase, putative (AT4G31180) mRNA, complete cds
0530-94-(6-8-06)_F04	1.00E-112	dbj|AK118255.1| Arabidopsis thaliana At3g29100 mRNA for putative vesicle transport protein, complete cds, clone: RAFL19-55-L11
0770-94-(6-14-06)_B05'	1.00E-35	gb|BT023476.1| Arabidopsis thaliana At4g13270 gene, complete cds
0276-94(5-31-06)_014	3.00E-104	gb|BT030465.1| Arabidopsis thaliana At5g37340 mRNA, complete cds
Contig\16	0	ref|NM_102198.3| Arabidopsis thaliana ATARF/ATARF1/ATARFA1A (ADP-RIBOSYLATION FACTOR 1); GTP binding / phospholipase activator/ protein binding (ATARF/ATARF1/ATARFA1A) mRNA, complete cds
Contig\174	5.00E-142	ref|NM_118359.3| Arabidopsis thaliana ATCES1 (ATCES1); catalytic (ATCES1) mRNA, complete cds
Contig\206	7.00E-134	ref|NM_111192.2| Arabidopsis thaliana ATEXPA13 (ARABIDOPSIS THALIANA EXPANSIN A13) (ATEXPA13) mRNA, complete cds
0922-94-(6-15-06)_A01	1.00E-85	ref|NM_125748.2| Arabidopsis thaliana ATFP3 (Arabidopsis thaliana farnesylated protein 3); metal ion binding (ATFP3) mRNA, complete cds
Contig\22	0	ref|NM_104734.2| Arabidopsis thaliana ATGOLS4 (ARABIDOPSIS THALIANA GALACTINOL SYNTHASE 4); transferase, transferring glycosyl groups / transferase, transferring he (ATGOLS4) mRNA, complete cds
0463-94-(6-16-06)_E05	3.00E-120	ref|NM_116494.4| Arabidopsis thaliana ATMLO1/MLO1 (MILDEW RESISTANCE LOCUS O 1); calmodulin binding (ATMLO1/MLO1) mRNA, complete cds
0465-94-(6-16-06)_G05	6.00E-179	ref|NM_101530.3| Arabidopsis thaliana ATMLO14 (ARABIDOPSIS THALIANA MILDEW RESISTANCE LOCUS O 14); NADH dehydrogenase (ubiquinone) (ATMLO14) mRNA, complete cds
0717-94-(6-7-06)_A03	9.00E-95	ref|NM_114748.2| Arabidopsis thaliana ATMP2 (ARABIDOPSIS THALIANA MEMBRANE-ASSOCIATED PROGESTERONE BINDING PROTEIN 3); heme binding / transition metal ion binding (ATMP2) mRNA, complete cds
0690-94-(6-6-06)_B12	1.00E-66	ref|NM_148121.2| Arabidopsis thaliana AtMYB82 (myb domain protein 82); DNA binding / transcription factor (AtMYB82) mRNA, complete cds
0847-94-(6-5-06)_G06	2.00E-77	ref|NM_122512.3| Arabidopsis thaliana ATP binding / protein kinase/ protein serine/threonine kinase (AT5G26110) mRNA, complete cds
0087-93-B03(4-21-06)	4.00E-57	ref|NM_121632.3| Arabidopsis thaliana ATRAD21.3 (Arabidopsis homolog of RAD21 3) (ATRAD21.3) mRNA, complete cds
0621-94-(6-6-06)_E03	0	ref|NM_118989.2| Arabidopsis thaliana AtRPN1b/RPN1B (26S proteasome regulatory subunit S2 1B); binding (AtRPN1b/RPN1B) mRNA, complete cds
0597-94-(6-8-06)_D11	1.00E-85	ref|NM_116051.3| Arabidopsis thaliana ATRSP31 (ARGININE/SERINE-RICH SPLICING FACTOR 31); RNA binding (ATRSP31) mRNA, complete cds
1064-94-(6-2-06)_F08	1.00E-104	ref|NM_180843.2| Arabidopsis thaliana ATRSP41 (Arabidopsis thaliana arginine/serine-rich splicing factor 41); RNA binding (ATRSP41) mRNA, complete cds
0726-94-(6-7-06)_B04	1.00E-105	ref|NM_104210.3| Arabidopsis thaliana AtTLP7 (TUBBY LIKE PROTEIN 7); phosphoric diester hydrolase/ transcription factor (AtTLP7) mRNA, complete cds
0595-94-(6-8-06)_B11	3.00E-69	ref|NM_105795.4| Arabidopsis thaliana ATWHY2 (A. THALIANA WHIRLY 2); DNA binding (ATWHY2) mRNA, complete cds
0311-94(5-31-06)_016	6.00E-176	ref|NM_125543.3| Arabidopsis thaliana autophagy 3 (APG3) (AT5G61500) mRNA, complete cds
0133-94-	0	ref|NM_106541.3| Arabidopsis thaliana AVP2 (ARABIDOPSIS VACUOLAR

E03(5-9-06)		H+-PYROPHOSPHATASE 2) (AVP2) mRNA, complete cds
Contig\85	0	ref|NM_126401.4| Arabidopsis thaliana band 7 family protein (AT2G03510) mRNA, complete cds
0799-94-(6-7-06)_F12	0	ref|NM_124536.3| Arabidopsis thaliana band 7 family protein (AT5G51570) mRNA, complete cds
Contig\66	3.00E-158	ref|NM_117209.4| Arabidopsis thaliana beta-adaptin, putative (AT4G11380) mRNA, complete cds
0527-94-(6-8-06)_C04	4.00E-93	ref|NM_124824.3| Arabidopsis thaliana binding (AT5G54440) mRNA, complete cds
0584-94-(6-8-06)_G09	1.00E-47	ref|NM_102394.2| Arabidopsis thaliana BSD domain-containing protein (AT1G26300) mRNA, complete cds
Contig\185	6.00E-173	ref|NM_121242.4| Arabidopsis thaliana carbon-nitrogen hydrolase family protein (AT5G12040) mRNA, complete cds
0666-94-(6-6-06)_B09	4.00E-48	ref|NM_116520.3| Arabidopsis thaliana catalytic (AT4G02860) mRNA, complete cds
0455-94-(6-16-06)_E04	1.00E-168	ref|NM_129358.3| Arabidopsis thaliana ceramidase family protein (AT2G38010) mRNA, complete cds
0200-94-A07(5-10-06)	2.00E-150	ref|NM_180700.3| Arabidopsis thaliana chaperone protein dnaJ-related (AT5G06130) mRNA, complete cds
1097-94-(6-2-06)_G12	0	ref|NM_121867.3| Arabidopsis thaliana CHR17 (CHROMATIN REMODELING FACTOR17); DNA-dependent ATPase (CHR17) mRNA, complete cds
0694-94-(6-6-06)_F12	1.00E-54	ref|NM_180719.3| Arabidopsis thaliana CIC7E11; protein binding / zinc ion binding (CIC7E11) mRNA, complete cds
0097-94-H09(4-28-06)	4.00E-133	ref|NM_105927.3| Arabidopsis thaliana cinnamyl-alcohol dehydrogenase, putative (AT1G72680) mRNA, complete cds
Contig\137	2.00E-127	ref|NM_122420.1| Arabidopsis thaliana CIPK25 (CBL-INTERACTING PROTEIN KINASE 25); kinase (CIPK25) mRNA, complete cds
Contig\93	4.00E-80	ref|NM_119709.1| Arabidopsis thaliana CLC-E (CHLORIDE CHANNEL E); voltage-gated chloride channel (CLC-E) mRNA, complete cds
0665-94-(6-6-06)_A09	7.00E-121	gb|AY084964.1| Arabidopsis thaliana clone 122943 mRNA, complete sequence
1032-94-(6-16-06)_D06	1.00E-137	gb|AY085017.1| Arabidopsis thaliana clone 12455 mRNA, complete sequence
0591-94-(6-8-06)_F10	2.00E-83	gb|AY086037.1| Arabidopsis thaliana clone 207684 mRNA, complete sequence
0106-94-A11(4-28-06)	4.00E-45	gb|AY086191.1| Arabidopsis thaliana clone 22246 mRNA, complete sequence
0749-94-(6-7-06)_A07	1.00E-125	gb|AY087677.1| Arabidopsis thaliana clone 37589 mRNA, complete sequence
0851-94-(6-5-06)_C07	3.00E-151	gb|AY087739.1| Arabidopsis thaliana clone 38096 mRNA, complete sequence
0704-94-(6-7-06)_D01	2.00E-102	ref|NM_117276.2| Arabidopsis thaliana Clp amino terminal domain-containing protein (AT4G12060) mRNA, complete cds
0652-94-(6-6-06)_D07	4.00E-143	ref|NM_105338.3| Arabidopsis thaliana CLPP3 (Clp protease proteolytic subunit 3); endopeptidase Clp (CLPP3) mRNA, complete cds
0029-94-D01(4-28-06)	6.00E-43	ref|NM_179526.3| Arabidopsis thaliana copine-related (AT1G67800) mRNA, complete cds
0915-94-(6-14-06)_B12	7.00E-26	ref|NM_106586.4| Arabidopsis thaliana copine-related (AT1G79380) mRNA, complete cds
0439-94-(6-16-06)_G02	7.00E-140	ref|NM_119688.3| Arabidopsis thaliana cyclase family protein (AT4G35220) mRNA, complete cds
0086-94-E08(4-28-06)	3.00E-66	ref|NM_121005.4| Arabidopsis thaliana cytochrome b5 domain-containing protein (AT5G09680) mRNA, complete cds

0732-94-(6-14-06)_A05	0	ref|NM_125507.2| Arabidopsis thaliana DEAD box RNA helicase, putative (AT5G61140) mRNA, complete cds
Contig\92	0	ref|NM_121158.3| Arabidopsis thaliana DEAD/DEAH box helicase, putative (AT5G11200) mRNA, complete cds
Contig\89	4.00E-150	ref|NM_125799.2| Arabidopsis thaliana dehydration-responsive protein-related (AT5G64030) mRNA, complete cds
Contig\21	6.00E-160	ref|NM_106375.1| Arabidopsis thaliana dehydration-responsive protein-related (AT1G77260) mRNA, complete cds
0801-94-(6-5-06)_A01	2.00E-103	ref|NM_203052.1| Arabidopsis thaliana dehydration-responsive protein-related (AT5G14430) mRNA, complete cds
0249-94(5-31-06)_007	7.00E-162	ref|NM_121923.3| Arabidopsis thaliana ECR1 (E1 C-TERMINAL RELATED 1); small protein activating enzyme (ECR1) mRNA, complete cds
0624-94-(6-6-06)_H03	0	ref|NM_112228.2| Arabidopsis thaliana endomembrane protein 70, putative (AT3G13772) mRNA, complete cds
0242-94-C12(5-10-06)	1.00E-178	ref|NM_126258.2| Arabidopsis thaliana endomembrane protein 70, putative (AT2G01970) mRNA, complete cds
0509-94-(6-8-06)_A02	3.00E-113	ref|NM_106062.3| Arabidopsis thaliana enolase, putative (AT1G74030) mRNA, complete cds
Contig\42	0	ref|NM_129716.2| Arabidopsis thaliana esterase, putative (AT2G41530) mRNA, complete cds
1108-94-(6-9-06)_H07	1.00E-87	ref|NM_121228.4| Arabidopsis thaliana eukaryotic translation initiation factor SUI1 family protein (AT5G11900) mRNA, complete cds
1151-94-(6-15-06)_C04	1.00E-163	ref|NM_105837.3| Arabidopsis thaliana F-actin capping protein beta subunit family protein (AT1G71790) mRNA, complete cds
0199-94(5-31-06)_008	9.00E-53	ref|NM_120858.2| Arabidopsis thaliana formin homology 2 domain-containing protein / FH2 domain-containing protein (AT5G07760) mRNA, complete cds
Contig\82	1.00E-43	emb|BX814086.1|CNS0AE0N Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB56ZD01 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress)
1308-94-(6-16-06)_B07	3.00E-88	emb|BX842281.1|CNS0A0DV Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTSIL91ZD04 of Silique of strain col-0 of Arabidopsis thaliana (thale cress)
1193-94-(6-15-06)_E07	6.00E-173	emb|BX829681.1|CNS0A1CB Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB2ZA11 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress)
0910-94-(6-14-06)_E11	2.00E-116	emb|BX814089.1|CNS0AC31 Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB56ZE07 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress)
0844-94-(6-5-06)_D06	7.00E-166	emb|BX824728.1|CNS0A6VN Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPGH68ZC04 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress)
0541-94-(6-8-06)_A06	5.00E-129	emb|BX815165.1|CNS0ACS6 Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTLS39ZG02 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress)
0239-94-H11(5-10-06)	3.00E-40	emb|BX827331.1|CNS0A4JV Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTLS40ZA10 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress)
1042-94-(6-15-06)_E12	5.00E-123	ref|NM_115978.3| Arabidopsis thaliana FUS6 (FUSCA 6) (FUS6) mRNA, complete cds
0398-94-(6-8-06)_F12	0	ref|NM_103026.4| Arabidopsis thaliana galactosyltransferase family protein (AT1G32930) mRNA, complete cds
Contig\55	8.00E-127	ref|NM_114727.2| Arabidopsis thaliana GAMMA CAL2 (GAMMA CARBONIC ANHYDRASE-LIKE 2); acyltransferase (GAMMA CAL2) mRNA, complete cds
Contig\32	2.00E	ref|NM_121381.3| Arabidopsis thaliana GCN5-related N-acetyltransferase,

