HAZELNUT GENOME AND TRANSCRIPTOME ANALYSIS UNDER BIOTIC AND ABIOTIC STRESS

by

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ABSTRACT

HAZELNUT GENOME AND TRANSCRIPTOME ANALYSIS UNDER BIOTIC AND ABIOTIC STRESS

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Molecular Biology, Genetics and Bioengineering, PhD Thesis, 2020

Supervised by: Prof. Dr. Levent Öztürk
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Keywords: Hazelnut, Genome and transcriptome assembly, Chilling stress, Chloroplast assembly

European hazel (*Corylus avellana* L.) is a crop tree of well-known health benefits and great economic importance, but only limited number of studies exist about it at the molecular level. The aim of this thesis to demonstrate the mechanisms of genes under biotic and abiotic stresses, and analysis of the cv ‘Tombul’ genome, one of the most important Turkish varieties. Firstly, the emerging powdery mildew pathogen, *Erysiphe corylacearum*, and the degree of genetic diversity within the growing epidemic were analyzed with DNA barcode analysis and molecular markers. No genetic variation was observed within these samples, suggesting that the current outbreak originated from a single recent transmission event. In order to utilize available hazelnut genetic resources for crop improvement, annotation for cv Tombul was carried through a fully assembled genome sequence produced with a hybrid sequencing strategy. The genome includes 27,270 high-confidence protein-coding genes, over 20,000 of which were functionally annotated based on homology to known plant proteins. Furthermore, the complete chloroplast genome was assembled and analyzed with multiple annotation tools, having a typical quadripartite structure. This can provide comprehensive genetic insight into the evolution of genus *Corylus*. Lastly, transcriptome analysis was conducted to obtain new insight on the genes and gene networks involved in chilling stress. A total of 2,440 differentially expressed transcripts were generated, and of these, 1,368 were upregulated under chilling stress. It may facilitate further study on freezing tolerance mechanisms which could be useful for breeding approaches in tree species.

ÖZET

BİYOTİK VE ABİYOTİK STRES KOŞULLARI ALTINDA FINDIK GENOM VE TRANSKRİPTOM ANALİZLERİ

Kadriye Kahraman

Moleküler Biyoloji, Genetik ve Biyomühendislik, Doktora Tezi, 2020

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Anahtar sözcükler: Fındık, Genom ve transkriptom analizleri, Soğuk stresi, Kloroplast dizimi

Avrupa fındığı, sağlık ve ekonomik önemi büyük olan bir ağaç türüdür. Tarımda önemli bir yere sahip olmasına rağmen moleküler düzeyde *C. avellana* ile ilgili sınırlı sayıda çalışma mevcuttur. Bu tezin amacı, biyotik ve abiyotik stresler altında genlerin mekanizmalarını ortaya koymak ve Türkiye'nin en önemli çeşitlerinden biri olan cv Tombul genomunun analizini yapmaktır. İlk olarak, yeni ortaya çıkan külleme patojeni *Erysiphe corylacearum* ve büyüyen salgın içindeki genetik çeşitlilik derecesi DNA barkod analizi ve moleküler belirteçler ile analiz edildi. Bu örneklerde herhangi bir genetik varyasyon gözlenmedi ve bu sonuçlar mevcut salgının yeni bir bulaşma olayından kaynaklandığını düşündürdü. Mahsul ıslahında mevcut fındık genetik kaynaklarından yararlanmak için, cv Tombul için gen anotasyonu, hibrit sekanslama stratejisi ile üretilmiş tamamen birleştirilmiş bir genom dizisi aracılığıyla gerçekleştirildi. Genom, 27.270 yüksek güvenilirlikli protein kodlama geni içerir; bunların 20.000'den fazlası, fonksiyonel olarak işlevselliği homolojiye dayalı bilinen bitki proteinleriyle açıklanmıştır. Bu genom dizileme projesinin bir parçası olarak, tam kloroplast genomu birden fazla anotasyon araçlarıyla analiz edildi. Tipik bir dört parçalı yapıya sahip olan tam kloroplast genomu oluşturuldu. Bu kloroplast genomu, *Corylus* cinsinin evrimi hakkında kapsamlı bir genetik kavrayış sağlayabilir. Son olarak, soğuma stresiyle ilgili genler ve gen ağları hakkında yeni bilgiler elde etmek için transkriptom analizi yapıldı. Toplam 2.440 farklı olarak ifade edilen gen tespit edildi ve bunlardan 1.368'i soğutma stresi altında yukarı regüle edildi. Bu çalışma ağaç türlerinde üreme yaklaşımları için faydalı olabilecek donma tolerans mekanizmaları üzerine daha fazla çalışmayı kolaylaştırabilir.

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This work is dedicated

To my family, **Mehmetali**, **Habibe** and **Fahri**,

To my chosen family, **The Leylas, Kafa nereye biz oraya** and **MATGRADS-Fam**,

Who always put their weight behind me and share their endless love.

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LIST OF ABBREVIATIONS

A	adenine
ABA	abscisic acid
ABA8ox	ABA 8'-hydroxylase
ABySS	Assembly By Short Sequence
AFLP	Amplified Fragment Length Polymorphism
AP2/EREBP	Apetala 2/ethylene-responsive element binding protein
AP2/ERF	Apetala 2/Ethylene responsive factor
ATAF	Arabidopsis transcription activation factor
bp	basepair
BAC	bacterial artificial chromosome
bHLH	basic helix-loop-helix
BR	brassinosteroid
BS	bootstrap
C	cytosine
C. avellana	*Corylus avellana*
CALP	cumulative alignment length percentage
CBF/DREB1	C-repeat binding factor/Dehydration responsive element-binding 1
Chl	chlorophyll
CIP	cumulative identity percentage
CK	cytokinin
CNS	conserved non-coding sequences

CO_2	carbon dioxide
cp	chloroplast
cpDNA	chloroplast DNA
CTAB	cetyltrimethyl ammonium bromide
cv	cultivar
C-to-U	cytosine to uracil
CUC	cup-shaped cotyledon
DET	differentially expressed transcript
EudicotReps	eudicot repetitive elements from RepBase
FAO	Food and Agriculture Organization
FPKM	fragments per kilobase of exon in per million fragments mapped reads
G	guanine
GA	gibberellin
GO	gene ontology
GST	glutathione S-transferase
HMG-CoA	3-Hydroxy-3-methylglutaryl-coenzyme A reductase
HSP	heat shock protein
IMEx-web	Imperfect Microsatellite Extraction Webserver
I	isoleucine
IR	inverted repeat
IRAP	inter-retrotransposon amplified polymorphism
ITS	internal transcribed spacer
JA	jasmonic acid

KEGG	Kyoto Encyclopedia of Genes and Genomes
LSC	large single copy
L	leucine
LINE/L1	long interspersal nuclear elements
LRR	leucine-rich repeat
LTR	long terminal repeat
M	methionine
MISA	MIcroSAtellite identification tool
ML	maximum likelihood
MLST	Multilocus Sequence Typing
MYB	my elob lastosis
NAC	NAM, ATAF and CUC
NAM	no apical meristem
NC	negative control
OG	ortholog group
PAGE	polyacrylamide gel electrophoresis
PCR	polymerase chain reaction
PHD	plant homeodomain zinc finger
PlantTFDB	plant transcription factor database
qRT-PCR	quantitative real-time PCR
RAPD	random amplified polymorphic DNA
REMAP	retrotransposon-microsatellite amplified polymorphism
rDNA	ribosomal DNA

RT-qPCR	reverse transcription quantitative polymerase chain reaction
ROS	reactive oxygen species
SA	salicylic acid
SGA	String Graph Assembler
SL	strigolactones
SOAPdenovo	Short Oligonucleotide Analysis Package
SSC	small single copy
SSR	simple sequence repeat
T	thymine
TBE	Tris/Borate/EDTA
TF	transcription factor
TNT	trinitrotoluene
TRIM	terminal repeats in miniature
U	uracil
U-to-C	uracil to cytosine
UV	ultraviolet
V	valine
WGS	whole genome shotgun
zf	zinc finger
ZFP	zinc finger protein

1. DEVELOPING METHODS FOR MOLECULAR CHARACTERIZATION OF POWDERY MILDEW IN HAZEL

1.1. INTRODUCTION

European hazel (*Corylus avellana* L.) is a crop tree of worldwide agronomic importance, which has been cultivated for human consumption for thousands of years (Casus-Agustench et al., 2011). When the nutritional value is considered, the nuts are high in unsaturated fats and contain many essential and minerals (USDA, 2014). Hazelnuts have a broad usage area, such as adding flavor and texture to dairy, bakery, confectionary and chocolate products. According to FAO report (2017), hazelnuts from Turkey account for 70-80% of the world market and are the country's most valuable agricultural export, with annual sales climbing above $1 billion in 2011. For many families of the Black Sea Region, the majority of income is supplied by hazel, and it is typically farmed as a monoculture (Gonenc et al., 2006). Therefore, pathogen outbreaks, along with environmental stresses such as drought and frost, could have a serious economic impact on both the region and the nation.

The common hazel belongs to the genus *Corylus*, placed in the family *Betulaceae* and classified in the order *Fagales*. There are about 26 species in the genus *Corylus*, including *Corylus avellana*, *Corylus colurna*, *Corylus chinensis*, and *Corylus americana* (Table 1.1) (https://www.treenames.net/ti/corylus). *Corylus avellana* is the species most extensively grown worldwide for its edible nuts and higher production rate. Hazel species are deciduous trees and some large shrubs that grow in the temperate regions of the northern hemisphere.

Table 1.1: List of *Corylus* species, and distribution of harvested area

Hazelnut Names and Distribution		
Botanical Name	**Common Name**	**Location**
Corylus americana	American Hazel, Hazelnut, American filbert	EN. America
Corylus avellana	Common Hazel, European hazel	Europe, Caucasus, W. Asia
Corylus avellana var. avellana		Europe to Caucasus
Corylus avellana var. pontica		N. Turkey, W. Transcaucasus
Corylus chinensis	Chinese Hazel	MS. China
Corylus californica	California hazel	S. British Columbia (Canada) to central California (USA)
Corylus colchica	Colchican Filbert	
Corylus colurna	Turkish Hazel	Balkans, Turkey and Georgia
Corylus × colurnoides	Trazel	Transcaucasus
Corylus cornuta	Beaked Hazel	Appalachian Mountains (USA) to Gaspè peninsula (Quebec) to central British Columbia (Canada)
Corylus cornuta ssp. californica	California Hazel	British Columbia to California
Corylus cornuta ssp. Cornuta		Canada, N. and E. U.S.A.
Corylus fargesii	Farges' Hazel, Paperbark Hazel	MS. China
Corylus ferox	Himalayan Hazel	SC. China to Tibet, Bhutan and Nepal
Corylus ferox var. ferox	Himalayan Hazel	C. Himalaya to Myanmar and Tibet
Corylus ferox var. thibetica	Tibetan Hazel	C. China
Corylus heterophylla	Asian Hazel, Siberian Hazel	NE. China, Japan, Korea, Russia
Corylus heterophylla var. heterophylla		SE. Siberia, S. Russian Far East, E. Mongolia, N. and NE. China, Korea, N. & C. Japan
Corylus heterophylla var. sutchuensis		China (Yunnan, Sichuan, Guizhou, Hubei, Hunan)
Corylus jacquemontii	Jacquemont's Hazel, Indian Hazel	Northern India and Pakistan
Corylus kweichowensis	Guizhou hazel	MS. China
Corylus maxima	Filbert, Giant Filbert, European Filbert	
Corylus potaninii		SC. China, (Szechuan; Hupeh; Kweichau; Yunnan.)
Corylus sieboldiana	Asian Beaked Hazel	Japan, Korea, NE. China, Russian far E.
Corylus sieboldiana var. mandshurica	Manchurian Hazelnut	SE. Siberia to N. & C. Japan
Corylus sieboldiana var. sieboldiana		S. Korea, Japan
Corylus wangii	Wang's Hazel	

Corylus wulingensis		China (Hunan)
Corylus yunnanensis	Yunnan Hazel	China

The European hazel is typically a shrub with generally 4-8 m tall and branched stems. The leaves are rounded, deciduous, hairy on both sides, and almost 6-12 cm long. The flowers are monoecious with wind-pollinated catkins. The female catkins are small with red, pink or yellow stigmas, whereas male catkins are mainly grouped together with yellowish-brown bracteoles. Nuts, the fruit of hazelnut, are roughly spherical, up to 2 cm long, and grouped in clusters (Enescu et al., 2016). Hazelnut grows best in moderate climate with high temperature during the growing season. Moreover, it can cope with cold temperatures or even frosts (Savill, 2013). In Turkey the temperature varies between 13 and 16 °C during the growing season, and enough rainfall provides optimal conditions (Ustaoglu and Karaca, 2014).

Powdery mildew, caused by *Erysiphe corylacearum*, is a fungal infection of current concern that could impact on productivity of *Corylus avellana* in Black Sea Region. The fungal pathogen forms a white powdery coating on leaves that can be observed by naked eye. The degree of disease can be classified with the observation of patches, but molecular identification is crucial to manage the disease. There are two main pathogens, *Erysiphe corylacearum* and *Phyllactinia guttata*, that cause powdery mildew on *C. avellana*. This study focused on the molecular identification of *Erysiphe corylacearum* and distinguishing genetic diversity between and within mildew strains.

Another major emerging disease in hazel was caused by the fungal pathogen *Anisogramma anomala* in the western USA in 1970. Since then it has spread steadily through the major hazel cultivation areas of the USA and Canada (Pinkerton et al., 1992). It became as a serious problem causing the loss of the hazelnut crop, and death of affected trees for almost all hazel cultivars in North America (Thompson et al., 1996). Horticultural and fungicide control measures have been used against this fungal disease. However, these applications were expensive, and they also caused the loss of yield. Therefore, identification of resistant germplasm and breeding resistant cultivars has been investigated in order to combat the disease (Chen et al., 2007).

Powdery mildew fungi are obligate, biotrophic parasites of the family *Erysiphaceae* of the phylum Ascomycota. Unlike most fungal pathogens, powdery mildew fungi tend to grow superficially, or epiphytically, on plant surfaces. During the growing season, hyphae are produced on both upper and lower leaf surfaces. Infections can also occur on stems, flowers, or fruit. Specialized absorption cells, termed haustoria, extend into the plant epidermal cells to obtain nutrition. Thereby, it can impair photosynthesis, stunt growth, and increase the rate of senescence of host tissue. The disease can cause slight economic losses, but if the plant is left untreated, it may result in severe economic losses on some crops (Heffer et al. 2006). On hazelnut, powdery mildew disease is usually caused by *Phyllactinia guttata*, and fungi infect stems and the underside of leaves, while causing a mottled lightening and yellowing of the upper surface (Hartney et al., 2005). This fungus can infect a diverse range of hard-shelled fruit bearing trees (Pscheidt et al. 2002) in addition to *C. avellana*, from the Betulaceae, Fagaceae and Juglandaceae families (MycoBank 2015). The infection rate of powdery mildew varies according to area of the Black Sea region. Whereas infection in the eastern Black Sea region has been found to be endemic, with up to 100% of trees infected in some areas (Halilbeyoglu, 1980), in the western part of the region it was found to be the most common disease, with up to 70% infection in hazel groves (Yurut et al., 1996). Although powdery mildew is the most widespread disease on Turkish hazel, treating the disease is often thought as unnecessary because it does not directly affect the nut crop. However infected leaves are compromised in their physiological activity, dry out, curl up and fall early, with a negative impact on both productivity and propagation if the disease is allowed to continue over a period of years. In addition to infection on leaves, infection on immature nut clusters leads to crop losses because of drying out and falling early. Destroying fallen leaves and ensuring good air circulation and sunlight penetration by pruning of hazel groves are some protective applications to minimize the infection (Anonymous, 2008).

However, in the last four years a new form of powdery mildew with much more severe disease symptoms has been reported in cultivated *C. avellana* in Turkey, and observations indicate that a high proportion of hazel cultivation areas have significant damage. Since 2016, all licensed provinces of hazelnut cultivation orchards have infected by the destructive powdery mildew agent, and it was rapidly spreading throughout Asia and Europe, including Iran, Azerbaijan, Ukraine, Switzerland and central Europe. This disease is caused by a fungus with different morphological features from *P. guttata,* which was previously observed to cause a mild infection, and recently determined to be *Erysiphe corylacearum* (Sezer et al., 2017). The causative agent of the powdery mildew disease is a different fungal species with morphological features of the genus Erysiphe, section Microsphaera (Braun and Takamatsu, 2000). Several fungi from this taxon, including *E. corylacearum* (Braun, 2002), *E. corylicola* and *E. ellisii* have been observed to parasitize various *Corylus* species (Farr and Rossman, 2014). None of these species were reported to infect *C. avellana*, and nor has any species from this taxon previously been observed in Turkey; therefore, the causative agent of the disease is not yet clearly characterized at the species level. Determining the genetic characteristics of pathogen by DNA sequencing is an effective method to distinguish between fungal species and strains. Takamatsu et al. (2007) studied powdery mildew from oak, and described 7 well-differentiated clades with phylogenetic analysis based on sequencing of the ribosomal DNA (rDNA). There are two sequenced genomes of fungi belonging to the genus *Erysiphe*, *Erysiphe pisi* (Spanu et al., 2010) and *Erysiphe necator* (Jones et al., 2014), which cause powdery mildew disease on pea and grape, respectively. These genomes are vital resources for developing molecular markers such as simple sequence repeats (SSRs) that are more useful to investigate differences between strains than rDNA sequences alone (Schwarzenbach et al., 2007). A few molecular genetics tools exist for *C. avellana*; for example, Mehlenbacher et al. (2004, 2006) developed over 250 RAPD loci and 30 SSR markers for genetic linkage map, and similarly RAPD markers are already being used in breeding for resistance to the fungal pathogen *Anisogramma anomala*. Although marker assisted selection can be applicable for disease resistance in hazel breeding, the resolution of the linkage map is limited, and the use of RAPD markers is hard to apply to genetically diverse varieties (Mehlenbacher et al. 2004, 2006). Therefore, development of new molecular markers will be beneficial, especially for cultivars grown in Turkey, and can be used to map prevalence of *E. corylacearum* in the Black Sea Region.

This study aimed to characterize this emerging disease at a molecular level, and develop markers that can be used to map its prevalence in the Black Sea Region. Moreover, no fungi from this taxon have previously been reported in Turkey, and the species that causes severe powdery mildew has not yet been fully characterized, and it would be investigated whether it is a single clone or a diverse population containing multiple strains. Moreover, this was the first molecular study of powdery mildew in the Betulaceae, and determination of new hazel pathogen characteristics would give information about its origin and possible natural reservoirs. The data generated would be of considerable novelty and broad significance for understanding plant host-pathogen interactions and for future forestry research.

1.2. MATERIALS AND METHODS

1.2.1. Determination of species of the newly emerging powdery mildew pathogen

1.2.1.1. Fungal DNA isolation

DNA was isolated from fungi growing on the surface of infected leaves from multiple locations, along with examples of the less severe infection caused by *Phyllactinia guttata*. DNA isolation was carried by Dr. Arzu Sezer, head of the Plant Health Division and from the plant cultivation technologies division, agricultural engineer Özlem Boztepe, at the Giresun Hazelnut Research Institute, who joined the project as researchers. Samples, collected from Ordu, Giresun and Trabzon, were sent to Sabanci University Nanotechnology Research and Application Center.

As DNA isolation from fungal tissues can be difficult, a variety of DNA extraction methods were tested to identify the one that gives the highest yield and quality, including the DNeasy Plant Mini Kit (Qiagen, Santa Clara, CA) following the manufacturer’s protocol, CTAB (cetyltrimethyl ammonium bromide) protocol modified for fungi (Jones et al. 2014), and others if necessary. The concentration and purity of isolated DNA was estimated by UV spectrophotometry at wavelengths of 260nm and 280 nm using the NanoDrop ND-2000c (Thermo Scientific, Wilmington, DE). In order to confirm that the DNA was not degraded and of sufficient quality for Sanger sequencing analysis, 2 aliquots of each sample were also analyzed by agarose gel electrophoresis, using TBE buffer and visualizing with GelGreen nucleic acid stain (Biotium Inc., Hayward, CA).

1.2.1.2. Molecular identification of powdery mildew fungus species

The genomes of *Erysiphe* species that have been characterized to date are between 100-150 Mb in size and include a high percentage of repetitive elements (Spanu et al., 2010, Jones et al., 2014). Each DNA sample was diluted to approximately 20 ng/µL for polymerase chain reaction using PCR primers designed to amplify regions that were known to distinguish between *Erysiphe* species for both ITS and 28S regions (Figure 1.1, Table 1.2). The PCR protocols used for DNA barcode analysis were given in Table 1.3 and 1.4 for 28S and ITS regions, respectively. (Braun et al., 2007).

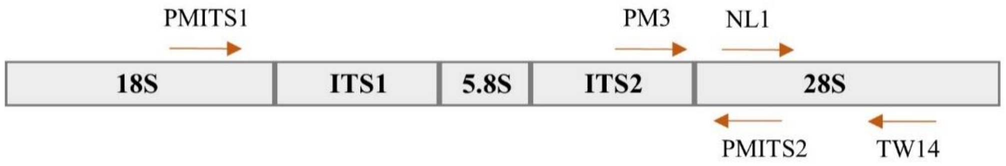


Figure 1.1: 28S and ITS regions of fungi kingdom and positions of universal primers. Forward and reverse primers are labelled at the top and the bottom, respectively.

Table 1.2: PCR primer sequences used for DNA barcode analysis

PRIMERS	SEQUENCES	ANNEALING TEMPERATURE (TM)	REFERENCE	TARGETED REGION	EXPECTED PCR LENGTH
PMITS1	TCGGACTGGCCCAGGGAGA	50 ºC	Cunnington et al. (2003)	ITS	600-650 nt
PMITS2	TCACTCGCCGTTACTGAGGT				
PM3	GKGCTYTMCGCGTAGT	50 ºC	Takamatsu and Kano (2001)	Outer part of 28S (used with TW14)	~850 nt
TW14	GCTATCCTGAGGGAAACTTC	50 ºC	Mori et al. (2000)	28S	~825 nt
NL1	AGTAACGGCGAGTGAAGCGG			Inner part of 28S (used with TW14)	

Table 1.3: PCR protocol used for 28S DNA barcode analysis

Reagents (20 µl)		PCR conditions			
10x PCR reaction buffer	2 µl	Pre-denaturation		95ºC, 5 sec	Touchdown
10 mM dNTP mix	0.4 µl	Denaturation		95ºC, 15 sec	
10 µM forward primer	0.4 µl	Annealing	16 cycles	60ºC, 25 sec	
10 µM reverse primer	0.4 µl	Extansion		72ºC, 45 sec	
Maximo Taq	0.1 µl	Denaturation		95ºC, 15 sec	
Template gDNA	1 µl	Annealing	9 cycles	52ºC*, 25 sec	
ddH$_2$O	15.7 µl	Extansion		72ºC, 45 sec	
		Final extansion		72ºC, 5 min	
		Storage		10ºC, ∞	

* Annealing temperatures for NL1 and PM3 is 55ºC and 52ºC, respectively.

Table 1.4: PCR protocol used for ITS DNA barcode analysis

Reagents (20 µl)		PCR conditions		
10x PCR reaction buffer[1]	2 µl	Pre-denaturation		95ºC, 2 min
10 mM dNTP mix	0.4 µl	Denaturation		95ºC, 30 sec
10 µM forward primer	0.4 µl	Annealing	35 cycles	58ºC, 30 sec
10 µM reverse primer	0.4 µl	Extansion		72ºC, 30 sec
Maximo Taq[1]	0.1 µl	Final extansion		72ºC, 5 min
Template gDNA	1 µl	Storage		4ºC, ∞
ddH$_2$O	15.7 µl			

The species of the newly emerging powdery mildew pathogen, determined as *Erysiphe corylacearum*, and the degree of genetic diversity within the growing epidemic was confirmed by DNA barcode analysis of the internal transcribed spacer (ITS) situated between the sequences encoding the small and large ribosomal RNA subunits and D1/D2 regions of its 28S ribosomal RNA (White et al., 1990; Figure 1.2). The PCR products were confirmed by agarose gel electrophoresis, using a 1% agarose gel in 0.5x TBE buffer, and the products visualized using non-toxic GelRed nucleic acid stain (Biotium, Hayward CA, USA). The resulting PCR products of samples collected from three different Turkish states in the Black Sea region, Giresun, Trabzon and Ordu, were then sent for Sanger sequencing of the barcode regions (BM Laboratuvar Sistemleri A.Ş., Ankara). Raw sequence data was compared with those previously reported using MEGA7 software, allowing the emerging hazel pathogen to be located in the phylogeny of *Erysiphe* species (Takamatsu et al., 2007), and aligned by ClustalW algorithm (Chenna et al., 2003). Evolutionary analyses were conducted in MEGA7 (Kumar et al., 2016).

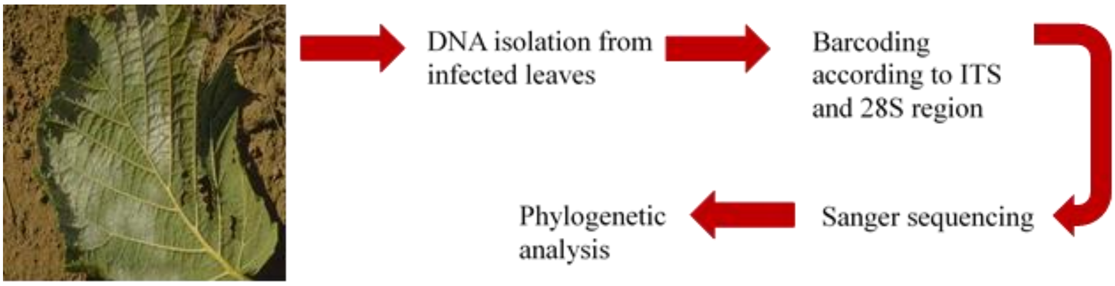


Figure 1.2: An overview of confirmation of the genetic diversity of *Erysiphe corylacearum* by DNA barcode analysis and evolutionary analysis

1.2.2. Designing molecular markers to distinguish genetic diversity between and within mildew strains

While differences between the rDNA and ITS regions are sufficient to distinguish between *Erysiphe* species, it would also be valuable to assess the genetic diversity within the emerging hazel pathogen. This could be achieved using simple sequence repeat (SSR) markers, which also have the advantage that polymorphisms can be readily detected on an agarose gel after normal PCR amplification (Schwarzenbach et al., 2007). Regions that contain SSRs in the previously sequenced *Erysiphe pisi* (ASM79871v1, European Nucleotide Archive (http://www.ebi.ac.uk/ena/data/view/GCA_000798715.1)) and *Erysiphe necator* (ASM20880v1, Max Planck Institute (http://www.mpipz.mpg.de/fungal-genomes/ downloads)) genomes were identified by bioinformatic methods (Kofler et al., 2007), and PCR primers were designed to flank these regions at 8 SSRs (Figure 1.3). These were then used to amplify the SSRs from each of the severe powdery mildew isolates collected above, and the PCR products separated and visualized by agarose gel electrophoresis, in order to determine the degree of polymorphism within the pathogenic fungus population (Table 1.5). The primer pairs that reveal the most polymorphism would be selected to carry out a geographical survey of the spread of the disease through the Black Sea Region.

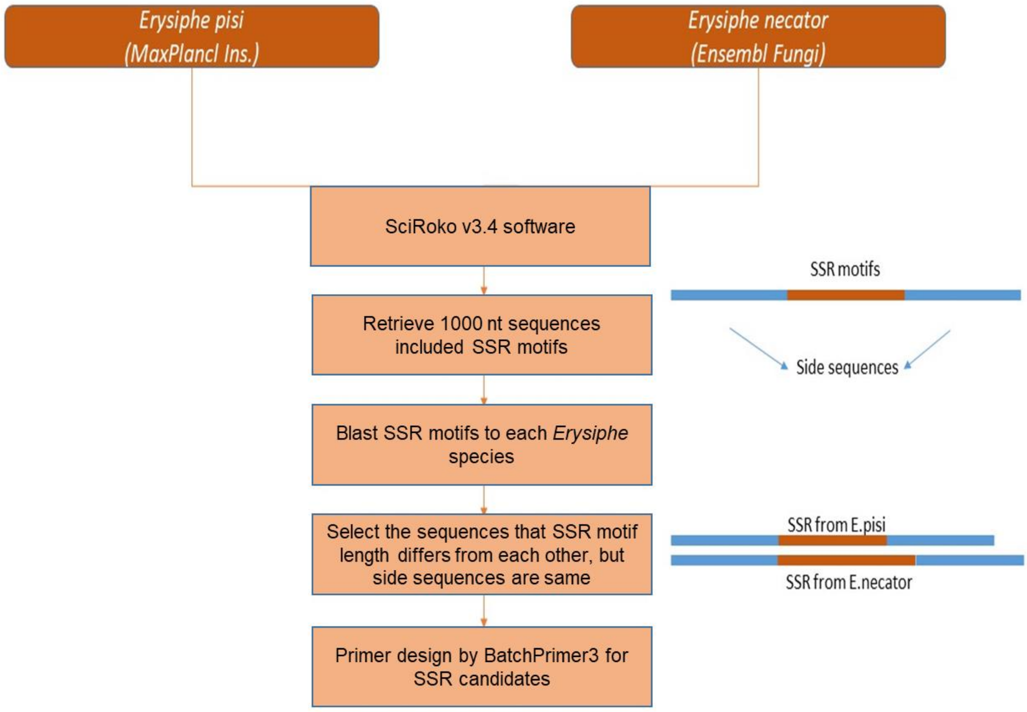


Figure 1.3: A generalized scheme of SSR marker design

Table 1.5: PCR protocol used for SSR genotyping

Reagents (20 µl)		**PCR conditions**		
10x PCR reaction buffer[1]	2 µl	Pre-denaturation		95ºC, 2 min
10 mM dNTP mix	0.4 µl	Denaturation	35 cycles	95ºC, 30 sec
10 µM forward primer	0.4 µl	Annealing		58ºC, 30 sec
10 µM reverse primer	0.4 µl	Extansion		72ºC, 30 sec
Maximo Taq[1]	0.1 µl	Final extansion		72ºC, 5 min
Template gDNA	1 µl	Storage		4ºC, ∞
ddH$_2$O	15.7 µl			

For SSR markers, SciRoKo v3.4 software was used to determine SSR motifs (Table 1.6) (Kofler et al., 2007), and PCR primers were designed by BatchPrimer3 software (https://probes.pw.usda.gov/batchprimer/). Eight selected SSR primers were listed in Table 1.7.

Table 1.6: SSR motifs for candidate SSR markers

SSR ID*	SSR	FULL MOTIF
EP10308	GCT	GCTGCTGCTGCTGCTGCTGC
EP12023	AAAT	AAATAAATAAATAAATAAATAA
EP12856	GCGCA	GCGCAGCGCAGCGCAG
EP00265	A	AAAAAAAAAAAAAAAAAA
EP01434	ATA	ATAATAATAATAATAATGATAATACTAATA
EP01989	TCTTCG	TCTTCGTCTTCGTCTTCGTCTTC
EP03113	AAG	AAGAAGAAGAAGAAGA
EP03497	AC	ACACACACACACACA

* SSR ID was given as based on *E.pisi* genome.

Table 1.7: Primers designed for common SSR motifs

SSR ID*	FORWARD PRIMER	REVERSE PRIMER	PCR PRODUCT LENGTH (BP)*
EP10308	TCTGAGCGAGATCCCTGCT	GATCCGATATGAAGATTGGCATAT	187
EP12023	ACTATTGACTACCCCAGCCT	TCAAATATTTTGAGGTTTGATGG	211
EP12856	AAAGCATCATTTGCCTTATCA	GTTATAGCAAATGCAGAATCAGT	182
EP00265	GATACCAGCATACCTTGCATGCT	TGGTCAACGATGCTCTAAACA	254
EP01434	AAGGAAAAGCAAATGTTCTTGC	CCTCTGTCAACTGTGAACCAT	152
EP01989	TGTATTTATCATATGTGATCTTAGT	AGCTCGAGCTAATTGTGTTG	293
EP03113	GTATTTCTTGAAGCTCTATCCAT	ATGGCCGACATATTGTAATGG	182
EP03497	GAGCGAAAGGATTCGGGTTG	CGGTGCTGGATGAACGAACA	209

* SSR ID and PCR product length were given as based on *E.pisi* genome.

Retroelements (retrotransposons) represent a major part of all the DNA in most plant and fungus genomes. These elements have very conserved genes within them, and create large and stable insertions in the genome. Therefore, they are used as an efficient tool for detecting the genomic changes associated with their activity to visualize the genetic diversity. Two marker systems, inter-retrotransposon amplified polymorphism (IRAP) and retrotransposon-microsatellite amplified polymorphism (REMAP) methods, were also developed to exploit polymorphisms within the pathogenic fungus population. In the IRAP method, amplification is carried out between the long terminal repeats (LTRs) of two retrotransposons with a single primer matching either the 5’ to 3’ end of LTR. REMAP method is similar to IRAP, but amplification is carried out between primers matching a LTR and a microsatellite domain (SSRs). LTRs from *Erysiphe pisi* and *Erysiphe necator* genomes were identified by bioinformatic methods, RepeatMasker, then common LTRs were retrieved and annotated to detect long terminal region, sequences used to design IRAP primers (Figure 1.4, Table 1.8). For REMAP primers, previously identified SSRs were used by adding a selective base at the 3'-end of repeat motifs (Kalendar and Schulman, 2006) (Figure 1.5, Table 1.8).

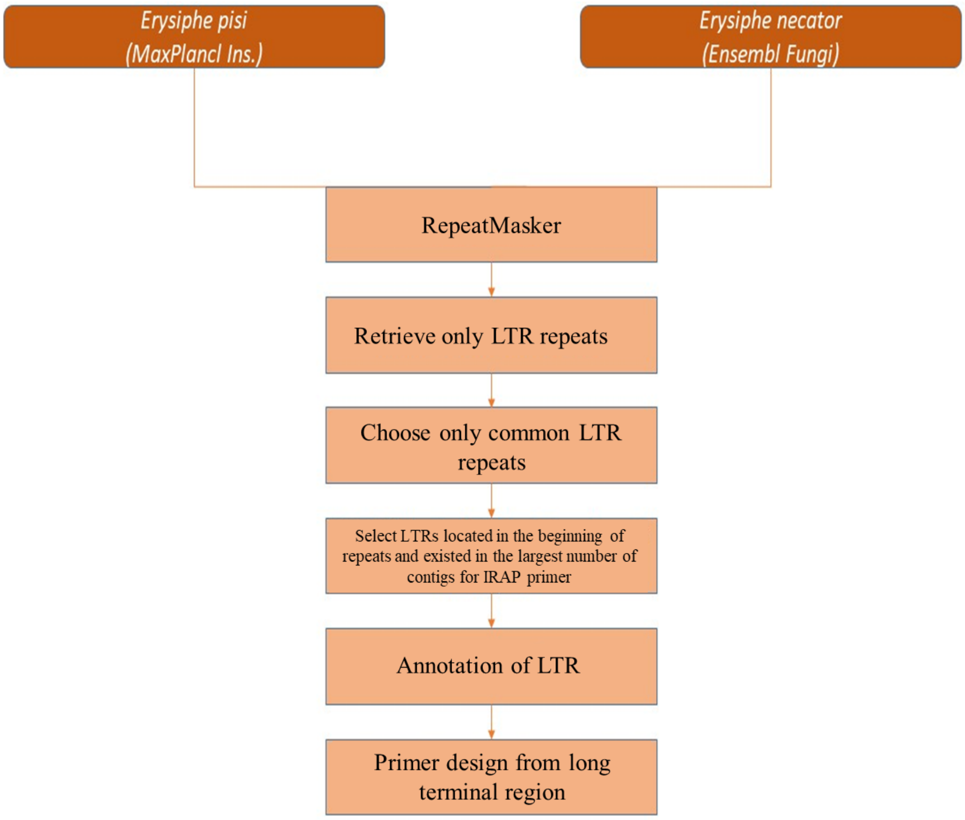


Figure 1.4: A generalized scheme of IRAP marker design

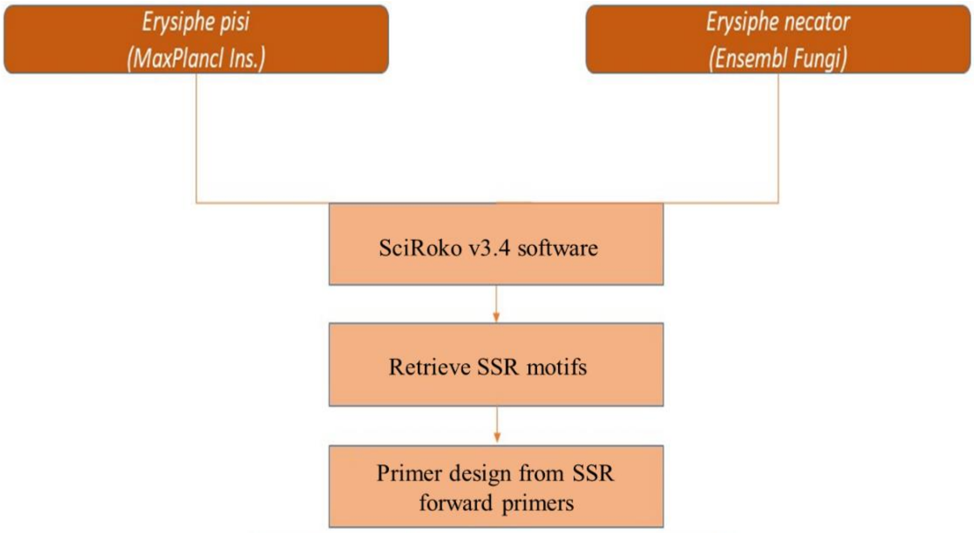


Figure 1.5: A generalized scheme of REMAP marker design

Table 1.8: Inter-retrotransposon amplified polymorphism (IRAP) and retrotransposon-microsatellite amplified polymorphism (REMAP) markers

IRAP ID	Primer sequences
Gypsy14_NN1	TGA AAC ACT TCG AAG GTG AAG
LTRa1_001_140	TTT TAC AGT TGT ACT GGA TAC
LTRa1_003_561	AAA CCC CGA CTC GGA AGA AG
LTRgm_14_4515	CCA ATG CCC TTT GGG GCT CT

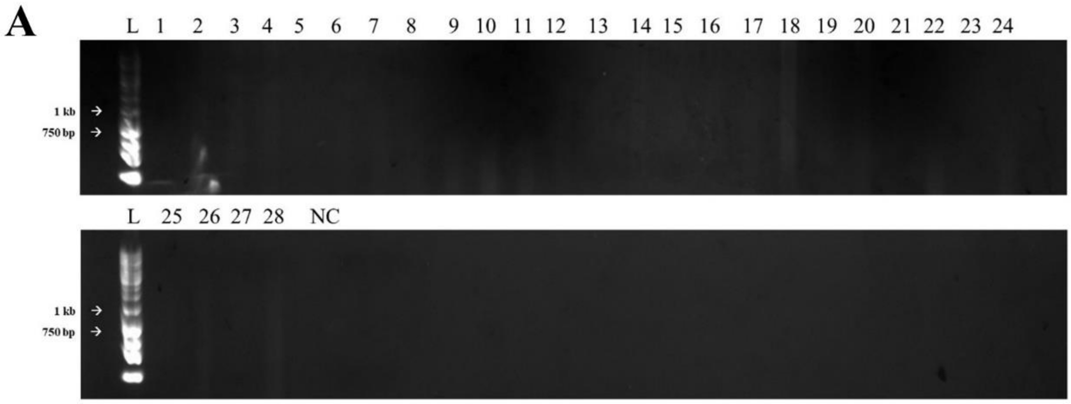
REMAP ID	Primer sequences
REMAP_10308	GCT GCT GCT GCT GCT GCT A
REMAP_12023	AAA TAA ATA AAT AAA TAA ATG
REMAP_12856	GCG CAG CGC AGC GCA T
REMAP_265	AAA AAA AAA AAA AAA AAA AAG
REMAP_1434	ATA ATA ATA ATA ATA ATA ATA G
REMAP_1989	TCT TCG TCT TCG TCT TCG A
REMAP_3113	AAG AAG AAG AAG AAG AAG AAG C
REMAP_3497	ACA CAC ACA CAC ACA CAC ACG

1.3. RESULTS

1.3.1. Molecular identification of powdery mildew fungus in hazelnut

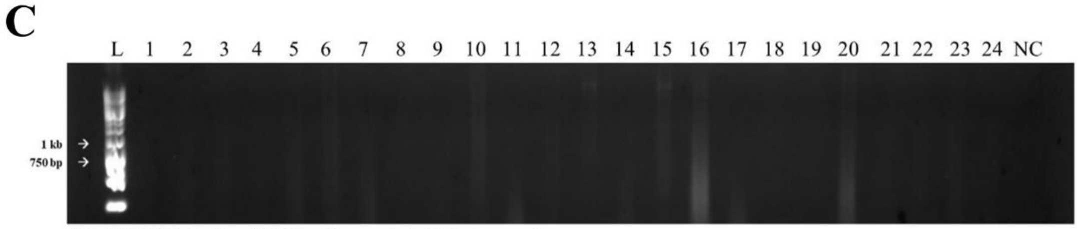
The species of the newly emerging powdery mildew pathogen, *Erysiphe corylacearum*, was confirmed by DNA barcode analysis of the internal transcribed spacer (ITS) situated between the sequences encoding the small and large ribosomal RNA subunits and the regions of two variable domains near the 5' end of the large subunit, the D1/D2 regions of the 28S ribosomal RNA. The isolated DNA samples contained both fungus and hazelnut DNA. To amplify barcode region belonging to only fungi, specific PCR primers were designed for both ITS and 28S regions (Figure 1.1, Table 1.2). A semi-nested PCR reaction was used for specific and abundant amplification of 28S region. Maximo Taq polymerase enzyme was used for all PCR reactions, and PCR products were confirmed by agarose gel electrophoresis, using a 1% agarose gel in 0.5x TBE buffer, and the products visualized using non-toxic GelRed nucleic acid stain.

PM3-TW14 primer pairs were used as first PCR reaction for 28S region amplification. Agarose gel images of Giresun, Ordu and Trabzon samples were shown in Figure 1.6. As expected, bands were not observed in almost all samples because of low DNA concentration in the first PCR. Then, PCR products were amplified with NL1-TW14 primer pairs. However, the band was observed in when negative control of first PCR product was used as template in second PCR as negative control (NC*) (Figure 1.7).



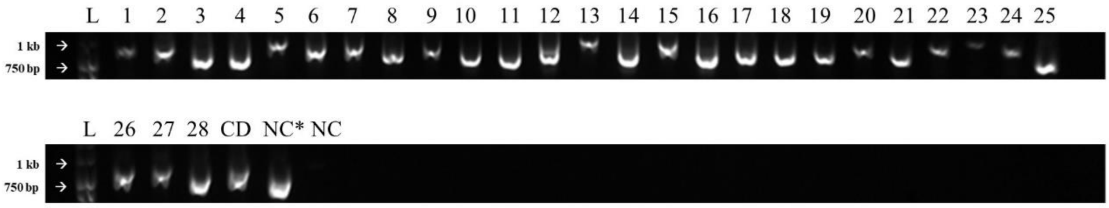
* L: 1 kb DNA ladder; NC: Negative control; Giresun samples

* L: 1 kb DNA Ladder; NC: Negative control; Ordu samples



* L: 1 kb DNA Ladder; NC: Negative control; Trabzon samples

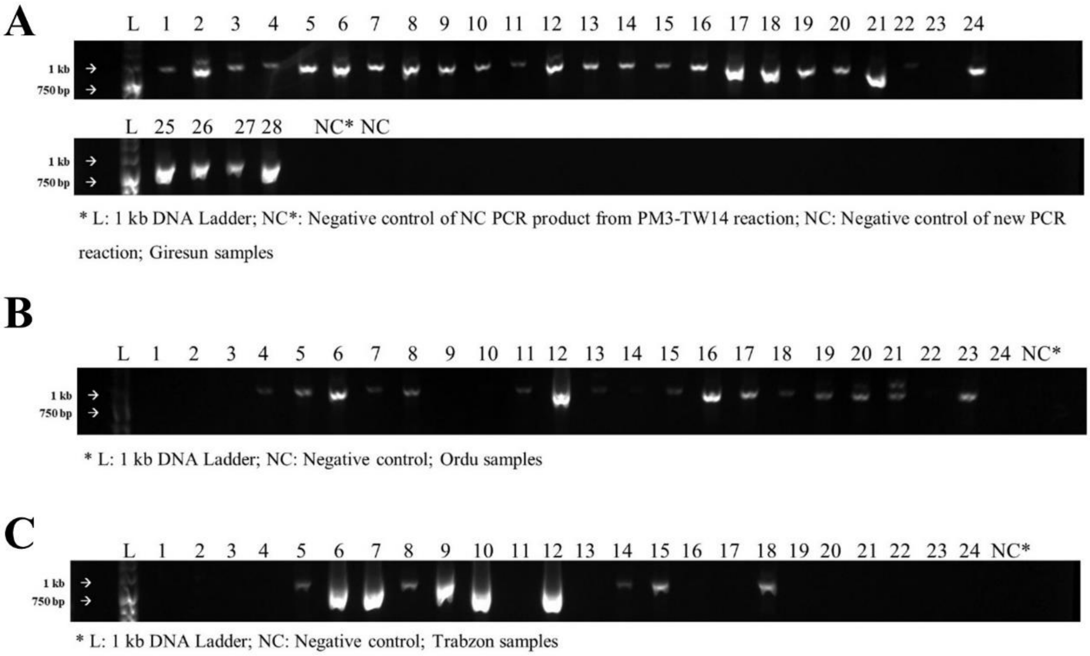
Figure 1.6: Agarose gel images of amplified PCR products with PM3-TW14 primer pairs of **a.** Giresun samples, **b.** Ordu samples, **c.** Trabzon samples



* L: 1 kb DNA ladder; CD: Control DNA; NC*: Negative control of NC PCR product from PM3-TW14 reaction; NC: Negative control; Giresun samples

Figure 1.7: Agarose gel image of amplified PCR products of Giresun samples with NL1-TW14 primer pairs

It was thought that the band observed in NC* was caused by non-specific binding, and literature research about PCR optimization was carried out for resolving the risk of contamination and off-target amplification (Roux, 2009). From this, the combination of nested PCR with touchdown PCR was selected for further PCR reactions. The PCR reaction was started with a high annealing temperature, which was decreased in the first 16 cycles by 0.5 °C during the amplification stage. Therefore, off-target primer binding was prevented in the early cycles, so that only the targeted region was amplified with decreasing temperature. No band was observed in when negative control of first PCR product was used as template in second PCR as negative control (NC*) (Figure 1.8).



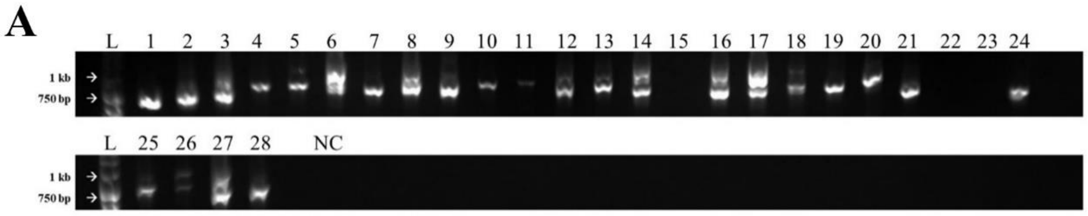
* L: 1 kb DNA Ladder; NC*: Negative control of NC PCR product from PM3-TW14 reaction; NC: Negative control of new PCR reaction; Giresun samples

* L: 1 kb DNA Ladder; NC: Negative control; Ordu samples

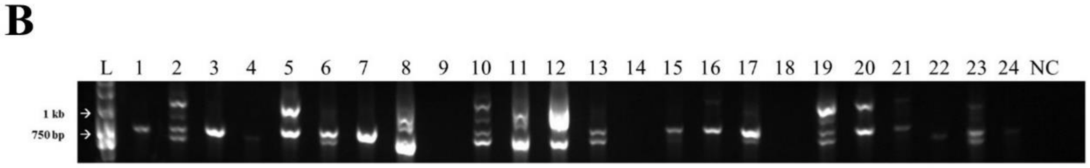
* L: 1 kb DNA Ladder; NC: Negative control; Trabzon samples

Figure 1.8: Agarose gel image of amplified PCR products with NL1-TW14 primer pairs of **a.** Giresun samples, **b.** Ordu samples, **c.** Trabzon samples (Combination of nested PCR with touchdown PCR)

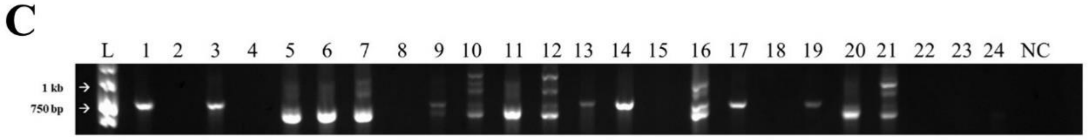
For amplification of the ITS region, the best favorable annealing temperature was determined by gradient PCR, and the samples were amplified with the PMITS1-PMITS2 primer pair in a single reaction (Figure 1.9).



* L: 1 kb DNA Ladder; NC: Negative control; Giresun samples



* L: 1 kb DNA Ladder; NC: Negative control; Ordu samples

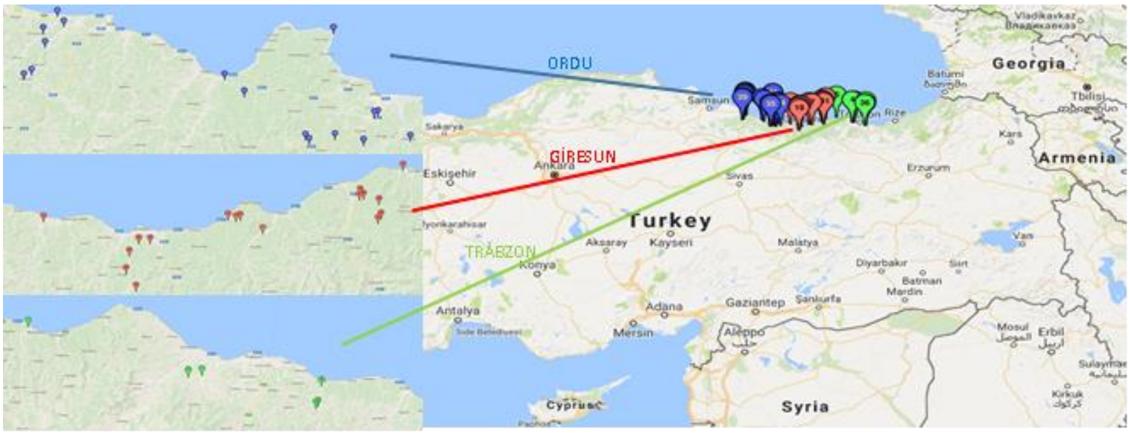


* L: 1 kb DNA Ladder; NC: Negative control; Trabzon samples

Figure 1.9: Agarose gel image of amplified PCR products with PMITS1-PMITS2 primer pair of **a.** Giresun samples, **b.** Ordu samples, **c.** Trabzon samples

PCR products for which a single, bright band was observed on the gel were sent for Sanger sequencing (Appendix A: Table S1.1-3). Products were sequenced from both ends using PMITS1-PMITS2, and NL1-TW14 primer pairs for ITS and 28S regions, respectively. Raw sequence data was compared with those previously reported using MEGA7 software, allowing the emerging hazel pathogen to be located in the phylogeny of *Erysiphe* species (Takamatsu et al., 2007), and aligned by ClustalW algorithm. Evolutionary analyses were conducted in MEGA7 (Kumar et al., 2016).

The powdery mildew samples were collected from three different cities, Giresun, Ordu and Trabzon, from the Black Sea Region. The coordinates of orchards are indicated in Figure 1.10. 110 samples collected from 44 orchards spread across the Eastern Black Sea Region were sequenced (Table 1.9). According to sequence alignment results, 108/110 samples were genetically identical in the barcode region. Typical results belonging to several identical samples are shown in Figure 1.11a. This finding may indicate that the newly emerging disease caused by *E. corylacearum* arose from a recent single transmission event. However, several nucleotide differences were detected in 2 samples collected in Ordu province (Figure 1.11b).



1 Akçaabat-Derecik Mah.
2 Akçaabat-Derecik Mah.
3 Akçaabat-Derecik Mah.(İbrahim Bey'in Bahçesi)
4 Akçaabat-Yeşilyurt Mah.
5 Beşikdüzü-Çeşmeönü Mah.
6 Bulancak-Pazarsuyu
7 Espiye-Kaşdibi Köyü
8 Fatsa-Ilıca
9 Fatsa-Ilıca (Yukarı Kesim)
10 Görele 1- Hastane Üstü
11 Keşap-Düzköy-Gelene Mah.
12 Keşap-Yolağzı
13 Keşap-Yolağzı-Cingiren
14 Merkez (Altınordu) Budama Proje Bahçesi
15 Merkez (Altınordu) Kuştepe
16 Merkez (Altınordu)-Kuştepe
17 Merkez (Altınordu)-Ulubey Yolu Üzeri
18 Merkez (Altınordu)-Ulubey Yolu Üzeri
19 Merkez-Elmatepesi
20 Merkez-Kemaliye Köyü
21 Merkez-Org.Sanayi Çıkışı
22 Merkez-Yukarıalınlı
23 Merkez-Çalış yolu-Kayadibi
24 Perşembe-Mersin Köyü
25 Perşembe-Çeşmeönü Mevkii
26 Perşembe-Çeşmeönü Mevkii
27 Tirebolu-Balçıkbelen-Merkez Mah
28 Tirebolu-Belenköyü-Göğceyazı
29 Tirebolu-Deeme Bahçesi Alt Kısmında
30 Tirebolu-Gençleştirme Bahçesi
31 Tirebolu-Kovanpınar
32 Tirebolu-Yağlıkuyumcu Köyü
33 Ulubey (Mezarlık Yanı)
34 Ulubey-Fındıklı Köyü
35 Ulubey-Sayaca Köyü
36 Yomra-Kömürcü Mah.
37 Yomra-Kömürcü Mah.
38 Yomra-Kömürcü Yolu Girişi
39 Çaybaşı
40 Çaybaşı (Giriş, Cami Yanı)
41 Ünye (Akçay Köprüsü Üst Tarafı)
42 Ünye (İkizce Yolu Girişi)
43 Ünye (Çatak Yolu Üzeri)
44 Ünye-Alan Mevkii

Figure 1.10: The coordinates of orchards where powdery mildew samples were collected. Orchards located in Ordu, Giresun and Trabzon were represented with blue, red and green color, respectively. The names of 44 orchards spread across the Eastern Black Sea Region were indicated below the map.

Table 1.9: Number of sequenced samples collected from three different location from Black Sea Region

	Number of sequenced samples	**Number of resembling sequences**	**Number of differential sequences**
Ordu	25	23	2
Giresun	54	54	-
Trabzon	16	16	-

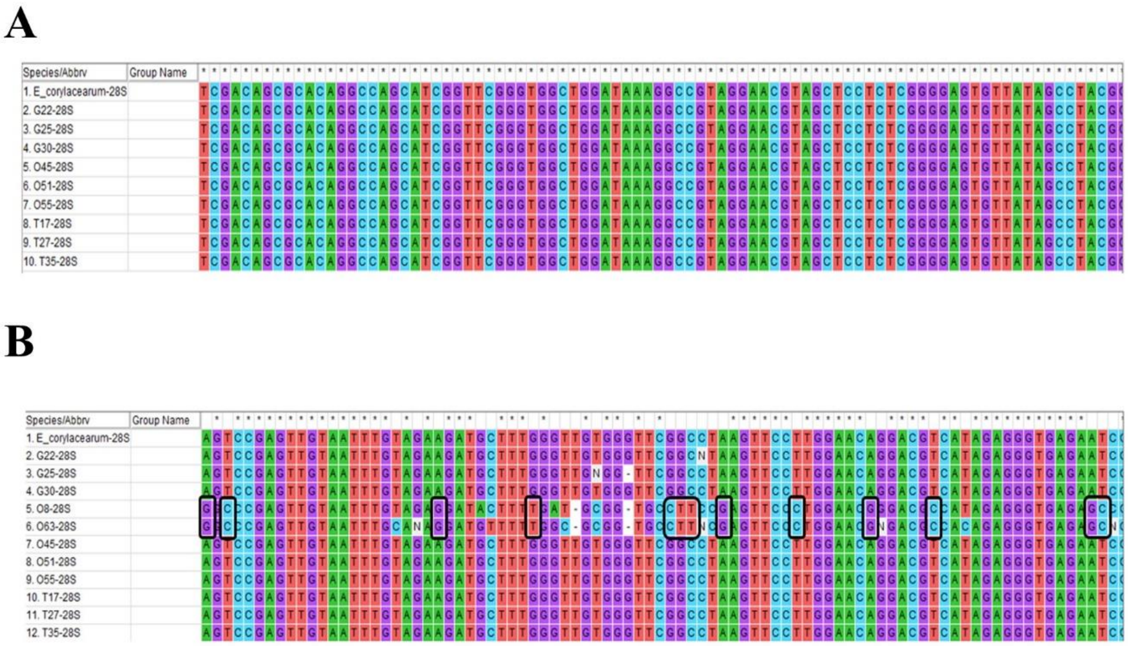


Figure 1.11: Typical alignment results for bases of the 28S barcode region of sequenced data. **a.** E_corylacearum-28S - original species sample collected in 2015 (GenBank Accession No. KX279887.1). All other samples - this study; G = Giresun province, O = Ordu province, T = Trabzon province **b.** Multiple sequence alignment that different nucleotides were remarked in two samples collected from Ordu province

The evolutionary history of these samples was inferred by using the Maximum Likelihood method based on the Tamura-Nei model (Kumar et al., 2016). Phylogenetic analysis including the closest fungi family according to BLAST+ results was carried out with several of the similar samples according to sequence alignment and two different samples. As stated in phylogenetic analysis, O8 and O63 were closely related to each other, and they formed a separate sub-group located between *Erysiphe corylacearum* and *Erysiphe quercicola* & *Erysiphe magnifica* (Figure 1.12). When sequences belonging to these two samples were investigated in UNITE fungi database (https://unite.ut.ee/), the closest species to O8 was *Gibberella avenacea* (97% identical), and O63 was *Melanconis alni* (95% identical). Further studies are required to determine which species they should be assigned to, or whether they could be hybrids.

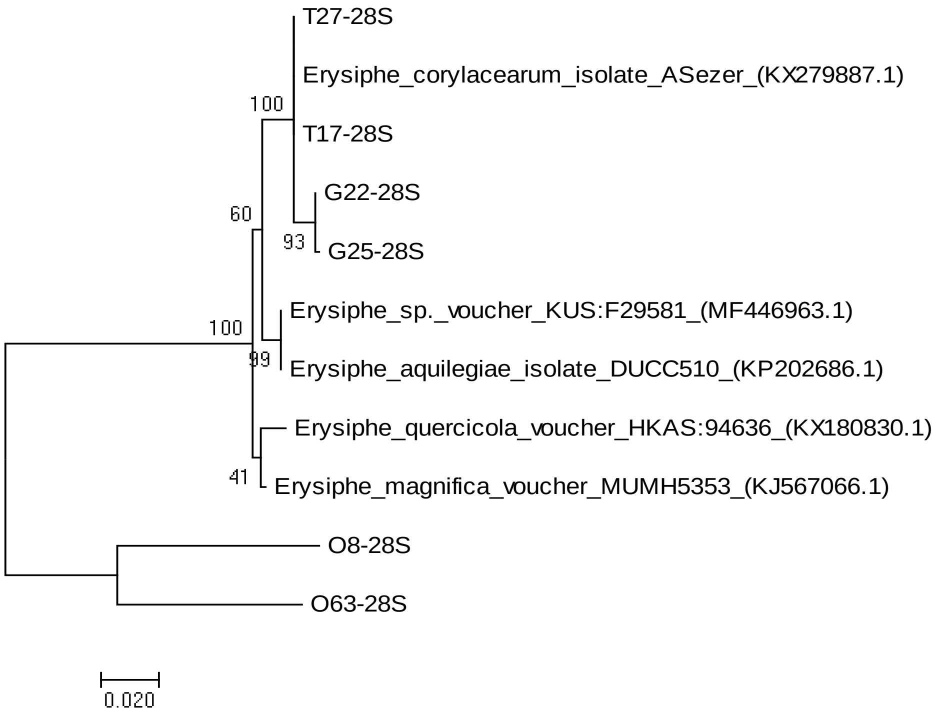
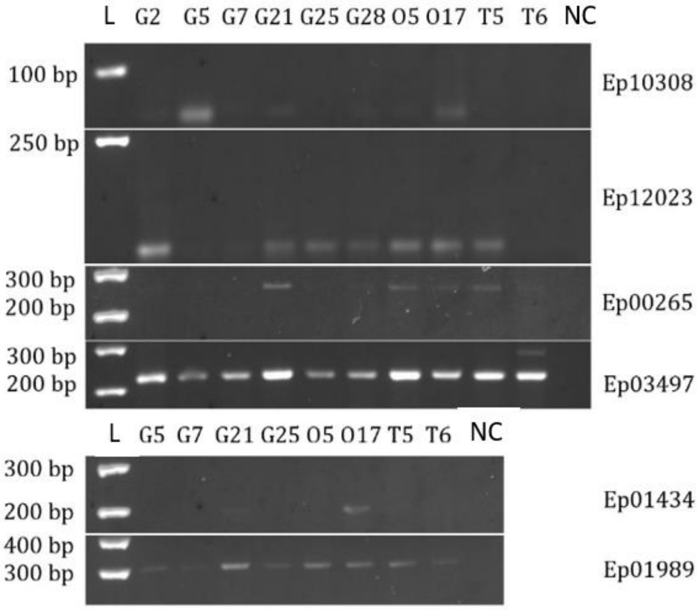


Figure 1.12: Molecular phylogenetic analysis by Maximum Likelihood method. In phylogenetic tree, node labels indicate the confidence of node assignments calculated by bootstrap analysis (500 replications). There were a total of 813 positions in the final dataset. Evolutionary analyses were conducted in MEGA7.

1.3.2. Designing molecular markers to distinguish genetic diversity between and within mildew strains

Genetic diversity of *E. corylacearum* was not observed in barcode sequencing. Therefore, molecular markers were developed to try to discover genetic diversity within the emerging hazel pathogen. Common sequences from previously sequenced *Erysiphe pisi* (Spanu et al., 2010) and *Erysiphe necator* (Jones et al., 2014) genomes were used to identify the molecular markers. Simple sequence repeat (SSR), inter-retrotransposon amplified polymorphism (IRAP), and retrotransposon-microsatellite amplified polymorphism (REMAP) markers were designed with this approach (Kalendar and Schulman, 2014). SSR and retrotransposons motifs were identified from *Erysiphe* genomes with SciRoKo (Kofler et al., 2007) and Repeatmasker (Smit et al. 2014) software, respectively. Common motifs for both *E. pisi* and *E. necator* genomes were selected for all 3 marker types, and PCR primers were designed to get PCR products of different lengths.

For SSR markers, SciRoKo v3.4 software was used to determine SSR motifs (Table 1.6). Then 1000 nt sequences including SSR motifs were retrieved by in-house perl program, and SSR motifs were blasted to each *Erysiphe* species by BLAST+ software (Camacho et al., 2009). The sequences for which the SSR motif length differed from each other, but side sequences were conserved were selected as candidate SSR markers, and PCR primers were designed by BatchPrimer3 software (https://probes.pw.usda.gov/batchprimer/). According to blast results, primers with hits to more than one region were eliminated, and 8 selected SSR primer pairs were listed in Table 1.7. These PCR primers were used in samples that had been shown to belong to *E. corylacearum* by the barcoding method. PCR products were confirmed by agarose gel electrophoresis, using a 2% agarose gel. Two primers, Ep12856 and Ep03113, were not amplified in all samples. The length of PCR product for Ep10308 and Ep12023 primers was smaller in *E. corylacearum* than in genome of *E. pisi*, and the length of PCR products was larger in *E. corylacearum* for other SSR candidates. The length differences could be caused by mutations in target sequences of primer binding sites or the quality of gDNA. According to the PCR results, polymorphism couldn't be detected among *E. corylacearum* samples, in other words no diversity was found with SSR markers among species (Figure 1.13).



*L: Ladder, NC: Negative control, Gx, Ox, Tx : Samples collected from Giresun, Ordu and Trabzon

Figure 1.13: PCR amplification for SSR motifs in *E. corylacearum* samples

Retroelements have very conserved genes within them, and create large and stable insertion in the genome. Therefore, they are used as an efficient tool for detecting the genomic changes associated with their activity to visualize the genetic diversity. Because of the lack of diversity detection with SSR markers, two other marker systems, inter-retrotransposon amplified polymorphism (IRAP) and retrotransposon-microsatellite amplified polymorphism (REMAP) methods, were also developed to exploit polymorphisms that may exist within the pathogenic fungus population. Long terminal repeats (LTRs) from *E. pisi* and *E. necator* genomes were identified by bioinformatic methods, RepeatMasker, then common LTRs were retrieved by Perl program from contig sequences. The LTRclassifier (Monat et al., 2016) web server was used for annotation to detect gene regions of transposons, and sequences were used to design IRAP primers that were suitable for long terminal region. For REMAP primers, previously identified SSRs were used by adding a selective base at the 3'-end of repeat motifs (Table 1.8). PCR products were visualized by agarose gel electrophoresis, using a 2% agarose gel in 0.5x TBE buffer, and the products visualized using non-toxic GelRed nucleic acid stain. However, these PCR primers amplified no markers in all samples.

1.4. DISCUSSION & CONCLUSIONS

1.4.1. Discussion

The Black Sea region is the major site of hazelnut production of Turkey. Because of the economic importance of agricultural exports, effects that cause production yield loss shoud be well understood to cope with the reduction. Since 2013, a severe powdery mildew disease was observed in this region. Furthermore, the disease was observed in almost all hazelnut groves tested in the eastern Black Sea region in July of 2016. According to observations of Lucas et al. (2018), the new powdery mildew caused by *Erysiphe corylacearum* was epidemic in the eastern Black Sea region, and it will probably cause reduction in hazelnut production due to effects on leaves, young shoots and immature nut clusters, especially in sensitive varieties. Therefore, molecular analysis has a crucial place to light on intervention approaches for the disease.

The DNA barcoding approach is widely used to identify and distinguish between and within morphologically similar species. In previous studies, the ITS region was selected as the standard fungal barcode (Schoch et al., 2012). However, secondary markers should also be used to reliably express an idea about genetic diversity in the case of low ITS interspecific variability. Sezer et al. (2017) determined and compared ITS and 28S regions from powdery mildew samples with previous datasets, deposited in GenBank (Accession No. KY082910 & KX279887 respectively), and the analysis was carried out with primers desigened using these datasets. In this study, samples from infected hazelnut orchards in Giresun, Ordu and Trabzon were collected, and the fungi found in these orchards were characterized by using DNA barcode analysis for two variable regions of the ribosomal RNA gene, 28S and ITS regions. Isolates were identified and distinguished whether they belonged to *E. corylacearum* or another fungus species. The ITS and 28S barcode regions amplified by PCR were also sequenced to assess whether a single or multiple strains existed in the current disease caused by *E. corylacearum*. For amplification of the 28S region, nested PCR was conducted, but a band was observed in negative control when it was used as template in the second step. Hence, touchdown PCR was combined with nested PCR, and the band was eliminated by enhancing specificity. Identical sequences were found in both regions for nearly all of the *E. corylacearum* isolates, indicating that they belong to the same species. With DNA barcode analysis, no sequence diversity was observed among the fungal isolates collected from the Black Sea region, thus molecular markers were developed to try to discover genetic diversity within the isolates. Since the *E. corylacearum* genome has not been sequenced yet, two previously sequenced *Erysiphe* genomes, *E.pisi* and *E. necator*, were used to develop SSR markers that could provide a more precise distinction between strains (Schwarzenbach et al., 2007). According to the PCR analysis, similar results were observed in nearly all the isolates and no genetic variation could be detected at SSR loci by agarose gel electrophoresis. To increase resolution, the samples could be visualized by polyacrylamide gel electrophoresis (PAGE) that can separate up to 5-500 bp fragments of DNA, to observe differences among samples. In addition, capillary electrophoresis could also be used because of its high sensitivity and precision to distinguish single base length variations. However, the PCR product length of SSR regions was readily detectable with agarose gel electrophoresis, and the DNA barcoding also found little or no variation. Pirondi et al. (2015) analyzed the genetic diversity of the cucurbit powdery mildew fungus *Podosphaera xanthii* using several PCR approaches. They concluded that no variations were observed in housekeeping gene fragments with Multilocus Sequence Typing (MLST) analysis, and high similarity was also found between isolates from Amplified Fragment Length Polymorphism (AFLP) data. Wyman et al. (2019) indicated that the low genetic diversity was observed among sampled dogwood powdery mildew caused by *Erysiphe pulchra* with both agarose gel and capillary electrophoresis systems. Hence, it could be expected that results would be similar with all techniques. Altogether, these results provide further evidence for limited genetic diversity among isolates collected from the Black Sea region in 2016-2017, and indicate that current outbreak was originated from a single recent transmission event. On other hand, it is possible that diversity has increased more recently.

1.4.2. Conclusions

The currently observed and damaging form of powdery mildew disease on hazelnut in Turkey was caused by *E. corylacearum*. In a few years it has rapidly spreading through the Black Sea region, and the infection is now ubiquitous throughout the region. According to observations of Lucas et al. (2018), almost all of the standard Turkish hazelnut varieties are susceptible to the new powdery mildew disease, hence the understanding the disease at a molecular level has become vital to prevent yield reduction. Herein, DNA barcoding and SSR markers were used for genetic characterization of powdery mildew fungus, and no genetic variations were detected among isolates collected in 2016-2017. This suggested that it comes through a single strain, and it would be much easier to find genetic resistance against the disease. As future aspects, molecular marker analysis could be carried on with the collected samples in more recent years to determine whether new mutations are leading to strain diversification or not.

2. GENOME DATA ANALYSIS AND GENE MODELLING OF TOMBUL CULTIVAR

2.1. INTRODUCTION

Due to great economic importance of European hazel (*Corylus avellana* L.), hazelnuts are a fundamental source of income for many families in the Black Sea Region. Even though it has a vital place in agriculture, the current knowledge of the hazelnut genome is very limited. The characterization of the hazel genome was the first aim of the TUBITAK project conducted by Asst. Dr. Stuart J. Lucas in which I was involved, and it produced the first fully assembled sequence of the genome, for the Turkish hazel cultivar, Tombul. This provided broad knowledge in understanding the genetics and biochemistry of this species, and may be a useful for breeders to produce more stable hazelnut for the future. Assembly and annotation of hazel genes was one of the parts of this study, and it provides an essential foundation for researchers in understanding hazel molecular biology, and developing molecular markers relevant to any trait of agricultural interest.

Even though hazelnut has a significant place in agriculture, the only available genome sequences for *C. avellana* at the start of this project was a draft genome for the American cultivar ‘Jefferson’ (Rowley et al. 2018). *C. avellana* was recently characterized by Falistocco and Marconi (2013) as having a diploid genome structure (2n = 22), and a genomic bacterial artificial chromosome (BAC) library has been constructed for the ‘Jefferson’ variety, as a basis for map-based cloning (Sathuvalli and Mehlenbacher, 2017). Although whole genome sequencing has been made much more affordable by next-generation technologies, to date only draft genome and transcriptome assemblies were available for European hazelnut, the latter consisting of 28,255 contigs that represented putative transcript sequences (Rowley et al. 2012). In addition, the transcriptome of *C. mandshurica*, a wild hazelnut species native to China, has been sequenced, and 37,846 contigs were generated. A little over half of these contigs (19,908) were mapped to the same genes in other species as *C. avellana* contigs. Another Chinese species, *C. heterophylla*, has also been transcriptome sequenced for identification of genes related to cold tolerance (Chen et al., 2014). In previous studies, a genetic linkage map and SSR markers have also been developed for *C. avellana* (Mehlenbacher et al., 2006; Bhattarai and Mehlenbacher, 2017; Colburn et al., 2017). In addition, genetic diversity between Turkish and European hazelnut varieties was characterized with SSR markers by using a partial genome sequencing approach (Öztürk et al., 2018).

2.2. MATERIALS AND METHODS

2.2.1. DNA extraction, sequencing, and assessment of genome assembly

Two-year old saplings of *C. avellana* L. cv Tombul were obtained from commercial nurseries and the shrubs cultivated on the Sabanci University campus. High molecular weight DNA was extracted from hazel tissues using a CTAB method optimized for Betulaceae (Wang et al., 2013). The concentration and purity of isolated nucleic acids were estimated by UV spectrophotometry at wavelengths of 260nm and 280 nm using the NanoDrop ND-2000c (Thermo Scientific, Wilmington, DE) and agarose gel electrophoresis was conducted to check for DNA degradation. Final DNA concentration was measured using a dsDNA-specific fluorescent dye (Quant-iT HS dsDNA Assay Kit, ThermoFisher, Waltham, MA, USA).

The same protocol was modified for RNA isolation. All buffers were newly prepared using nuclease-free water. Fresh buds were picked, flash frozen in liquid nitrogen, and ground using 3 mm steel beads in a Tissue Lyser II (Qiagen, Santa Clara, CA). During the 2 x CTAB incubation, RNAse A was not applied; nucleic acids were subsequently recovered by extraction with 24:1 chloroform:isoamyl alcohol. The RNA-containing aqueous phase from this extraction was precipitated using isopropanol. The pellet was cleaned by resuspension first in high salt TE buffer, then in TE without added salt, with ethanol precipitation after each step. The final total RNA was resuspended in 60 µl TE and residual DNA eliminated using RNAse-free DNAse I. In order to confirm that the RNA was not degraded and of sufficient quality for RNA sequencing (RNA-Seq) analysis, 2 aliquots of each sample were also analyzed by agarose gel electrophoresis.

Whole genome shotgun libraries were prepared using TruSeq Library Preparation kits and selected for an insert size of 700-800 nt. Paired-end sequencing was carried out on

Illumina HiSeq4000, and Illumina library preparation and sequencing were carried out by Macrogen (Seoul, S Korea). Reads were deposited in the European Nucleotide Archive (Project accession: PRJEB31933). In addition to genome sequencing, single-molecule and proximity ligation sequencing were carried out obtaining a better complete assembly. For single-molecule sequencing, whole genomic DNA was physically disrupted into ~8kb fragments using a Covaris g-TUBE (Covaris, Woburn, MA, USA) and then NanoPore sequencing was prepared on the MinION platform using R9.4 flowcells and the Ligation Sequencing Kit 1D according to the manufacturer’s protocols (Oxford NanoPore Technologies, Oxford, UK). Proximity ligation sequencing was carried out by Dovetail Genomics (Santa Cruz, CA) using their proprietary Chicago & HiC protocols.

The raw sequence reads were assembled using different *de novo* assembly methods, including String Graph Assembler (SGA) (Simpson and Durbin, 2012), Short Oligonucleotide Analysis Package (SOAPdenovo) (Luo et al, 2012), and Assembly By Short Sequence (ABySS) (Simpson et al, 2009).

For transcriptome shotgun sequencing, the RNA-Seq library was constructed using a TruSeq RNA sample preparation kit from Illumina platform (BMLabosis). The sequencing library was prepared by random fragmentation of the cDNA sample, followed by 5' and 3' adapter ligation. Adapter-ligated fragments were then PCR amplified and gel purified. The library was loaded into a flow cell where fragments were captured on a lawn of surface-bound oligos complementary to the library adapters. Each fragment was then amplified into distinct, clonal clusters through bridge amplification. When cluster generation was complete, the templates were ready for sequencing. Paired-end sequencing was carried out on the Illumina HiSeq 4000 platform (Illumina, San Diego, CA, USA). For transcriptome mapping, raw RNA-seq reads were processed with Trimmomatic to remove adapters. Trimmed reads were aligned to the genome using HISAT2 2.1.0, using recommended alignment parameters for distinguishing between genotypic variants (Pertea et al., 2016). StringTie 1.3.4 was employed to assemble the transcripts from RNA-seq reads aligned to the genome, and compute their abundance (Pertea et al., 2016).

2.2.2. Annotation of non-coding elements in the *C. avellana* genome

Repetitive elements were identified using RepeatMasker 4.0.7 and a custom repeat database combining novel repeats detected in the Tombul genome with eudicot repetitive elements from RepBase (EudicotReps) Update 22.08 (5,913 elements) and mipsREdat 9.3 (26,123 elements) (Jurka et al., 2005; Nussbaumer et al., 2012; Smit et al., 2019). Analysis of tRNA types were identified by tRNAscan-SE 2.0.0 using the unmasked and repeat-masked genome sequences (Chan and Lowe, 2019). The results were compared with genomes from *B. pendula* (NCBI Genome accession no. GCA_900184695.1), *J. regia* (GCF_001411555.1) and *P. trichocarpa* (Pop_tri_v3 assembly, obtained from EnsemblPlants). tRNA predictions for *A. thaliana* were taken from GtRNAdb (Chan and Lowe, 2009).

2.2.3. Protein-coding gene identification and annotation

Prediction of gene models was carried out by Augustus, an *ab initio* gene predictor based on Hidden Markov Models (Stanke and Waack, 2003). Augustus was run on the masked Tombul genome using parameters optimised for *Arabidopsis thaliana* (Stanke and Waack, 2003). High-confidence genes were then identified by aligning gene models to the Tombul transcriptome using BLASTN, and retaining hits with ≥90% sequence identity and ≥25% query coverage (Camacho et al. 2009). The gene models were also assigned to the Viridiplantae conserved ortholog groups (OGs) recorded in OrthoMCL-DB (Chen et al., 2006). Multiple BLAST hits between different segments of the same pair of sequences were merged using a custom Perl script to calculate the ‘Cumulative Identity Percentage’ (CIP) and ‘Cumulative Alignment Length Percentage’ (CALP). Low-quality hits were eliminated based on the following criteria: CIP < 90%, CALP <60% for transcript matches, and CIP < 70%, CALP < 60% for ortholog matches. Gene models were selected as ‘high-confidence’ if they were supported by a good quality match to a transcript sequence and/or to an ortholog from other plant species. Functional annotation of the gene models was carried out using Mercator4, and TRAPID2 with default parameters, and GO term plots were produced using REVIGO (Lohse et al., 2014; Van Bel et al., 2013; Supek et al., 2011).

2.3. RESULTS

2.3.1. Assessment of genome assembly

The Tombul genome sequences were analyzed as described in study of Lucas et al. (2014) on wheat. First of all, the raw sequence reads were assembled using three different *de novo* assembly methods, including SGA (Simpson and Durbin, 2012), SOAPdenovo (Luo et al, 2012), and ABySS (Simpson et al, 2009). After comparison of assembly tools, ABySS was selected for an initial survey of the 'Tombul' hazelnut genome, and high-coverage Illumina 150 bp paired-end reads were obtained for their low error rate and cost-effectiveness. However, the assembly was highly fragmented and 25-30% larger than previous estimates of the *C. avellana* genome size (378 Mb, calculated from flow cytometry data). Hence, it was decided to facilitate a hybrid sequencing approach for the complete assembly of the hazelnut genome. The genome assembly was improved by incorporating low-coverage, long single-molecule reads (Oxford NanoPore), and information about physically adjacent sequences produced using proximity ligation sequencing (Dovetail Genomics). This part was carried out by Asst. Prof. Dr. Stuart J. Lucas. After NanoPore data was combined with the Illumina data, the assembly eliminated duplicated sequences and the majority of gaps in assembled scaffolds, giving a final assembly size of 383 Mb, very close to the expected genome size. However, it was still too fragmented to allow large-scale structural comparisons, for example with hazelnut genetic maps and other genomes from other species. The combination of hybrid assembly with Dovetail data resulted that the assembly consisted of 11 chromosome-sized pseudomolecules ranging from 22.42 – 50.95 Mb in length, in total accounting for 97.8% of the predicted genome size; the remaining unplaced scaffolds were 1 kb – 400 kb in size and had a total length of 13.6 Mb.

Assembly parameters were fine-tuned to obtain an assembly that has a total length (contigs + unassembled reads) similar to the estimated size of the *C. avellana* genome. This assembly was used to calculate general genome structural characteristics such as GC content, and then screened against databases of known plant repetitive elements using RepeatMasker software (Smit et al, 2019) to identify and mask sequences derived from transposable elements and other repeats.

2.3.2. Assessment of transcriptome assembly

For transcriptome assembly, two RNA-seq libraries were generated from total RNA isolated from leaf buds, and were sequenced by following Illumina protocols. After quality control and trimming, the reads were aligned to the chromosome pseudomolecules using HISAT2 (Pertea et al., 2016). Aligned reads were assembled using StringTie individually for each sample, and then redundant transcript contigs from both samples were combined, using StringTie's 'merge' function; at this step, putative transcript isoforms with very low expression levels (<1% of all expression for that transcript) (Pertea et al., 2016). The final assembly included 57,315 distinct transcripts arising from 47,250 transcribed genes (Table 2.1). This was expected to be greater than the number of protein-coding genes in the genome, because it included non-coding RNAs; also, heterozygous alleles may be assembled twice by this method, into different genes.

Table 2.1: Sequencing and assembly statistics for RNA-seq libraries (Paired end, 2 x 100 nt)

Sample ID	Total read bases (bp)	Total reads	GC(%)	AT(%)	Q20(%)	Q30(%)
Library_T1	6,677,685,902	66,115,702	46.310	53.69	98.763	95.400
Library_T2	7,017,024,288	69,475,488	46.084	53.92	98.163	95.286
Mapping & assembly	**Filtered reads**	**Reads mapped & paired**	**% Properly paired**	**Assembled transcript contigs**	**Merged isoforms**	**Final 'genes'**
Library_T1	65,937,538	61,974,596	94.0	76,540	57,315	47,250
Library_T2	69,238,960	62,411,216	90.1	77,602		

2.3.3. Repetitive elements in the genome

In the cv Tombul assembly, 7.32% of the genome consisted of repeat elements that represented conserved repeats found in many other plant genomes (Table 2.2). The most abundant repeat family wa identified as long terminal repeat (LTR) retrotransposons. Gypsy- and Copia-like long terminal repeat retrotransposons and long interspersal nuclear elements (LINE/L1) have been determined as other three largest repeat sub-families (Figure 2.1).

Table 2.2: Summary and categorization of conserved repetitive elements found in cv Tombul genome

	Number of elements	Length occupied (bp)	Percentage of sequences (%)
Retroelements	68,379	27,139,883	7.32
SINEs:	1	85	0
LINEs:	8,032	4,066,434	1.1
-RTE/Bov-B	99	22,350	0.01
-L1/CIN4	7,281	3,967,752	1.07
LTR elements:	60,346	23,073,364	6.23
-Ty1/Copia	13,593	9,610,917	2.59
-Gypsy/DIRS1	20,706	8,983,505	2.42
Retroviral	0	0	0
DNA transposons:	7,443	2,762,009	0.75
-hobo-Activator	2,879	1,242,613	0.34
-En-Spm	104	32,530	0.01
-MuDR-IS905	1,350	305,664	0.08
-Tourist/Harbinger	605	157,409	0.04
Unclassified:	2,573	994,645	0.27
Total interspersed repeats:		30,896,537	8.34
Small RNA:	418	44,116	0.01
Satellites:	76	5,090	0
Simple repeats:	0	0	0
Low complexity:	0	0	0

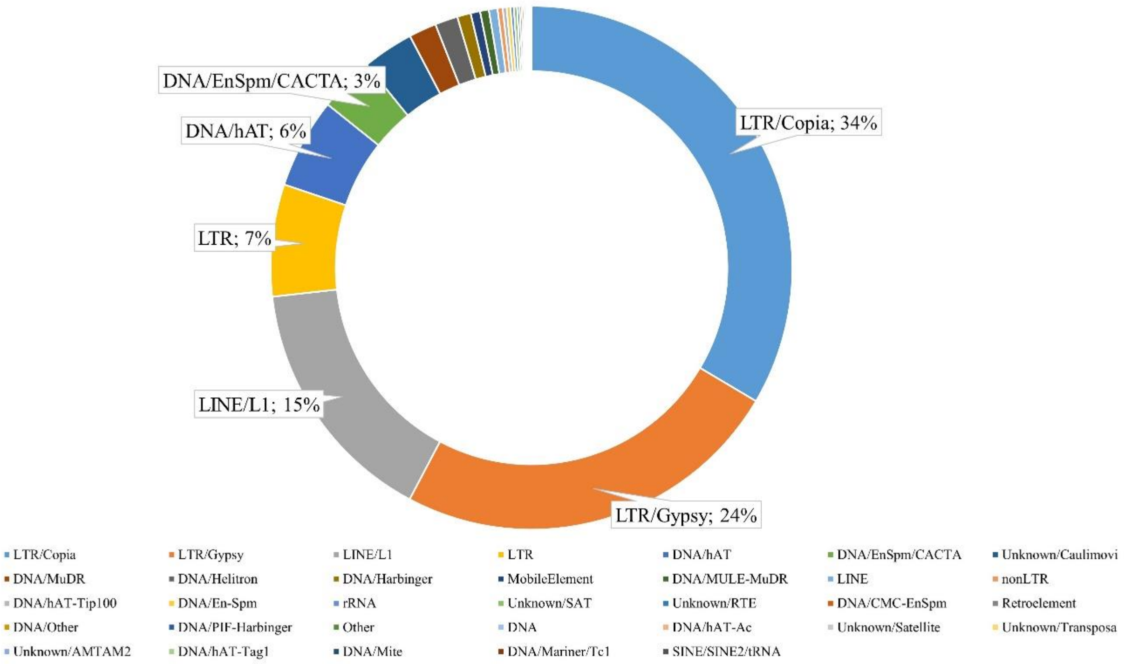


Figure 2.1: Relative abundance of interspersed repeat families in the cv Tombul genome

Furthermore, repeat-type specific prediction tools, including LTRharvest/LTRdigest for LTRs and TRIMs and SINE-finder for SINEs, were used for identification of candidate novel retrotransposons (Ellinghaus et al., 2008; Steinbiss et al., 2009; Wenke et al., 2011). Arrays of short tandem repeats were eliminated using TRF (Benson, 1999). These newly identified repeats were combined with known eudicot repetitive elements from RepBase Update 22.08 (5,913 elements) and mipsREdat 9.3 (26,123 elements) to create a custom repeat library. For subsequent identification of protein-coding genes and other functional elements, the –nolow option was used to leave simple repeats and low-complexity regions unmasked. In total, the chromosome pseudomolecules were found to consist of 35.72% interspersed repeats, the large majority of which were LTR retrotransposons, and 2.41% simple repeats, as summarized in Table 2.3 (Lucas et al., 2020). The identification of candidate novel retrotransposons was carried by Asst. Dr. Stuart J. Lucas.

Table 2.3: Summary of predicted repeat elements identified in *C. avellana* genome

	Number of elements	**Length occupied (bp)**	**Percentage of sequence (%)**
Retroelements	350,766	131,114,230	35.38
SINEs:	239	14,731	0.00
LINEs:	620	103,692	0.03
- RTE/Bov-B	96	19,947	0.01
- L1/CIN4	551	99,487	0.03
LTR elements:	349,907	130,995,807	35.35
- Ty1/Copia	101,052	32,516,429	8.78
- Ty3/Gypsy/DIRS1	50,068	25,164,581	6.79
Retroviral	0	0	0
DNA transposons	2,397	1,123,336	0.30
hobo-Activator	787	354,147	0.10
En-Spm/CACTA	385	164,418	0.04
MuDR-IS905	438	182,472	0.05
Tourist/Harbinger	234	98,731	0.03
Helitron	488	269,216	0.07
Unclassified:	589	106,975	0.03
Total interspersed repeats:		132,344,541	35.72
Small RNA:	399	41,681	0.01
Satellites:	7	579	0.00
Simple repeats:	208820	7,134,639	1.93
Low complexity:	36677	1,756,537	0.47
Total simple repeats:		8,933,436	2.41
Total repetitive content:		141,262,718	38.13

2.3.4. Annotation and inter-species comparison of tRNA genes

tRNA loci was defined using tRNA-scan SE (Chan and Lowe, 2019). All twenty amino acids and 54 possible anti-codon tRNAs were detected in masked cv Tombul genome. In addition, ten putative suppressor tRNAs, with anti-codons complementary to the TGA (9) or TAA (1) stop codons were included. A total of 477 predicted tRNA genes and 40 tRNA pseudogenes, with an average length of 75 nt, were listed in Table S2.1. Of these 27 tRNA genes were predicted to contain introns, chiefly some of those encoding Gly, Met & Tyr. Codon frequencies for tRNA genes in *C.avellana* were calculated and compared with other tree species and *Arabidopsis* (Figure 2.2, Appendix B: Table S2.2). The codon preference was generally reflected by GC composition, which means G or C was prefered at the third position of codons in GC-rich genomes, whereas the AT-rich genomes prefered A or T. Various differences could be detected among equivalent codons. The results showed that Tombul preferred TCT or TCA for Serine while *Populus trichocarpa* preferred TCG or TCC.

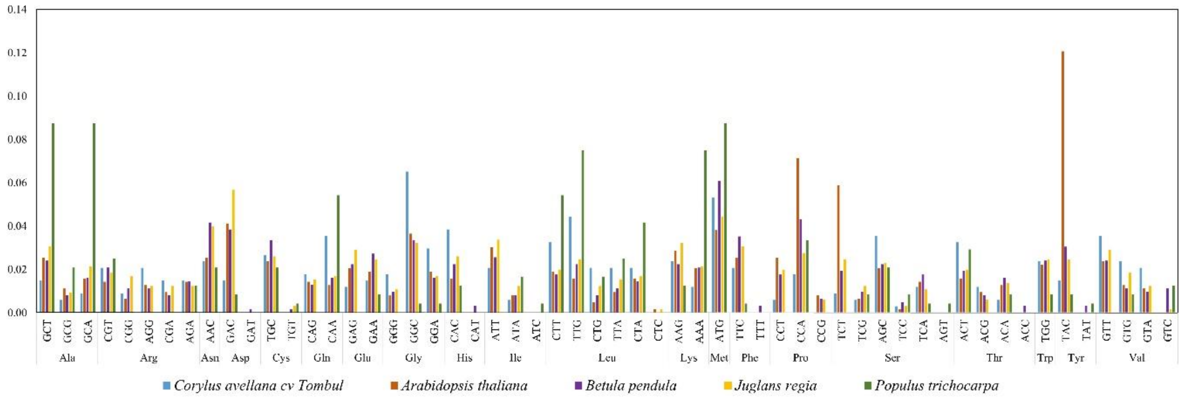


Figure 2.2: Relative frequency of tRNA anticodons in *C. avellana* cv Tombul and other plant genomes

2.3.5. Protein-coding genes and annotation

Augustus software was used to generate *ab initio* gene predictions from the masked cv Tombul genome based on Hidden Markov Models optimised for *Arabidopsis thaliana* (Stanke and Waack, 2003). These predictions were tested by aligning the gene models with the Tombul transcriptome assembly, to provide evidence for gene expression. However, because our RNA-seq libraries were only generated from green buds under normal growth conditions, many tissue- and stress specific genes would not have been expressed. Therefore the gene models were also assigned to the Viridiplantae ortholog groups (OGs) conserved recorded in OrthoMCL-DB (Chen et al., 2006). According to the *ab initio* gene finder, 50,761 genes have been predicted from Tombul masked genome. Of our models, 12,516 (25%) were not found in any other plant species searched. Gene models were considered to be of low confidence if they did not have orthologs in other species, and if they did not have BLAST matches in the cv Tombul bud transcriptome assembly or a match to a paralog that did match a transcript (thresholds were CIP < 90%, CALP <60% for transcript matches, and CIP < 70%, CALP < 60% for ortholog matches).

As a consequence, 27,270 high-confidence protein-coding gene models remained, of which 16,521 were supported by high transcript coverage under normal growth conditions. There were 2,844 high-confidence gene models that were expressed in leaf buds but had no homologs outside of hazelnut, suggesting that these are *Corylus*-specific genes. Furthermore, over 20,000 of the high-confidence protein-coding gene models were functionally annotated based on homology to known plant proteins using BLAST+ (Camacho et al., 2009). Functional analysis and annotation of predicted genes were carried out by Mercator4 (Lohse et al., 2014). During automated annotation, InterPro protein domains were identified in 88.77% of gene models (24,208), while 82.38% of gene models (22,466) were identified with one or more GO terms, and 49.07% (13,381) were assigned to MapMan functional bins representing plant-specific molecular components and pathways (Table 2.4). Only 2,332 gene models (8.55%) were not assigned functional annotation by any of these approaches. The most significant proportion of classified proteins, 13.79%, were annotated with enzyme classifications, including transferases, oxidoreductases, hydrolases and lyases. RNA biosynthesis and solute transport functions were following with 13.79% and 9.64%, respectively.

Table 2.4: Assignment of *C.avellana* predicted proteins to MapMan functional Bins.

Bin Description	Number of MapMan Bin
Enzyme classification	1845
RNA biosynthesis	1844
Solute transport	1290
Protein modification	1240
Protein homeostasis	925
Protein biosynthesis	606
RNA processing	521
Phytohormone action	483
Lipid metabolism	450
Cell cycle organisation	418
Vesicle trafficking	413
Cell wall organisation	405
Chromatin organisation	269
Cytoskeleton organisation	255
External stimuli response	247
Carbohydrate metabolism	236
Amino acid metabolism	233
Photosynthesis	229
Secondary metabolism	227
Coenzyme metabolism	206
Multi-process regulation	196
Protein translocation	186
Cellular respiration	164
Nutrient uptake	146
Redox homeostasis	114
Nucleotide metabolism	101
DNA damage response	99
Polyamine metabolism	33

Protein-coding genes have also been annotated with GO-terms, and GO-enrichment analysis has been carried out with the selected transcripts. With respect to the 3 main GO categories, Biological Process GO terms were assigned to 15,425, Cellular Component terms to 15,313, and Molecular Function terms to 16,473 gene models. For each gene model, the most specific (highest level) GO terms assigned for each category were recorded in the additional file (Appendix B: Table S2.3).

The most abundant conserved protein domain has been detected as from a variety of protein kinases; e.g. 1,401 gene models were annotated with IPR000719, ‘protein kinase catalytic domain', accounting for almost 5% of all high-confidence gene models; this is similar to the abundance observed in other sequenced plant genomes and indicates the importance of signal transduction in controlling many aspects of plant biology. Apart from highly prevalent domain structures that were found in proteins with diverse functions (e.g. NAD(P)-binding, Pentatricopeptide repeat, Zinc finger, WD40, and Armadillo domains) other notable abundant domains included the NB-ARC motif, found in 279 gene models, the large majority of which also contained leucine-rich repeats (LRRs). These genes belong to the NB-LRR family of pattern recognition receptors, which play a critical role in the plant response to pathogens. Homeobox-like and Cytochrome P450 domains were each found in over 300 gene models, making these the most abundant transcription factor and enzyme families respectively in the hazelnut genome.

2.4. DISCUSSION & CONCLUSIONS

2.4.1. Discussion

Even though hazelnut is a fundamental crop species, limited genome data has been available. To date only a draft transcriptome assembly was available for European hazelnut, the American cultivar 'Jefferson', consisting of 28,255 contigs that represented putative transcript sequences. It provided to identify the majority of gene sequences, however the chromosomal locations of the genes could not be determined. The aim of the study to produce a chromosome-level genome assembly for the Turkish cultivar 'Tombul' in a time and cost-effective manner, in order to identify structural relationships between genes and facilitate rapid mapping of candidate genes from molecular markers for traits of interest. When raw sequence reads were individually assembled using 3 different methods, including Illumina paired-end, NanoPore and Dovetail, a fully assembled sequence of the genome could not be achieved; thereby a hybrid sequencing approach was facilitated for the complete assembly of the hazelnut genome. As a consequence, the assembly accounted for 97.8% of the predicted genome size, and the chromosomes were found to be highly consistent with existing cytogenetic data and genetic maps (Lucas et al., 2020).

According to *ab initio* gene finder, 27,270 high-confidence protein-coding genes have been predicted, and the number of genes annotated in cv Tombul genome was very similar to *B. pendula* (28,153) and a little less than walnut & pistachio (~32,000 each). The different gene families that have undergone lineage-specific expansion have been determined among plant genomes, and may indicate their functional importance to their species. Martínez-García et al. (2016) showed that *J. regia* has an unusually large complement of genes for polyphenol synthesis. In this, 147 gene families were specifically expanded in *C. avellana*, and the largest of these families included pattern recognition receptors and protein kinases involved in defense against pathogens response. The genes related with the vesicle trafficking and RNA biosynthesis pathways were also enriched gene functions, hence it was suggested that suggest that *C. avellana* has developed diverse systems for regulating protein function at both transcriptional and post-transcriptional levels. The other abundant gene families were involved in stress and defense responses, and closer examination of these gene families could reveal important aspects of the response to infection of hazelnut. Moreover, 20 and 34 genes were the most significantly enriched gene functions that were related to melatonin biosynthesis and breakdown of 2,4,6-trinitrotoluene (TNT)-containing compounds, respectively. Although melatonin were more widely known as an animal hormone and antioxidant, it has been reported to regulate diverse processes in plants in the last few years, and is also gaining popularity as a health supplement (Arnao and Hernández-Ruiz, 2018). TNT is a toxic soil pollutant resulting from use of explosives that is highly resistant to biodegradation (Rylott et al., 2014). Therefore, closer examination of these gene families could reveal important new uses for *C. avellana*, either in production of nuts with increased nutritional benefits, and for bio-remediation of contaminated soil.

About a third of the cv Tombul genome was found to consist of LTR retrotransposons. In total the chromosome pseudomolecules were found to consist of 35.72% interspersed repeats, and 2.41% simple repeats. The overall abundance of repetitive elements was similar to the rice genome that consisted of 35-40% repeats (Mahesh et al. 2016). However, it was lower than that of the slightly larger silver birch genome, *Betula pendula* L., consisted of 51.35% repeats (Salojarvi et al., 2017). Over half of the LTR elements were too diversified to be positively assigned to a sub-family. Copia elements were almost twice as abundant as Gypsy elements, but the total number of bases covered by both families was comparable because of their shorter average length. TRIMs (Terminal

Repeats In Miniature) were a relatively recently described class of short, non-autonomous LTR retroelements, that are thought to replicate using the enzymes encoded by related Copia or Gypsy LTRs (Gao et al 2016). TRIMs were found to be highly abundant in the *B. pendula* genome with over 82,000 copies, but their copy number in *C. avellana* was only 8,712, which is within the typical range observed for other plant genomes (Gao et al. 2016). DNA transposons, which were again highly abundant in *B. pendula*, were notably scarce in *C. avellana*. These observations suggested that the expansion of these repeat families in *Betula* took place after the ancestors of the *Betula* and *Corylus* lineages diverged.

Various differences in abundance between tRNA genes for particular amino acids, and codons for the same amino acid, were observed in the analysis. tRNAs for codons ending "–AT" were non-existent or rare in all the plant genomes examined. Some species-specific differences were also noted. *C.avellana* has a higher abundance of tRNAs for all Glycine codons, and especially GGC, than the other plant genomes, whereas *P. trichocarpa* has an increased number of all Alanine and Leucine tRNAs. Among the Serine codons, *C. avellana* has a greater abundance of tRNAs for AGC than the other tree species, whereas *Arabidopsis* favours TCT. Further study would be useful to determine whether these differences are correlated to codon frequeuncies in protein-coding genes, or influence translation efficiency in different plant species. However, overall there were few species- or lineage-specific variations in tRNA abundance.

2.4.2. Conclusions

Herein, we present a chromosome-level reference genome assembly and annotation for European hazelnut, *C. avellana* cv. Tombul. Using a combination of short-read, long-read and proximity ligation sequencing we produced a genome of similar quality to those obtained by anchoring contigs to high-density genetic maps, making this to our knowledge the most complete tree nut genome published to date. The genes and functional elements identified here provide a foundation for ensuring the sustainability of future hazelnut production, for example by identifying targets for breeding or gene knockout that could confer resistance to several abiotic and biotic stresses.

3. COMPARISON OF DIFFERENT ANNOTATION TOOLS FOR CHARACTERIZATION OF THE COMPLETE CHLOROPLAST GENOME OF *CORYLUS AVELLANA* CV TOMBUL

3.1. INTRODUCTION

Corylus is a phylogenetically and economically important genus with 16-20 species in the family Betulaceae. Study of this genus contributes to both science and the economy because of commercial and ornamental values of *Corylus* species. Even though European hazel (*Corylus avellana* L.) has a significant place in agriculture, a limited number of studies exist about *C. avellana* at the molecular level. Until recently the only available genome sequences for *C. avellana* were a draft genome for the American cultivar 'Jefferson' (Rowley et al., 2018). In addition to Jefferson genome, Lucas and coworkers recently published a reference nuclear genome sequence for *C. avellana* cv Tombul (Lucas et al., 2020). There are several bioinformatics tools that have been designed for assembly and annotation of chloroplast (cp) genomes, hence it is difficult to decide which is most useful and applicable to a specific case. With enhancing the number of plant genomes, cp genomes can be accurately obtained from whole genome shotgun (WGS) sequences, and it is the most powerful approach to assemble cp genome in comparison to purifying the leaf chloroplast, because the obtaining cp genome by purifying leaf cp is little difficult to provide homogeneity in quantities necessary for near-complete cataloging of proteins. Here, I made attempts to assemble the complete cp genome sequences of Tombul cultivar, the most widely grown Turkish variety, from next generation WGS sequences by using several computational methods.

The cp performs a vital photosynthetic function and is the central node of enzymatic mechanisms for carbohydrate and lipid biosynthesis in plants, hence it is in charge of much of the world's primary productivity. The main energy-input into living cells by the conversion of sunlight into chemical energy is provided by photosynthesis which takes place in cp, thereby agriculture is obviously dependent upon the cp. Chloroplast genomes have a simple circular, quadripartite structure, including two copies of an inverted repeat (IR) that separate the large and small single copy regions (LSC and SSC), that contribute to plant systematics and evolutionary studies (Lee et al., 2006; Green, 2011; Daniell et al., 2016). Chloroplast DNA (cpDNA) fragments are often used as 'DNA barcodes' in inter-species phylogenetic analysis due to their universal presence and abundance in plant cells. However, Yang et al. (2018) indicated that the cpDNA fragments most commonly used in phylogenetic analysis such as *matK*, *rbcL* and *trnH-psbA*, have little sequence divergence in genus *Corylus*, thus it is hard to precisely resolve the phylogenetic relationships within genus *Corylus* using these fragments (Yang et al., 2018). Especially in the phylogeny of land plants, studies demonstrated that complete cp genomes provide more reliable information than cpDNA barcode sequences, and eliminate problems associated with barcoding, such as primer design and amplification (Suo et al., 2012; Dong et al., 2016; Wang et al., 2017; Xu et al., 2017; Percy et al., 2014). The cp genomes are useful and cost-effective for resolving phylogenetic relationship at both high and low taxonomic levels because of containing both conserved and variable protein-coding genes; also, compared to the nuclear genome cp genomes exhibit a slower evolutionary rate and mostly uniparental inheritance (Jansen et al., 2007; Moore et al.. 2007; Moore et al., 2010; Drouin et al., 2008; Parks et al., 2009; Carbonell-Caballero et al.; 2015; Smith, 2015). Limited sequence variation has led to the use of cp genomes mostly in studies at the interspecific and interfamilial levels (Jansen et al., 2007; Moore et al.2007; Xi et al., 2012; Barrett et al., 2013). In addition, the cp genes provide deeper information for phylogeny reconstruction of *Corylus* species in comparison with previous studies, including RAPD (Galderisi et al., 1999), SSR (Zhao et al., 2015; Beltramo et al., 2016), SRAP (Di et al., 2014), ISSR (Essadki et al., 2006; Ferreira et al., 2009), AFLP (Zong et al., 2015), and DNA fragments such as ITS regions and cpDNA fragments (Zong et al., 2015; Erdogan and Mehlenbacher, 2000; Leinemann et al., 2013). The whole cp genome is also useful for identification of plant varieties by allowing selection of highly variable non-genic markers for DNA barcoding (Taberlet et al., 2007; Kane et al., 2012).

Bakker et al. (2016) indicate that next generation whole genome shotgun (WGS) sequences from plants typically contain 5% or more reads derived from the chloroplast (Bakker et al., 2016). Thus, the sequenced genome data of plant species can be used to obtain cp genomes without prior isolation of cpDNA. Due to the development of next generation sequencing technology, an increasing number of WGS datasets are available for cp genome assembly. Wang et al. (2018) revealed the complete cp genomes of *Fagopyrum dibotrys* from high-throughput sequencing datasets, and obtained reliable cp genomes (Wang et al., 2018). Osuna-Mascaró et al. (2018) also retrieved the cp genome of *Erysimum* (Brassicaceae) species from a genomic library, and achieved similar cp genomes in terms of overall size, structure and composition (Osuna-Mascaró et al., 2018). Besides *de novo* assembly of complete cp genome, alignment-based methods can also be used to obtain cp assemblies from WGS reads by mapping them onto a reference cp genome (Vinga et al., 2012). However, this latter method relies on the availability of a high quality cp genome from a related species.

Herein, I present the complete cp genome of *Corylus avellana* cv Tombul. In particular, the aim of the study was to compare different available annotation tools, develop an optimized pipeline for cp assembly and annotation from WGS sequences, and examine the cp genome structure, gene content and gene order of Turkish hazelnut. Although there is a chloroplast genome for *C. avellana* in NCBI GenBank (accession no. KX822768), there is no detailed information about the construction of this genome or which variety of hazelnut it originates from. Therefore, I chose to generate a new annotation for one of the most commercially important Turkish hazelnut cultivars, 'Tombul'. Moreover, simple sequence repeats (SSRs) are investigated in cv Tombul cp genome, and phylogenetic relationships are predicted among the Fagales, including genera Betulaceae, Fagaceae and Juglandaceae.

3.2. MATERIALS AND METHODS

3.2.1. DNA extraction and sequencing

DNA extraction and sequencing was carried out as part of an ongoing *C. avellana* genome sequencing project. High molecular weight DNA was extracted from young leaf buds using a CTAB method optimized for Betulaceae (Wang et al., 2013). Whole genome shotgun libraries were prepared using TruSeq kits and selected for an insert size of 600-800 nt. Paired-end sequencing was carried out on a Illumina HiSeq4000 and reads were deposited in the European Nucleotide Archive (Project accession: PRJEB31933).

NanoPore sequencing reads were also obtained for the same cv Tombul genome project. Nano-Pore sequencing was carried out on the MinION platform using R9.4 flowcells and

Ligation Sequencing Kit 1D, according to the manufacturer's protocols (Oxford NanoPore Technologies, Oxford, UK).

3.2.2. Chloroplast genome assembly and annotation

Whole genome Illumina paired-end raw data without adapters were used in *de novo* assembler NOVOPlasty, a seed-extend based assembler (Dierckxsens et al., 2017) (Figure 3.1). The cp genome was assembled from WGS data, initiated by a seed sequence, which is iteratively extended bidirectionally, to obtain the circular genome. Using a reference genome is optional in the pipeline, but can be useful to obtain a single circular genome, and to eliminate manual adjustments. The assembled data was obtained based on *Arabidopsis thaliana* (KX551970.1) and *Corylus avellana* complete cpDNA sequences (KX822768.2) as seed and reference genomes, respectively. The parameters were specified as in the following: automatic insert size detection, a genome size range from 120,000 to 200,000, a K-mer value of 39, an insert range of 1.8, a strict insert range of 1.3, and the paired-end reads option. Moreover, the contig was checked using BLAST+ searches against the available complete cp sequence of KX822768 (Camacho et al., 2009; Wang et al., 2018). Relative positions were manually curated according to the reference genome, and the complete cp genome for Tombul cultivar was finally acquired for further analysis. In addition, Illumina paired-end raw sequence reads were processed by Trimmomatic to remove adapters, and trimmed sequences were assembled using ABySS 1.9 (Simpson et al., 2009; Bolger et al., 2014). Then, the cv Tombul cp genome obtained from NOVOplasty was aligned to the ABySS contigs using BLAST.

The Tombul cp genome was annotated through three different online programs, including GeSeq, CpGAVAS and DOGMA with default parameters (Tillich et al., 2017; Liu et al., 2012; Shi et al., 2019; Wyman et al., 2004). For annotation file, the gene locations were compared and determined when it matched to the same position at least two annotation tools. MEGA pairwise alignment was additionally used to confirm the genes among closely related taxa, and the gene locations were verified from cv Tombul cp genome sequences. In addition, protein-coding and tRNA genes found by only one tool were not included in the map. The visual image of annotation was illustrated with the help of

OGDRAW (Greiner et al., 2019). The final assembly was submitted to GenBank (MN082371).

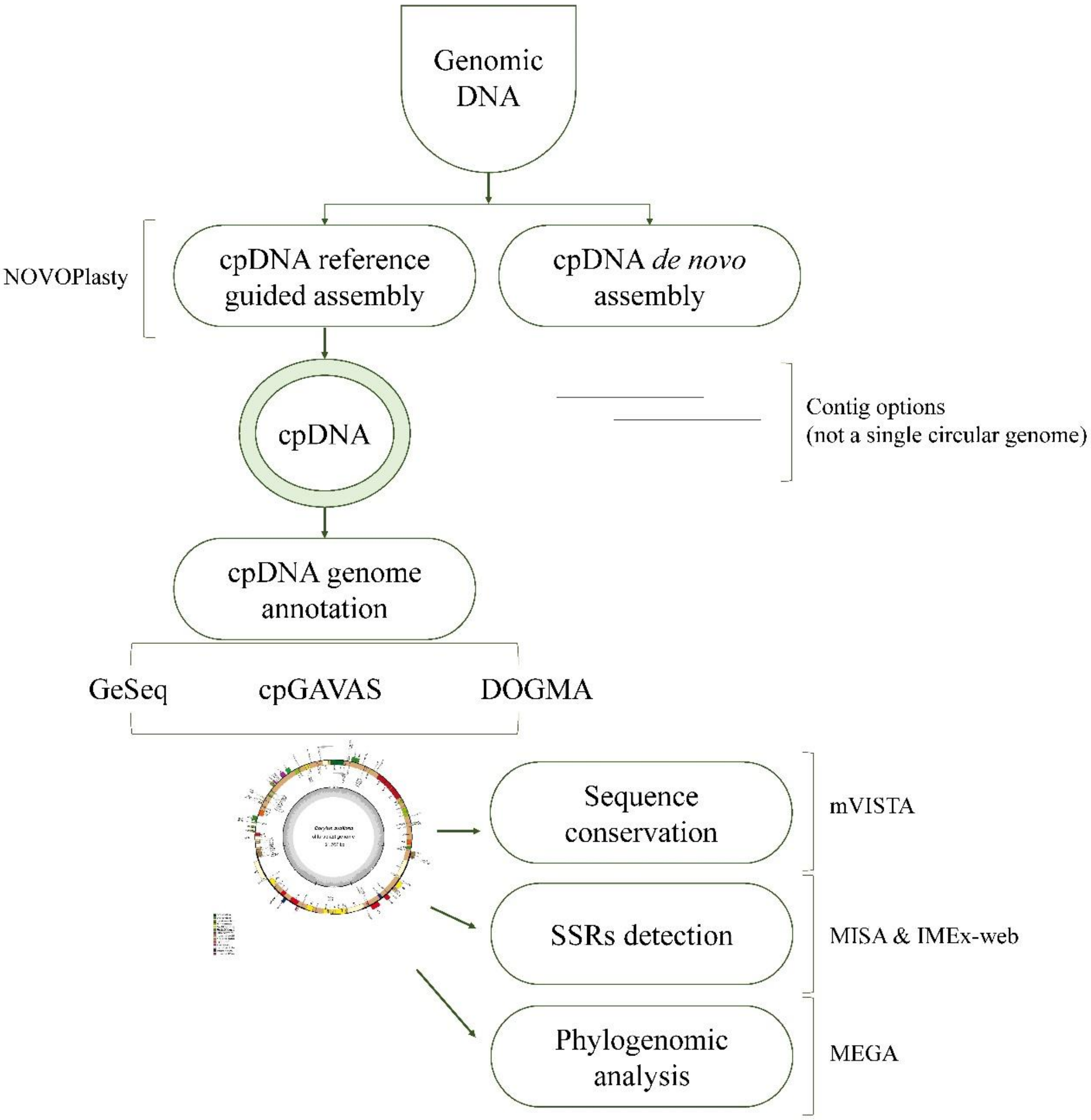


Figure 3.1: Flow chart describing the optimized bioinformatics pipeline for cp genome assembly

3.2.3. Comparative chloroplast genomic analysis

Complete cp genomes of seven species, including *Corylus avellana* (GenBank accession number: KX822768.2), *Betula nana* (GenBank accession number: NC_033978.1), *Juglans regia* (GenBank accession number: MF167463.1), *Populus trichocarpa* (GenBank accession number: EF489041.1), *Quercus rubra* (GenBank accession number: JX970937.1), *Glycine max* (GenBank accession number: NC_007942.1) and *Arabidopsis thaliana* (GenBank accession number: KX551970.1), were downloaded from NCBI, in order to compare the overall similarities among different cp genomes with Tombul cultivar. Pairwise alignments were implemented in the LAGAN alignment program included in mVISTA program with default parameters (Frazer et al., 2004) using the annotation of *Corylus avellana* cv Tombul (Betulaceae, Fagales; GenBank accession number: MN082371) as the reference.

3.2.4. Simple sequence repeats analysis

Simple sequence repeats (SSRs) were detected using two different microsatellite identification web tools, including MISA (MIcroSAtellite identification tool) and IMEx-web (Imperfect Microsatellite Extraction Webserver) by setting the minimum number of repeats to 10, 5, 4, 3, 3 and 3 for mono-, di-, tri-, tetra-, penta- and hexanucleotides, respectively (Beier et al., 2017; Mudunuri and Nagarajaram, 2007).

3.2.5. Phylogenomic analysis

The complete cp genome sequences of twenty-two species from Fagales were used for phylogenetic analysis, including representatives of genera of Betulaceae, Fagaceae, and Juglandaceae. The cp genomes of species were aligned with multiple sequence alignment tool, MUSCLE (Edgar, 2004). Positions with gaps in all sequences were excluded after alignment in the analysis. The evolutionary history was inferred by using the Maximum Likelihood method and Tamura-Nei model and analyses were conducted in MEGA X (Tamura and Nei, 1993; Kumar et al., 2018). The bootstrap consensus tree inferred from 500 replicates was taken to represent the evolutionary history of the taxa analyzed. All positions with less than 90% site coverage were eliminated, i.e., fewer than 10%

alignment gaps, missing data, and ambiguous bases were allowed at any position (partial deletion option).

3.3. RESULTS

3.3.1. Size, gene content, order and organization of the hazelnut chloroplast genome

Initial assembly using the NOVOplasty assembler with raw *C. avellana* cv ‘Tombul’ WGS sequences produced a single 200,017 bp contig (Dierckxsens et al., 2017). The length of this contig was significantly longer than the *C. avellana* cp genome previously published in GenBank (Accession no: KX822768). Therefore, the raw contig was aligned to the KX822768 cp genome, and it was observed that the last part, starting from 161,667 bp, consisted of repeats of sequences from the rest of the Tombul chloroplast genome. To demonstrate whether the extra part, located after 161,667 bp, was genuine or not, Nanopore sequencing reads belonging to cv Tombul were also aligned to the contig. Although a subset of reads matched these additional parts in two segments, the mapped read depth of the these segments was approximately half of that of the rest of the cp genome. Moreover, BLAST alignment found that the additional part was 100% identical to two regions in the first 161 kb of the cv Tombul cp genome (Figure 3.2) (Camacho et al., 2009). These observations suggested that the extra 39 kb in our initial contig was an artefact of the NOVOplasty assembly algorithm, where the duplicated segments were incorporated twice, perhaps due to sequence variation at their boundaries.

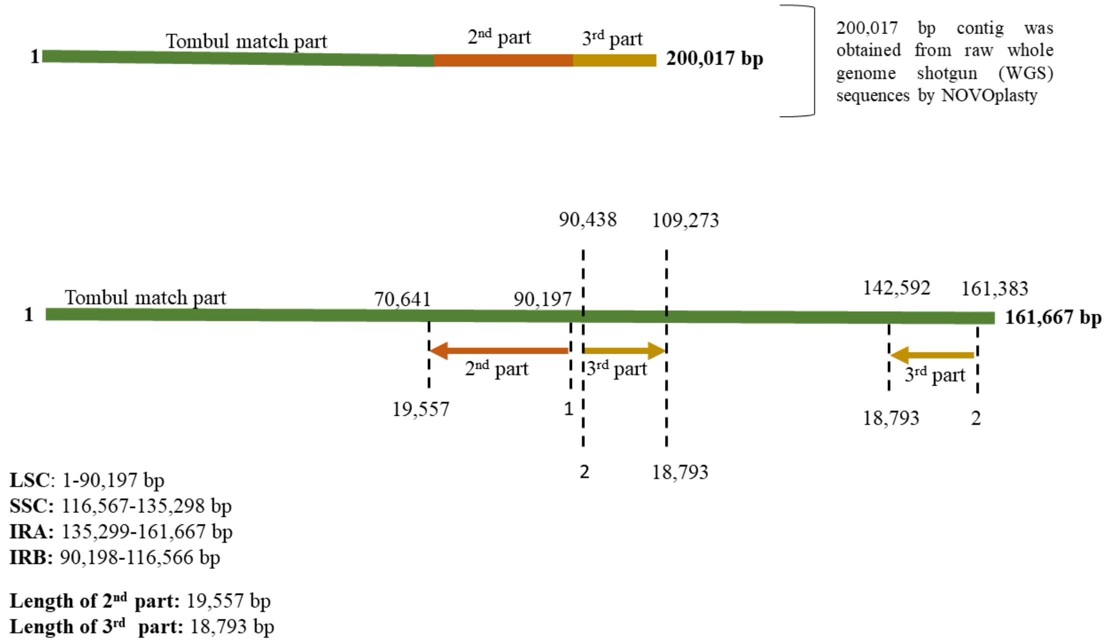


Figure 3.2: Schematic that explains the structure of cv Tombul chloroplast genome. The green part showed high similarity to the KX822768 cp genome, and used for further analysis. The orange and mustard segments were artefacts of the NOVOplasty assembly algorithm.

In addition, we examined whether a single circular cp genome could be retrieved using a standard whole genome assembly algorithm, rather than one specific to the chloroplast. For this test, trimmed WGS sequences were assembled using ABySS assembler (Simpson et al., 2009), and then the cv Tombul cp genome constructed by NOVOplasty and the KX822768 cp genome were mapped to these contigs of cv Tombul genome using BLAST. Multiple contigs from the whole genome assembly matched the chloroplast sequences, but they were overlapping and fragmented (data not shown). Therefore it was concluded that using an assembler specialized for organellar genomes is advantageous for cp genome construction; further analysis was carried out using the first 161,667 bp of the genome assembly obtained from NOVOplasty, which also showed high similarity to the KX822768 cp genome.

The Tombul complete cp genome had a length of 161,667 bp, and includes a pair of inverted repeats 26,368 bp long, separated by a small and a large single copy region of 18,733 bp and 90,198 bp, respectively (Figure 3.3). The overall GC content of cv Tombul cp genome was 36.40%, and GC contents of the LSC and the SSC regions were 34.17 and 30.25%, respectively. The GC content of IR region was much higher than that of the

LSC and SSC regions with 42.37%, due to its relatively abundant GC-rich tRNA and rRNA genes.

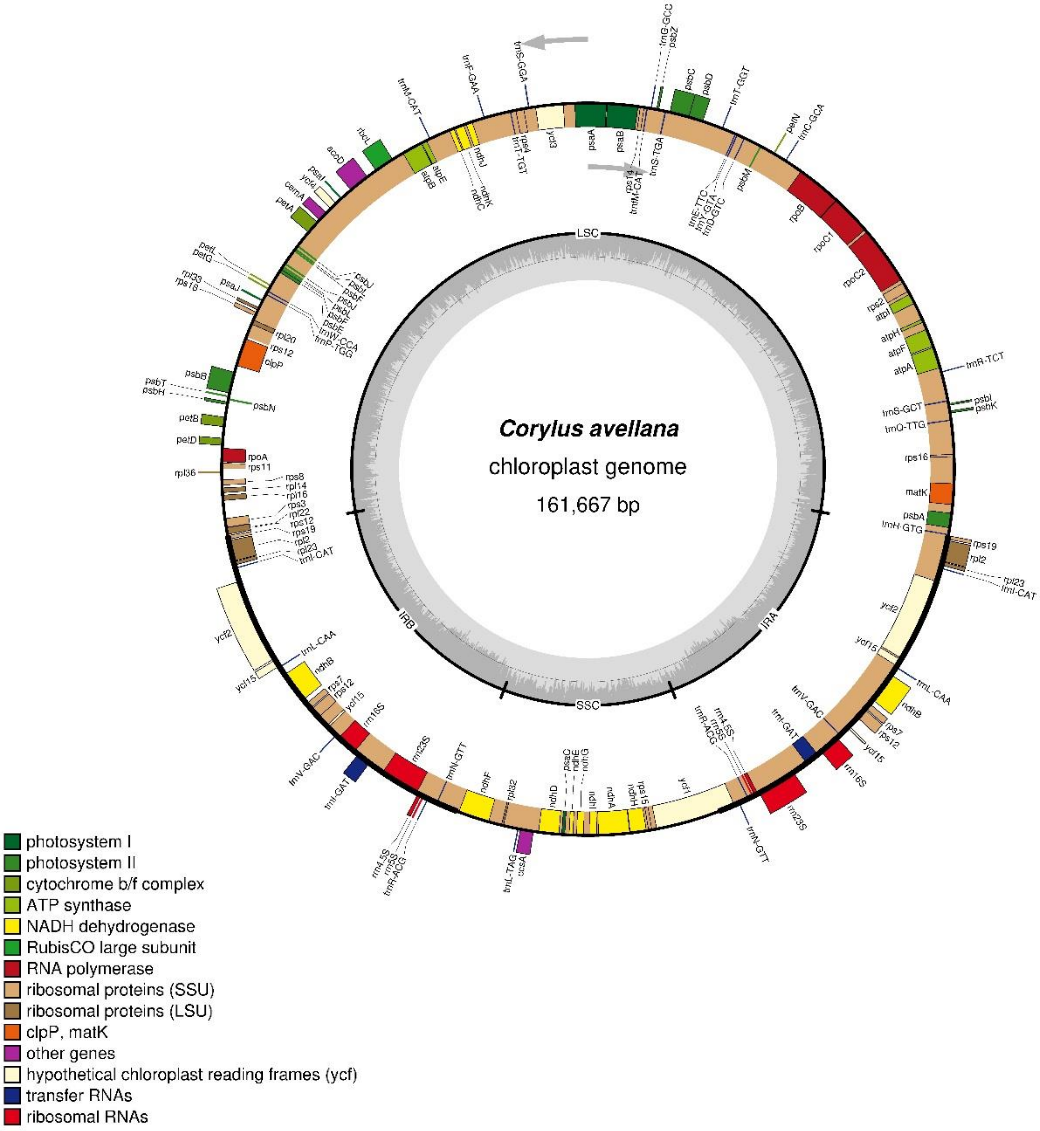


Figure 3.3: The chloroplast genome map of *Corylus avellana* cv Tombul species. Genes lying outside the circle are transcribed in the counter clockwise direction, while those inside are transcribed in clockwise direction. The colored bars indicted different functional groups. The darker gray area in the inner circle denotes GC content while the lighter gray corresponds to the AT content of the genome. LSC, large single copy; SSC, small single copy; IR, inverted repeat.

For annotation of functional genes, three different prediction tools, namely GeSeq, cpGAVAS, and DOGMA, were compared, and agreed with each other for the majority of the content and order of genes (Tillich et al., 2017; Liu et al., 2012; Shi et al., 2019; Wyman et al., 2004). Generally, genes were included in the final map when at least 2 of the tools gave matching predictions. A total of 125 predicted functional genes were encoded within the *Corylus avellana* cv Tombul cp genome. Among them, 88 genes were unique, while 17 genes were duplicated in the IR region (IRA and IRB). Furthermore, the 105 distinct genes comprised 76 protein-coding, 25 tRNA and 4 rRNA genes. Seven protein coding genes (*ndhB, rpl2, rpl23, rps7, rps12, rps19,* and *ycf2*), six of the tRNA genes (*trnI-CAT, trnI-GAT, trnL-CAA, trnN-GTT*, *trnR-ACG,* and *trnV-GAC*) and all rRNA genes (*rrn16, rrn23, rrn5* and *rrn4.5*) were duplicated within the IR. Although the 3 annotation tools gave similar gene predictions, a few differences were detected, especially in tRNA genes. The genes for *trnA-TGC* (duplicated in IR), *trnK-TTT*, *trnL-TAA* and *trnV-TAC* were only annotated by DOGMA, therefore they were not included in the final map. Fifty seven protein-coding genes and 18 tRNA genes were contained in the LSC region, while 12 protein-coding genes and one tRNA gene were identified in the SSC region. Three open reading frames (*orf42*, *orf56*, and *orf188*) and an addition hypothetical chloroplast reading frame (*ycf68*) were also identified with the DOGMA tool. Moreover, one gene, *ycf1* located in the IRA/SSC junction, extended the IRA region by several bases. A *ycf*-like gene was also reported in the IRB region, one of the two IRs, with two annotation tools, DOGMA and GeSeq, but it was a truncated fragment of *ycf1* gene, and thus not included in the genome map. Of the 76 unique protein-coding genes, five genes (*atpF*, *ndhA*, *ndhB*, *rpl2*, and *rpoC1*) contained one intron, while two protein-coding genes (*clpP* and *ycf3*) contained two introns each. The gene *rps12* was annotated as trans-spliced gene of which the 5′-end exon was located in the LSC region while its intron and 3′- end exon were situated in the IR region (Appendix C: Table S3.1, S3.2).

RNA editing, a post-transcriptional process, exists in chloroplasts to encode appropriate amino acids by correcting the codons, and maintain conserved protein functions by correcting codons, especially by alteration of nucleotides from cytosine to uracil (C-to-U) and less frequently from uracil to cytosine (U-to-C) (Tillich et al., 2006; Chateigner-Boutin and Small, 2010; Rodrigues et al., 2017). Wang et al. (2018) indicated that several changes were observed in protein-coding transcripts from chloroplasts, including C to U, along with G to A and C to G, A to G and G to A (Wang et al., 2018). Several nucleotide alterations are required to provide functional start codons in a handful of the genes annotated in the present study (Table 3.1). RNA editing at these sites has not previously been confirmed in the Betulaceae, thereby further RNA sequence analysis should be carried out to determine whether these modifications occur, and to elucidate the uncertainty.

Table 3.1: Nucleotide, codon and amino acid changes in protein-coding genes

Genes	Nucleotide Change	Codon Change	Aminoacid Change
ndhD	A > G	AUA > AUG	I > M
petN			
psbH			
ycf2	U > G	AUU > AUG	I > M
rpl32			
psbI	C > G	AUC > AUG	I > M
psbT			
rpl16			
rps16			
rpl36	C > A	CUG > AUG	L > M
rps19	G > A	GUG > AUG	V > M

Comparing the results of the annotation tools, ten genes (*atpF*, *clpP*, *ndhA*, *ndhB*, *ndhK*, *petA*, *rpl2*, *rpoC1*, *ycf3*, *ycf15*) were erroneously reported twice as 2 gene fragments by DOGMA and GeSeq, whereas they were correctly reported as a single gene containing an intron by cpGAVAS (Table 3.2). These fragments were used to determine the locations of the exons and introns of a gene. When the annotated genes were compared with those previously reported in other species' chloroplast sequences, the GeSeq tool gave the most accurate results for gene locations, including starting and end points of the CDS. DOGMA did not define the start and end point of exons, therefore start and stop codons had to be manually checked, and added from the cp genome. All of the genome and annotation information is shown in Figure 3.3.

Table 3.2: Differences between annotation tools

		Annotation Tools		
		cpGAVAS	**Dogma**	**GeSeq**
Genes	*atpF*	No gap	One gap	One gap
	clpP	No gap	Two gap	Two gap
	ndhA	No gap	One gap	One gap
	ndhB	No gap	One gap	One gap
	ndhK	No gap	One gap	No gap
	petA	No gap	One gap	No gap
	rpl2	No gap	One gap	One gap
	rpoC1	No gap	One gap	One gap
	ycf3	No gap	Two gap	Two gap
	ycf15	No gap	One gap	-
tRNAs	*trnA-TGC*	-	+	-
	trnfM-CAT	+	+	-
	trnI-CAT	+	+	-
	trnI-GAT	-	+	+
	trnK-TTT	-	+	-
	trnL-TAA	-	+	-
	trnV-TAC	-	+	-

* - : not found; +: found

Prediction of the *C. avellana* cv Tombul cp gene functions was based on homology, and they were mostly involved in photosynthesis and other metabolic processes as expected. The genes were classified into three broad categories based on their functions: photosynthesis, self-replication and other genes. While 42 protein-coding genes participated in photosynthesis, 25 protein-coding genes were involved in the chloroplast self-replication processes, and 5 genes represented other functions, all of which were summarized in Table 3.3.

Table 3.3: Gene contents and functional classification of cv Tombul chloroplast genome

Category	Group of Genes	Code of Genes	List of Genes
Genes for photosynthesis	Subunits of ATP synthase	atp	atpA, atpB, atpE, atpF, atpH, atpI
	Subunits of NADH-dehydrogenase	ndh	ndhA, ndhB, ndhC, ndhD, ndhE, ndhF, ndhG, ndhH, ndhI, ndhJ, ndhK
	Subunits of cytochrome b/f complex	pet	petD, petG, petL, petN
	Subunits of photosystem I	psa	psaA, psaB, psaC, psaI, psaJ
	Subunits of photosystem II	psb	psbA, psbB, psbC, psbD, psbE, psbF, psbH, psbI, psbJ, psbK, psbL, psbM, psbN, psbT, psbZ
	Subunit of rubisco	rbc	rbcL
Self-replication	Large subunit of ribosome	rpl	rpl2,rpl14,rpl16, rpl20, rpl22, rpl23, rpl32, rpl33, rpl36
	DNA dependent RNA polymerase	rpo	rpoA, rpoB, rpoC1, rpoC2
	Small subunit of ribosome	rps	rps2, rps3, rps4, rps7, rps8, rps11, rps12, rps14, rps15, rps16, rps18, rps19
	rRNA Genes	rrn	rrn4.5S, rrn5S, rrn16S, rrn23S
	tRNA Genes	trn	trnC-GCA, trnD-GTC, trnE-TTC, trnF-GAA, trnfM-CAT, trnG-GCC, trnH-GTG, trnM-CAT, trnP-TGG, trnQ-TTG, trnR-TCT, trnS-GCT, trnS-GGA, trnS-TGA, trnT-GGT, trnT-TGT, trnW-CCA, trnY-GTA, trnL-TAG, trnI-CAT, trnI-GAT, trnL-CAA, trnN-GTT, trnR-ACG, trnV-GAC
Other genes	Subunit of Acetyl-CoA-carboxylase	acc	accD
	c-type cytochrome synthesis gene	ccs	ccsA
	Envelop membrane protein	cem	cemA
	Protease	clp	clpP
	Maturase	mat	matK
Genes of unkown function	Conserved open reading frames	ycf	ycf1, ycf2, ycf3, ycf4

Based on a sequence similarity search of the whole genome, *C.avellana* cv Tombul chloroplast was most similar to chloroplast genomes belonging to the *Corylus* family with a range from 99.46 (*Corylus wangii*, Accesion: MH628454.1) to 99.88% (*Corylus heterophylla* var. sutchuenensis, Accesion: MF996573.1) identity via Basic Local Alignment Search Tool (BLAST) search in NCBI website (http://blast.ncbi.nlm.nih.gov/) against Viridiplantae (taxid: 33090) (Camacho et al., 2009). In addition, *Carpinus* and *Ostrya* families also showed high similarity with cv Tombul cp genome with nearly 98.91 and 99.21% identity, respectively (Appendix C: Table S3.3).

3.3.2. Comparison of chloroplast genome sequences with other species

The similarities and differences of the cp genome between *C. avellana* cv Tombul and other species, including representatives of the Malpighiales, Fabales and Brassicales, were determined by a global alignment program, mVISTA (Frazer et al., 2004). The chloroplast genome sequences were aligned to each other and plotted using *C. avellana* cv Tombul as a reference (Figure 3.4). Tombul had a similar cp genome size to the other species, which range from 152,217 bp to 161,303 bp (Tombul cp genome size is 161,667 bp). In addition, the alignment revealed a very high level of identity in the global patterns of sequence similarities with KX822768, an accession of an unspecified *C. avellana* variety found in China, and *Betula nana* with 99.8 and 96.6% identity, respectively. As expected, coding regions were more highly conserved than non-coding regions. The highest polymorphism was observed in intergenic regions (such as *rps16-psbK*, *psbI-atpA*, *psbM-psbD*), but the *ycf1* gene had higher variability regions, especially between distant species. Dong et al. (2015) also indicated that *ycf1* gene was the most variable plastid genome region and could serve as a barcode of land plants. At the species level, nucleotide substitution could more rapidly occur in intergenic regions, and these regions with high levels of divergence could have high potential for developing molecular markers for population genetic analysis between varieties. Furthermore, a region was detected in the cv Tombul cp genome from ~ 68 to 69 kb that was conserved with KX822768 but none of the other species presented in the global alignment. This region contained duplicates of the *psbF*, *psbJ* and *psbL* genes from the adjacent region, and an unprocessed *petA* gene. This could be a tandem duplication specific to the hazelnut lineage; further *Corylus* chloroplast genomes should be explored to determine whether it is found in other species from this genus.

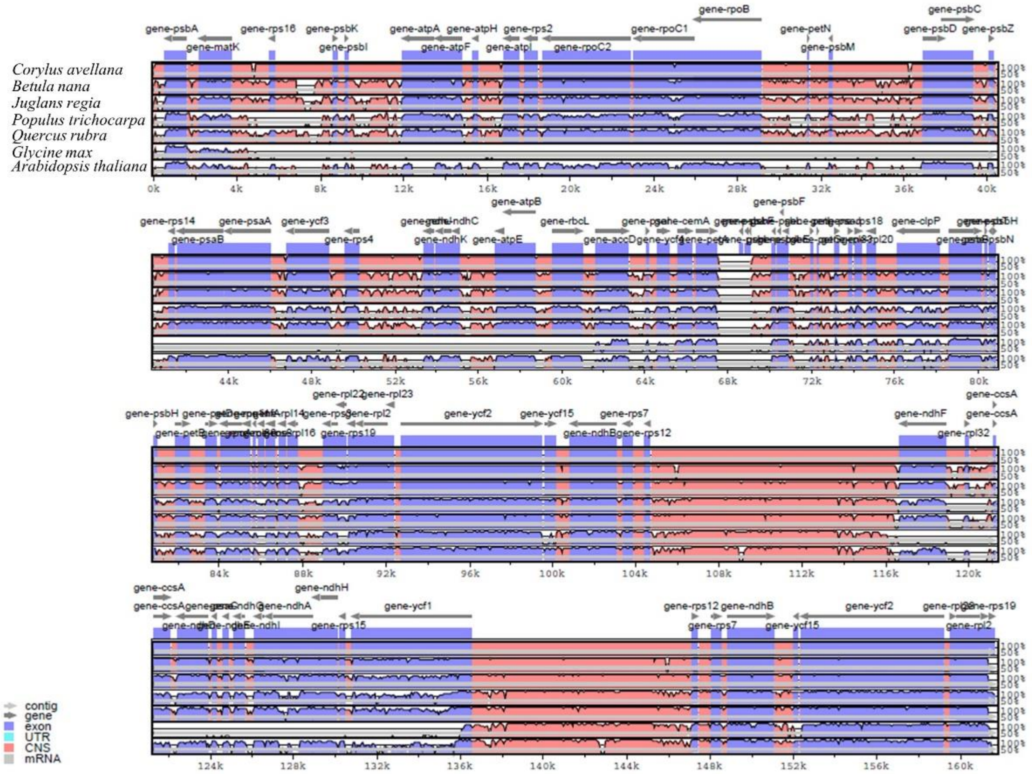


Figure 3.4: Sequence alignment of 8 chloroplast genomes using mVISTA tool with *Corylus avellana* cv Tombul as a reference. Grey arrows above the alignment indicate the transcriptional directions of genes. Genome regions, exon and conserved non-coding sequences (CNS), are color coded as blue and red, respectively. Multiple alignment was carried by LAGAN option, and a cut-off of 50% identity was used for the plots. The Y-axis indicated the percent identity between 50 and 100%.