	-103	putative (AT5G13780) mRNA, complete cds
0539-94-(6-8-06)_G05	5.00E-167	ref|NM_106409.3| Arabidopsis thaliana glucose-6-phosphate/phosphate translocator-related (AT1G77610) mRNA, complete cds
Contig\120	3.00E-81	ref|NM_116196.2| Arabidopsis thaliana glutamate binding (AT3G63310) mRNA, complete cds
0506-94-(6-8-06)_F01	0	ref|NM_124073.2| Arabidopsis thaliana glycine-rich protein (AT5G47020) mRNA, complete cds
Contig\154	5.00E-111	ref|NM_120865.4| Arabidopsis thaliana glycosyl hydrolase family 79 N-terminal domain-containing protein (AT5G07830) mRNA, complete cds
0866-94-(6-5-06)_B09	5.00E-79	ref|NM_119941.2| Arabidopsis thaliana HAT22 (homeobox-leucine zipper protein 22); transcription factor (HAT22) mRNA, complete cds
1101-94-(6-9-06)_A07	2.00E-38	ref|NM_180278.3| Arabidopsis thaliana HDA15 (histone deacetylase 15); histone deacetylase (HDA15) mRNA, complete cds
0185-94-B05(5-10-06)	5.00E-120	ref|NM_111475.1| Arabidopsis thaliana homeotic gene regulator, putative (AT3G06010) mRNA, complete cds
0245-94-F12(5-10-06)	2.00E-157	ref|NM_118250.4| Arabidopsis thaliana HSA32 (HEAT-STRESS-ASSOCIATED 32) (HSA32) mRNA, complete cds
0701-94-(6-7-06)_A01	1.00E-105	ref|NM_105955.3| Arabidopsis thaliana HTH (HOTHEAD); aldehyde-lyase (HTH) mRNA, complete cds
Contig\54	3.00E-119	ref|NM_130060.2| Arabidopsis thaliana HUB1 (HISTONE MONO-UBIQUITINATION 1); protein binding / zinc ion binding (HUB1) mRNA, complete cds
1137-94-(6-9-06)_E11	3.00E-100	ref|NM_126486.5| Arabidopsis thaliana IBR5 (INDOLE-3-BUTYRIC ACID RESPONSE 5); protein tyrosine/serine/threonine phosphatase (IBR5) mRNA, complete cds
1090-94-(6-2-06)_H11	3.00E-177	ref|NM_118900.3| Arabidopsis thaliana importin beta-2 subunit family protein (AT4G27640) mRNA, complete cds
0724-94-(6-7-06)_H03	1.00E-136	ref|NM_103934.4| Arabidopsis thaliana indigoidine synthase A family protein (AT1G50510) mRNA, complete cds
0566-94-(6-8-06)_A08	1.00E-155	ref|NM_101685.4| Arabidopsis thaliana ketose-bisphosphate aldolase class-II family protein (AT1G18270) mRNA, complete cds
Contig\10	6.00E-40	ref|NM_124685.3| Arabidopsis thaliana KH domain-containing protein (AT5G53060) mRNA, complete cds
0763-94-(6-7-06)_G08	0	ref|NM_129178.1| Arabidopsis thaliana kinesin motor protein-related (AT2G36200) mRNA, complete cds
1116-94-(6-9-06)_H08	4.00E-54	ref|NM_121067.3| Arabidopsis thaliana leucine-rich repeat family protein / protein kinase family protein (AT5G10290) mRNA, complete cds
0583-94-(6-8-06)_F09	1.00E-131	ref|NM_105440.1| Arabidopsis thaliana leucine-rich repeat family protein / protein kinase family protein (AT1G67720) mRNA, complete cds
Contig\102	0	ref|NM_102881.4| Arabidopsis thaliana leucine-rich repeat transmembrane protein kinase, putative (AT1G31420) mRNA, complete cds
1192-94-(6-15-06)_D07	2.00E-65	ref|NM_112263.3| Arabidopsis thaliana lipase class 3 family protein (AT3G14075) mRNA, complete cds
0137-94-A04(5-9-06)	1.00E-126	ref|NM_202415.1| Arabidopsis thaliana LPAT4; acyltransferase (LPAT4) mRNA, complete cds
1019-94-(6-2-06)_B03	0	ref|NM_001084696.1| Arabidopsis thaliana LPD1 (LIPOAMIDE DEHYDROGENASE 1) (LPD1) mRNA, complete cds
0929-94-(6-15-06)_H01	8.00E-95	ref|NM_103939.2| Arabidopsis thaliana lysine decarboxylase family protein (AT1G50575) mRNA, complete cds
Contig\36	4.00E-144	ref|NM_112003.3| Arabidopsis thaliana lysyl-tRNA synthetase, putative / lysine--tRNA ligase, putative (AT3G11710) mRNA, complete cds
0048-94-G03(4-28-06)	6.00E-74	ref|NM_106508.2| Arabidopsis thaliana mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein (AT1G78610) mRNA, complete cds

1144-94-(6-9-06)_D12	7.00E-64	ref|NM_124426.4| Arabidopsis thaliana MEMB12 (Golgi SNARE protein membrin 12); v-SNARE (MEMB12) mRNA, complete cds
0908-94-(6-14-06)_C11	2.00E-72	ref|NM_202089.1| Arabidopsis thaliana methyladenine glycosylase family protein (AT1G13635) mRNA, complete cds
0148-94-D05(5-9-06)	0	ref|NM_111566.3| Arabidopsis thaliana MFP2 (MULTIFUNCTIONAL PROTEIN); enoyl-CoA hydratase (MFP2) mRNA, complete cds
1029-94-(6-2-06)_D04	3.00E-107	ref|NM_102557.1| Arabidopsis thaliana microtubule associated protein (MAP65/ASE1) family protein (AT1G27920) mRNA, complete cds
0447-94-(6-16-06)_F03	3.00E-125	ref|NM_128068.2| Arabidopsis thaliana MIR domain-containing protein (SDF2) mRNA, complete cds
0807-94-(6-5-06)_G01	1.00E-48	ref|NM_125994.1| Arabidopsis thaliana MLO10 (MILDEW RESISTANCE LOCUS O 10); calmodulin binding (MLO10) mRNA, complete cds
Contig\111	2.00E-142	dbj|AK228873.1| Arabidopsis thaliana mRNA for hypothetical protein, complete cds, clone: RAFL16-19-K11
0925-94-(6-16-06)_C11	3.00E-88	dbj|AK229460.1| Arabidopsis thaliana mRNA for hypothetical protein, complete cds, clone: RAFL16-83-O15
0747-94-(6-7-06)_G06	1.00E-125	dbj|AK226330.1| Arabidopsis thaliana mRNA for hypothetical protein, complete cds, clone: RAFL05-14-F21
0733-94-(6-7-06)_A05	9.00E-120	dbj|AK227325.1| Arabidopsis thaliana mRNA for hypothetical protein, complete cds, clone: RAFL14-02-A12
0691-94-(6-6-06)_C12	2.00E-84	dbj|AK228115.1| Arabidopsis thaliana mRNA for hypothetical protein, complete cds, clone: RAFL14-59-H03
0643-94-(6-6-06)_C06	1.00E-36	dbj|AK228494.1| Arabidopsis thaliana mRNA for hypothetical protein, complete cds, clone: RAFL15-12-I18
0363-94-(6-12-06)_H07	9.00E-120	dbj|AK230280.1| Arabidopsis thaliana mRNA for hypothetical protein, partial cds, clone: RAFL24-02-C11
0209-94-B08(5-10-06)	6.00E-169	dbj|AK230070.1| Arabidopsis thaliana mRNA for hypothetical protein, partial cds, clone: RAFL22-69-F03
1170-94-(6-15-06)_H05	5.00E-167	dbj|AK226691.1| Arabidopsis thaliana mRNA for ubiquitin-specific protease 8, complete cds, clone: RAFL07-56-I10
0752-94-(6-7-06)_D07	6.00E-122	dbj|AK226405.1| Arabidopsis thaliana mRNA for vesicle-associated membrane protein 7C, complete cds, clone: RAFL06-07-E23
1159-94-(6-15-06)_A05	5.00E-148	dbj|AK228585.1| Arabidopsis thaliana mRNA for zinc finger like protein, complete cds, clone: RAFL15-36-C08
Contig\115	0	ref|NM_118907.3| Arabidopsis thaliana MSP1 protein, putative / intramitochondrial sorting protein, putative (AT4G27680) mRNA, complete cds
0336-94-(6-9-06)_D03	0	ref|NM_102799.5| Arabidopsis thaliana MUR4 (MURUS 4); catalytic (MUR4) mRNA, complete cds
Contig\160	0	ref|NM_129427.4| Arabidopsis thaliana MVD1 (mevalonate diphosphate decarboxylase 1) (MVD1) mRNA, complete cds
Contig\68	2.00E-51	ref|NM_001035880.2| Arabidopsis thaliana MYB88 (myb domain protein 88); DNA binding / transcription factor (MYB88) mRNA, complete cds
Contig\124	9.00E-76	ref|NM_111180.3| Arabidopsis thaliana NADH:ubiquinone oxidoreductase family protein (AT3G03100) mRNA, complete cds
1172-94-(6-15-06)_B06	2.00E-52	ref|NM_130337.4| Arabidopsis thaliana NADH-ubiquinone oxidoreductase-related (AT2G47690) mRNA, complete cds
Contig\155	1.00E-74	ref|NM_111998.2| Arabidopsis thaliana NHL1 (NDR1/HIN1-like 1) (NHL1) mRNA, complete cds
Contig\35	5.00E-130	ref|NM_121605.2| Arabidopsis thaliana NIK1 (NSP-INTERACTING KINASE 1); kinase (NIK1) mRNA, complete cds
Contig\88	6.00E-160	ref|NM_122656.4| Arabidopsis thaliana nucleoside-triphosphatase/ nucleotide binding (AT5G27740) mRNA, complete cds
0297-94(5-31-06)_007	1.00E-120	ref|NM_123565.3| Arabidopsis thaliana ORMDL family protein (AT5G42000) mRNA, complete cds

Contig\195	2.00E-89	ref|NM_179213.3| Arabidopsis thaliana oxidoreductase, 2OG-Fe(II) oxygenase family protein (AT4G16765) mRNA, complete cds
Contig\95	1.00E-169	ref|NM_103435.2| Arabidopsis thaliana patched family protein (AT1G42470) mRNA, complete cds
0227-94-D10(5-10-06)	2.00E-130	ref|NM_129424.4| Arabidopsis thaliana PECT1 (PHOSPHORYLETHANOLAMINE CYTIDYLYLTRANSFERASE 1); ethanolamine-phosphate cytidylyltransferase (PECT1) mRNA, complete cds
0282-94(5-31-06)_009	9.00E-161	ref|NM_115179.4| Arabidopsis thaliana pectate lyase family protein (AT3G53190) mRNA, complete cds
1084-94-(6-2-06)_B11	7.00E-20	ref|NM_118901.4| Arabidopsis thaliana PEL1 (PELOTA); translation release factor (PEL1) mRNA, complete cds
0305-94(5-31-06)_004	7.00E-137	ref|NM_119662.3| Arabidopsis thaliana peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative (AT4G34960) mRNA, complete cds
Contig\71	8.00E-70	ref|NM_128192.2| Arabidopsis thaliana PEX10 (peroxin 10); protein binding / zinc ion binding (PEX10) mRNA, complete cds
Contig\191	2.00E-90	ref|NM_113082.3| Arabidopsis thaliana PEX22 (PEROXIN 22); protein binding (PEX22) mRNA, complete cds
Contig\94	0	ref|NM_120089.4| Arabidopsis thaliana phenylalanyl-tRNA synthetase, putative / phenylalanine--tRNA ligase, putative (AT4G39280) mRNA, complete cds
1111-94-(6-9-06)_C08	6.00E-84	ref|NM_127277.2| Arabidopsis thaliana phosphate-responsive 1 family protein (AT2G17230) mRNA, complete cds
1018-94-(6-2-06)_A03	3.00E-113	ref|NM_124155.2| Arabidopsis thaliana phosphofructokinase family protein (AT5G47810) mRNA, complete cds
0901-94-(6-14-06)_D10	1.00E-74	ref|NM_114912.3| Arabidopsis thaliana phosphoglycerate/bisphosphoglycerate mutase family protein (AT3G50520) mRNA, complete cds
0272-94(5-31-06)_006	0	gb|U72711.1|ATU72711 Arabidopsis thaliana proline iminopeptidase mRNA, complete cds
1078-94-(6-2-06)_D10	7.00E-96	ref|NM_101916.3| Arabidopsis thaliana protein kinase (AT1G20650) mRNA, complete cds
Contig\125	0	ref|NM_119744.4| Arabidopsis thaliana protein kinase family protein (AT4G35780) mRNA, complete cds
1187-94-(6-15-06)_B07	9.00E-120	ref|NM_129570.3| Arabidopsis thaliana protein kinase family protein (AT2G40120) mRNA, complete cds
0464-94-(6-16-06)_F05	0	ref|NM_102133.2| Arabidopsis thaliana protein kinase family protein (AT1G22870) mRNA, complete cds
Contig\69	3.00E-56	ref|NM_116091.3| Arabidopsis thaliana protein phosphatase 2C, putative / PP2C, putative (AT3G62260) mRNA, complete cds
0823-94-(6-5-06)_G03	1.00E-136	ref|NM_129214.3| Arabidopsis thaliana pyruvate kinase, putative (AT2G36580) mRNA, complete cds
0284-94(5-31-06)_013	3.00E-115	ref|NM_113418.4| Arabidopsis thaliana QUA1 (QUASIMODO1); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferas (QUA1) mRNA, complete cds
Contig\65	0	ref|NM_101843.3| Arabidopsis thaliana regulator of chromosome condensation (RCC1) family protein (AT1G19880) mRNA, complete cds
1171-94-(6-15-06)_A06	2.00E-179	ref|NM_120884.1| Arabidopsis thaliana replication protein, putative (AT5G08020) mRNA, complete cds
Contig\194	3.00E-76	ref|NM_105082.4| Arabidopsis thaliana reticulon family protein (RTNLB3) (AT1G64090) mRNA, complete cds
0360-94-(6-12-06)_E07	9.00E-139	ref|NM_124142.3| Arabidopsis thaliana RNA binding / tRNA methyltransferase (AT5G47680) mRNA, complete cds
0729-94-(6-7-06)_E04	8.00E-70	ref|NM_130244.3| Arabidopsis thaliana RNA recognition motif (RRM)-containing protein (AT2G46780) mRNA, complete cds
0225-94-B10(5-10-06)	0	ref|NM_128872.2| Arabidopsis thaliana SAR1 (SYNAPTOBREVIN-RELATED PROTEIN 1) (SAR1) mRNA, complete cds

0835-94-(6-5-06)_C05	4.00E-112	ref|NM_121275.4| Arabidopsis thaliana SEC10 (EXOCYST COMPLEX COMPONENT SEC10) (SEC10) mRNA, complete cds
Contig\101	0	ref|NM_117916.4| Arabidopsis thaliana SH3 domain-containing protein 3 (SH3P3) (AT4G18060) mRNA, complete cds
0434-94-(6-16-06)_B02	0	ref|NM_117467.3| Arabidopsis thaliana SHM4 (SERINE HYDROXYMETHYLTRANSFERASE 4); glycine hydroxymethyltransferase (SHM4) mRNA, complete cds
0612-94-(6-6-06)_D02	0	ref|NM_125590.2| Arabidopsis thaliana signal recognition particle-related / SRP-related (AT5G61970) mRNA, complete cds
Contig\196	1.00E-118	ref|NM_106265.3| Arabidopsis thaliana SKS5 (SKU5 Similar 5); copper ion binding / oxidoreductase (SKS5) mRNA, complete cds
0656-94-(6-6-06)_H07	1.00E-104	ref|NM_100773.3| Arabidopsis thaliana SNF4 (Sucrose NonFermenting 4) (SNF4) mRNA, complete cds
0112-94-(6-12-06)_D04	3.00E-148	ref|NM_100276.3| Arabidopsis thaliana SNF7 family protein (AT1G03950) mRNA, complete cds
0210-94-C08(5-10-06)	9.00E-110	ref|NM_103995.4| Arabidopsis thaliana synbindin, putative (AT1G51160) mRNA, complete cds
0232-94-A11(5-10-06)	2.00E-155	ref|NM_100300.3| Arabidopsis thaliana tetratricopeptide repeat (TPR)-containing protein (AT1G04190) mRNA, complete cds
1126-94-(6-9-06)_B10	9.00E-158	ref|NM_179234.1| Arabidopsis thaliana TMT2 (TONOPLAST MONOSACCHARIDE TRANSPORTER2); carbohydrate transporter/ nucleoside transporter/ sugar porter (TMT2) mRNA, complete cds
1047-94-(6-2-06)_F06	3.00E-94	ref|NM_179658.3| Arabidopsis thaliana transducin family protein / WD-40 repeat family protein (AT2G19430) mRNA, complete cds
0459-94-(6-16-06)_A05	3.00E-132	ref|NM_105842.2| Arabidopsis thaliana transducin family protein / WD-40 repeat family protein (AT1G71840) mRNA, complete cds
0393-94-(6-8-06)_B12	0	ref|NM_105153.3| Arabidopsis thaliana translational activator family protein (AT1G64790) mRNA, complete cds
1143-94-(6-9-06)_C12	3.00E-163	ref|NM_112984.2| Arabidopsis thaliana translocation protein-related (AT3G20920) mRNA, complete cds
Contig\131	5.00E-168	ref|NM_100564.4| Arabidopsis thaliana transporter-related (AT1G06890) mRNA, complete cds
1145-94-(6-9-06Truncated)_E12	8.00E-51	ref|NM_115324.3| Arabidopsis thaliana TTN8 (TITAN8); ATP binding (TTN8) mRNA, complete cds
1015-94-(6-2-06)_F02	2.00E-122	ref|NM_103932.3| Arabidopsis thaliana UBC20 (ubiquitin-conjugating enzyme 20); ubiquitin-protein ligase (UBC20) mRNA, complete cds
Contig\86	3.00E-62	ref|NM_100818.3| Arabidopsis thaliana unknown protein (AT1G09470) mRNA, complete cds
1058-94-(6-2-06)_H07	2.00E-76	ref|NM_101208.2| Arabidopsis thaliana unknown protein (AT1G13380) mRNA, complete cds
1032-94-(6-2-06)_G04	7.00E-26	ref|NM_101446.2| Arabidopsis thaliana unknown protein (AT1G15780) mRNA, complete cds
0549-94-(6-12-06)_F10	2.00E-122	ref|NM_103483.2| Arabidopsis thaliana unknown protein (AT1G43580) mRNA, complete cds
1096-94-(6-2-06)_F12	3.00E-94	ref|NM_105176.2| Arabidopsis thaliana unknown protein (AT1G65020) mRNA, complete cds
0180-94-E04(5-10-06)	6.00E-43	ref|NM_105780.3| Arabidopsis thaliana unknown protein (AT1G71110) mRNA, complete cds
0777-94-(6-7-06)_B10	7.00E-39	ref|NM_129147.3| Arabidopsis thaliana unknown protein (AT2G35880) mRNA, complete cds
Contig\169	5.00E-22	ref|NM_129190.2| Arabidopsis thaliana unknown protein (AT2G36330) mRNA, complete cds
0895-94-(6-5-06)_G12	9.00E-38	ref|NM_129617.4| Arabidopsis thaliana unknown protein (AT2G40550) mRNA, complete cds