3.3.3. Simple sequence repeats analysis

Simple sequence repeats (SSR) are useful in characterization of genetic diversity. According to the MISA web tool, a total of 83 SSRs were identified in the cv Tombul cp genome (Beier et al., 2017). Among these SSRs, there were 44, 19, 4, 13, 2, 1 for mono-, di-, tri-, tetra- and penta- nucleotide repeats, respectively (Appendix C: Table S3.4). The largest proportion of simple repeats was classified as mononucleotides (48.2%). While most of the mononucleotides were composed of A/T (90.9%), most of the dinucleotides were AT/TA (84.2%) (Fig. 5). Similar results were obtained from IMEx-web server (Mudunuri and Nagarajaram, 2007). Only a few differences were shown in the direction of SSRs (Appendix C: Table S3.5). These SSR regions may be useful in developing markers useful to elucidate genome evolution and chloroplast rearrangements among species.

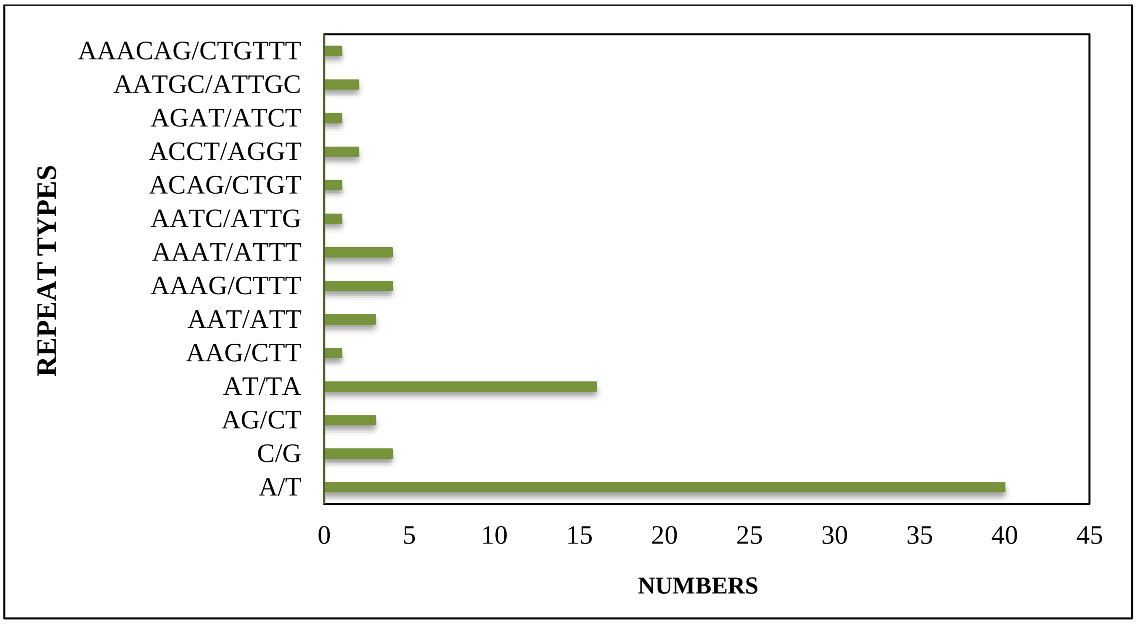


Figure 3.5: Number of classified SSR repeat types (considering complementary sequences)

3.3.4. Phylogeny inference

The complete cp genome sequences of 22 species from Fagales order were obtained from the NCBI and used for phylogenetic analysis, including representatives of genera of Betulaceae, Fagaceae, and Juglandaceae. As chloroplast protein sequences showed high similarity among related species, the phylogenetic analysis was carried out using the whole cp genome nucleotide sequences. Tree construction was carried out using the maximum likelihood method with 500 replicates. All nodes of these phylogenetic trees were strongly supported by bootstrap values (BS). The 22 taxa were classified into four major clades. A monophyletic group was observed incorporating the *Corylus*, *Betula* and *Juglans* species. *Fagus* and the sister group of *Quercus* and *Castanopsis* were located at the basal position. Moreover, within the Betulaceae, *Carpinus* and *Ostrya* clustered into a clade which was the sister to the clade *Corylus* and showed greater divergence from the clade formed by *Betula* species. As stated in the literature, *Corylus* was closest to

Carpinus and *Ostrya* species, and then relatively close to *Betula*, which is consistent with their taxonomic classification but provides greater insight into the relatedness of these genera (Figure 3.6) (Chen et al., 1999; Yang et al., 2019).

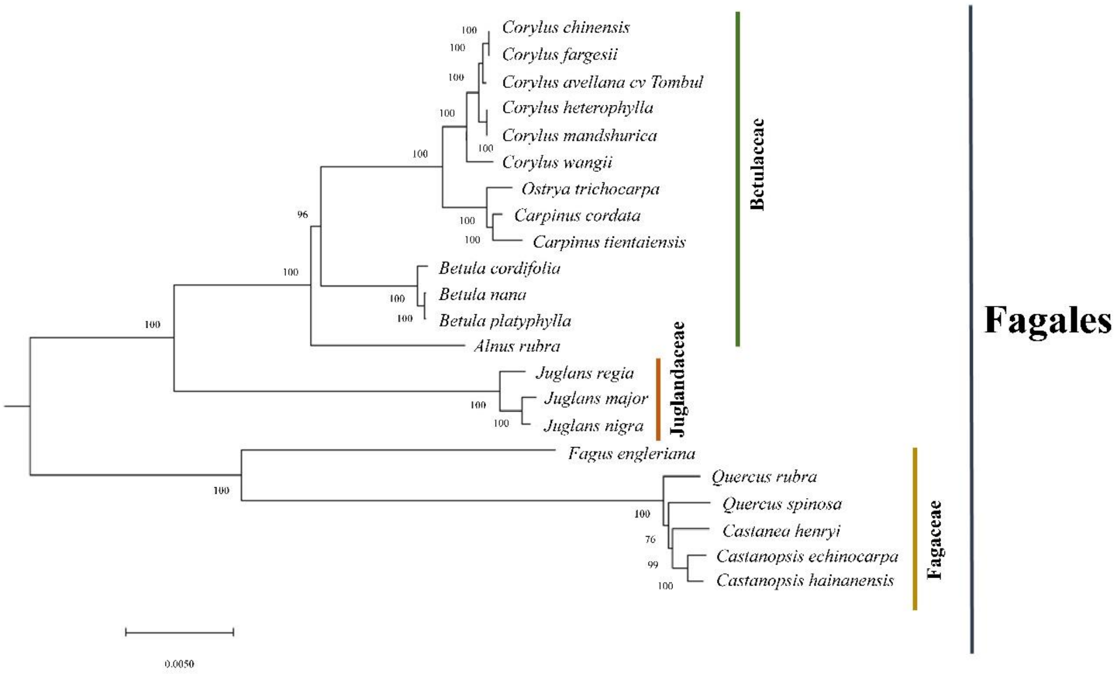


Figure 3.6: Phylogenetic position of *Corylus avellana* cv Tombul inferred by maximum likelihood (ML) analysis of 22 complete cp genomes. Numbers above each node indicate the bootstrap values based on 500 replicates.

In the clade *Corylus*, 6 species were divided into four subclades. *C. wangii* was located at the basal position, while *C. mandshurica* and *C. heterophylla* clustered into a sister group, while *C. fargesii* and *C. chinensis* clustered together. The phylogenetic tree indicated that cv Tombul, although it formed a distinct subclade, exhibited a closer relationship with *C. fargesii* and *C. chinensis* than the other varieties (Fig. 3.6) (Hu et al., 2016a,b).

3.4. DISCUSSION & CONCLUSIONS

3.4.1. Discussion

3.4.1.1. Comparison of methods for assembling cp sequences from WGS data

The assembly of cp genomes derived from whole genome shotgun (WGS) sequences is a useful strategy to characterize cp functional elements and provide extensive analysis of phylogenetic and evolutionary relationships among related species. Multiple tools have been developed to construct and annotate cp genomes. This study reported a complete cp genome sequence of *Corylus avellana* cv Tombul, annotated by different available annotation tools (Figure 3.1) (Dierckxsens et al., 2017). Initially, *de novo* assembler NOVOPlasty was used to reconstitute the Tombul cp genome. A single 200,017 bp contig was obtained from raw WGS sequences by NOVOplasty. When the contig was compared with the KX822768 cp genome published in GenBank, it indicated that the last part of the sequence, (161,667–200,017 bp), was nearly identical to other segments of the Tombul chloroplast genome. Nanopore sequencing reads belonging to cv Tombul, were aligned to the contig, and a subset of reads matched these additional parts. Therefore, we considered the possibility that the cp genome of cv Tombul could be physically larger than the reported *C. avellana* cp genome. However, BLAST results indicated that this part consisted of two segments, each of which was 100% identical to region in the first 161 kb of the cv Tombul cp genome (Figure 3.2) (Wang et al., 2018). Furthermore, the mapped read depth of the duplicated segments was approximately half of that of the rest of the cp genome. Hence, we concluded that the additional 39 kb was an artefact of the NOVOplasty assembly algorithm. Further analysis was carried out using the first 161,667 bp of the genome assembly, which also showed 99.8% similarity to the KX822768 cp genome.

3.4.1.2. Comparison of methods for annotation of cp genome for cv Tombul

The cv Tombul cp genome represented similar characteristics with angiosperm cp genomes. In addition, it exhibited some differences between closely related species. There is a previously reported sequence for *C. avellana* deposited in Genbank (KX822768), cultivated in China, but no varietal information was provided for this accession. Whereas the general characteristics of cv Tombul cp genome are highly consistent with KX822768, a few differences were detected at the gene level. Two genes, *atpF* and *clpP*, were reported as unprocessed in the older sequence, however full-length protein sequences were predicted for these genes in the cv Tombul cp genome. Furthermore, the genes *accD*, *psbM*, and *trnI-GAT*, were not annotated in the KX822768, but they were present in the cv Tombul cp genome. In addition, the analysis of these genes among the KX822768 using BLAST+ software showed that the annotation of KX822768 just missed them even though they existed in the cp genome. Lastly, *psbF*, *psbJ* and *psbL* genes were found twice in the cv Tombul cp genome (Appendix C: Table S3.6). The length of the cv Tombul cp genome was found to be similar to other *Corylus* and *Quercus* species, but a difference was indicated with *Populus* and *Juglans* species (Hu et al., 2016a,b; Yang et al., 2016; Dong et al., 2017; Zong et al., 2019). Although the length differed among species, the GC contents were very similar in angiosperm cp genomes (Appendix C: Table S3.7) (Cheng et al., 2018).

Two hypothetical chloroplast protein coding sequences, *ycf15* and *ycf68*, were also identified in our annotation process. Whereas they were represented as functional protein-coding gene in some studies (Raubeson et al., 2007), they were classified as pseudogenes in our map because of containing several internal stop codons in their coding sequences as indicated in several other species (Yang et al., 2018; Lu et al., 2017). Moreover, the gene *ycf15* was annotated between *rps7* and *trnV-GAC* in some studies, while some others revealed that it was located between *ycf2* and *trnL-CAA1*. (Choi et al., 2015; Williams et al., 2015). In the present study, the gene *ycf15* was detected in both positions, thereby further studies are required to clarify whether either of these is expressed.

The annotation of cv Tombul cp genome was carried out using three different tools, cpGAVAS, DOGMA and GeSeq (Tillich et al., 2017; Liu et al., 2012; Shi et al., 2019; Wyman et al., 2004). In terms of gene contents, similar results were obtained from all tools. A number of genes were annotated as fragmented by DOGMA and GeSeq, whereas they were found as a single gene in cpGAVAS containing introns in specific locations. Additionally, more tRNA genes were detected using the DOGMA tool than the other two (Table 2). The GeSeq annotation tool provides more precise results for gene locations, which may be because it chooses a broad range of BLAT reference sequences, including closely related taxa. Because it is not suitable for defining the start and end of exons, the

DOGMA annotation needs manual editing, and additionally the identification of the IR region was not supported by this tool. CpGAVAS results showed high similarity with the GeSeq findings. If a cp genome belonging to a closely related taxon is available, the GeSeq annotation tool is the most useful for the analysis. In other cases, the annotation with both GeSeq and cpGAVAS, followed by comparison of the results from both tools, provides the most precise information about functional genes and locations with minimal configuration.

Due to the properties of cp genome that has a small size, single-parental inheritance, haploid nature, low nucleotide substitution rate, and highly conserved genomic structure, the Tombul cp genome showed high similarities with other species (Palmer et al., 1988; Yang et al., 2013). Highly conserved structure, similar gene content and order were determined by comparative genome analysis of cv Tombul genome with six different species, indicating that cv Tombul cp genome contains largely the same coding genes, tRNAs and rRNAs. However, Tombul cp genome showed a difference with *Glycine max*. Although the cp genomes of plants are highly conserved in regard to gene structure, content and order, rearrangements of plastid gene order and gene losses have been observed in legumes, for instance one of the IR-region has been completely lost in several legumes, and an inversion of the LSC was pointed out in *Glycine* species (Palmer et al., 1987; Tangphatsornruang et al., 2010; Asaf et al., 2017). Moreover, the length of the cp genome from cv Tombul slightly differed from the published sequence KX822768 in GenBank, from which it could be inferred that some genetic differences exist even between cultivars.

3.4.1.3. Repeat analysis

Simple sequence repeats (SSR) are useful for characterization of genetic diversity and development of molecular markers for phylogenetic studies and breeding. Herein, I identified several microsatellite sequences in the *C. avellana* cv Tombul cp genome, most of which were distributed in the intergenic regions, although some SSRs were detected in several coding genes. Multiple SSR types were detected in the *ycf1* protein-coding gene, confirming the results of comparative genome analysis that *ycf1* contains high variability regions. The majority of simple repeats from the cv Tombul cp genome were classified as mononucleotides and dinucleotides, which were mainly composed of adenine (A) or thymine (T) repeats, and rarely contained guanine (G) or cytosine (C) repeats. Our findings presented similar results to previous studies (Yang et al., 2018; Qian et al., 2013; Jiang et al., 2017). These features could provide deeper information for phylogenetic research of *Corylus* by allowing development of species- and variety-specific molecular markers.

3.4.1.4. Phylogenetic analysis

Previous studies have resolved the relationships of Betulaceae family, and the most taxonomists have agreed that the Betulaceae family is divided into two subfamilies, named as Betuloideae (genera: *Alnus* and *Betula*) and Coryloideae (genera: *Corylus*, *Carpinus*, *Ostrya*, and *Ostryopsis*) (Chen et al., 1999). The generic relationships within Coryloideae were studied by molecular markers including *matK* and *rbcL* genes, and ITS regions (Chen et al., 1999; Bousquet et al., 1992; Kato et al., 1998; Hufford et al., 2001). We found a similar grouping within the cp genome phylogeny, including *Corylus* formed a monophyletic group and had a close relationship with *Carpinus* and *Ostrya*: the results of our analyses supported the previous studies (Yang et al., 2019). *Ostrya* formed a sister group with *Carpinus*, and these genera together constituted a sister group to *Corylus*. Whereas relationships between sub-families have fairly well resolved, the inter-specific relationships within *Corylus* have not been completely determined due to lack of information about taxon sampling for *Corylus* species, and limited studies at molecular level, such as molecular markers (Zong et al., 2015). Our results about the relationship of *Corylus* species supported those by Yang et al. (2018), and *Corylus avellana* cv Tombul exhibited close relationship to the sister group of *C. fargesii* and *C. chinensis*, which are tree species in *Corylus* family, and the most distant to primitive species, *C. wangii*. Helmstetter et al. (2019) found clades similar to found by Yang et al. (2018) but they noted that *C. avellana* is placed either closely related to the Colurnae subsection that was not present in our study. Similarly, Helmstetter et al. (2019) represented that *C. heterophylla* and *C. sieboldiana var. mandshurica* formed a sister pair in the cpDNA tree. As briefly stated, the complete cp genomes provide more in-depth information about both inter- and intraspecific relationships, and for evolutionary studies.

3.4.2. Conclusions

Corylus is a phylogenetically and economically important genus with 16–20 species, in the family Betulaceae. Because of commercial and ornamental values of *Corylus* species, greater study of this genus can contribute to both science and the economy. In summary, we assembled the cv Tombul cp genome by using WGS sequences generated as part of a whole genome sequencing project. The cp genome of cv Tombul has a typical cp genome structure that has a simple circular, quadripartite structure, including two copies of an inverted repeat (IR) that separate the large and small single copy regions (LSC and SSC), and is highly similar to other cp genomes of *Betulaceae* family. Our results confirm that complete and highly-accurate chloroplast genome assemblies can be simply obtained from next generation whole genome shotgun data, but that assembly and annotation tools must be carefully selected and cross-checked for potential errors. Although the results were similar in all annotation tools in terms of gene content, GeSeq and cpGAVAS provided better results for gene locations. If the location information of exons and introns of a gene was needed for further analysis, annotation should be carried by using GeSeq. According to phylogenetic analysis, it was observed that *Corylus avellana* cv Tombul had a close relationship to *C. fargesii* and *C. chinensis*. Therefore, these two *Corylus* species may be especially useful for crossbreeding and grafting with *C. avellana*, in order to produce resilient and productive varieties. The interspecific relationships of genus *Corylus* could be more precisely understood with enhanced taxon sampling. In the future, we are considering wider cp genome sampling of other widely grown varieties, to investigate whether cultivar specific markers exist or not, and focus on the development of molecular markers for deeper information about phylogeny.

4. WHOLE TRANSCRIPTOME SHOTGUN SEQUENCING AND TRANSCRIPTOME ASSEMBLY FOR CONTROL AND STRESS APPLIED SAMPLES, AND HOW CHILLING STRESS AFFECTS THE GENE EXPRESSION OF HAZELNUT

4.1. INTRODUCTION

Environmental conditions are one of the major limiting factors for plant growth and development. Due to their sessile nature, plants have to cope with diverse environmental stresses by adaptive mechanisms throughout the year and abiotic stresses are one of the main reasons for crop failure by affecting plant survival and growth. Climate studies indicate that extreme weather conditions will become more frequent in the near future, and it is expected the changes will have a big impact on year-to-year yield variability and crop production (Foresight, 2011). Therefore, increasing our knowledge about plant mechanisms to adapt to adverse conditions is becoming much more important to sustain productivity worldwide. Emerging technology, including genome and transcriptome sequencing, allows us to analyze plant responses to stress conditions, transcript abundance profiles under abiotic stresses, stress-responsive genes and gene networks, transcription factors and hormones controlling stress-induced signaling pathways (Kreps et al., 2002; Shinozaki and Yamaguchi- Shinozaki, 2007; Shanker and Venkateswarlu, 2011).

Low temperature, termed as “chilling stress,” is the exposure to low non-freezing temperatures generally ranging from 0-15°C, is one of the inevitable environmental challenges that has an impact on plant growth, development and productivity (Kim et al., 2011). Especially in higher altitude mountain areas, low temperature is one of the most frequently faced stresses during life cycles. Low non-freezing temperatures have altered plant species in their developmental, morphological, physiological, cellular and biochemical processes (Hausman et al., 2000; Maestrini et al., 2009). Alterations in membrane properties and protein structure, impairment of metabolic processes, and tissue damage have been observed under chilling stress, and the extent of damage was dependent on the duration of the stress (Hirt and Shinozaki, 2004). Alongside alteration of physiological and metabolic processes, a reduction occurred in yield quantity and quality. Seed germination and seedling growth were also hampered under chilling stress (Ding et al., 2017; Farooq et al., 2017; Sheteiwy et al., 2017). Chilling treatment has a range of negative effects, including reduction of net/maximal photosynthetic rates and carbohydrate metabolism, induction of photochemical efficiency loss, destruction of chloroplast structures, and restriction of electron transport and enzyme activity (Kratsch and Wise 2000; Marian et al. 2004; Renaut et al. 2004). Moreover, Yadav (2010) indicated that the reduction of water and mineral uptake, stomatal conductance, and photosynthesis under chilling stress caused the impairment of plant growth and development. Chilling stress damaged thylakoid membranes and also chlorophyll (Chl) pigment formation, and it directly affected the photosynthetic apparatus. CO_2 fixation was also altered because of imbalanced stomatal movement, causing excess sugar accumulation and lipid peroxidation. In addition, water potential and photosynthesis rate were disturbed due to the lower CO_2 fixation. Reduction of root growth was also observed under chilling stress, and was directly linked with low water and mineral nutrient uptake, resulting in nutrient deficiency in plants (Farooq et al., 2017). Moreover, imbalanced metabolic processes due to chilling stress also caused overproduction of ROS, and oxidative damage to DNA, protein, and lipid (Ding et al., 2017).

Plants withstand chilling stress by inducing gene expression and alteration of metabolic mechanisms, a process called cold acclimation (Renaut et al. 2004). There were several studies related to transcription factors, involved in activation or repression of specific cold-responsive genes, including CBF/DREB1, WRKY, AP2/ERF, MYB, and bHLH (Ramsay and Glover 2005; Chen et al. 2009; Maestrini et al. 2009; Li et al. 2003, 2011). Song et al. (2013) reported the gene expression in poplar, *Populus simonii*, in response to chilling stress. They identified 1,085 differentially expressed genes in cold stress that were involved in photosynthesis, signal transduction, and regulation of transcription. These findings may also provide insight into the molecular mechanisms of chilling tolerance for other woody plants. Although environmental factors such as chilling stress are known to affect the production of hazelnut, no transcriptome studies exist exploring gene expression in chilling stress induced hazel.

Corylus avellana, commonly called European hazel, is a prevalent crop tree grown across much of Europe, western Asia and northern Africa. Black Sea region of Turkey provides almost 70% of the world’s hazelnut production. This species historically had a wide usage area including wood, furniture, coppices, flavor and texture in a variety of food products. Besides the nuts are very valuable for human nutrition, hazelnut also serves as an important food supply to several animals and birds (Gökirmak, Mehlenbacher, & Bassil, 2008; Enescu et al., 2016). Kavas et al. (2019) indicated that the hazelnut production considerably decreased due to cold temperature in 2012 and 2013. Hazelnut yields were also significantly reduced spring frosts and summer droughts (Ustaoglu, 2012; Helmstetter et al., 2019). Hence, it is crucial to identify genes and gene networks related with low temperature for improvement of hazelnut cultivars.

Herein, I presented the transcriptome analysis of *Corylus avellana* cv Tombul and Cakildak, the most widely grown Turkish varieties. The aim of current study was to obtain new insight on the genes and gene networks involved in chilling stress, and to see how sudden chilling affected them. Plants can modify their physiological and cellular states, and change gene expression levels to adjust to stress conditions in order to survive. The results generated through transcriptome sequencing will provide a broad knowledge about stress-responsive genes in hazelnut, and highlighting their expression profile under stress. For the world’s food production and security, it is crucial to understand the genes and gene networks involved in abiotic stress resistance, and this study will be useful for the future genetic improvement of hazelnut in order to better tolerate chilling stress.

4.2. MATERIALS AND METHODS

4.2.1. Chilling-stress treatment and RNA isolation

Corylus avellana cv Tombul and Cakildak branches with buds used in the study were collected from one-year-old trees of Sabanci University. Branches around 3-4 cm with buds were cut from hazelnut trees, and placed in the 50 ml falcon tubes containing water. One set of tubes was kept in the 4 °C cold room for 7 days for chilling treatment. Other set of tubes was stored at room temperature as control.

The total RNA was extracted from young leaf buds using a cetyltrimethylammonium ammonium bromide (CTAB) method optimized for Betulaceae (Wang et al., 2013). Buds (~100 mg sample) were frozen in liquid nitrogen and then grounded into powder using 3 mm steel beads in a TissueLyser II (Qiagen, Santa Clarita, CA). After homogenization, polysaccharides were extracted from the tissues by two successive incubations on ice with TNE buffer (200 mM Tris-HCl, 250 mM NaCl, 50 mM EDTA), followed by precipitation of proteins using a modified CTAB protocol: RNAse A was not applied and removal of lipids achieved by an extraction with 24:1 chloroform:isoamyl alcohol. The aqueous phase from this extraction was then recovered by two successive ethanol precipitations at high and low salt concentrations. The final total RNA was resuspended in 60 µl TE and residual DNA eliminated using RNAse-free DNAse I. The concentration and purity of isolated RNA were estimated by UV spectrophotometry at wavelengths of 260nm and 280 nm using the NanoDrop ND-2000c (Thermo Scientific, Wilmington, DE). In order to confirm that the RNA was not degraded and of sufficient quality for RNA sequencing (RNA-Seq) analysis, 2 aliquots of each sample were also analyzed by agarose gel electrophoresis.

4.2.2. RNA-Seq library construction and whole transcriptome shotgun sequencing

The RNA-Seq library was constructed using a TruSeq RNA sample preparation kit from Illumina platform (BMLabosis). The sequencing library was prepared by random fragmentation of the cDNA sample, followed by 5' and 3' adapter ligation. Adapter-ligated fragments were then PCR amplified and gel purified. The library was loaded into a flow cell where fragments were captured on a lawn of surface-bound oligos complementary to the library adapters. Each fragment was then amplified into distinct, clonal clusters through bridge amplification. When cluster generation was complete, the templates were ready for sequencing. Paired-end sequencing was carried out on the Illumina HiSeq 4000 platform (Illumina, San Diego, CA, USA). Whole transcriptome shotgun sequencing was carried by Macrogen (Seoul, South Korea; https://www.macrogen.com)

4.2.3. Transcriptome assembly and sequence annotation

The adaptor region of the raw data generated via Illumina sequencing was trimmed using CutAdapt (Martin M., 2011). The quality of obtained raw reads was checked by the

FastQC tool (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/). Following preprocessing, the trimmed reads were then mapped back onto the *Corylus avellana* genome (Accession number: GCA_ 901000735) with the HISAT2 aligner (Pertea et al., 2016). The alignment results were coordinate-sorted with SAMtools and used in the StringTie assembly (Li et al., 2009). Furthermore, the differentially expressed transcripts were determined with Ballgown software (Pertea et al., 2016) (Figure 4.1). All assembled transcripts were searched against Viridiplantae and Swissprot databases using the BLASTx program with an E-value cut-off of 1.0e–5 (Camacho et al., 2009). Gene Ontology (GO) annotation for the transcripts was analyzed by using the TRAPID program, based on three major categories of biological process, molecular function, and cellular component (Van Bel at al., 2013).

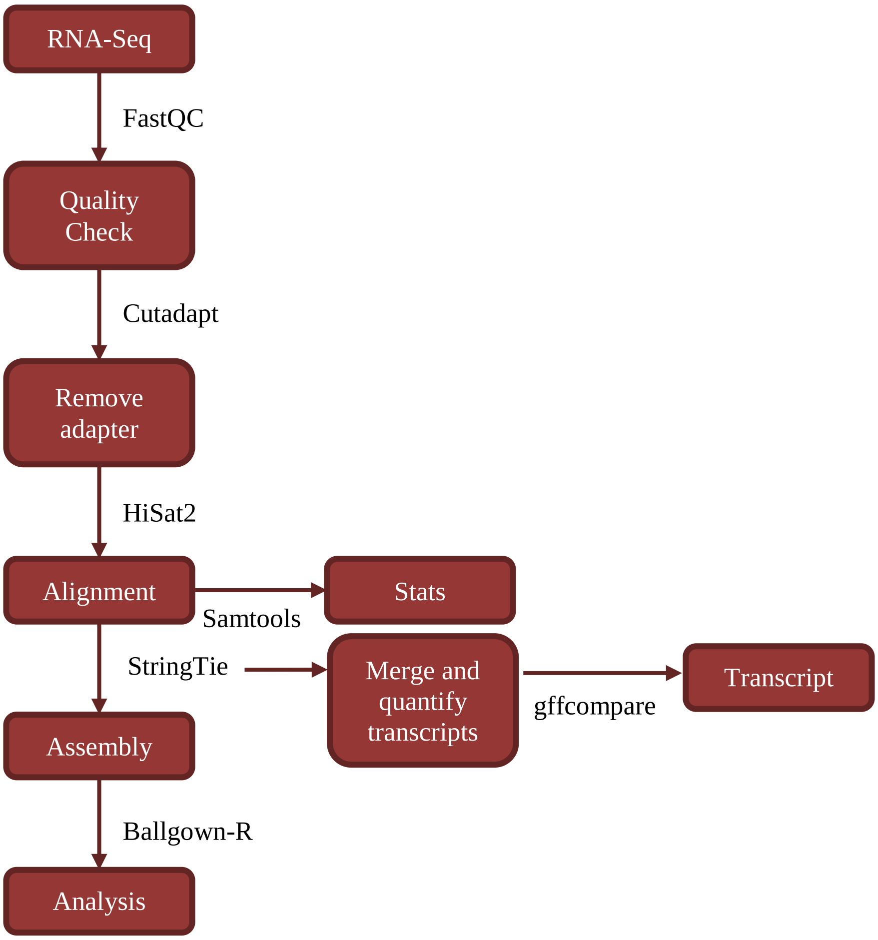


Figure 4.1: Flowchart of transcriptome assembly

4.2.4. Analysis and functional enrichment of differentially expressed transcripts

The expression level of each transcript was measured by the numbers of fragments per kilobase of exon in per million fragments mapped reads (FPKM). Adjusted p-value ≤ 0.05, fold change (FC)>2 and FC<0.5 were employed as criteria for identifying differentially expressed transcripts (DETs) with Ballgown software. Beside Ballgown analysis, the analysis of differential expression was based on the count of expression level of each transcripts in control and chilling treated samples using DESeq2 R package in IDEP web-server (Ge et al., 2018).

4.2.5. qRT-PCR analysis of gene expression

Total RNA was extracted from each *Corylus avellana* bud samples using CTAB method and reverse-transcribed (Wang et al., 2013). The first strand cDNA was synthesized using Transcriptor First Strand cDNA Synthesis Kit (Roche Life Science), and cDNA diluted 10-fold with RNase free water was used as a template for qRT-PCR (Chao et al. 2018). One of the transcripts, mapped to HMG-CoA genes of *Corylus avellana*, was used as an internal control, and six differentially expressed transcripts were randomly selected to analyze the expression level (Table 4.1). The qRT-PCR was performed in a LightCycler 480 Real-Time PCR System (Roche Life Science). Each 20 µL reaction mixture contained 10 µL SYBR® Green Real-time PCR Master Mix (Roche Life Science), 5 µL cDNA template (equivalent to 100 ng of total RNA), and 0.5 µM of each forward and reverse primer. The following cycling parameters were applied for amplification: 95 °C for 5 m followed by 45 cycles of 95 °C for 10 s, 58 °C for 10 s, 72 °C for 30 s, then 1 s at 81 °C for plate reading. The experiments were designed with three replication to ensure the reproducibility of qRT-PCR results. The relative expression levels were calculated using the $2^{-\Delta\Delta CT}$ method (Livak and Schmittgen, 2001).

Table 4.1: Selected transcripts and primer properties for qRT analysis

Transcript name	Primer (L: Left, R: Right)	Tm	GC%	Product size
MSTRG.11796.95	L: GACAAGTCTCCGTTGCTTCC	59.85	55.00	202
	R: CCCCAAAGTAAGGCTTGTCA	60.10	50.00	
MSTRG.31160.5	L: CCATACCCAACGGAAGAAGA	59.93	50.00	204
	R: CTCATCCAATCCGTCCAGTT	59.93	50.00	
MSTRG.41294.1	L: AGCCCGTCAACATATTCCTG	59.96	50.00	200
	R: CAGGCCATCCAGACTTGAAT	60.07	50.00	
MSTRG.45264.1	L: CCTCGGGTCACAAAGAGAGA	60.38	55.00	204
	R: GGCCTTCTCCACCATAATGA	59.89	50.00	
MSTRG.23250.2	L: CAAGCCACTTCTCCAAGCAT	60.40	50.00	209
	R: GCCATTCGAATTCCGTCTTA	60.04	45.00	
MSTRG.10583.2	L: GCTTGGAGTTGCAGGACTTC	60.00	55.00	212
	R: TCTTGCCAGAAGACCCTGTT	59.84	50.00	

4.2.6. Analysis of TF and hormone-related DETs from RNAseq data

The plant transcription factor database (PlantTFDB) (http://plntfdb.bio.uni-potsdam.de/v3.0/) was used to predict transcription factors. Transcription factor (TF) prediction was performed with BLAST+ under a threshold E-value ≤ 10−5 (Camacho et al., 2009). For plant hormone-related DETs prediction, genes related to hormone metabolic pathways in *Arabidopsis thaliana* were downloaded from RIKEN Plant Hormone Research Network website (http://hormones.psc.riken.jp/). DETs from two groups were compared with nucleotide and protein sequences of Arabidopsis hormone using Blastn, and Blastx, respectively (E-value ≤ 10−5).

4.3. RESULTS

4.3.1. Sequencing and transcriptome assembly

In the present study, total RNA was extracted from the buds of *Corylus avellana* to explore differentially expressed transcripts under chilling stress. RNA sequencing of two different cultivars from the control and chilling-treated samples was then performed on the Illumina HiSeq 4000 platform. From eight libraries, a total of 693,044,652 raw reads were obtained. After filtering out low-quality reads, 74,695,406, 68,030,232, 65,937,538, and 69,238,960 clean reads with more than 95% Q30 bases were acquired for the control samples (Table 4.2). For the chilling-treated samples, 113,756,106, 91,238,730, 106,029,446, and 101,621,024 clean reads with more than 94% Q30 bases were acquired (Table 4.2). The GC content was approximately 47% in all samples with the exception of C1 control.

Table 4.2: Sequencing the *Corylus avellana* transcriptome in eight bud samples for both control and chilling treated

Sample	Read		GC(%)	Q20(%)	Q30(%)
	Raw Data	Clean data			
C1 control	75,169,522	74,695,406	51.147	98.196	95.299
C1 chilling	114,162,372	113,756,106	46.997	98.002	95.021
C2 control	68,322,282	68,030,232	47.163	98.186	95.351
C2 chilling	91,521,458	91,238,730	46.954	97.834	94.688
T1 control	66,115,702	65,937,538	46.310	98.763	95.400
T1 chilling	106,347,136	106,029,446	46.854	98.164	95.389
T2 control	69,475,488	69,238,960	46.084	98.163	95.286
T2 chilling	101,930,692	101,621,024	46.440	97.900	94.814

*C: Cakildak cv, T: Tombul cv, GC(%): The percentage of guanine and cytosine out of four bases, Q20: The probability that the base was miscalled is 1%, Q30: The probability that the base was miscalled is 0.1%.

To generate a comprehensive transcriptome, the filtered clean reads were mapped to the *Corylus avellana* reference genome with Hisat2, and then assembled using the Stringtie program. The clean reads that successfully mapped to the reference genome ranged from 91.15% to 95.17% (Table 4.3). The obtained valid reads were assembled to generate 48,873 genes with 74,489 transcripts in four samples (Figure 4.2a). The minimum and maximum length of transcripts were 200 and 16,724 bp, respectively. Total lengths extended to 106,568,850 bp with an N50 value of 19,372 bp. In total, 61,806 transcripts (82.97%) were longer than 500 bp, and 44,571 transcripts (59.84%) were longer than 1 kb (Figure 4.2b, Table 4.4). The transcripts that could not be identified by squence comparison with known protein databases were classified as novel transcripts.

Table 4.3: Alignment summary

Sample	Total reads	Total mapped	Overall alignment rate (%)
C1 control	74,695,406	71,084,982	95.17
C1 chilling	113,756,106	106,111,980	93.28
C2 control	68,030,232	62,009,182	91.15
C2 chilling	91,238,730	84,889,928	93.04
T1 control	65,937,538	63,745,092	96.67
T1 chilling	106,029,446	100,581,355	94.86
T2 control	69,238,960	65,028,383	93.92
T2 chilling	101,621,024	95,410,099	93.89

Table 4.4: Summary of transcript data

All (≥200)	74,489
≥500	61,806
≥1000	44,571
N50 (bp)	19,372
N90 (bp)	51,851
Total length (bp)	106,568,850
Max length (bp)	16,724
Minimum length (bp)	200
Average length (bp)	1,431

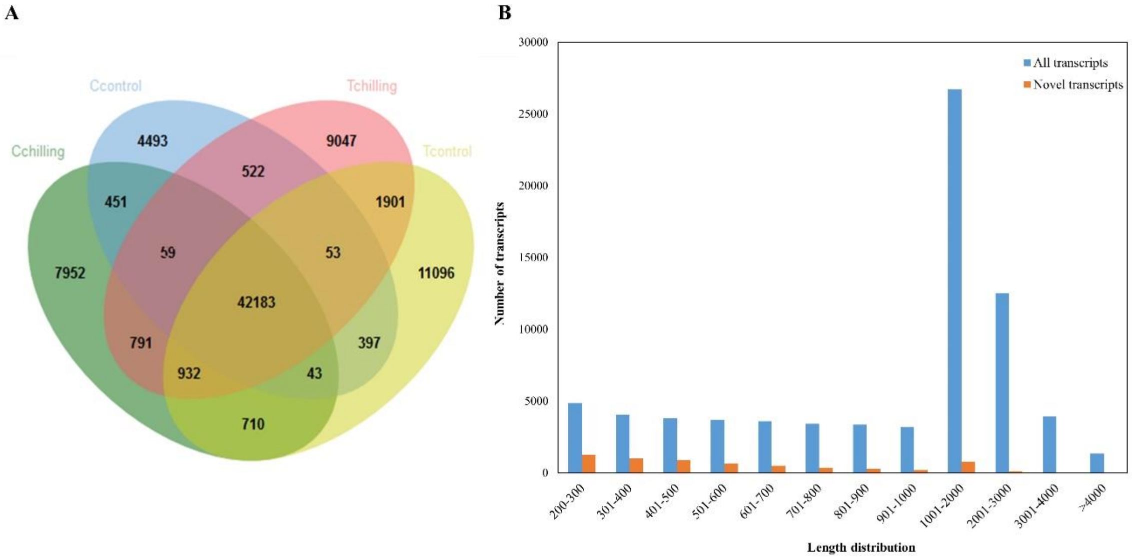


Figure 4.2: Statistics of transcripts detected by NGS from four samples**. a.** Venn diagram of transcripts detected in the four samples. **b.** Length distributions of all and novel transcripts detected in RNA-Seq.

4.3.2. Annotation and classification of *Corylus avellana* transcripts

The putative functions of *Corylus avellana* transcripts were identified by several complementary methods. The assembled transcripts were searched against the Viridiplantae proteins, UniProtKB/Swiss-Prot, and String databases using the BLAST+ software, with a cutoff E-value≤10−5. In addition, GO and KEGG analysis were performed through web server. In total, 54,221 (72.8%) transcripts were annotated against the SwissProt/UniProt database, and among the 50,005 proteins predicted with Transdecoder, 45,121 (90.2%) were annotated. Moreover, 66,944 (89.9%) transcripts were annotated to known proteins in Viridiplantae database, 50,005 (67.2%) to the Pfam database, 15,380 (20.7%) to the KEGG database, 67,087 (90.1%) to the String database, and 67,188 (90.2%) to the GO database (Figure 4.3a). According to analysis of taxonomic composition, most of the transcripts had a closest homolog that belonged to the Fagales, followed by the Rosales (Figure 4.3b). By searching the Viridiplantae database, the matches with the largest number of transcripts were found to be leucine-rich repeat transmembrane protein kinases, heat shock proteins, and NAM (no apical meristem), ATAF (Arabidopsis transcription activation factor), and CUC (cup-shaped cotyledon) (NAC) domain-containing proteins. Moreover, each transcript was classified by GO analysis. In total, 67,188 transcripts were successfully annotated with 8,395 GO terms, which were classified into three groups: biological processes, cellular components, and molecular functions (Appendix D: Table S4.1). Of the biological processes, the three largest categories were cellular process, metabolic process, and response to stimulus. The dominant cellular components were organelle, nucleus, and plastid. For molecular functions, the dominant terms were binding and catalytic activity (Figure 4.3c). The three largest groups of KEGG analysis annotations were glutathione S-transferase (GST), transcription factor MYB (MYBP), and HSP20 family protein (HSP20), as shown in Figure 4.3d.

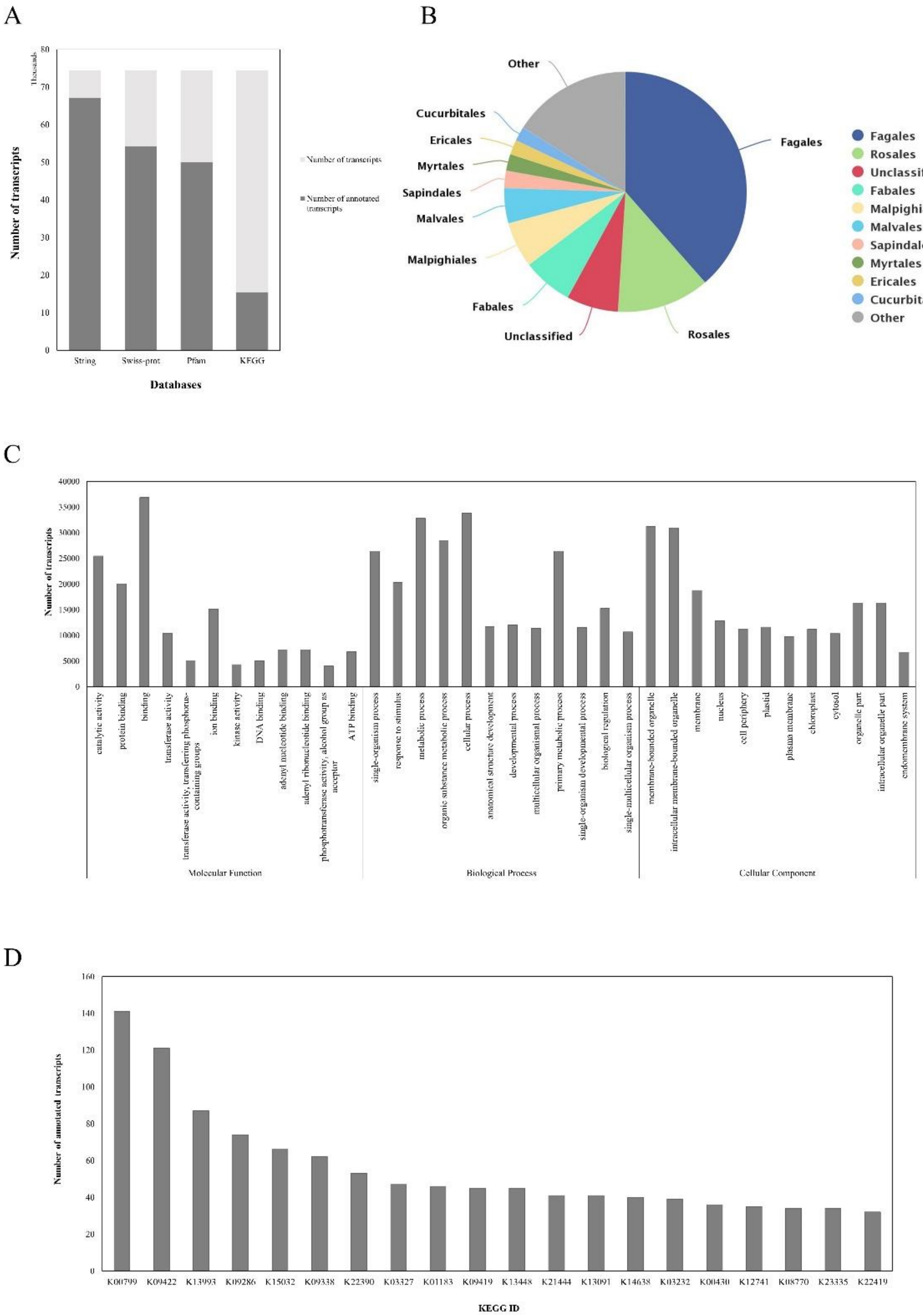


Figure 4.3: Classification of *Corylus avellana* transcripts. **a.** Number of annotated transcripts or putative proteins mapping to public databases, including String, SwissProt, pfam and KEGG. **b.** Distribution of annotated species according to order composition. The proportions of each species was showed with different colors that represent different species. **c.** Gene Ontology classification of transcripts that were annotated in three categories: molecular functions, biological processes and cellular components. **d.** Top 20 KEGG annotations.

4.3.3. Analysis and identification of differentially expressed transcripts under chilling stress

The expression abundance of the transcripts were calculated utilizing the FPKM approach and a total of 2,440 DETs were generated using Ballgown software. Of these, 1,368 were upregulated and 1,072 were downregulated under chilling stress (Appendix D: Table S4.2, 4.3). In addition to Ballgown analysis, the transcripts with p-value < 0.05 were analyzed by DESeq2 to identify DETs between cultivars. There were 4,888 and 5,886 DETs in the Chilling/Control Cakildak and Chilling/Control Tombul, respectively. In the Chilling/Control Cakildak group, 2,305 transcripts were upregulated, and 2,583 transcripts were downregulated (Figure 4.4a, Appendix D: Table S4.4, S4.5). In the Chilling/Control Tombul group, 2,859 transcripts were upregulated, and 3,027 transcripts were downregulated (Figure 4.4b, Appendix D: Table S4.6, S4.7). Moreover, 299 transcripts were differentially expressed between chilling Cakildak and Tombul (Figure 4.4c, Appendix D: Table S4.8). There were 1,468 DETs in the Control Cakildak vs Tombul (Figure 4.4d, Appendix D: Table S4.9). The numbers of up and down regulated transcripts in different ranges can be found in Figure 4.4e. Notably, 104 and 198 transcripts were upregulated very significantly (log2FC>10) in chilling samples cv Cakildak and cv Tombul in comparison with control samples, respectively.

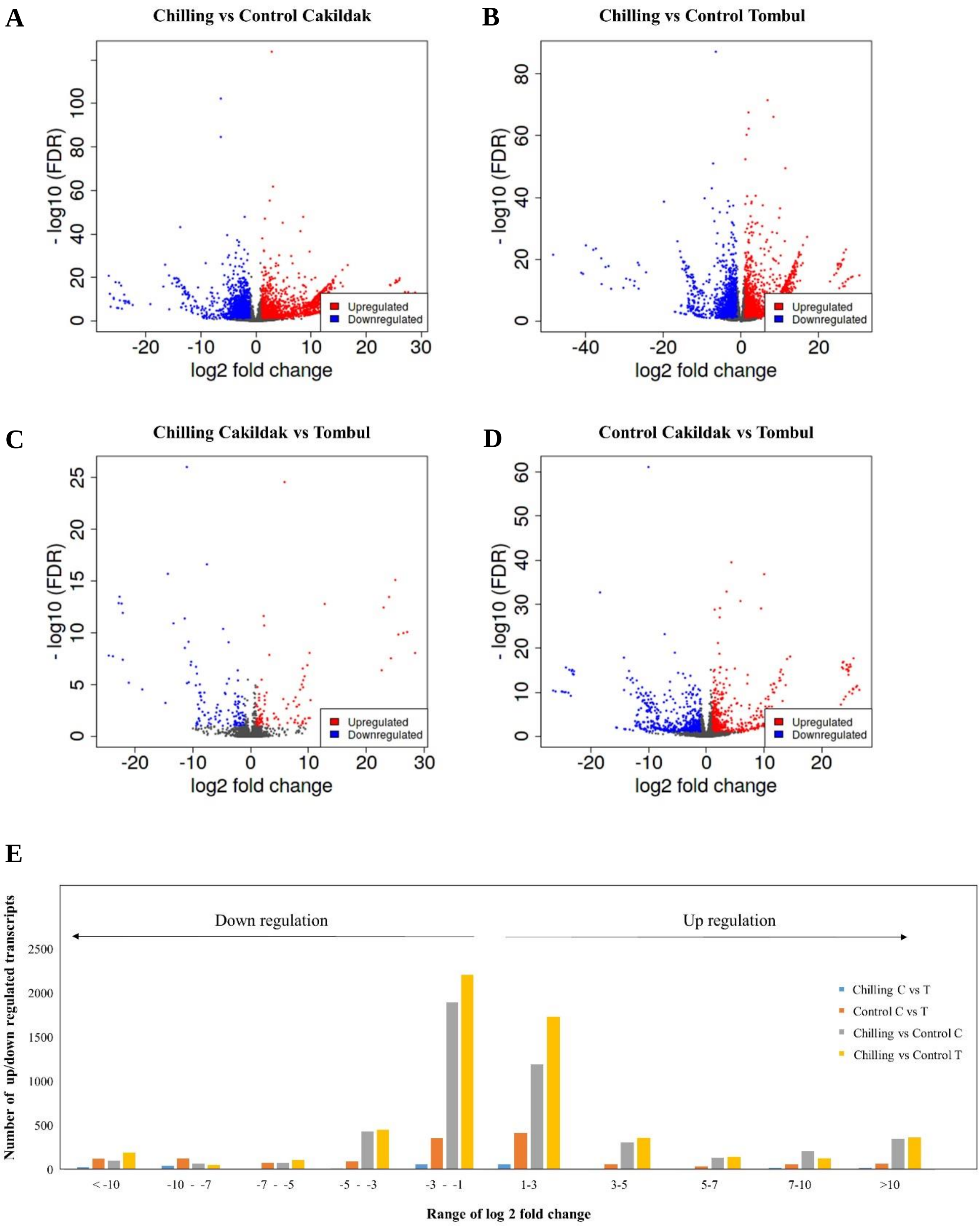


Figure 4.4: Different expression profile of transcriptome. A-D) Volcano plots of differentially expressed transcripts between **a.** chilling and control of cv Cakildak **b.** chilling and control of cv Tombul **c.** chilling cv Cakildak and Tombul **d.** control cv Cakildak and Tombul **e.** Number of up- and down-regulated transcripts among groups.

Hierarchical clustering was conducted to identify expression pattern of the transcripts in both chilling treated and control samples of cv Cakildak and cv Tombul. The transcripts were vertically clustered into 2 groups as up regulation and down regulation in each sample. A slight difference was observed in the control group of cv Cakildak (Figure 4.5).

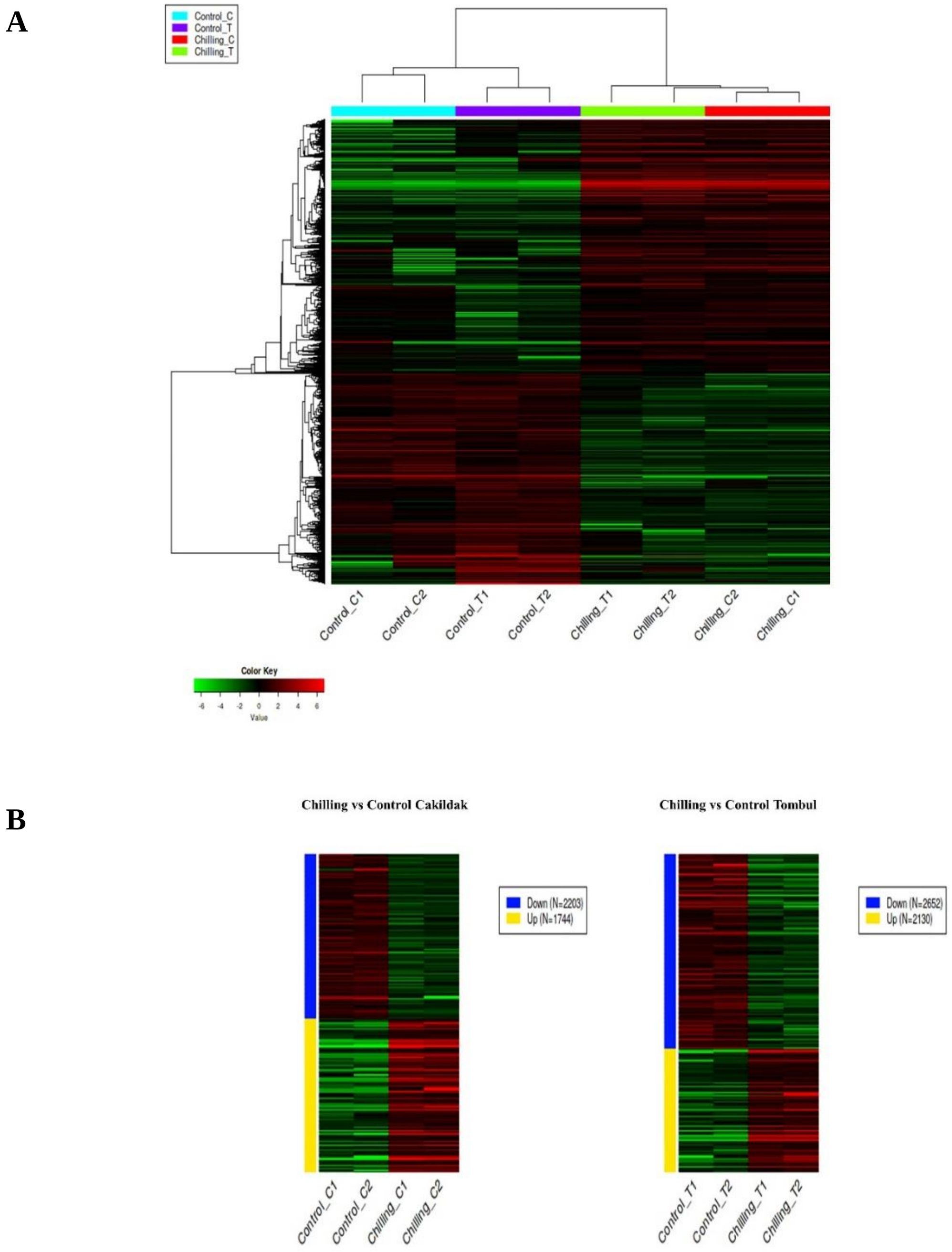


Figure 4.5: Hierarchical clustering map of differentially transcripts between chilling treated and control group of *Corylus avellana*. **a.** The heatmap of transcripts for all samples. **b.** The separate heatmaps of cv Cakildak and cv Tombul.

4.3.4. Transcription factor analysis and plant hormone-related DETs between control and chilling-treated samples

The Arabidopsis hormone database from RIKEN Plant Hormone Research Network was used to predict plant hormone DETs. There were 212 DETs predicted to be involved in plant hormone responses, including abscisic acid (ABA), auxin, brassinosteroid (BR), cytokinin (CK), ethylene, gibberellin (GA), jasmonic acid (JA), salicylic acid (SA) and strigolactones (SL) (Table 4.5). ABA is one of the major plant hormone involved in plant responses to abiotic stresses. ABA 8'-hydroxylase (ABA8ox) genes are involved in the deactivation of ABA, and 30 ABA8ox homolog transcripts were downregulated in chilling-treated samples.

Table 4.5: Number of differentially expressed transcripts involved in plant hormones

Hormone	**DETs Chilling vs Control**	
	Up regulated	**Down regulated**
ABA	30	53
Auxin	26	30
BR	50	51
CK	48	55
Ethylene	8	17
GA	29	50
JA	5	24
SA	36	27
SL	16	26

* p-value<0.05

Based on the plant transcription factor database (PlantTFDB), 69 domains of trancription factor were predicted with BLAST+, and were related with 740 transcripts. Top 20 TF domains were shown in Figure 4.6. The largest third TF families were zinc finger CCCH-type (zf-CCCH), plant homeodomain zinc finger (PHD) and myeloblastosis (MYB)-related transcription factors.

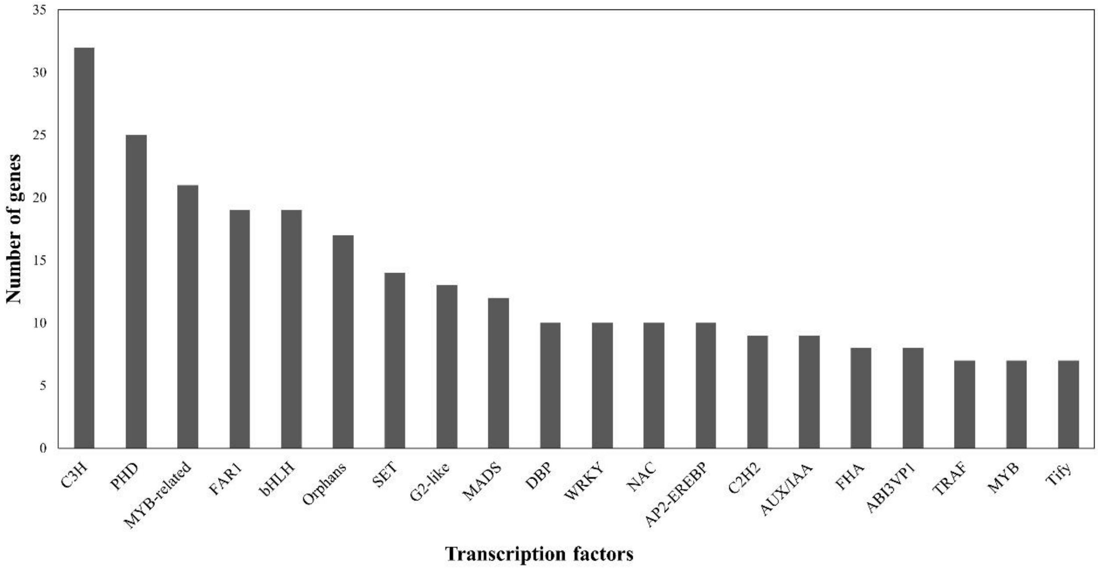


Figure 4.6: Top 20 transcription factor families of *Corylus avellana*.

4.3.5. qRT-PCR validation of RNA-Seq-based DETs under chilling stress

Differentially expressed transcripts under chilling stress identified by RNA-Seq were confirmed by quantitative real-time PCR (qRT-PCR). A total of 6 DETs were randomly selected as candidates to assess the validity of the key RNA-Seq results, and those DETs showed significant up- or downregulation in response to low-temperature stresses. Their expression levels were analyzed in chilling treated and control samples. For internal control, housekeeping primers were designed from transcripts that were mapping to HMG-CoA genes of *Corylus avellana* (Lucas et al., 2020). The expression patterns of some of these transcripts using qRT-PCR were correlated with the results obtained with RNA-seq analysis (Figure 4.7). One of them was chilling induced, and three of the selected transcripts were chilling repressed. The expression patterns of two of the transcripts were different among cultivars.

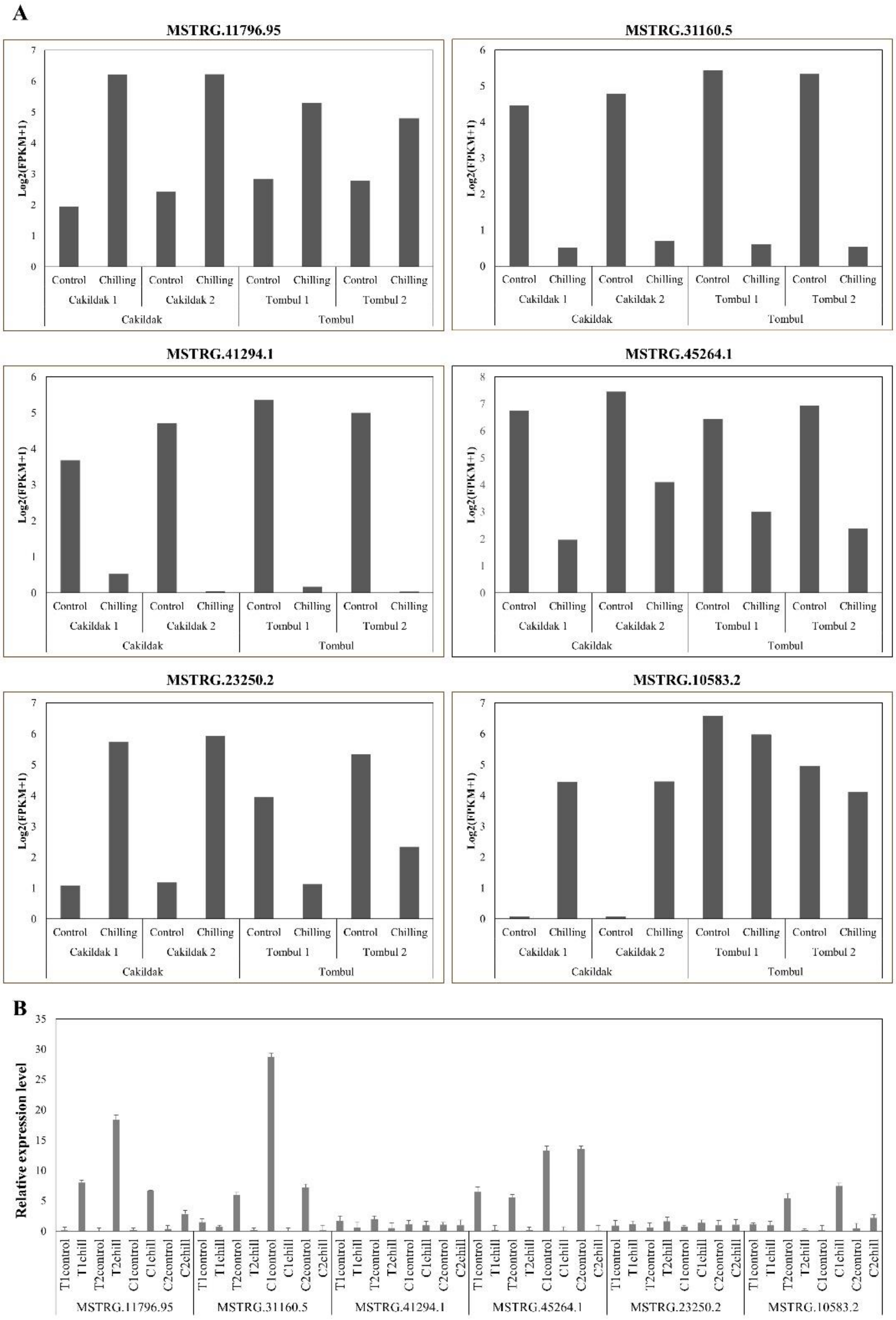


Figure 4.7: Expression profiles of validation genes in normal- and chilling-treated *Corylus avellana* cv Tombul buds by qRT-PCR analysis. Relative levels of gene expression were calculated using HMG-CoA. The X-axis indicates the eight samples. The Y-axis shows the expression levels: **a.** FPKM; **b.** qRT-PCR. All PCR reactions were performed with three technical replicates. Error bars represent the standard deviation of the mean.

4.4. DISCUSSION & CONCLUSIONS

4.4.1. Discussion

Chilling stress is one of the inevitable environmental challenges that have impact on plant growth, development and productivity (Kim et al., 2011). European hazelnut has been commercially cultivated in temperate maritime climate regions, and the accumulation of chilling hours is required to initiate the breaking of dormancy of vegetative buds, and then to trigger pollen shed and female anthesis (Mehlenbacher et al., 1991). Tiyayon (2008) indicated that post-chill warmth was required for catkin elongation, and the optimum temperature was 15 °C. Although hazelnut required chilling to commence flower development with breaking of the period of endodormancy, chilling should be followed by warmth to initiate development (Mehlenbacher et al., 1991). With alteration of temperature periods, it is thought that changing climatic conditions could cause negative impacts on crop yield. Farmers have reported the adverse influence of chilling stress after flower development has started on hazelnut production. In this study, transcriptome profiling was used in order to understand the chilling stress defense mechanisms in *Corylus avellana*, and there was no previous research on expression patterns of transcripts under low temperature conditions in this species. To further explore chilling response mechanisms in *C. avellana*, numerous chilling-related transcripts were identified and their expression patterns were investigated. Eight transcriptome libraries were constructed and sequenced for two hazelnut cultivars, Tombul and Cakildak. Tombul was selected as the most important Turkish hazelnut variety, and Cakildak was another important cultivar used extensively in hazelnut cultivation. It was reported that Cakildak begins flowering later than Tombul, and is much more resistant to environmental stresses (Islam, 2018). The transcriptome sequences were assembled into 74,489 transcripts, of which 90.2% were annotated. These annotations give will insight into the processes and pathways of *Corylus avellana* buds under both normal and chilling conditions.

Branches from trees with no leaves were cut in 3-4 cm, and placed in the falcon tubes containing water. The experiment was carried out in the dark conditions. Charrier et al. (2011) also applied similar chilling treatment to walnut trees examine the budburst dates, and dormancy. Although the stress we applied was not exactly same from chilling in the field, we suggested that any additional stress caused by cutting the twigs should be the same across all groups and so not affect the DETs. Due to the metabolism should be slow and minimal photosynthesis takes place in buds, the results will mainly be due to chilling stress, and a significant difference in order to gene expression would not be observed because of placing the cuttings in the dark.

More RNA-seq reads were observed in all of the chilling samples compared to controls, and this could show some genes involved in stress pathways were turned on under low temperature conditions, and shut off in control samples. It was also known that the RNA quality has widespread effects in the read number, and possibly on measurements of gene expression levels. In the study, the RNA quality was similar in all samples, and RNA-Seq expression was measured using FPKM that stands for ' Fragments per Kilobase of transcript per Million mapped reads’, and is a normalised estimation of gene expression based on RNA-seq data. This allowed to reliably compare experiments with different raw counts; thereby it was not likely to affect the quantification results. A total of 2,440 DETs were identified in the comparison between the chilling treated and the control group by Ballgown analysis. In addition, gene ontology analysis showed that 3,996 transcripts were mainly involved in cold responses. Among these transcripts, 473 transcripts were differentially expressed under chilling conditions. QRT results validated the data from the RNA-Seq analysis, however it would be better to analyze with much more transcripts to demonstrate the reliability of the DETs identified from RNA-Seq results.

Description of the role of genes was provided by GO analysis. Based on GO analysis of DETs, several enriched GO terms in the biological processes, cellular component and molecular function ontologies were identified to give insight into the possible molecular mechanisms underlying the chilling stress response in *C. avellana*. In the study, many DETs were enriched in GO terms such as cellular process, metabolic process, response to stimulus, membrane and catalytic activity. A crucial interface for cell-cell interaction is represented by the plasma membrane, and damage to the plasma membrane was one of the first symptoms of chilling (Cooper, 2000; Hirt and Shinozaki, 2004). There were 318 DETs that were associated with the plasma membrane, and almost half of them were repressed under chilling stress. Further analysis of these transcripts could provide information about the loss of functionality of plasma membrane due to the damage of *C. avellana* under low temperature. In addition, 778 DETs were involved in response to stimulus. Most of these DETs were chilling-induced, and further analysis may insight into the response pathways of *C. avellana* under chilling stress.

The gene transcription processes were regulated by transcription factors, which have been reported as involved in plant resistance against several stresses, and described as important regulators in plant responses. TFs are molecular switches that connect signal transduction pathways and gene expression, and initiate the transcription of defence genes associated in immune system of plant to cope with the various stresses. There are several transcription factors involved in stress resistance systems, including zinc finger proteins (ZFPs), C-repeat binding factor/dehydration responsive element binding factor (CBF/DREB), myeloblastosis (MYB), Apetala 2/ethylene-responsive element binding protein (AP2/EREBP) and basic helix-loop-helix (bHLH) (Liu et al., 1998; Zhai et al., 2010; Du et al., 2012; Luo et al., 2012; Licausi et al., 2013). According to the results of this study, 270 differentially expressed genes that encoded TFs encompassing 58 families were detected and classified by using PlantTFDB. Whereas some members of a TF family were induced during chilling conditions, some members of same TF family were repressed. AP2-like proteins are one of the important TF families that regulate stress responses (Mizoi et al., 2012; Yang et al., 2019). A total of ten genes related to AP2/EREBP members were detected, eight of which were upregulated and two of which were downregulated under chilling stress. In previous studies, MYB proteins were also involved in chilling stress in Arabidopsis (Agarwal et al., 2006; Chen et al., 2006). Yang et al. (2019) indicated that three MYB members, one cold-induced and two cold-repressed, were detected in *Populus tomentosa* under cold stress. In this study, seven genes were observed in the MYB family. While two of them were upregulated during low-temperature stress, five genes were cold-repressed. Twenty-three genes were also found to encode MYB-related transcription factors. Feng et al. (2012) showed that the bHLH gene family, the second largest transcription factor familiy in plant genomes, was induced in response to cold stress, and could improve cold tolerance. Our transcriptome data also suggest that nine upregulated genes encoded bHLH TFs that may function under low temperature conditions. Multiple studies showed that NAC TF family members were involved in various molecular mechanisms during temperature fluctuations (Puranik et al., 2012; Javed et al., 2020). Seven genes related with NAC transcription factor were induced by chilling conditions. This study could enhance the knowledge about mechanism of TFs involved in *Corylus avellana* under chilling conditions, and so provide to understand adaptation mechanism to low temperature stress at the molecular level.

Several plant hormones have been demonstrated to modulate response to stresses and adaptation to an altered environment by inducing stress responsive genes (Belkhadir and Chory, 2006). Action mechanisms of plant hormones could provide enhancement of plant tolerance against abiotic stresses. A large number of DETs were identified in the plant hormone signal transduction pathways, including BR, CK, ABA and GA etc. Bajguz and Hayat (2009) showed that BRs can play role in resistance of plants to several stresses. In the study, 50 BR related DETs were chilling induced. GA is another important phytohormone during life cycle of plants. Yamauchi et al. (2004) showed low temperature caused to activate GA biosynthesis during seed inhibition of *Arabidopsis thaliana*. GA deactivation was triggered by GA-2 oxidase, an enzyme involved in GA synthesis (Thomas et al., 1999). In this study, seven transcripts encoding GA-2 oxidase were upregulated, whereas the expression level of 15 DETs were dowregulated during chilling conditions. Furthermore, ABA is one of the vital hormones regulating cold resistance in several plants (Janowiak et al., 2003; Hou et al., 2010). While the expression level of 30 transcripts encoding ABA 8'-hydroxylase (ABA8ox) were downregulated, 8 transcripts were induced by chilling stress. Three transcripts involved in the conversion of xanthoxin to ABA were also upregulated under stress conditions.

4.4.2. Conclusions

This study provided a first comprehensive analysis via transcriptome sequencing between two *Corylus avellana* cultivars, Cakildak and Tombul, under low temperatures. A number of DETs related to chilling stress were identified using the Illumina sequencing, and the expression patterns of 6 randomly selected DETs were further validated by qRT-PCR. These DETs are involved in multiple biological functions, including cellular response to oxygen-containing compounds, abscisic acid metabolic process, amino acid homeostasis, response to stimulus, gibberellin and chitin. This study has provided comprehensive insight into the gene expression profiles in buds from two different *Corylus avellana* cultivars with contrasting responses to chilling stress. Further research will focus on the functional characterization of these important candidate DETs discovered in this study under low-temperature stress conditions, and may facilitate further study on chilling tolerance mechanisms that could be useful for guiding breeding approaches in tree species.

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APPENDIX A

Table S1.1 Selected samples and plate design for Sanger sequencing

	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**
A	G2 NL1-TW14	G5 NL1-TW14	G6 NL1-TW14	G7 NL1-TW14	G8 NL1-TW14	G9 NL1-TW14	G12 NL1-TW14	G13 NL1-TW14	G14 NL1-TW14	G16 NL1-TW14	G17 NL1-TW14	G18 NL1-TW14
B	G19 NL1-TW14	G21 NL1-TW14	G24 NL1-TW14	G25 NL1-TW14	G26 NL1-TW14	G28 NL1-TW14	O5 NL1-TW14	O6 NL1-TW14	O12 NL1-TW14	O16 NL1-TW14	O17 NL1-TW14	T5 NL1-TW14
C	T6 NL1-TW14	T7 NL1-TW14	T9 NL1-TW14	T10 NL1-TW14	T12 NL1-TW14							
D												
E	G1 PMITS1-PMITS2	G2 PMITS1-PMITS2	G3 PMITS1-PMITS2	G5 PMITS1-PMITS2	G7 PMITS1-PMITS2	G9 PMITS1-PMITS2	G13 PMITS1-PMITS2	G19 PMITS1-PMITS2	G20 PMITS1-PMITS2	G21 PMITS1-PMITS2	G24 PMITS1-PMITS2	G25 PMITS1-PMITS2
F	G28 PMITS1-PMITS2	O3 PMITS1-PMITS2	O5 PMITS1-PMITS2	O7 PMITS1-PMITS2	O16 PMITS1-PMITS2	O17 PMITS1-PMITS2	T1 PMITS1-PMITS2	T3 PMITS1-PMITS2	T5 PMITS1-PMITS2	T6 PMITS1-PMITS2	T7 PMITS1-PMITS2	T10 PMITS1-PMITS2
G	T11 PMITS1-PMITS2	T12 PMITS1-PMITS2	T14 PMITS1-PMITS2	T17 PMITS1-PMITS2	T20 PMITS1-PMITS2							
H												

*G: Giresun samples; O: Ordu samples; T: Trabzon samples

Table S1.2 Selected samples and plate design for Sanger sequencing

	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**
A	O6 NL1-TW14	O8 NL1-TW14	O9 NL1-TW14	O10 NL1-TW14	O11 NL1-TW14	O12 NL1-TW14	O13 NL1-TW14	O14 NL1-TW14	O19 NL1-TW14	O44 NL1-TW14	O45 NL1-TW14	O46 NL1-TW14
B	O47 NL1-TW14	O48 NL1-TW14	O49 NL1-TW14	O50 NL1-TW14	O51 NL1-TW14	O52 NL1-TW14	O53 NL1-TW14	O54 NL1-TW14	O55 NL1-TW14	O56 NL1-TW14	O57 NL1-TW14	O58 NL1-TW14
C	O60 NL1-TW14	O63 NL1-TW14	O65 NL1-TW14	O78 NL1-TW14	O81 NL1-TW14							
D												
E												
F												
G												
H												

* O: Ordu samples

Table S1.3 Selected samples and plate design for Sanger sequencing

	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**
A	G1 NL1-TW14	G2 NL1-TW14	G3 NL1-TW14	G4 NL1-TW14	G5 NL1-TW14	G7 NL1-TW14	G8 NL1-TW14	G9 NL1-TW14	G10 NL1-TW14	G11 NL1-TW14	G12 NL1-TW14	G13 NL1-TW14
B	G14 NL1-TW14	G15 NL1-TW14	G16 NL1-TW14	G17 NL1-TW14	G18 NL1-TW14	G19 NL1-TW14	G20 NL1-TW14	G21 NL1-TW14	G22 NL1-TW14	G24 NL1-TW14	G25 NL1-TW14	G26 NL1-TW14
C	G27 NL1-TW14	G28 NL1-TW14	G29 NL1-TW14	G30 NL1-TW14	G34 NL1-TW14	G36 NL1-TW14	G38 NL1-TW14	G39 NL1-TW14	G42 NL1-TW14	G43 NL1-TW14	G44 NL1-TW14	G45 NL1-TW14
D	G46 NL1-TW14	G47 NL1-TW14	G48 NL1-TW14	G49 NL1-TW14	G51 NL1-TW14	G52 NL1-TW14	G53 NL1-TW14	G54 NL1-TW14	G55 NL1-TW14	G56 NL1-TW14	G57 NL1-TW14	G58 NL1-TW14
E	G59 NL1-TW14	G60 NL1-TW14	G61 NL1-TW14	G62 NL1-TW14	G63 NL1-TW14	G64 NL1-TW14	G70 NL1-TW14	G71 NL1-TW14	G72 NL1-TW14	G73 NL1-TW14	G75 NL1-TW14	G76 NL1-TW14
F	G77 NL1-TW14	G79 NL1-TW14	G81 NL1-TW14									
G	T4 NL1-TW14	T8 NL1-TW14	T9 NL1-TW14	T10 NL1-TW14	T11 NL1-TW14	T12 NL1-TW14	T13 NL1-TW14	T14 NL1-TW14	T16 NL1-TW14	T17 NL1-TW14	T18 NL1-TW14	T19 NL1-TW14
H	T26 NL1-TW14	T27 NL1-TW14	T30 NL1-TW14	T34 NL1-TW14	T35 NL1-TW14	T37 NL1-TW14						

*G: Giresun samples; T: Trabzon samples

APPENDIX B

Table S2.1: Identity and locations of predicted tRNA genes in *C. avellana* genome

tRNA ID	Chromosome	Start	End	Type	Anti-codon	Intron start	Intron end	Score	Notes
Cav_tRNA_pchr01-1	pchr01	3391931	3392016	Met	CAT	3391969	3391980	64.2	
Cav_tRNA_pchr01-2	pchr01	4793996	4794080	Met	CAT	4794034	4794044	64.3	
Cav_tRNA_pchr01-3	pchr01	4821116	4821200	Met	CAT	4821154	4821164	64.3	
Cav_tRNA_pchr01-4	pchr01	5963344	5963415	Trp	CCA	0	0	75.8	
Cav_tRNA_pchr01-5	pchr01	8840675	8840747	Ala	TGC	0	0	65.5	
Cav_tRNA_pchr01-6	pchr01	9736225	9736295	Gly	GCC	0	0	66.5	
Cav_tRNA_pchr01-7	pchr01	9746967	9747037	Gly	GCC	0	0	66.5	
Cav_tRNA_pchr01-8	pchr01	11005140	11005215	Undet	NNN	0	0	31.6	
Cav_tRNA_pchr01-9	pchr01	11583856	11583927	Pro	AGG	0	0	67.4	
Cav_tRNA_pchr01-10	pchr01	11739601	11739672	Asn	GTT	0	0	37.2	pseudo
Cav_tRNA_pchr01-11	pchr01	13900927	13900997	Gly	CCC	0	0	65.4	
Cav_tRNA_pchr01-12	pchr01	26685886	26685956	Arg	TCG	0	0	20.7	pseudo
Cav_tRNA_pchr01-13	pchr01	26765631	26765704	Arg	TCG	0	0	81.9	
Cav_tRNA_pchr01-14	pchr01	28131738	28131811	Ile	AAT	0	0	81.8	
Cav_tRNA_pchr01-15	pchr01	28156495	28156568	Ile	AAT	0	0	81.8	
Cav_tRNA_pchr01-16	pchr01	34033105	34033177	Glu	CTC	0	0	78.9	
Cav_tRNA_pchr01-17	pchr01	35199032	35199100	Gln	CTG	0	0	37.2	pseudo
Cav_tRNA_pchr01-18	pchr01	35675244	35675315	Asp	GTC	0	0	69.8	
Cav_tRNA_pchr01-19	pchr01	38527992	38528074	Leu	TAA	0	0	68.4	
Cav_tRNA_pchr01-20	pchr01	38686521	38686593	Arg	TCT	0	0	68.1	

Cav_tRNA_pchr01-21	pchr01	39157027	39157099	Arg	CCT	0	0	69.1	
Cav_tRNA_pchr01-22	pchr01	44577060	44577132	Arg	ACG	0	0	72.9	
Cav_tRNA_pchr01-23	pchr01	46494718	46494799	Ser	GCT	0	0	80.5	
Cav_tRNA_pchr01-24	pchr01	50061997	50061925	Lys	TTT	0	0	88.7	
Cav_tRNA_pchr01-25	pchr01	46632165	46632094	Asn	GTT	0	0	42.8	pseudo
Cav_tRNA_pchr01-26	pchr01	45769107	45769035	Arg	TCT	0	0	70.3	
Cav_tRNA_pchr01-27	pchr01	45465289	45465218	Gly	TCC	0	0	71	
Cav_tRNA_pchr01-28	pchr01	43008042	43007969	Val	CAC	0	0	81.5	
Cav_tRNA_pchr01-29	pchr01	42435249	42435178	Trp	CCA	0	0	75.8	
Cav_tRNA_pchr01-30	pchr01	39264948	39264876	Gln	TTG	0	0	55.9	
Cav_tRNA_pchr01-31	pchr01	35485130	35485053	Ile	AAT	0	0	20	pseudo
Cav_tRNA_pchr01-32	pchr01	35261581	35261508	Ile	AAT	0	0	55.8	
Cav_tRNA_pchr01-33	pchr01	34700961	34700890	Glu	TTC	0	0	72	
Cav_tRNA_pchr01-34	pchr01	33238059	33237987	Glu	CTC	0	0	78.9	
Cav_tRNA_pchr01-35	pchr01	33140501	33140429	Glu	CTC	0	0	78.9	
Cav_tRNA_pchr01-36	pchr01	32898832	32898749	Leu	CAA	0	0	81	
Cav_tRNA_pchr01-37	pchr01	32127931	32127859	Glu	CTC	0	0	78.9	
Cav_tRNA_pchr01-38	pchr01	24732418	24732334	Met	CAT	24732380	24732370	64.2	
Cav_tRNA_pchr01-39	pchr01	24637011	24636927	Met	CAT	24636973	24636963	64.2	
Cav_tRNA_pchr01-40	pchr01	18728799	18728728	Thr	TGT	0	0	84.3	
Cav_tRNA_pchr01-41	pchr01	18665021	18664940	Ser	GCT	0	0	80.5	
Cav_tRNA_pchr01-42	pchr01	14893364	14893293	His	GTG	0	0	63	
Cav_tRNA_pchr01-43	pchr01	14870632	14870561	His	GTG	0	0	63	
Cav_tRNA_pchr01-44	pchr01	12279853	12279780	Thr	AGT	0	0	76	
Cav_tRNA_pchr01-45	pchr01	11605498	11605427	Pro	TGG	0	0	68.5	
Cav_tRNA_pchr01-46	pchr01	7483517	7483443	Leu	CAA	0	0	20	pseudo
Cav_tRNA_pchr01-47	pchr01	4820558	4820487	Gln	TTG	0	0	74	

Cav_tRNA_pchr01-48	pchr01	4793441	4793370	Gln	TTG	0	0	74	
Cav_tRNA_pchr01-49	pchr01	3099775	3099696	Leu	TAG	0	0	69.5	
Cav_tRNA_pchr01-50	pchr01	2872349	2872278	Trp	CCA	0	0	75.8	
Cav_tRNA_pchr01-51	pchr01	2849528	2849458	Gly	CCC	0	0	61.2	
Cav_tRNA_pchr01-52	pchr01	2696564	2696492	Ala	CGC	0	0	68.3	
Cav_tRNA_pchr01-53	pchr01	1049666	1049595	iMet	CAT	0	0	58.3	
Cav_tRNA_pchr01-54	pchr01	276270	276187	Leu	CAA	0	0	77.7	
Cav_tRNA_pchr02-1	pchr02	1581876	1581949	Ile	AAT	0	0	81.8	
Cav_tRNA_pchr02-2	pchr02	2092686	2092758	Glu	CTC	0	0	78.9	
Cav_tRNA_pchr02-3	pchr02	2175490	2175561	Pro	CGG	0	0	68.5	
Cav_tRNA_pchr02-4	pchr02	2647353	2647425	Ala	CGC	0	0	68.3	
Cav_tRNA_pchr02-5	pchr02	2677283	2677355	Arg	CCT	0	0	69.1	
Cav_tRNA_pchr02-6	pchr02	3183532	3183605	Asn	GTT	0	0	81.1	
Cav_tRNA_pchr02-7	pchr02	3791236	3791327	Tyr	GTA	3791273	3791291	74.2	
Cav_tRNA_pchr02-8	pchr02	3987484	3987557	Ile	TAT	0	0	85.9	
Cav_tRNA_pchr02-9	pchr02	4518346	4518418	Ala	AGC	0	0	63.4	
Cav_tRNA_pchr02-10	pchr02	4527686	4527757	Pro	CGG	0	0	69.6	
Cav_tRNA_pchr02-11	pchr02	5062561	5062632	Glu	TTC	0	0	72	
Cav_tRNA_pchr02-12	pchr02	5203012	5203082	Gly	CCC	0	0	65.4	
Cav_tRNA_pchr02-13	pchr02	5217885	5217956	Pro	TGG	0	0	68.5	
Cav_tRNA_pchr02-14	pchr02	6105535	6105616	Ser	TGA	0	0	80.7	
Cav_tRNA_pchr02-15	pchr02	12153728	12153800	Lys	TTT	0	0	88.7	
Cav_tRNA_pchr02-16	pchr02	13563221	13563293	Ala	TGC	0	0	69.1	
Cav_tRNA_pchr02-17	pchr02	13697726	13697797	Pro	AGG	0	0	67.4	
Cav_tRNA_pchr02-18	pchr02	14616327	14616398	Asp	GTC	0	0	69.8	
Cav_tRNA_pchr02-19	pchr02	14622897	14622968	Asp	GTC	0	0	69.8	
Cav_tRNA_pchr02-20	pchr02	15612597	15612668	Undet	NNN	0	0	24.9	pseudo

Cav_tRNA_pchr02-21	pchr02	16895844	16895916	Phe	GAA	0	0	78.3	
Cav_tRNA_pchr02-22	pchr02	16919991	16920063	Phe	GAA	0	0	78.3	
Cav_tRNA_pchr02-23	pchr02	17144306	17144378	Phe	GAA	0	0	78.3	
Cav_tRNA_pchr02-24	pchr02	25171848	25171922	His	ATG	0	0	28.6	
Cav_tRNA_pchr02-25	pchr02	25184939	25185013	His	ATG	0	0	28.6	
Cav_tRNA_pchr02-26	pchr02	25197687	25197761	His	GTG	0	0	40.9	
Cav_tRNA_pchr02-27	pchr02	25659152	25659224	Arg	ACG	0	0	71.3	
Cav_tRNA_pchr02-28	pchr02	25659308	25659391	Leu	CAA	0	0	78.6	
Cav_tRNA_pchr02-29	pchr02	29821953	29822023	Sup	TCA	0	0	43.3	
Cav_tRNA_pchr02-30	pchr02	32069506	32069580	Leu	CAA	0	0	28.1	
Cav_tRNA_pchr02-31	pchr02	35107498	35107570	Lys	CTT	0	0	50.8	
Cav_tRNA_pchr02-32	pchr02	37258907	37258982	Undet	NNN	0	0	33.9	pseudo
Cav_tRNA_pchr02-33	pchr02	37262381	37262456	Undet	NNN	0	0	22.1	pseudo
Cav_tRNA_pchr02-34	pchr02	37795204	37795277	Ile	AAT	0	0	81.8	
Cav_tRNA_pchr02-35	pchr02	37834105	37834178	Ile	AAT	0	0	81.8	
Cav_tRNA_pchr02-36	pchr02	39200613	39200683	Gly	GCC	0	0	66.5	
Cav_tRNA_pchr02-37	pchr02	39644230	39644302	Leu	CAA	0	0	30.3	pseudo
Cav_tRNA_pchr02-38	pchr02	45369292	45369365	Thr	AGT	0	0	73.6	
Cav_tRNA_pchr02-39	pchr02	47599049	47599122	Val	CAC	0	0	81.5	
Cav_tRNA_pchr02-40	pchr02	47680677	47680756	Leu	TAG	0	0	69.5	
Cav_tRNA_pchr02-41	pchr02	50399805	50399734	Thr	CGT	0	0	80.2	
Cav_tRNA_pchr02-42	pchr02	48375665	48375593	Phe	GAA	0	0	78.3	
Cav_tRNA_pchr02-43	pchr02	47958231	47958160	Trp	CCA	0	0	75.8	
Cav_tRNA_pchr02-44	pchr02	44203659	44203585	Pro	TGG	0	0	33.7	
Cav_tRNA_pchr02-45	pchr02	44203421	44203348	Trp	CCA	0	0	61.7	
Cav_tRNA_pchr02-46	pchr02	43267278	43267206	Val	TAC	0	0	71.5	
Cav_tRNA_pchr02-47	pchr02	43182887	43182815	Val	TAC	0	0	75.3	

Cav_tRNA_pchr02-48	pchr02	42502237	42502167	Gly	GCC	0	0	66.5
Cav_tRNA_pchr02-49	pchr02	42502154	42502082	Phe	GAA	0	0	78.3
Cav_tRNA_pchr02-50	pchr02	42500075	42500005	Gly	GCC	0	0	66.5
Cav_tRNA_pchr02-51	pchr02	42499993	42499921	Phe	GAA	0	0	78.3
Cav_tRNA_pchr02-52	pchr02	42478691	42478621	Gly	GCC	0	0	66.5
Cav_tRNA_pchr02-53	pchr02	42478608	42478536	Phe	GAA	0	0	78.3
Cav_tRNA_pchr02-54	pchr02	42476875	42476805	Gly	GCC	0	0	66.5
Cav_tRNA_pchr02-55	pchr02	42476793	42476721	Phe	GAA	0	0	78.3
Cav_tRNA_pchr02-56	pchr02	41436584	41436512	Ala	TGC	0	0	65.5
Cav_tRNA_pchr02-57	pchr02	40550891	40550819	Glu	CTC	0	0	78.9
Cav_tRNA_pchr02-58	pchr02	33592286	33592215	Asp	ATC	0	0	50.9
Cav_tRNA_pchr02-59	pchr02	30056607	30056537	Sup	TCA	0	0	66.1
Cav_tRNA_pchr02-60	pchr02	29875258	29875188	Sup	TCA	0	0	56.4
Cav_tRNA_pchr02-61	pchr02	29870569	29870499	Sup	TCA	0	0	56.4
Cav_tRNA_pchr02-62	pchr02	29863960	29863891	Sup	TCA	0	0	55.8
Cav_tRNA_pchr02-63	pchr02	29795506	29795436	Sup	TCA	0	0	66.1
Cav_tRNA_pchr02-64	pchr02	29791967	29791897	Sup	TCA	0	0	43.3
Cav_tRNA_pchr02-65	pchr02	27974904	27974832	Val	TAC	0	0	71.5
Cav_tRNA_pchr02-66	pchr02	26475794	26475715	Leu	TAG	0	0	69.5
Cav_tRNA_pchr02-67	pchr02	25204047	25203968	Leu	TAG	0	0	69.5
Cav_tRNA_pchr02-68	pchr02	25182757	25182683	His	GTG	0	0	40.9
Cav_tRNA_pchr02-69	pchr02	16179572	16179501	His	GTG	0	0	63
Cav_tRNA_pchr02-70	pchr02	14746097	14746027	Gly	CCC	0	0	66
Cav_tRNA_pchr02-71	pchr02	14256476	14256404	Arg	ACG	0	0	72.9
Cav_tRNA_pchr02-72	pchr02	14235430	14235358	Arg	ACG	0	0	72.9
Cav_tRNA_pchr02-73	pchr02	13698090	13698019	Pro	TGG	0	0	68.5
Cav_tRNA_pchr02-74	pchr02	11532202	11532131	Undet	NNN	0	0	24.3

Cav_tRNA_pchr02-75	pchr02	7081962	7081892	Cys	GCA	0	0	52.9	
Cav_tRNA_pchr02-76	pchr02	6063929	6063848	Ser	TGA	0	0	80.7	
Cav_tRNA_pchr02-77	pchr02	4628890	4628817	Thr	AGT	0	0	76	
Cav_tRNA_pchr02-78	pchr02	4152886	4152813	Ile	AAT	0	0	75.7	
Cav_tRNA_pchr02-79	pchr02	3975860	3975788	Phe	GAA	0	0	78.3	
Cav_tRNA_pchr02-80	pchr02	2405728	2405657	His	GTG	0	0	63	
Cav_tRNA_pchr02-81	pchr02	2175693	2175623	Gly	GCC	0	0	66.5	
Cav_tRNA_pchr03-1	pchr03	593503	593584	Leu	AAG	0	0	62.5	
Cav_tRNA_pchr03-2	pchr03	686137	686218	Ser	TGA	0	0	80.7	
Cav_tRNA_pchr03-3	pchr03	1012474	1012545	Gln	TTG	0	0	73.5	
Cav_tRNA_pchr03-4	pchr03	1909849	1909920	Glu	TTC	0	0	72	
Cav_tRNA_pchr03-5	pchr03	2505771	2505851	Leu	AAG	0	0	72.6	
Cav_tRNA_pchr03-6	pchr03	4572102	4572172	Sup	TCA	0	0	24.7	
Cav_tRNA_pchr03-7	pchr03	5546346	5546417	Thr	TGT	0	0	79.3	
Cav_tRNA_pchr03-8	pchr03	7010377	7010450	Asp	GTC	0	0	37.2	pseudo
Cav_tRNA_pchr03-9	pchr03	7234932	7235005	Ile	AAT	0	0	81.8	
Cav_tRNA_pchr03-10	pchr03	7250523	7250596	Ile	AAT	0	0	81.8	
Cav_tRNA_pchr03-11	pchr03	7641129	7641201	Arg	CCG	0	0	65.5	
Cav_tRNA_pchr03-12	pchr03	8368729	8368800	Gly	GCC	0	0	26.4	pseudo
Cav_tRNA_pchr03-13	pchr03	8383112	8383182	Gly	GCC	0	0	66.5	
Cav_tRNA_pchr03-14	pchr03	8653863	8653949	Ser	TGA	0	0	43.2	
Cav_tRNA_pchr03-15	pchr03	13199592	13199676	Met	CAT	13199630	13199640	64.3	
Cav_tRNA_pchr03-16	pchr03	14434953	14435024	iMet	CAT	0	0	58.3	
Cav_tRNA_pchr03-17	pchr03	14786578	14786670	Tyr	GTA	14786615	14786634	74.2	
Cav_tRNA_pchr03-18	pchr03	15011708	15011779	Trp	CCA	0	0	75.8	
Cav_tRNA_pchr03-19	pchr03	21203211	21203284	Asn	GTT	0	0	70.6	
Cav_tRNA_pchr03-20	pchr03	22241484	22241555	Asp	GTC	0	0	55.4	

Cav_tRNA_pchr03-21	pchr03	24380724	24380795	iMet	CAT	0	0	58.3	
Cav_tRNA_pchr03-22	pchr03	25013245	25013316	Gly	TCC	0	0	71	
Cav_tRNA_pchr03-23	pchr03	28353426	28353496	Gly	GCC	0	0	66.5	
Cav_tRNA_pchr03-24	pchr03	28354854	28354924	Gly	GCC	0	0	66.5	
Cav_tRNA_pchr03-25	pchr03	28711571	28711651	Leu	AAG	0	0	74	
Cav_tRNA_pchr03-26	pchr03	29365944	29366017	Val	AAC	0	0	72.6	
Cav_tRNA_pchr03-27	pchr03	29769851	29769923	Lys	CTT	0	0	87.7	
Cav_tRNA_pchr03-28	pchr03	30003593	30003664	Gln	CTG	0	0	74.3	
Cav_tRNA_pchr03-29	pchr03	30160799	30160871	Ala	CGC	0	0	68.3	
Cav_tRNA_pchr03-30	pchr03	30189321	30189393	Ala	CGC	0	0	68.3	
Cav_tRNA_pchr03-31	pchr03	30351141	30351212	Gln	CTG	0	0	74.3	
Cav_tRNA_pchr03-32	pchr03	31626385	31626457	Ala	TGC	0	0	65.5	
Cav_tRNA_pchr03-33	pchr03	34055046	34055128	Leu	TAG	0	0	26.9	pseudo
Cav_tRNA_pchr03-34	pchr03	36753519	36753589	Gly	CCC	0	0	66	
Cav_tRNA_pchr03-35	pchr03	37033654	37033727	Met	CAT	0	0	59.2	
Cav_tRNA_pchr03-36	pchr03	38868337	38868409	Phe	GAA	0	0	78.3	
Cav_tRNA_pchr03-37	pchr03	39136837	39136908	iMet	CAT	0	0	57.5	
Cav_tRNA_pchr03-38	pchr03	39593946	39593875	Trp	CCA	0	0	75.8	
Cav_tRNA_pchr03-39	pchr03	37349382	37349310	Phe	GAA	0	0	78.3	
Cav_tRNA_pchr03-40	pchr03	35612767	35612686	Ser	AGA	0	0	78.7	
Cav_tRNA_pchr03-41	pchr03	35384960	35384888	Phe	GAA	0	0	78.3	
Cav_tRNA_pchr03-42	pchr03	35260836	35260764	Phe	GAA	0	0	78.3	
Cav_tRNA_pchr03-43	pchr03	33362143	33362070	Ile	TAT	0	0	85.9	
Cav_tRNA_pchr03-44	pchr03	31816611	31816544	Met	CAT	0	0	30.1	pseudo
Cav_tRNA_pchr03-45	pchr03	30927998	30927925	Val	AAC	0	0	73.2	
Cav_tRNA_pchr03-46	pchr03	28322172	28322099	Val	AAC	0	0	69.9	
Cav_tRNA_pchr03-47	pchr03	26620255	26620184	Thr	TGT	0	0	84.3	

Cav_tRNA_pchr03-48	pchr03	25586991	25586919	Ala	AGC	0	0	63.4	
Cav_tRNA_pchr03-49	pchr03	25561374	25561302	Ala	AGC	0	0	63.4	
Cav_tRNA_pchr03-50	pchr03	25303622	25303539	Leu	CAA	0	0	77.7	
Cav_tRNA_pchr03-51	pchr03	25300165	25300082	Leu	CAA	0	0	77.7	
Cav_tRNA_pchr03-52	pchr03	22505797	22505726	Asp	GTC	0	0	60.7	
Cav_tRNA_pchr03-53	pchr03	14986617	14986546	Trp	CCA	0	0	75.8	
Cav_tRNA_pchr03-54	pchr03	14827036	14826964	Glu	CTC	0	0	78.9	
Cav_tRNA_pchr03-55	pchr03	14754942	14754850	Tyr	GTA	14754905	14754886	74.2	
Cav_tRNA_pchr03-56	pchr03	13717163	13717092	Cys	GCA	0	0	82.1	
Cav_tRNA_pchr03-57	pchr03	12661398	12661319	Leu	TAG	0	0	50.7	
Cav_tRNA_pchr03-58	pchr03	8987449	8987359	Tyr	GTA	8987412	8987395	74.3	
Cav_tRNA_pchr03-59	pchr03	6853814	6853743	Asp	GTC	0	0	69.8	
Cav_tRNA_pchr03-60	pchr03	6619201	6619130	Thr	CGT	0	0	77.8	
Cav_tRNA_pchr03-61	pchr03	2885608	2885536	Ala	AGC	0	0	63.4	
Cav_tRNA_pchr03-62	pchr03	2871594	2871522	Ala	AGC	0	0	63.4	
Cav_tRNA_pchr03-63	pchr03	2492125	2492045	Leu	CAG	0	0	69.5	
Cav_tRNA_pchr04-1	pchr04	1621668	1621740	Arg	CCT	0	0	72.2	
Cav_tRNA_pchr04-2	pchr04	2619150	2619222	Lys	CTT	0	0	87.7	
Cav_tRNA_pchr04-3	pchr04	3303969	3304042	Asn	GTT	0	0	81.1	
Cav_tRNA_pchr04-4	pchr04	15949465	15949536	Asn	GTT	0	0	23.6	pseudo
Cav_tRNA_pchr04-5	pchr04	17196916	17196987	Asp	ATC	0	0	49.6	
Cav_tRNA_pchr04-6	pchr04	20175107	20175188	Ser	AGA	0	0	80.6	
Cav_tRNA_pchr04-7	pchr04	20189748	20189829	Ser	AGA	0	0	80.6	
Cav_tRNA_pchr04-8	pchr04	22297822	22297895	Ile	AAT	0	0	81.8	
Cav_tRNA_pchr04-9	pchr04	26952656	26952737	Ser	AGA	0	0	78.4	
Cav_tRNA_pchr04-10	pchr04	27024063	27024135	Lys	CTT	0	0	87.7	
Cav_tRNA_pchr04-11	pchr04	28245708	28245789	Tyr	ATA	0	0	61.2	

Cav_tRNA_pchr04-12	pchr04	28455042	28455108	Undet	NNN	0	0	29.1	
Cav_tRNA_pchr04-13	pchr04	28806330	28806411	Ser	AGA	0	0	77.2	
Cav_tRNA_pchr04-14	pchr04	29444622	29444694	Lys	CTT	0	0	87.7	
Cav_tRNA_pchr04-15	pchr04	30254499	30254570	Pro	AGG	0	0	67.4	
Cav_tRNA_pchr04-16	pchr04	30711014	30711085	His	GTG	0	0	63.3	
Cav_tRNA_pchr04-17	pchr04	31193536	31193607	Asp	GTC	0	0	69.8	
Cav_tRNA_pchr04-18	pchr04	31359062	31359133	Thr	CGT	0	0	76.1	
Cav_tRNA_pchr04-19	pchr04	31424995	31425068	Asn	GTT	0	0	80	
Cav_tRNA_pchr04-20	pchr04	31425137	31425210	Asn	GTT	0	0	84.5	
Cav_tRNA_pchr04-21	pchr04	31425288	31425361	Asn	GTT	0	0	80	
Cav_tRNA_pchr04-22	pchr04	31486587	31486659	Ala	TGC	0	0	69.1	
Cav_tRNA_pchr04-23	pchr04	31623551	31623624	Thr	AGT	0	0	75	
Cav_tRNA_pchr04-24	pchr04	31629399	31629472	Thr	AGT	0	0	75	
Cav_tRNA_pchr04-25	pchr04	33304902	33304974	Arg	ACG	0	0	72.9	
Cav_tRNA_pchr04-26	pchr04	33361456	33361529	Val	AAC	0	0	73.2	
Cav_tRNA_pchr04-27	pchr04	33527722	33527801	Lys	TTT	0	0	27.3	pseudo
Cav_tRNA_pchr04-28	pchr04	35422145	35422216	iMet	CAT	0	0	56.4	
Cav_tRNA_pchr04-29	pchr04	35439416	35439498	Leu	TAA	0	0	68.4	
Cav_tRNA_pchr04-30	pchr04	35723438	35723518	Leu	AAG	0	0	72.6	
Cav_tRNA_pchr04-31	pchr04	35846149	35846230	Ser	TGA	0	0	80.7	
Cav_tRNA_pchr04-32	pchr04	36176944	36177015	Gln	TTG	0	0	73.5	
Cav_tRNA_pchr04-33	pchr04	36340551	36340623	Lys	CTT	0	0	87.7	
Cav_tRNA_pchr04-34	pchr04	36591247	36591327	Leu	AAG	0	0	74	
Cav_tRNA_pchr04-35	pchr04	35424495	35424423	Lys	CTT	0	0	87.7	
Cav_tRNA_pchr04-36	pchr04	34967544	34967473	Cys	GCA	0	0	82.1	
Cav_tRNA_pchr04-37	pchr04	33349519	33349446	Asn	GTT	0	0	82.7	
Cav_tRNA_pchr04-38	pchr04	32030440	32030367	Lys	CTT	0	0	25.6	pseudo

Cav_tRNA_pchr04-39	pchr04	31744367	31744296	Trp	CCA	0	0	75.8	
Cav_tRNA_pchr04-40	pchr04	30292589	30292518	Thr	TGT	0	0	79.3	
Cav_tRNA_pchr04-41	pchr04	28520478	28520385	Tyr	GTA	28520441	28520421	74.2	
Cav_tRNA_pchr04-42	pchr04	26949779	26949706	Lys	CTT	0	0	23.6	
Cav_tRNA_pchr04-43	pchr04	25836947	25836866	Ser	AGA	0	0	77.7	
Cav_tRNA_pchr04-44	pchr04	25156404	25156331	Asn	GTT	0	0	80	
Cav_tRNA_pchr04-45	pchr04	20098245	20098173	Asp	GTC	0	0	42.6	pseudo
Cav_tRNA_pchr04-46	pchr04	13187297	13187224	Asn	GTT	0	0	81.1	
Cav_tRNA_pchr04-47	pchr04	9332152	9332069	Leu	CAA	0	0	78.6	
Cav_tRNA_pchr04-48	pchr04	4999992	4999919	Val	AAC	0	0	73.2	
Cav_tRNA_pchr04-49	pchr04	3663536	3663465	Pro	TGG	0	0	68.5	
Cav_tRNA_pchr04-50	pchr04	3660651	3660580	Pro	TGG	0	0	68.5	
Cav_tRNA_pchr04-51	pchr04	1716408	1716336	Glu	CTC	0	0	78.9	
Cav_tRNA_pchr04-52	pchr04	1703985	1703913	Arg	TCT	0	0	68.5	
Cav_tRNA_pchr05-1	pchr05	1815230	1815310	Leu	CAG	0	0	68.4	
Cav_tRNA_pchr05-2	pchr05	6859044	6859115	Asn	GTT	0	0	46.4	pseudo
Cav_tRNA_pchr05-3	pchr05	7513692	7513773	Ser	TGA	0	0	80.7	
Cav_tRNA_pchr05-4	pchr05	8545067	8545138	Asp	GTC	0	0	69.8	
Cav_tRNA_pchr05-5	pchr05	8556326	8556397	Asp	GTC	0	0	69.8	
Cav_tRNA_pchr05-6	pchr05	9324990	9325062	Lys	TTT	0	0	88.4	
Cav_tRNA_pchr05-7	pchr05	9332922	9332994	Lys	TTT	0	0	88.4	
Cav_tRNA_pchr05-8	pchr05	9349791	9349863	Val	TAC	0	0	71.2	
Cav_tRNA_pchr05-9	pchr05	9765723	9765808	Leu	CAA	0	0	34.3	
Cav_tRNA_pchr05-10	pchr05	11114374	11114455	Leu	TAG	0	0	20.2	pseudo
Cav_tRNA_pchr05-11	pchr05	12454818	12454889	Asp	GTC	0	0	48.6	
Cav_tRNA_pchr05-12	pchr05	20977601	20977674	Trp	CCA	0	0	70.1	
Cav_tRNA_pchr05-13	pchr05	23842142	23842215	Val	AAC	0	0	72.5	

Cav_tRNA_pchr05-14	pchr05	26544910	26544983	Ile	TAT	0	0	85.9	
Cav_tRNA_pchr05-15	pchr05	26671787	26671858	Pro	TGG	0	0	68.9	
Cav_tRNA_pchr05-16	pchr05	26673824	26673895	Pro	TGG	0	0	68.5	
Cav_tRNA_pchr05-17	pchr05	26674616	26674687	Pro	TGG	0	0	68.5	
Cav_tRNA_pchr05-18	pchr05	26675300	26675371	Pro	TGG	0	0	68.5	
Cav_tRNA_pchr05-19	pchr05	28201431	28201511	Val	CAC	0	0	21.4	pseudo
Cav_tRNA_pchr05-20	pchr05	28227937	28228017	Val	CAC	0	0	23.2	pseudo
Cav_tRNA_pchr05-21	pchr05	28242832	28242912	Val	CAC	0	0	21.4	pseudo
Cav_tRNA_pchr05-22	pchr05	28247539	28247614	Val	CAC	0	0	21.5	pseudo
Cav_tRNA_pchr05-23	pchr05	29460370	29460450	Leu	CAG	0	0	69.5	
Cav_tRNA_pchr05-24	pchr05	31372403	31372476	Ile	AAT	0	0	81.8	
Cav_tRNA_pchr05-25	pchr05	31392722	31392793	Asp	GTC	0	0	69.8	
Cav_tRNA_pchr05-26	pchr05	31782560	31782631	Thr	CGT	0	0	80.5	
Cav_tRNA_pchr05-27	pchr05	35029856	35029927	Thr	TGT	0	0	81.6	
Cav_tRNA_pchr05-28	pchr05	35058947	35059018	Pro	AGG	0	0	67.4	
Cav_tRNA_pchr05-29	pchr05	35776755	35776835	Leu	AAG	0	0	62.9	
Cav_tRNA_pchr05-30	pchr05	36023689	36023760	Glu	TTC	0	0	72	
Cav_tRNA_pchr05-31	pchr05	35704039	35703968	Pro	TGG	0	0	68.5	
Cav_tRNA_pchr05-32	pchr05	34829184	34829113	Asp	GTC	0	0	69.8	
Cav_tRNA_pchr05-33	pchr05	34226048	34225977	Pro	TGG	0	0	66.3	
Cav_tRNA_pchr05-34	pchr05	33659587	33659514	Val	AAC	0	0	73.2	
Cav_tRNA_pchr05-35	pchr05	33209756	33209684	Ala	AGC	0	0	63.4	
Cav_tRNA_pchr05-36	pchr05	32100929	32100857	Ala	TGC	0	0	70	
Cav_tRNA_pchr05-37	pchr05	31911473	31911402	Pro	AGG	0	0	67.4	
Cav_tRNA_pchr05-38	pchr05	29626403	29626323	Leu	CAG	0	0	68.4	
Cav_tRNA_pchr05-39	pchr05	26673617	26673546	Pro	TGG	0	0	68.5	
Cav_tRNA_pchr05-40	pchr05	26629170	26629097	Asn	GTT	0	0	81.1	

Cav_tRNA_pchr05-41	pchr05	26185990	26185919	Val	GAC	0	0	53.3	
Cav_tRNA_pchr05-42	pchr05	23847969	23847896	Val	AAC	0	0	72.5	
Cav_tRNA_pchr05-43	pchr05	22225377	22225306	Asp	GTC	0	0	30.5	pseudo
Cav_tRNA_pchr05-44	pchr05	16134645	16134572	Gly	GCC	16134609	16134607	37.7	pseudo
Cav_tRNA_pchr05-45	pchr05	14449949	14449877	iMet	CAT	0	0	33.9	
Cav_tRNA_pchr05-46	pchr05	11837485	11837405	Leu	CAA	0	0	27	pseudo
Cav_tRNA_pchr05-47	pchr05	9575023	9574951	Glu	CTC	0	0	80	
Cav_tRNA_pchr05-48	pchr05	9569245	9569173	Glu	CTC	0	0	78.9	
Cav_tRNA_pchr05-49	pchr05	6354355	6354274	Ser	CGA	0	0	76.5	
Cav_tRNA_pchr05-50	pchr05	6350492	6350399	Tyr	GTA	6350455	6350435	74.2	
Cav_tRNA_pchr05-51	pchr05	6005071	6004999	Ala	AGC	0	0	63.4	
Cav_tRNA_pchr05-52	pchr05	3889925	3889852	Asn	GTT	0	0	80	
Cav_tRNA_pchr06-1	pchr06	1257365	1257437	Arg	CCT	0	0	72.6	
Cav_tRNA_pchr06-2	pchr06	1514614	1514686	Phe	GAA	0	0	78.3	
Cav_tRNA_pchr06-3	pchr06	3951684	3951754	Gly	GCC	0	0	66.5	
Cav_tRNA_pchr06-4	pchr06	5731187	5731258	Glu	TTC	0	0	72	
Cav_tRNA_pchr06-5	pchr06	7060904	7060977	Ile	AAT	0	0	81.8	
Cav_tRNA_pchr06-6	pchr06	7446890	7446961	Asp	GTC	0	0	69.8	
Cav_tRNA_pchr06-7	pchr06	7633156	7633227	Undet	NNN	0	0	27	pseudo
Cav_tRNA_pchr06-8	pchr06	11199715	11199789	Leu	CAA	0	0	23.7	pseudo
Cav_tRNA_pchr06-9	pchr06	12641463	12641536	Ile	AAT	0	0	78.2	
Cav_tRNA_pchr06-10	pchr06	12646107	12646180	Ile	AAT	0	0	81.8	
Cav_tRNA_pchr06-11	pchr06	16098448	16098519	Pro	TGG	0	0	49.9	
Cav_tRNA_pchr06-12	pchr06	17240191	17240263	Phe	GAA	0	0	75.4	
Cav_tRNA_pchr06-13	pchr06	17789608	17789679	Pro	TGG	0	0	68.5	
Cav_tRNA_pchr06-14	pchr06	19804927	19805008	Ser	TGA	0	0	80.7	
Cav_tRNA_pchr06-15	pchr06	20334586	20334666	Leu	CAG	0	0	68.4	

Cav_tRNA_pchr06-16	pchr06	28584928	28584855	Thr	AGT	0	0	74.7	
Cav_tRNA_pchr06-17	pchr06	17897898	17897826	Ala	CGC	0	0	68.2	
Cav_tRNA_pchr06-18	pchr06	7085060	7084987	Ile	AAT	0	0	81.8	
Cav_tRNA_pchr06-19	pchr06	5681003	5680925	Arg	GCG	0	0	33.5	
Cav_tRNA_pchr06-20	pchr06	5516049	5515977	Ala	AGC	0	0	63.4	
Cav_tRNA_pchr06-21	pchr06	5480659	5480586	Asn	GTT	0	0	80.4	
Cav_tRNA_pchr06-22	pchr06	2717701	2717630	Gln	TTG	0	0	73.5	
Cav_tRNA_pchr06-23	pchr06	2645796	2645726	Gly	GCC	0	0	66.5	
Cav_tRNA_pchr06-24	pchr06	805813	805741	Val	TAC	0	0	75.7	
Cav_tRNA_pchr06-25	pchr06	392014	391941	Ile	AAT	0	0	79.3	
Cav_tRNA_pchr07-1	pchr07	1036037	1036108	Glu	TTC	0	0	72	
Cav_tRNA_pchr07-2	pchr07	1746173	1746245	Glu	CTC	0	0	21.2	pseudo
Cav_tRNA_pchr07-3	pchr07	2321140	2321213	Thr	AGT	0	0	74.7	
Cav_tRNA_pchr07-4	pchr07	3826167	3826240	Arg	TCG	0	0	81.9	
Cav_tRNA_pchr07-5	pchr07	3896673	3896744	Glu	TTC	0	0	72	
Cav_tRNA_pchr07-6	pchr07	4229095	4229166	Pro	TGG	0	0	68.5	
Cav_tRNA_pchr07-7	pchr07	5145709	5145792	Leu	CAA	0	0	77.7	
Cav_tRNA_pchr07-8	pchr07	5849334	5849406	Ala	AGC	0	0	63.4	
Cav_tRNA_pchr07-9	pchr07	6054604	6054675	Gln	CTG	0	0	73.7	
Cav_tRNA_pchr07-10	pchr07	7854104	7854176	Lys	CTT	0	0	87.7	
Cav_tRNA_pchr07-11	pchr07	13990780	13990854	Leu	CAA	0	0	20.6	pseudo
Cav_tRNA_pchr07-12	pchr07	16845878	16845950	Arg	TCT	0	0	69.7	
Cav_tRNA_pchr07-13	pchr07	17228043	17228124	Ser	CGA	0	0	78.9	
Cav_tRNA_pchr07-14	pchr07	18692335	18692418	Leu	CAA	0	0	73.4	
Cav_tRNA_pchr07-15	pchr07	23376282	23376362	Leu	AAG	0	0	74	
Cav_tRNA_pchr07-16	pchr07	23586132	23586204	Ala	TGC	0	0	65.9	
Cav_tRNA_pchr07-17	pchr07	23917882	23917972	Tyr	GTA	23917919	23917936	74.3	

Cav_tRNA_pchr07-18	pchr07	25021809	25021880	Asp	GTC	0	0	69.8	
Cav_tRNA_pchr07-19	pchr07	27076604	27076675	Cys	GCA	0	0	82.1	
Cav_tRNA_pchr07-20	pchr07	27171034	27171105	His	GTG	0	0	63	
Cav_tRNA_pchr07-21	pchr07	27171837	27171909	Arg	CCG	0	0	81.6	
Cav_tRNA_pchr07-22	pchr07	27412818	27412890	Lys	CTT	0	0	87.7	
Cav_tRNA_pchr07-23	pchr07	27476370	27476442	Lys	TTT	0	0	90.5	
Cav_tRNA_pchr07-24	pchr07	27476536	27476608	Lys	TTT	0	0	90.5	
Cav_tRNA_pchr07-25	pchr07	27476703	27476775	Lys	TTT	0	0	90.5	
Cav_tRNA_pchr07-26	pchr07	28352197	28352268	Pro	AGG	0	0	67.4	
Cav_tRNA_pchr07-27	pchr07	28699331	28699403	Lys	CTT	0	0	87.7	
Cav_tRNA_pchr07-28	pchr07	28588231	28588159	Arg	CCT	0	0	65.6	
Cav_tRNA_pchr07-29	pchr07	28351435	28351364	Asp	GTC	0	0	69.8	
Cav_tRNA_pchr07-30	pchr07	28014975	28014902	Val	CAC	0	0	81.5	
Cav_tRNA_pchr07-31	pchr07	27190727	27190656	Pro	AGG	0	0	67.4	
Cav_tRNA_pchr07-32	pchr07	26049504	26049433	Pro	AGG	0	0	67.4	
Cav_tRNA_pchr07-33	pchr07	25006503	25006430	Val	AAC	0	0	73.2	
Cav_tRNA_pchr07-34	pchr07	23376170	23376090	Leu	AAG	0	0	74	
Cav_tRNA_pchr07-35	pchr07	23332435	23332365	Leu	CAG	0	0	25	pseudo
Cav_tRNA_pchr07-36	pchr07	22434255	22434172	Leu	CAA	0	0	77.7	
Cav_tRNA_pchr07-37	pchr07	19276685	19276604	Ser	AGA	0	0	75.4	
Cav_tRNA_pchr07-38	pchr07	19239851	19239767	Leu	CAA	0	0	31.7	pseudo
Cav_tRNA_pchr07-39	pchr07	18984733	18984660	Arg	TCG	0	0	82.3	
Cav_tRNA_pchr07-40	pchr07	17202810	17202736	Lys	CTT	0	0	21.9	
Cav_tRNA_pchr07-41	pchr07	16333979	16333908	Lys	TTT	0	0	92.3	
Cav_tRNA_pchr07-42	pchr07	11596683	11596611	Ala	TGC	0	0	63.7	
Cav_tRNA_pchr07-43	pchr07	10893681	10893600	Ser	GCT	0	0	80.5	
Cav_tRNA_pchr07-44	pchr07	6764465	6764394	Cys	GCA	0	0	80.9	

Cav_tRNA_pchr07-45	pchr07	6279526	6279453	Val	AAC	0	0	73.2	
Cav_tRNA_pchr07-46	pchr07	6182943	6182873	Gly	CCC	0	0	66	
Cav_tRNA_pchr07-47	pchr07	5420857	5420786	iMet	CAT	0	0	58.3	
Cav_tRNA_pchr07-48	pchr07	5397520	5397449	iMet	CAT	0	0	58.3	
Cav_tRNA_pchr07-49	pchr07	5206618	5206547	Gly	TCC	0	0	71	
Cav_tRNA_pchr07-50	pchr07	4258303	4258230	Val	CAC	0	0	82.4	
Cav_tRNA_pchr07-51	pchr07	4236994	4236923	Cys	GCA	0	0	82.1	
Cav_tRNA_pchr07-52	pchr07	3390274	3390202	Arg	TCT	0	0	69.9	
Cav_tRNA_pchr07-53	pchr07	3388183	3388111	Lys	TTT	0	0	89.6	
Cav_tRNA_pchr07-54	pchr07	2531096	2531025	iMet	CAT	0	0	58.3	
Cav_tRNA_pchr07-55	pchr07	1317154	1317083	Asp	GTC	0	0	53	
Cav_tRNA_pchr07-56	pchr07	1313476	1313360	Asp	GTC	1313439	1313395	37.9	
Cav_tRNA_pchr07-57	pchr07	1297913	1297834	Asp	GTC	0	0	32.5	pseudo
Cav_tRNA_pchr07-58	pchr07	1292508	1292437	Asp	GTC	0	0	69.8	
Cav_tRNA_pchr07-59	pchr07	1285275	1285204	Asp	GTC	0	0	69.8	
Cav_tRNA_pchr07-60	pchr07	955795	955716	Undet	NNN	0	0	27.2	
Cav_tRNA_pchr07-61	pchr07	947788	947709	Undet	NNN	0	0	27.2	
Cav_tRNA_pchr07-62	pchr07	893043	892972	Gln	CTG	0	0	74.7	
Cav_tRNA_pchr07-63	pchr07	520759	520678	Ser	GCT	0	0	80.5	
Cav_tRNA_pchr08-1	pchr08	3703490	3703570	Leu	AAG	0	0	74	
Cav_tRNA_pchr08-2	pchr08	3818947	3819025	Arg	ACG	0	0	53.9	
Cav_tRNA_pchr08-3	pchr08	5265333	5265414	Sup	TTA	5265366	5265375	22.6	
Cav_tRNA_pchr08-4	pchr08	8972131	8972203	Arg	ACG	0	0	72.6	
Cav_tRNA_pchr08-5	pchr08	8981323	8981404	Lys	CTT	0	0	33.2	pseudo
Cav_tRNA_pchr08-6	pchr08	16488057	16488132	Leu	CAG	0	0	26.1	pseudo
Cav_tRNA_pchr08-7	pchr08	20012702	20012774	Lys	CTT	0	0	87.7	
Cav_tRNA_pchr08-8	pchr08	20016994	20017066	Lys	CTT	0	0	87.7	

Cav_tRNA_pchr08-9	pchr08	21410870	21410941	Asp	GTC	0	0	69.8	
Cav_tRNA_pchr08-10	pchr08	23157816	23157888	Glu	CTC	0	0	78.9	
Cav_tRNA_pchr08-11	pchr08	23191017	23191089	Glu	CTC	0	0	79.2	
Cav_tRNA_pchr08-12	pchr08	24782019	24782091	Glu	CTC	0	0	78.9	
Cav_tRNA_pchr08-13	pchr08	25283649	25283720	Asp	GTC	0	0	69.8	
Cav_tRNA_pchr08-14	pchr08	25390158	25390074	Met	CAT	25390120	25390110	64.2	
Cav_tRNA_pchr08-15	pchr08	25310179	25310108	Trp	CCA	0	0	75.1	
Cav_tRNA_pchr08-16	pchr08	23960669	23960598	Glu	TTC	0	0	62.8	
Cav_tRNA_pchr08-17	pchr08	23339672	23339600	Phe	GAA	0	0	78.3	
Cav_tRNA_pchr08-18	pchr08	23163757	23163685	Glu	CTC	0	0	78.9	
Cav_tRNA_pchr08-19	pchr08	22862146	22862063	Leu	CAA	0	0	81	
Cav_tRNA_pchr08-20	pchr08	21935172	21935099	Glu	TTC	0	0	42	
Cav_tRNA_pchr08-21	pchr08	21725856	21725783	Thr	AGT	0	0	76	
Cav_tRNA_pchr08-22	pchr08	21724091	21724018	Thr	AGT	0	0	76	
Cav_tRNA_pchr08-23	pchr08	20647157	20647085	Ala	CGC	0	0	68.3	
Cav_tRNA_pchr08-24	pchr08	20268237	20268141	Tyr	GTA	20268200	20268177	74	
Cav_tRNA_pchr08-25	pchr08	4796848	4796777	Gly	TCC	0	0	71	
Cav_tRNA_pchr08-26	pchr08	3703712	3703640	Arg	CCG	0	0	67.8	
Cav_tRNA_pchr08-27	pchr08	2658048	2657975	Thr	AGT	0	0	74.7	
Cav_tRNA_pchr08-28	pchr08	1669481	1669400	Lys	CTT	0	0	32.3	pseudo
Cav_tRNA_pchr08-29	pchr08	765690	765600	Tyr	GTA	765653	765636	66.3	
Cav_tRNA_pchr08-30	pchr08	756999	756909	Tyr	GTA	756962	756945	74.3	
Cav_tRNA_pchr09-1	pchr09	5884384	5884455	Cys	GCA	0	0	82.1	
Cav_tRNA_pchr09-2	pchr09	5921123	5921194	Cys	GCA	0	0	82.1	
Cav_tRNA_pchr09-3	pchr09	6098924	6099005	Ser	GCT	0	0	80.5	
Cav_tRNA_pchr09-4	pchr09	6100867	6100948	Ser	GCT	0	0	80.5	
Cav_tRNA_pchr09-5	pchr09	6101679	6101760	Ser	GCT	0	0	80.5	

Cav_tRNA_pchr09-6	pchr09	6326981	6327062	Ser	GCT	0	0	80.5
Cav_tRNA_pchr09-7	pchr09	6449623	6449694	Gly	TCC	0	0	71
Cav_tRNA_pchr09-8	pchr09	6760536	6760609	Asn	GTT	0	0	75.3
Cav_tRNA_pchr09-9	pchr09	6783623	6783695	Arg	CCT	0	0	68.1
Cav_tRNA_pchr09-10	pchr09	7750320	7750391	Undet	NNN	0	0	24.4
Cav_tRNA_pchr09-11	pchr09	7757631	7757702	Undet	NNN	0	0	24.4
Cav_tRNA_pchr09-12	pchr09	15389106	15389177	His	GTG	0	0	63
Cav_tRNA_pchr09-13	pchr09	18277034	18277107	Arg	TCG	0	0	82.3
Cav_tRNA_pchr09-14	pchr09	18637847	18637918	Cys	GCA	0	0	79.9
Cav_tRNA_pchr09-15	pchr09	18974971	18975043	Lys	CTT	0	0	87.7
Cav_tRNA_pchr09-16	pchr09	19239850	19239922	Lys	TTT	0	0	89.6
Cav_tRNA_pchr09-17	pchr09	20164024	20164094	Gly	GCC	0	0	66.5
Cav_tRNA_pchr09-18	pchr09	20175819	20175891	Ala	AGC	0	0	63.4
Cav_tRNA_pchr09-19	pchr09	20175969	20176050	Ser	AGA	0	0	73.2
Cav_tRNA_pchr09-20	pchr09	20196942	20197013	Pro	AGG	0	0	67.4
Cav_tRNA_pchr09-21	pchr09	21466723	21466795	Ala	AGC	0	0	63.4
Cav_tRNA_pchr09-22	pchr09	21746507	21746579	Lys	CTT	0	0	87.7
Cav_tRNA_pchr09-23	pchr09	22152178	22152249	Gln	TTG	0	0	73.5
Cav_tRNA_pchr09-24	pchr09	22657523	22657610	Tyr	GTA	22657560	22657574	74.4
Cav_tRNA_pchr09-25	pchr09	22970805	22970878	Ile	AAT	0	0	81.8
Cav_tRNA_pchr09-26	pchr09	22636817	22636734	Leu	TAA	0	0	62.7
Cav_tRNA_pchr09-27	pchr09	21842038	21841957	Ser	CGA	0	0	76.5
Cav_tRNA_pchr09-28	pchr09	20523515	20523443	Glu	CTC	0	0	78.9
Cav_tRNA_pchr09-29	pchr09	20195162	20195091	Asp	GTC	0	0	69.8
Cav_tRNA_pchr09-30	pchr09	20052200	20052127	Val	CAC	0	0	81.5
Cav_tRNA_pchr09-31	pchr09	18671925	18671852	Val	AAC	0	0	60.9
Cav_tRNA_pchr09-32	pchr09	17418959	17418887	Ala	TGC	0	0	63.7

Cav_tRNA_pchr09-33	pchr09	17236593	17236522	Pro	AGG	0	0	67.4	
Cav_tRNA_pchr09-34	pchr09	15777574	15777501	Ile	AAT	0	0	81.8	
Cav_tRNA_pchr09-35	pchr09	13177830	13177759	Ser	CGA	0	0	20.2	pseudo
Cav_tRNA_pchr09-36	pchr09	10911858	10911788	Gly	GCC	0	0	62.2	
Cav_tRNA_pchr09-37	pchr09	6682266	6682194	Ala	TGC	0	0	63.7	
Cav_tRNA_pchr09-38	pchr09	5909170	5909098	Ala	TGC	0	0	65.5	
Cav_tRNA_pchr09-39	pchr09	2523318	2523239	Leu	TAG	0	0	69.5	
Cav_tRNA_pchr09-40	pchr09	2416337	2416266	Pro	CGG	0	0	68.5	
Cav_tRNA_pchr09-41	pchr09	1454167	1454085	Leu	TAA	0	0	71.4	
Cav_tRNA_pchr10-1	pchr10	581088	581159	iMet	CAT	0	0	58.3	
Cav_tRNA_pchr10-2	pchr10	878504	878576	Ala	AGC	0	0	63.4	
Cav_tRNA_pchr10-3	pchr10	3120032	3120104	Arg	ACG	0	0	72	
Cav_tRNA_pchr10-4	pchr10	4537672	4537743	Gln	CTG	0	0	75.3	
Cav_tRNA_pchr10-5	pchr10	6080297	6080379	Leu	TAA	0	0	70.7	
Cav_tRNA_pchr10-6	pchr10	6272500	6272572	Arg	TCT	0	0	67.3	
Cav_tRNA_pchr10-7	pchr10	9271683	9271753	Sup	TCA	0	0	66.1	
Cav_tRNA_pchr10-8	pchr10	15665768	15665840	Lys	CTT	0	0	87.7	
Cav_tRNA_pchr10-9	pchr10	18404365	18404436	Gly	TCC	0	0	71	
Cav_tRNA_pchr10-10	pchr10	19364257	19364330	Val	CAC	0	0	81.5	
Cav_tRNA_pchr10-11	pchr10	19498802	19498883	Ser	AGA	0	0	79	
Cav_tRNA_pchr10-12	pchr10	20553020	20553092	Lys	TTT	0	0	88.7	
Cav_tRNA_pchr10-13	pchr10	21119022	21119093	His	GTG	0	0	63	
Cav_tRNA_pchr10-14	pchr10	21292734	21292806	Glu	CTC	0	0	79.2	
Cav_tRNA_pchr10-15	pchr10	22356796	22356868	Arg	CCT	0	0	60.5	
Cav_tRNA_pchr10-16	pchr10	22190082	22190012	Gly	GCC	0	0	50.6	
Cav_tRNA_pchr10-17	pchr10	21444909	21444828	Ser	CGA	0	0	76.5	
Cav_tRNA_pchr10-18	pchr10	21297440	21297369	Glu	TTC	0	0	72	

Cav_tRNA_pchr10-19	pchr10	21264660	21264587	Ile	TAT	0	0	85.9	
Cav_tRNA_pchr10-20	pchr10	19828901	19828830	Gly	TCC	0	0	71	
Cav_tRNA_pchr10-21	pchr10	19516970	19516899	Asp	GTC	0	0	69.8	
Cav_tRNA_pchr10-22	pchr10	19516810	19516739	Asp	GTC	0	0	69.8	
Cav_tRNA_pchr10-23	pchr10	17795502	17795429	Val	AAC	0	0	73.2	
Cav_tRNA_pchr10-24	pchr10	17465913	17465842	His	GTG	0	0	63	
Cav_tRNA_pchr10-25	pchr10	12734586	12734515	Asp	GTC	0	0	63.4	
Cav_tRNA_pchr10-26	pchr10	8918821	8918744	His	GTG	0	0	38.3	pseudo
Cav_tRNA_pchr10-27	pchr10	6250697	6250616	Ser	GCT	0	0	80.5	
Cav_tRNA_pchr10-28	pchr10	6080513	6080442	Gly	TCC	0	0	71	
Cav_tRNA_pchr10-29	pchr10	5967369	5967289	Leu	AAG	0	0	74	
Cav_tRNA_pchr10-30	pchr10	5677788	5677715	Phe	GAA	0	0	27.7	pseudo
Cav_tRNA_pchr10-31	pchr10	3993240	3993168	Ala	TGC	0	0	65.6	
Cav_tRNA_pchr10-32	pchr10	3152751	3152680	Glu	TTC	0	0	72	
Cav_tRNA_pchr10-33	pchr10	673406	673335	Gly	TCC	0	0	71	
Cav_tRNA_pchr10-34	pchr10	669356	669240	Gly	TCC	669319	669275	50.7	
Cav_tRNA_pchr10-35	pchr10	666892	666780	Gly	TCC	666855	666815	56	
Cav_tRNA_pchr11-1	pchr11	879005	879075	Gly	GCC	0	0	66.5	
Cav_tRNA_pchr11-2	pchr11	1623230	1623314	Met	CAT	1623268	1623278	64.3	
Cav_tRNA_pchr11-3	pchr11	2289064	2289136	Ala	TGC	0	0	59.2	
Cav_tRNA_pchr11-4	pchr11	3820888	3820972	Met	CAT	3820926	3820936	64.3	
Cav_tRNA_pchr11-5	pchr11	4155096	4155168	Arg	ACG	0	0	72.9	
Cav_tRNA_pchr11-6	pchr11	6234553	6234626	Ile	AAT	0	0	81.8	
Cav_tRNA_pchr11-7	pchr11	20558573	20558644	Pro	TGG	0	0	69.2	
Cav_tRNA_pchr11-8	pchr11	21935869	21935788	Ser	GCT	0	0	80.5	
Cav_tRNA_pchr11-9	pchr11	18715211	18715131	Leu	AAG	0	0	74	
Cav_tRNA_pchr11-10	pchr11	17274012	17273931	Ser	AGA	0	0	80.3	

Cav_tRNA_pchr11-11	pchr11	6189875	6189804	His	GTG	0	0	63
Cav_tRNA_pchr11-12	pchr11	6189795	6189705	Tyr	GTA	6189758	6189741	74.3
Cav_tRNA_pchr11-13	pchr11	5704670	5704600	Gly	GCC	0	0	66.5
Cav_tRNA_pchr11-14	pchr11	5605468	5605396	Thr	AGT	0	0	66.4
Cav_tRNA_pchr11-15	pchr11	5601326	5601253	Thr	AGT	0	0	61.2
Cav_tRNA_pchr11-16	pchr11	5033782	5033709	Val	CAC	0	0	81.5
Cav_tRNA_pchr11-17	pchr11	4583777	4583705	Ala	AGC	0	0	63.4
Cav_tRNA_pchr11-18	pchr11	4327914	4327830	Met	CAT	4327876	4327866	64.2
Cav_tRNA_pchr11-19	pchr11	3545283	3545211	Phe	GAA	0	0	76.1
Cav_tRNA_pchr11-20	pchr11	2942515	2942434	Ser	TGA	0	0	80.7
Cav_tRNA_pchr11-21	pchr11	1231372	1231300	Arg	CCG	0	0	67

Table S2.2: Comparison of tRNA gene codon frequencies.

tRNA type	Codon	Species	Codon frequency	tRNA type	Codon	Species	Codon frequency
Ala	GCT	*C. avellana cv. 'Tombul'*	0.015	Leu	TTA	*C. avellana cv. 'Tombul'*	0.021
		Arabidopsis thaliana	0.025			*Arabidopsis thaliana*	0.010
		Betula pendula	0.024			*Betula pendula*	0.011
		Juglans regia	0.031			*Juglans regia*	0.015
		Populus trichocarpa	0.088			*Populus trichocarpa*	0.025
	GCG	*C. avellana cv. 'Tombul'*	0.006		CTA	*C. avellana cv. 'Tombul'*	0.021
		Arabidopsis thaliana	0.011			*Arabidopsis thaliana*	0.016
		Betula pendula	0.008			*Betula pendula*	0.014
		Juglans regia	0.009			*Juglans regia*	0.017
		Populus trichocarpa	0.021			*Populus trichocarpa*	0.042
	GCA	*C. avellana cv. 'Tombul'*	0.009		CTC	*C. avellana cv. 'Tombul'*	0.000
		Arabidopsis thaliana	0.016			*Arabidopsis thaliana*	0.002
		Betula pendula	0.016			*Betula pendula*	0.000
		Juglans regia	0.021			*Juglans regia*	0.002
		Populus trichocarpa	0.088			*Populus trichocarpa*	0.000
Arg	CGT	*C. avellana cv. 'Tombul'*	0.021	Lys	AAG	*C. avellana cv. 'Tombul'*	0.024
		Arabidopsis thaliana	0.014			*Arabidopsis thaliana*	0.029
		Betula pendula	0.021			*Betula pendula*	0.022
		Juglans regia	0.018			*Juglans regia*	0.032
		Populus trichocarpa	0.025			*Populus trichocarpa*	0.013
	CGG	*C. avellana cv. 'Tombul'*	0.009		AAA	*C. avellana cv. 'Tombul'*	0.012

		Arabidopsis thaliana	0.006			*Arabidopsis thaliana*	0.021
		Betula pendula	0.011			*Betula pendula*	0.021
		Juglans regia	0.017			*Juglans regia*	0.021
		Populus trichocarpa	0.000			*Populus trichocarpa*	0.075
	AGG	*C. avellana cv. 'Tombul'*	0.021	Met	ATG	*C. avellana cv. 'Tombul'*	0.053
		Arabidopsis thaliana	0.013			*Arabidopsis thaliana*	0.038
		Betula pendula	0.011			*Betula pendula*	0.061
		Juglans regia	0.012			*Juglans regia*	0.044
		Populus trichocarpa	0.000			*Populus trichocarpa*	0.088
	CGA	*C. avellana cv. 'Tombul'*	0.015	Phe	TTC	*C. avellana cv. 'Tombul'*	0.021
		Arabidopsis thaliana	0.010			*Arabidopsis thaliana*	0.025
		Betula pendula	0.008			*Betula pendula*	0.035
		Juglans regia	0.012			*Juglans regia*	0.031
		Populus trichocarpa	0.000			*Populus trichocarpa*	0.004
	AGA	*C. avellana cv. 'Tombul'*	0.015		TTT	*C. avellana cv. 'Tombul'*	0.000
		Arabidopsis thaliana	0.014			*Arabidopsis thaliana*	0.000
		Betula pendula	0.014			*Betula pendula*	0.003
		Juglans regia	0.012			*Juglans regia*	0.000
		Populus trichocarpa	0.013			*Populus trichocarpa*	0.000
Asn	AAC	*C. avellana cv. 'Tombul'*	0.024	Pro	CCT	*C. avellana cv. 'Tombul'*	0.006
		Arabidopsis thaliana	0.025			*Arabidopsis thaliana*	0.025
		Betula pendula	0.042			*Betula pendula*	0.018
		Juglans regia	0.040			*Juglans regia*	0.020
		Populus trichocarpa	0.021			*Populus trichocarpa*	0.000