Contig\104	3.00E -76	ref|NM_130051.2| Arabidopsis thaliana unknown protein (AT2G44870) mRNA, complete cds
0164-94-D07(5-5-06)	5.00E -63	ref|NM_111275.3| Arabidopsis thaliana unknown protein (AT3G04040) mRNA, complete cds
Contig\198	1.00E -87	ref|NM_111589.4| Arabidopsis thaliana unknown protein (AT3G07090) mRNA, complete cds
0534-94-(6-8-06)_B05	4.00E -118	ref|NM_111856.2| Arabidopsis thaliana unknown protein (AT3G10210) mRNA, complete cds
0658-94-(6-6-06)_B08	8.00E -70	ref|NM_180669.2| Arabidopsis thaliana unknown protein (AT3G11560) mRNA, complete cds
Contig\63	2.00E -70	ref|NM_112699.2| Arabidopsis thaliana unknown protein (AT3G18165) mRNA, complete cds
Contig\52	6.00E -122	ref|NM_115270.4| Arabidopsis thaliana unknown protein (AT3G54100) mRNA, complete cds
Contig\117	6.00E -34	ref|NM_115417.3| Arabidopsis thaliana unknown protein (AT3G55600) mRNA, complete cds
0179-94-D04(5-10-06)	1.00E -51	ref|NM_115541.2| Arabidopsis thaliana unknown protein (AT3G56820) mRNA, complete cds
0683-94-(6-6-06)_C11	2.00E -58	ref|NM_116580.3| Arabidopsis thaliana unknown protein (AT4G03420) mRNA, complete cds
0306-94(5-31-06)_006	9.00E -66	ref|NM_117051.2| Arabidopsis thaliana unknown protein (AT4G09830) mRNA, complete cds
0710-94-(6-7-06)_B02	2.00E -140	ref|NM_117530.2| Arabidopsis thaliana unknown protein (AT4G14500) mRNA, complete cds
0708-94-(6-7-06)_H01	2.00E -110	ref|NM_118617.3| Arabidopsis thaliana unknown protein (AT4G24840) mRNA, complete cds
0687-94-(6-6-06)_G11	2.00E -71	ref|NM_118774.3| Arabidopsis thaliana unknown protein (AT4G26410) mRNA, complete cds
0884-94-(6-5-06)_D11	0	ref|NM_118911.3| Arabidopsis thaliana unknown protein (AT4G27720) mRNA, complete cds
0250-94(5-31-06)_009	8.00E -130	ref|NM_119739.3| Arabidopsis thaliana unknown protein (AT4G35730) mRNA, complete cds
0778-94-(6-7-06)_C10	0	ref|NM_121443.4| Arabidopsis thaliana unknown protein (AT5G14390) mRNA, complete cds
1073-94-(6-2-06)_G09	2.00E -90	ref|NM_122380.4| Arabidopsis thaliana unknown protein (AT5G24710) mRNA, complete cds
0507-94-(6-8-06)_G01	4.00E -118	gb|AY128810.1| Arabidopsis thaliana unknown protein (At5g27970) mRNA, complete cds
0531-94-(6-8-06)_G04	3.00E -87	ref|NM_123621.2| Arabidopsis thaliana unknown protein (AT5G42570) mRNA, complete cds
0916-94-(6-14-06)_C12	2.00E -07	ref|NM_123838.4| Arabidopsis thaliana unknown protein (AT5G44710) mRNA, complete cds
0260-94(5-31-06)_014	2.00E -87	ref|NM_124361.4| Arabidopsis thaliana unknown protein (AT5G49830) mRNA, complete cds
0773-94-(6-7-06)_G09	7.00E -83	ref|NM_124462.3| Arabidopsis thaliana unknown protein (AT5G50840) mRNA, complete cds
0738-94-(6-7-06)_F05	5.00E -104	ref|NM_125694.3| Arabidopsis thaliana unknown protein (AT5G63000) mRNA, complete cds
0107-94-(6-12-06)_A04	4.00E -133	ref|NM_123480.3| Arabidopsis thaliana UVH1 (ULTRAVIOLET HYPERSENSITIVE 1) (UVH1) mRNA, complete cds
1125-94-(6-9-06)_A10	8.00E -127	ref|NM_102430.3| Arabidopsis thaliana VTI12 (VESICAL TRANSPORT V-SNARE 12, vesical transport v-SNARE 12); SNARE binding / receptor (VTI12) mRNA, complete cds
0223-94-H09(5-10-06)	6.00E -112	ref|NM_122467.3| Arabidopsis thaliana zinc finger (C3HC4-type RING finger) family protein (AT5G25560) mRNA, complete cds

0780-94-(6-7-06)_E10	2.00E-152	gb|DQ887086.1| Arachis hypogaea ubiquitin-conjugating enzyme mRNA, complete cds
1305-94-(6-16-06)_G06	8.00E-127	gb|AF203882.1|AF203882 Astragalus sinicus dynamin homolog (DH1) mRNA, complete cds
0143-94(5-31-06)_013	0	gb|DQ235254.1| Betula pendula xyloglucan endotransglucosylase mRNA, complete cds
Contig\12	0	gb|AY860952.1| Betula platyphylla caffeoyl CoA 3-O-methyltransferase mRNA, complete cds
Contig\168	4.00E-29	gb|DQ226583.1| Boechera divaricarpa isolate SLW-2-F07 mRNA sequence
0378-94-(6-12-06)_E09	0	dbj|D63166.1| Brassica napus mRNA for CTP:phosphocholine cytidylyltransferase, complete cds
Contig\59	2.00E-72	gb|EF110927.1| Brassica rapa clone 321 unknown mRNA
0920-94-(6-14-06)_G12	7.00E-58	gb|AC189305.1| Brassica rapa subsp. pekinensis clone KBrB031O20, complete sequence
0436-94-(6-16-06)_D02	5.00E-22	gb|AC189362.1| Brassica rapa subsp. pekinensis clone KBrB045I17, complete sequence
1188-94-(6-15-06)_C07	1.00E-162	gb|AC189500.1| Brassica rapa subsp. pekinensis clone KBrB086N06, complete sequence
0192-94-A06(5-10-06)	0	dbj|AB043960.2| Bruguiera gymnorhiza psbO mRNA for oxygen evolving enhancer protein 1 precursor, complete cds
0128-94(5-31-06)_009	9.00E-85	dbj|AB037929.2| Bruguiera sexangula mang-1 mRNA for mangrin, complete cds
1089-94-(6-2-06)_G11	0	gb|DQ869862.1| Camellia sinensis 26S proteasome regulatory particle non-ATPase subunit 12 mRNA, complete cds
0938-94-(6-15-06)_A03	2.00E-08	gb|AC188639.6| Canis Familiaris chromosome 10, clone XX-332P23, complete sequence
0394-94-(6-8-06)_C12	0	gb|AF108891.1|AF108891 Capsicum annuum ADP-ribosylation factor mRNA, complete cds
Contig\74	4.00E-124	gb|DQ672569.1| Capsicum annuum CCR4 associated factor 1-related protein (CAF1) mRNA, complete cds
0815-94-(6-14-06)_E05	0	gb|EF512303.1| Carica papaya clone Cp45 hypersensitive-induced response protein mRNA, complete cds
0313-94-(6-9-06)_B01	1.00E-165	emb|AJ010227.1|CAR010227 Cicer arietinum mRNA for 40S ribosomal protein S6, partial
0657-94-(6-6-06)_A08	8.00E-127	emb|AJ004961.1|CAA004961 Cicer arietinum mRNA for cytoplasmic ribosomal protein L18
Contig\172	3.00E-176	emb|AJ005836.1|CAR5836 Cicer arietinum mRNA for GDP dissociation inhibitor (gdi)
Contig\156	7.00E-20	emb|AJ012681.1|CAR012681 Cicer arietinum mRNA for hypothetical protein, clone Can137
0387-94-(6-12-06)_D10	4.00E-150	emb|AJ012686.1|CAR012686 Cicer arietinum mRNA for nucleolar protein, partial
Contig\128	0	emb|AJ299063.1|CAR299063 Cicer arietinum partial mRNA for putative mitochondrial glyoxalase II (ORF1), clone CanGLXII
0010-94_005(5-31-06)	3.00E-116	dbj|AB212224.1| Citrullus lanatus GAT mRNA for glutamate N-acetyltransferase, complete cds
0010-93-G12(4-21-06)	1.00E-19	dbj|AB212224.1| Citrullus lanatus GAT mRNA for glutamate N-acetyltransferase, complete cds
Contig\201	0	gb|AY428798.1| Citrus junos dicarboxylate/tricarboxylate carrier (dtc) mRNA, complete cds; mitochondrial
0449-94-(6-27-06)_G06	0	emb|AJ001304.1|CPHYPOTHE Citrus paradisi mRNA for hypothetical protein

Contig\139	0	emb|Z97064.1|CPDUNCAN Citrus paradisi mRNA for hypothetical protein
0513-94-(6-8-06)_E02	0	gb|DQ083540.1| Citrus sinensis pyruvate decarboxylase mRNA, partial cds
0855-94-(6-5-06)_G07	0	dbj|AB022091.1| Citrus unshiu CitSUSA mRNA for sucrose synthase, complete cds
0660-94-(6-6-06)_D08	0	gb|AY561840.1| Citrus unshiu fructokinase mRNA, complete cds
Contig\98	9.00E-38	gb|DQ415921.1| Cleome spinosa clone BAC Cs2, complete sequence
0091-94-B09(4-28-06)	6.00E-144	gb|DQ845760.1| Cloning vector pExpress-1, complete sequence
Contig\6	0	emb|X65304.3|CVPGEM3Z Cloning vector pGEM-3Z
Contig\49	0	dbj|AB243086.1| Codonopsis lanceolata mRNA for sulfite oxidase, complete cds
0709-94-(6-7-06)_A02	0	emb|AJ295617.1|CAV295617 Corylus avellana mRNA for putative luminal binding protein
1152-94-(6-15-06)_D04	0	emb|AJ417435.1|CSA417435 Cucumis sativus partial mRNA for phosphoenolpyruvate carboxylase (pepc1 gene)
1039-94-(6-2-06)_F05	0	dbj|AB070626.1| Cucurbita sp. cv. Kurokawa Amakuri pAPX mRNA for peroxisomal ascorbate peroxidase, complete cds
0793-94-(6-14-06)_C05	0	gb|DQ650638.1| Dimocarpus longan peroxidase (POD1) mRNA, complete cds
Contig\19	0	gb|EF445894.1| Escherichia coli isolate E81 disrupted tna operon, complete sequence; and insertion sequence IS1, complete sequence
0607-94-(6-6-06)_G01	3.00E-107	gb|DQ376138.1| Eucalyptus globulus subsp. globulus pectate lyase (PL1) mRNA, partial cds
0714-94-(6-7-06)_F02	9.00E-82	emb|AM231807.1| Fagus sylvatica mRNA for GASA protein (gasa4 gene), from seed tissue
Contig\114	0	emb|AJ420192.1|FSY420192 Fagus sylvatica mRNA for gibberellin 20-oxidase 1 (ga20ox1 gene)
Contig\61	7.00E-172	emb|AJ130885.1|FSY130885 Fagus sylvatica mRNA for xyloglucan endotransglycosylase 1
Contig\157	0	emb|AJ130885.1|FSY130885 Fagus sylvatica mRNA for xyloglucan endotransglycosylase 1
Contig\109	0	emb|AJ298828.1|FSY298828 Fagus sylvatica partial mRNA for protein phosphatase (pp1-1 gene)
1174-94-(6-15-06)_D06	0	gb|DQ166522.1| Fagus sylvatica putative 3-dehydroquinate synthase mRNA, complete cds
0755-94-(6-7-06)_G07	0	gb|DQ166527.1| Fagus sylvatica putative chorismate mutase mRNA, complete cds
0842-94-(6-5-06)_B06	0	emb|AJ001451.2|FVAJ1451 Fragaria vesca partial mRNA for putative cystathionine gamma synthase
Contig\175	4.00E-30	emb|AJ001448.1|FVAJ1448 Fragaria vesca partial mRNA for ripening-induced protein, clone 2.5.R1
0626-94-(6-6-06)_B04	5.00E-155	gb|EU024845.1| Fragaria vesca subsp. americana clone fosmid 32L07, complete sequence
0365-94-(6-12-06)_B08	3.00E-25	emb|AJ870451.1| Fragaria x ananassa microsatellite DNA, locus UFFa10D08
Contig\171	5.00E-117	emb|Z46955.1|GMHSF31 G.max mRNA for heat shock transcription factor 31
0919-94-(6-14-06)_F12	1.00E-169	gb|U92876.1|GMU92876 Garcinia mangsotana acyl-ACP thioesterase (FatA1) mRNA, nuclear gene encoding chloroplast protein, complete cds
0369-94-(6-12-06)_F08	1.00E-85	gb|AF205859.1|AF205859 Gentiana lutea FtsZ protein (ftsZ) mRNA, complete cds; nuclear gene for chloroplast product

0833-94-(6-5-06)_A05	1.00E-104	gb|EF640322.1| Glycine max acyl-CoA oxidase mRNA, complete cds
Contig\143	0	gb|L22162.1|SOYMER5HOM Glycine max brassinosteroid-regulated protein mRNA, complete cds
1036-94-(6-2-06)_C05	1.00E-93	gb|DQ787076.1| Glycine max bZIP transcription factor bZIP43 (bZIP43) mRNA, partial cds
1105-94-(6-9-06)_E07	4.00E-93	gb|AC159804.18| Glycine max clone gmp1-34b24, complete sequence
0042-93-G08(4-21-06)	4.00E-19	gb|AC198447.7| Glycine max clone gmw2-48a19, complete sequence
0611-94-(6-6-06)_C02	0	gb|EF433423.1| Glycine max cysteine synthase (OAS-TL7) mRNA, complete cds
Contig\166	0	gb|AF475939.1| Glycine max elongation factor 1-gamma mRNA, complete cds
1139-94-(6-9-06)_G11	0	gb|EF521872.1| Glycine max endonuclease (EN1) mRNA, complete cds
Contig\192	0	gb|AF516880.1| Glycine max expansin (EXP2) mRNA, complete cds
1002-94-(6-2-06)_B01	8.00E-146	gb|AY126715.1| Glycine max galactinol synthase mRNA, complete cds
Contig\81	0	dbj|AB196933.1| Glycine max Gm cnx-1 mRNA for calnexin, complete cds
0750-94-(6-7-06)_B07	7.00E-109	gb|AY458843.1| Glycine max heat shock factor protein hsf8-related mRNA, complete cds
0861-94-(6-5-06)_E08	1.00E-118	gb|AF249913.1|AF249913 Glycine max In2-1 protein mRNA, complete cds
0361-94-(6-12-06)_F07	0	gb|AY230156.1| Glycine max leaf ubiquitous urease mRNA, complete cds
Contig\197	2.00E-165	emb|AJ871580.1| Glycine max mRNA for beta-amylase (bmy1 gene)
0943-94-(6-16-06)_F12	0	dbj|AB016063.1| Glycine max mRNA for mitochondrial phosphate transporter, complete cds
0215-94(5-31-06)_012	0	emb|AM238658.1| Glycine max mRNA for putative beta-glycosidase (sfr2 gene), from leaf tissue
0359-94-(6-12-06)_D07	1.00E-136	emb|AJ518837.1|GMA518837 Glycine max mRNA for putative phosphatase (nod33 gene)
0696-94-(6-6-06)_H12	8.00E-70	dbj|AB083028.1| Glycine max mRNA for syringolide-induced protein 1-3-1B, complete cds
0587-94-(6-8-06)_B10	0	gb|AF160197.1|AF160197 Glycine max Ni-binding urease accessory protein UreG (Eu3) mRNA, complete cds
Contig\9	2.00E-115	gb|DQ224372.1| Glycine max ornithine aminotransferase mRNA, complete cds
0523-94-(6-8-06)_G03	6.00E-147	gb|U51193.1|GMU51193 Glycine max peroxidase (sEPb1) mRNA, partial cds
0323-94-(6-9-06)_C02	0	gb|AY942816.1| Glycine max putative plastid glucose 6 phosphate/phosphate translocator mRNA, complete cds; nuclear gene for plastid product
Contig\48	2.00E-153	gb|AF532622.1| Glycine max ubiquitin-conjugation enzyme gene, complete cds
1163-94-(6-15-06)_C05	0	gb|U53418.1|GMU53418 Glycine max UDP-glucose dehydrogenase mRNA, complete cds
0017-94_004(5-31-06)	3.00E-122	gb|EU019586.1| Glycine max WRKY50 (WRKY50) mRNA, partial cds
Contig\203	2.00E-103	gb|AY429438.1| Gossypium barbadense fiber protein Fb34 mRNA, complete cds
Contig\205	5.00E-104	gb|AY337616.1| Gossypium barbadense Gbiaa-Re (iaa-re) mRNA, complete cds

0332-94-(6-9-06)_A03	0	gb|U73746.2|GHU73746 Gossypium hirsutum annexin (AnnGh1) mRNA, partial cds
0300-94(5-31-06)_013	6.00E-93	gb|AY283056.1| Gossypium hirsutum central motor kinesin 1 (CMK1) mRNA, complete cds
Contig\152	0	gb|EF432568.1| Gossypium hirsutum kinesin-related protein (kch2) mRNA, complete cds
0858-94-(6-5-06)_B08	0	gb|DQ004685.1| Hevea brasiliensis 12-oxophytodienoate reductase (opr) mRNA, complete cds
1169-94-(6-15-06)_G05	0	gb|AF521007.1| Hevea brasiliensis heat shock protein mRNA, complete cds
Contig\83	0	gb|AY297039.1| Hevea brasiliensis latex cyanogenic beta glucosidase mRNA, complete cds
0016-93-A12(4-21-06)	2.00E-11	dbj|AK000414.1| Homo sapiens cDNA FLJ20407 fis, clone KAT01658
1147-94-(6-9-06Truncated)_G12	6.00E-27	dbj|AK123523.1| Homo sapiens cDNA FLJ41529 fis, clone BRTHA2014792, weakly similar to ENHANCER OF ZESTE
0806-94-(6-5-06)_F01	0	ref|NM_016656.2| Homo sapiens Ras-related GTP binding B (RRAGB), transcript variant RAGBl, mRNA
0792-94-(6-7-06)_H11	4.00E-92	dbj|AK248503.1| Hordeum vulgare subsp. vulgare cDNA clone: FLbaf31a24, mRNA sequence
1004-94(6-2-06Truncated)_D01	2.00E-84	dbj|AB290349.1| Humulus lupulus DFR mRNA for dihydroflavonol 4-reductase, complete cds
0130-94-B03(5-9-06)	4.00E-178	gb|AF302496.1| Hybrid poplar (Populus trichocarpa x P. deltoides) NADPH-cytochrome P450 oxydoreductase isoform 1 mRNA, complete cds
0917-94-(6-14-06)_D12	3.00E-132	dbj|AB125890.1| Ipomoea batatas SRF6 mRNA for leucine-rich repeat receptor-like kinase, complete cds
0654-94-(6-6-06)_F07	4.00E-143	gb|EU106891.1| Jatropha curcas chloroplast acyl-ACP thioesterase mRNA, complete cds; nuclear gene for chloroplast product
0568-94-(6-8-06)_C08	0	gb|DQ026508.1| Juglans regia hexose transporter 1 mRNA, complete cds
0437-94-(6-16-06)_E02	0	emb|Z34527.1|LESSRPSPR L.esculentum (UC82-B) mRNA for 54-kD signal recognition particle (SRP) specific protein
Contig\190	4.00E-162	emb|X80840.1|LEGDL L.esculentum mRNA for glutamate decarboxylase-like protein
0911-94-(6-14-06)_F11	0	emb|Z73932.1|LJRAB1C L.japonicus mRNA for small GTP-binding protein, RAB1C
Contig\173	0	emb|Z73962.1|LJRAC2 L.japonicus mRNA for small GTP-binding protein, RAC2
0648-94(6-6-06)_H06	0	gb|DQ139264.1| Lotus corniculatus var. japonicus pyridoxine biosynthesis protein mRNA, complete cds
Contig\188	4.00E-125	dbj|AP004956.1| Lotus japonicus genomic DNA, chromosome 1, clone:LjT34I04, TM0133, complete sequence
1104-94-(6-9-06)_D07	3.00E-63	dbj|AP004965.1| Lotus japonicus genomic DNA, chromosome 1, clone:LjT20J05, TM0143b, complete sequence
1054-94-(6-2-06)_E07	4.00E-92	dbj|AP004968.1| Lotus japonicus genomic DNA, chromosome 1, clone:LjT43O24, TM0145, complete sequence
0748-94-(6-7-06)_H06	6.00E-116	dbj|AP006427.1| Lotus japonicus genomic DNA, chromosome 1, clone:LjT45A23, TM0318, complete sequence
0226-94-C10(5-10-06)	4.00E-45	dbj|AP009073.1| Lotus japonicus genomic DNA, chromosome 1, clone:LjT43J08, TM1255, complete sequence
0124-94-D02(5-9-06)	3.00E-14	dbj|AP004941.1| Lotus japonicus genomic DNA, chromosome 1, clone:LjT25N10, TM0109, complete sequence

Contig\75	2.00E-148	dbj|AP004579.1| Lotus japonicus genomic DNA, chromosome 2, clone:LjT11E23, TM0557
1050-94-(6-2-06)_A07	2.00E-121	dbj|AP006864.1| Lotus japonicus genomic DNA, chromosome 3, clone:LjT18I21, TM1144, complete sequence
0849-94-(6-5-06)_A07	1.00E-09	dbj|AP004505.1| Lotus japonicus genomic DNA, chromosome 3, clone:LjT10E18, TM0035, complete sequence
0628-94-(6-6-06)_D04	1.00E-36	dbj|AP004977.1| Lotus japonicus genomic DNA, chromosome 3, clone:LjT12A10, TM0160, complete sequence
Contig\41	4.00E-144	dbj|AP004512.1| Lotus japonicus genomic DNA, chromosome 4, clone:LjT10L16, TM0042, complete sequence
1182-94-(6-15-06)_H06	2.00E-95	dbj|AP004536.1| Lotus japonicus genomic DNA, chromosome 4, clone:LjT15N19, TM0097b, complete sequence
0671-94-(6-6-06)_G09	2.00E-172	dbj|AP004911.1| Lotus japonicus genomic DNA, chromosome 4, clone:LjT13O11, TM0069, complete sequence
0211-94-D08(5-10-06)	9.00E-91	dbj|AP006382.1| Lotus japonicus genomic DNA, chromosome 4, clone:LjT32J05, TM0238, complete sequence
Contig\142	2.00E-72	dbj|AP006127.1| Lotus japonicus genomic DNA, chromosome 5, clone:LjT48O21, TM0211, complete sequence
Contig\26	8.00E-51	dbj|AP006731.1| Lotus japonicus genomic DNA, chromosome 6, clone:LjT45B09, TM0885c, complete sequence
1180-94-(6-15-06)_G06	4.00E-55	dbj|AP006412.1| Lotus japonicus genomic DNA, chromosome 6, clone:LjT29C05, TM0301c, complete sequence
0598-94-(6-8-06)_E11	1.00E-99	dbj|AP004960.1| Lotus japonicus genomic DNA, chromosome 6, clone:LjT19B18, TM0139, complete sequence
0427-94-(6-16-06)_C01	0	dbj|AB167408.1| Lotus japonicus LjM3Kalpha mRNA for mitogen-activated kinase kinase kinase alpha, complete cds
0099-94-B10(4-28-06)	6.00E-163	gb|EF640319.1| Lupinus albus GDP-dissociation inhibitor mRNA, complete cds
Contig\129	0	emb|AJ344108.1|LAL344108 Lupinus albus mRNA for ATP citrate lyase b-subunit (aclb gene)
0860-94-(6-5-06)_D08	7.00E-178	emb|AJ421012.3|LLU421012 Lupinus luteus mRNA for putative metallophosphatase (ppd4 gene)
0307-94-(6-12-06)_F05	3.00E-96	gb|U19099.1|LCU19099 Lycopersicon chilense unknown protein (LC15) mRNA, complete cds
1142-94-(6-9-06)_B12	0	gb|AY656837.1| Lycopersicon esculentum arginase 1 (ARG1) mRNA, complete cds
Contig\146	9.00E-139	gb|AF233745.1|AF233745 Lycopersicon esculentum chaperonin 21 precursor, mRNA, complete cds; nuclear gene for chloroplast product
0159-94(5-31-06)_004	0	gb|BT012805.1| Lycopersicon esculentum clone 113821R, mRNA sequence
0032-93-A10(4-21-06)	8.00E-111	gb|BT012808.1| Lycopersicon esculentum clone 113828F, mRNA sequence
0533-94-(6-8-06)_A05	4.00E-124	gb|BT012822.1| Lycopersicon esculentum clone 113871F, mRNA sequence
0814-94-(6-5-06)_F02	0	gb|BT012845.1| Lycopersicon esculentum clone 113921R, mRNA sequence
0515-94-(6-8-06)_G02	0	gb|BT012881.1| Lycopersicon esculentum clone 113982F, mRNA sequence
0429-94-(6-27-06)_B06	0	gb|BT012988.1| Lycopersicon esculentum clone 114208R, mRNA sequence
0570-94-(6-8-06)_E08	4.00E-149	gb|BT012992.1| Lycopersicon esculentum clone 114212R, mRNA sequence
0445-94-(6-16-06)_D03	6.00E-147	gb|BT013010.1| Lycopersicon esculentum clone 114247F, mRNA sequence

0605-94-(6-6-06)_E01	8.00E-146	gb|BT013017.1| Lycopersicon esculentum clone 114255R, mRNA sequence
0547-94-(6-8-06)_G06	3.00E-164	gb|BT013054.1| Lycopersicon esculentum clone 114310R, mRNA sequence
0921-94-(6-14-06)_H12	2.00E-103	gb|BT013092.1| Lycopersicon esculentum clone 114358R, mRNA sequence
0898-94-(6-14-06)_H07	2.00E-166	gb|BT013422.1| Lycopersicon esculentum clone 132061R, mRNA sequence
0235-94-D11(5-10-06)	2.00E-22	gb|BT013475.1| Lycopersicon esculentum clone 132142R, mRNA sequence
0319-94-(6-9-06)_G01	0	gb|BT013490.1| Lycopersicon esculentum clone 132174R, mRNA sequence
0888-94-(6-5-06)_H11	0	gb|BT013497.1| Lycopersicon esculentum clone 132183F, mRNA sequence
0811-94-(6-5-06)_C02	8.00E-108	gb|BT013508.1| Lycopersicon esculentum clone 132199F, mRNA sequence
006-94-E05(4-28-06)	3.00E-180	gb|BT013569.1| Lycopersicon esculentum clone 132307R, mRNA sequence
0872-94-(6-5-06)_H09	7.00E-83	gb|BT013653.1| Lycopersicon esculentum clone 132472F, mRNA sequence
0247-94(5-31-06)_003	0	gb|BT013673.1| Lycopersicon esculentum clone 132492F, mRNA sequence
0259-94(5-31-06)_012	2.00E-168	gb|BT013729.1| Lycopersicon esculentum clone 132589F, mRNA sequence
0661-94-(6-6-06)_E08	1.00E-143	gb|BT013770.1| Lycopersicon esculentum clone 132655R, mRNA sequence
0390-94-(6-8-06)_G11	3.00E-163	gb|BT013787.1| Lycopersicon esculentum clone 132681F, mRNA sequence
1081-94-(6-2-06)_G10	0	gb|BT013793.1| Lycopersicon esculentum clone 132713F, mRNA sequence
0640-94-(6-6-06)_H05	7.00E-83	gb|BT013820.1| Lycopersicon esculentum clone 132742F, mRNA sequence
0918-94-(6-14-06)_E12	0	gb|BT013889.1| Lycopersicon esculentum clone 132874R, mRNA sequence
0902-94-(6-14-06)_E10	1.00E-28	gb|BT013931.1| Lycopersicon esculentum clone 132929R, mRNA sequence
0255-94(5-31-06)_004	2.00E-118	gb|BT013943.1| Lycopersicon esculentum clone 132966F, mRNA sequence
1031-94-(6-2-06)_F04	2.00E-165	gb|BT013978.1| Lycopersicon esculentum clone 133023F, mRNA sequence
0698-94-(6-12-06)_G12	0	gb|BT014017.1| Lycopersicon esculentum clone 133079F, mRNA sequence
0450-94-(6-16-06)_H03	1.00E-130	gb|BT014025.1| Lycopersicon esculentum clone 133087R, mRNA sequence
1179-94-(6-15-06)_F06	5.00E-136	gb|BT014125.1| Lycopersicon esculentum clone 133233F, mRNA sequence
0727-94-(6-7-06)_C04	0	gb|BT014132.1| Lycopersicon esculentum clone 133248R, mRNA sequence
0797-94-(6-7-06)_E12	0	gb|BT014209.1| Lycopersicon esculentum clone 133386F, mRNA sequence
0857-94-(6-5-06)_A08	4.00E-111	gb|BT014286.1| Lycopersicon esculentum clone 133525F, mRNA sequence
0123-94-C02(5-9-06)	6.00E-112	gb|BT014350.1| Lycopersicon esculentum clone 133626F, mRNA sequence