Asp	GAC	*C. avellana cv. 'Tombul'*	0.015		CCA	*C. avellana cv. 'Tombul'*	0.018
		Arabidopsis thaliana	0.041			*Arabidopsis thaliana*	0.071
		Betula pendula	0.038			*Betula pendula*	0.043
		Juglans regia	0.057			*Juglans regia*	0.028
		Populus trichocarpa	0.008			*Populus trichocarpa*	0.033
	GAT	*C. avellana cv. 'Tombul'*	0.000		CCG	*C. avellana cv. 'Tombul'*	0.000
		Arabidopsis thaliana	0.000			*Arabidopsis thaliana*	0.008
		Betula pendula	0.002			*Betula pendula*	0.006
		Juglans regia	0.000			*Juglans regia*	0.006
		Populus trichocarpa	0.000			*Populus trichocarpa*	0.000
Cys	TGC	*C. avellana cv. 'Tombul'*	0.027	Ser	TCT	*C. avellana cv. 'Tombul'*	0.009
		Arabidopsis thaliana	0.024			*Arabidopsis thaliana*	0.059
		Betula pendula	0.034			*Betula pendula*	0.019
		Juglans regia	0.026			*Juglans regia*	0.025
		Populus trichocarpa	0.021			*Populus trichocarpa*	0.000
	TGT	*C. avellana cv. 'Tombul'*	0.000		TCG	*C. avellana cv. 'Tombul'*	0.006
		Arabidopsis thaliana	0.000			*Arabidopsis thaliana*	0.006
		Betula pendula	0.002			*Betula pendula*	0.010
		Juglans regia	0.003			*Juglans regia*	0.012
		Populus trichocarpa	0.004			*Populus trichocarpa*	0.008
Gln	CAG	*C. avellana cv. 'Tombul'*	0.018		AGC	*C. avellana cv. 'Tombul'*	0.036
		Arabidopsis thaliana	0.014			*Arabidopsis thaliana*	0.021
		Betula pendula	0.013			*Betula pendula*	0.022

		Juglans regia	0.015			*Juglans regia*	0.023
		Populus trichocarpa	0.000			*Populus trichocarpa*	0.021
	CAA	*C. avellana cv. 'Tombul'*	0.036		TCC	*C. avellana cv. 'Tombul'*	0.003
		Arabidopsis thaliana	0.013			*Arabidopsis thaliana*	0.002
		Betula pendula	0.016			*Betula pendula*	0.005
		Juglans regia	0.017			*Juglans regia*	0.003
		Populus trichocarpa	0.054			*Populus trichocarpa*	0.008
Glu	GAG	*C. avellana cv. 'Tombul'*	0.012		TCA	*C. avellana cv. 'Tombul'*	0.012
		Arabidopsis thaliana	0.021			*Arabidopsis thaliana*	0.014
		Betula pendula	0.022			*Betula pendula*	0.018
		Juglans regia	0.029			*Juglans regia*	0.011
		Populus trichocarpa	0.000			*Populus trichocarpa*	0.004
	GAA	*C. avellana cv. 'Tombul'*	0.015		AGT	*C. avellana cv. 'Tombul'*	0.000
		Arabidopsis thaliana	0.019			*Arabidopsis thaliana*	0.000
		Betula pendula	0.027			*Betula pendula*	0.000
		Juglans regia	0.025			*Juglans regia*	0.000
		Populus trichocarpa	0.008			*Populus trichocarpa*	0.004
Gly	GGG	*C. avellana cv. 'Tombul'*	0.018	Thr	ACT	*C. avellana cv. 'Tombul'*	0.033
		Arabidopsis thaliana	0.008			*Arabidopsis thaliana*	0.016
		Betula pendula	0.010			*Betula pendula*	0.019
		Juglans regia	0.011			*Juglans regia*	0.020
		Populus trichocarpa	0.000			*Populus trichocarpa*	0.029
	GGC	*C. avellana cv. 'Tombul'*	0.065		ACG	*C. avellana cv. 'Tombul'*	0.012

		Arabidopsis thaliana	0.037			*Arabidopsis thaliana*	0.010
		Betula pendula	0.034			*Betula pendula*	0.008
		Juglans regia	0.032			*Juglans regia*	0.006
		Populus trichocarpa	0.004			*Populus trichocarpa*	0.000
	GGA	*C. avellana cv. 'Tombul'*	0.030		ACA	*C. avellana cv. 'Tombul'*	0.006
		Arabidopsis thaliana	0.019			*Arabidopsis thaliana*	0.013
		Betula pendula	0.016			*Betula pendula*	0.016
		Juglans regia	0.017			*Juglans regia*	0.014
		Populus trichocarpa	0.004			*Populus trichocarpa*	0.008
His	CAC	*C. avellana cv. 'Tombul'*	0.038		ACC	*C. avellana cv. 'Tombul'*	0.000
		Arabidopsis thaliana	0.016			*Arabidopsis thaliana*	0.000
		Betula pendula	0.022			*Betula pendula*	0.003
		Juglans regia	0.026			*Juglans regia*	0.000
		Populus trichocarpa	0.013			*Populus trichocarpa*	0.000
	CAT	*C. avellana cv. 'Tombul'*	0.000	Trp	TGG	*C. avellana cv. 'Tombul'*	0.024
		Arabidopsis thaliana	0.000			*Arabidopsis thaliana*	0.022
		Betula pendula	0.003			*Betula pendula*	0.024
		Juglans regia	0.000			*Juglans regia*	0.025
		Populus trichocarpa	0.000			*Populus trichocarpa*	0.008
Ile	ATT	*C. avellana cv. 'Tombul'*	0.021	Tyr	TAC	*C. avellana cv. 'Tombul'*	0.015
		Arabidopsis thaliana	0.030			*Arabidopsis thaliana*	0.121
		Betula pendula	0.026			*Betula pendula*	0.030
		Juglans regia	0.034			*Juglans regia*	0.025
		Populus trichocarpa	0.000			*Populus trichocarpa*	0.008

	ATA	*C. avellana cv. 'Tombul'*	0.006		TAT	*C. avellana cv. 'Tombul'*	0.000
		Arabidopsis thaliana	0.008			*Arabidopsis thaliana*	0.000
		Betula pendula	0.008			*Betula pendula*	0.003
		Juglans regia	0.012			*Juglans regia*	0.000
		Populus trichocarpa	0.017			*Populus trichocarpa*	0.004
	ATC	*C. avellana cv. 'Tombul'*	0.000	Val	GTT	*C. avellana cv. 'Tombul'*	0.036
		Arabidopsis thaliana	0.000			*Arabidopsis thaliana*	0.000
		Betula pendula	0.000			*Betula pendula*	0.024
		Juglans regia	0.000			*Juglans regia*	0.029
		Populus trichocarpa	0.004			*Populus trichocarpa*	0.000
Leu	CTT	*C. avellana cv. 'Tombul'*	0.033		GTG	*C. avellana cv. 'Tombul'*	0.024
		Arabidopsis thaliana	0.019			*Arabidopsis thaliana*	0.013
		Betula pendula	0.018			*Betula pendula*	0.011
		Juglans regia	0.020			*Juglans regia*	0.018
		Populus trichocarpa	0.054			*Populus trichocarpa*	0.008
	TTG	*C. avellana cv. 'Tombul'*	0.044		GTA	*C. avellana cv. 'Tombul'*	0.021
		Arabidopsis thaliana	0.016			*Arabidopsis thaliana*	0.011
		Betula pendula	0.022			*Betula pendula*	0.010
		Juglans regia	0.025			*Juglans regia*	0.012
		Populus trichocarpa	0.075			*Populus trichocarpa*	0.000
	CTG	*C. avellana cv. 'Tombul'*	0.021		GTC	*C. avellana cv. 'Tombul'*	0.000
		Arabidopsis thaliana	0.005			*Arabidopsis thaliana*	0.024
		Betula pendula	0.008			*Betula pendula*	0.011

		Juglans regia	0.012			*Juglans regia*	0.002
		Populus trichocarpa	0.017			*Populus trichocarpa*	0.013

Table S2.3: Significantly enriched GO terms in gene families that are specifically expanded in the *Corylus* lineage

GO term ID	Domain	Term	Occurences in expanded gene families	Occurences in whole genome	Fisher's exact test p-value	FDR adjusted p-value
GO:0030186	Biological Process	melatonin metabolic process	16	20	5.40E-63	1.30E-60
GO:0030187	Biological Process	melatonin biosynthetic process	16	20	5.40E-63	1.30E-60
GO:0048544	Biological Process	recognition of pollen	44	196	1.30E-37	2.00E-35
GO:0008037	Biological Process	cell recognition	44	198	4.20E-37	5.00E-35
GO:0010071	Biological Process	root meristem specification	12	19	2.50E-36	2.40E-34
GO:0009875	Biological Process	pollen-pistil interaction	44	212	9.50E-34	7.60E-32
GO:0000956	Biological Process	nuclear-transcribed mRNA catabolic process	21	62	2.40E-31	1.70E-29
GO:0019326	Biological Process	nitrotoluene metabolic process	15	34	1.30E-30	4.30E-29
GO:0018973	Biological Process	trinitrotoluene metabolic process	15	34	1.30E-30	4.30E-29
GO:0018974	Biological Process	2,4,6-trinitrotoluene metabolic process	15	34	1.30E-30	4.30E-29
GO:0072490	Biological Process	toluene-containing compound metabolic process	15	34	1.30E-30	4.30E-29
GO:0072491	Biological Process	toluene-containing compound catabolic process	15	34	1.30E-30	4.30E-29
GO:0046256	Biological Process	2,4,6-trinitrotoluene catabolic process	15	34	1.30E-30	4.30E-29
GO:0046260	Biological Process	trinitrotoluene catabolic process	15	34	1.30E-30	4.30E-29
GO:0046263	Biological Process	nitrotoluene catabolic process	15	34	1.30E-30	4.30E-29
GO:0034754	Biological Process	cellular hormone metabolic process	16	42	1.50E-27	4.40E-26
GO:0042537	Biological Process	benzene-containing compound metabolic process	15	38	6.20E-27	1.70E-25
GO:0006402	Biological Process	mRNA catabolic process	21	71	1.40E-26	3.80E-25
GO:0009635	Biological Process	response to herbicide	14	39	1.60E-22	4.00E-21
GO:0046348	Biological Process	amino sugar catabolic process	18	63	6.40E-22	1.30E-20

GO:0006026	Biological Process	aminoglycan catabolic process	18	63	6.40E-22	1.30E-20
GO:1901072	Biological Process	glucosamine-containing compound catabolic process	18	63	6.40E-22	1.30E-20
GO:0006030	Biological Process	chitin metabolic process	18	63	6.40E-22	1.30E-20
GO:0006032	Biological Process	chitin catabolic process	18	63	6.40E-22	1.30E-20
GO:2000083	Biological Process	negative regulation of L-ascorbic acid biosynthetic process	8	14	2.20E-21	4.00E-20
GO:0046137	Biological Process	negative regulation of vitamin metabolic process	8	14	2.20E-21	4.00E-20
GO:0031087	Biological Process	deadenylation-independent decapping of nuclear-transcribed mRNA	12	31	4.50E-21	7.20E-20
GO:0006022	Biological Process	aminoglycan metabolic process	18	65	4.30E-21	7.20E-20
GO:1901071	Biological Process	glucosamine-containing compound metabolic process	18	65	4.30E-21	7.20E-20
GO:0031086	Biological Process	nuclear-transcribed mRNA catabolic process, deadenylation-independent decay	12	31	4.50E-21	7.20E-20
GO:0090487	Biological Process	secondary metabolite catabolic process	17	63	2.50E-19	3.80E-18
GO:0009407	Biological Process	toxin catabolic process	17	63	2.50E-19	3.80E-18
GO:0006401	Biological Process	RNA catabolic process	21	92	4.10E-19	6.00E-18
GO:0001578	Biological Process	microtubule bundle formation	7	12	5.40E-19	7.70E-18
GO:0006580	Biological Process	ethanolamine metabolic process	8	16	1.60E-18	2.20E-17
GO:0006040	Biological Process	amino sugar metabolic process	18	75	1.30E-17	1.80E-16
GO:0042435	Biological Process	indole-containing compound biosynthetic process	22	107	2.30E-17	3.00E-16
GO:0042439	Biological Process	ethanolamine-containing compound metabolic process	8	17	2.40E-17	3.10E-16
GO:2000082	Biological Process	regulation of L-ascorbic acid biosynthetic process	8	18	2.70E-16	3.30E-15

GO:0010072	Biological Process	primary shoot apical meristem specification	12	41	3.40E-15	4.00E-14
GO:0006749	Biological Process	glutathione metabolic process	13	48	5.80E-15	6.80E-14
GO:0034655	Biological Process	nucleobase-containing compound catabolic process	21	112	1.20E-14	1.40E-13
GO:0051289	Biological Process	protein homotetramerization	7	16	6.00E-14	6.70E-13
GO:0019439	Biological Process	aromatic compound catabolic process	41	335	6.90E-14	7.50E-13
GO:0000289	Biological Process	nuclear-transcribed mRNA poly(A) tail shortening	6	12	1.10E-13	1.20E-12
GO:1901361	Biological Process	organic cyclic compound catabolic process	41	342	2.20E-13	2.30E-12
GO:0048629	Biological Process	trichome patterning	7	17	4.70E-13	4.80E-12
GO:1901160	Biological Process	primary amino compound metabolic process	8	22	4.80E-13	4.80E-12
GO:0045168	Biological Process	cell-cell signaling involved in cell fate commitment	7	18	2.90E-12	2.80E-11
GO:0009057	Biological Process	macromolecule catabolic process	55	556	5.70E-12	5.50E-11
GO:0090421	Biological Process	embryonic meristem initiation	12	50	6.20E-12	5.80E-11
GO:0002239	Biological Process	response to oomycetes	24	163	1.20E-11	1.10E-10
GO:0006468	Biological Process	protein phosphorylation	128	1758	2.70E-11	2.40E-10
GO:0009404	Biological Process	toxin metabolic process	17	96	4.00E-11	3.60E-10
GO:0007267	Biological Process	cell-cell signaling	7	20	6.40E-11	5.60E-10
GO:0030656	Biological Process	regulation of vitamin metabolic process	8	26	8.40E-11	7.20E-10
GO:0016310	Biological Process	phosphorylation	134	1912	2.00E-10	1.70E-09
GO:0010014	Biological Process	meristem initiation	12	56	2.40E-10	2.00E-09
GO:0002229	Biological Process	defense response to oomycetes	22	156	4.50E-10	3.70E-09
GO:1902456	Biological Process	regulation of stomatal opening	11	50	7.40E-10	5.90E-09
GO:0000288	Biological Process	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	6	17	2.00E-09	1.60E-08

GO:0006561	Biological Process	proline biosynthetic process	6	17	2.00E-09	1.60E-08
GO:0010726	Biological Process	positive regulation of hydrogen peroxide metabolic process	7	23	2.40E-09	1.80E-08
GO:0015074	Biological Process	DNA integration	8	30	3.70E-09	2.80E-08
GO:1990069	Biological Process	stomatal opening	11	54	6.10E-09	4.50E-08
GO:0048508	Biological Process	embryonic meristem development	12	63	6.80E-09	5.00E-08
GO:1901136	Biological Process	carbohydrate derivative catabolic process	18	124	8.50E-09	6.10E-08
GO:0042430	Biological Process	indole-containing compound metabolic process	22	171	1.00E-08	7.30E-08
GO:0009856	Biological Process	pollination	51	587	1.70E-08	1.20E-07
GO:0044706	Biological Process	multi-multicellular organism process	51	587	1.70E-08	1.20E-07
GO:1901575	Biological Process	organic substance catabolic process	82	1104	2.00E-08	1.30E-07
GO:0045087	Biological Process	innate immune response	64	814	4.80E-08	3.20E-07
GO:0006955	Biological Process	immune response	64	825	8.90E-08	5.90E-07
GO:0042631	Biological Process	cellular response to water deprivation	16	113	1.20E-07	8.00E-07
GO:0071462	Biological Process	cellular response to water stimulus	16	114	1.50E-07	9.90E-07
GO:0006002	Biological Process	fructose 6-phosphate metabolic process	6	21	1.80E-07	1.10E-06
GO:0034308	Biological Process	primary alcohol metabolic process	8	37	3.80E-07	2.40E-06
GO:0010115	Biological Process	regulation of abscisic acid biosynthetic process	6	22	4.30E-07	2.60E-06
GO:0042446	Biological Process	hormone biosynthetic process	16	120	5.60E-07	3.40E-06
GO:2000379	Biological Process	positive regulation of reactive oxygen species metabolic process	7	30	6.80E-07	4.00E-06
GO:0051262	Biological Process	protein tetramerization	7	30	6.80E-07	4.00E-06
GO:0044265	Biological Process	cellular macromolecule catabolic process	37	417	7.70E-07	4.50E-06
GO:0006575	Biological Process	cellular modified amino acid metabolic process	13	90	1.50E-06	8.70E-06
GO:0006952	Biological Process	defense response	118	1885	1.60E-06	9.30E-06

GO:0002376	Biological Process	immune system process	64	884	1.80E-06	1.00E-05
GO:0009056	Biological Process	catabolic process	84	1249	2.00E-06	1.10E-05
GO:0090305	Biological Process	nucleic acid phosphodiester bond hydrolysis	12	84	5.20E-06	2.90E-05
GO:0046700	Biological Process	heterocycle catabolic process	21	207	1.30E-05	7.40E-05
GO:0044270	Biological Process	cellular nitrogen compound catabolic process	21	210	1.90E-05	0.0001
GO:2000030	Biological Process	regulation of response to red or far red light	13	103	2.20E-05	0.00012
GO:0044703	Biological Process	multi-organism reproductive process	54	763	2.40E-05	0.00013
GO:0010565	Biological Process	regulation of cellular ketone metabolic process	17	158	3.20E-05	0.00017
GO:0009688	Biological Process	abscisic acid biosynthetic process	6	29	3.50E-05	0.00018
GO:0009816	Biological Process	defense response to bacterium, incompatible interaction	17	159	3.70E-05	0.00019
GO:0007154	Biological Process	cell communication	127	2189	3.80E-05	0.00019
GO:0009636	Biological Process	response to toxic substance	14	120	4.50E-05	0.00022
GO:0051704	Biological Process	multi-organism process	153	2727	4.50E-05	0.00022
GO:0019853	Biological Process	L-ascorbic acid biosynthetic process	8	49	4.80E-05	0.00023
GO:0019852	Biological Process	L-ascorbic acid metabolic process	8	49	4.80E-05	0.00023
GO:0043207	Biological Process	response to external biotic stimulus	115	1964	5.40E-05	0.00026
GO:0051707	Biological Process	response to other organism	115	1964	5.40E-05	0.00026
GO:0006796	Biological Process	phosphate-containing compound metabolic process	138	2444	7.20E-05	0.00034
GO:0006560	Biological Process	proline metabolic process	6	31	8.40E-05	0.00039
GO:0006793	Biological Process	phosphorus metabolic process	138	2470	0.00012	0.00055
GO:0009607	Biological Process	response to biotic stimulus	115	2003	0.00013	0.00059
GO:0042742	Biological Process	defense response to bacterium	55	852	0.00036	0.0016

GO:0009409	Biological Process	response to cold	48	724	0.00043	0.0019
GO:0009266	Biological Process	response to temperature stimulus	63	1026	0.00065	0.0029
GO:0043622	Biological Process	cortical microtubule organization	7	48	0.00067	0.0029
GO:0010187	Biological Process	negative regulation of seed germination	7	49	0.00084	0.0037
GO:0009084	Biological Process	glutamine family amino acid biosynthetic process	6	38	0.00089	0.0039
GO:0031122	Biological Process	cytoplasmic microtubule organization	7	50	0.0011	0.0045
GO:0030865	Biological Process	cortical cytoskeleton organization	7	51	0.0013	0.0055
GO:0009620	Biological Process	response to fungus	50	799	0.0015	0.0063
GO:0006464	Biological Process	cellular protein modification process	136	2581	0.0015	0.0064
GO:0036211	Biological Process	protein modification process	136	2581	0.0015	0.0064
GO:0010310	Biological Process	regulation of hydrogen peroxide metabolic process	7	52	0.0016	0.0066
GO:0042445	Biological Process	hormone metabolic process	16	185	0.0021	0.0087
GO:0006576	Biological Process	cellular biogenic amine metabolic process	8	67	0.0024	0.0096
GO:0009759	Biological Process	indole glucosinolate biosynthetic process	6	42	0.0024	0.0096
GO:0016144	Biological Process	S-glycoside biosynthetic process	6	42	0.0024	0.0096
GO:0051260	Biological Process	protein homooligomerization	7	55	0.0028	0.011
GO:0009933	Biological Process	meristem structural organization	12	126	0.003	0.012
GO:0009605	Biological Process	response to external stimulus	130	2499	0.003	0.012
GO:0006414	Biological Process	translational elongation	5	33	0.0044	0.017
GO:0009617	Biological Process	response to bacterium	57	986	0.0053	0.02
GO:0042180	Biological Process	cellular ketone metabolic process	17	215	0.0054	0.02
GO:0044248	Biological Process	cellular catabolic process	60	1052	0.0058	0.022
GO:0009687	Biological Process	abscisic acid metabolic process	6	47	0.0065	0.024
GO:0008219	Biological Process	cell death	28	424	0.0082	0.03
GO:0010091	Biological Process	trichome branching	7	62	0.0084	0.031

GO:0043531	Molecular Function	ADP binding	106	284	3.10E-163	5.10E-161
GO:0008843	Molecular Function	endochitinase activity	18	27	2.90E-58	1.60E-56
GO:0035885	Molecular Function	exochitinase activity	18	27	2.90E-58	1.60E-56
GO:0017096	Molecular Function	acetylserotonin O-methyltransferase activity	22	43	4.70E-53	1.90E-51
GO:0008171	Molecular Function	O-methyltransferase activity	38	124	3.50E-49	1.10E-47
GO:0047763	Molecular Function	caffeate O-methyltransferase activity	16	29	5.50E-42	1.50E-40
GO:0030145	Molecular Function	manganese ion binding	34	120	4.70E-40	1.10E-38
GO:0004523	Molecular Function	RNA-DNA hybrid ribonuclease activity	13	23	6.20E-35	1.30E-33
GO:0045735	Molecular Function	nutrient reservoir activity	34	137	9.60E-34	1.70E-32
GO:0032559	Molecular Function	adenyl ribonucleotide binding	252	3068	9.80E-27	1.60E-25
GO:0030554	Molecular Function	adenyl nucleotide binding	252	3070	1.10E-26	1.60E-25
GO:0008569	Molecular Function	ATP-dependent microtubule motor activity, minus-end-directed	7	9	1.00E-25	1.40E-24
GO:0097367	Molecular Function	carbohydrate derivative binding	270	3463	2.40E-24	3.00E-23
GO:0047501	Molecular Function	(+)-neomenthol dehydrogenase activity	6	7	5.00E-24	5.10E-23
GO:0047504	Molecular Function	(-)-menthol dehydrogenase activity	6	7	5.00E-24	5.10E-23
GO:0010301	Molecular Function	xanthoxin dehydrogenase activity	6	7	5.00E-24	5.10E-23
GO:0070009	Molecular Function	serine-type aminopeptidase activity	7	10	5.10E-23	4.90E-22
GO:0050162	Molecular Function	oxalate oxidase activity	14	40	7.30E-22	6.60E-21
GO:0001883	Molecular Function	purine nucleoside binding	252	3336	4.10E-21	3.20E-20
GO:0032555	Molecular Function	purine ribonucleotide binding	252	3336	4.10E-21	3.20E-20
GO:0032550	Molecular Function	purine ribonucleoside binding	252	3336	4.10E-21	3.20E-20
GO:0017076	Molecular Function	purine nucleotide binding	252	3338	4.50E-21	3.30E-20
GO:0032549	Molecular Function	ribonucleoside binding	252	3345	6.10E-21	4.30E-20
GO:0001882	Molecular Function	nucleoside binding	252	3347	6.60E-21	4.50E-20
GO:1990939	Molecular Function	ATP-dependent microtubule motor activity	7	11	8.00E-21	5.20E-20

GO:0032553	Molecular Function	ribonucleotide binding	252	3357	1.00E-20	6.40E-20
GO:1900750	Molecular Function	oligopeptide binding	15	48	1.80E-20	1.10E-19
GO:0043295	Molecular Function	glutathione binding	15	48	1.80E-20	1.10E-19
GO:0004568	Molecular Function	chitinase activity	18	67	2.60E-20	1.50E-19
GO:0072341	Molecular Function	modified amino acid binding	15	53	3.80E-18	2.10E-17
GO:0008061	Molecular Function	chitin binding	18	74	6.60E-18	3.50E-17
GO:1901681	Molecular Function	sulfur compound binding	15	56	5.80E-17	3.00E-16
GO:0030246	Molecular Function	carbohydrate binding	50	416	5.00E-16	2.40E-15
GO:0000166	Molecular Function	nucleotide binding	252	3676	1.50E-15	7.00E-15
GO:1901265	Molecular Function	nucleoside phosphate binding	252	3676	1.50E-15	7.00E-15
GO:0004364	Molecular Function	glutathione transferase activity	15	60	1.50E-15	7.00E-15
GO:0016623	Molecular Function	oxidoreductase activity, acting on the aldehyde or oxo group of donors, oxygen as acceptor	14	55	6.80E-15	3.00E-14
GO:0036094	Molecular Function	small molecule binding	252	3736	1.00E-14	4.50E-14
GO:0004252	Molecular Function	serine-type endopeptidase activity	24	143	3.70E-14	1.50E-13
GO:0016891	Molecular Function	endoribonuclease activity, producing 5'-phosphomonoesters	13	54	6.10E-13	2.50E-12
GO:1901363	Molecular Function	heterocyclic compound binding	437	7386	1.10E-12	4.50E-12
GO:0097159	Molecular Function	organic cyclic compound binding	437	7406	1.60E-12	6.30E-12
GO:0004022	Molecular Function	alcohol dehydrogenase (NAD) activity	7	18	2.90E-12	1.10E-11
GO:0016893	Molecular Function	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	13	58	8.00E-12	3.00E-11
GO:0004672	Molecular Function	protein kinase activity	128	1737	1.00E-11	3.80E-11
GO:0008168	Molecular Function	methyltransferase activity	40	358	1.60E-11	5.60E-11
GO:0042277	Molecular Function	peptide binding	15	80	1.00E-10	3.60E-10

GO:0016773	Molecular Function	phosphotransferase activity, alcohol group as acceptor	134	1904	1.40E-10	4.90E-10
GO:0016741	Molecular Function	transferase activity, transferring one-carbon groups	40	376	1.60E-10	5.40E-10
GO:0002020	Molecular Function	protease binding	7	21	2.40E-10	7.80E-10
GO:0008757	Molecular Function	S-adenosylmethionine-dependent methyltransferase activity	22	157	5.70E-10	1.80E-09
GO:0004674	Molecular Function	protein serine/threonine kinase activity	50	538	1.10E-09	3.40E-09
GO:0046914	Molecular Function	transition metal ion binding	125	1801	1.40E-09	4.20E-09
GO:0016301	Molecular Function	kinase activity	134	1981	2.60E-09	7.70E-09
GO:0005488	Molecular Function	binding	728	14031	2.20E-08	6.40E-08
GO:0033218	Molecular Function	amide binding	15	97	3.40E-08	9.80E-08
GO:0004521	Molecular Function	endoribonuclease activity	13	77	3.80E-08	1.10E-07
GO:0003872	Molecular Function	6-phosphofructokinase activity	6	21	1.80E-07	5.00E-07
GO:0008106	Molecular Function	alcohol dehydrogenase (NADP+) activity	6	21	1.80E-07	5.00E-07
GO:0019899	Molecular Function	enzyme binding	31	318	3.70E-07	1.00E-06
GO:0004033	Molecular Function	aldo-keto reductase (NADP) activity	6	22	4.30E-07	1.10E-06
GO:0008443	Molecular Function	phosphofructokinase activity	6	22	4.30E-07	1.10E-06
GO:0017171	Molecular Function	serine hydrolase activity	24	221	4.70E-07	1.20E-06
GO:0008236	Molecular Function	serine-type peptidase activity	24	221	4.70E-07	1.20E-06
GO:0016765	Molecular Function	transferase activity, transferring alkyl or aryl (other than methyl) groups	18	144	5.50E-07	1.40E-06
GO:0046983	Molecular Function	protein dimerization activity	60	817	2.10E-06	5.20E-06
GO:0016772	Molecular Function	transferase activity, transferring phosphorus-containing groups	134	2214	2.60E-06	6.40E-06
GO:0016903	Molecular Function	oxidoreductase activity, acting on the aldehyde or oxo group of donors	14	107	4.80E-06	1.20E-05
GO:0004518	Molecular Function	nuclease activity	21	199	5.30E-06	1.30E-05

GO:0004519	Molecular Function	endonuclease activity	14	110	8.50E-06	2.00E-05
GO:0004867	Molecular Function	serine-type endopeptidase inhibitor activity	6	27	1.20E-05	2.80E-05
GO:0009055	Molecular Function	electron carrier activity	19	178	1.20E-05	2.80E-05
GO:0051015	Molecular Function	actin filament binding	8	45	1.30E-05	2.90E-05
GO:0016740	Molecular Function	transferase activity	227	4233	2.80E-05	6.10E-05
GO:0004177	Molecular Function	aminopeptidase activity	7	39	4.80E-05	0.0001
GO:0061135	Molecular Function	endopeptidase regulator activity	7	39	4.80E-05	0.0001
GO:0004866	Molecular Function	endopeptidase inhibitor activity	7	39	4.80E-05	0.0001
GO:0008408	Molecular Function	3'-5' exonuclease activity	7	39	4.80E-05	0.0001
GO:0004540	Molecular Function	ribonuclease activity	13	110	7.30E-05	0.00015
GO:0061134	Molecular Function	peptidase regulator activity	7	41	9.60E-05	0.00019
GO:0030414	Molecular Function	peptidase inhibitor activity	7	41	9.60E-05	0.00019
GO:0005524	Molecular Function	ATP binding	153	2795	0.00015	0.0003
GO:0030247	Molecular Function	polysaccharide binding	15	153	0.00049	0.00095
GO:0001871	Molecular Function	pattern binding	15	153	0.00049	0.00095
GO:0031625	Molecular Function	ubiquitin protein ligase binding	6	37	0.00067	0.0013
GO:0044389	Molecular Function	ubiquitin-like protein ligase binding	6	37	0.00067	0.0013
GO:0008270	Molecular Function	zinc ion binding	56	895	0.00078	0.0015
GO:0004527	Molecular Function	exonuclease activity	8	65	0.0017	0.0032
GO:0003746	Molecular Function	translation elongation factor activity	5	30	0.0019	0.0035
GO:0046872	Molecular Function	metal ion binding	137	2621	0.002	0.0036
GO:0004175	Molecular Function	endopeptidase activity	25	338	0.0021	0.0038
GO:0043169	Molecular Function	cation binding	137	2672	0.0041	0.0072
GO:0003690	Molecular Function	double-stranded DNA binding	22	300	0.0047	0.0082
GO:0032403	Molecular Function	protein complex binding	8	74	0.0065	0.011
GO:0035639	Molecular Function	purine ribonucleoside triphosphate binding	153	3063	0.0067	0.012
GO:0070008	Molecular Function	serine-type exopeptidase activity	7	62	0.0084	0.014

GO:0003779	Molecular Function	actin binding	8	77	0.0093	0.016
GO:0019200	Molecular Function	carbohydrate kinase activity	6	50	0.011	0.018
GO:0004553	Molecular Function	hydrolase activity, hydrolyzing O-glycosyl compounds	32	524	0.017	0.028
GO:0005506	Molecular Function	iron ion binding	28	446	0.018	0.029
GO:0003676	Molecular Function	nucleic acid binding	171	3560	0.018	0.029
GO:0005515	Molecular Function	protein binding	343	7503	0.019	0.031
GO:0043167	Molecular Function	ion binding	137	2819	0.023	0.036
GO:0072686	Cellular Component	mitotic spindle	7	13	1.90E-17	1.90E-15
GO:0031012	Cellular Component	extracellular matrix	14	59	1.20E-13	5.80E-12
GO:0044421	Cellular Component	extracellular region part	14	85	2.00E-08	5.50E-07
GO:0000932	Cellular Component	cytoplasmic mRNA processing body	12	66	2.30E-08	5.50E-07
GO:0035770	Cellular Component	ribonucleoprotein granule	12	69	7.00E-08	1.10E-06
GO:0036464	Cellular Component	cytoplasmic ribonucleoprotein granule	12	69	7.00E-08	1.10E-06
GO:0055028	Cellular Component	cortical microtubule	7	46	0.00041	0.0056
GO:0005881	Cellular Component	cytoplasmic microtubule	7	47	0.00053	0.0063
GO:0030981	Cellular Component	cortical microtubule cytoskeleton	7	48	0.00067	0.0071
GO:0030863	Cellular Component	cortical cytoskeleton	7	49	0.00084	0.0081

APPENDIX C

Table S3.1 Comparison of three different annotation tools in terms of protein-coding gene content

cpGAVAS				**Dogma**				**GeSeq**			
Genes	**Start**	**End**	**Strand**	**Genes**	**Start**	**End**	**Strand**	**Genes**	**Start**	**End**	**Strand**
accD	61672	63231	+	*accD*	61672	63207	+	*accD*	61709	63205	+
atpA	11893	13416	-	*atpA*	11899	13416	-	*atpA*	11891	13417	-
atpB	57234	58735	-	*atpB*	57266	58735	-	*atpB*	57234	58735	-
atpE	56839	57237	-	*atpE*	56842	57237	-	*atpE*	56841	57237	-
atpF	13485	14789	-	*atpF*	13488	13955	-	*atpF*	13486	13895	-
				atpF	14631	14789	-	*atpF*	14645	14789	-
atpH	15314	15559	-	*atpH*	15317	15559	-	*atpH*	15314	15559	-
atpI	16779	17525	-	*atpI*	16782	17525	-	*atpI*	16780	17525	-
ccsA	121141	122097	+	*ccsA*	121141	122094	+	*ccsA*	121141	122088	+
cemA	65565	66254	+	*cemA*	65565	66251	+	*cemA*	65506	66254	+
clpP	76125	78145	-	*clpP*	76128	76352	-	*clpP*	76966	77264	-
				clpP	76966	77259	-	*clpP*	76125	76352	-
				clpP	78077	78145	-	*clpP*	78074	78145	-
infA	85877	86110	-	*infA*	85880	86110	-	*infA*	85878	86106	-
matK	2172	3686	-	*matK*	2175	3686	-	*matK*	2172	3686	-
ndhA	126653	128887	-	*ndhA*	126656	127192	-	*ndhA*	126654	127193	-
				ndhA	128336	128887	-	*ndhA*	128320	128887	-
ndhB	100825	103049	-	*ndhB*	100828	101586	-	*ndhB*	100826	101586	-
ndhB	148816	151040	+	*ndhB*	102273	103049	-	*ndhB*	102272	103049	-
				ndhB	148816	149592	+	*ndhB*	148816	149593	+
				ndhB	150279	151037	+	*ndhB*	150279	151039	+

								ndhB	117887	118194	-
ndhC	54736	55098	-	*ndhC*	54739	55098	-	*ndhC*	54737	55098	-
ndhD	122428	123921	-	*ndhD*	122425	123924	-	*ndhD*	122425	123924	-
								ndhD	117870	118170	-
ndhE	124586	124891	-	*ndhE*	124589	124891	-	*ndhE*	124587	124891	-
ndhF	116655	118883	-	*ndhF*	116658	118883	-	*ndhF*	116659	118883	-
								ndhF	122910	123269	-
ndhG	125123	125653	-	*ndhG*	125126	125653	-	*ndhG*	125121	125653	-
ndhH	128889	130070	-	*ndhH*	128892	130070	-	*ndhH*	128889	130069	-
ndhI	126079	126570	-	*ndhI*	126076	126570	-	*ndhI*	126075	126570	-
ndhJ	53367	53843	-	*ndhJ*	53370	53843	-	*ndhJ*	53368	53842	-
ndhK	53998	54856	-	*ndhK*	54001	54714	-	*ndhK*	53999	54677	-
ndhK	53998	54678	-	*ndhK*	54692	54856	-				
								pbf1	80504	80635	-
petA	66468	67434	+	*petA*	66468	67139	+	*petA*	66468	67434	+
				petA	67114	67431	+				
petB	81835	82538	+	*petB*	81885	82535	+	*petB*	81895	82537	+
petD	83326	83871	+	*petD*	83326	83868	+	*petD*	83375	83849	+
petG	72234	72347	+	*petG*	72234	72344	+	*petG*	72234	72348	+
petL	71964	72059	+	*petL*	71964	72056	+	*petL*	71964	72059	+
petN	31354	31452	+	*petN*	31357	31449	+	*petN*	31363	31452	+
psaA	43785	46037	-	*psaA*	43788	46037	-	*psaA*	43786	46037	-
								psaA	41712	43727	-
psaB	41555	43759	-	*psaB*	41558	43759	-	*psaB*	41556	43759	-
								psaB	43815	45914	-
psaC	124066	124311	-	*psaC*	124069	124311	-	*psaC*	124066	124311	-
psaI	64061	64174	+	*psaI*	64061	64171	+	*psaI*	64061	64173	+
psaJ	73140	73274	+	*psaJ*	73140	73271	+	*psaJ*	73140	73269	+

								psb30	45897	45938	+
psbA	530	1591	-	*psbA*	533	1591	-	*psbA*	530	1591	-
								psbA	162197	163258	-
								psbA	37213	37777	+
psbB	78611	80137	+	*psbB*	78611	80131	+	*psbB*	78611	80137	+
psbC	37856	39319	+	*psbC*	37856	39316	+	*psbC*	37934	39318	+
psbD	36889	37950	+	*psbD*	36889	37947	+	*psbD*	36889	37950	+
								psbD	698	1247	-
								psbD	162365	162914	-
psbE	70641	70892	-	*psbE*	70644	70892	-	*psbE*	70641	70892	-
								psbE	26478	26593	-
psbF	68982	69101	-	*psbF*	68985	69101	-	*psbF*	68982	69101	-
psbF	70512	70631	-	*psbF*	70515	70631	-	*psbF*	70512	70631	-
psbH	80742	80972	+	*psbH*	80751	80969	+	*psbH*	80751	80972	+
psbI	9175	9330	+	*psbI*	9175	9327	+	*psbI*	9220	9330	+
psbJ	68581	68703	-	*psbJ*	68584	68703	-	*psbJ*	68582	68703	-
psbJ	70111	70233	-	*psbJ*	70114	70233	-	*psbJ*	70112	70233	-
psbK	8617	8808	+	*psbK*	8623	8805	+	*psbK*	8623	8808	+
psbL	68843	68959	-	*psbL*	68846	68959	-	*psbL*	68844	68959	-
psbL	70373	70489	-	*psbL*	70376	70489	-	*psbL*	70374	70489	-
psbM	32408	32521	-	*psbM*	32420	32521	-	*psbM*	32418	32520	-
psbN	80504	80635	-	*psbN*	80507	80635	-				
psbT	80315	80431	+	*psbT*	80315	80428	+	*psbT*	80324	80428	+
psbZ	40087	40275	+	*psbZ*	40087	40272	+	*psbZ*	40087	40275	+
rbcL	59556	60983	+	*rbcL*	59556	60980	+	*rbcL*	59556	60982	+
rpl2	90542	92054	-	*rpl2*	90545	91012	-	*rpl2*	90544	90981	-
rpl2	159811	161323	+	*rpl2*	91662	92054	-	*rpl2*	91664	92054	-
				rpl2	159811	160203	+	*rpl2*	159811	160201	+

				rpl2	160853	161320	+	*rpl2*	160884	161321	+
rpl14	86816	87184	-	*rpl14*	86819	87184	-	*rpl14*	86817	87184	-
rpl16	87328	87738	-	*rpl16*	87331	87729	-	*rpl16*	87331	87729	-
rpl20	74693	75046	-	*rpl20*	74696	75046	-	*rpl20*	74694	75046	-
rpl22	89622	90131	-	*rpl22*	89625	90131	-	*rpl22*	89757	90126	-
rpl23	92073	92354	-	*rpl23*	92076	92354	-	*rpl23*	92075	92354	-
rpl23	159511	159792	+	*rpl23*	159511	159789	+	*rpl23*	159511	159790	+
rpl32	119796	119959	-	*rpl32*	119796	119945	+	*rpl32*	119796	119937	+
rpl33	73754	73975	+	*rpl33*	73754	73972	+	*rpl33*	73754	73974	+
rpl36	85643	85756	+	*rpl36*	85646	85756	-	*rpl36*	85643	85756	-
rpoA	84019	85014	-	*rpoA*	84040	85014	-	*rpoA*	84024	85014	-
rpoB	25934	29146	-	*rpoB*	25937	29146	-	*rpoB*	25935	29146	-
rpoC1	23021	25928	-	*rpoC1*	23024	24646	-	*rpoC1*	23022	24641	-
				rpoC1	25467	25907	-	*rpoC1*	25467	25907	-
rpoC2	18671	22855	-	*rpoC2*	18674	22855	-	*rpoC2*	18674	22843	-
rps2	17746	18450	-	*rps2*	17749	18450	-	*rps2*	17748	18450	-
rps3	88981	89637	-	*rps3*	88984	89637	-	*rps3*	88984	89637	-
rps4	49624	50229	-	*rps4*	49627	50229	-	*rps4*	49625	50229	-
rps7	103369	103836	-	*rps7*	103372	103836	-	*rps7*	103370	103836	-
rps7	148029	148496	+	*rps7*	148029	148493	+	*rps7*	148029	148495	+
rps8	86237	86641	-	*rps8*	86240	86641	-	*rps8*	86237	86641	-
rps11	85084	85500	-	*rps11*	85087	85500	-	*rps11*	85085	85500	-
rps12	75840	75986	-	*rps12*	75873	75986	-	*rps12*	75872	75986	-
rps12	104447	104755	-	*rps12*	104450	104689	-	*rps12*	103892	103921	-
rps12	147110	147418	+	*rps12*	147176	147415	+	*rps12*	104456	104690	-
				rps12_3end	104438	104689	-	*rps12*	147175	147409	+
rps14	41122	41424	-	*rps14*	41125	41424	-	*rps14*	41123	41424	-
rps15	130193	130465	-	*rps15*	130196	130492	-	*rps15*	130194	130465	-

rps16	5540	5773	-	*rps16*	5570	5773	-	*rps16*	5559	5773	-
								rps16	6643	6690	-
								rps16	167226	167440	-
								rps16	168310	168357	-
rps18	74117	74474	+	*rps18*	74117	74419	+	*rps18*	74118	74418	+
rps19	90198	90476	-	*rps19*	90201	90476	-	*rps19*	90199	90476	-
				rps19	161389	161664	+	*rps19*	161389	161666	+
ycf1	131190	136511	-	*ycf1*	130791	136511	-	*ycf1*	130784	136511	-
				ycf1	115354	116562	+	*ycf1*	115354	116563	+
ycf2	93513	99503	+	*ycf2*	92682	99500	+	*ycf2*	92682	99505	+
ycf2	152362	158352	-	*ycf2*	152365	159183	-	*ycf2*	152360	159183	-
ycf3	46825	48817	-	*ycf3*	46828	46977	-	*ycf3*	46827	46982	-
				ycf3	47753	47980	-	*ycf3*	47753	47982	-
				ycf3	48692	48817	-	*ycf3*	48691	48817	-
ycf4	64588	65142	+	*ycf4*	64588	65139	+	*ycf4*	64589	65142	+
ycf15	99594	100135	+	*ycf15*	99645	99776	+				
ycf15	105501	105677	-	*ycf15*	99752	99874	+				
ycf15	146188	146364	+	*ycf15*	151991	152113	-				
ycf15	151988	152220	-	*ycf15*	152089	152220	-				
				ycf68	108683	108991	+				
				ycf68	142874	143182	-				

Table S3.2 Comparison of three different annotation tools in terms of transfer and ribosomal RNA gene content

cpGAVAS				Dogma				GeSeq			
tRNA	**Start**	**End**	**Strand**	**tRNA**	**Start**	**End**	**Strand**	**tRNA**	**Start**	**End**	**Strand**
				trnA-TGC	109564	109601	+				
				trnA-TGC	110411	110445	+				
				trnA-TGC	141420	141454	-				
				trnA-TGC	142264	142301	-				
trnC-GCA	30414	30484	+	*trnC-GCA*	30414	30493	+	*trnC-GCA*	30414	30484	+
trnD-GTC	33706	33779	-	*trnD-GTC*	33706	33779	-	*trnD-GTC*	33706	33779	-
trnE-TTC	34408	34480	-	*trnE-TTC*	34408	34480	-	*trnE-TTC*	34408	34480	-
trnF-GAA	52451	52523	+	*trnF-GAA*	52451	52523	+	*trnF-GAA*	52451	52523	+
trnfM-CAT	40885	40958	-	*trnfM-CAT*	40885	40958	-				
trnG-GCC	40604	40674	+	*trnG-GCC*	40604	40674	+	*trnG-GCC*	40604	40674	+
				trnG-TCC	11207	11243	+				
trnH-GTG	17	90	-	*trnH-GTG*	17	91	-	*trnH-GTG*	17	90	-
								trnH-GTG	161684	161757	-
trnI-CAT	92520	92593	-	*trnI-CAT*	92520	92593	-				
trnI-CAT	159272	159345	+	*trnI-CAT*	159272	159345	+				
				trnI-GAT	108472	108513	+	*trnI-GAT*	108472	108559	+
				trnI-GAT	109465	109499	+	*trnI-GAT*	143306	143393	-
				trnI-GAT	142366	142400	-				
				trnI-GAT	143352	143393	-				
				trnK-TTT	4442	4478	-				
trnL-CAA	100167	100247	-	*trnL-CAA*	100167	100247	-	*trnL-CAA*	100167	100247	-
trnL-CAA	151618	151698	+	*trnL-CAA*	151618	151698	+	*trnL-CAA*	151618	151698	+
trnL-TAG	120950	121029	+	*trnL-TAG*	120950	121029	+	*trnL-TAG*	120950	121029	+
				trnL-TAA	51438	51474	+				
				trnL-TAA	52012	52061	+				

trnM-CAT	56543	56615	+	*trnM-CAT*	56544	56615	+	*trnM-CAT*	56543	56615	+
				trnM-CAT	35416	35474	+	*trnM-CAT*	40885	40958	-
								trnM-CAT	92520	92593	-
								trnM-CAT	159272	159345	+
trnN-GTT	114958	115029	-	*trnN-GTT*	114958	115029	-	*trnN-GTT*	136836	136907	+
trnN-GTT	136836	136907	+	*trnN-GTT*	136836	136907	+	*trnN-GTT*	114958	115029	-
trnP-TGG	72661	72734	-	*trnP-TGG*	72661	72734	-	*trnP-TGG*	72661	72734	-
				trnP-GGG	72663	72733	-				
trnQ-TTG	8107	8178	-	*trnQ-TTG*	8107	8178	-	*trnQ-TTG*	8107	8178	-
								trnQ-TTG	169774	169845	-
trnR-ACG	114255	114328	+	*trnR-ACG*	114255	114328	+	*trnR-ACG*	114255	114328	+
trnR-ACG	137537	137610	-	*trnR-ACG*	137537	137610	-	*trnR-ACG*	137537	137610	-
trnR-TCT	11552	11623	+	*trnR-TCT*	11552	11623	+	*trnR-TCT*	11552	11623	+
trnS-GCT	9479	9566	-	*trnS-GCT*	9479	9566	-	*trnS-GCT*	9479	9566	-
trnS-TGA	39570	39662	-	*trnS-TGA*	39570	39662	-	*trnS-TGA*	39570	39662	-
trnS-GGA	49229	49315	+	*trnS-GGA*	49229	49315	+	*trnS-GGA*	49229	49315	+
								trnS-GCT	171146	171233	-
trnT-GGT	35410	35481	+	*trnT-GGT*	35410	35481	+	*trnT-GGT*	35410	35481	+
trnT-TGT	50563	50635	-	*trnT-TGT*	50563	50635	-	*trnT-TGT*	50563	50635	-
				trnT-GGT	56549	56607	+				
trnV-GAC	106388	106459	+	*trnV-GAC*	106388	106459	+	*trnV-GAC*	106388	106459	+
trnV-GAC	145406	145477	-	*trnV-GAC*	145406	145477	-	*trnV-GAC*	145406	145477	-
				trnV-TAC	55655	55690	-				
				trnV-TAC	56332	56369	-				
trnW-CCA	72423	72496	-	*trnW-CCA*	72423	72496	-	*trnW-CCA*	72423	72496	-
trnY-GTA	34264	34347	-	*trnY-GTA*	34264	34347	-	*trnY-GTA*	34264	34347	-
rrn4.5S	113510	113780	+	*rrn4.5*	113510	113612	+	*rrn4.5*	113511	113612	+

rrn4.5S	138085	138355	-	*rrn4.5*	138253	138355	-	*rrn4.5*	138253	138354	-
rrn5S	113872	113993	+	*rrn5*	113873	113993	+	*rrn5*	113873	113993	+
rrn5S	137872	137993	-	*rrn5*	137872	137992	-	*rrn5*	137872	137992	-
rrn16S	106687	108177	-	*rrn16*	106687	108177	+	*rrn16*	106687	108177	+
rrn16S	143688	145178	+	*rrn16*	143688	145178	-	*rrn16*	143688	145178	-
rrn23S	109977	113410	-	*rrn23*	110603	113411	+	*rrn23*	110603	113411	+
rrn23S	138455	141888	+	*rrn23*	138454	141262	-	*rrn23*	138454	141262	-

Table S3.3 BLAST result of the cv Tombul chloroplast genome against Viridiplantae (best 100 hits)

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Corylus heterophylla var. sutchuenensis chloroplast, complete genome	1.07E+05	3.96E+05	100%	0	99.88%	MF996573.1
Corylus avellana chloroplast, complete genome	1.07E+05	3.94E+05	99%	0	99.84%	KX822768.2
Corylus fargesii chloroplast, complete genome	1.26E+05	3.95E+05	100%	0	99.69%	KX822767.2
Corylus chinensis chloroplast, complete genome	1.26E+05	3.95E+05	100%	0	99.69%	KX814336.2
Corylus mandshurica chloroplast, complete genome	1.26E+05	3.92E+05	99%	0	99.60%	NC_039127.1
Corylus mandshurica chloroplast, complete genome	1.26E+05	3.93E+05	99%	0	99.60%	MF375334.1
Corylus heterophylla chloroplast, complete genome	1.26E+05	3.94E+05	100%	0	99.53%	KX822769.2
Corylus ferox var. thibetica chloroplast, complete genome	1.26E+05	3.92E+05	99%	0	99.51%	NC_039128.1
Corylus ferox var. thibetica chloroplast, complete genome	1.26E+05	3.93E+05	99%	0	99.51%	MF375335.1
Corylus yunnanensis chloroplast, complete genome	93982	3.89E+05	99%	0	99.51%	NC_039129.1
Corylus yunnanensis chloroplast, complete genome	93982	3.90E+05	99%	0	99.51%	MF375336.1
Corylus wangii chloroplast, complete genome	93882	3.89E+05	99%	0	99.46%	NC_040995.1
Corylus wangii chloroplast, complete genome	93882	3.89E+05	99%	0	99.46%	MH628454.1
Carpinus putoensis chloroplast, complete genome	61658	3.76E+05	98%	0	99.31%	KX695124.1
Ostrya japonica isolate Oja15 chloroplast, complete genome	81131	3.49E+05	88%	0	99.25%	MG662143.1
Ostrya japonica isolate Oja18 chloroplast, complete genome	81131	3.49E+05	88%	0	99.25%	MG662142.1
Ostrya japonica isolate Oja26 chloroplast, complete genome	81126	3.49E+05	88%	0	99.25%	MG662137.1
Ostrya japonica chloroplast, complete genome	81109	3.40E+05	85%	0	99.24%	MG386375.1
Ostrya japonica isolate Oja01 chloroplast, complete genome	81107	3.49E+05	88%	0	99.24%	MG662148.1
Ostrya chinensis isolate Och13 chloroplast, complete genome	81091	3.49E+05	88%	0	99.23%	MG662150.1
Ostrya japonica isolate Oja02 chloroplast, complete genome	81091	3.49E+05	88%	0	99.23%	MG662147.1
Ostrya japonica isolate Oja19 chloroplast, complete genome	81091	3.49E+05	88%	0	99.23%	MG662141.1
Ostrya rehderiana isolate Ore01 chloroplast, complete genome	81091	3.49E+05	88%	0	99.23%	MG662135.1
Ostrya rehderiana isolate Ore03 chloroplast, complete genome	81091	3.49E+05	88%	0	99.23%	MG662133.1

Ostrya chinensis isolate Och02 chloroplast, complete genome	81085	3.49E+05	88%	0	99.23%	MG662154.1
Ostrya chinensis isolate Och03 chloroplast, complete genome	81085	3.49E+05	88%	0	99.23%	MG662153.1
Ostrya chinensis isolate Och12 chloroplast, complete genome	81085	3.49E+05	88%	0	99.23%	MG662151.1
Ostrya japonica isolate Oja08 chloroplast, complete genome	81085	3.49E+05	88%	0	99.23%	MG662145.1
Ostrya japonica isolate Oja20 chloroplast, complete genome	81085	3.49E+05	88%	0	99.23%	MG662140.1
Ostrya japonica isolate Oja21 chloroplast, complete genome	81085	3.49E+05	88%	0	99.23%	MG662139.1
Ostrya rehderiana isolate Ore02 chloroplast, complete genome	81085	3.49E+05	88%	0	99.23%	MG662134.1
Ostrya rehderiana isolate Ore04 chloroplast, complete genome	81085	3.49E+05	88%	0	99.23%	MG662132.1
Ostrya japonica isolate Oja06 chloroplast, complete genome	81083	3.49E+05	88%	0	99.23%	MG662146.1
Ostrya rehderiana chloroplast, complete genome	81078	3.71E+05	96%	0	99.23%	KT454094.1
Ostrya japonica isolate Oja23 chloroplast, complete genome	81074	3.49E+05	88%	0	99.23%	MG662138.1
Ostrya chinensis isolate Och09 chloroplast, complete genome	81030	3.44E+05	86%	0	99.21%	MG662152.1
Ostrya chinensis isolate Och08 chloroplast, complete genome	80993	3.44E+05	86%	0	99.19%	MG662156.1
Ostrya trichocarpa isolate Otr07 chloroplast, complete genome	80923	3.49E+05	88%	0	99.18%	MG662128.1
Ostrya chinensis isolate Och14 chloroplast, complete genome	80965	3.44E+05	86%	0	99.17%	NC_039817.1
Ostrya chinensis isolate Och14 chloroplast, complete genome	80965	3.44E+05	86%	0	99.17%	MG662149.1
Ostrya japonica isolate Oja27 chloroplast, complete genome	85464	3.48E+05	88%	0	99.16%	NC_039816.1
Ostrya japonica isolate Oja27 chloroplast, complete genome	85464	3.48E+05	88%	0	99.16%	MG662136.1
Ostrya japonica isolate Oja09 chloroplast, complete genome	85452	3.48E+05	88%	0	99.16%	MG662144.1
Ostrya japonica isolate Oja10 chloroplast, complete genome	85443	3.48E+05	88%	0	99.16%	MG662157.1
Ostrya trichocarpa isolate Otr04 chloroplast, complete genome	80941	3.49E+05	88%	0	99.16%	MG662129.1
Ostrya trichocarpa isolate Otr03 chloroplast, complete genome	80936	3.49E+05	88%	0	99.16%	MG662130.1
Ostrya chinensis isolate Och01 chloroplast, complete genome	80926	3.49E+05	88%	0	99.16%	MG662155.1
Carpinus betulus chloroplast, complete genome	85253	3.63E+05	92%	0	99.12%	NC_039934.1
Carpinus betulus chloroplast, complete genome	85253	3.81E+05	99%	0	99.12%	MF977767.1
Ostrya trichocarpa isolate Otr01 chloroplast, complete genome	85340	3.49E+05	88%	0	99.11%	MG662131.1
Carpinus tientaiensis chloroplast, complete genome	86756	3.75E+05	98%	0	99.01%	KY174338.1

Carpinus tientaiensis chloroplast, complete genome	86756	3.75E+05	99%	0	99.01%	KY117036.1
Carpinus caroliniana chloroplast, complete genome	84958	3.76E+05	98%	0	99.01%	NC_039935.1
Carpinus caroliniana chloroplast, complete genome	84958	3.78E+05	99%	0	99.01%	MF977768.1
Carpinus fangiana chloroplast, complete genome	91526	3.61E+05	92%	0	99.00%	MG386371.1
Carpinus cordata chloroplast, complete genome	92414	3.77E+05	98%	0	98.99%	MF977769.1
Carpinus fargesiana chloroplast, complete genome	91445	3.67E+05	95%	0	98.99%	NC_039937.1
Carpinus fargesiana chloroplast, complete genome	91445	3.80E+05	99%	0	98.99%	MF977771.1
Carpinus fangiana chloroplast, complete genome	92374	3.79E+05	99%	0	98.97%	NC_039936.1
Carpinus fangiana chloroplast, complete genome	92374	3.80E+05	99%	0	98.97%	MF977770.1
Carpinus cordata chloroplast, complete genome	91491	3.79E+05	99%	0	98.97%	KY312849.1
Ostrya trichocarpa chloroplast, complete genome	84963	3.71E+05	97%	0	98.97%	KY088271.1
Carpinus oblongifolia chloroplast, complete genome	92202	3.78E+05	98%	0	98.92%	NC_038092.1
Carpinus oblongifolia chloroplast, complete genome	92202	3.77E+05	98%	0	98.92%	MG720817.1
Carpinus tschonoskii chloroplast, complete genome	92189	3.68E+05	95%	0	98.92%	NC_039938.1
Carpinus tschonoskii chloroplast, complete genome	92189	3.79E+05	99%	0	98.92%	MF977772.1
Ostrya trichocarpa isolate Otr08 chloroplast, complete genome	71278	3.55E+05	91%	0	98.92%	MG662127.1
Carpinus polyneura chloroplast, complete genome	92195	3.68E+05	95%	0	98.91%	NC_039998.1
Carpinus polyneura chloroplast, complete genome	92195	3.68E+05	95%	0	98.91%	MG386373.1
Ostrya trichocarpa isolate Otr12 chloroplast, complete genome	71267	3.55E+05	91%	0	98.91%	MG662125.1
Ostrya trichocarpa isolate Otr11 chloroplast, complete genome	71263	3.55E+05	91%	0	98.91%	MG662126.1
Carpinus monbeigiana chloroplast, complete genome	92124	3.67E+05	95%	0	98.89%	NC_039997.1
Carpinus monbeigiana chloroplast, complete genome	92124	3.61E+05	92%	0	98.89%	MG386372.1
Carpinus rupestris chloroplast, complete genome	92078	3.66E+05	94%	0	98.87%	NC_039999.1
Carpinus rupestris chloroplast, complete genome	92078	3.53E+05	89%	0	98.87%	MG386374.1
Carpinus purpurinervis chloroplast, complete genome	91901	3.77E+05	98%	0	98.80%	NC_038093.1
Carpinus purpurinervis chloroplast, complete genome	91901	3.77E+05	98%	0	98.80%	MG720818.1
Carpinus viminea chloroplast, complete genome	91899	3.66E+05	94%	0	98.80%	NC_039939.1

Carpinus viminea chloroplast, complete genome	91899	3.77E+05	98%	0	98.80%	MF977773.1
Carpinus hebestroma chloroplast, complete genome	53168	3.78E+05	98%	0	98.77%	NC_038131.1
Carpinus hebestroma chloroplast, complete genome	53168	3.77E+05	98%	0	98.77%	MG720819.1
Alnus nitida isolate 1998-654 (K) chloroplast, complete genome	57269	3.58E+05	99%	0	98.40%	MF136513.1
Alnus glutinosa chloroplast, complete genome	52503	3.11E+05	79%	0	98.37%	NC_039930.1
Ostryopsis davidiana chloroplast, complete genome	81288	3.78E+05	98%	0	98.05%	MH628451.1
Ostryopsis davidiana chloroplast, complete genome	81207	3.81E+05	99%	0	98.03%	NC_039130.1
Ostryopsis davidiana chloroplast, complete genome	81207	3.82E+05	99%	0	98.03%	MF375337.1
Ostryopsis davidiana chloroplast, complete genome	81166	3.71E+05	96%	0	97.99%	MG386376.1
Alnus jorullensis subsp. jorullensis isolate 2014-40 (K) chloroplast, complete genome	62560	3.59E+05	99%	0	97.99%	MF136508.1
Alnus rubra chloroplast, complete genome	62550	3.59E+05	99%	0	97.99%	MG356709.1
Alnus rubra isolate 1979-786 (K) chloroplast, complete genome	62550	3.59E+05	99%	0	97.99%	MF136515.1
Ostryopsis intermedia chloroplast, complete genome	76179	3.77E+05	98%	0	97.97%	NC_040000.1
Ostryopsis intermedia chloroplast, complete genome	76179	3.77E+05	98%	0	97.97%	MG386377.1
Ostryopsis nobilis chloroplast, complete genome	76112	3.71E+05	96%	0	97.95%	NC_040001.1
Ostryopsis nobilis chloroplast, complete genome	76112	3.71E+05	96%	0	97.95%	MG386378.1
Alnus japonica isolate 1999-155 (K) chloroplast, complete genome	62508	3.61E+05	99%	0	97.95%	MF136507.1
Ostrya rehderiana chloroplast, complete genome	55950	3.76E+05	98%	0	97.41%	MG584735.1
Fagus sylvatica chloroplast, complete genome	53404	2.31E+05	55%	0	96.47%	NC_041437.1
Fagus sylvatica chloroplast, complete genome	53404	2.31E+05	55%	0	96.47%	MK598696.1
Fagus crenata chloroplast, complete genome	53372	2.31E+05	55%	0	96.44%	NC_041252.1
Fagus crenata chloroplast, complete genome	53372	2.68E+05	72%	0	96.44%	MH171101.1

Table S3.4 Simple sequence repeats within the cv Tombul chloroplast genome

No	SSR type	Size	Region	Start	End
1	(GAAA)3	12	LSC	361	372
2	(AAT)4	12	LSC	3061	3072
3	(T)10	10	LSC	4236	4245
4	(T)10	10	LSC	4712	4721
5	(A)11	11	LSC	5221	5231
6	(C)11	11	LSC	5507	5517
7	(T)11	11	LSC	7498	7508
8	(T)10	10	LSC	7734	7743
9	(A)12	12	LSC	8015	8026
10	(A)12	12	LSC	8491	8502
11	(TCTT)3	12	LSC	9627	9638
12	(TA)7	14	LSC	9827	9840
13	(A)10	10	LSC	10653	10662
14	(AT)6	12	LSC	11275	11286
15	(GTCT)3	12	LSC	12896	12907
16	(A)10	10	LSC	13455	13464
17	(T)10	10	LSC	14022	14031
18	(T)11	11	LSC	14162	14172
19	(T)11	11	LSC	18473	18483
20	(A)12	12	LSC	18633	18644
21	(T)10	10	LSC	20573	20582
22	(T)11	11	LSC	20701	20711
23	(T)12	12	LSC	21239	21250
24	(AT)5	10	LSC	22080	22089

25	(T)10	10	LSC	28501	28510
26-27	(C)14(A)12*	26	LSC	30355	30380
28	(G)13	13	LSC	30562	30574
29	(T)11	11	LSC	31681	31691
30	(AATA)3	12	LSC	33583	33594
31	(AT)5	10	LSC	35341	35350
32	(TAT)4	12	LSC	35687	35698
33	(TCTA)3	12	LSC	39775	39786
34	(A)12	12	LSC	40536	40547
35	(A)10	10	LSC	40810	40819
36	(A)10	10	LSC	46508	46517
37	(T)10	10	LSC	52331	52340
38	(AT)5	10	LSC	55283	55292
39	(T)11	11	LSC	55574	55584
40	(T)10	10	LSC	58680	58689
41	(T)10	10	LSC	59165	59174
42	(AACAGA)3	18	LSC	62346	62363
43	(AT)5	10	LSC	63730	63739
44	(T)11	11	LSC	65168	65178
45	(TC)5	10	LSC	65632	65641
46-47	(AT)5tattggtatattgtgattgtgtcctccagaaaaaacaaggggggggtcgagtga(TTCT)3	76	LSC	68217	68292
48-49	(AT)5tattggtatattgtgattgtgtcctccagaaaaaacaaggggggggtcgagtga(TTCT)3	76	LSC	69747	69822
50	(T)11	11	LSC	72990	73000
51	(TA)8	16	LSC	74035	74050
52	(TTTA)3	12	LSC	76645	76656
53	(A)13	13	LSC	76844	76856
54	(A)10	10	LSC	78274	78283

55	(TA)5	10	LSC	86701	86710
56	(A)10	10	LSC	87228	87237
57	(TA)6	12	IRB	91109	91120
58	(GCAAT)3	15	IRB	105664	105678
59	(AGGT)3	12	IRB	112256	112267
60	(AG)5	10	IRB	114151	114160
61	(ATT)4	12	SSC	117369	117380
62-63	(AAAT)3aaaaatcttttatttttaattaactgtttctgattcaccagctctta(T)11gaaaggaatcagttaataaaaaaattaaaatatataaaact(A)10	121	SSC	118886	119006
64	(A)10	10	SSC	119529	119538
65	(A)11	11	SSC	120076	120086
66-67	(TATT)3atatttatata(AT)5	33	SSC	120291	120323
68	(AT)5	10	SSC	120456	120465
69	(A)12	12	SSC	120580	120591
70	(C)11	11	SSC	121101	121111
71	(AT)5	10	SSC	122136	122145
72	(TTGA)3	12	SSC	124603	124614
73	(T)10	10	SSC	126075	126084
74	(TTC)4	12	SSC	128068	128079
75	(AT)7	14	SSC	130508	130521
76	(T)11	11	SSC	131628	131638
77	(T)10	10	SSC	133593	133602
78	(A)10	10	SSC	134962	134971
79	(CT)5	10	IRA	137705	137714
80	(CTAC)3	12	IRA	139596	139607
81	(CATTG)3	15	IRA	146186	146200
82	(AT)6	12	IRA	160744	160755

Table S3.5 Comparison of two SSR identification tools for the cv Tombul chloroplast genome

IMEx-web						MISA					
No	**SSR type**	**Size**	**Region**	**Start**	**End**	**No**	**SSR type**	**Size**	**Region**	**Start**	**End**
30	(TAAA)3	12	LSC	33585	33596	30	(AATA)3	12	LSC	33583	33594
-	-	-	-	-	-	52	(TTTA)3	12	LSC	76645	76656
72	(TGAT)3	12	SSC	124604	124615	72	(TTGA)3	12	SSC	124603	124614
74	(TCT)4	12	SSC	128069	128080	74	(TTC)4	12	SSC	128068	128079

Table S3.6 Differences between cv Tombul and KX822768 cp genome published in GenBank

Differences	**Genes**
Unprocessed genes in KX822768, but found in cv Tombul	*atpF*, *clpP*
Not found in KX822768	*accD*, *psbM*, *trnI-GAT*
Found twice in cv Tombul	*psbF*, *psbJ*, *psbL*

Table S3.7 The features of Fagales and Malpighiales plastomes

Species	Size (bp)	LSC (bp)	SSC (bp)	IR (bp)	Number of protein-coding gene	Number of tRNA genes	Number of rRNA genes	GC content (%)
Corylus avellana cv Tombul	161,667	90,198	18,733	26,368	86	31	8	36.40
Corylus chinensis Franch	159,915	88,115	17,822	26,989	95	29	8	36.49
Corylus fargesii	159,856	88,313	18,339	26,602	94	29	8	36.51
Betula nana L.	160,579	89,492	19,343	25,872	86	40	8	36.10
Castanea mollissima	160,869	90,497	18,970	25,701	86	37	8	36.75
Juglans regia	160,352	89,871	18,413	26,034	80	36	8	36.10
Populus cathayana	156,789	84,851	16,594	27,672	85	37	8	36.70
Populus schneideri	156,513	84,778	16,495	27,620	85	37	8	36.70
Quercus aliena	161,150	90,444	19,054	25,826	86	40	8	36.83

APPENDIX D

Table S4.1: Functional annotation of DETs

Type	GO	Enrichment	p-value	Subset-ratio	Description
MF	GO:0000166	0.002796117	0.0139699	15.24099666	nucleotide binding
MF	GO:0001071	0.005371241	0.0484904	3.014160256	nucleic acid binding transcription factor activity
MF	GO:0003677	0.005083746	7.47063E-06	8.615290353	DNA binding
MF	GO:0003824	0.004005128	4.15E-22	43.30110967	catalytic activity
MF	GO:0004672	0.005371241	0.00012209	5.926203281	protein kinase activity
MF	GO:0005215	0.004479819	0.0175613	5.519436313	transporter activity
MF	GO:0005488	0.00273852	1.28E-18	62.61488188	binding
MF	GO:0005515	0.004508583	3.41E-21	34.07481789	protein binding
MF	GO:0005524	0.004307222	3.34762E-05	11.59370958	ATP binding
MF	GO:0015075	0.005371241	0.0445718	3.06011301	ion transmembrane transporter activity
MF	GO:0016301	0.005371241	7.00638E-06	7.355844509	kinase activity
MF	GO:0016740	0.005227501	1.23848E-14	17.67138675	transferase activity
MF	GO:0016772	0.005371241	3.76708E-07	8.679964599	transferase activity, transferring phosphorus-containing groups
MF	GO:0016773	0.005371241	1.91955E-05	6.85547008	phosphotransferase activity, alcohol group as acceptor
MF	GO:0016787	0.00345832	0.000770944	14.1704677	hydrolase activity
MF	GO:0017076	0.003386356	0.00161734	13.67179522	purine nucleotide binding
MF	GO:0022857	0.005371241	0.00213472	4.571448022	transmembrane transporter activity
MF	GO:0022891	0.005371241	0.0130069	3.679624209	substrate-specific transmembrane transporter activity
MF	GO:0022892	0.004781814	0.03451	4.237865069	substrate-specific transporter activity
MF	GO:0030554	0.004364757	1.10369E-05	12.25236572	adenyl nucleotide binding
MF	GO:0032553	0.003415142	0.00129334	13.82156716	ribonucleotide binding

MF	GO:0032555	0.003386356	0.00161309	13.65988154	purine ribonucleotide binding
MF	GO:0032559	0.004364757	1.11538E-05	12.24045204	adenyl ribonucleotide binding
MF	GO:0035639	0.003299995	0.0041198	13.01313908	purine ribonucleoside triphosphate binding
MF	GO:0036094	0.002968895	0.00315482	16.39151746	small molecule binding
MF	GO:0043167	0.003271206	7.16762E-07	25.78970658	ion binding
MF	GO:0043168	0.002968895	0.00323851	16.36939206	anion binding
MF	GO:0043169	0.004077061	0.000179979	11.44563959	cation binding
MF	GO:0043565	0.005371241	0.0299389	3.267751379	sequence-specific DNA binding
MF	GO:0046872	0.004033901	0.000337036	11.08482538	metal ion binding
MF	GO:0046914	0.00368858	0.0431588	7.282660494	transition metal ion binding
MF	GO:0046983	0.005371241	0.0266245	3.329021717	protein dimerization activity
MF	GO:0097367	0.00345832	0.000844952	14.11089931	carbohydrate derivative binding
MF	GO:1901265	0.002796117	0.0139699	15.24099666	nucleoside phosphate binding
BP	GO:0000003	0.004954354	5.69674E-08	12.09238205	reproduction
BP	GO:0001101	0.003947579	0.00109892	10.37511063	response to acid chemical
BP	GO:0003006	0.004896843	1.2644E-06	10.55721969	developmental process involved in reproduction
BP	GO:0005975	0.004407906	0.0340038	5.138198652	carbohydrate metabolic process
BP	GO:0006139	0.003314389	5.95964E-05	19.11294166	nucleobase-containing compound metabolic process
BP	GO:0006351	0.004594872	5.78011E-05	9.542855198	transcription, DNA-templated
BP	GO:0006355	0.004508583	0.000393076	8.523384846	regulation of transcription, DNA-templated
BP	GO:0006464	0.005371241	2.39696E-09	10.96058275	cellular protein modification process
BP	GO:0006468	0.005371241	9.43333E-05	6.04534005	protein phosphorylation
BP	GO:0006508	0.005371241	0.0048657	4.1629791	proteolysis
BP	GO:0006629	0.004393523	0.0374229	5.07522636	lipid metabolic process
BP	GO:0006725	0.003616628	3.27818E-07	22.36877936	cellular aromatic compound metabolic process
BP	GO:0006793	0.005126874	2.82361E-07	10.16066444	phosphorus metabolic process
BP	GO:0006796	0.005112498	5.23609E-07	9.869630336	phosphate-containing compound metabolic process

BP	GO:0006807	0.003026483	1.94822E-10	39.85124923	nitrogen compound metabolic process
BP	GO:0006950	0.004235301	2.91642E-10	21.71012322	response to stress
BP	GO:0006952	0.003515888	0.0447665	7.953230308	defense response
BP	GO:0006970	0.00456611	0.00628168	6.096398666	response to osmotic stress
BP	GO:0006979	0.005371241	0.00630836	4.026822793	response to oxidative stress
BP	GO:0006996	0.00506937	1.98496E-05	8.097896385	organelle organization
BP	GO:0007154	0.005371241	1.08785E-07	9.248417183	cell communication
BP	GO:0007165	0.005371241	1.20208E-05	7.071618218	signal transduction
BP	GO:0007275	0.004810572	3.23135E-11	17.62373204	multicellular organism development
BP	GO:0008152	0.002896907	1.34E-16	55.76621962	metabolic process
BP	GO:0009056	0.003890027	0.0363909	6.673361018	catabolic process
BP	GO:0009058	0.001903102	0.0453321	24.75151474	biosynthetic process
BP	GO:0009266	0.004939977	0.00241135	5.660698482	response to temperature stimulus
BP	GO:0009314	0.005371241	2.79866E-05	6.637619988	response to radiation
BP	GO:0009409	0.005371241	0.0075176	3.9417251	response to cold
BP	GO:0009414	0.005371241	0.0162129	3.572401116	response to water deprivation
BP	GO:0009415	0.005371241	0.0154476	3.59622847	response to water
BP	GO:0009416	0.005371241	3.39946E-05	6.535502757	response to light stimulus
BP	GO:0009605	0.003789307	0.00161407	10.87888896	response to external stimulus
BP	GO:0009617	0.005371241	0.00160859	4.711008237	response to bacterium
BP	GO:0009628	0.004925599	2.01964E-11	16.82381374	response to abiotic stimulus
BP	GO:0009651	0.004465437	0.0208341	5.429232759	response to salt stress
BP	GO:0009653	0.004997486	0.000388152	6.583157465	anatomical structure morphogenesis
BP	GO:0009719	0.00414899	5.75022E-05	12.11110355	response to endogenous stimulus
BP	GO:0009725	0.00414899	5.83331E-05	12.07706447	response to hormone
BP	GO:0009755	0.005371241	0.00523861	4.122132208	hormone-mediated signaling pathway
BP	GO:0009791	0.004939977	1.63592E-07	11.55286269	post-embryonic development

BP	GO:0009888	0.005371241	0.00135426	4.789298114	tissue development
BP	GO:0009889	0.003976353	0.000766136	10.60657635	regulation of biosynthetic process
BP	GO:0009908	0.005371241	0.0175496	3.534958132	flower development
BP	GO:0009987	0.002637719	2.00686E-14	57.49540472	cellular process
BP	GO:0010033	0.004206531	1.85922E-06	14.8376336	response to organic substance
BP	GO:0010035	0.004005128	0.00279984	9.03907686	response to inorganic substance
BP	GO:0010154	0.004451054	0.0220718	5.388385867	fruit development
BP	GO:0010468	0.003976353	0.000850125	10.53679624	regulation of gene expression
BP	GO:0010556	0.004350373	0.00024467	9.655184151	regulation of macromolecule biosynthetic process
BP	GO:0016049	0.005371241	0.0359054	3.175845871	cell growth
BP	GO:0016070	0.004192146	2.6009E-06	14.66403431	RNA metabolic process
BP	GO:0016310	0.005371241	2.28113E-05	6.755054803	phosphorylation
BP	GO:0018130	0.004580491	1.2818E-06	12.50595684	heterocycle biosynthetic process
BP	GO:0019219	0.004580491	7.57159E-05	9.391381306	regulation of nucleobase-containing compound metabolic process
BP	GO:0019222	0.004321606	1.61586E-06	14.09898564	regulation of metabolic process
BP	GO:0019438	0.004609253	5.64536E-07	12.91953162	aromatic compound biosynthetic process
BP	GO:0019538	0.003141652	0.000265981	18.7793587	protein metabolic process
BP	GO:0022414	0.004954354	5.91761E-08	12.06515079	reproductive process
BP	GO:0022622	0.005371241	0.00654274	4.0081013	root system development
BP	GO:0023052	0.005371241	9.50837E-06	7.20096671	signaling
BP	GO:0030154	0.005371241	0.00834238	3.890666485	cell differentiation
BP	GO:0031323	0.004594872	1.05514E-06	12.60467016	regulation of cellular metabolic process
BP	GO:0031326	0.004422289	5.86981E-05	10.41425557	regulation of cellular biosynthetic process
BP	GO:0032501	0.004853708	7.02229E-13	19.34440738	multicellular organismal process
BP	GO:0032502	0.004767435	5.15967E-13	20.47110082	developmental process
BP	GO:0032774	0.004594872	5.80726E-05	9.553066921	RNA biosynthetic process
BP	GO:0032870	0.005371241	0.000959509	4.949281775	cellular response to hormone stimulus

BP	GO:0033554	0.004163375	0.026564	6.104908435	cellular response to stress
BP	GO:0034641	0.002191232	0.00896509	24.72258152	cellular nitrogen compound metabolic process
BP	GO:0034654	0.004451054	3.43034E-05	10.72401116	nucleobase-containing compound biosynthetic process
BP	GO:0036211	0.005371241	2.39696E-09	10.96058275	protein modification process
BP	GO:0040007	0.004810572	0.027895	4.35359793	growth
BP	GO:0042221	0.004048288	1.68856E-08	20.47450473	response to chemical
BP	GO:0042742	0.005371241	0.00622571	4.035332562	defense response to bacterium
BP	GO:0043170	0.003127256	2.40902E-09	35.11300974	macromolecule metabolic process
BP	GO:0043412	0.005371241	1.66201E-10	12.14684458	macromolecule modification
BP	GO:0044237	0.002536911	5.18174E-09	46.02423582	cellular metabolic process
BP	GO:0044238	0.003069672	7.13553E-13	44.84988767	primary metabolic process
BP	GO:0044260	0.0029401	2.79173E-07	32.35414256	cellular macromolecule metabolic process
BP	GO:0044267	0.00286811	0.00489529	16.66893594	cellular protein metabolic process
BP	GO:0044281	0.003242417	0.0258091	10.38872626	small molecule metabolic process
BP	GO:0044699	0.003832474	3.61E-21	44.89924433	single-organism process
BP	GO:0044700	0.005371241	9.63922E-06	7.189053033	single organism signaling
BP	GO:0044702	0.004911221	7.45185E-07	10.81591667	single organism reproductive process
BP	GO:0044707	0.004824951	9.45386E-12	18.178569	single-multicellular organism process
BP	GO:0044710	0.003314389	1.21573E-05	21.49737899	single-organism metabolic process
BP	GO:0044763	0.003415142	3.39955E-08	27.59547961	single-organism cellular process
BP	GO:0044765	0.004853708	0.0125777	4.784192253	single-organism transport
BP	GO:0044767	0.004738676	2.98852E-12	19.66777861	single-organism developmental process
BP	GO:0046483	0.00353028	1.59962E-06	21.43270475	heterocycle metabolic process
BP	GO:0048316	0.004422289	0.0316928	5.17734359	seed development
BP	GO:0048364	0.005371241	0.00663007	3.999591531	root development
BP	GO:0048366	0.005371241	0.041685	3.094152087	leaf development
BP	GO:0048367	0.005371241	5.75145E-05	6.292123358	shoot system development

BP	GO:0048518	0.004609253	0.00349391	6.42147185	positive regulation of biological process
BP	GO:0048522	0.005371241	0.00273997	4.443801484	positive regulation of cellular process
BP	GO:0048580	0.005371241	0.0214637	3.436244809	regulation of post-embryonic development
BP	GO:0048583	0.005371241	0.000259798	5.580706651	regulation of response to stimulus
BP	GO:0048608	0.00483933	2.00504E-05	9.176935122	reproductive structure development
BP	GO:0048731	0.004997486	3.97225E-09	13.30587514	system development
BP	GO:0048827	0.005371241	0.00798074	3.912791885	phyllome development
BP	GO:0048856	0.004868087	2.11985E-13	19.88733066	anatomical structure development
BP	GO:0048869	0.004896843	0.00524543	5.245421744	cellular developmental process
BP	GO:0050789	0.004033901	2.83038E-10	24.00265505	regulation of biological process
BP	GO:0050793	0.004911221	0.00373333	5.42072299	regulation of developmental process
BP	GO:0050794	0.004019515	3.335E-08	20.13411396	regulation of cellular process
BP	GO:0050896	0.004235301	2.57E-18	34.47307509	response to stimulus
BP	GO:0051171	0.004479819	2.26459E-05	10.98270815	regulation of nitrogen compound metabolic process
BP	GO:0051239	0.005371241	0.0021865	4.557832392	regulation of multicellular organismal process
BP	GO:0051252	0.004537347	0.000222193	8.836544353	regulation of RNA metabolic process
BP	GO:0051704	0.003890027	0.000526898	11.57839199	multi-organism process
BP	GO:0051716	0.004652395	1.01447E-07	13.78752808	cellular response to stimulus
BP	GO:0055085	0.004810572	0.0257771	4.404656546	transmembrane transport
BP	GO:0060255	0.004120219	9.24811E-05	11.81836749	regulation of macromolecule metabolic process
BP	GO:0061458	0.00483933	2.00504E-05	9.176935122	reproductive system development
BP	GO:0065007	0.004134604	5.786E-12	25.94458438	biological regulation
BP	GO:0065008	0.005371241	0.000694123	5.117775206	regulation of biological quality
BP	GO:0070887	0.00502624	0.000123061	7.149908094	cellular response to chemical stimulus
BP	GO:0071229	0.005371241	0.00960402	3.820886378	cellular response to acid chemical
BP	GO:0071310	0.004968732	0.000955054	6.132139696	cellular response to organic substance
BP	GO:0071495	0.005371241	0.000908382	4.983320852	cellular response to endogenous stimulus

BP	GO:0071704	0.003184838	7.54E-16	48.4733474	organic substance metabolic process
BP	GO:0080090	0.004522965	8.4847E-06	11.53924706	regulation of primary metabolic process
BP	GO:0080134	0.005371241	0.0446971	3.056709102	regulation of response to stress
BP	GO:0090304	0.00304088	0.00161299	16.89189189	nucleic acid metabolic process
BP	GO:0090567	0.005371241	0.0123227	3.708557424	reproductive shoot system development
BP	GO:0097659	0.004594872	5.78011E-05	9.542855198	nucleic acid-templated transcription
BP	GO:0099402	0.005371241	8.44204E-06	7.263939002	plant organ development
BP	GO:1901360	0.003659799	9.93682E-08	23.06147457	organic cyclic compound metabolic process
BP	GO:1901362	0.004652395	1.24445E-07	13.67519913	organic cyclic compound biosynthetic process
BP	GO:1901564	0.003199233	1.25216E-06	26.05180747	organonitrogen compound metabolic process
BP	GO:1901565	0.005371241	0.0220995	3.420927224	organonitrogen compound catabolic process
BP	GO:1901700	0.004220916	1.46561E-05	12.91272381	response to oxygen-containing compound
BP	GO:1901701	0.005371241	0.000915454	4.976513037	cellular response to oxygen-containing compound
BP	GO:1902578	0.004868087	0.00955099	4.923752468	single-organism localization
BP	GO:1903506	0.004508583	0.000393076	8.523384846	regulation of nucleic acid-templated transcription
BP	GO:1905392	0.005371241	0.0375067	3.152018517	plant organ morphogenesis
BP	GO:2000026	0.005371241	0.00371853	4.292327592	regulation of multicellular organismal development
BP	GO:2000112	0.004350373	0.000258803	9.617741167	regulation of cellular macromolecule biosynthetic process
BP	GO:2001141	0.004508583	0.0003914	8.531894615	regulation of RNA biosynthetic process
CC	GO:0005634	0.004364757	4.33775E-11	21.88712642	nucleus
CC	GO:0005739	0.004177761	0.00276883	8.273197631	mitochondrion
CC	GO:0005794	0.00456611	0.00628168	6.096398666	Golgi apparatus
CC	GO:0005829	0.004393523	9.72934E-09	17.59650078	cytosol
CC	GO:0005886	0.004781814	2.76791E-10	16.6076656	plasma membrane
CC	GO:0005911	0.004824951	2.75482E-05	8.991422153	cell-cell junction
CC	GO:0009506	0.004824951	2.75482E-05	8.991422153	plasmodesma
CC	GO:0009507	0.004465437	5.03205E-10	19.01422833	chloroplast

CC	GO:0009532	0.004192146	0.0212451	6.246170604	plastid stroma
CC	GO:0009536	0.004494201	1.08592E-10	19.78691538	plastid
CC	GO:0009570	0.004163375	0.0267572	6.09810062	chloroplast stroma
CC	GO:0012505	0.004508583	9.7784E-06	11.45074546	endomembrane system
CC	GO:0016020	0.004134604	1.209E-15	31.92695214	membrane
CC	GO:0016021	0.005371241	0.000122282	5.929607189	integral component of membrane
CC	GO:0030054	0.004824951	2.75482E-05	8.991422153	cell junction
CC	GO:0031224	0.005371241	2.32673E-05	6.741439172	intrinsic component of membrane
CC	GO:0031410	0.005371241	0.0406243	3.107767717	cytoplasmic vesicle
CC	GO:0031974	0.004623634	0.00275211	6.561032065	membrane-enclosed lumen
CC	GO:0031981	0.00456611	0.00614967	6.11171625	nuclear lumen
CC	GO:0031982	0.005371241	0.0384376	3.136700933	vesicle
CC	GO:0043227	0.003933191	2.94E-29	53.06521887	membrane-bounded organelle
CC	GO:0043231	0.003918803	6.33E-29	52.63462455	intracellular membrane-bounded organelle
CC	GO:0043233	0.004623634	0.00275211	6.561032065	organelle lumen
CC	GO:0044422	0.003328782	7.91938E-08	27.74354959	organelle part
CC	GO:0044425	0.003818085	0.00432478	9.519027844	membrane part
CC	GO:0044428	0.004709916	0.000552037	7.423922663	nuclear part
CC	GO:0044434	0.004436672	4.41813E-05	10.58955681	chloroplast part
CC	GO:0044435	0.004465437	2.81506E-05	10.83123426	plastid part
CC	GO:0044446	0.003328782	8.093E-08	27.71972224	intracellular organelle part
CC	GO:0055044	0.004824951	2.75482E-05	8.991422153	symplast
CC	GO:0070013	0.004623634	0.00278073	6.544012526	intracellular organelle lumen
CC	GO:0071944	0.004594872	6.29213E-11	19.16910613	cell periphery
CC	GO:0097708	0.005371241	0.0402042	3.114575533	intracellular vesicle
CC	GO:0098805	0.003918803	0.0315986	6.768670434	whole membrane

Table S4.2: Upregulated transcripts under control conditions

Transcript ID	FC	pval	qval	Transcript ID	FC	pval	qval
MSTRG.10041.15427	3.6526	0.0001	0.0070	MSTRG.31043.47304	2.7694	0.0015	0.0278
MSTRG.10042.15430	3.0023	0.0016	0.0293	MSTRG.31061.47330	4.8563	0.0030	0.0405
MSTRG.10045.15438	4.6887	0.0001	0.0066	MSTRG.31106.47389	4.2803	0.0026	0.0373
MSTRG.10045.15439	2.4735	0.0005	0.0167	MSTRG.31160.47473	3.0969	0.0000	0.0017
MSTRG.10061.15459	4.0559	0.0008	0.0205	MSTRG.31160.47474	12.0358	0.0000	0.0005
MSTRG.10062.15460	3.9747	0.0009	0.0219	MSTRG.31160.47478	25.3659	0.0000	0.0002
MSTRG.10085.15489	2.4403	0.0009	0.0226	MSTRG.31169.47489	2.3558	0.0014	0.0268
MSTRG.10092.15496	2.5273	0.0009	0.0223	MSTRG.31174.47499	2.4171	0.0038	0.0467
MSTRG.10164.15597	4.2871	0.0004	0.0153	MSTRG.31215.47564	8.8998	0.0001	0.0087
MSTRG.10188.15632	2.3063	0.0032	0.0423	MSTRG.31237.47620	3.1793	0.0037	0.0462
MSTRG.10209.15658	2.0295	0.0031	0.0419	MSTRG.31245.47630	3.0629	0.0001	0.0088
MSTRG.10283.15838	2.5116	0.0016	0.0290	MSTRG.31314.47729	4.0785	0.0003	0.0128
MSTRG.10285.15840	2.3222	0.0005	0.0161	MSTRG.31365.47814	7.9765	0.0020	0.0329
MSTRG.10295.15853	3.2584	0.0021	0.0330	MSTRG.31368.47817	2.3216	0.0009	0.0219
MSTRG.10368.15957	4.9172	0.0017	0.0302	MSTRG.31490.47990	2.9496	0.0005	0.0161
MSTRG.10369.15960	3.4856	0.0039	0.0472	MSTRG.31498.48001	3.2246	0.0005	0.0166
MSTRG.10381.15973	2.5725	0.0040	0.0477	MSTRG.31499.48002	4.5050	0.0001	0.0073
MSTRG.10475.16109	3.2121	0.0010	0.0235	MSTRG.31551.48110	6.3289	0.0000	0.0019
MSTRG.10477.16112	2.1977	0.0034	0.0437	MSTRG.31553.48122	2.5511	0.0001	0.0086
MSTRG.10538.16200	8.1927	0.0000	0.0011	MSTRG.31555.48119	2.5636	0.0001	0.0065
MSTRG.10545.16208	2.3461	0.0042	0.0488	MSTRG.31583.48157	2.0545	0.0031	0.0419
MSTRG.10557.16243	4.5975	0.0004	0.0140	MSTRG.31609.48202	7.7581	0.0018	0.0311
MSTRG.10563.16233	5.3193	0.0001	0.0071	MSTRG.31621.48219	2.8852	0.0037	0.0462
MSTRG.10575.16286	3.5867	0.0001	0.0074	MSTRG.3163.4699	7.0591	0.0016	0.0290
MSTRG.10621.16344	2.7799	0.0002	0.0110	MSTRG.31667.48281	3.0210	0.0031	0.0416

MSTRG.10622.16345	5.0560	0.0003	0.0119
MSTRG.10685.16425	2.5828	0.0042	0.0487
MSTRG.10685.16427	2.2693	0.0006	0.0176
MSTRG.10685.16439	3.4095	0.0007	0.0198
MSTRG.10689.16446	2.2256	0.0007	0.0192
MSTRG.10690.16447	4.1375	0.0005	0.0160
MSTRG.10692.16450	3.8434	0.0001	0.0076
MSTRG.10694.16452	2.8704	0.0003	0.0119
MSTRG.107.154	2.7190	0.0019	0.0317
MSTRG.1075.1606	35.1529	0.0000	0.0005
MSTRG.10807.16614	2.3963	0.0019	0.0320
MSTRG.10813.16623	2.1157	0.0018	0.0307
MSTRG.10819.16629	2.2832	0.0021	0.0332
MSTRG.10886.16711	4.7337	0.0000	0.0047
MSTRG.10886.16714	5.0638	0.0002	0.0112
MSTRG.10909.16758	2.4912	0.0024	0.0359
MSTRG.10961.16829	2.1716	0.0003	0.0119
MSTRG.10987.16874	2.7105	0.0001	0.0080
MSTRG.11010.16905	2.9929	0.0006	0.0182
MSTRG.11042.16949	2.7815	0.0007	0.0194
MSTRG.1128.1684	2.1458	0.0019	0.0321
MSTRG.11290.17305	2.7191	0.0005	0.0172
MSTRG.11354.17391	2.4265	0.0013	0.0262
MSTRG.11356.17396	2.3258	0.0039	0.0472
MSTRG.11405.17474	3.0210	0.0001	0.0071
MSTRG.11419.17492	2.2172	0.0004	0.0156
MSTRG.11435.17508	2.7394	0.0005	0.0161
MSTRG.31727.48361	2.2171	0.0004	0.0148
MSTRG.31751.48399	3.4139	0.0022	0.0344
MSTRG.31788.48444	9.5256	0.0003	0.0122
MSTRG.31823.48500	4.6569	0.0024	0.0359
MSTRG.31863.48560	2.3683	0.0027	0.0386
MSTRG.31898.48615	3.1344	0.0002	0.0107
MSTRG.31898.48622	3.1613	0.0010	0.0227
MSTRG.31920.48653	2.6206	0.0012	0.0260
MSTRG.31952.48703	7.5233	0.0000	0.0051
MSTRG.31969.48730	3.3878	0.0014	0.0271
MSTRG.32002.48770	2.7038	0.0001	0.0080
MSTRG.32016.48796	11.0929	0.0000	0.0051
MSTRG.32031.48819	2.5101	0.0034	0.0441
MSTRG.32032.48821	2.3552	0.0010	0.0231
MSTRG.32037.48829	2.6938	0.0023	0.0349
MSTRG.32045.48843	4.3562	0.0019	0.0318
MSTRG.32158.49007	4.1344	0.0018	0.0310
MSTRG.32213.49094	2.0106	0.0009	0.0223
MSTRG.32269.49172	2.0824	0.0030	0.0409
MSTRG.32275.49188	2.4596	0.0008	0.0201
MSTRG.32310.49256	2.1127	0.0009	0.0218
MSTRG.32336.49296	9.4441	0.0011	0.0248
MSTRG.32612.49709	2.4278	0.0012	0.0253
MSTRG.32613.49710	2.3684	0.0004	0.0146
MSTRG.32730.49872	2.4802	0.0033	0.0434
MSTRG.32793.49947	2.2601	0.0001	0.0069
MSTRG.32952.50165	2.4281	0.0002	0.0108

MSTRG.11450.17524	2.2180	0.0000	0.0029	MSTRG.33007.50244	2.1670	0.0034	0.0437
MSTRG.11605.17743	3.2521	0.0018	0.0307	MSTRG.33007.50245	2.8082	0.0042	0.0489
MSTRG.11784.18066	4.0921	0.0023	0.0349	MSTRG.33054.50327	2.4661	0.0015	0.0287
MSTRG.11784.18159	8.2212	0.0040	0.0478	MSTRG.33118.50436	2.1021	0.0001	0.0092
MSTRG.11888.18317	2.7904	0.0004	0.0152	MSTRG.33120.50437	2.4777	0.0004	0.0155
MSTRG.12012.18476	3.0609	0.0009	0.0217	MSTRG.33171.50524	2.0266	0.0023	0.0348
MSTRG.12025.18491	2.8016	0.0031	0.0413	MSTRG.33174.50530	7.3520	0.0008	0.0213
MSTRG.12074.18549	4.3502	0.0008	0.0214	MSTRG.33174.50542	2.6458	0.0034	0.0437
MSTRG.12074.18550	3.1832	0.0010	0.0231	MSTRG.33175.50532	3.2517	0.0014	0.0270
MSTRG.12132.18640	3.5668	0.0020	0.0324	MSTRG.33225.50617	3.3250	0.0032	0.0425
MSTRG.12272.18858	19.2689	0.0002	0.0112	MSTRG.33266.50668	3.0975	0.0001	0.0080
MSTRG.12298.18901	3.3256	0.0037	0.0462	MSTRG.33269.50671	3.4103	0.0001	0.0092
MSTRG.12426.19095	2.4274	0.0003	0.0121	MSTRG.33285.50695	4.0676	0.0029	0.0403
MSTRG.12443.19122	3.4067	0.0016	0.0297	MSTRG.33307.50733	4.6093	0.0041	0.0481
MSTRG.12456.19143	2.7064	0.0017	0.0302	MSTRG.33353.50794	3.0718	0.0005	0.0158
MSTRG.12557.19328	4.3102	0.0004	0.0153	MSTRG.33354.50798	2.6170	0.0020	0.0326
MSTRG.1260.1873	4.8339	0.0002	0.0114	MSTRG.33386.50837	5.7293	0.0004	0.0154
MSTRG.12660.19489	2.6506	0.0008	0.0214	MSTRG.33411.50867	3.1635	0.0008	0.0207
MSTRG.12662.19491	3.0722	0.0005	0.0168	MSTRG.33510.50995	2.1720	0.0011	0.0249
MSTRG.12712.19555	4.7118	0.0007	0.0188	MSTRG.33667.51212	2.4225	0.0013	0.0262
MSTRG.12758.19618	3.9050	0.0022	0.0345	MSTRG.33679.51227	14.4343	0.0007	0.0198
MSTRG.12765.19631	2.4086	0.0015	0.0284	MSTRG.33697.51256	2.6056	0.0043	0.0495
MSTRG.12785.19665	2.8650	0.0039	0.0473	MSTRG.33732.51316	2.3308	0.0009	0.0224
MSTRG.12787.19666	3.3322	0.0020	0.0321	MSTRG.33757.51348	3.6317	0.0001	0.0074
MSTRG.1282.1910	2.2122	0.0026	0.0381	MSTRG.33833.51464	2.1521	0.0022	0.0343
MSTRG.12828.19723	4.0930	0.0028	0.0391	MSTRG.33912.51566	2.5017	0.0005	0.0161
MSTRG.12859.19768	19.1095	0.0031	0.0417	MSTRG.33915.51569	2.5397	0.0037	0.0460

MSTRG.12860.19770	2.2531	0.0035	0.0450
MSTRG.13030.20013	8.0574	0.0023	0.0349
MSTRG.13055.20049	4.5625	0.0005	0.0167
MSTRG.13091.20097	3.1039	0.0014	0.0274
MSTRG.1323.1963	2.4484	0.0036	0.0453
MSTRG.1330.1973	3.0998	0.0017	0.0303
MSTRG.13367.20534	2.3221	0.0001	0.0094
MSTRG.13380.20549	4.0412	0.0023	0.0356
MSTRG.13381.20550	8.2015	0.0005	0.0163
MSTRG.13382.20551	2.8772	0.0006	0.0184
MSTRG.13489.20737	3.1443	0.0003	0.0119
MSTRG.13515.20771	3.3172	0.0000	0.0046
MSTRG.13548.20823	2.3958	0.0002	0.0103
MSTRG.13559.20836	3.5361	0.0005	0.0160
MSTRG.13592.20878	4.4824	0.0038	0.0466
MSTRG.13596.20884	2.7727	0.0001	0.0086
MSTRG.13597.20883	2.7097	0.0003	0.0133
MSTRG.13622.20929	2.5824	0.0006	0.0184
MSTRG.13653.20976	2.6954	0.0004	0.0137
MSTRG.13655.20980	2.1928	0.0001	0.0087
MSTRG.13676.21003	2.2245	0.0043	0.0497
MSTRG.13717.21048	5.1863	0.0004	0.0152
MSTRG.13825.21229	2.0561	0.0019	0.0320
MSTRG.1383.2046	3.1157	0.0014	0.0272
MSTRG.13959.21421	3.3208	0.0001	0.0074
MSTRG.14001.21497	2.2799	0.0015	0.0286
MSTRG.14024.21543	2.8994	0.0018	0.0307
MSTRG.33918.51573	12.5116	0.0013	0.0266
MSTRG.33933.51605	4.5924	0.0024	0.0363
MSTRG.33957.51635	3.1561	0.0027	0.0385
MSTRG.34005.51737	2.3762	0.0034	0.0440
MSTRG.34108.51911	4.5567	0.0025	0.0364
MSTRG.34151.51980	2.2486	0.0010	0.0231
MSTRG.34226.52077	3.0150	0.0036	0.0452
MSTRG.34226.52096	4.1089	0.0009	0.0217
MSTRG.34243.52110	5.4069	0.0002	0.0094
MSTRG.34301.52187	2.6310	0.0020	0.0325
MSTRG.34303.52190	2.3478	0.0010	0.0232
MSTRG.34391.52326	2.3634	0.0009	0.0223
MSTRG.34424.52380	3.7500	0.0001	0.0087
MSTRG.34473.52449	3.0551	0.0028	0.0389
MSTRG.34562.52568	3.3187	0.0007	0.0189
MSTRG.34572.52583	3.1336	0.0039	0.0470
MSTRG.34594.52611	3.7454	0.0002	0.0110
MSTRG.34691.52756	2.4439	0.0012	0.0253
MSTRG.3475.5191	3.0289	0.0017	0.0304
MSTRG.34901.53144	7.6678	0.0036	0.0453
MSTRG.34910.53158	5.1827	0.0041	0.0483
MSTRG.34997.53306	6.1634	0.0009	0.0217
MSTRG.35094.53450	2.4547	0.0007	0.0197
MSTRG.35218.53631	2.9272	0.0032	0.0426
MSTRG.35238.53662	2.2722	0.0011	0.0243
MSTRG.3529.5251	2.9499	0.0001	0.0068
MSTRG.35294.53748	6.9564	0.0003	0.0129

MSTRG.14027.21533	3.6243	0.0027	0.0382	MSTRG.3530.5254	3.0655	0.0006	0.0177
MSTRG.14027.21534	4.0095	0.0016	0.0296	MSTRG.35392.53908	2.1805	0.0035	0.0442
MSTRG.14027.21535	4.0635	0.0012	0.0252	MSTRG.35503.54061	3.1365	0.0019	0.0316
MSTRG.14027.21536	3.2451	0.0030	0.0407	MSTRG.35507.54065	3.4020	0.0003	0.0122
MSTRG.14225.21814	2.3600	0.0010	0.0236	MSTRG.35527.54095	4.3534	0.0001	0.0071
MSTRG.14420.22071	2.3774	0.0003	0.0119	MSTRG.35528.54098	2.4725	0.0015	0.0285
MSTRG.14446.22103	217.4467	0.0000	0.0002	MSTRG.35536.54111	2.6431	0.0022	0.0344
MSTRG.14612.22374	2.9231	0.0018	0.0307	MSTRG.35565.54154	4.8763	0.0001	0.0065
MSTRG.14631.22394	3.4157	0.0004	0.0138	MSTRG.3559.5293	4.4418	0.0017	0.0304
MSTRG.14704.22499	5.8481	0.0007	0.0196	MSTRG.35591.54205	2.2345	0.0038	0.0463
MSTRG.14725.22538	3.0956	0.0003	0.0119	MSTRG.35599.54213	3.0610	0.0023	0.0348
MSTRG.14743.22559	3.1813	0.0013	0.0267	MSTRG.35611.54239	2.1561	0.0032	0.0423
MSTRG.1479.2204	2.0262	0.0003	0.0119	MSTRG.35611.54240	2.9915	0.0028	0.0395
MSTRG.14790.22627	5.2637	0.0002	0.0106	MSTRG.35690.54361	2.8362	0.0015	0.0279
MSTRG.14790.22628	4.5051	0.0014	0.0270	MSTRG.35724.54407	2.2361	0.0004	0.0141
MSTRG.14792.22632	2.4968	0.0006	0.0175	MSTRG.35751.54451	7.0184	0.0018	0.0310
MSTRG.14796.22640	2.0200	0.0037	0.0460	MSTRG.35752.54452	5.2255	0.0027	0.0387
MSTRG.14803.22653	2.4473	0.0004	0.0149	MSTRG.35876.54665	2.1430	0.0026	0.0373
MSTRG.1487.2214	2.4013	0.0015	0.0283	MSTRG.3591.5341	2.8549	0.0006	0.0178
MSTRG.14963.22915	2.3293	0.0039	0.0470	MSTRG.35980.54821	3.0369	0.0002	0.0098
MSTRG.14974.22933	3.1387	0.0023	0.0349	MSTRG.35999.54850	3.1755	0.0041	0.0481
MSTRG.14975.22930	2.4280	0.0029	0.0402	MSTRG.36044.54925	2.7282	0.0041	0.0481
MSTRG.1504.2246	3.6770	0.0001	0.0077	MSTRG.36044.54926	7.1902	0.0018	0.0314
MSTRG.15059.23032	4.3208	0.0002	0.0096	MSTRG.36066.54960	2.9270	0.0037	0.0456
MSTRG.15073.23051	2.9345	0.0003	0.0137	MSTRG.3609.5379	2.0889	0.0016	0.0294
MSTRG.15136.23137	2.7056	0.0037	0.0461	MSTRG.36103.55015	2.4510	0.0034	0.0441
MSTRG.15179.23185	4.1473	0.0008	0.0204	MSTRG.36141.55090	7.8713	0.0038	0.0463

MSTRG.15180.23187	2.6582	0.0027	0.0387	MSTRG.36238.55252	2.0890	0.0036	0.0451
MSTRG.1534.2294	3.1302	0.0004	0.0149	MSTRG.36311.55401	2.3289	0.0027	0.0386
MSTRG.15415.23530	3.6274	0.0036	0.0453	MSTRG.36359.55473	2.5492	0.0032	0.0424
MSTRG.15460.23590	3.1342	0.0003	0.0126	MSTRG.36396.55521	2.5713	0.0000	0.0012
MSTRG.15481.23634	23.4105	0.0039	0.0468	MSTRG.36473.55628	4.5395	0.0010	0.0238
MSTRG.15492.23653	2.2852	0.0021	0.0336	MSTRG.36585.55803	3.4085	0.0005	0.0170
MSTRG.15599.23796	2.0074	0.0001	0.0086	MSTRG.36631.55865	3.3767	0.0001	0.0066
MSTRG.156.221	3.4715	0.0010	0.0238	MSTRG.36663.55914	2.3062	0.0032	0.0425
MSTRG.15603.23804	3.0017	0.0020	0.0326	MSTRG.36678.55946	2.5263	0.0001	0.0089
MSTRG.15672.23900	3.0644	0.0011	0.0247	MSTRG.3671.5457	2.1341	0.0043	0.0497
MSTRG.15690.23938	4.6659	0.0038	0.0466	MSTRG.36756.56040	3.2869	0.0001	0.0084
MSTRG.15722.23981	2.2273	0.0002	0.0096	MSTRG.36783.56078	5.0512	0.0010	0.0238
MSTRG.15724.23983	4.4299	0.0021	0.0330	MSTRG.36802.56107	2.8158	0.0013	0.0267
MSTRG.15838.24122	3.4087	0.0001	0.0069	MSTRG.36820.56143	3.1077	0.0006	0.0186
MSTRG.15841.24126	3.2352	0.0013	0.0266	MSTRG.36820.56144	5.5453	0.0003	0.0119
MSTRG.15859.24156	17.9082	0.0002	0.0102	MSTRG.36975.56344	2.9468	0.0005	0.0158
MSTRG.15860.24155	30.7974	0.0015	0.0281	MSTRG.371.536	2.5460	0.0004	0.0149
MSTRG.15998.24377	14.4581	0.0000	0.0043	MSTRG.37188.56673	5.7400	0.0039	0.0468
MSTRG.16006.24386	2.5075	0.0024	0.0361	MSTRG.37287.56815	4.5678	0.0024	0.0357
MSTRG.1603.2399	2.1667	0.0004	0.0142	MSTRG.37287.56817	2.0394	0.0022	0.0338
MSTRG.16133.24569	5.1287	0.0022	0.0342	MSTRG.37326.56861	3.7152	0.0010	0.0234
MSTRG.16178.24636	7.1919	0.0000	0.0024	MSTRG.37389.57018	2.8851	0.0004	0.0154
MSTRG.16222.24709	3.4564	0.0028	0.0395	MSTRG.37403.57035	2.2629	0.0000	0.0056
MSTRG.16284.24807	3.3149	0.0006	0.0177	MSTRG.37450.57118	4.2746	0.0005	0.0167
MSTRG.16309.24847	3.6463	0.0011	0.0245	MSTRG.37454.57125	2.4133	0.0005	0.0166
MSTRG.16385.24953	2.4375	0.0025	0.0372	MSTRG.37459.57132	2.8480	0.0021	0.0333
MSTRG.1640.2461	2.9272	0.0019	0.0316	MSTRG.37503.57203	2.3887	0.0004	0.0155

MSTRG.16428.25025	2.5286	0.0012	0.0257	MSTRG.37504.57204	2.8283	0.0004	0.0149
MSTRG.16474.25084	4.2786	0.0004	0.0139	MSTRG.37553.57263	2.8049	0.0006	0.0176
MSTRG.16511.25130	2.5491	0.0012	0.0255	MSTRG.37558.57270	2.1897	0.0017	0.0302
MSTRG.16529.25153	2.3325	0.0038	0.0466	MSTRG.37667.57445	2.4437	0.0010	0.0235
MSTRG.16650.25342	2.4165	0.0011	0.0242	MSTRG.37981.57874	3.4169	0.0039	0.0473
MSTRG.16725.25453	4.4397	0.0000	0.0029	MSTRG.38003.57906	2.1054	0.0002	0.0112
MSTRG.16726.25455	11.3036	0.0000	0.0026	MSTRG.38051.57979	3.4235	0.0007	0.0192
MSTRG.16797.25545	5.5745	0.0000	0.0044	MSTRG.38051.57980	2.2159	0.0025	0.0367
MSTRG.16805.25563	3.2665	0.0011	0.0249	MSTRG.38102.58046	3.4080	0.0009	0.0222
MSTRG.16864.25677	6.4470	0.0001	0.0067	MSTRG.38136.58094	6.0743	0.0007	0.0194
MSTRG.16892.25720	3.0445	0.0020	0.0326	MSTRG.38166.58144	7.8479	0.0005	0.0159
MSTRG.1696.2538	2.9348	0.0003	0.0130	MSTRG.38207.58205	4.9304	0.0000	0.0037
MSTRG.17268.26337	2.5241	0.0004	0.0154	MSTRG.38207.58206	6.3584	0.0001	0.0066
MSTRG.17270.26338	4.1397	0.0010	0.0226	MSTRG.38208.58213	3.7364	0.0005	0.0163
MSTRG.17289.26367	3.6115	0.0025	0.0368	MSTRG.38242.58264	2.4603	0.0013	0.0264
MSTRG.17294.26373	4.9215	0.0013	0.0264	MSTRG.38244.58270	6.0779	0.0019	0.0315
MSTRG.17407.26551	2.6276	0.0000	0.0044	MSTRG.38245.58271	4.4849	0.0013	0.0266
MSTRG.17415.26562	2.6691	0.0019	0.0320	MSTRG.38262.58299	2.7209	0.0020	0.0329
MSTRG.17440.26600	9.3341	0.0017	0.0302	MSTRG.38344.58405	2.3283	0.0010	0.0231
MSTRG.17513.26694	2.5484	0.0006	0.0186	MSTRG.38363.58432	5.2395	0.0001	0.0071
MSTRG.17517.26705	2.9994	0.0007	0.0188	MSTRG.38501.58636	2.2274	0.0012	0.0258
MSTRG.17596.26818	2.4678	0.0011	0.0239	MSTRG.38708.58914	2.0259	0.0010	0.0232
MSTRG.17611.26869	6.8263	0.0002	0.0108	MSTRG.38739.58975	2.1041	0.0022	0.0344
MSTRG.17621.26896	5.1401	0.0000	0.0019	MSTRG.38742.58978	3.3520	0.0003	0.0132
MSTRG.17728.27056	2.6289	0.0040	0.0478	MSTRG.38797.59058	2.8591	0.0029	0.0403
MSTRG.17878.27320	5.0146	0.0010	0.0235	MSTRG.38812.59084	3.6455	0.0029	0.0403
MSTRG.17880.27322	2.7488	0.0042	0.0487	MSTRG.38933.59273	4.9545	0.0002	0.0096

MSTRG.18032.27566	2.8681	0.0028	0.0389	MSTRG.38934.59275	13.5735	0.0007	0.0188
MSTRG.18036.27570	4.8578	0.0002	0.0099	MSTRG.38934.59276	6.1547	0.0008	0.0204
MSTRG.18160.27747	4.1901	0.0003	0.0119	MSTRG.38962.59324	2.5359	0.0002	0.0110
MSTRG.18168.27774	15.9855	0.0026	0.0373	MSTRG.39061.59469	3.3572	0.0009	0.0223
MSTRG.18251.27910	2.3923	0.0016	0.0289	MSTRG.39086.59538	2.9212	0.0038	0.0463
MSTRG.1826.2717	2.1837	0.0037	0.0456	MSTRG.39151.59639	5.7685	0.0002	0.0110
MSTRG.1826.2723	3.9953	0.0027	0.0386	MSTRG.39184.59696	3.6620	0.0025	0.0371
MSTRG.18281.27949	7.1047	0.0004	0.0154	MSTRG.3925.5848	191.4355	0.0020	0.0325
MSTRG.18292.27965	2.2460	0.0006	0.0178	MSTRG.39353.59956	2.6359	0.0000	0.0030
MSTRG.18327.28003	2.9727	0.0032	0.0425	MSTRG.39439.60100	2.7619	0.0032	0.0425
MSTRG.18631.28447	2.2005	0.0041	0.0486	MSTRG.39440.60102	2.9816	0.0035	0.0447
MSTRG.18637.28460	2.1510	0.0021	0.0336	MSTRG.39491.60179	4.7941	0.0002	0.0107
MSTRG.18726.28580	3.3481	0.0012	0.0260	MSTRG.39667.60441	6.2631	0.0000	0.0053
MSTRG.18754.28618	8.3707	0.0001	0.0068	MSTRG.39674.60448	3.1611	0.0000	0.0049
MSTRG.18763.28638	2.1738	0.0033	0.0432	MSTRG.39708.60489	3.1712	0.0011	0.0240
MSTRG.18764.28639	5.2979	0.0012	0.0258	MSTRG.39710.60494	3.3745	0.0002	0.0113
MSTRG.18764.28641	4.5425	0.0009	0.0216	MSTRG.3989.5952	3.0712	0.0020	0.0325
MSTRG.18812.28705	3.0875	0.0013	0.0266	MSTRG.39901.60776	3.5300	0.0012	0.0250
MSTRG.18813.28706	2.9873	0.0009	0.0223	MSTRG.39910.60788	9.4667	0.0007	0.0200
MSTRG.18894.28813	3.5281	0.0003	0.0133	MSTRG.39911.60789	6.7888	0.0016	0.0292
MSTRG.18895.28814	2.6634	0.0012	0.0260	MSTRG.39931.60825	2.4592	0.0002	0.0098
MSTRG.18911.28838	16.8287	0.0041	0.0482	MSTRG.39964.60873	2.9359	0.0043	0.0498
MSTRG.18911.28839	7.2501	0.0002	0.0096	MSTRG.39964.60874	2.4605	0.0036	0.0451
MSTRG.18912.28840	2.3097	0.0002	0.0100	MSTRG.40008.60938	2.1207	0.0013	0.0266
MSTRG.18976.28935	3.0371	0.0002	0.0108	MSTRG.40097.61094	3.1524	0.0001	0.0081
MSTRG.18991.28950	2.4657	0.0009	0.0216	MSTRG.40098.61089	2.7079	0.0009	0.0219
MSTRG.190.271	2.3911	0.0012	0.0258	MSTRG.40145.61156	2.6261	0.0023	0.0353

MSTRG.19049.29038	5.9162	0.0026	0.0373	MSTRG.4033.6047	2.4948	0.0008	0.0208
MSTRG.19054.29052	2.6945	0.0028	0.0392	MSTRG.40428.61567	2.5935	0.0011	0.0243
MSTRG.19057.29055	2.2953	0.0011	0.0239	MSTRG.40450.61605	2.9471	0.0020	0.0327
MSTRG.19071.29081	4.7228	0.0003	0.0133	MSTRG.40506.61696	3.0828	0.0011	0.0248
MSTRG.19077.29090	2.0680	0.0021	0.0338	MSTRG.40531.61736	4.7835	0.0005	0.0161
MSTRG.19086.29099	2.0733	0.0019	0.0319	MSTRG.40533.61741	2.9695	0.0004	0.0156
MSTRG.1910.2838	2.8673	0.0009	0.0225	MSTRG.40552.61771	4.4370	0.0000	0.0030
MSTRG.19124.29156	3.3684	0.0004	0.0138	MSTRG.40557.61779	2.3049	0.0037	0.0456
MSTRG.19225.29333	2.4331	0.0040	0.0478	MSTRG.40561.61785	3.4834	0.0003	0.0136
MSTRG.19295.29429	2.2010	0.0019	0.0318	MSTRG.40585.61903	3.0045	0.0000	0.0040
MSTRG.19330.29490	2.4296	0.0013	0.0267	MSTRG.40652.62011	8.6372	0.0001	0.0065
MSTRG.19363.29547	2.3161	0.0000	0.0051	MSTRG.40653.62013	2.6752	0.0009	0.0225
MSTRG.19388.29585	15.1718	0.0000	0.0044	MSTRG.40667.62035	3.4160	0.0002	0.0100
MSTRG.19487.29714	2.7929	0.0043	0.0498	MSTRG.40816.62249	3.4413	0.0005	0.0164
MSTRG.19488.29715	2.5436	0.0012	0.0260	MSTRG.40932.62404	2.8107	0.0019	0.0315
MSTRG.19584.29863	2.4647	0.0031	0.0416	MSTRG.41072.62591	6.6973	0.0001	0.0081
MSTRG.19626.29904	5.4854	0.0032	0.0423	MSTRG.41079.62607	2.1268	0.0036	0.0452
MSTRG.19636.29927	2.3941	0.0005	0.0166	MSTRG.41080.62608	2.3728	0.0026	0.0381
MSTRG.19636.29929	2.0428	0.0027	0.0386	MSTRG.41111.62651	3.5365	0.0010	0.0236
MSTRG.19715.30034	2.5307	0.0012	0.0253	MSTRG.41112.62652	2.6570	0.0026	0.0381
MSTRG.19716.30035	2.6345	0.0022	0.0345	MSTRG.41118.62659	7.3151	0.0006	0.0180
MSTRG.19810.30167	5.2519	0.0002	0.0096	MSTRG.4115.6164	3.4620	0.0000	0.0018
MSTRG.19910.30295	3.5624	0.0004	0.0138	MSTRG.4116.6166	2.8684	0.0000	0.0035
MSTRG.19948.30345	3.7295	0.0038	0.0467	MSTRG.41193.62764	3.0582	0.0002	0.0098
MSTRG.2005.2975	2.7197	0.0010	0.0227	MSTRG.41224.62806	2.9892	0.0040	0.0478
MSTRG.20116.30611	3.1008	0.0016	0.0292	MSTRG.41269.62872	5.5054	0.0024	0.0362
MSTRG.20183.30692	2.5353	0.0039	0.0471	MSTRG.41294.62915	29.4900	0.0000	0.0009

MSTRG.20256.30794	3.3380	0.0002	0.0110	MSTRG.4138.6190	3.0183	0.0030	0.0407
MSTRG.20337.30892	2.7532	0.0014	0.0273	MSTRG.41495.63217	2.0672	0.0002	0.0102
MSTRG.20368.30936	2.3263	0.0000	0.0019	MSTRG.41606.63400	19.3556	0.0003	0.0136
MSTRG.20368.30938	2.2476	0.0040	0.0478	MSTRG.41747.63610	2.8729	0.0003	0.0121
MSTRG.20368.30940	2.3549	0.0040	0.0477	MSTRG.41778.63665	6.3438	0.0041	0.0481
MSTRG.20437.31050	13.3432	0.0038	0.0463	MSTRG.41930.63880	5.8751	0.0024	0.0360
MSTRG.20451.31074	3.1807	0.0000	0.0053	MSTRG.41931.63881	2.1320	0.0022	0.0344
MSTRG.20491.31160	5.2519	0.0001	0.0086	MSTRG.41945.63899	2.0535	0.0032	0.0426
MSTRG.20491.31161	6.0539	0.0002	0.0097	MSTRG.41961.63920	2.4563	0.0001	0.0061
MSTRG.20491.31162	3.6368	0.0000	0.0040	MSTRG.41980.63963	2.4459	0.0008	0.0203
MSTRG.20515.31193	2.0680	0.0010	0.0231	MSTRG.42060.64088	2.7553	0.0012	0.0260
MSTRG.20532.31214	5.8829	0.0023	0.0351	MSTRG.42072.64108	2.4793	0.0005	0.0158
MSTRG.20533.31215	3.2877	0.0002	0.0110	MSTRG.4208.6292	14.5060	0.0006	0.0177
MSTRG.20582.31276	10.4489	0.0000	0.0027	MSTRG.42227.64409	3.1981	0.0022	0.0342
MSTRG.20585.31280	4.9534	0.0000	0.0045	MSTRG.42248.64438	4.0161	0.0000	0.0051
MSTRG.206.298	2.7276	0.0001	0.0091	MSTRG.42302.64514	4.8001	0.0002	0.0110
MSTRG.2062.3052	2.7215	0.0006	0.0179	MSTRG.42306.64528	10.7436	0.0003	0.0123
MSTRG.20772.31560	9.9830	0.0025	0.0368	MSTRG.42306.64529	6.7654	0.0012	0.0252
MSTRG.20908.31783	2.8261	0.0003	0.0135	MSTRG.42308.64532	2.4219	0.0020	0.0329
MSTRG.20944.31827	2.8334	0.0024	0.0361	MSTRG.42308.64537	2.8397	0.0018	0.0307
MSTRG.20945.31828	2.5812	0.0014	0.0270	MSTRG.42341.64584	3.0801	0.0016	0.0294
MSTRG.20945.31829	4.7184	0.0007	0.0190	MSTRG.42342.64585	6.9894	0.0028	0.0395
MSTRG.21108.32105	3.6548	0.0008	0.0208	MSTRG.42343.64586	4.2436	0.0028	0.0389
MSTRG.21177.32211	2.9884	0.0000	0.0023	MSTRG.42350.64595	3.2703	0.0001	0.0075
MSTRG.21202.32257	2.4599	0.0002	0.0102	MSTRG.42381.64635	4.2799	0.0028	0.0389
MSTRG.21203.32258	2.1158	0.0006	0.0183	MSTRG.42482.64784	4.1896	0.0009	0.0217
MSTRG.21240.32340	3.9801	0.0038	0.0463	MSTRG.42527.64838	2.6666	0.0030	0.0406

MSTRG.21266.32375	2.1470	0.0016	0.0292	MSTRG.42536.64855	8.7097	0.0007	0.0196
MSTRG.21291.32409	3.6728	0.0037	0.0456	MSTRG.42597.64945	7.0440	0.0000	0.0027
MSTRG.21293.32412	4.9461	0.0007	0.0188	MSTRG.4265.6370	2.5770	0.0015	0.0281
MSTRG.21415.32687	3.2165	0.0006	0.0183	MSTRG.42657.65038	3.7961	0.0028	0.0393
MSTRG.21536.32856	2.5947	0.0019	0.0318	MSTRG.42730.65143	3.6818	0.0027	0.0381
MSTRG.21574.32909	5.1455	0.0016	0.0292	MSTRG.42751.65173	2.5299	0.0020	0.0329
MSTRG.21616.32978	2.0059	0.0020	0.0325	MSTRG.42756.65191	2.6264	0.0004	0.0139
MSTRG.21626.32991	2.1536	0.0015	0.0283	MSTRG.42757.65192	2.1766	0.0024	0.0363
MSTRG.21652.33025	3.4803	0.0001	0.0071	MSTRG.42759.65194	2.0529	0.0011	0.0243
MSTRG.21789.33211	2.7862	0.0021	0.0334	MSTRG.42802.65267	2.8598	0.0009	0.0216
MSTRG.21796.33222	2.2277	0.0012	0.0255	MSTRG.42831.65309	2.5644	0.0032	0.0426
MSTRG.21842.33294	3.5191	0.0026	0.0376	MSTRG.42833.65328	2.7143	0.0020	0.0325
MSTRG.21860.33322	4.8302	0.0006	0.0179	MSTRG.42875.65393	2.4020	0.0009	0.0219
MSTRG.2192.3240	2.4910	0.0042	0.0488	MSTRG.42963.65538	2.0437	0.0016	0.0292
MSTRG.21946.33448	2.4119	0.0013	0.0266	MSTRG.42989.65583	2.8203	0.0011	0.0248
MSTRG.22004.33520	3.7701	0.0002	0.0096	MSTRG.43032.65634	3.4426	0.0033	0.0432
MSTRG.22100.33647	3.8681	0.0025	0.0364	MSTRG.43082.65707	5.6820	0.0008	0.0212
MSTRG.22118.33670	3.2369	0.0024	0.0361	MSTRG.43116.65759	3.1412	0.0028	0.0393
MSTRG.22119.33671	2.9467	0.0007	0.0194	MSTRG.43143.65797	3.5925	0.0011	0.0240
MSTRG.2212.3268	4.4691	0.0013	0.0261	MSTRG.4320.6450	3.2053	0.0000	0.0046
MSTRG.2212.3273	2.4704	0.0008	0.0209	MSTRG.43261.65979	2.8829	0.0040	0.0478
MSTRG.22166.33746	18.7017	0.0001	0.0072	MSTRG.434.623	3.0200	0.0012	0.0253
MSTRG.2219.3286	4.3570	0.0041	0.0485	MSTRG.43401.66201	2.5335	0.0032	0.0421
MSTRG.2226.3304	3.7217	0.0000	0.0051	MSTRG.43471.66294	3.4103	0.0031	0.0417
MSTRG.22291.33940	2.2993	0.0009	0.0225	MSTRG.43491.66330	2.7213	0.0010	0.0231
MSTRG.22309.33975	29.6427	0.0004	0.0137	MSTRG.43517.66364	2.5951	0.0009	0.0217
MSTRG.22348.34039	2.3770	0.0017	0.0302	MSTRG.43572.66428	2.7621	0.0002	0.0096

MSTRG.22350.34041	2.1615	0.0013	0.0268	MSTRG.437.629	10.5494	0.0001	0.0061
MSTRG.22374.34073	2.5871	0.0025	0.0371	MSTRG.43722.66681	2.5946	0.0008	0.0202
MSTRG.22562.34380	2.5946	0.0009	0.0226	MSTRG.43763.66727	2.2583	0.0040	0.0479
MSTRG.22569.34388	2.6078	0.0003	0.0135	MSTRG.43766.66731	3.7503	0.0041	0.0481
MSTRG.22658.34533	3.3140	0.0005	0.0171	MSTRG.43881.66887	3.8369	0.0017	0.0304
MSTRG.22664.34558	4.4840	0.0008	0.0201	MSTRG.43931.66960	2.5030	0.0001	0.0075
MSTRG.22678.34568	3.2897	0.0000	0.0025	MSTRG.44018.67117	2.4755	0.0006	0.0176
MSTRG.22745.34670	2.3318	0.0006	0.0182	MSTRG.44041.67153	7.2853	0.0000	0.0036
MSTRG.22747.34669	2.0703	0.0004	0.0138	MSTRG.4406.6599	4.5307	0.0012	0.0251
MSTRG.2277.3372	3.2209	0.0000	0.0032	MSTRG.44168.67328	3.9529	0.0018	0.0311
MSTRG.22830.34815	3.3377	0.0003	0.0119	MSTRG.44293.67509	2.6162	0.0001	0.0075
MSTRG.22830.34818	3.3615	0.0042	0.0486	MSTRG.44323.67546	3.7509	0.0021	0.0335
MSTRG.22830.34826	2.3974	0.0030	0.0406	MSTRG.44325.67548	2.8907	0.0004	0.0149
MSTRG.22845.34848	3.1342	0.0002	0.0096	MSTRG.44327.67550	3.9182	0.0032	0.0425
MSTRG.22859.34889	3.0500	0.0000	0.0031	MSTRG.44329.67553	2.8929	0.0003	0.0119
MSTRG.22908.34972	4.3052	0.0011	0.0244	MSTRG.4437.6638	2.7674	0.0017	0.0302
MSTRG.22927.34998	5.7353	0.0016	0.0290	MSTRG.4465.6691	4.2982	0.0001	0.0066
MSTRG.22985.35094	2.9855	0.0016	0.0296	MSTRG.44663.68040	2.6695	0.0000	0.0046
MSTRG.22992.35104	2.5703	0.0002	0.0107	MSTRG.44672.68050	5.2715	0.0021	0.0331
MSTRG.23009.35128	5.0413	0.0021	0.0331	MSTRG.44749.68167	2.2669	0.0027	0.0386
MSTRG.23072.35206	8.7542	0.0006	0.0180	MSTRG.44753.68188	38.2370	0.0000	0.0035
MSTRG.23093.35237	2.1639	0.0001	0.0071	MSTRG.44824.68296	5.4093	0.0040	0.0477
MSTRG.23169.35343	15.0968	0.0000	0.0029	MSTRG.44897.68405	2.9216	0.0010	0.0236
MSTRG.2319.3445	4.0425	0.0001	0.0071	MSTRG.44936.68466	4.5049	0.0001	0.0059
MSTRG.23216.35406	5.7360	0.0008	0.0201	MSTRG.44967.68506	2.0148	0.0025	0.0364
MSTRG.23230.35425	3.3949	0.0003	0.0119	MSTRG.45078.68709	2.0030	0.0001	0.0066
MSTRG.23232.35426	6.1472	0.0006	0.0176	MSTRG.45078.68710	3.4114	0.0011	0.0239

MSTRG.23237.35432	3.0614	0.0041	0.0484	MSTRG.45165.68857	2.9378	0.0003	0.0136
MSTRG.23238.35433	2.6231	0.0015	0.0283	MSTRG.45264.68999	16.0574	0.0013	0.0263
MSTRG.23359.35640	15.2659	0.0004	0.0143	MSTRG.45309.69068	2.9209	0.0001	0.0087
MSTRG.234.334	14.1282	0.0001	0.0077	MSTRG.45380.69172	2.1132	0.0040	0.0480
MSTRG.23400.35702	9.1053	0.0000	0.0035	MSTRG.45394.69189	2.6381	0.0012	0.0256
MSTRG.23419.35724	2.3908	0.0001	0.0072	MSTRG.45455.69273	6.3852	0.0040	0.0479
MSTRG.23448.35790	2.1388	0.0042	0.0487	MSTRG.45467.69303	5.9746	0.0001	0.0065
MSTRG.23485.35846	2.9439	0.0026	0.0375	MSTRG.45504.69350	10.3155	0.0017	0.0297
MSTRG.23655.36094	3.3944	0.0024	0.0359	MSTRG.45519.69377	2.2047	0.0028	0.0391
MSTRG.23852.36394	4.6770	0.0000	0.0052	MSTRG.45546.69410	2.6752	0.0007	0.0194
MSTRG.23960.36536	3.4248	0.0007	0.0194	MSTRG.45549.69413	2.0301	0.0014	0.0273
MSTRG.23965.36541	2.4656	0.0005	0.0158	MSTRG.45566.69466	3.3964	0.0036	0.0453
MSTRG.23977.36561	2.3399	0.0037	0.0461	MSTRG.45567.69468	3.9929	0.0035	0.0450
MSTRG.24048.36685	2.2397	0.0022	0.0346	MSTRG.45567.69481	6.5308	0.0003	0.0125
MSTRG.24194.36888	2.4072	0.0004	0.0149	MSTRG.45571.69486	7.0033	0.0005	0.0164
MSTRG.24196.36889	5.6848	0.0000	0.0046	MSTRG.45571.69487	5.7142	0.0013	0.0260
MSTRG.24197.36890	2.7145	0.0000	0.0033	MSTRG.45598.69539	2.4431	0.0032	0.0421
MSTRG.24199.36892	2.9922	0.0002	0.0102	MSTRG.45795.69814	2.1344	0.0000	0.0046
MSTRG.24214.36909	10.0661	0.0007	0.0193	MSTRG.45797.69816	2.1206	0.0009	0.0225
MSTRG.24233.36933	6.0918	0.0013	0.0262	MSTRG.45803.69822	4.8893	0.0001	0.0065
MSTRG.24238.36942	5.0556	0.0019	0.0314	MSTRG.45851.69897	4.4934	0.0000	0.0033
MSTRG.24291.37015	3.6611	0.0022	0.0345	MSTRG.45970.70082	3.4690	0.0018	0.0306
MSTRG.24308.37035	7.1816	0.0000	0.0042	MSTRG.46112.70295	2.1321	0.0001	0.0058
MSTRG.2432.3607	4.0037	0.0007	0.0194	MSTRG.46376.70728	2.3608	0.0035	0.0442
MSTRG.24373.37133	3.2284	0.0001	0.0075	MSTRG.46394.70755	2.7440	0.0003	0.0120
MSTRG.24431.37220	2.8687	0.0018	0.0306	MSTRG.46394.70756	3.0759	0.0031	0.0416
MSTRG.24442.37237	3.5702	0.0004	0.0154	MSTRG.46394.70761	2.8295	0.0010	0.0232

MSTRG.24454.37257	2.3145	0.0027	0.0381	MSTRG.46397.70778	6.6239	0.0007	0.0199
MSTRG.24458.37262	3.6780	0.0002	0.0110	MSTRG.4646.6950	4.3686	0.0001	0.0084
MSTRG.24462.37267	2.8382	0.0004	0.0143	MSTRG.4646.6954	4.3481	0.0001	0.0061
MSTRG.24465.37273	3.7279	0.0034	0.0436	MSTRG.46574.71042	3.7683	0.0003	0.0121
MSTRG.24469.37279	3.0892	0.0013	0.0266	MSTRG.46574.71043	3.5878	0.0004	0.0149
MSTRG.24722.37679	3.2483	0.0031	0.0419	MSTRG.46669.71160	3.0902	0.0002	0.0113
MSTRG.24736.37697	4.8974	0.0001	0.0072	MSTRG.46693.71193	2.7532	0.0038	0.0463
MSTRG.24739.37705	3.0071	0.0020	0.0325	MSTRG.46893.71512	2.5847	0.0034	0.0437
MSTRG.2480.3672	74.5173	0.0026	0.0380	MSTRG.46983.71636	2.0867	0.0032	0.0427
MSTRG.24876.37877	2.2689	0.0014	0.0268	MSTRG.47158.71880	3.4772	0.0025	0.0372
MSTRG.24910.37918	6.4213	0.0007	0.0194	MSTRG.47209.71939	16.0467	0.0005	0.0170
MSTRG.24917.37930	2.9690	0.0008	0.0203	MSTRG.473.681	2.0059	0.0044	0.0499
MSTRG.25073.38238	4.6750	0.0019	0.0321	MSTRG.47320.72083	2.7592	0.0016	0.0290
MSTRG.251.368	4.0344	0.0004	0.0138	MSTRG.47364.72151	2.0500	0.0012	0.0253
MSTRG.25114.38297	3.1938	0.0008	0.0207	MSTRG.47375.72163	3.1371	0.0006	0.0184
MSTRG.25120.38307	5.0064	0.0033	0.0432	MSTRG.47422.72240	3.7733	0.0001	0.0071
MSTRG.25120.38308	2.2170	0.0004	0.0138	MSTRG.47541.72431	5.4651	0.0004	0.0138
MSTRG.25120.38309	2.5854	0.0014	0.0270	MSTRG.47615.72536	5.4698	0.0000	0.0010
MSTRG.25121.38306	2.1663	0.0013	0.0266	MSTRG.47658.72608	2.0122	0.0013	0.0260
MSTRG.25304.38546	15.8975	0.0000	0.0032	MSTRG.4766.7138	2.9995	0.0002	0.0110
MSTRG.2533.3758	3.3436	0.0002	0.0118	MSTRG.4766.7144	8.0518	0.0039	0.0473
MSTRG.25330.38587	2.5485	0.0035	0.0444	MSTRG.47660.72610	2.3653	0.0015	0.0287
MSTRG.25354.38625	4.2584	0.0034	0.0439	MSTRG.47664.72614	5.4535	0.0025	0.0369
MSTRG.25371.38651	5.6904	0.0000	0.0019	MSTRG.477.687	2.4452	0.0009	0.0221
MSTRG.25428.38732	2.3391	0.0006	0.0185	MSTRG.48079.73257	4.1164	0.0022	0.0346
MSTRG.25442.38748	7.2410	0.0022	0.0345	MSTRG.48080.73260	4.5328	0.0016	0.0292
MSTRG.2545.3770	2.1734	0.0030	0.0411	MSTRG.48096.73296	4.5978	0.0036	0.0454