0736-94-(6-7-06)_D05	3.00E-107	gb|BT014372.1| Lycopersicon esculentum clone 133660F, mRNA sequence
1307-94-(6-16-06)_A07	2.00E-95	gb|BT014397.1| Lycopersicon esculentum clone 133702F, mRNA sequence
0451-94-(6-16-06)_A04	2.00E-89	gb|BT014430.1| Lycopersicon esculentum clone 133748R, mRNA sequence
1148-94-(6-9-06)_H12	6.00E-27	gb|BT014542.1| Lycopersicon esculentum clone 133957R, mRNA sequence
0373-94-(6-12-06)_A09	4.00E-175	gb|BT013152.1| Lycopersicon esculentum clone 134156F, mRNA sequence
0759-94-(6-7-06)_C08	8.00E-152	gb|BT013369.1| Lycopersicon esculentum clone 135389F, mRNA sequence
0312-94-(6-9-06)_A01	6.00E-157	gb|BT013399.1| Lycopersicon esculentum clone 135708R, mRNA sequence
0926-94-(6-16-06)_D11	0	gb|AY240231.1| Lycopersicon esculentum gamma-aminobutyrate transaminase subunit precursor isozyme 3 mRNA, complete cds
Contig\25	0	gb|AY368907.1| Lycopersicon esculentum molecular chaperone Hsp90-2 mRNA, complete cds
Contig\18	4.00E-80	emb|X90695.1|MSRNAPE02 M.sativa mRNA for peroxidase 2
Contig\4	1.00E-11	emb|CT963076.3| M.truncatula DNA sequence from clone MTH2-22P7 on chromosome 3, complete sequence
0462-94-(6-16-06)_D05	5.00E-60	emb|CU457801.7| M.truncatula DNA sequence from clone MTH2-38N16 on chromosome 3, complete sequence
Contig\130	2.00E-47	emb|CU062624.10| M.truncatula DNA sequence from clone MTH2-77J21 on chromosome 3, complete sequence
Contig\103	5.00E-174	emb|CT961058.16| M.truncatula DNA sequence from clone MTH2-80N17 on chromosome 3, complete sequence
0766-94-(6-7-06)_A09	0	gb|AF039709.1|AF039709 Maackia amurensis 14-3-3 protein homolog mRNA, complete cds
1008-94-(6-2-06)_H01	3.00E-176	gb|AF153828.1|AF153828 Malus domestica alpha-amylase mRNA, complete cds
Contig\7	0	gb|U80269.1|MDU80269 Malus domestica translation initiation factor 2 beta (eIF-2beta) mRNA, partial cds
0026-94-(6-12-06)_A01	8.00E-98	gb|DQ279909.1| Malus pumila CXE carboxylesterase (CXE8) mRNA, complete cds
Contig\150	0	gb|DQ221207.1| Malus x domestica cytosolic malate dehydrogenase mRNA, complete cds
0672-94-(6-6-06)_H09	0	gb|AY787586.1| Malus x domestica L-galactose-1-phosphate phosphatase mRNA, complete cds
1107-94-(6-9-06)_G07	5.00E-72	gb|DQ074461.1| Malus x domestica MYB6 mRNA, complete cds
0825-94-(6-5-06)_A04	0	gb|DQ184951.1| Malus x domestica putative receptor kinase (DIPM4) mRNA, complete cds
Contig\91	2.00E-104	emb|AM040280.1| Mangifera indica partial mRNA for beta-galactosidase (pman11 gene)
Contig\176	5.00E-111	gb|DQ122779.1| Medicago sativa clone C4 unknown mRNA
1052-94-(6-2-06)_C07	3.00E-138	gb|DQ122777.1| Medicago sativa clone RF4 histidyl-tRNA synthetase mRNA, partial cds
Contig\135	6.00E-167	gb|AF020272.1|AF020272 Medicago sativa cytosolic malate dehydrogenase (cmdh) mRNA, complete cds
0630-94-(6-6-06)_F04	1.00E-66	emb|Y16672.1|MSY16672 Medicago sativa mRNA for putative arginine/serine-rich splicing factor, (sclp gene)

0745-94-(6-7-06)_E06	4.00E-168	gb|AY247272.1| Medicago truncatula AKIN beta2 mRNA, complete cds
0071_F06(For 4-28-06)	5.00E-50	gb|AC169124.2| Medicago truncatula chromosome 2 BAC clone mte1-34m3, complete sequence
0309-94(5-31-06)_012	1.00E-76	gb|AC186295.3| Medicago truncatula chromosome 2 BAC clone mth2-26g6, complete sequence
Contig\77	1.00E-05	emb|CT025844.1| Medicago truncatula chromosome 5 clone mte1-41h18, COMPLETE SEQUENCE
1130-94-(6-9-06)_F10	2.00E-110	emb|CT963115.2| Medicago truncatula chromosome 5 clone mte1-43g8, COMPLETE SEQUENCE
Contig\46	3.00E-31	emb|CR954197.2| Medicago truncatula chromosome 5 clone mte1-80m7, COMPLETE SEQUENCE
0914-94-(6-14-06)_A12	2.00E-38	emb|CR931728.1| Medicago truncatula chromosome 5 clone mth2-175g3, COMPLETE SEQUENCE
0382-94-(6-12-06)_A10	5.00E-22	emb|CU302329.1| Medicago truncatula chromosome 5 clone mth2-171p15, COMPLETE SEQUENCE
0779-94-(6-7-06)_D10	9.00E-63	emb|CT573508.2| Medicago truncatula chromosome 5 clone mth2-29p15, COMPLETE SEQUENCE
0562-94-(6-8-06)_H07	2.00E-19	emb|CU302347.1| Medicago truncatula chromosome 5 clone mth2-5p5, COMPLETE SEQUENCE
Contig\67	5.00E-60	emb|CR936324.2| Medicago truncatula chromosome 5 clone mth2-62a22, COMPLETE SEQUENCE
1079-94-(6-2-06)_E10	4.00E-93	emb|CR962131.2| Medicago truncatula chromosome 5 clone mth2-69b10, COMPLETE SEQUENCE
Contig\123	2.00E-72	emb|CU179920.2| Medicago truncatula chromosome 5 clone mth4-25c2, COMPLETE SEQUENCE
1160-94-(6-15-06)_B05	7.00E-71	gb|AC146307.24| Medicago truncatula chromosome 6 clone mth2-9p17, complete sequence
Contig\64	2.00E-07	gb|AC171533.3| Medicago truncatula chromosome 7 BAC clone mth2-82b20, complete sequence
Contig\189	2.00E-26	gb|AC144483.10| Medicago truncatula chromosome 8 clone mth2-12f13, complete sequence
1071-94-(6-2-06)_E09	2.00E-116	gb|AC146862.24| Medicago truncatula chromosome 8 clone mth2-174p12, complete sequence
0431-94-(6-16-06)_G01	3.00E-177	gb|EF128059.1| Medicago truncatula class II KNOX homeobox transcription factor (KNOX4) mRNA, complete cds
1088-94-(6-2-06)_F11	1.00E-180	gb|AC152920.17| Medicago truncatula clone mth2-101o15, complete sequence
Contig\144	2.00E-109	gb|AC152921.8| Medicago truncatula clone mth2-102h2, complete sequence
0006-94-C05(4-20-06)	9.00E-161	gb|AC148097.7| Medicago truncatula clone mth2-15a20, complete sequence
Contig\57	2.00E-46	gb|AC136974.11| Medicago truncatula clone mth2-22e9, complete sequence
0007for_D05'	7.00E-23	gb|AC144389.22| Medicago truncatula clone mth2-25e14, complete sequence
Contig\3	3.00E-62	gb|AC140035.9| Medicago truncatula clone mth2-25n18, complete sequence
0271-94(5-31-06)_004	2.00E-23	gb|AC137669.12| Medicago truncatula clone mth2-27m3, complete sequence
1060-94-(6-2-06)_B08	3.00E-87	gb|AC126012.22| Medicago truncatula clone mth2-27p4, complete sequence
1087-94-(6-2-06)_E11	2.00E-121	gb|AC128638.34| Medicago truncatula clone mth2-36h10, complete sequence

Contig\73	0	gb|AC148818.15| Medicago truncatula clone mth2-39c7, complete sequence
Contig\31	1.00E-68	gb|AC151426.32| Medicago truncatula clone mth2-6o22, complete sequence
1077-94-(6-2-06)_C10	2.00E-96	gb|AC126786.22| Medicago truncatula clone mth2-8c2, complete sequence
0644-94-(6-6-06)_D06	4.00E-35	gb|AC146567.10| Medicago truncatula clone mth2-99p24, complete sequence
0641-94-(6-6-06)_A06	0	emb|AJ430609.1|MTR430609 Medicago truncatula mRNA for squalene monooxygenase 1 (sqp1 gene)
0927-94-(6-15-06)_F01	6.00E-08	gb|AC192090.4| Mus musculus BAC clone RP23-408O7 from chromosome 3, complete sequence
0521-94-(6-8-06)_E03	2.00E-08	gb|AC127583.4| Mus musculus BAC clone RP24-121M11 from 13, complete sequence
Contig\121	4.00E-42	emb|AJ697696.1| Nicotiana benthamiana mRNA for ALY protein (ALY617 allele)
Contig\116	0	gb|DQ121388.1| Nicotiana benthamiana PHB2 mRNA, complete cds
1016-94-(6-2-06)_G02	0	emb|AJ272011.1|NPL272011 Nicotiana plumbaginifolia mRNA for oligouridylate binding protein (ubp1 gene)
1086-94-(6-2-06)_D11	1.00E-104	gb|DQ231577.1| Nicotiana sylvestris cryptochrome 2 (cry2) mRNA, complete cds
0679-94-(6-6-06)_G10	6.00E-135	gb|AY578143.2| Nicotiana tabacum 3-dehydroquinate dehydratase / shikimate dehydrogenase isoform 2 mRNA, complete cds
Contig\40	2.00E-153	gb|AY775048.1| Nicotiana tabacum Avr9/Cf-9 rapidly elicited protein 271 (ACRE271) mRNA, partial cds
0105-94-H10(4-28-06)	6.00E-157	gb|AF190657.1|AF190657 Nicotiana tabacum clone 7 poly(A)-binding protein (PABP) mRNA, partial cds
1035-94-(6-14-06)_G08	5.00E-117	gb|AF154645.1| Nicotiana tabacum clone PR26 mRNA sequence
0942-94-(6-15-06)_E03	6.00E-141	gb|AF191497.1|AF191497 Nicotiana tabacum DnaJ-like protein mRNA, complete cds
Contig\29	0	emb|AJ319873.1|NTA319873 Nicotiana tabacum mRNA for carbamoyl phosphate synthase small subunit
0217-94-(6-16-06)_B09	0	emb|AJ249883.1|NTA249883 Nicotiana tabacum mRNA for N-acetylglucosaminyltransferase I (GntI gene), clone A9
0556-94-(6-12-06)_H10	0	emb|AJ291738.1|NTA291738 Nicotiana tabacum mRNA for putative alpha7 proteasome subunit (a7 gene)
Contig\126	0	dbj|AB079020.1| Nicotiana tabacum mRNA for ras-related protein RAB8-1, complete cds
1005-94-(6-2-06)_E01	0	emb|AJ011576.1|NTA011576 Nicotiana tabacum mRNA for RNA-directed RNA polymerase
Contig\202	0	dbj|AB036735.1| Nicotiana tabacum NtADH mRNA for allyl alcohol dehydrogenase, complete cds
0079-93-B04(4-21-06)	4.00E-108	emb|AJ299251.1|NTA299251 Nicotiana tabacum partial mRNA for lysyl-tRNA synthetase (lysRS gene)
Contig\100	0	gb|AF190655.1|AF190655 Nicotiana tabacum poly(A)-binding protein (PABP) mRNA, complete cds
0065-94-H05(4-28-06)	0	gb|AY619952.1| Nicotiana tabacum putative UDP-glucuronate decarboxylase 3 mRNA, complete cds
0110-94-E11(4-28-06)	1.00E-134	gb|AF055910.2| Orobanche ramosa NADPH-dependent mannose 6-phosphate reductase (M6PR) mRNA, complete cds
Contig\72	6.00E-65	emb|CT829234.1| Oryza sativa (indica cultivar-group) cDNA clone:OSIGCEA047B09, full insert sequence
Contig\147	1.00E-156	emb|CT837671.1| Oryza sativa (indica cultivar-group) cDNA clone:OSIGCEA046L07, full insert sequence

0536-94-(6-8-06)_D05	6.00E-147	emb|CT830199.1| Oryza sativa (indica cultivar-group) cDNA clone:OSIGCRA126P24, full insert sequence
Contig\96	0	dbj|AK064791.1| Oryza sativa (japonica cultivar-group) cDNA clone:J013000C08, full insert sequence
Contig\70	3.00E-152	dbj|AK069870.1| Oryza sativa (japonica cultivar-group) cDNA clone:J023039C20, full insert sequence
Contig\39	3.00E-139	dbj|AK100610.1| Oryza sativa (japonica cultivar-group) cDNA clone:J023107L11, full insert sequence
Contig\162	8.00E-32	dbj|AK067094.1| Oryza sativa (japonica cultivar-group) cDNA clone:J013098P05, full insert sequence
1141-94-(6-9-06)_A12	2.00E-147	ref|NM_001049454.1| Oryza sativa (japonica cultivar-group) Os01g0328900 (Os01g0328900) mRNA, complete cds
1127-94-(6-9-06Truncated)_C10	2.00E-07	ref|NM_001073481.1| Oryza sativa (japonica cultivar-group) Os12g0540700 (Os12g0540700) mRNA, complete cds
1118-94-(6-9-06)_B09	9.00E-101	ref|NM_001049151.1| Oryza sativa (japonica cultivar-group) Os01g0254100 (Os01g0254100) mRNA, complete cds
0744-94-(6-7-06)_D06	1.00E-136	ref|NM_001053454.1| Oryza sativa (japonica cultivar-group) Os02g0506500 (Os02g0506500) mRNA, complete cds
0663-94-(6-6-06)_G08	2.00E-72	ref|NM_001063520.1| Oryza sativa (japonica cultivar-group) Os06g0182500 (Os06g0182500) mRNA, complete cds
0599-94-(6-8-06)_F11	5.00E-117	ref|NM_001055284.1| Oryza sativa (japonica cultivar-group) Os03g0115100 (Os03g0115100) mRNA, complete cds
0577-94-(6-8-06)_B09	6.00E-78	ref|NM_001068166.1| Oryza sativa (japonica cultivar-group) Os08g0359500 (Os08g0359500) mRNA, complete cds
0571-94-(6-8-06)_F08	6.00E-52	ref|NM_001065116.1| Oryza sativa (japonica cultivar-group) Os06g0715100 (Os06g0715100) mRNA, complete cds
0457-94-(6-16-06)_G04	5.00E-66	ref|NM_001065908.1| Oryza sativa (japonica cultivar-group) Os07g0280200 (Os07g0280200) mRNA, complete cds
0346-94-(6-9-06)_D04	6.00E-166	ref|NM_001062092.1| Oryza sativa (japonica cultivar-group) Os05g0415700 (Os05g0415700) mRNA, complete cds
0440-94-(6-16-06)_H02	1.00E-156	emb|Z68506.1|PSIEP110 P.sativum mRNA for 110 kD chloroplast inner envelope protein IEP110
Contig\8	1.00E-163	gb|DQ781308.1| Pachysandra terminalis chloroplast carbonic anhydrase mRNA, complete cds; nuclear gene for chloroplast product
0905-94-(6-14-06)_H10	2.00E-84	gb|AF492816.1| Phaseolus vulgaris cyclic nucleotide-gated channel A (CNGC-A) mRNA, partial cds
0699-94-(6-12-06)_H12	0	gb|AF492818.1| Phaseolus vulgaris cyclic nucleotide-gated channel C (CNGC-C) mRNA, partial cds
0350-94-(6-9-06)_G04	8.00E-165	emb|Z99953.1|PVZ99953 Phaseolus vulgaris Moldavian encoding cysteine proteinase precursor (clone cp41)
Contig\149	0	emb|AJ288895.1|PVU288895 Phaseolus vulgaris mRNA for peroxiredoxin (2-Cys PRx gene)
1040-94-(6-2-06)_G05	2.00E-21	gb|AF363809.1|AF363809 Phaseolus vulgaris Pto-like kinase SG2 gene, partial cds
0261-94(5-31-06)_016	3.00E-08	gb|AF461687.1| Pinus pinaster putative ubiquitin mRNA, partial cds
0520-94-(6-8-06)_D03	0	gb|AF397903.1| Pisum sativum AAA-metalloprotease FtsH (FTSH) mRNA, complete cds; nuclear gene for mitochondrial product
Contig\136	0	gb|L36856.1|PEAIAP34A Pisum sativum GTP-binding protein (IAP34) mRNA, complete cds
Contig\105	0	dbj|D86494.1| Pisum sativum mRNA for diminuto, complete cds
1113-94-(6-9-06)_E08	0	emb|X59773.1|PSGDPP Pisum sativum mRNA for P protein, a part of glycine cleavage complex