MSTRG.25547.38893	3.2326	0.0010	0.0231	MSTRG.48246.73511	2.6174	0.0010	0.0228
MSTRG.25555.38913	5.3690	0.0014	0.0274	MSTRG.48251.73527	11.5274	0.0000	0.0046
MSTRG.25613.39011	2.2491	0.0008	0.0215	MSTRG.48472.73864	2.4794	0.0005	0.0161
MSTRG.25656.39061	9.0327	0.0038	0.0464	MSTRG.48496.73889	2.2641	0.0002	0.0096
MSTRG.25671.39087	2.5365	0.0004	0.0146	MSTRG.48497.73890	3.3321	0.0003	0.0126
MSTRG.25672.39088	2.5138	0.0015	0.0281	MSTRG.48519.73928	3.2512	0.0001	0.0082
MSTRG.2575.3815	5.1525	0.0002	0.0110	MSTRG.48566.74018	2.1355	0.0024	0.0360
MSTRG.25798.39256	2.7797	0.0037	0.0456	MSTRG.48583.74048	2.3200	0.0002	0.0100
MSTRG.25829.39307	4.7938	0.0008	0.0203	MSTRG.48602.74070	24.0854	0.0001	0.0067
MSTRG.25851.39341	7.0020	0.0041	0.0484	MSTRG.48635.74127	3.5236	0.0003	0.0119
MSTRG.25884.39391	2.6870	0.0012	0.0250	MSTRG.48651.74148	4.6035	0.0036	0.0453
MSTRG.2592.3843	2.8675	0.0014	0.0269	MSTRG.48696.74210	2.1144	0.0011	0.0240
MSTRG.2599.3850	2.8310	0.0040	0.0475	MSTRG.48697.74212	2.2157	0.0020	0.0324
MSTRG.26036.39628	3.8284	0.0031	0.0418	MSTRG.4870.7320	2.6209	0.0000	0.0034
MSTRG.26040.39632	2.9722	0.0008	0.0203	MSTRG.48758.74298	5.6098	0.0000	0.0019
MSTRG.26042.39634	2.1572	0.0011	0.0239	MSTRG.48760.74303	5.8312	0.0001	0.0094
MSTRG.26065.39668	12.5277	0.0000	0.0056	MSTRG.48760.74304	5.4309	0.0015	0.0284
MSTRG.26066.39669	8.1247	0.0000	0.0019	MSTRG.48769.74320	2.0546	0.0020	0.0329
MSTRG.2613.3872	2.7077	0.0005	0.0167	MSTRG.494.715	15.0335	0.0005	0.0160
MSTRG.26139.39778	4.3256	0.0018	0.0312	MSTRG.5025.7577	3.3211	0.0044	0.0499
MSTRG.2626.3890	3.6273	0.0020	0.0327	MSTRG.503.729	2.6472	0.0004	0.0137
MSTRG.26282.39985	4.0850	0.0007	0.0194	MSTRG.5040.7593	2.4111	0.0002	0.0106
MSTRG.26328.40044	4.1056	0.0001	0.0071	MSTRG.5041.7594	2.6603	0.0014	0.0270
MSTRG.26329.40045	7.7956	0.0002	0.0117	MSTRG.508.735	4.8010	0.0004	0.0141
MSTRG.26344.40063	2.5572	0.0001	0.0092	MSTRG.508.749	4.9350	0.0000	0.0034
MSTRG.26361.40083	4.5581	0.0010	0.0233	MSTRG.509.736	2.6057	0.0005	0.0171
MSTRG.26466.40252	9.5669	0.0002	0.0103	MSTRG.511.741	6.2690	0.0019	0.0318

MSTRG.26480.40274	2.7287	0.0018	0.0309	MSTRG.511.743	3.9382	0.0006	0.0186
MSTRG.26576.40423	2.6178	0.0014	0.0273	MSTRG.511.744	3.3098	0.0016	0.0295
MSTRG.26647.40554	2.9634	0.0018	0.0311	MSTRG.5155.7776	2.0324	0.0018	0.0313
MSTRG.26679.40597	3.4460	0.0021	0.0331	MSTRG.5191.7836	2.7330	0.0001	0.0075
MSTRG.26704.40636	2.3737	0.0039	0.0472	MSTRG.5193.7830	3.9907	0.0002	0.0118
MSTRG.2671.3958	4.6425	0.0026	0.0379	MSTRG.5193.7832	3.9337	0.0029	0.0404
MSTRG.26713.40653	2.2101	0.0014	0.0272	MSTRG.5213.7863	3.3229	0.0038	0.0466
MSTRG.26738.40691	3.6328	0.0001	0.0074	MSTRG.5316.8025	2.2755	0.0012	0.0258
MSTRG.26753.40710	4.6571	0.0006	0.0178	MSTRG.5394.8143	3.6487	0.0031	0.0413
MSTRG.26842.40862	3.5153	0.0023	0.0349	MSTRG.5482.8275	20.3374	0.0000	0.0012
MSTRG.26843.40863	4.0755	0.0003	0.0130	MSTRG.5497.8298	2.3523	0.0003	0.0125
MSTRG.26901.40962	7.3991	0.0007	0.0198	MSTRG.5601.8467	4.5524	0.0002	0.0102
MSTRG.26907.40985	3.4072	0.0017	0.0302	MSTRG.5712.8638	4.5124	0.0000	0.0030
MSTRG.2696.4000	2.0005	0.0013	0.0266	MSTRG.5720.8664	2.9523	0.0042	0.0490
MSTRG.27007.41160	9.3468	0.0019	0.0320	MSTRG.5740.8692	2.7360	0.0032	0.0424
MSTRG.27047.41219	2.1662	0.0005	0.0168	MSTRG.5773.8755	2.1226	0.0005	0.0170
MSTRG.27109.41321	6.6666	0.0009	0.0216	MSTRG.5835.8833	2.1814	0.0022	0.0344
MSTRG.27111.41324	3.5043	0.0003	0.0129	MSTRG.5902.8929	2.6296	0.0019	0.0318
MSTRG.27163.41407	8.4068	0.0006	0.0186	MSTRG.5959.9013	4.0552	0.0002	0.0113
MSTRG.27164.41408	2.4796	0.0012	0.0252	MSTRG.598.895	3.0182	0.0033	0.0432
MSTRG.273.406	7.4043	0.0033	0.0431	MSTRG.5985.9057	3.1726	0.0002	0.0107
MSTRG.27418.41771	2.8561	0.0033	0.0432	MSTRG.5988.9061	2.7016	0.0040	0.0477
MSTRG.27422.41776	6.1971	0.0000	0.0020	MSTRG.5997.9090	6.2966	0.0002	0.0095
MSTRG.27428.41785	3.0698	0.0005	0.0170	MSTRG.6104.9272	2.6024	0.0008	0.0209
MSTRG.27430.41789	2.1224	0.0001	0.0078	MSTRG.611.914	2.5073	0.0016	0.0296
MSTRG.27465.41840	3.2798	0.0005	0.0170	MSTRG.6115.9284	13.8607	0.0002	0.0117
MSTRG.27541.41967	2.6344	0.0010	0.0231	MSTRG.6122.9296	4.2599	0.0000	0.0039

MSTRG.27592.42058	2.2906	0.0021	0.0333	MSTRG.6152.9357	5.2300	0.0030	0.0407
MSTRG.27731.42263	4.8081	0.0019	0.0315	MSTRG.6182.9392	4.5219	0.0017	0.0298
MSTRG.27827.42407	2.2406	0.0008	0.0214	MSTRG.6182.9398	5.2498	0.0030	0.0409
MSTRG.27828.42408	2.2424	0.0008	0.0214	MSTRG.6182.9399	5.8440	0.0012	0.0255
MSTRG.27842.42433	2.3053	0.0024	0.0359	MSTRG.6182.9409	2.8149	0.0012	0.0260
MSTRG.27844.42436	11.2436	0.0000	0.0035	MSTRG.6184.9395	2.6054	0.0013	0.0266
MSTRG.27861.42458	3.7837	0.0001	0.0086	MSTRG.6186.9402	3.7936	0.0013	0.0264
MSTRG.27867.42468	3.1808	0.0016	0.0292	MSTRG.6254.9518	3.0017	0.0001	0.0091
MSTRG.27870.42473	2.6362	0.0030	0.0411	MSTRG.6391.9751	2.0645	0.0030	0.0411
MSTRG.27958.42591	17.0267	0.0000	0.0043	MSTRG.6421.9797	2.3227	0.0018	0.0306
MSTRG.27987.42649	3.5549	0.0019	0.0316	MSTRG.6505.9978	2.3371	0.0032	0.0421
MSTRG.28015.42694	4.0541	0.0001	0.0076	MSTRG.656.968	5.0150	0.0042	0.0486
MSTRG.28036.42721	2.3424	0.0007	0.0188	MSTRG.657.974	10.7258	0.0001	0.0076
MSTRG.28037.42722	2.7121	0.0018	0.0306	MSTRG.6577.10119	6.5089	0.0018	0.0311
MSTRG.28043.42728	2.3495	0.0010	0.0226	MSTRG.6587.10134	12.9859	0.0001	0.0087
MSTRG.28069.42777	22.0340	0.0007	0.0194	MSTRG.6633.10206	3.6845	0.0018	0.0307
MSTRG.28090.42809	6.5126	0.0000	0.0035	MSTRG.6660.10269	3.5509	0.0004	0.0154
MSTRG.28121.42856	6.1149	0.0016	0.0297	MSTRG.675.994	3.9004	0.0012	0.0258
MSTRG.28131.42873	5.0104	0.0003	0.0128	MSTRG.6762.10437	17.8697	0.0000	0.0022
MSTRG.28145.42889	2.2834	0.0017	0.0304	MSTRG.6894.10653	13.8815	0.0008	0.0209
MSTRG.28194.42956	2.4436	0.0012	0.0252	MSTRG.6918.10687	2.2963	0.0009	0.0217
MSTRG.28273.43064	13.0708	0.0000	0.0046	MSTRG.7076.10977	3.3751	0.0006	0.0183
MSTRG.28412.43275	2.4161	0.0001	0.0086	MSTRG.7095.11003	3.0016	0.0000	0.0035
MSTRG.28491.43391	2.7242	0.0013	0.0266	MSTRG.7111.11028	2.4174	0.0035	0.0444
MSTRG.28530.43464	2.8180	0.0002	0.0096	MSTRG.7122.11042	6.3561	0.0000	0.0044
MSTRG.28698.43709	5.0451	0.0022	0.0345	MSTRG.7128.11054	11.9042	0.0006	0.0184
MSTRG.28704.43716	3.0675	0.0035	0.0447	MSTRG.7297.11298	2.0319	0.0011	0.0242

MSTRG.28745.43766	2.1859	0.0003	0.0128	MSTRG.7302.11303	8.2615	0.0007	0.0190
MSTRG.28758.43787	4.0468	0.0005	0.0157	MSTRG.7303.11304	7.7162	0.0009	0.0217
MSTRG.28784.43824	4.5933	0.0017	0.0302	MSTRG.7349.11389	2.7740	0.0011	0.0249
MSTRG.2880.4286	2.8106	0.0028	0.0394	MSTRG.7407.11458	2.0309	0.0001	0.0059
MSTRG.28811.43868	5.1506	0.0007	0.0200	MSTRG.7446.11502	4.4524	0.0011	0.0242
MSTRG.28891.43997	2.0610	0.0003	0.0119	MSTRG.7457.11518	5.1595	0.0004	0.0141
MSTRG.28913.44036	5.2362	0.0004	0.0154	MSTRG.7558.11655	5.3644	0.0003	0.0133
MSTRG.28913.44037	4.2122	0.0021	0.0334	MSTRG.757.1150	2.1013	0.0018	0.0307
MSTRG.28916.44040	3.3567	0.0009	0.0217	MSTRG.7580.11685	2.8256	0.0017	0.0305
MSTRG.28932.44057	2.7340	0.0002	0.0110	MSTRG.7581.11688	10.8046	0.0000	0.0007
MSTRG.28973.44115	4.1408	0.0041	0.0486	MSTRG.7629.11763	2.0787	0.0011	0.0248
MSTRG.28975.44118	5.7362	0.0037	0.0458	MSTRG.7645.11779	2.1310	0.0000	0.0054
MSTRG.29020.44187	3.1629	0.0002	0.0107	MSTRG.7663.11797	4.2838	0.0009	0.0218
MSTRG.29023.44190	3.3378	0.0000	0.0036	MSTRG.7668.11805	7.3028	0.0015	0.0283
MSTRG.29050.44230	2.2408	0.0021	0.0336	MSTRG.7672.11811	4.8405	0.0025	0.0369
MSTRG.29145.44434	2.4058	0.0038	0.0466	MSTRG.770.1166	7.8994	0.0040	0.0477
MSTRG.29167.44461	8.1576	0.0001	0.0077	MSTRG.7710.11867	2.5541	0.0002	0.0114
MSTRG.29191.44507	4.3592	0.0003	0.0137	MSTRG.7710.11872	6.1286	0.0035	0.0444
MSTRG.29255.44641	2.3072	0.0018	0.0306	MSTRG.7710.11874	3.1632	0.0012	0.0260
MSTRG.29257.44643	2.0767	0.0027	0.0384	MSTRG.7710.11878	2.0692	0.0036	0.0453
MSTRG.29266.44654	2.5049	0.0009	0.0217	MSTRG.7765.11946	2.1284	0.0014	0.0274
MSTRG.29294.44710	4.0644	0.0001	0.0086	MSTRG.783.1180	2.0867	0.0039	0.0473
MSTRG.29297.44708	4.5763	0.0021	0.0334	MSTRG.7888.12132	3.1265	0.0025	0.0371
MSTRG.29401.44857	3.8841	0.0028	0.0394	MSTRG.7892.12143	5.9475	0.0001	0.0083
MSTRG.29420.44894	5.7056	0.0021	0.0334	MSTRG.792.1195	2.6136	0.0022	0.0346
MSTRG.2945.4372	2.3203	0.0006	0.0188	MSTRG.7930.12198	3.1826	0.0002	0.0100
MSTRG.295.438	3.0317	0.0002	0.0108	MSTRG.7936.12209	6.1347	0.0019	0.0314

MSTRG.29567.45096	3.9217	0.0007	0.0194	MSTRG.7943.12222	5.1596	0.0001	0.0061
MSTRG.29598.45146	2.3350	0.0013	0.0266	MSTRG.7980.12278	3.7922	0.0017	0.0302
MSTRG.29602.45151	2.3237	0.0030	0.0407	MSTRG.7981.12279	3.9360	0.0014	0.0274
MSTRG.29678.45266	2.5042	0.0003	0.0136	MSTRG.8078.12423	2.3346	0.0038	0.0463
MSTRG.29709.45333	5.0438	0.0001	0.0076	MSTRG.8082.12432	2.0998	0.0005	0.0171
MSTRG.29721.45351	2.2741	0.0015	0.0285	MSTRG.8083.12438	2.5321	0.0017	0.0300
MSTRG.29722.45353	2.3842	0.0008	0.0209	MSTRG.819.1248	2.6182	0.0001	0.0087
MSTRG.29812.45482	2.2998	0.0019	0.0318	MSTRG.8234.12665	19.1613	0.0000	0.0001
MSTRG.29812.45485	2.9257	0.0037	0.0456	MSTRG.8349.12830	2.8711	0.0007	0.0198
MSTRG.29849.45540	4.4201	0.0037	0.0460	MSTRG.8350.12832	2.9098	0.0015	0.0286
MSTRG.29858.45549	2.4980	0.0025	0.0366	MSTRG.8355.12838	3.4222	0.0036	0.0452
MSTRG.29869.45570	2.0155	0.0040	0.0477	MSTRG.8356.12840	3.5644	0.0024	0.0356
MSTRG.29872.45575	2.8370	0.0004	0.0137	MSTRG.8399.12911	2.3417	0.0018	0.0314
MSTRG.29951.45698	3.6133	0.0007	0.0199	MSTRG.8413.12926	4.9582	0.0001	0.0078
MSTRG.29955.45704	2.6427	0.0015	0.0285	MSTRG.8499.13056	2.3106	0.0013	0.0266
MSTRG.29969.45721	4.4848	0.0013	0.0262	MSTRG.8506.13063	2.6935	0.0001	0.0069
MSTRG.29969.45723	2.5212	0.0034	0.0437	MSTRG.8516.13082	2.1502	0.0040	0.0478
MSTRG.29979.45737	4.6579	0.0020	0.0324	MSTRG.8556.13161	6.3562	0.0009	0.0215
MSTRG.301.444	9.2148	0.0011	0.0248	MSTRG.8581.13193	4.8460	0.0002	0.0100
MSTRG.30131.45938	2.6658	0.0002	0.0108	MSTRG.8598.13214	2.5020	0.0044	0.0499
MSTRG.30138.45947	3.6066	0.0006	0.0180	MSTRG.8760.13444	3.7608	0.0003	0.0136
MSTRG.30220.46053	3.2913	0.0001	0.0069	MSTRG.8783.13486	2.2195	0.0007	0.0200
MSTRG.30222.46055	3.0268	0.0022	0.0345	MSTRG.8789.13493	4.3079	0.0001	0.0069
MSTRG.30280.46135	5.7719	0.0029	0.0400	MSTRG.8796.13508	12.4494	0.0004	0.0147
MSTRG.30294.46169	2.1395	0.0042	0.0489	MSTRG.8842.13578	2.2013	0.0006	0.0186
MSTRG.30323.46207	2.4679	0.0007	0.0194	MSTRG.8855.13596	2.6220	0.0010	0.0236
MSTRG.30439.46376	2.5343	0.0004	0.0144	MSTRG.8881.13634	2.9907	0.0034	0.0441

MSTRG.30441.46378	2.8577	0.0020	0.0323	MSTRG.8889.13651	2.1116	0.0015	0.0280
MSTRG.30490.46481	3.0986	0.0013	0.0267	MSTRG.8914.13696	2.5437	0.0019	0.0316
MSTRG.30490.46482	2.6154	0.0011	0.0248	MSTRG.895.1366	6.4859	0.0000	0.0018
MSTRG.30490.46483	2.6094	0.0005	0.0164	MSTRG.9078.13949	13.3811	0.0000	0.0022
MSTRG.30505.46509	2.6834	0.0010	0.0236	MSTRG.9099.13976	2.9258	0.0028	0.0394
MSTRG.30515.46523	2.6770	0.0006	0.0181	MSTRG.9123.14003	2.1652	0.0000	0.0043
MSTRG.30555.46585	2.3429	0.0004	0.0154	MSTRG.92.132	12.4568	0.0000	0.0016
MSTRG.30558.46588	2.0788	0.0026	0.0379	MSTRG.9221.14162	11.7825	0.0000	0.0034
MSTRG.30561.46596	2.6742	0.0001	0.0071	MSTRG.9236.14201	2.7436	0.0043	0.0494
MSTRG.30568.46605	2.2661	0.0010	0.0235	MSTRG.928.1416	5.2146	0.0005	0.0170
MSTRG.30615.46676	3.0641	0.0017	0.0305	MSTRG.9285.14266	3.8158	0.0004	0.0149
MSTRG.30656.46742	3.3769	0.0023	0.0349	MSTRG.9411.14469	2.7619	0.0003	0.0123
MSTRG.30656.46750	2.5037	0.0006	0.0175	MSTRG.9411.14471	4.0314	0.0000	0.0027
MSTRG.30657.46744	4.9455	0.0007	0.0197	MSTRG.9429.14500	3.7572	0.0042	0.0488
MSTRG.30657.46746	2.4274	0.0024	0.0356	MSTRG.9653.14837	2.6609	0.0018	0.0310
MSTRG.30691.46800	2.5611	0.0003	0.0132	MSTRG.9653.14838	2.5560	0.0006	0.0186
MSTRG.30781.46932	9.8533	0.0000	0.0037	MSTRG.9664.14852	3.8426	0.0001	0.0067
MSTRG.30783.46934	2.5416	0.0013	0.0260	MSTRG.9679.14894	3.8682	0.0001	0.0073
MSTRG.30857.47039	9.6555	0.0034	0.0440	MSTRG.970.1469	4.6133	0.0004	0.0150
MSTRG.30877.47066	2.1027	0.0005	0.0172	MSTRG.972.1471	4.5272	0.0005	0.0158
MSTRG.30913.47110	3.0800	0.0019	0.0314	MSTRG.9775.15071	13.4355	0.0002	0.0102
MSTRG.30949.47162	3.9380	0.0000	0.0028	MSTRG.9776.15069	2.9130	0.0014	0.0271
MSTRG.30971.47193	5.4286	0.0019	0.0318	MSTRG.9777.15073	2.0795	0.0011	0.0244
MSTRG.31036.47292	4.6118	0.0005	0.0165	MSTRG.9816.15125	8.0105	0.0000	0.0033
MSTRG.31036.47303	4.0136	0.0004	0.0150	MSTRG.9934.15286	2.4147	0.0034	0.0439

Table S4.3: Downregulated transcripts under control conditions

Transcript ID	fc	pval	qval	Transcript ID	fc	pval	qval
MSTRG.44654.68029	0.3238	7.50E-10	0.0000	MSTRG.35014.53320	0.4249	0.0008	0.0202
MSTRG.17055.26020	0.2214	9.83E-10	0.0000	MSTRG.38150.58121	0.3339	0.0008	0.0202
MSTRG.6762.10439	0.0337	1.51E-09	0.0000	MSTRG.32045.48847	0.3646	0.0008	0.0203
MSTRG.32016.48799	0.0669	1.21E-08	0.0001	MSTRG.5696.8612	0.4248	0.0008	0.0203
MSTRG.4339.6476	0.0327	1.65E-08	0.0001	MSTRG.14249.21844	0.2349	0.0008	0.0203
MSTRG.374.544	0.2333	2.76E-08	0.0001	MSTRG.17059.26025	0.2325	0.0008	0.0204
MSTRG.24964.38068	0.2876	2.79E-08	0.0001	MSTRG.16218.24702	0.1578	0.0008	0.0204
MSTRG.19349.29531	0.3418	3.24E-08	0.0001	MSTRG.4068.6102	0.4633	0.0008	0.0204
MSTRG.18754.28619	0.0724	3.61E-08	0.0001	MSTRG.16492.25109	0.3226	0.0008	0.0206
MSTRG.17415.26564	0.0483	3.84E-08	0.0001	MSTRG.1323.1964	0.1448	0.0008	0.0206
MSTRG.2613.3874	0.1007	4.05E-08	0.0001	MSTRG.6527.10019	0.4829	0.0008	0.0207
MSTRG.29954.45703	0.1654	5.68E-08	0.0002	MSTRG.25640.39043	0.0955	0.0008	0.0207
MSTRG.12456.19144	0.0257	6.34E-08	0.0002	MSTRG.38887.59199	0.1078	0.0008	0.0207
MSTRG.437.630	0.1086	9.07E-08	0.0002	MSTRG.30138.45948	0.1499	0.0008	0.0209
MSTRG.31952.48705	0.0512	1.03E-07	0.0002	MSTRG.16880.25695	0.4506	0.0008	0.0209
MSTRG.9221.14161	0.0564	1.04E-07	0.0002	MSTRG.44567.67882	0.4428	0.0008	0.0210
MSTRG.92.133	0.1080	1.42E-07	0.0002	MSTRG.18044.27583	0.4107	0.0008	0.0211
MSTRG.36.57	0.1333	1.48E-07	0.0002	MSTRG.32517.49576	0.1177	0.0008	0.0211
MSTRG.31143.47450	0.1061	1.54E-07	0.0002	MSTRG.25264.38492	0.2391	0.0008	0.0212
MSTRG.2002.2973	0.1364	1.77E-07	0.0003	MSTRG.42272.64471	0.1367	0.0008	0.0213
MSTRG.32762.49912	0.0576	1.88E-07	0.0003	MSTRG.9229.14183	0.4993	0.0008	0.0213
MSTRG.31160.47477	0.0836	1.99E-07	0.0003	MSTRG.19886.30258	0.4544	0.0008	0.0213
MSTRG.7581.11690	0.1057	2.05E-07	0.0003	MSTRG.42037.64053	0.3900	0.0008	0.0214
MSTRG.3396.5069	0.2336	2.52E-07	0.0003	MSTRG.20677.31425	0.3090	0.0008	0.0214
MSTRG.10580.16291	0.0744	2.74E-07	0.0003	MSTRG.36011.54870	0.3479	0.0008	0.0214

MSTRG.12272.18861	0.1392	3.26E-07	0.0004	MSTRG.3570.5309	0.3539	0.0008	0.0214
MSTRG.17938.27438	0.4182	4.78E-07	0.0005	MSTRG.9214.14152	0.3318	0.0008	0.0214
MSTRG.45260.68996	0.0212	5.11E-07	0.0005	MSTRG.32148.48994	0.1869	0.0009	0.0215
MSTRG.6123.9297	0.4442	5.87E-07	0.0006	MSTRG.24396.37178	0.3867	0.0009	0.0215
MSTRG.17523.26713	0.0918	7.62E-07	0.0007	MSTRG.26154.39794	0.3850	0.0009	0.0215
MSTRG.29705.45326	0.2238	7.62E-07	0.0007	MSTRG.43663.66666	0.3535	0.0009	0.0215
MSTRG.44997.68557	0.0102	7.69E-07	0.0007	MSTRG.45681.69646	0.4800	0.0009	0.0216
MSTRG.16098.24516	0.2179	8.38E-07	0.0008	MSTRG.31476.47969	0.2001	0.0009	0.0216
MSTRG.37195.56688	0.0233	8.64E-07	0.0008	MSTRG.7276.11270	0.4516	0.0009	0.0216
MSTRG.8234.12670	0.0375	8.92E-07	0.0008	MSTRG.16450.25051	0.3083	0.0009	0.0216
MSTRG.13959.21422	0.0671	9.49E-07	0.0008	MSTRG.29833.45514	0.3155	0.0009	0.0216
MSTRG.24120.36788	0.1246	9.86E-07	0.0008	MSTRG.14017.21517	0.2059	0.0009	0.0216
MSTRG.11863.18283	0.0846	9.95E-07	0.0008	MSTRG.9344.14369	0.4173	0.0009	0.0217
MSTRG.41118.62658	0.1022	1.03E-06	0.0008	MSTRG.16160.24602	0.3406	0.0009	0.0217
MSTRG.819.1250	0.1219	1.04E-06	0.0008	MSTRG.47615.72537	0.1140	0.0009	0.0217
MSTRG.498.721	0.1000	1.05E-06	0.0008	MSTRG.46210.70458	0.4018	0.0009	0.0217
MSTRG.7340.11381	0.0816	1.07E-06	0.0008	MSTRG.10108.15518	0.3904	0.0009	0.0217
MSTRG.30319.46201	0.0896	1.08E-06	0.0008	MSTRG.29572.45104	0.3122	0.0009	0.0217
MSTRG.16864.25665	0.3384	1.15E-06	0.0008	MSTRG.12730.19580	0.2937	0.0009	0.0217
MSTRG.41275.62883	0.2429	1.19E-06	0.0008	MSTRG.47678.72631	0.3914	0.0009	0.0218
MSTRG.29167.44464	0.0125	1.36E-06	0.0009	MSTRG.39015.59411	0.4576	0.0009	0.0219
MSTRG.19299.29434	0.2104	1.41E-06	0.0009	MSTRG.10411.16018	0.3603	0.0009	0.0219
MSTRG.28672.43677	0.0614	1.43E-06	0.0009	MSTRG.29710.45336	0.2695	0.0009	0.0219
MSTRG.15405.23517	0.0562	1.44E-06	0.0009	MSTRG.7197.11159	0.4611	0.0009	0.0219
MSTRG.22166.33739	0.0090	1.63E-06	0.0010	MSTRG.45698.69668	0.3173	0.0009	0.0219
MSTRG.494.714	0.0738	1.72E-06	0.0010	MSTRG.10349.15922	0.4599	0.0009	0.0221
MSTRG.33356.50801	0.1962	1.76E-06	0.0010	MSTRG.19309.29466	0.0748	0.0009	0.0221

MSTRG.26538.40360	0.4675	1.83E-06	0.0010	MSTRG.9724.14995	0.1737	0.0009	0.0222
MSTRG.36057.54943	0.0792	2.07E-06	0.0011	MSTRG.40246.61319	0.2139	0.0009	0.0222
MSTRG.41862.63788	0.1300	2.17E-06	0.0011	MSTRG.38364.58433	0.2575	0.0009	0.0222
MSTRG.28811.43871	0.1381	2.19E-06	0.0011	MSTRG.35432.53958	0.3242	0.0009	0.0223
MSTRG.11131.17085	0.4022	2.23E-06	0.0011	MSTRG.31053.47320	0.3383	0.0009	0.0224
MSTRG.15087.23067	0.3837	2.24E-06	0.0011	MSTRG.14133.21687	0.2352	0.0009	0.0224
MSTRG.46184.70424	0.0651	2.32E-06	0.0011	MSTRG.25296.38534	0.2586	0.0009	0.0224
MSTRG.12558.19331	0.3008	2.48E-06	0.0012	MSTRG.46959.71607	0.4190	0.0009	0.0224
MSTRG.28575.43531	0.1961	2.54E-06	0.0012	MSTRG.36207.55202	0.2869	0.0009	0.0225
MSTRG.32702.49826	0.2184	2.57E-06	0.0012	MSTRG.12465.19163	0.3792	0.0009	0.0226
MSTRG.13786.21170	0.1437	2.58E-06	0.0012	MSTRG.15171.23176	0.3922	0.0009	0.0226
MSTRG.40585.61905	0.2132	2.62E-06	0.0012	MSTRG.24151.36824	0.4869	0.0009	0.0226
MSTRG.6522.10012	0.3442	2.67E-06	0.0012	MSTRG.3819.5675	0.2441	0.0010	0.0226
MSTRG.35197.53600	0.1003	2.68E-06	0.0012	MSTRG.17601.26836	0.3992	0.0010	0.0226
MSTRG.29835.45517	0.1516	2.80E-06	0.0012	MSTRG.3964.5913	0.2162	0.0010	0.0226
MSTRG.42456.64743	0.1722	2.87E-06	0.0012	MSTRG.18701.28550	0.0982	0.0010	0.0227
MSTRG.16356.24911	0.0281	3.25E-06	0.0014	MSTRG.18526.28296	0.3579	0.0010	0.0228
MSTRG.5602.8479	0.3958	3.25E-06	0.0014	MSTRG.9301.14288	0.2969	0.0010	0.0229
MSTRG.20211.30727	0.3044	3.36E-06	0.0014	MSTRG.42597.64949	0.0998	0.0010	0.0229
MSTRG.20660.31395	0.1323	3.89E-06	0.0016	MSTRG.32678.49787	0.3571	0.0010	0.0229
MSTRG.29979.45739	0.1508	3.92E-06	0.0016	MSTRG.12820.19712	0.4149	0.0010	0.0229
MSTRG.11246.17237	0.1714	4.34E-06	0.0017	MSTRG.17754.27107	0.1421	0.0010	0.0229
MSTRG.35174.53563	0.2812	4.41E-06	0.0017	MSTRG.44753.68189	0.0439	0.0010	0.0231
MSTRG.45401.69199	0.1455	4.65E-06	0.0018	MSTRG.11260.17265	0.1045	0.0010	0.0231
MSTRG.45563.69470	0.1052	4.80E-06	0.0018	MSTRG.30549.46579	0.3744	0.0010	0.0231
MSTRG.17621.26895	0.1289	5.12E-06	0.0019	MSTRG.14331.21945	0.1761	0.0010	0.0231
MSTRG.9533.14641	0.0704	5.30E-06	0.0019	MSTRG.12300.18913	0.2495	0.0010	0.0235

MSTRG.42682.65074	0.1982	5.38E-06	0.0019	MSTRG.987.1490	0.2298	0.0010	0.0235
MSTRG.12272.18860	0.1591	5.40E-06	0.0019	MSTRG.8725.13397	0.3225	0.0010	0.0235
MSTRG.9696.14961	0.3046	5.48E-06	0.0019	MSTRG.5909.8941	0.4703	0.0010	0.0235
MSTRG.21027.31980	0.0028	5.49E-06	0.0019	MSTRG.32621.49721	0.4735	0.0010	0.0236
MSTRG.1193.1766	0.4291	5.54E-06	0.0019	MSTRG.41593.63378	0.1086	0.0010	0.0236
MSTRG.1323.1965	0.0661	5.78E-06	0.0019	MSTRG.16690.25392	0.0782	0.0010	0.0236
MSTRG.2545.3772	0.1145	5.85E-06	0.0019	MSTRG.10888.16718	0.4079	0.0010	0.0236
MSTRG.34289.52170	0.2317	5.86E-06	0.0019	MSTRG.36389.55509	0.4421	0.0010	0.0237
MSTRG.28025.42707	0.1368	6.04E-06	0.0019	MSTRG.374.545	0.3725	0.0010	0.0238
MSTRG.14708.22506	0.4216	6.24E-06	0.0019	MSTRG.25434.38739	0.4453	0.0011	0.0239
MSTRG.37767.57578	0.1458	6.26E-06	0.0019	MSTRG.23763.36257	0.0820	0.0011	0.0240
MSTRG.42166.64314	0.0247	6.33E-06	0.0019	MSTRG.15420.23535	0.3735	0.0011	0.0240
MSTRG.22569.34390	0.0631	6.57E-06	0.0020	MSTRG.1083.1623	0.4507	0.0011	0.0240
MSTRG.36311.55402	0.0820	6.67E-06	0.0020	MSTRG.36378.55496	0.4977	0.0011	0.0240
MSTRG.15895.24217	0.2303	7.48E-06	0.0022	MSTRG.25624.39023	0.2552	0.0011	0.0240
MSTRG.27418.41773	0.0918	8.21E-06	0.0023	MSTRG.115.178	0.4291	0.0011	0.0240
MSTRG.18251.27912	0.1234	8.45E-06	0.0023	MSTRG.32397.49387	0.4246	0.0011	0.0241
MSTRG.21861.33325	0.1667	9.15E-06	0.0025	MSTRG.11796.18188	0.1569	0.0011	0.0241
MSTRG.35048.53381	0.0142	9.30E-06	0.0025	MSTRG.5164.7786	0.4777	0.0011	0.0241
MSTRG.8403.12915	0.1397	9.46E-06	0.0025	MSTRG.11901.18341	0.4389	0.0011	0.0241
MSTRG.36311.55400	0.2336	9.64E-06	0.0026	MSTRG.16229.24716	0.3216	0.0011	0.0242
MSTRG.2252.3339	0.4245	9.81E-06	0.0026	MSTRG.41883.63819	0.3872	0.0011	0.0243
MSTRG.21972.33481	0.1438	9.88E-06	0.0026	MSTRG.40252.61330	0.4632	0.0011	0.0243
MSTRG.29585.45130	0.1742	9.96E-06	0.0026	MSTRG.8105.12475	0.2803	0.0011	0.0244
MSTRG.14059.21591	0.3325	1.02E-05	0.0026	MSTRG.26799.40776	0.2872	0.0011	0.0245
MSTRG.23615.36030	0.3466	1.04E-05	0.0026	MSTRG.16292.24818	0.4046	0.0011	0.0245
MSTRG.16289.24815	0.1002	1.07E-05	0.0027	MSTRG.25100.38277	0.1517	0.0011	0.0245

MSTRG.537.813	0.1579	1.08E-05	0.0027	MSTRG.18737.28594	0.1167	0.0011	0.0245
MSTRG.1295.1930	0.0447	1.08E-05	0.0027	MSTRG.15967.24333	0.3471	0.0011	0.0247
MSTRG.4951.7449	0.2731	1.13E-05	0.0027	MSTRG.27749.42288	0.2036	0.0011	0.0248
MSTRG.33428.50895	0.4581	1.14E-05	0.0027	MSTRG.747.1126	0.3047	0.0011	0.0249
MSTRG.14155.21712	0.2627	1.20E-05	0.0029	MSTRG.18179.27791	0.4583	0.0011	0.0249
MSTRG.47826.72841	0.1796	1.26E-05	0.0029	MSTRG.11796.18186	0.1319	0.0012	0.0250
MSTRG.1982.2946	0.2948	1.30E-05	0.0030	MSTRG.35443.53974	0.3985	0.0012	0.0250
MSTRG.24231.36931	0.3606	1.31E-05	0.0030	MSTRG.5447.8224	0.3476	0.0012	0.0251
MSTRG.27429.41790	0.1604	1.32E-05	0.0030	MSTRG.42439.64717	0.3260	0.0012	0.0252
MSTRG.41931.63883	0.2477	1.33E-05	0.0030	MSTRG.40868.62319	0.4810	0.0012	0.0252
MSTRG.1914.2843	0.2017	1.35E-05	0.0030	MSTRG.6690.10328	0.4306	0.0012	0.0252
MSTRG.33108.50424	0.4558	1.35E-05	0.0030	MSTRG.4080.6118	0.4234	0.0012	0.0253
MSTRG.12859.19769	0.0903	1.38E-05	0.0030	MSTRG.3590.5340	0.3276	0.0012	0.0253
MSTRG.46492.70915	0.4780	1.39E-05	0.0030	MSTRG.25519.38855	0.3765	0.0012	0.0253
MSTRG.21030.32001	0.1991	1.40E-05	0.0030	MSTRG.45272.69014	0.4667	0.0012	0.0253
MSTRG.1670.2497	0.0590	1.41E-05	0.0030	MSTRG.40371.61491	0.2466	0.0012	0.0253
MSTRG.1295.1929	0.0540	1.41E-05	0.0030	MSTRG.43512.66358	0.3292	0.0012	0.0253
MSTRG.7651.11785	0.3367	1.42E-05	0.0030	MSTRG.7401.11453	0.4437	0.0012	0.0253
MSTRG.23072.35208	0.0657	1.47E-05	0.0030	MSTRG.25091.38266	0.3730	0.0012	0.0253
MSTRG.5048.7608	0.1325	1.48E-05	0.0030	MSTRG.26225.39891	0.4132	0.0012	0.0254
MSTRG.13409.20602	0.4911	1.50E-05	0.0031	MSTRG.41852.63775	0.2704	0.0012	0.0255
MSTRG.32217.49099	0.4620	1.52E-05	0.0031	MSTRG.10412.16019	0.4138	0.0012	0.0256
MSTRG.22547.34347	0.1450	1.53E-05	0.0031	MSTRG.4012.6025	0.3085	0.0012	0.0257
MSTRG.7419.11473	0.3609	1.58E-05	0.0032	MSTRG.24252.36964	0.4086	0.0012	0.0258
MSTRG.27531.41954	0.1134	1.60E-05	0.0032	MSTRG.25861.39355	0.4744	0.0012	0.0258
MSTRG.24917.37928	0.1431	1.62E-05	0.0032	MSTRG.4178.6244	0.2787	0.0012	0.0260
MSTRG.27795.42361	0.1284	1.76E-05	0.0033	MSTRG.22622.34481	0.1831	0.0012	0.0260

MSTRG.28645.43642	0.2111	1.78E-05	0.0034	MSTRG.14245.21840	0.4682	0.0012	0.0260
MSTRG.23596.35999	0.2901	1.81E-05	0.0034	MSTRG.3963.5909	0.4137	0.0012	0.0260
MSTRG.17651.26943	0.3316	1.83E-05	0.0034	MSTRG.36847.56176	0.3888	0.0012	0.0260
MSTRG.28124.42865	0.3244	1.87E-05	0.0034	MSTRG.35651.54306	0.3799	0.0012	0.0260
MSTRG.18368.28078	0.0979	1.87E-05	0.0034	MSTRG.32541.49612	0.4071	0.0012	0.0260
MSTRG.1899.2818	0.0137	1.90E-05	0.0034	MSTRG.19064.29066	0.1049	0.0012	0.0260
MSTRG.10563.16237	0.0841	1.90E-05	0.0034	MSTRG.23400.35703	0.3678	0.0012	0.0260
MSTRG.37134.56586	0.1301	1.96E-05	0.0035	MSTRG.15639.23856	0.2217	0.0013	0.0260
MSTRG.8981.13779	0.1569	1.99E-05	0.0035	MSTRG.4091.6133	0.3597	0.0013	0.0260
MSTRG.39151.59641	0.0922	2.05E-05	0.0035	MSTRG.48297.73589	0.4006	0.0013	0.0260
MSTRG.22489.34257	0.0435	2.05E-05	0.0035	MSTRG.28323.43141	0.1401	0.0013	0.0261
MSTRG.36707.55983	0.1765	2.08E-05	0.0035	MSTRG.46305.70609	0.3842	0.0013	0.0261
MSTRG.5213.7865	0.0626	2.12E-05	0.0036	MSTRG.42417.64686	0.4278	0.0013	0.0262
MSTRG.35194.53590	0.1490	2.19E-05	0.0036	MSTRG.19959.30362	0.3527	0.0013	0.0262
MSTRG.35294.53752	0.0963	2.23E-05	0.0036	MSTRG.7592.11714	0.3947	0.0013	0.0262
MSTRG.37295.56827	0.1343	2.43E-05	0.0039	MSTRG.37457.57130	0.3772	0.0013	0.0262
MSTRG.9728.15003	0.1273	2.44E-05	0.0039	MSTRG.26580.40430	0.0686	0.0013	0.0262
MSTRG.31890.48598	0.0456	2.56E-05	0.0040	MSTRG.8960.13753	0.3013	0.0013	0.0264
MSTRG.1430.2130	0.1609	2.62E-05	0.0041	MSTRG.47826.72840	0.4640	0.0013	0.0264
MSTRG.23766.36263	0.0278	2.63E-05	0.0041	MSTRG.6214.9455	0.2452	0.0013	0.0265
MSTRG.3894.5805	0.1118	2.72E-05	0.0042	MSTRG.36669.55935	0.2456	0.0013	0.0265
MSTRG.11209.17194	0.2243	2.78E-05	0.0042	MSTRG.35704.54379	0.4597	0.0013	0.0265
MSTRG.17311.26397	0.4213	2.79E-05	0.0043	MSTRG.48009.73124	0.2404	0.0013	0.0265
MSTRG.42248.64440	0.1691	2.92E-05	0.0043	MSTRG.35341.53840	0.4619	0.0013	0.0265
MSTRG.33321.50757	0.1689	2.93E-05	0.0043	MSTRG.44148.67301	0.3046	0.0013	0.0266
MSTRG.43401.66202	0.1801	3.01E-05	0.0044	MSTRG.13393.20563	0.1579	0.0013	0.0266
MSTRG.32085.48903	0.0880	3.07E-05	0.0044	MSTRG.37607.57345	0.4059	0.0013	0.0266

MSTRG.37329.56865	0.4294	3.08E-05	0.0044	MSTRG.32895.50079	0.3509	0.0013	0.0266
MSTRG.29050.44231	0.1587	3.08E-05	0.0044	MSTRG.3004.4471	0.3048	0.0013	0.0266
MSTRG.1083.1622	0.2726	3.09E-05	0.0044	MSTRG.7309.11311	0.4714	0.0013	0.0266
MSTRG.8139.12527	0.0900	3.10E-05	0.0044	MSTRG.1143.1700	0.3509	0.0013	0.0266
MSTRG.10850.16665	0.1609	3.11E-05	0.0044	MSTRG.25477.38805	0.1972	0.0013	0.0266
MSTRG.26802.40782	0.1212	3.16E-05	0.0045	MSTRG.27622.42114	0.1598	0.0013	0.0266
MSTRG.7492.11571	0.0729	3.21E-05	0.0045	MSTRG.33643.51184	0.2345	0.0013	0.0266
MSTRG.21530.32850	0.0552	3.31E-05	0.0046	MSTRG.16498.25117	0.3937	0.0013	0.0267
MSTRG.46108.70291	0.4430	3.34E-05	0.0046	MSTRG.38151.58125	0.3420	0.0013	0.0267
MSTRG.9221.14163	0.2874	3.35E-05	0.0046	MSTRG.11756.17970	0.4353	0.0013	0.0267
MSTRG.11357.17397	0.4409	3.35E-05	0.0046	MSTRG.23144.35310	0.2326	0.0014	0.0268
MSTRG.38267.58306	0.2044	3.37E-05	0.0046	MSTRG.34216.52065	0.4808	0.0014	0.0268
MSTRG.11488.17570	0.3561	3.39E-05	0.0046	MSTRG.38001.57904	0.2266	0.0014	0.0268
MSTRG.8636.13275	0.3998	3.44E-05	0.0046	MSTRG.45939.70029	0.2648	0.0014	0.0269
MSTRG.37419.57066	0.2319	3.44E-05	0.0046	MSTRG.44898.68406	0.4486	0.0014	0.0269
MSTRG.2989.4450	0.2400	3.45E-05	0.0046	MSTRG.40341.61456	0.2533	0.0014	0.0269
MSTRG.12808.19691	0.4375	3.62E-05	0.0047	MSTRG.16180.24643	0.2797	0.0014	0.0269
MSTRG.8631.13269	0.3578	3.64E-05	0.0047	MSTRG.27932.42561	0.2946	0.0014	0.0269
MSTRG.8278.12721	0.2974	3.66E-05	0.0047	MSTRG.29359.44794	0.3943	0.0014	0.0269
MSTRG.42257.64452	0.3475	3.73E-05	0.0048	MSTRG.16697.25404	0.2053	0.0014	0.0269
MSTRG.39971.60892	0.1453	3.74E-05	0.0048	MSTRG.13468.20700	0.3952	0.0014	0.0269
MSTRG.2270.3363	0.1484	3.86E-05	0.0049	MSTRG.38424.58522	0.4053	0.0014	0.0270
MSTRG.5960.9017	0.1318	4.04E-05	0.0051	MSTRG.2100.3113	0.1791	0.0014	0.0270
MSTRG.1295.1927	0.1599	4.05E-05	0.0051	MSTRG.15139.23140	0.2201	0.0014	0.0270
MSTRG.18283.27954	0.3662	4.05E-05	0.0051	MSTRG.24281.37004	0.2847	0.0014	0.0270
MSTRG.26196.39853	0.1749	4.12E-05	0.0051	MSTRG.11221.17207	0.4546	0.0014	0.0271
MSTRG.42912.65442	0.1262	4.17E-05	0.0051	MSTRG.11230.17219	0.4731	0.0014	0.0271

MSTRG.38022.57935	0.2722	4.19E-05	0.0051	MSTRG.33679.51230	0.1103	0.0014	0.0272
MSTRG.46644.71133	0.3863	4.22E-05	0.0051	MSTRG.27326.41651	0.4095	0.0014	0.0273
MSTRG.33984.51681	0.2066	4.22E-05	0.0051	MSTRG.48026.73149	0.2632	0.0014	0.0273
MSTRG.34610.52631	0.2475	4.27E-05	0.0051	MSTRG.22511.34301	0.4454	0.0014	0.0273
MSTRG.17422.26571	0.1871	4.30E-05	0.0052	MSTRG.24048.36687	0.3557	0.0014	0.0273
MSTRG.23401.35704	0.2966	4.32E-05	0.0052	MSTRG.7333.11371	0.3254	0.0014	0.0273
MSTRG.2376.3529	0.0940	4.39E-05	0.0052	MSTRG.25249.38472	0.3353	0.0014	0.0273
MSTRG.44731.68148	0.2044	4.41E-05	0.0052	MSTRG.21715.33116	0.1480	0.0014	0.0273
MSTRG.41392.63058	0.0866	4.58E-05	0.0054	MSTRG.36983.56354	0.2422	0.0014	0.0274
MSTRG.39881.60749	0.3448	4.63E-05	0.0054	MSTRG.10390.15985	0.1520	0.0014	0.0275
MSTRG.36585.55804	0.2759	4.72E-05	0.0055	MSTRG.38553.58704	0.2967	0.0014	0.0275
MSTRG.11258.17261	0.2786	4.88E-05	0.0056	MSTRG.19310.29464	0.1878	0.0015	0.0278
MSTRG.29234.44610	0.2141	4.91E-05	0.0056	MSTRG.21880.33353	0.3509	0.0015	0.0278
MSTRG.20412.31008	0.2276	4.94E-05	0.0056	MSTRG.9996.15369	0.3100	0.0015	0.0279
MSTRG.24160.36847	0.3465	5.09E-05	0.0057	MSTRG.23448.35792	0.2876	0.0015	0.0279
MSTRG.39731.60525	0.1946	5.18E-05	0.0058	MSTRG.3208.4765	0.4696	0.0015	0.0279
MSTRG.1411.2087	0.0615	5.19E-05	0.0058	MSTRG.26799.40779	0.3016	0.0015	0.0279
MSTRG.1464.2186	0.3579	5.26E-05	0.0059	MSTRG.23154.35325	0.3839	0.0015	0.0279
MSTRG.9296.14282	0.4058	5.38E-05	0.0059	MSTRG.27525.41945	0.3453	0.0015	0.0280
MSTRG.34851.53081	0.2755	5.62E-05	0.0061	MSTRG.12957.19911	0.4130	0.0015	0.0281
MSTRG.30535.46555	0.2385	5.65E-05	0.0061	MSTRG.25092.38267	0.4914	0.0015	0.0281
MSTRG.41294.62918	0.1060	5.71E-05	0.0061	MSTRG.24281.37003	0.3073	0.0015	0.0281
MSTRG.10124.15536	0.2502	5.87E-05	0.0063	MSTRG.4382.6557	0.3737	0.0015	0.0281
MSTRG.92.130	0.1688	5.94E-05	0.0063	MSTRG.22176.33757	0.0701	0.0015	0.0281
MSTRG.35648.54302	0.2624	6.02E-05	0.0064	MSTRG.43871.66872	0.3690	0.0015	0.0281
MSTRG.44981.68535	0.1405	6.05E-05	0.0064	MSTRG.20033.30478	0.4708	0.0015	0.0282
MSTRG.34864.53096	0.1427	6.19E-05	0.0065	MSTRG.27976.42614	0.4641	0.0015	0.0283

MSTRG.21240.32342	0.1458	6.21E-05	0.0065	MSTRG.23464.35813	0.2549	0.0015	0.0283
MSTRG.41603.63394	0.1009	6.29E-05	0.0065	MSTRG.30840.47005	0.3292	0.0015	0.0283
MSTRG.33214.50601	0.1209	6.31E-05	0.0065	MSTRG.17129.26119	0.2981	0.0015	0.0284
MSTRG.35049.53384	0.0359	6.49E-05	0.0066	MSTRG.25965.39516	0.1433	0.0015	0.0284
MSTRG.44688.68074	0.3722	6.50E-05	0.0066	MSTRG.39971.60890	0.3253	0.0015	0.0285
MSTRG.14810.22663	0.2852	6.60E-05	0.0066	MSTRG.3088.4594	0.3111	0.0015	0.0285
MSTRG.15606.23810	0.1164	6.62E-05	0.0066	MSTRG.29395.44849	0.2260	0.0015	0.0285
MSTRG.48255.73533	0.1662	6.69E-05	0.0067	MSTRG.7823.12024	0.3709	0.0015	0.0285
MSTRG.17049.26006	0.2813	6.71E-05	0.0067	MSTRG.15351.23441	0.1849	0.0015	0.0286
MSTRG.18245.27891	0.2949	6.79E-05	0.0067	MSTRG.23098.35243	0.4695	0.0015	0.0287
MSTRG.17688.27007	0.2341	6.86E-05	0.0067	MSTRG.40523.61724	0.2452	0.0016	0.0288
MSTRG.8393.12904	0.4296	6.87E-05	0.0067	MSTRG.6149.9340	0.4755	0.0016	0.0288
MSTRG.37128.56569	0.1312	6.88E-05	0.0067	MSTRG.25264.38491	0.4053	0.0016	0.0288
MSTRG.45972.70088	0.1911	6.92E-05	0.0067	MSTRG.12377.19004	0.3712	0.0016	0.0288
MSTRG.20099.30590	0.3799	6.92E-05	0.0067	MSTRG.445.642	0.1997	0.0016	0.0289
MSTRG.39280.59846	0.2827	6.93E-05	0.0067	MSTRG.6666.10300	0.2263	0.0016	0.0289
MSTRG.46792.71350	0.3535	6.99E-05	0.0067	MSTRG.14458.22117	0.4369	0.0016	0.0289
MSTRG.21871.33335	0.3922	7.00E-05	0.0067	MSTRG.35133.53504	0.0762	0.0016	0.0289
MSTRG.13592.20879	0.1338	7.01E-05	0.0067	MSTRG.42858.65361	0.3065	0.0016	0.0290
MSTRG.7955.12250	0.3347	7.04E-05	0.0067	MSTRG.41986.63975	0.2590	0.0016	0.0290
MSTRG.34161.51993	0.1838	7.07E-05	0.0067	MSTRG.2778.4122	0.2167	0.0016	0.0290
MSTRG.20313.30860	0.4337	7.16E-05	0.0068	MSTRG.10333.15903	0.2660	0.0016	0.0292
MSTRG.37345.56965	0.2756	7.31E-05	0.0068	MSTRG.47741.72735	0.3845	0.0016	0.0292
MSTRG.13819.21223	0.3676	7.31E-05	0.0068	MSTRG.32826.49988	0.4393	0.0016	0.0292
MSTRG.44394.67651	0.1058	7.34E-05	0.0068	MSTRG.48736.74269	0.2979	0.0016	0.0292
MSTRG.41950.63906	0.0664	7.34E-05	0.0068	MSTRG.14087.21628	0.3610	0.0016	0.0294
MSTRG.26017.39605	0.3676	7.35E-05	0.0068	MSTRG.8783.13487	0.1620	0.0016	0.0295

MSTRG.28456.43329	0.2308	7.55E-05	0.0069	MSTRG.12652.19481	0.2971	0.0016	0.0295
MSTRG.11357.17398	0.3584	7.55E-05	0.0069	MSTRG.5003.7549	0.4298	0.0016	0.0295
MSTRG.15230.23261	0.3494	7.58E-05	0.0069	MSTRG.8468.13013	0.2361	0.0016	0.0296
MSTRG.26059.39661	0.1026	7.65E-05	0.0069	MSTRG.15472.23619	0.3316	0.0016	0.0296
MSTRG.352.515	0.2010	7.68E-05	0.0069	MSTRG.38650.58833	0.3994	0.0016	0.0296
MSTRG.14305.21914	0.4270	7.75E-05	0.0070	MSTRG.2022.2995	0.2616	0.0016	0.0297
MSTRG.26461.40242	0.4528	7.82E-05	0.0070	MSTRG.17876.27312	0.3809	0.0016	0.0297
MSTRG.24167.36854	0.3552	7.86E-05	0.0070	MSTRG.1929.2862	0.2722	0.0017	0.0298
MSTRG.28630.43620	0.4825	7.96E-05	0.0071	MSTRG.25284.38517	0.4318	0.0017	0.0299
MSTRG.19270.29400	0.0696	8.01E-05	0.0071	MSTRG.6637.10212	0.2493	0.0017	0.0299
MSTRG.18281.27951	0.1557	8.02E-05	0.0071	MSTRG.16646.25338	0.4453	0.0017	0.0300
MSTRG.6528.10021	0.4945	8.26E-05	0.0071	MSTRG.30750.46890	0.1882	0.0017	0.0300
MSTRG.28090.42808	0.3384	8.27E-05	0.0071	MSTRG.6856.10577	0.4434	0.0017	0.0301
MSTRG.13870.21289	0.1651	8.33E-05	0.0071	MSTRG.37483.57172	0.0781	0.0017	0.0301
MSTRG.11796.18185	0.2087	8.50E-05	0.0072	MSTRG.45237.68964	0.3609	0.0017	0.0301
MSTRG.36013.54876	0.3395	8.76E-05	0.0073	MSTRG.36119.55046	0.3571	0.0017	0.0302
MSTRG.23252.35472	0.1343	8.77E-05	0.0073	MSTRG.31027.47282	0.1334	0.0017	0.0302
MSTRG.27979.42624	0.0129	9.03E-05	0.0074	MSTRG.20380.30958	0.3036	0.0017	0.0302
MSTRG.7914.12173	0.3276	9.12E-05	0.0075	MSTRG.6018.9124	0.3602	0.0017	0.0302
MSTRG.45045.68663	0.3990	9.26E-05	0.0075	MSTRG.24183.36874	0.3749	0.0017	0.0302
MSTRG.34995.53276	0.2237	9.26E-05	0.0075	MSTRG.33475.50948	0.4889	0.0017	0.0302
MSTRG.15158.23161	0.2164	9.29E-05	0.0075	MSTRG.35774.54514	0.3339	0.0017	0.0302
MSTRG.6591.10143	0.1501	9.56E-05	0.0076	MSTRG.23433.35767	0.1198	0.0017	0.0302
MSTRG.33886.51535	0.1871	9.58E-05	0.0076	MSTRG.39348.59947	0.3929	0.0017	0.0302
MSTRG.35668.54329	0.1536	9.72E-05	0.0077	MSTRG.36123.55049	0.1791	0.0017	0.0303
MSTRG.28745.43769	0.2418	9.80E-05	0.0077	MSTRG.27526.41944	0.4132	0.0017	0.0304
MSTRG.46705.71208	0.3157	9.81E-05	0.0077	MSTRG.43600.66465	0.3110	0.0017	0.0304

MSTRG.40570.61886	0.2091	9.91E-05	0.0077	MSTRG.38312.58361	0.3867	0.0017	0.0304
MSTRG.32999.50235	0.2288	9.92E-05	0.0077	MSTRG.37774.57586	0.1383	0.0017	0.0305
MSTRG.43193.65881	0.3228	1.01E-04	0.0078	MSTRG.3402.5078	0.3651	0.0017	0.0305
MSTRG.9728.15002	0.2993	1.01E-04	0.0078	MSTRG.29876.45579	0.2002	0.0017	0.0305
MSTRG.7333.11365	0.3479	1.01E-04	0.0078	MSTRG.25836.39317	0.1112	0.0017	0.0305
MSTRG.5674.8585	0.4768	1.01E-04	0.0078	MSTRG.35823.54583	0.3823	0.0017	0.0306
MSTRG.38545.58694	0.1316	1.02E-04	0.0078	MSTRG.26536.40358	0.3173	0.0018	0.0306
MSTRG.7521.11614	0.4294	1.02E-04	0.0078	MSTRG.9692.14955	0.1572	0.0018	0.0306
MSTRG.21536.32861	0.3348	1.02E-04	0.0078	MSTRG.28845.43919	0.3040	0.0018	0.0306
MSTRG.21092.32083	0.1373	1.02E-04	0.0078	MSTRG.27844.42437	0.1491	0.0018	0.0306
MSTRG.35716.54394	0.3082	1.03E-04	0.0078	MSTRG.835.1273	0.2666	0.0018	0.0306
MSTRG.1096.1636	0.2185	1.03E-04	0.0078	MSTRG.42740.65156	0.2246	0.0018	0.0306
MSTRG.47795.72802	0.3267	1.03E-04	0.0078	MSTRG.7915.12174	0.2731	0.0018	0.0307
MSTRG.21166.32198	0.1574	1.04E-04	0.0078	MSTRG.34031.51776	0.2540	0.0018	0.0307
MSTRG.9322.14335	0.3265	1.05E-04	0.0079	MSTRG.29929.45663	0.3501	0.0018	0.0307
MSTRG.36718.55997	0.2518	1.06E-04	0.0080	MSTRG.20778.31568	0.4626	0.0018	0.0308
MSTRG.30138.45951	0.1187	1.07E-04	0.0080	MSTRG.18127.27706	0.4941	0.0018	0.0308
MSTRG.45198.68908	0.2664	1.08E-04	0.0080	MSTRG.29509.45017	0.3305	0.0018	0.0309
MSTRG.43710.66642	0.3293	1.08E-04	0.0080	MSTRG.41796.63706	0.4652	0.0018	0.0310
MSTRG.21030.32002	0.1766	1.09E-04	0.0080	MSTRG.35887.54681	0.2788	0.0018	0.0310
MSTRG.9908.15245	0.0331	1.10E-04	0.0081	MSTRG.10336.15902	0.4185	0.0018	0.0310
MSTRG.27261.41549	0.2773	1.11E-04	0.0081	MSTRG.8419.12934	0.4460	0.0018	0.0311
MSTRG.8691.13351	0.4772	1.11E-04	0.0081	MSTRG.33805.51428	0.2394	0.0018	0.0311
MSTRG.1670.2495	0.3136	1.12E-04	0.0081	MSTRG.459.660	0.2975	0.0018	0.0311
MSTRG.19799.30154	0.3180	1.12E-04	0.0081	MSTRG.48718.74239	0.2484	0.0018	0.0311
MSTRG.28382.43237	0.3621	1.13E-04	0.0082	MSTRG.36388.55508	0.3905	0.0018	0.0312
MSTRG.21647.33016	0.1609	1.13E-04	0.0082	MSTRG.39685.60463	0.4934	0.0018	0.0313

MSTRG.25093.38269	0.4127	1.14E-04	0.0082	MSTRG.43053.65669	0.4847	0.0018	0.0313
MSTRG.1404.2077	0.4597	1.14E-04	0.0082	MSTRG.12707.19548	0.2967	0.0018	0.0314
MSTRG.14338.21954	0.3824	1.15E-04	0.0082	MSTRG.12585.19390	0.2299	0.0019	0.0314
MSTRG.3797.5643	0.4993	1.15E-04	0.0082	MSTRG.26187.39836	0.4943	0.0019	0.0314
MSTRG.7315.11336	0.4360	1.17E-04	0.0083	MSTRG.39656.60429	0.0813	0.0019	0.0315
MSTRG.45342.69111	0.2660	1.18E-04	0.0083	MSTRG.22687.34593	0.2717	0.0019	0.0315
MSTRG.46297.70601	0.4812	1.21E-04	0.0085	MSTRG.26802.40781	0.3408	0.0019	0.0316
MSTRG.10837.16649	0.1317	1.21E-04	0.0085	MSTRG.28761.43790	0.4839	0.0019	0.0316
MSTRG.7941.12218	0.3022	1.22E-04	0.0085	MSTRG.35980.54824	0.2427	0.0019	0.0316
MSTRG.15661.23882	0.1743	1.23E-04	0.0085	MSTRG.1227.1809	0.4107	0.0019	0.0317
MSTRG.47541.72434	0.0253	1.23E-04	0.0085	MSTRG.47056.71748	0.4175	0.0019	0.0317
MSTRG.17199.26214	0.3496	1.23E-04	0.0086	MSTRG.2532.3757	0.4048	0.0019	0.0317
MSTRG.46788.71345	0.1833	1.24E-04	0.0086	MSTRG.39181.59693	0.4701	0.0019	0.0318
MSTRG.8641.13281	0.1016	1.27E-04	0.0086	MSTRG.27366.41706	0.4400	0.0019	0.0318
MSTRG.2134.3163	0.3900	1.28E-04	0.0087	MSTRG.17129.26118	0.2798	0.0019	0.0318
MSTRG.3938.5875	0.1010	1.30E-04	0.0087	MSTRG.7842.12055	0.3733	0.0019	0.0318
MSTRG.2645.3917	0.1451	1.30E-04	0.0087	MSTRG.44967.68507	0.2440	0.0019	0.0318
MSTRG.4001.6022	0.1799	1.31E-04	0.0087	MSTRG.41604.63396	0.4804	0.0019	0.0319
MSTRG.2093.3103	0.2144	1.31E-04	0.0087	MSTRG.38092.58033	0.4422	0.0019	0.0319
MSTRG.29671.45257	0.3593	1.32E-04	0.0088	MSTRG.31599.48186	0.4267	0.0019	0.0320
MSTRG.5534.8375	0.1095	1.34E-04	0.0088	MSTRG.42868.65377	0.3564	0.0019	0.0320
MSTRG.13746.21103	0.2519	1.37E-04	0.0090	MSTRG.48775.74330	0.3521	0.0019	0.0321
MSTRG.8909.13690	0.3536	1.39E-04	0.0091	MSTRG.41989.63982	0.3712	0.0020	0.0321
MSTRG.35882.54673	0.2898	1.40E-04	0.0091	MSTRG.40927.62399	0.1418	0.0020	0.0322
MSTRG.6855.10576	0.2263	1.41E-04	0.0092	MSTRG.9692.14936	0.2087	0.0020	0.0322
MSTRG.34324.52231	0.0467	1.41E-04	0.0092	MSTRG.17358.26478	0.3906	0.0020	0.0322
MSTRG.47864.72898	0.3744	1.41E-04	0.0092	MSTRG.1345.1993	0.4377	0.0020	0.0322

MSTRG.39350.59950	0.3049	1.43E-04	0.0092	MSTRG.25164.38369	0.3917	0.0020	0.0323
MSTRG.43238.65934	0.4915	1.44E-04	0.0092	MSTRG.45007.68572	0.1319	0.0020	0.0323
MSTRG.18580.28365	0.2637	1.45E-04	0.0092	MSTRG.40066.61025	0.2597	0.0020	0.0323
MSTRG.34063.51833	0.2385	1.45E-04	0.0092	MSTRG.37437.57104	0.1894	0.0020	0.0324
MSTRG.46131.70322	0.1069	1.45E-04	0.0092	MSTRG.36896.56235	0.1954	0.0020	0.0324
MSTRG.28512.43435	0.3020	1.46E-04	0.0092	MSTRG.47655.72605	0.3785	0.0020	0.0324
MSTRG.28716.43729	0.1636	1.49E-04	0.0094	MSTRG.28897.44013	0.4339	0.0020	0.0324
MSTRG.1715.2566	0.3516	1.51E-04	0.0094	MSTRG.6338.9661	0.4106	0.0020	0.0325
MSTRG.21992.33504	0.1178	1.51E-04	0.0094	MSTRG.23205.35387	0.2467	0.0020	0.0326
MSTRG.23649.36084	0.2047	1.55E-04	0.0096	MSTRG.14850.22733	0.1806	0.0020	0.0327
MSTRG.22668.34548	0.2916	1.56E-04	0.0096	MSTRG.29842.45531	0.3773	0.0020	0.0328
MSTRG.7520.11613	0.3619	1.56E-04	0.0096	MSTRG.44953.68491	0.4624	0.0020	0.0328
MSTRG.39181.59694	0.1083	1.58E-04	0.0096	MSTRG.7285.11283	0.4850	0.0020	0.0328
MSTRG.11632.17789	0.2306	1.59E-04	0.0096	MSTRG.6146.9332	0.2135	0.0020	0.0328
MSTRG.17118.26104	0.1783	1.59E-04	0.0096	MSTRG.33957.51636	0.2708	0.0021	0.0331
MSTRG.1628.2446	0.0917	1.60E-04	0.0096	MSTRG.37014.56391	0.4065	0.0021	0.0331
MSTRG.18463.28213	0.1562	1.60E-04	0.0096	MSTRG.16832.25608	0.2439	0.0021	0.0331
MSTRG.40121.61130	0.4291	1.61E-04	0.0096	MSTRG.47653.72604	0.0812	0.0021	0.0331
MSTRG.39147.59634	0.4572	1.61E-04	0.0096	MSTRG.490.706	0.3638	0.0021	0.0331
MSTRG.14887.22794	0.4636	1.64E-04	0.0097	MSTRG.441.637	0.2707	0.0021	0.0331
MSTRG.10882.16705	0.3650	1.65E-04	0.0098	MSTRG.15170.23175	0.4228	0.0021	0.0331
MSTRG.22976.35078	0.0560	1.67E-04	0.0098	MSTRG.30419.46342	0.4127	0.0021	0.0332
MSTRG.4775.7162	0.4482	1.67E-04	0.0098	MSTRG.10272.15822	0.4489	0.0021	0.0332
MSTRG.29464.44951	0.2761	1.67E-04	0.0098	MSTRG.44703.68095	0.3659	0.0021	0.0332
MSTRG.456.657	0.2422	1.68E-04	0.0098	MSTRG.36473.55630	0.1082	0.0021	0.0332
MSTRG.42733.65146	0.3057	1.69E-04	0.0099	MSTRG.28128.42870	0.2745	0.0021	0.0332
MSTRG.48647.74143	0.2902	1.71E-04	0.0100	MSTRG.48819.74430	0.4639	0.0021	0.0332

MSTRG.6942.10724	0.3487	1.72E-04	0.0100	MSTRG.33606.51136	0.3561	0.0021	0.0332
MSTRG.42298.64509	0.3576	1.74E-04	0.0100	MSTRG.25558.38916	0.3215	0.0021	0.0332
MSTRG.24185.36876	0.3329	1.74E-04	0.0100	MSTRG.7212.11179	0.4573	0.0021	0.0333
MSTRG.24391.37171	0.0683	1.75E-04	0.0101	MSTRG.6546.10070	0.2444	0.0021	0.0334
MSTRG.48080.73258	0.2746	1.78E-04	0.0102	MSTRG.31239.47622	0.4666	0.0021	0.0334
MSTRG.25512.38847	0.3210	1.79E-04	0.0102	MSTRG.14592.22331	0.3927	0.0021	0.0334
MSTRG.396.575	0.2095	1.79E-04	0.0102	MSTRG.27973.42609	0.4705	0.0021	0.0334
MSTRG.25811.39274	0.4777	1.80E-04	0.0102	MSTRG.47042.71728	0.3550	0.0021	0.0334
MSTRG.21173.32206	0.3850	1.80E-04	0.0102	MSTRG.29185.44498	0.3286	0.0021	0.0335
MSTRG.22313.33981	0.4547	1.87E-04	0.0105	MSTRG.29609.45159	0.4519	0.0021	0.0336
MSTRG.42418.64687	0.4022	1.89E-04	0.0106	MSTRG.10642.16366	0.2374	0.0021	0.0338
MSTRG.3839.5707	0.3012	1.90E-04	0.0106	MSTRG.18196.27817	0.1196	0.0021	0.0338
MSTRG.2626.3892	0.2145	1.91E-04	0.0106	MSTRG.4012.6021	0.2593	0.0022	0.0340
MSTRG.39849.60696	0.0880	1.93E-04	0.0107	MSTRG.6886.10643	0.3923	0.0022	0.0340
MSTRG.44923.68450	0.4278	1.93E-04	0.0107	MSTRG.16840.25627	0.1736	0.0022	0.0340
MSTRG.41358.63015	0.0341	1.94E-04	0.0107	MSTRG.3970.5923	0.2607	0.0022	0.0340
MSTRG.26679.40599	0.2033	1.94E-04	0.0107	MSTRG.36262.55316	0.1100	0.0022	0.0341
MSTRG.7916.12175	0.3971	1.96E-04	0.0107	MSTRG.12278.18870	0.1055	0.0022	0.0342
MSTRG.6820.10518	0.3308	1.97E-04	0.0107	MSTRG.39504.60196	0.3468	0.0022	0.0342
MSTRG.22965.35058	0.1111	1.98E-04	0.0108	MSTRG.38670.58869	0.2748	0.0022	0.0342
MSTRG.4154.6211	0.0056	1.99E-04	0.0108	MSTRG.1897.2815	0.1212	0.0022	0.0343
MSTRG.11097.17033	0.3705	1.99E-04	0.0108	MSTRG.37177.56661	0.3224	0.0022	0.0343
MSTRG.19810.30168	0.2876	2.00E-04	0.0108	MSTRG.24151.36826	0.4436	0.0022	0.0343
MSTRG.17652.26944	0.2299	2.01E-04	0.0108	MSTRG.24719.37675	0.4316	0.0022	0.0343
MSTRG.14488.22166	0.3053	2.02E-04	0.0108	MSTRG.40113.61119	0.4615	0.0022	0.0345
MSTRG.25832.39310	0.3282	2.03E-04	0.0108	MSTRG.19801.30157	0.3619	0.0022	0.0345
MSTRG.44978.68532	0.4161	2.04E-04	0.0108	MSTRG.204.296	0.3015	0.0022	0.0345