0907-94-(6-14-06)_B11	7.00E-102	emb|AJ251828.1|PSA251828 Pisum sativum partial mRNA for putative cysteine protease (plp gene)
1115-94-(6-9-06)_G08	3.00E-63	dbj|AB021873.1| Pisum sativum RSP mRNA for ribosome-sedimenting protein, complete cds
0944-94-(6-15-06)_G03	2.00E-122	gb|DQ181626.1| Pisum sativum unknown mRNA
0613-94-(6-6-06)_E02	3.00E-170	emb|AM111319.1| Plantago major partial mRNA for Nucleoside-Diphopshate-Sugar Dehydratase (nsd1 gene)
0265-94(5-31-06)_007	2.00E-67	emb|AM293621.1| Platanus x acerifolia partial ORF5 mRNA for hypothetical protein, clone Q8E
0863-94-(6-5-06)_G08	5.00E-117	emb|CT028878.1| Poplar cDNA sequences
0739-94-(6-7-06)_G05	1.00E-92	emb|CT028623.1| Poplar cDNA sequences
0616-94-(6-6-06)_H02	1.00E-150	emb|CT028457.1| Poplar cDNA sequences
0886-94-(6-5-06)_F11	0	gb|AY230139.1| Populus alba cyclin D mRNA, complete cds
Contig\193	0	gb|AY755413.1| Populus alba x Populus tremula homeodomain protein ARBORKNOX1 (ARBORKNOX1) mRNA, complete cds
Contig\5	0	emb|AJ744954.1| Populus alba x Populus tremula mRNA for putative auxin-amidohydrolase precursor (Iar3 gene)
Contig\161	0	gb|DQ131179.1| Populus deltoides lipoxygenase LOX2 (LOX2) mRNA, complete cds
Contig\182	2.00E-178	gb|DQ517530.1| Populus euphratica Na+/H+ antiporter (sos1) mRNA, complete cds
Contig\199	3.00E-139	gb|AY501392.1| Populus tomentosa MADS box transcription factor (MADS1) mRNA, complete cds
Contig\165	0	gb|EF035039.1| Populus tremula x Populus alba LIM domain protein WLIM1b (WLIM1b) mRNA, complete cds
Contig\153	0	gb|EF035040.1| Populus tremula x Populus alba LIM domain protein WLIM2a (WLIM2a) mRNA, complete cds
Contig\158	0	gb|EF501824.1| Populus tremula x Populus alba secondary wall-associated glycosyltransferase family 8D (GT8D) mRNA, complete cds
0325-94-(6-14-06)_E02	7.00E-162	gb|EF035036.1| Populus tremula x Populus alba strain INRA717-1B4 LIM domain protein GLIM1b (GLIM1b) mRNA, complete cds
0890-94-(6-14-06)_E07	2.00E-97	emb|AJ306828.1|PTR306828 Populus tremula x Populus tremuloides mRNA for aux/IAA protein (IAA5 gene)
Contig\148	3.00E-177	gb|AF373100.1| Populus tremula x Populus tremuloides auxin-regulated protein (IAA1) mRNA, complete cds
0453-94-(6-16-06)_C04	0	gb|AY935506.1| Populus tremula x Populus tremuloides secondary cell wall-related glycosyltransferase family 47 mRNA, complete cds
Contig\90	0	gb|EF194056.1| Populus tremula x Populus tremuloides xyloglucan endotransglycosylase/hydrolase precursor XTH-17 mRNA, complete cds
0177-94-B04(5-10-06)	8.00E-168	gb|AF377868.1| Populus tremuloides MADS-box protein PTM5 mRNA, complete cds
0195-94-D06(5-10-06)	3.00E-66	gb|DQ536148.1| Populus trichocarpa clone 15623897 auxin-regulated protein-like protein mRNA, complete cds
0544-94-(6-8-06)_D06	0	gb|AC210650.1| Populus trichocarpa clone POP004-K01, complete sequence
0548-94-(6-8-06)_H06	1.00E-123	gb|AC210505.1| Populus trichocarpa clone POP021-M24, complete sequence
0767-94-(6-7-06)_B09	2.00E-167	gb|AC210335.1| Populus trichocarpa clone POP024-E12, complete sequence

0930-94-(6-16-06)_F11	6.00E-46	gb|AC149300.1| Populus trichocarpa clone Pop1-040E01, complete sequence
0052-94-C04(4-28-06)	1.00E-13	gb|AC185353.2| Populus trichocarpa clone Pop1-100A20, complete sequence
0818-94-(6-5-06)_B03	4.00E-36	gb|AC187865.2| Populus trichocarpa clone Pop1-4F12, complete sequence
0381-94-(6-12-06)_H09	1.00E-118	gb|AC184077.2| Populus trichocarpa clone Pop1-53L15, complete sequence
1080-94-(6-2-06)_F10	4.00E-131	gb|AC184091.2| Populus trichocarpa clone Pop1-64B3, complete sequence
Contig\99	5.00E-98	gb|AC182701.2| Populus trichocarpa clone Pop1-74K8, complete sequence
0329-94-(6-27-06)_H03	3.00E-96	gb|AC182701.2| Populus trichocarpa clone Pop1-74K8, complete sequence
0468-94-(6-16-06)_B06	0	gb|AC182714.2| Populus trichocarpa clone Pop1-86K15, complete sequence
0619-94-(6-6-06)_C03	1.00E-48	gb|EU130560.1| Populus trichocarpa GAGA-motif binding transcriptional activator (BBR/BPC1) mRNA, complete cds
0283-94(5-31-06)_011	0	gb|AF139498.1|AF139498 Prunus armeniaca porin (mPOR) mRNA, nuclear gene encoding mitochondrial product, complete cds
0198-94-(6-16-06)_H08	9.00E-161	gb|DQ222998.1| Prunus armeniaca temperature-induced lipocalin (TIL) mRNA, complete cds
0234-94-C11(5-10-06)	0	emb|AJ862887.1| Prunus avium mRNA for putative auxin influx carrier protein (lax1 gene)
1085-94-(6-2-06)_C11	6.00E-166	gb|AC154901.1| Prunus persica (peach) BAC clone 82I18, complete sequence
0454-94-(6-16-06)_D04	3.00E-88	gb|AF467900.1| Prunus persica clone pPn31C7 hypothetical proteins, and hypothetical transcription factor genes, complete cds
Contig\167	0	gb|AF039598.1| Prunus persica light harvesting chlorophyll A/B binding protein (Lhcb-Pp2) mRNA, complete cds
0871-94-(6-14-06)_G06	0	dbj|AB047518.1| Prunus persica PpExp2 mRNA for expansin, complete cds
0525-94-(6-8-06)_A04	2.00E-178	gb|AF386521.1|AF386521 Pyrus communis putative Tub family protein mRNA, partial cds
0446-94-(6-16-06)_E03	6.00E-160	dbj|AB239590.1| Pyrus pyrifolia var. culta PsS-AIV2 mRNA for soluble acid invertase, complete cds
0684-94-(6-6-06)_D11	0	emb|AJ577264.1|QRO577264 Quercus robur partial mRNA for expansin-like protein (ORF1)
1166-94-(6-15-06)_E05	9.00E-25	gb|AY526717.1| Quercus suber resistance protein (RPc) gene, RPc-a allele, partial cds
0303-94(5-31-06)_002	0	emb|Z81012.1|RCUNKN R.communis mRNA for unknown protein
0278-94(5-31-06)_001	3.00E-154	emb|AJ007579.1|RNI7579 Ribes nigrum mRNA for putative cysteine proteinase, partial
1030-94-(6-2-06)_E04	0	gb|DQ300357.1| Ricinus communis ACS1 mRNA, partial cds
0074-94-A07(4-28-06)	0	gb|U72693.1|RCU72693 Ricinus communis phospholipase D gene, complete cds
0074-93-G04(4-21-06)	2.00E-144	gb|L33686.1|RCCPLD Ricinus communis phospholipase D mRNA, complete cds
0785-94-(6-7-06)_B11	1.00E-168	gb|DQ007449.1| Ruta graveolens UDP-N-acetyl glucosamine-dolichyl phosphate transferase mRNA, partial sequence
1046-94-(6-2-06)_E06	0	dbj|AB003137.1| Salix gilgiana mRNA for DnaJ homolog protein, complete cds

Contig\13	0	gb|AF326321.1|AF326321 Shuttle vector pBHad-CMV, complete plasmid sequence
0743-94-(6-7-06)_C06	0	gb|EF447217.1| Solanum chacoense ovule receptor-like kinase 28 (ORK28) mRNA, complete cds
0606-94-(6-6-06)_F01	0	dbj|AK246627.1| Solanum lycopersicum cDNA, clone: FC17BE09, HTC in fruit
0642-94-(6-6-06)_B06	8.00E-127	dbj|AK246647.1| Solanum lycopersicum cDNA, clone: FC18AD04, HTC in fruit
0444-94-(6-16-06)_C03	4.00E-93	dbj|AK224815.2| Solanum lycopersicum cDNA, clone: FC18BH03, HTC in fruit
0162-94-B07(5-5-06)	9.00E-72	dbj|AK246659.1| Solanum lycopersicum cDNA, clone: FC18CA01, HTC in fruit
0824-94-(6-5-06)_H03	2.00E-141	dbj|AK246759.1| Solanum lycopersicum cDNA, clone: FC23AF10, HTC in fruit
0115-94-B12(4-28-06)	6.00E-157	dbj|AK246844.1| Solanum lycopersicum cDNA, clone: FC26AC04, HTC in fruit
0263-94(5-31-06)_003	4.00E-76	dbj|AK246968.1| Solanum lycopersicum cDNA, clone: LEFL1005BD01, HTC in leaf
0768-94-(6-7-06)_C09	0	dbj|AK247440.1| Solanum lycopersicum cDNA, clone: LEFL1021DD06, HTC in leaf
0681-94-(6-6-06)_A11	7.00E-26	dbj|AK247103.1| Solanum lycopersicum cDNA, clone: LEFL1035AD05, HTC in leaf
0221-94-F09(5-10-06)	8.00E-168	dbj|AK247264.1| Solanum lycopersicum cDNA, clone: LEFL1078BG09, HTC in leaf
0725-94-(6-7-06)_A04	5.00E-66	dbj|AK247284.1| Solanum lycopersicum cDNA, clone: LEFL1086AG10, HTC in leaf
0208-94-A08(5-10-06)	7.00E-143	dbj|AK247687.1| Solanum lycopersicum cDNA, clone: LEFL1092AE12, HTC in leaf
0030-94-E01(4-28-06)	2.00E-131	dbj|AK247932.1| Solanum lycopersicum cDNA, clone: LEFL2051C01, HTC in fruit
Contig\60	7.00E-134	gb|DQ206630.1| Solanum tuberosum ABA 8'-hydroxylase CYP707A1 mRNA, complete cds
0119-94-F12(4-28-06)	1.00E-151	gb|AF193845.1|AF193845 Solanum tuberosum branched-chain amino acid aminotransferase (BCAT1) mRNA, complete cds
Contig\186	8.00E-108	gb|DQ241861.1| Solanum tuberosum clone 021G11 translocon-associated protein beta family protein-like mRNA, complete cds
Contig\44	3.00E-170	gb|DQ200374.1| Solanum tuberosum clone 059F12 unknown mRNA
Contig\78	0	gb|DQ222496.1| Solanum tuberosum clone 104F01 triose phosphate isomerase cytosolic isoform-like mRNA, complete cds
Contig\127	0	gb|DQ222522.1| Solanum tuberosum clone 129C03 Ran/TC4-like protein mRNA, complete cds
Contig\145	0	gb|DQ268839.1| Solanum tuberosum clone 130D11 40S ribosomal protein S4-like protein mRNA, complete cds
Contig\17	6.00E-116	gb|DQ235163.1| Solanum tuberosum clone 153D02 CAPIP1-like mRNA, complete cds
Contig\76	3.00E-138	gb|DQ235192.1| Solanum tuberosum clone 167F07 unknown mRNA
Contig\20	2.00E-28	gb|DQ241827.1| Solanum tuberosum clone 172C11 hypothetical protein mRNA, complete cds
0923-94-(6-15-06)_B01	3.00E-176	gb|DQ294277.1| Solanum tuberosum clone 172G04 60S ribosomal protein L19-like protein mRNA, complete cds
0294-94(5-31-06)_001	0	gb|AY690423.1| Solanum tuberosum cultivar USW 2230 glucose-6-phosphate isomerase (GPI) mRNA, complete cds

Contig\133	0	emb|AJ000265.1|SOJ00265 Spinacia oleracea mRNA (nuclear-encoded) for chloroplast glucose-6-phosphate isomerase
Contig\15	9.00E-101	gb|AF266551.1|AF266551 Staphylococcus capitis clone 4b shotgun library fragment
Contig\200	0	emb|AJ313385.1|TCA313385 Theobroma cacao mRNA for aspartic proteinase (ap2 gene)
0020-94_010(5-31-06)	0	emb|AJ313384.1|TCA313384 Theobroma cacao mRNA for aspartic proteinase (ap1 gene)
0233-94-B11(5-10-06)	0	gb|AY570507.1| Theobroma cacao somatic embryogenesis receptor-like kinase (SERK) mRNA, partial cds
0734-94-(6-7-06)_B05	0	gb|AY445630.1| Trifolium pratense GTP-binding protein TypA mRNA, complete cds
0576-94-(6-12-06)_E11	3.00E-151	dbj|AB236802.1| Trifolium pratense RNA for hypothetical protein, complete cds, clone: C1966
0347-94-(6-12-06)_F06	2.00E-166	dbj|AB236792.1| Trifolium pratense RNA for putative DNA binding protein, partial cds, clone: C1861
0298-94(5-31-06)_009	1.00E-145	gb|AY192361.1| Trifolium repens cysteine protease 14 mRNA, complete cds
Contig\163	3.00E-126	emb|AJ867392.1| Triticum aestivum mRNA for glycosyltransferase (a1 gene)
0762-94-(6-7-06)_F08	0	emb|Y08624.1|VUTED2 V.unguiculata mRNA for Ted2 protein
Contig\138	0	gb|AF047173.1| Vernicia fordii aquaporin mRNA, complete cds
0839-94-(6-14-06)_C06	0	gb|AY819699.1| Vernicia fordii NADH:cytochrome b5 reductase (CBR1A) mRNA, complete cds
Contig\27	5.00E-168	gb|AF141898.1|AF141898 Vitis berlandieri x Vitis rupestris putative aquaporin PIP1-2 (PIP1-2) mRNA, complete cds
0817-94-(6-5-06)_A03	5.00E-148	gb|DQ354157.1| Vitis pseudoreticulata clone EST-443 unknown mRNA
0529-94-(6-8-06)_E04	3.00E-170	gb|DQ336282.1| Vitis pseudoreticulata L-isoaspartate-O-methyl transferase mRNA, complete cds
1310-94-(6-16-06)_D07	0	gb|L34836.1|VIIMDN Vitis vinifera (clone pGME1) malate dehydrogenase mRNA, complete cds
Contig\112	0	gb|AY839872.2| Vitis vinifera aquaporin (TIP1;1) mRNA, complete cds
0645-94-(6-6-06)_E06	3.00E-49	emb|AM432629.2| Vitis vinifera contig VV78X000634.80, whole genome shotgun sequence
0013-94_011(5-31-06)	3.00E-58	emb|AM484093.2| Vitis vinifera contig VV78X003218.11, whole genome shotgun sequence
0838-94-(6-5-06)_F05	1.00E-137	emb|AM448978.2| Vitis vinifera contig VV78X005403.16, whole genome shotgun sequence
0713-94-(6-7-06)_E02	0	emb|AM484571.2| Vitis vinifera contig VV78X010579.6, whole genome shotgun sequence
0804-94-(6-5-06)_D01	1.00E-85	emb|AM467308.2| Vitis vinifera contig VV78X011524.4, whole genome shotgun sequence
0379-94-(6-12-06)_F09	6.00E-46	emb|AM467727.2| Vitis vinifera contig VV78X011652.21, whole genome shotgun sequence
1134-94-(6-9-06)_B11	2.00E-83	emb|AM437239.1| Vitis vinifera contig VV78X018020.2, whole genome shotgun sequence
0543-94-(6-8-06)_C06	5.00E-09	emb|AM440497.2| Vitis vinifera contig VV78X018685.4, whole genome shotgun sequence
0054-94-E04(4-28-06)	5.00E-88	emb|AM482958.2| Vitis vinifera contig VV78X019958.11, whole genome shotgun sequence

0686-94-(6-6-06)_F11	2.00E-134	emb|AM466389.2| Vitis vinifera contig VV78X020180.8, whole genome shotgun sequence
Contig\37	2.00E-97	emb|AM458094.1| Vitis vinifera contig VV78X024267.14, whole genome shotgun sequence
0127-94(5-31-06)_007	5.00E-63	emb|AM437734.2| Vitis vinifera contig VV78X024535.5, whole genome shotgun sequence
0214-94(5-31-06)_010	3.00E-84	emb|AM447494.2| Vitis vinifera contig VV78X024983.11, whole genome shotgun sequence
0172-94-E03(5-10-06)	0	emb|AM466191.1| Vitis vinifera contig VV78X027829.4, whole genome shotgun sequence
0136-94(5-31-06)_011	9.00E-66	emb|AM446570.2| Vitis vinifera contig VV78X034573.14, whole genome shotgun sequence
0388-94-(6-12-06)_E10	7.00E-96	emb|AM479658.1| Vitis vinifera contig VV78X035251.11, whole genome shotgun sequence
1120-94-(6-9-06)_D09	3.00E-43	emb|AM441534.1| Vitis vinifera contig VV78X035471.3, whole genome shotgun sequence
0362-94-(6-12-06)_G07	6.00E-116	emb|AM440961.2| Vitis vinifera contig VV78X037392.6, whole genome shotgun sequence
Contig\132	4.00E-169	emb|AM486046.1| Vitis vinifera contig VV78X042566.6, whole genome shotgun sequence
0315-94-(6-9-06)_D01	2.00E-98	emb|AM426422.2| Vitis vinifera contig VV78X044419.14, whole genome shotgun sequence
Contig\177	4.00E-23	emb|AM470132.1| Vitis vinifera contig VV78X044452.23, whole genome shotgun sequence
0695-94-(6-6-06)_G12	2.00E-33	emb|AM468846.1| Vitis vinifera contig VV78X046391.5, whole genome shotgun sequence
0149-94-E05(5-9-06)	6.00E-55	emb|AM476574.1| Vitis vinifera contig VV78X048877.7, whole genome shotgun sequence
0141-94-E04(5-9-06)	7.00E-105	emb|AM430425.2| Vitis vinifera contig VV78X049119.5, whole genome shotgun sequence
0904-94-(6-14-06)_G10	4.00E-10	emb|AM423655.1| Vitis vinifera contig VV78X050837.6, whole genome shotgun sequence
0789-94-(6-7-06)_E11	2.00E-127	emb|AM442180.2| Vitis vinifera contig VV78X054778.6, whole genome shotgun sequence
0756-94-(6-7-06)_H07	3.00E-49	emb|AM462727.2| Vitis vinifera contig VV78X055060.11, whole genome shotgun sequence
Contig\110	5.00E-09	emb|AM474715.1| Vitis vinifera contig VV78X055193.7, whole genome shotgun sequence
0594-94-(6-8-06)_A11	4.00E-17	emb|AM427820.2| Vitis vinifera contig VV78X055578.7, whole genome shotgun sequence
0016-94_002(5-31-06)	6.00E-62	emb|AM465666.2| Vitis vinifera contig VV78X057834.10, whole genome shotgun sequence
0846-94-(6-5-06)_F06	1.00E-149	emb|AM443511.2| Vitis vinifera contig VV78X059386.8, whole genome shotgun sequence
0625-94-(6-6-06)_A04	1.00E-123	emb|AM463368.2| Vitis vinifera contig VV78X059861.10, whole genome shotgun sequence
0295-94(5-31-06)_003	5.00E-88	emb|AM451060.2| Vitis vinifera contig VV78X060552.11, whole genome shotgun sequence
0826-94-(6-5-06)_B04	3.00E-68	emb|AM460476.2| Vitis vinifera contig VV78X063991.7, whole genome shotgun sequence
0252-94(5-31-06)_013	5.00E-139	emb|AM428631.2| Vitis vinifera contig VV78X064996.4, whole genome shotgun sequence
0503-94-(6-8-06)_C01	3.00E-06	emb|AM470530.2| Vitis vinifera contig VV78X066539.5, whole genome shotgun sequence

0546-94-(6-8-06)_F06	8.00E-171	emb|AM445156.2| Vitis vinifera contig VV78X067066.11, whole genome shotgun sequence
0537-94-(6-8-06)_E05	0	emb|AM445156.2| Vitis vinifera contig VV78X067066.11, whole genome shotgun sequence
0795-94-(6-7-06)_C12	4.00E-67	emb|AM486698.2| Vitis vinifera contig VV78X068997.3, whole genome shotgun sequence
0822-94-(6-5-06)_F03	2.00E-46	emb|AM451408.2| Vitis vinifera contig VV78X073445.2, whole genome shotgun sequence
0596-94-(6-8-06)_C11	0	emb|AM443064.1| Vitis vinifera contig VV78X073525.10, whole genome shotgun sequence
0328-94-(6-9-06)_G02	8.00E-41	emb|AM470860.1| Vitis vinifera contig VV78X074716.3, whole genome shotgun sequence
0316-94-(6-9-06)_E01	2.00E-93	emb|AM448784.2| Vitis vinifera contig VV78X077229.13, whole genome shotgun sequence
Contig\204	6.00E-53	emb|AM424498.1| Vitis vinifera contig VV78X081526.43, whole genome shotgun sequence
0511-94-(6-8-06)_C02	2.00E-71	emb|AM425004.2| Vitis vinifera contig VV78X083605.8, whole genome shotgun sequence
0668-94-(6-6-06)_D09	2.00E-77	emb|AM443416.1| Vitis vinifera contig VV78X083609.33, whole genome shotgun sequence
0545-94-(6-8-06)_E06	1.00E-47	emb|AM425275.2| Vitis vinifera contig VV78X087688.7, whole genome shotgun sequence
0836-94-(6-5-06)_D05	4.00E-48	emb|AM469471.2| Vitis vinifera contig VV78X090243.7, whole genome shotgun sequence
0063-94-F05(4-28-06)	6.00E-68	emb|AM459605.2| Vitis vinifera contig VV78X091834.13, whole genome shotgun sequence
0514-94-(6-8-06)_F02	3.00E-145	emb|AM476887.2| Vitis vinifera contig VV78X092610.11, whole genome shotgun sequence
0870-94-(6-5-06)_F09	2.00E-115	emb|AM458473.1| Vitis vinifera contig VV78X094999.4, whole genome shotgun sequence
1082-94-(6-2-06)_H10	1.00E-142	emb|AM436998.1| Vitis vinifera contig VV78X098497.33, whole genome shotgun sequence
0896-94-(6-5-06)_H12	4.00E-169	emb|AM460819.2| Vitis vinifera contig VV78X099670.6, whole genome shotgun sequence
0614-94-(6-6-06)_F02	0	emb|AM476761.1| Vitis vinifera contig VV78X102785.4, whole genome shotgun sequence
0667-94-(6-6-06)_C09	2.00E-70	emb|AM471679.2| Vitis vinifera contig VV78X104105.11, whole genome shotgun sequence
0163-94-C07(5-5-06)	3.00E-166	emb|AM456450.2| Vitis vinifera contig VV78X104795.20, whole genome shotgun sequence
0526-94-(6-8-06)_B04	6.00E-78	emb|AM465028.1| Vitis vinifera contig VV78X105028.7, whole genome shotgun sequence
0524-94-(6-8-06)_H03	1.00E-55	emb|AM459051.1| Vitis vinifera contig VV78X105510.28, whole genome shotgun sequence
0887-94-(6-5-06)_G11	7.00E-90	emb|AM465307.2| Vitis vinifera contig VV78X110587.5, whole genome shotgun sequence
0790-94-(6-7-06)_F11	3.00E-81	emb|AM446906.2| Vitis vinifera contig VV78X112185.9, whole genome shotgun sequence
Contig\50	4.00E-17	emb|AM426844.1| Vitis vinifera contig VV78X115678.10, whole genome shotgun sequence
0352-94-(6-27-06)_H04	2.00E-65	emb|AM440904.2| Vitis vinifera contig VV78X119347.17, whole genome shotgun sequence
1063-94-(6-2-06)_E08	9.00E-101	emb|AM436746.1| Vitis vinifera contig VV78X120047.5, whole genome shotgun sequence

0244-94-E12(5-10-06)	7.00E-42	emb|AM427983.2| Vitis vinifera contig VV78X123551.5, whole genome shotgun sequence
0753-94-(6-7-06)_E07	7.00E-159	emb|AM435130.2| Vitis vinifera contig VV78X123562.7, whole genome shotgun sequence
0693-94-(6-6-06)_E12	4.00E-54	emb|AM440507.2| Vitis vinifera contig VV78X124639.7, whole genome shotgun sequence
0580-94-(6-8-06)_D09	1.00E-98	emb|AM428739.2| Vitis vinifera contig VV78X124967.7, whole genome shotgun sequence
0653-94-(6-6-06)_E07	1.00E-98	emb|AM441566.2| Vitis vinifera contig VV78X129319.10, whole genome shotgun sequence
0385-94-(6-12-06)_B10	0	emb|AM423527.2| Vitis vinifera contig VV78X129999.11, whole genome shotgun sequence
0885-94-(6-5-06)_E11	5.00E-28	emb|AM424169.2| Vitis vinifera contig VV78X130502.3, whole genome shotgun sequence
1128-94-(6-9-06Truncated)_D10	2.00E-76	emb|AM463089.1| Vitis vinifera contig VV78X133512.3, whole genome shotgun sequence
0735-94-(6-7-06)_C05	2.00E-109	emb|AM454394.2| Vitis vinifera contig VV78X133763.7, whole genome shotgun sequence
0175-94-H03(5-10-06)	9.00E-34	emb|AM459902.1| Vitis vinifera contig VV78X135233.9, whole genome shotgun sequence
0567-94-(6-8-06)_B08	2.00E-121	emb|AM451466.2| Vitis vinifera contig VV78X135650.3, whole genome shotgun sequence
0219-94-D09(5-10-06)	8.00E-60	emb|AM467027.2| Vitis vinifera contig VV78X136834.9, whole genome shotgun sequence
0254-94-(6-16-06)_B10	2.00E-49	emb|AM453065.2| Vitis vinifera contig VV78X136997.8, whole genome shotgun sequence
0655-94-(6-6-06)_G07	1.00E-85	emb|AM481573.2| Vitis vinifera contig VV78X141279.3, whole genome shotgun sequence
1102-94-(6-9-06)_B07	5.00E-136	emb|AM458581.1| Vitis vinifera contig VV78X141303.10, whole genome shotgun sequence
0046-94-E03(4-28-06)	5.00E-31	emb|AM485344.2| Vitis vinifera contig VV78X146798.9, whole genome shotgun sequence
0788-94-(6-7-06)_D11	2.00E-115	emb|AM475102.2| Vitis vinifera contig VV78X148227.11, whole genome shotgun sequence
0229-94-F10(5-10-06)	6.00E-43	emb|AM438403.1| Vitis vinifera contig VV78X148954.8, whole genome shotgun sequence
0522-94-(6-8-06)_F03	4.00E-99	emb|AM454880.2| Vitis vinifera contig VV78X149779.3, whole genome shotgun sequence
1083-94-(6-2-06)_A11	5.00E-47	emb|AM426394.1| Vitis vinifera contig VV78X150841.10, whole genome shotgun sequence
0581-94-(6-8-06)_E09	2.00E-167	emb|AM467891.2| Vitis vinifera contig VV78X155293.3, whole genome shotgun sequence
0377-94-(6-12-06)_D09	4.00E-175	emb|AM467891.2| Vitis vinifera contig VV78X155293.3, whole genome shotgun sequence
0131-94-C03(5-9-06)	5.00E-94	emb|AM430014.2| Vitis vinifera contig VV78X155605.7, whole genome shotgun sequence
0796-94-(6-7-06)_D12	2.00E-89	emb|AM454175.1| Vitis vinifera contig VV78X156050.2, whole genome shotgun sequence
0045-94-D03(4-28-06)	8.00E-22	emb|AM485844.1| Vitis vinifera contig VV78X158554.4, whole genome shotgun sequence
0433-94-(6-27-06)_D06	1.00E-22	emb|AM476024.2| Vitis vinifera contig VV78X159831.9, whole genome shotgun sequence
0720-94-(6-7-06)_D03	2.00E-21	emb|AM478428.2| Vitis vinifera contig VV78X160122.36, whole genome shotgun sequence

0609-94-(6-6-06)_A02	0	emb|AM466336.2| Vitis vinifera contig VV78X161177.4, whole genome shotgun sequence
0129-94-A03(5-9-06)	3.00E-78	emb|AM462739.2| Vitis vinifera contig VV78X161821.7, whole genome shotgun sequence
0121-94-H12(4-28-06)	4.00E-127	emb|AM447198.2| Vitis vinifera contig VV78X163338.7, whole genome shotgun sequence
0262-94(5-31-06)_001	2.00E-29	emb|AM445448.2| Vitis vinifera contig VV78X163861.25, whole genome shotgun sequence
0803-94-(6-5-06)_C01	4.00E-35	emb|AM457140.2| Vitis vinifera contig VV78X164259.5, whole genome shotgun sequence
0296-94(5-31-06)_005	2.00E-106	emb|AM446364.2| Vitis vinifera contig VV78X167880.8, whole genome shotgun sequence
0746-94-(6-7-06)_F06	3.00E-56	emb|AM477118.1| Vitis vinifera contig VV78X175812.10, whole genome shotgun sequence
0358-94-(6-12-06)_C07	4.00E-149	emb|AM428538.2| Vitis vinifera contig VV78X176556.9, whole genome shotgun sequence
0071_B05(Rev 4-21-06)	6.00E-43	emb|AM436525.2| Vitis vinifera contig VV78X179149.4, whole genome shotgun sequence
0831-94-(6-5-06)_G04	8.00E-70	emb|AM443236.2| Vitis vinifera contig VV78X183120.5, whole genome shotgun sequence
0140-94-D04(5-9-06)	6.00E-49	emb|AM470478.2| Vitis vinifera contig VV78X183888.10, whole genome shotgun sequence
0737-94-(6-7-06)_E05	3.00E-44	emb|AM488642.2| Vitis vinifera contig VV78X187737.9, whole genome shotgun sequence
0688-94-(6-6-06)_H11	1.00E-105	emb|AM487076.1| Vitis vinifera contig VV78X188132.3, whole genome shotgun sequence
Contig\24	2.00E-116	emb|AM451805.1| Vitis vinifera contig VV78X191383.8, whole genome shotgun sequence
0280-94(5-31-06)_005	4.00E-32	emb|AM425853.2| Vitis vinifera contig VV78X191886.14, whole genome shotgun sequence
0095-93-B02(4-21-06)	3.00E-122	emb|AM488253.2| Vitis vinifera contig VV78X192978.4, whole genome shotgun sequence
0636-94-(6-6-06)_D05	2.00E-33	emb|AM467064.2| Vitis vinifera contig VV78X193621.4, whole genome shotgun sequence
0147-94-C05(5-9-06)	1.00E-134	emb|AM451838.2| Vitis vinifera contig VV78X195455.4, whole genome shotgun sequence
0856-94-(6-5-06)_H07	3.00E-100	emb|AM479197.1| Vitis vinifera contig VV78X202850.5, whole genome shotgun sequence
0072-94-F01(5-9-06)	0	emb|AM459753.2| Vitis vinifera contig VV78X203315.8, whole genome shotgun sequence
Contig\80	1.00E-23	emb|AM468138.1| Vitis vinifera contig VV78X205727.5, whole genome shotgun sequence
0438-94-(6-16-06)_F02	2.00E-102	emb|AM487966.2| Vitis vinifera contig VV78X206601.18, whole genome shotgun sequence
0134-94-F03(5-9-06)	3.00E-84	emb|AM464998.2| Vitis vinifera contig VV78X209295.9, whole genome shotgun sequence
1072-94-(6-2-06)_F09	0	emb|AM425413.1| Vitis vinifera contig VV78X215139.6, whole genome shotgun sequence
0019-94_008(5-31-06)	2.00E-24	emb|AM461381.2| Vitis vinifera contig VV78X216117.38, whole genome shotgun sequence
0649-94-(6-6-06)_A07	2.00E-178	emb|AM432430.2| Vitis vinifera contig VV78X216460.7, whole genome shotgun sequence

1076-94-(6-2-06)_B10	1.00E-28	emb|AM473670.1| Vitis vinifera contig VV78X216657.3, whole genome shotgun sequence
0702-94-(6-7-06)_B01	2.00E-103	emb|AM446335.2| Vitis vinifera contig VV78X216922.15, whole genome shotgun sequence
0120-94-A02(5-9-06)	3.00E-52	emb|AM486571.2| Vitis vinifera contig VV78X217783.9, whole genome shotgun sequence
1003-94-(6-2-06)_C01	6.00E-97	emb|AM441201.1| Vitis vinifera contig VV78X218938.3, whole genome shotgun sequence
0220-94E09(5-10-06)	7.00E-42	emb|AM428720.2| Vitis vinifera contig VV78X223874.4, whole genome shotgun sequence
0528-94-(6-8-06)_D04	0	emb|AM479280.2| Vitis vinifera contig VV78X229922.9, whole genome shotgun sequence
0356-94-(6-12-06)_A07	0	emb|AM479280.2| Vitis vinifera contig VV78X229922.9, whole genome shotgun sequence
0859-94-(6-5-06)_C08	1.00E-118	emb|AM452448.2| Vitis vinifera contig VV78X230125.6, whole genome shotgun sequence
0426-94-(6-16-06)_B01	5.00E-41	emb|AM452222.2| Vitis vinifera contig VV78X230407.7, whole genome shotgun sequence
1194-94-(6-15-06)_F07	0	emb|AM475919.1| Vitis vinifera contig VV78X233722.8, whole genome shotgun sequence
0894-94-(6-5-06)_F12	8.00E-89	emb|AM451964.2| Vitis vinifera contig VV78X237314.10, whole genome shotgun sequence
0829-94-(6-5-06)_E04	3.00E-101	emb|AM463121.1| Vitis vinifera contig VV78X245121.18, whole genome shotgun sequence
0021-94_012(5-31-06)	2.00E-24	emb|AM453785.2| Vitis vinifera contig VV78X245887.19, whole genome shotgun sequence
0774-94-(6-7-06)_H09	0	emb|AM489278.2| Vitis vinifera contig VV78X249588.41, whole genome shotgun sequence
1178-94-(6-15-06)_E06	3.00E-158	emb|AM488387.1| Vitis vinifera contig VV78X249904.9, whole genome shotgun sequence
0285-94(5-31-06)_015	2.00E-61	emb|AM426326.2| Vitis vinifera contig VV78X251338.3, whole genome shotgun sequence
0257-94(5-31-06)_008	5.00E-126	emb|AM481020.2| Vitis vinifera contig VV78X251561.7, whole genome shotgun sequence
0800-94-(6-7-06)_G12	4.00E-42	emb|AM466875.2| Vitis vinifera contig VV78X252678.5, whole genome shotgun sequence
0380-94-(6-12-06)_G09	2.00E-45	emb|AM450130.2| Vitis vinifera contig VV78X253621.4, whole genome shotgun sequence
0075-94-B07(4-28-06)	8.00E-79	emb|AM459438.2| Vitis vinifera contig VV78X255329.11, whole genome shotgun sequence
0678-94-(6-6-06)_F10	1.00E-156	emb|AM453037.2| Vitis vinifera contig VV78X255915.8, whole genome shotgun sequence
0535-94-(6-8-06)_C05	5.00E-117	emb|AM458018.2| Vitis vinifera contig VV78X262152.22, whole genome shotgun sequence
0111-94-F11(4-28-06)	4.00E-45	emb|AM471702.1| Vitis vinifera contig VV78X263217.13, whole genome shotgun sequence
0230-94(5-31-06)_014	3.00E-110	emb|AM470409.1| Vitis vinifera contig VV78X265552.16, whole genome shotgun sequence
Contig\151	4.00E-67	emb|AM443902.1| Vitis vinifera contig VV78X271086.9, whole genome shotgun sequence
1017-94-(6-2-06)_H02	6.00E-59	emb|AM443902.1| Vitis vinifera contig VV78X271086.9, whole genome shotgun sequence

0830-94-(6-5-06)_F04	7.00E-77	emb|AM456848.2| Vitis vinifera contig VV78X271989.8, whole genome shotgun sequence
0635-94-(6-6-06)_C05	2.00E-59	emb|AM463419.2| Vitis vinifera contig VV78X272673.7, whole genome shotgun sequence
0588-94-(6-8-06)_C10	3.00E-18	emb|AM449982.2| Vitis vinifera contig VV78X275557.3, whole genome shotgun sequence
0721-94-(6-7-06)_E03	1.00E-42	emb|AM456273.1| Vitis vinifera contig VV79X000559.3, whole genome shotgun sequence
Contig\97	0	gb|AY849388.1| Vitis vinifera cultivar Riesling cyc07 mRNA, partial cds
0540-94-(6-8-06)_H05	3.00E-126	gb|DQ843600.1| Vitis vinifera galacturonic acid reductase mRNA, complete cds
0810-94-(6-5-06)_B02	0	gb|EU016366.1| Vitis vinifera GEM-like 1 mRNA, complete cds
0740-94-(6-7-06)_H05	2.00E-95	gb|DQ673106.1| Vitis vinifera germin-like protein 2 mRNA, complete cds
Contig\14	0	gb|AY826350.1| Vitis vinifera homogentisate geranylgeranyl transferase (HGGT) mRNA, complete cds
0270-94(5-31-06)_002	1.00E-38	emb|AJ237987.1|VVI237987 Vitis vinifera mRNA for putative ripening-related protein (grip68 gene)
0603-94-(6-6-06)_C01	1.00E-180	dbj|AB001375.1| Vitis vinifera mRNA for soluble NSF attachment protein homologue, complete cds
Contig\84	2.00E-84	emb|AM441575.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X044576.17, clone ENTAV 115
Contig\62	3.00E-107	emb|AM467202.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X053926.11, clone ENTAV 115
Contig\58	7.00E-134	emb|AM440204.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X034340.4, clone ENTAV 115
Contig\53	4.00E-36	emb|AM462469.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X137813.10, clone ENTAV 115
Contig\43	5.00E-98	emb|AM454265.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X025044.6, clone ENTAV 115
Contig\38	0	emb|AM472270.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X008189.5, clone ENTAV 115
Contig\33	5.00E-35	emb|AM439204.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X204419.5, clone ENTAV 115
Contig\28	4.00E-80	emb|AM438267.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X076653.8, clone ENTAV 115
Contig\2	5.00E-111	emb|AM471131.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X100743.10, clone ENTAV 115
Contig\187	1.00E-112	emb|AM436189.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X023655.4, clone ENTAV 115
Contig\179	2.00E-70	emb|AM434350.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X178339.3, clone ENTAV 115
Contig\141	1.00E-74	emb|AM486383.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X003670.12, clone ENTAV 115
Contig\140	0	emb|AM486694.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X086249.3, clone ENTAV 115
Contig\119	3.00E-24	emb|AM486598.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X039063.5, clone ENTAV 115
Contig\118	0	emb|AM481936.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X234341.8, clone ENTAV 115
Contig\113	2.00E-32	emb|AM485598.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X145389.17, clone ENTAV 115
Contig\108	9.00E	emb|AM459219.1| Vitis vinifera, whole genome shotgun sequence, contig

	-171	VV78X157061.3, clone ENTAV 115
Contig\1	1.00E-62	emb|AM472126.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X142339.3, clone ENTAV 115
1167-94-(6-15-06)_F05	2.00E-14	emb|AM473925.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X242545.11, clone ENTAV 115
1138-94-(6-9-06)_F11	0	emb|AM455759.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X260371.5, clone ENTAV 115
1094-94-(6-2-06)_D12	2.00E-45	emb|AM431485.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X232794.5, clone ENTAV 115
1092-94-(6-2-06)_B12	2.00E-32	emb|AM437104.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X270786.13, clone ENTAV 115
1075-94-(6-2-06)_A10	1.00E-30	emb|AM464667.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X179256.5, clone ENTAV 115
1067-94-(6-2-06)_A09	1.00E-87	emb|AM458760.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X269648.9, clone ENTAV 115
1061-94-(6-2-06)_C08	6.00E-40	emb|AM466264.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X243603.3, clone ENTAV 115
1041-94-(6-2-06)_H05	8.00E-57	emb|AM459477.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X049524.43, clone ENTAV 115
1026-94-(6-2-06)_A04	6.00E-97	emb|AM486579.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X266421.7, clone ENTAV 115
1021-94-(6-2-06)_D03	6.00E-173	emb|AM480357.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X015768.4, clone ENTAV 115
1014-94-(6-2-06)_E02	4.00E-35	emb|AM486193.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X160992.3, clone ENTAV 115
1010-94-(6-2-06)_B02	0	emb|AM432127.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X012423.11, clone ENTAV 115
1007-94-(6-2-06)_G01	1.00E-137	emb|AM487366.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X151885.15, clone ENTAV 115
1006-94-(6-2-06)_F01	1.00E-80	emb|AM448628.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X106645.3, clone ENTAV 115
0945-94-(6-15-06)_H03	1.00E-61	emb|AM477926.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X077994.18, clone ENTAV 115
0936-94-(6-16-06)_D12	7.00E-58	emb|AM450097.1| Vitis vinifera, whole genome shotgun sequence, contig VV79X002210.3, clone ENTAV 115
0931-94-(6-16-06)_G11	3.00E-37	emb|AM464603.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X204536.4, clone ENTAV 115
0892-94-(6-5-06)_D12	6.00E-46	emb|AM445420.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X111264.5, clone ENTAV 115
0883-94-(6-5-06)_C11	6.00E-65	emb|AM437120.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X031623.28, clone ENTAV 115
0881-94-(6-5-06)_A11	2.00E-65	emb|AM454427.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X215478.32, clone ENTAV 115
0854-94-(6-5-06)_F07	3.00E-176	emb|AM454398.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X038686.5, clone ENTAV 115
0841-94-(6-5-06)_A06	5.00E-41	emb|AM457144.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X154954.16, clone ENTAV 115
0834-94-(6-15-06bad)_H10	5.00E-79	emb|AM438763.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X110917.28, clone ENTAV 115
0821-94-(6-5-06)_E03	3.00E-125	emb|AM453537.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X199310.5, clone ENTAV 115
0813-94-(6-5-06)_E02	0	emb|AM473297.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X024334.9, clone ENTAV 115

0808-94-(6-5-06)_H01	5.00E-180	emb|AM453481.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X069400.5, clone ENTAV 115
0802-94-(6-5-06)_B01	1.00E-54	emb|AM465073.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X218558.56, clone ENTAV 115
0782-94-(6-7-06)_G10	3.00E-157	emb|AM437104.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X270786.13, clone ENTAV 115
0728-94-(6-7-06)_D04	5.00E-34	emb|AM456979.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X064852.7, clone ENTAV 115
0716-94-(6-14-06)_H04	3.00E-170	emb|AM463258.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X156046.15, clone ENTAV 115
0707-94-(6-7-06)_G01	5.00E-110	emb|AM483437.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X127436.12, clone ENTAV 115
0676-94-(6-6-06)_D10	2.00E-33	emb|AM488688.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X230051.13, clone ENTAV 115
0664-94-(6-6-06)_H08	2.00E-70	emb|AM461269.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X200864.8, clone ENTAV 115
0639-94-(6-6-06)_G05	3.00E-107	emb|AM473297.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X024334.9, clone ENTAV 115
0578-94-(6-8-06)_C09	2.00E-97	emb|AM463789.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X118074.3, clone ENTAV 115
0572-94-(6-8-06)_G08	6.00E-147	emb|AM435225.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X240850.2, clone ENTAV 115
0538-94-(6-8-06)_F05	0	emb|AM464367.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X086416.13, clone ENTAV 115
0519-94-(6-8-06)_C03	6.00E-103	emb|AM440217.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X156061.11, clone ENTAV 115
0372-94-(6-12-06)_H08	1.00E-47	emb|AM460409.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X135834.21, clone ENTAV 115
0349-94-(6-9-06)_F04	8.00E-114	emb|AM451877.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X227014.6, clone ENTAV 115
0326-94-(6-14-06)_F02	0	emb|AM448264.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X002540.12, clone ENTAV 115
0275-94(5-31-06)_012	0	emb|AM470358.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X080993.6, clone ENTAV 115
0269-94(5-31-06)_015	1.00E-13	emb|AM471515.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X220202.6, clone ENTAV 115
0228-94-E10(5-10-06)	9.00E-110	emb|AM433542.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X095695.20, clone ENTAV 115
0144-94(5-31-06)_015	5.00E-120	emb|AM456234.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X271524.3, clone ENTAV 115
0118-94-E12(4-28-06)	1.00E-70	emb|AM458229.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X029806.3, clone ENTAV 115
0085-94-D08(4-28-06)	1.00E-31	emb|AM449507.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X221633.8, clone ENTAV 115
0047-93-B08(4-21-06)	4.00E-57	emb|AM480404.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X094129.12, clone ENTAV 115
0024-94(5-31-06)_001	1.00E-45	emb|AM479304.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X064570.20, clone ENTAV 115
0012-94_009(5-31-06)	3.00E-115	emb|AM455467.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X047292.4, clone ENTAV 115
0008-94-G05(4-20-06)	0	emb|AM469149.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X027578.8, clone ENTAV 115
0006-93-B05(4-20-06)	1.00E-134	emb|AM456651.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X249037.7, clone ENTAV 115

0400-94-(6-8-06)_H12	2.00E-173	gb|AY226583.1| X Citrofortunella mitis leucine-rich repeat protein mRNA, complete cds
Contig\170	0	gb|EF036511.1| YAC construction vector pRML2, complete sequence
1135-94-(6-9-06)_C11	4.00E-149	gb|DQ245286.1| Zea mays clone 14308 mRNA sequence
0117-94-D12(4-28-06)	2.00E-17	gb|DQ245711.1| Zea mays clone 19741 mRNA sequence
Contig\180	7.00E-77	gb|BT017347.1| Zea mays clone EL01N0323E09.c mRNA sequence
0843-94-(6-5-06)_C06	3.00E-56	gb|BT017608.1| Zea mays clone EL01N0432F07.c mRNA sequence
1028-94-(6-2-06)_C04	0	gb|BT024115.1| Zea mays clone EL01N0513A07 mRNA sequence
1301-94-(6-16-06)_C06	8.00E-57	gb|AY105876.1| Zea mays PCO109868 mRNA sequence
0032-94-G01(4-28-06)	0	gb|AY104603.1| Zea mays PCO113315 mRNA sequence
0430-94-(6-16-06)_F01	2.00E-128	gb|AY106247.1| Zea mays PCO128311 mRNA sequence