MSTRG.36025.54899	0.2635	2.04E-04	0.0108	MSTRG.8722.13393	0.4904	0.0022	0.0345
MSTRG.39491.60183	0.0934	2.04E-04	0.0108	MSTRG.12679.19509	0.1873	0.0022	0.0345
MSTRG.3073.4570	0.4697	2.04E-04	0.0108	MSTRG.3951.5893	0.1950	0.0022	0.0346
MSTRG.33856.51498	0.2109	2.06E-04	0.0109	MSTRG.36759.56043	0.4146	0.0023	0.0346
MSTRG.46112.70296	0.2467	2.08E-04	0.0110	MSTRG.39669.60443	0.4533	0.0023	0.0346
MSTRG.41576.63353	0.4597	2.08E-04	0.0110	MSTRG.37501.57201	0.3608	0.0023	0.0349
MSTRG.835.1276	0.2857	2.10E-04	0.0110	MSTRG.11796.18184	0.1691	0.0023	0.0351
MSTRG.44180.67347	0.2923	2.11E-04	0.0110	MSTRG.6577.10120	0.1478	0.0023	0.0351
MSTRG.35542.54123	0.3468	2.12E-04	0.0110	MSTRG.6203.9435	0.2925	0.0023	0.0351
MSTRG.658.970	0.3738	2.12E-04	0.0110	MSTRG.15278.23340	0.4380	0.0023	0.0351
MSTRG.17876.27311	0.1619	2.12E-04	0.0110	MSTRG.10450.16083	0.4466	0.0023	0.0352
MSTRG.44951.68489	0.4436	2.15E-04	0.0110	MSTRG.34450.52421	0.2655	0.0023	0.0353
MSTRG.12838.19740	0.3298	2.18E-04	0.0111	MSTRG.20833.31651	0.4683	0.0023	0.0353
MSTRG.9692.14937	0.2069	2.19E-04	0.0112	MSTRG.44567.67884	0.2823	0.0023	0.0353
MSTRG.11477.17559	0.3305	2.20E-04	0.0112	MSTRG.18550.28326	0.4312	0.0023	0.0354
MSTRG.29055.44258	0.0782	2.21E-04	0.0112	MSTRG.36977.56347	0.4056	0.0023	0.0356
MSTRG.45914.69982	0.3162	2.21E-04	0.0112	MSTRG.42000.64002	0.2360	0.0024	0.0356
MSTRG.46397.70776	0.3020	2.23E-04	0.0112	MSTRG.1470.2194	0.3797	0.0024	0.0356
MSTRG.32899.50088	0.1950	2.25E-04	0.0113	MSTRG.47729.72718	0.3796	0.0024	0.0356
MSTRG.38742.58980	0.3236	2.26E-04	0.0113	MSTRG.7862.12082	0.2921	0.0024	0.0356
MSTRG.343.502	0.4504	2.27E-04	0.0113	MSTRG.37483.57175	0.3360	0.0024	0.0356
MSTRG.41719.63564	0.3418	2.28E-04	0.0113	MSTRG.1305.1941	0.4921	0.0024	0.0356
MSTRG.46645.71134	0.4829	2.29E-04	0.0114	MSTRG.6346.9673	0.3521	0.0024	0.0358
MSTRG.20167.30675	0.2930	2.30E-04	0.0114	MSTRG.10763.16554	0.4105	0.0024	0.0358
MSTRG.10725.16504	0.3520	2.30E-04	0.0114	MSTRG.44996.68555	0.3004	0.0024	0.0358
MSTRG.8925.13714	0.0832	2.32E-04	0.0114	MSTRG.4014.6023	0.2694	0.0024	0.0358
MSTRG.9484.14573	0.1640	2.36E-04	0.0115	MSTRG.47139.71858	0.1737	0.0024	0.0359

MSTRG.27358.41692	0.2766	2.36E-04	0.0115	MSTRG.15323.23402	0.3117	0.0024	0.0359
MSTRG.17212.26256	0.1551	2.37E-04	0.0115	MSTRG.33662.51204	0.4144	0.0024	0.0360
MSTRG.5001.7542	0.4721	2.37E-04	0.0115	MSTRG.36157.55116	0.2648	0.0024	0.0360
MSTRG.42788.65242	0.4825	2.38E-04	0.0116	MSTRG.21905.33375	0.4150	0.0024	0.0360
MSTRG.16988.25914	0.2977	2.39E-04	0.0116	MSTRG.9054.13896	0.3152	0.0024	0.0361
MSTRG.13216.20332	0.4989	2.41E-04	0.0117	MSTRG.16369.24925	0.2777	0.0024	0.0361
MSTRG.36720.55999	0.3586	2.41E-04	0.0117	MSTRG.20007.30437	0.3953	0.0024	0.0361
MSTRG.45044.68661	0.4014	2.43E-04	0.0117	MSTRG.9050.13888	0.4674	0.0024	0.0361
MSTRG.6562.10093	0.2194	2.43E-04	0.0117	MSTRG.22846.34854	0.3174	0.0024	0.0363
MSTRG.22675.34563	0.3633	2.43E-04	0.0117	MSTRG.33660.51202	0.3767	0.0024	0.0363
MSTRG.36744.56028	0.2589	2.44E-04	0.0117	MSTRG.13389.20558	0.4891	0.0025	0.0364
MSTRG.32899.50084	0.3460	2.46E-04	0.0118	MSTRG.9104.13983	0.1823	0.0025	0.0364
MSTRG.45389.69183	0.4287	2.50E-04	0.0119	MSTRG.13521.20778	0.4411	0.0025	0.0364
MSTRG.21536.32863	0.4505	2.52E-04	0.0119	MSTRG.488.703	0.2878	0.0025	0.0364
MSTRG.29825.45505	0.2297	2.52E-04	0.0119	MSTRG.20289.30834	0.3581	0.0025	0.0365
MSTRG.32213.49093	0.2118	2.52E-04	0.0119	MSTRG.27913.42527	0.1316	0.0025	0.0365
MSTRG.25270.38500	0.3000	2.54E-04	0.0119	MSTRG.45912.69979	0.4748	0.0025	0.0366
MSTRG.17850.27268	0.3176	2.54E-04	0.0119	MSTRG.11144.17104	0.4627	0.0025	0.0366
MSTRG.44667.68046	0.1809	2.55E-04	0.0119	MSTRG.17843.27256	0.1758	0.0025	0.0366
MSTRG.33683.51236	0.3417	2.55E-04	0.0119	MSTRG.34057.51824	0.1815	0.0025	0.0369
MSTRG.20425.31036	0.3101	2.57E-04	0.0119	MSTRG.11719.17920	0.4243	0.0025	0.0369
MSTRG.30187.46006	0.2863	2.57E-04	0.0119	MSTRG.38156.58132	0.3335	0.0025	0.0369
MSTRG.43050.65665	0.3061	2.57E-04	0.0119	MSTRG.43501.66345	0.4711	0.0025	0.0371
MSTRG.41083.62614	0.1483	2.58E-04	0.0119	MSTRG.45015.68582	0.4969	0.0025	0.0371
MSTRG.9592.14734	0.2737	2.58E-04	0.0119	MSTRG.47283.72043	0.1880	0.0025	0.0371
MSTRG.20618.31329	0.3251	2.58E-04	0.0119	MSTRG.37694.57482	0.1098	0.0025	0.0371
MSTRG.21664.33040	0.4106	2.58E-04	0.0119	MSTRG.46844.71430	0.4368	0.0025	0.0371

MSTRG.44175.67337	0.4905	2.59E-04	0.0119	MSTRG.33004.50240	0.3615	0.0025	0.0372
MSTRG.37941.57818	0.1683	2.59E-04	0.0119	MSTRG.26427.40192	0.3926	0.0026	0.0372
MSTRG.13287.20429	0.2101	2.61E-04	0.0119	MSTRG.41576.63354	0.3462	0.0026	0.0372
MSTRG.20744.31514	0.1698	2.61E-04	0.0119	MSTRG.36093.55002	0.3395	0.0026	0.0373
MSTRG.28784.43827	0.2299	2.61E-04	0.0119	MSTRG.14879.22784	0.4958	0.0026	0.0373
MSTRG.23560.35957	0.1725	2.61E-04	0.0119	MSTRG.24151.36823	0.4825	0.0026	0.0374
MSTRG.5191.7828	0.2617	2.65E-04	0.0120	MSTRG.20247.30784	0.4947	0.0026	0.0375
MSTRG.23612.36025	0.3484	2.65E-04	0.0120	MSTRG.34503.52487	0.1843	0.0026	0.0375
MSTRG.1304.1940	0.4270	2.66E-04	0.0120	MSTRG.44840.68315	0.1952	0.0026	0.0375
MSTRG.17764.27127	0.4835	2.68E-04	0.0121	MSTRG.31582.48156	0.3927	0.0026	0.0378
MSTRG.10348.15921	0.2903	2.69E-04	0.0121	MSTRG.11802.18189	0.2142	0.0026	0.0379
MSTRG.11743.17955	0.4552	2.70E-04	0.0121	MSTRG.1185.1755	0.4758	0.0026	0.0379
MSTRG.23754.36237	0.2366	2.72E-04	0.0122	MSTRG.21518.32833	0.3710	0.0026	0.0380
MSTRG.39963.60872	0.0866	2.73E-04	0.0122	MSTRG.14262.21860	0.4430	0.0026	0.0380
MSTRG.38411.58503	0.3677	2.74E-04	0.0122	MSTRG.15364.23457	0.3580	0.0026	0.0381
MSTRG.22718.34631	0.3717	2.74E-04	0.0122	MSTRG.41897.63845	0.3884	0.0026	0.0381
MSTRG.19173.29274	0.1899	2.75E-04	0.0122	MSTRG.9028.13845	0.2552	0.0027	0.0381
MSTRG.23390.35691	0.1828	2.77E-04	0.0123	MSTRG.15894.24216	0.4361	0.0027	0.0381
MSTRG.1707.2553	0.1992	2.77E-04	0.0123	MSTRG.19931.30325	0.3176	0.0027	0.0382
MSTRG.31707.48335	0.2950	2.80E-04	0.0123	MSTRG.17118.26103	0.3848	0.0027	0.0382
MSTRG.12700.19537	0.0624	2.82E-04	0.0124	MSTRG.17790.27158	0.2406	0.0027	0.0383
MSTRG.6816.10514	0.2637	2.83E-04	0.0124	MSTRG.23234.35441	0.3518	0.0027	0.0383
MSTRG.18957.28907	0.1756	2.85E-04	0.0125	MSTRG.4364.6531	0.3885	0.0027	0.0383
MSTRG.38383.58467	0.3586	2.87E-04	0.0125	MSTRG.43193.65883	0.2283	0.0027	0.0383
MSTRG.47158.71884	0.2540	2.89E-04	0.0126	MSTRG.37895.57760	0.2600	0.0027	0.0384
MSTRG.15967.24330	0.4106	2.90E-04	0.0126	MSTRG.13902.21334	0.1393	0.0027	0.0384
MSTRG.31495.47998	0.4474	2.90E-04	0.0126	MSTRG.42859.65362	0.3867	0.0027	0.0385

MSTRG.4380.6552	0.2362	2.91E-04	0.0126	MSTRG.45900.69965	0.4575	0.0027	0.0385
MSTRG.24336.37064	0.0365	2.91E-04	0.0126	MSTRG.22846.34855	0.3406	0.0027	0.0385
MSTRG.25964.39513	0.4669	2.93E-04	0.0127	MSTRG.36718.55996	0.0902	0.0027	0.0385
MSTRG.38553.58705	0.2109	2.93E-04	0.0127	MSTRG.10602.16316	0.1747	0.0027	0.0385
MSTRG.5858.8865	0.3099	2.94E-04	0.0127	MSTRG.25327.38583	0.2346	0.0027	0.0386
MSTRG.40921.62391	0.3212	2.94E-04	0.0127	MSTRG.9692.14920	0.2348	0.0027	0.0386
MSTRG.13319.20475	0.4027	2.97E-04	0.0128	MSTRG.107.152	0.4445	0.0027	0.0386
MSTRG.25161.38366	0.2767	2.98E-04	0.0128	MSTRG.14669.22449	0.4265	0.0027	0.0386
MSTRG.24044.36679	0.3403	2.99E-04	0.0128	MSTRG.41719.63565	0.2324	0.0028	0.0388
MSTRG.41439.63123	0.1609	3.01E-04	0.0128	MSTRG.37442.57108	0.3336	0.0028	0.0393
MSTRG.25756.39202	0.4594	3.04E-04	0.0129	MSTRG.33317.50751	0.1862	0.0028	0.0393
MSTRG.6807.10504	0.1969	3.09E-04	0.0130	MSTRG.6207.9457	0.4782	0.0028	0.0393
MSTRG.36025.54901	0.3239	3.10E-04	0.0130	MSTRG.15625.23836	0.3380	0.0028	0.0394
MSTRG.21299.32420	0.3624	3.12E-04	0.0131	MSTRG.2966.4393	0.4089	0.0028	0.0394
MSTRG.22719.34632	0.3155	3.14E-04	0.0132	MSTRG.32003.48783	0.3939	0.0028	0.0394
MSTRG.46141.70333	0.4652	3.20E-04	0.0133	MSTRG.15055.23029	0.4006	0.0028	0.0394
MSTRG.31505.48011	0.1237	3.20E-04	0.0133	MSTRG.27906.42520	0.1418	0.0029	0.0396
MSTRG.33317.50750	0.2911	3.28E-04	0.0135	MSTRG.25669.39084	0.2334	0.0029	0.0396
MSTRG.31890.48596	0.2966	3.28E-04	0.0135	MSTRG.14256.21852	0.4311	0.0029	0.0396
MSTRG.28035.42720	0.0482	3.29E-04	0.0135	MSTRG.35778.54530	0.4506	0.0029	0.0396
MSTRG.5155.7775	0.2106	3.31E-04	0.0136	MSTRG.728.1097	0.2456	0.0029	0.0398
MSTRG.32942.50144	0.1200	3.32E-04	0.0136	MSTRG.46266.70552	0.4955	0.0029	0.0398
MSTRG.24390.37169	0.0674	3.32E-04	0.0136	MSTRG.7929.12196	0.4996	0.0029	0.0399
MSTRG.37632.57398	0.2105	3.32E-04	0.0136	MSTRG.33748.51336	0.3342	0.0029	0.0402
MSTRG.38102.58047	0.2649	3.33E-04	0.0136	MSTRG.17768.27132	0.3560	0.0029	0.0403
MSTRG.29055.44254	0.0585	3.33E-04	0.0136	MSTRG.23164.35337	0.3827	0.0029	0.0403
MSTRG.37150.56620	0.2728	3.34E-04	0.0136	MSTRG.10018.15399	0.4613	0.0029	0.0403

MSTRG.22492.34259	0.3398	3.35E-04	0.0136	MSTRG.6263.9529	0.3660	0.0029	0.0404
MSTRG.6873.10614	0.3104	3.37E-04	0.0136	MSTRG.19867.30238	0.1012	0.0029	0.0404
MSTRG.22846.34861	0.2980	3.38E-04	0.0136	MSTRG.14250.21845	0.3571	0.0030	0.0405
MSTRG.37677.57459	0.4343	3.40E-04	0.0137	MSTRG.32517.49574	0.0098	0.0030	0.0406
MSTRG.22867.34899	0.3263	3.41E-04	0.0137	MSTRG.44417.67682	0.2195	0.0030	0.0406
MSTRG.23479.35836	0.3910	3.43E-04	0.0137	MSTRG.23153.35324	0.4125	0.0030	0.0406
MSTRG.42455.64739	0.3470	3.43E-04	0.0137	MSTRG.11762.17976	0.2400	0.0030	0.0406
MSTRG.47423.72242	0.3334	3.44E-04	0.0137	MSTRG.1534.2288	0.2866	0.0030	0.0407
MSTRG.6893.10652	0.0667	3.45E-04	0.0137	MSTRG.40555.61879	0.0791	0.0030	0.0407
MSTRG.13797.21186	0.0964	3.47E-04	0.0137	MSTRG.24937.37953	0.2806	0.0030	0.0407
MSTRG.18036.27574	0.3102	3.48E-04	0.0137	MSTRG.30576.46621	0.3501	0.0030	0.0408
MSTRG.1804.2687	0.1255	3.48E-04	0.0137	MSTRG.13615.20919	0.3077	0.0030	0.0408
MSTRG.14922.22843	0.0704	3.48E-04	0.0137	MSTRG.14171.21735	0.3068	0.0030	0.0408
MSTRG.533.799	0.2171	3.50E-04	0.0137	MSTRG.44885.68371	0.4783	0.0030	0.0408
MSTRG.17894.27338	0.2557	3.51E-04	0.0137	MSTRG.47893.72957	0.0726	0.0030	0.0409
MSTRG.14246.21841	0.2785	3.52E-04	0.0138	MSTRG.42634.64999	0.2003	0.0030	0.0409
MSTRG.38725.58945	0.1505	3.59E-04	0.0139	MSTRG.21856.33313	0.2455	0.0030	0.0411
MSTRG.48090.73284	0.4809	3.66E-04	0.0141	MSTRG.28735.43750	0.2831	0.0030	0.0412
MSTRG.8282.12725	0.1960	3.67E-04	0.0141	MSTRG.23766.36260	0.0261	0.0031	0.0413
MSTRG.36631.55866	0.1374	3.68E-04	0.0141	MSTRG.13927.21368	0.4809	0.0031	0.0413
MSTRG.26943.41039	0.3352	3.68E-04	0.0141	MSTRG.8983.13783	0.3919	0.0031	0.0414
MSTRG.728.1096	0.1954	3.69E-04	0.0141	MSTRG.11564.17682	0.1896	0.0031	0.0414
MSTRG.38098.58043	0.3861	3.76E-04	0.0143	MSTRG.20745.31518	0.1924	0.0031	0.0415
MSTRG.22735.34654	0.3599	3.78E-04	0.0143	MSTRG.32286.49215	0.1675	0.0031	0.0415
MSTRG.21089.32078	0.4461	3.80E-04	0.0144	MSTRG.34467.52443	0.3095	0.0031	0.0415
MSTRG.23430.35760	0.0902	3.82E-04	0.0144	MSTRG.12101.18584	0.4130	0.0031	0.0416
MSTRG.38094.58035	0.4106	3.87E-04	0.0146	MSTRG.16439.25039	0.3379	0.0031	0.0418

MSTRG.42709.65116	0.4970	3.90E-04	0.0146	MSTRG.6682.10318	0.0160	0.0031	0.0418
MSTRG.36587.55805	0.2574	3.91E-04	0.0146	MSTRG.31479.47986	0.1793	0.0031	0.0419
MSTRG.29626.45179	0.2696	3.93E-04	0.0147	MSTRG.31413.47876	0.3846	0.0031	0.0419
MSTRG.8137.12523	0.3735	3.94E-04	0.0147	MSTRG.15408.23520	0.1046	0.0031	0.0419
MSTRG.47254.71996	0.2811	3.95E-04	0.0147	MSTRG.8407.12920	0.2725	0.0032	0.0421
MSTRG.47555.72448	0.3032	3.95E-04	0.0147	MSTRG.21028.31994	0.2785	0.0032	0.0421
MSTRG.25516.38851	0.2257	4.03E-04	0.0149	MSTRG.1239.1840	0.1525	0.0032	0.0421
MSTRG.3632.5404	0.2161	4.05E-04	0.0149	MSTRG.1918.2848	0.3736	0.0032	0.0421
MSTRG.5353.8075	0.3959	4.06E-04	0.0149	MSTRG.45234.68960	0.3322	0.0032	0.0421
MSTRG.6018.9125	0.3794	4.06E-04	0.0149	MSTRG.41762.63633	0.2414	0.0032	0.0421
MSTRG.34691.52757	0.3082	4.07E-04	0.0149	MSTRG.41773.63652	0.2169	0.0032	0.0422
MSTRG.688.1010	0.2319	4.08E-04	0.0149	MSTRG.3884.5775	0.1951	0.0032	0.0423
MSTRG.10245.15758	0.2901	4.09E-04	0.0149	MSTRG.28556.43497	0.2955	0.0032	0.0425
MSTRG.29196.44536	0.2387	4.10E-04	0.0149	MSTRG.31511.48018	0.3509	0.0032	0.0425
MSTRG.17602.26837	0.2541	4.15E-04	0.0151	MSTRG.32447.49474	0.3540	0.0032	0.0426
MSTRG.17021.25964	0.3615	4.19E-04	0.0152	MSTRG.33338.50776	0.4766	0.0032	0.0426
MSTRG.21470.32773	0.2030	4.19E-04	0.0152	MSTRG.38100.58044	0.3909	0.0032	0.0427
MSTRG.32238.49129	0.1865	4.19E-04	0.0152	MSTRG.45838.69875	0.4142	0.0032	0.0427
MSTRG.27935.42566	0.4927	4.22E-04	0.0152	MSTRG.30341.46229	0.3048	0.0033	0.0428
MSTRG.48738.74271	0.1807	4.22E-04	0.0152	MSTRG.29710.45338	0.4250	0.0033	0.0428
MSTRG.28556.43502	0.2891	4.25E-04	0.0153	MSTRG.9031.13861	0.3423	0.0033	0.0428
MSTRG.17028.25974	0.4372	4.26E-04	0.0153	MSTRG.44642.68011	0.4310	0.0033	0.0429
MSTRG.10011.15388	0.4991	4.29E-04	0.0154	MSTRG.18788.28675	0.2291	0.0033	0.0429
MSTRG.15071.23059	0.1990	4.31E-04	0.0154	MSTRG.9924.15267	0.1518	0.0033	0.0429
MSTRG.26891.40940	0.3559	4.32E-04	0.0154	MSTRG.40236.61306	0.3757	0.0033	0.0429
MSTRG.32517.49573	0.0448	4.32E-04	0.0154	MSTRG.27326.41649	0.2681	0.0033	0.0431
MSTRG.25518.38854	0.1265	4.33E-04	0.0154	MSTRG.6090.9250	0.2350	0.0033	0.0431

MSTRG.24382.37161	0.1359	4.34E-04	0.0154	MSTRG.24963.38067	0.1512	0.0033	0.0431
MSTRG.20745.31517	0.1631	4.35E-04	0.0154	MSTRG.18395.28121	0.1316	0.0033	0.0431
MSTRG.8783.13485	0.3686	4.35E-04	0.0154	MSTRG.31920.48652	0.3192	0.0033	0.0432
MSTRG.45735.69717	0.4932	4.37E-04	0.0154	MSTRG.28114.42840	0.2733	0.0033	0.0433
MSTRG.46203.70448	0.2918	4.39E-04	0.0155	MSTRG.24813.37787	0.4430	0.0033	0.0433
MSTRG.44191.67365	0.2946	4.45E-04	0.0156	MSTRG.23379.35678	0.4561	0.0033	0.0433
MSTRG.35099.53457	0.1498	4.50E-04	0.0157	MSTRG.40480.61658	0.2658	0.0033	0.0433
MSTRG.42763.65202	0.1191	4.53E-04	0.0157	MSTRG.15194.23204	0.4813	0.0033	0.0434
MSTRG.42143.64287	0.4623	4.53E-04	0.0157	MSTRG.35958.54790	0.3336	0.0033	0.0435
MSTRG.37694.57479	0.2841	4.53E-04	0.0157	MSTRG.13383.20552	0.2920	0.0034	0.0436
MSTRG.27550.41978	0.0746	4.53E-04	0.0157	MSTRG.13241.20361	0.4071	0.0034	0.0437
MSTRG.15229.23260	0.4269	4.60E-04	0.0158	MSTRG.11603.17737	0.3467	0.0034	0.0437
MSTRG.20243.30767	0.0999	4.61E-04	0.0158	MSTRG.4419.6618	0.4892	0.0034	0.0437
MSTRG.9478.14563	0.1513	4.61E-04	0.0158	MSTRG.2906.4318	0.3565	0.0034	0.0437
MSTRG.17318.26408	0.1597	4.61E-04	0.0158	MSTRG.43700.66625	0.4103	0.0034	0.0437
MSTRG.32447.49472	0.1440	4.62E-04	0.0158	MSTRG.29708.45325	0.3787	0.0034	0.0438
MSTRG.11568.17686	0.4867	4.62E-04	0.0158	MSTRG.11761.17975	0.2680	0.0034	0.0438
MSTRG.9033.13866	0.3418	4.62E-04	0.0158	MSTRG.42657.65036	0.2083	0.0034	0.0438
MSTRG.28987.44132	0.4061	4.62E-04	0.0158	MSTRG.15952.24304	0.2652	0.0034	0.0439
MSTRG.9158.14054	0.2658	4.66E-04	0.0159	MSTRG.48564.74012	0.3472	0.0034	0.0440
MSTRG.26939.41033	0.1181	4.68E-04	0.0159	MSTRG.45669.69631	0.1780	0.0034	0.0441
MSTRG.21568.32904	0.2723	4.69E-04	0.0160	MSTRG.22626.34490	0.1112	0.0034	0.0441
MSTRG.30341.46230	0.2024	4.75E-04	0.0161	MSTRG.7021.10868	0.3553	0.0034	0.0441
MSTRG.1942.2881	0.4829	4.78E-04	0.0161	MSTRG.26446.40223	0.0788	0.0034	0.0441
MSTRG.28553.43494	0.3540	4.78E-04	0.0161	MSTRG.19071.29082	0.3144	0.0035	0.0442
MSTRG.11863.18284	0.2450	4.86E-04	0.0163	MSTRG.45580.69502	0.4050	0.0035	0.0444
MSTRG.27910.42523	0.4501	4.87E-04	0.0163	MSTRG.40866.62317	0.3537	0.0035	0.0444

MSTRG.35979.54820	0.1556	4.93E-04	0.0164	MSTRG.38737.58968	0.4471	0.0035	0.0444
MSTRG.9285.14268	0.1790	4.93E-04	0.0164	MSTRG.16180.24642	0.1315	0.0035	0.0444
MSTRG.47309.72073	0.1407	4.95E-04	0.0164	MSTRG.16018.24401	0.3713	0.0035	0.0444
MSTRG.2626.3889	0.1657	4.95E-04	0.0164	MSTRG.21789.33209	0.2783	0.0035	0.0444
MSTRG.39769.60578	0.2007	4.98E-04	0.0164	MSTRG.29055.44253	0.1266	0.0035	0.0445
MSTRG.8473.13022	0.4966	5.01E-04	0.0165	MSTRG.1459.2173	0.2984	0.0035	0.0445
MSTRG.43163.65828	0.3016	5.03E-04	0.0166	MSTRG.18649.28476	0.3372	0.0035	0.0447
MSTRG.38899.59218	0.2947	5.06E-04	0.0166	MSTRG.4184.6251	0.3628	0.0035	0.0447
MSTRG.39848.60695	0.3420	5.07E-04	0.0166	MSTRG.42867.65378	0.0766	0.0035	0.0447
MSTRG.24979.38086	0.4492	5.09E-04	0.0166	MSTRG.20821.31637	0.0607	0.0035	0.0447
MSTRG.44945.68482	0.1886	5.09E-04	0.0166	MSTRG.24759.37726	0.3731	0.0035	0.0447
MSTRG.11273.17283	0.3212	5.11E-04	0.0167	MSTRG.14399.22042	0.4572	0.0035	0.0450
MSTRG.13620.20927	0.3874	5.13E-04	0.0167	MSTRG.42318.64548	0.3057	0.0036	0.0450
MSTRG.4951.7448	0.2173	5.13E-04	0.0167	MSTRG.3131.4651	0.4151	0.0036	0.0450
MSTRG.18341.28030	0.3499	5.15E-04	0.0167	MSTRG.24596.37495	0.3680	0.0036	0.0451
MSTRG.22490.34256	0.0537	5.16E-04	0.0167	MSTRG.1205.1779	0.4876	0.0036	0.0452
MSTRG.25791.39248	0.3165	5.28E-04	0.0170	MSTRG.9312.14316	0.1964	0.0036	0.0452
MSTRG.37596.57334	0.4762	5.33E-04	0.0171	MSTRG.30112.45909	0.2470	0.0036	0.0452
MSTRG.3401.5077	0.3596	5.39E-04	0.0172	MSTRG.8023.12334	0.4181	0.0036	0.0452
MSTRG.16474.25086	0.1805	5.46E-04	0.0174	MSTRG.21222.32288	0.4992	0.0036	0.0453
MSTRG.29102.44333	0.3637	5.46E-04	0.0174	MSTRG.42632.64995	0.3252	0.0036	0.0453
MSTRG.25339.38604	0.4610	5.47E-04	0.0174	MSTRG.23679.36131	0.2195	0.0036	0.0453
MSTRG.37351.56975	0.2524	5.48E-04	0.0174	MSTRG.10529.16186	0.4763	0.0036	0.0453
MSTRG.29315.44734	0.3520	5.49E-04	0.0174	MSTRG.16824.25589	0.0557	0.0036	0.0453
MSTRG.32997.50230	0.3208	5.52E-04	0.0174	MSTRG.16382.24947	0.4728	0.0036	0.0453
MSTRG.25377.38661	0.1923	5.53E-04	0.0175	MSTRG.16485.25101	0.4031	0.0036	0.0453
MSTRG.10541.16203	0.2950	5.57E-04	0.0175	MSTRG.11796.18187	0.1557	0.0036	0.0454

MSTRG.9404.14458	0.4647	5.61E-04	0.0176	MSTRG.48503.73898	0.2496	0.0036	0.0454
MSTRG.35860.54639	0.2960	5.65E-04	0.0176	MSTRG.40782.62207	0.4018	0.0037	0.0456
MSTRG.22054.33594	0.2172	5.66E-04	0.0177	MSTRG.18116.27693	0.4814	0.0037	0.0458
MSTRG.33048.50317	0.3594	5.68E-04	0.0177	MSTRG.46511.70960	0.3035	0.0037	0.0459
MSTRG.2566.3804	0.3909	5.69E-04	0.0177	MSTRG.9649.14825	0.4717	0.0037	0.0462
MSTRG.47044.71730	0.2905	5.72E-04	0.0178	MSTRG.18942.28883	0.4227	0.0037	0.0462
MSTRG.33283.50689	0.1846	5.75E-04	0.0178	MSTRG.6546.10069	0.3638	0.0038	0.0463
MSTRG.27758.42304	0.4536	5.76E-04	0.0178	MSTRG.37940.57817	0.3903	0.0038	0.0463
MSTRG.48074.73304	0.4903	5.76E-04	0.0178	MSTRG.42104.64209	0.0538	0.0038	0.0463
MSTRG.33510.50997	0.2263	5.78E-04	0.0178	MSTRG.36739.56021	0.2782	0.0038	0.0463
MSTRG.27755.42298	0.4790	5.84E-04	0.0179	MSTRG.7843.12059	0.1455	0.0038	0.0463
MSTRG.15350.23440	0.1004	5.85E-04	0.0179	MSTRG.2093.3101	0.4286	0.0038	0.0463
MSTRG.18603.28407	0.2548	5.85E-04	0.0179	MSTRG.30294.46168	0.2914	0.0038	0.0463
MSTRG.31217.47572	0.4152	5.87E-04	0.0180	MSTRG.47574.72475	0.2834	0.0038	0.0463
MSTRG.29521.45042	0.3543	5.88E-04	0.0180	MSTRG.40745.62146	0.4528	0.0038	0.0463
MSTRG.37326.56862	0.2807	5.88E-04	0.0180	MSTRG.43462.66282	0.3361	0.0038	0.0464
MSTRG.40555.61854	0.0176	5.90E-04	0.0180	MSTRG.3644.5422	0.4500	0.0038	0.0465
MSTRG.26059.39656	0.4481	5.91E-04	0.0180	MSTRG.1194.1767	0.0590	0.0038	0.0465
MSTRG.7954.12249	0.3720	5.93E-04	0.0180	MSTRG.48010.73126	0.4829	0.0038	0.0465
MSTRG.47927.73012	0.4631	5.93E-04	0.0180	MSTRG.15409.23521	0.4370	0.0038	0.0466
MSTRG.21453.32749	0.3362	5.95E-04	0.0180	MSTRG.32719.49853	0.3956	0.0038	0.0466
MSTRG.28145.42890	0.2760	5.97E-04	0.0181	MSTRG.38647.58827	0.4295	0.0038	0.0466
MSTRG.46277.70571	0.3106	6.05E-04	0.0182	MSTRG.31351.47777	0.4581	0.0038	0.0466
MSTRG.37674.57460	0.2922	6.07E-04	0.0183	MSTRG.13750.21109	0.3729	0.0038	0.0466
MSTRG.17653.26945	0.3597	6.08E-04	0.0183	MSTRG.15676.23918	0.4589	0.0038	0.0467
MSTRG.27934.42565	0.3658	6.09E-04	0.0183	MSTRG.21156.32174	0.1013	0.0038	0.0467
MSTRG.6752.10425	0.3723	6.12E-04	0.0183	MSTRG.25387.38673	0.4416	0.0038	0.0467

MSTRG.47823.72836	0.4770	6.16E-04	0.0184	MSTRG.9179.14084	0.2931	0.0038	0.0467
MSTRG.36066.54958	0.3867	6.17E-04	0.0184	MSTRG.21890.33360	0.1771	0.0039	0.0467
MSTRG.14253.21849	0.3395	6.23E-04	0.0185	MSTRG.13068.20064	0.3873	0.0039	0.0467
MSTRG.36127.55060	0.2431	6.28E-04	0.0186	MSTRG.32912.50106	0.4613	0.0039	0.0468
MSTRG.38398.58488	0.1886	6.31E-04	0.0186	MSTRG.38056.57986	0.3233	0.0039	0.0470
MSTRG.37374.57002	0.3123	6.34E-04	0.0186	MSTRG.21390.32575	0.2741	0.0039	0.0470
MSTRG.36025.54903	0.3180	6.36E-04	0.0186	MSTRG.38412.58506	0.3598	0.0039	0.0470
MSTRG.10934.16793	0.3122	6.37E-04	0.0186	MSTRG.15353.23444	0.4007	0.0039	0.0470
MSTRG.12848.19751	0.4371	6.37E-04	0.0186	MSTRG.29817.45494	0.4178	0.0039	0.0471
MSTRG.31601.48190	0.4015	6.38E-04	0.0186	MSTRG.15536.23714	0.1149	0.0039	0.0472
MSTRG.22309.33974	0.3265	6.40E-04	0.0186	MSTRG.21682.33067	0.4069	0.0039	0.0473
MSTRG.5494.8293	0.2448	6.42E-04	0.0187	MSTRG.39024.59421	0.0731	0.0039	0.0473
MSTRG.14403.22046	0.4576	6.43E-04	0.0187	MSTRG.3542.5269	0.2172	0.0039	0.0473
MSTRG.19309.29465	0.1876	6.50E-04	0.0188	MSTRG.9542.14665	0.4567	0.0039	0.0473
MSTRG.35396.53914	0.1152	6.51E-04	0.0188	MSTRG.8751.13431	0.1374	0.0039	0.0474
MSTRG.9477.14562	0.1371	6.53E-04	0.0188	MSTRG.18261.27925	0.4462	0.0039	0.0474
MSTRG.39770.60580	0.2205	6.55E-04	0.0188	MSTRG.3642.5419	0.3514	0.0040	0.0476
MSTRG.24657.37587	0.2043	6.55E-04	0.0188	MSTRG.22264.33894	0.3866	0.0040	0.0477
MSTRG.36327.55432	0.2398	6.57E-04	0.0188	MSTRG.41083.62617	0.2619	0.0040	0.0478
MSTRG.42295.64506	0.2408	6.64E-04	0.0189	MSTRG.27223.41500	0.3261	0.0040	0.0478
MSTRG.33969.51660	0.2039	6.65E-04	0.0189	MSTRG.13886.21317	0.3832	0.0040	0.0478
MSTRG.42919.65457	0.1534	6.71E-04	0.0190	MSTRG.19145.29182	0.3698	0.0040	0.0478
MSTRG.47281.72037	0.1276	6.74E-04	0.0191	MSTRG.12765.19633	0.2885	0.0040	0.0478
MSTRG.30120.45926	0.4295	6.76E-04	0.0192	MSTRG.46838.71422	0.1499	0.0040	0.0479
MSTRG.1727.2592	0.3311	6.78E-04	0.0192	MSTRG.14245.21839	0.3664	0.0040	0.0480
MSTRG.3988.6074	0.1601	6.80E-04	0.0192	MSTRG.36076.54974	0.4142	0.0040	0.0480
MSTRG.37294.56829	0.4673	6.80E-04	0.0192	MSTRG.46491.70914	0.3846	0.0040	0.0480

MSTRG.45572.69489	0.3852	6.82E-04	0.0192	MSTRG.9405.14459	0.3611	0.0041	0.0480
MSTRG.17680.26996	0.4290	6.83E-04	0.0192	MSTRG.24962.38065	0.0351	0.0041	0.0480
MSTRG.41934.63888	0.2912	6.85E-04	0.0193	MSTRG.29764.45427	0.1988	0.0041	0.0481
MSTRG.39214.59753	0.3988	6.90E-04	0.0194	MSTRG.11632.17788	0.2214	0.0041	0.0481
MSTRG.4547.6817	0.3868	6.94E-04	0.0194	MSTRG.14629.22391	0.4177	0.0041	0.0481
MSTRG.24394.37175	0.3494	6.94E-04	0.0194	MSTRG.17967.27478	0.4490	0.0041	0.0481
MSTRG.9691.14916	0.2078	6.95E-04	0.0194	MSTRG.41125.62668	0.2332	0.0041	0.0481
MSTRG.25626.39026	0.3138	6.96E-04	0.0194	MSTRG.13436.20643	0.3884	0.0041	0.0481
MSTRG.26540.40363	0.4957	6.97E-04	0.0194	MSTRG.46706.71211	0.4064	0.0041	0.0481
MSTRG.42733.65147	0.2757	6.97E-04	0.0194	MSTRG.10253.15797	0.1005	0.0041	0.0483
MSTRG.18039.27600	0.0786	6.99E-04	0.0194	MSTRG.42504.64811	0.3006	0.0041	0.0485
MSTRG.579.874	0.3622	7.02E-04	0.0194	MSTRG.10934.16792	0.3927	0.0041	0.0485
MSTRG.29929.45656	0.1747	7.03E-04	0.0194	MSTRG.2422.3597	0.0725	0.0041	0.0486
MSTRG.10727.16506	0.4959	7.05E-04	0.0194	MSTRG.13865.21283	0.3400	0.0042	0.0486
MSTRG.36107.55024	0.3034	7.06E-04	0.0194	MSTRG.22382.34087	0.3857	0.0042	0.0486
MSTRG.40652.62010	0.4080	7.10E-04	0.0195	MSTRG.46839.71423	0.4320	0.0042	0.0486
MSTRG.12850.19753	0.4808	7.15E-04	0.0196	MSTRG.20787.31580	0.3090	0.0042	0.0487
MSTRG.26241.39925	0.1201	7.16E-04	0.0196	MSTRG.12765.19632	0.4073	0.0042	0.0488
MSTRG.13404.20582	0.3040	7.20E-04	0.0197	MSTRG.41960.63918	0.1604	0.0042	0.0488
MSTRG.15623.23833	0.0726	7.21E-04	0.0197	MSTRG.17720.27045	0.2169	0.0042	0.0488
MSTRG.3286.4892	0.1856	7.21E-04	0.0197	MSTRG.1717.2569	0.3185	0.0042	0.0488
MSTRG.43385.66178	0.4139	7.22E-04	0.0197	MSTRG.25057.38215	0.3569	0.0042	0.0491
MSTRG.39926.60820	0.4597	7.25E-04	0.0197	MSTRG.38091.58031	0.4175	0.0042	0.0491
MSTRG.21997.33509	0.2217	7.31E-04	0.0198	MSTRG.26976.41103	0.4350	0.0042	0.0491
MSTRG.40008.60939	0.4678	7.32E-04	0.0198	MSTRG.5904.8932	0.2656	0.0042	0.0492
MSTRG.3958.5899	0.3262	7.34E-04	0.0199	MSTRG.36220.55222	0.2192	0.0043	0.0493
MSTRG.21892.33362	0.1657	7.36E-04	0.0199	MSTRG.12128.18634	0.4876	0.0043	0.0495

MSTRG.24688.37628	0.3130	7.39E-04	0.0199	MSTRG.8021.12331	0.1663	0.0043	0.0495
MSTRG.17462.26628	0.2604	7.40E-04	0.0199	MSTRG.19992.30414	0.2239	0.0043	0.0496
MSTRG.9897.15231	0.0651	7.42E-04	0.0199	MSTRG.32617.49715	0.2271	0.0043	0.0496
MSTRG.42350.64593	0.3837	7.47E-04	0.0200	MSTRG.22424.34153	0.4355	0.0043	0.0497
MSTRG.24382.37160	0.0927	7.48E-04	0.0200	MSTRG.20739.31509	0.3742	0.0043	0.0497
MSTRG.8848.13588	0.0530	7.48E-04	0.0200	MSTRG.1895.2809	0.4823	0.0043	0.0497
MSTRG.34667.52706	0.3822	7.49E-04	0.0200	MSTRG.5649.8550	0.2059	0.0043	0.0497
MSTRG.27754.42297	0.4082	7.53E-04	0.0201	MSTRG.1100.1648	0.1088	0.0043	0.0497
MSTRG.27867.42467	0.2452	7.54E-04	0.0201	MSTRG.34074.51858	0.2959	0.0043	0.0497
MSTRG.34527.52517	0.3600	7.55E-04	0.0201	MSTRG.14154.21713	0.3435	0.0043	0.0497
MSTRG.4055.6080	0.1201	7.55E-04	0.0201	MSTRG.2736.4070	0.3424	0.0044	0.0499

Table S4.4: Upregulated transcripts under chilling conditions in *Corylus avellana* cv Cakildak with iDEP

Transcript ID	log2 FoldChange	Transcript ID	log2 FoldChange	Transcript ID	log2 FoldChange
MSTRG.24960.10	29.096	MSTRG.20514.2	4.682	MSTRG.6273.1	1.791
MSTRG.19068.1	28.529	MSTRG.32827.2	4.678	MSTRG.4749.1	1.789
MSTRG.29607.2	27.751	MSTRG.11802.5	4.675	MSTRG.2749.1	1.789
MSTRG.21027.3	27.417	MSTRG.27833.4	4.675	MSTRG.34031.1	1.788
MSTRG.34788.6	27.152	MSTRG.92.1	4.663	MSTRG.7520.1	1.783
MSTRG.16116.2	27.069	MSTRG.15351.1	4.640	MSTRG.45019.1	1.782
MSTRG.31177.1	26.811	MSTRG.5191.5	4.628	MSTRG.14488.3	1.782
MSTRG.4504.7	26.454	MSTRG.12730.3	4.621	MSTRG.20744.1	1.782
MSTRG.19068.2	26.418	MSTRG.9582.1	4.619	MSTRG.36765.2	1.778
MSTRG.18109.2	26.407	MSTRG.9583.1	4.619	MSTRG.16369.2	1.775
MSTRG.27264.2	26.330	MSTRG.24963.1	4.605	MSTRG.36025.1	1.774
MSTRG.17903.3	26.081	MSTRG.9645.1	4.592	MSTRG.27163.4	1.773
MSTRG.23455.2	25.891	MSTRG.23612.2	4.560	MSTRG.43119.1	1.773
MSTRG.46200.1	25.822	MSTRG.11253.10	4.534	MSTRG.20744.2	1.773
MSTRG.27578.5	25.566	MSTRG.11477.2	4.530	MSTRG.17790.1	1.772
MSTRG.12565.1	24.974	MSTRG.15623.1	4.522	MSTRG.35882.1	1.770
MSTRG.35565.3	24.777	MSTRG.38149.4	4.479	MSTRG.20871.1	1.770
MSTRG.44005.5	24.593	MSTRG.40248.1	4.477	MSTRG.17715.1	1.768
MSTRG.2524.1	24.386	MSTRG.29835.2	4.473	MSTRG.36186.2	1.768
MSTRG.40563.24	16.888	MSTRG.32999.3	4.472	MSTRG.30112.1	1.767
MSTRG.22166.4	16.731	MSTRG.36896.4	4.470	MSTRG.29732.1	1.766
MSTRG.23434.1	15.837	MSTRG.17359.2	4.463	MSTRG.41762.2	1.766
MSTRG.44997.2	15.781	MSTRG.1628.5	4.455	MSTRG.26803.1	1.765
MSTRG.27979.3	15.444	MSTRG.8521.20	4.442	MSTRG.36718.2	1.763

MSTRG.4339.2	14.536	MSTRG.44493.3	4.433	MSTRG.34057.1	1.762
MSTRG.44753.12	14.396	MSTRG.27832.1	4.426	MSTRG.38091.1	1.760
MSTRG.29351.3	14.223	MSTRG.1899.1	4.418	MSTRG.23816.1	1.759
MSTRG.35048.4	14.172	MSTRG.27031.2	4.416	MSTRG.10292.1	1.757
MSTRG.8234.5	14.125	MSTRG.18729.1	4.413	MSTRG.31897.2	1.757
MSTRG.37195.2	14.102	MSTRG.32517.3	4.412	MSTRG.40784.1	1.754
MSTRG.12456.2	14.084	MSTRG.40568.2	4.404	MSTRG.26562.1	1.753
MSTRG.14922.2	14.030	MSTRG.13287.2	4.402	MSTRG.24260.1	1.749
MSTRG.29946.3	14.019	MSTRG.6697.2	4.395	MSTRG.26594.1	1.749
MSTRG.42166.2	13.968	MSTRG.29055.1	4.374	MSTRG.22286.1	1.748
MSTRG.20821.3	13.951	MSTRG.27833.2	4.374	MSTRG.45418.2	1.745
MSTRG.16356.3	13.911	MSTRG.29050.2	4.372	MSTRG.31897.1	1.744
MSTRG.24390.2	13.834	MSTRG.23432.1	4.367	MSTRG.7521.1	1.744
MSTRG.32942.3	13.775	MSTRG.32702.1	4.362	MSTRG.12388.1	1.742
MSTRG.23072.4	13.681	MSTRG.41931.2	4.342	MSTRG.22680.3	1.741
MSTRG.24336.2	13.677	MSTRG.7627.3	4.338	MSTRG.2966.1	1.732
MSTRG.1295.3	13.669	MSTRG.21890.1	4.331	MSTRG.38862.1	1.732
MSTRG.2376.2	13.647	MSTRG.17768.1	4.330	MSTRG.33113.2	1.732
MSTRG.1295.5	13.513	MSTRG.3894.2	4.327	MSTRG.24252.1	1.730
MSTRG.31890.4	13.462	MSTRG.11863.1	4.303	MSTRG.9406.1	1.730
MSTRG.18039.3	13.460	MSTRG.27358.1	4.301	MSTRG.21156.1	1.729
MSTRG.9897.2	13.448	MSTRG.37411.5	4.295	MSTRG.40563.27	1.727
MSTRG.42867.2	13.444	MSTRG.26446.4	4.287	MSTRG.32777.1	1.726
MSTRG.28035.1	13.344	MSTRG.8722.1	4.275	MSTRG.20139.1	1.724
MSTRG.47893.3	13.254	MSTRG.4055.1	4.270	MSTRG.20745.1	1.720
MSTRG.32762.3	13.223	MSTRG.1727.2	4.250	MSTRG.46203.1	1.719
MSTRG.17415.3	13.205	MSTRG.41083.2	4.243	MSTRG.34289.2	1.717

MSTRG.22377.3	13.196	MSTRG.39971.6	4.235	MSTRG.44688.1	1.717
MSTRG.18368.4	13.079	MSTRG.41782.4	4.217	MSTRG.28553.1	1.716
MSTRG.46018.3	13.034	MSTRG.5415.1	4.215	MSTRG.747.1	1.715
MSTRG.39963.2	13.023	MSTRG.42633.1	4.212	MSTRG.4380.1	1.713
MSTRG.27057.2	13.018	MSTRG.21530.3	4.175	MSTRG.41270.1	1.711
MSTRG.13020.5	13.016	MSTRG.4092.1	4.164	MSTRG.48737.1	1.711
MSTRG.6762.2	12.991	MSTRG.7842.1	4.154	MSTRG.37674.3	1.710
MSTRG.22569.3	12.970	MSTRG.10245.3	4.150	MSTRG.32981.1	1.706
MSTRG.33389.2	12.967	MSTRG.9382.3	4.147	MSTRG.14249.1	1.704
MSTRG.42923.2	12.961	MSTRG.5574.3	4.142	MSTRG.44996.1	1.698
MSTRG.39491.5	12.950	MSTRG.22176.2	4.139	MSTRG.3958.1	1.698
MSTRG.40537.4	12.933	MSTRG.21892.1	4.131	MSTRG.31351.1	1.695
MSTRG.29702.4	12.903	MSTRG.21972.2	4.128	MSTRG.48061.6	1.693
MSTRG.42763.4	12.876	MSTRG.28939.3	4.121	MSTRG.21978.1	1.692
MSTRG.22976.2	12.870	MSTRG.42740.3	4.121	MSTRG.33980.1	1.691
MSTRG.11260.3	12.851	MSTRG.1227.3	4.114	MSTRG.42350.1	1.690
MSTRG.35197.6	12.845	MSTRG.32213.1	4.110	MSTRG.41355.2	1.690
MSTRG.31505.2	12.836	MSTRG.14884.1	4.106	MSTRG.13882.1	1.689
MSTRG.9908.2	12.798	MSTRG.23448.2	4.098	MSTRG.36013.1	1.683
MSTRG.22166.7	12.794	MSTRG.20458.1	4.096	MSTRG.12681.1	1.681
MSTRG.13959.2	12.723	MSTRG.28897.7	4.096	MSTRG.36025.3	1.679
MSTRG.34443.4	12.716	MSTRG.31584.2	4.096	MSTRG.27109.1	1.679
MSTRG.41593.4	12.666	MSTRG.25886.2	4.089	MSTRG.30576.1	1.678
MSTRG.26939.4	12.652	MSTRG.1083.3	4.065	MSTRG.7651.1	1.674
MSTRG.27372.3	12.648	MSTRG.23425.1	4.064	MSTRG.22165.1	1.673
MSTRG.32016.6	12.644	MSTRG.29652.2	4.052	MSTRG.11743.1	1.673
MSTRG.37494.5	12.632	MSTRG.22490.1	4.037	MSTRG.1529.1	1.671

MSTRG.11719.2	12.529	MSTRG.25189.2	4.025	MSTRG.11220.1	1.670
MSTRG.1100.3	12.529	MSTRG.33984.1	4.024	MSTRG.47999.1	1.670
MSTRG.22965.6	12.521	MSTRG.24917.3	4.020	MSTRG.9054.1	1.670
MSTRG.599.2	12.476	MSTRG.10253.21	4.017	MSTRG.13217.1	1.668
MSTRG.27418.2	12.446	MSTRG.22889.1	4.002	MSTRG.41960.1	1.668
MSTRG.38725.6	12.436	MSTRG.27031.1	4.000	MSTRG.35753.12	1.665
MSTRG.32517.1	12.432	MSTRG.47139.2	3.996	MSTRG.8403.1	1.663
MSTRG.37959.2	12.405	MSTRG.17077.1	3.991	MSTRG.14059.2	1.663
MSTRG.39849.2	12.403	MSTRG.20381.5	3.990	MSTRG.39878.3	1.662
MSTRG.28672.5	12.396	MSTRG.21568.4	3.977	MSTRG.14650.1	1.661
MSTRG.39656.2	12.384	MSTRG.8783.1	3.976	MSTRG.13393.4	1.661
MSTRG.10413.4	12.347	MSTRG.32286.3	3.964	MSTRG.41815.1	1.658
MSTRG.33317.5	12.338	MSTRG.15350.2	3.961	MSTRG.8726.1	1.654
MSTRG.16697.6	12.303	MSTRG.42302.2	3.952	MSTRG.11076.1	1.654
MSTRG.25999.2	12.282	MSTRG.25836.3	3.949	MSTRG.38398.3	1.653
MSTRG.20660.4	12.276	MSTRG.24391.1	3.937	MSTRG.38582.1	1.650
MSTRG.37694.4	12.269	MSTRG.25270.1	3.928	MSTRG.47648.2	1.649
MSTRG.17873.2	12.222	MSTRG.16824.6	3.924	MSTRG.11357.1	1.648
MSTRG.10530.2	12.210	MSTRG.17876.2	3.906	MSTRG.39977.4	1.647
MSTRG.3172.2	12.209	MSTRG.25272.1	3.905	MSTRG.4663.1	1.644
MSTRG.30138.4	12.190	MSTRG.32899.5	3.901	MSTRG.32145.4	1.641
MSTRG.34450.2	12.169	MSTRG.27795.1	3.895	MSTRG.37677.1	1.640
MSTRG.43405.1	12.154	MSTRG.8882.3	3.877	MSTRG.38887.3	1.639
MSTRG.12430.3	12.149	MSTRG.35980.4	3.875	MSTRG.45198.1	1.637
MSTRG.41294.4	12.147	MSTRG.41897.3	3.875	MSTRG.47795.1	1.634
MSTRG.31541.1	12.142	MSTRG.17422.1	3.874	MSTRG.16997.1	1.634
MSTRG.13786.5	12.132	MSTRG.6591.1	3.867	MSTRG.25624.2	1.634

MSTRG.22965.7	12.129	MSTRG.21992.2	3.849	MSTRG.26799.2	1.634
MSTRG.13515.2	12.127	MSTRG.27034.1	3.846	MSTRG.31351.6	1.630
MSTRG.22487.3	12.115	MSTRG.17843.2	3.845	MSTRG.17021.4	1.629
MSTRG.26923.1	12.112	MSTRG.41083.3	3.839	MSTRG.42809.2	1.625
MSTRG.29876.2	12.107	MSTRG.29671.1	3.837	MSTRG.46491.1	1.624
MSTRG.36631.2	12.060	MSTRG.835.4	3.834	MSTRG.23705.1	1.624
MSTRG.27651.2	12.055	MSTRG.40513.1	3.821	MSTRG.46838.2	1.622
MSTRG.43315.2	12.037	MSTRG.28412.2	3.811	MSTRG.35648.1	1.618
MSTRG.33679.4	12.029	MSTRG.28737.1	3.811	MSTRG.46542.1	1.616
MSTRG.46788.2	12.003	MSTRG.17665.2	3.789	MSTRG.13964.1	1.614
MSTRG.36547.3	11.998	MSTRG.42306.5	3.778	MSTRG.28066.1	1.614
MSTRG.10769.9	11.995	MSTRG.9478.1	3.778	MSTRG.16154.1	1.612
MSTRG.41439.2	11.990	MSTRG.40745.1	3.771	MSTRG.23674.1	1.608
MSTRG.44394.3	11.975	MSTRG.23434.6	3.766	MSTRG.26059.6	1.608
MSTRG.36311.3	11.971	MSTRG.24048.4	3.757	MSTRG.22968.3	1.608
MSTRG.2626.2	11.966	MSTRG.16832.1	3.755	MSTRG.4778.1	1.605
MSTRG.47574.3	11.943	MSTRG.44180.5	3.750	MSTRG.39657.1	1.604
MSTRG.13512.2	11.935	MSTRG.29916.2	3.739	MSTRG.29713.1	1.604
MSTRG.32349.2	11.928	MSTRG.11258.2	3.737	MSTRG.45580.1	1.604
MSTRG.29929.2	11.928	MSTRG.38303.2	3.737	MSTRG.33683.1	1.602
MSTRG.38361.2	11.928	MSTRG.28383.2	3.736	MSTRG.17251.3	1.602
MSTRG.32293.5	11.897	MSTRG.42632.1	3.733	MSTRG.39897.1	1.601
MSTRG.23763.7	11.883	MSTRG.28437.1	3.733	MSTRG.25682.1	1.600
MSTRG.26849.2	11.869	MSTRG.8023.1	3.727	MSTRG.21208.1	1.598
MSTRG.36207.6	11.843	MSTRG.29572.1	3.726	MSTRG.20100.1	1.598
MSTRG.14213.2	11.841	MSTRG.41989.1	3.723	MSTRG.38412.2	1.598
MSTRG.42248.4	11.834	MSTRG.36289.1	3.706	MSTRG.27234.1	1.593

MSTRG.44684.3	11.809	MSTRG.11148.6	3.699	MSTRG.42536.7	1.588
MSTRG.14511.3	11.807	MSTRG.29710.2	3.683	MSTRG.37774.1	1.587
MSTRG.10580.2	11.794	MSTRG.31619.1	3.679	MSTRG.41000.1	1.587
MSTRG.16690.3	11.787	MSTRG.1430.1	3.678	MSTRG.42318.4	1.585
MSTRG.21715.2	11.784	MSTRG.3088.1	3.669	MSTRG.32912.1	1.583
MSTRG.5071.2	11.780	MSTRG.44749.4	3.655	MSTRG.3988.7	1.582
MSTRG.36123.1	11.766	MSTRG.28512.3	3.652	MSTRG.46706.1	1.581
MSTRG.42733.2	11.764	MSTRG.29359.1	3.650	MSTRG.25036.1	1.581
MSTRG.34467.2	11.756	MSTRG.9477.1	3.635	MSTRG.17940.1	1.579
MSTRG.21562.2	11.755	MSTRG.43871.1	3.630	MSTRG.7197.1	1.579
MSTRG.437.4	11.736	MSTRG.27526.1	3.630	MSTRG.6752.3	1.577
MSTRG.24962.2	11.728	MSTRG.4382.12	3.626	MSTRG.32769.3	1.576
MSTRG.872.3	11.721	MSTRG.15420.2	3.626	MSTRG.35615.1	1.575
MSTRG.43336.3	11.710	MSTRG.37632.8	3.624	MSTRG.48074.8	1.575
MSTRG.41079.2	11.694	MSTRG.26261.1	3.624	MSTRG.22719.1	1.574
MSTRG.36057.2	11.682	MSTRG.16823.3	3.618	MSTRG.728.1	1.573
MSTRG.29234.2	11.674	MSTRG.29702.3	3.617	MSTRG.7955.1	1.573
MSTRG.2545.3	11.673	MSTRG.2942.1	3.615	MSTRG.25153.2	1.572
MSTRG.9158.2	11.668	MSTRG.15350.1	3.612	MSTRG.40783.1	1.572
MSTRG.35294.3	11.664	MSTRG.27154.2	3.612	MSTRG.37801.1	1.572
MSTRG.33191.3	11.660	MSTRG.38553.2	3.611	MSTRG.17870.5	1.571
MSTRG.15225.10	11.641	MSTRG.14331.1	3.610	MSTRG.32003.8	1.570
MSTRG.7581.4	11.639	MSTRG.28811.2	3.608	MSTRG.10404.3	1.570
MSTRG.21030.7	11.629	MSTRG.28556.5	3.601	MSTRG.34191.1	1.570
MSTRG.45401.2	11.620	MSTRG.11796.95	3.595	MSTRG.37838.5	1.568
MSTRG.27844.3	11.615	MSTRG.15262.1	3.593	MSTRG.2018.2	1.567
MSTRG.13592.2	11.554	MSTRG.14154.2	3.588	MSTRG.39325.1	1.566

MSTRG.23702.2	11.547	MSTRG.17075.1	3.586	MSTRG.17252.6	1.565
MSTRG.10348.3	11.542	MSTRG.41240.4	3.586	MSTRG.17938.1	1.562
MSTRG.30149.1	11.538	MSTRG.11863.2	3.583	MSTRG.14338.3	1.562
MSTRG.13811.8	11.532	MSTRG.39015.2	3.582	MSTRG.15536.1	1.562
MSTRG.27749.2	11.526	MSTRG.31042.1	3.569	MSTRG.47929.1	1.560
MSTRG.48409.3	11.512	MSTRG.1487.2	3.566	MSTRG.27550.1	1.560
MSTRG.22846.12	11.501	MSTRG.5679.2	3.562	MSTRG.19853.1	1.560
MSTRG.37577.5	11.500	MSTRG.9020.1	3.561	MSTRG.11899.5	1.557
MSTRG.21861.2	11.500	MSTRG.13045.2	3.554	MSTRG.12101.1	1.556
MSTRG.32327.4	11.467	MSTRG.16867.1	3.553	MSTRG.35240.1	1.556
MSTRG.48009.8	11.465	MSTRG.7333.3	3.550	MSTRG.6338.1	1.555
MSTRG.688.2	11.453	MSTRG.4012.3	3.542	MSTRG.28735.1	1.554
MSTRG.41719.4	11.449	MSTRG.25516.1	3.533	MSTRG.10404.1	1.551
MSTRG.21647.4	11.433	MSTRG.9484.2	3.532	MSTRG.48337.2	1.548
MSTRG.36473.3	11.417	MSTRG.42515.1	3.530	MSTRG.11480.1	1.547
MSTRG.17621.4	11.403	MSTRG.38566.3	3.527	MSTRG.41982.5	1.546
MSTRG.20618.2	11.393	MSTRG.47281.3	3.524	MSTRG.32917.1	1.544
MSTRG.16474.7	11.389	MSTRG.27531.2	3.522	MSTRG.27111.1	1.544
MSTRG.28323.3	11.385	MSTRG.36870.1	3.520	MSTRG.12465.8	1.542
MSTRG.22547.2	11.375	MSTRG.46999.1	3.514	MSTRG.44687.1	1.541
MSTRG.10602.3	11.364	MSTRG.36871.1	3.508	MSTRG.7419.1	1.540
MSTRG.48255.2	11.364	MSTRG.33414.6	3.498	MSTRG.22681.1	1.539
MSTRG.37437.2	11.363	MSTRG.17606.4	3.495	MSTRG.17653.1	1.535
MSTRG.42428.3	11.360	MSTRG.25284.1	3.494	MSTRG.15158.2	1.534
MSTRG.43965.6	11.356	MSTRG.39931.3	3.492	MSTRG.11901.1	1.529
MSTRG.27429.4	11.354	MSTRG.34802.2	3.485	MSTRG.31734.1	1.529
MSTRG.20243.2	11.352	MSTRG.46510.1	3.483	MSTRG.23434.5	1.528

MSTRG.36983.2	11.351	MSTRG.24241.1	3.472	MSTRG.28189.1	1.528
MSTRG.26802.2	11.348	MSTRG.24095.1	3.464	MSTRG.9696.1	1.526
MSTRG.819.4	11.341	MSTRG.27777.6	3.460	MSTRG.22681.2	1.524
MSTRG.6562.3	11.340	MSTRG.27432.1	3.438	MSTRG.7915.1	1.524
MSTRG.3819.2	11.338	MSTRG.7843.1	3.426	MSTRG.38138.1	1.521
MSTRG.11787.16	11.330	MSTRG.186.5	3.425	MSTRG.41883.1	1.521
MSTRG.12272.4	11.327	MSTRG.36127.2	3.418	MSTRG.43485.7	1.520
MSTRG.19418.2	11.315	MSTRG.35472.1	3.410	MSTRG.10598.1	1.517
MSTRG.3437.3	11.308	MSTRG.23599.1	3.410	MSTRG.16492.1	1.516
MSTRG.18942.7	11.304	MSTRG.20739.1	3.405	MSTRG.4069.1	1.515
MSTRG.13748.2	11.295	MSTRG.15071.2	3.399	MSTRG.39769.1	1.513
MSTRG.11632.4	11.293	MSTRG.40652.2	3.398	MSTRG.27755.1	1.512
MSTRG.34687.2	11.277	MSTRG.40555.62	3.397	MSTRG.34126.2	1.510
MSTRG.5960.4	11.276	MSTRG.12838.6	3.394	MSTRG.11986.1	1.509
MSTRG.29667.1	11.274	MSTRG.8294.1	3.386	MSTRG.43320.1	1.508
MSTRG.43388.2	11.263	MSTRG.34049.1	3.379	MSTRG.23451.3	1.507
MSTRG.35194.2	11.263	MSTRG.36587.1	3.367	MSTRG.6178.2	1.507
MSTRG.42013.2	11.256	MSTRG.24183.1	3.351	MSTRG.2495.1	1.506
MSTRG.47826.2	11.246	MSTRG.31599.1	3.350	MSTRG.33606.2	1.506
MSTRG.35002.2	11.243	MSTRG.14145.2	3.343	MSTRG.16439.1	1.505
MSTRG.28544.2	11.232	MSTRG.35432.1	3.342	MSTRG.27754.1	1.505
MSTRG.7953.2	11.200	MSTRG.47611.1	3.341	MSTRG.45272.1	1.503
MSTRG.29817.4	11.173	MSTRG.27979.7	3.340	MSTRG.31413.1	1.501
MSTRG.39723.2	11.169	MSTRG.37134.4	3.339	MSTRG.6699.1	1.501
MSTRG.42682.2	11.165	MSTRG.19706.1	3.328	MSTRG.18580.1	1.500
MSTRG.24382.8	11.154	MSTRG.9728.2	3.326	MSTRG.43096.8	1.499
MSTRG.2002.2	11.154	MSTRG.10324.1	3.324	MSTRG.15409.1	1.499

MSTRG.24964.2	11.135	MSTRG.45991.2	3.323	MSTRG.33139.1	1.496
MSTRG.32341.4	11.128	MSTRG.38056.2	3.322	MSTRG.27867.1	1.495
MSTRG.41755.2	11.111	MSTRG.24394.1	3.318	MSTRG.8468.4	1.495
MSTRG.2626.3	11.109	MSTRG.23560.2	3.315	MSTRG.2100.3	1.494
MSTRG.41950.2	11.108	MSTRG.9074.4	3.314	MSTRG.45021.1	1.494
MSTRG.46271.2	11.082	MSTRG.27521.2	3.313	MSTRG.7916.1	1.492
MSTRG.12773.2	11.075	MSTRG.6546.2	3.303	MSTRG.7333.2	1.492
MSTRG.45563.4	11.049	MSTRG.9211.2	3.302	MSTRG.7315.3	1.491
MSTRG.38109.4	11.049	MSTRG.23438.1	3.298	MSTRG.6214.1	1.491
MSTRG.31143.2	11.038	MSTRG.41473.1	3.293	MSTRG.36430.1	1.491
MSTRG.41655.4	11.018	MSTRG.14511.2	3.289	MSTRG.30120.1	1.489
MSTRG.38492.6	11.015	MSTRG.47653.2	3.286	MSTRG.23037.1	1.488
MSTRG.33317.4	11.006	MSTRG.11802.6	3.286	MSTRG.20675.1	1.487
MSTRG.41613.2	11.005	MSTRG.17082.1	3.267	MSTRG.15998.1	1.486
MSTRG.33321.2	10.993	MSTRG.38015.1	3.263	MSTRG.15086.1	1.486
MSTRG.37483.2	10.984	MSTRG.19145.1	3.257	MSTRG.48105.1	1.486
MSTRG.48061.8	10.981	MSTRG.37469.5	3.234	MSTRG.22313.1	1.484
MSTRG.30475.5	10.976	MSTRG.4091.3	3.232	MSTRG.47744.1	1.484
MSTRG.33856.3	10.976	MSTRG.43600.1	3.230	MSTRG.6528.1	1.483
MSTRG.37457.1	10.974	MSTRG.35716.3	3.224	MSTRG.31351.2	1.483
MSTRG.15639.2	10.973	MSTRG.7759.2	3.216	MSTRG.15230.1	1.482
MSTRG.43401.2	10.964	MSTRG.42295.1	3.214	MSTRG.36388.1	1.482
MSTRG.23679.2	10.960	MSTRG.35604.1	3.210	MSTRG.42455.3	1.482
MSTRG.35565.4	10.942	MSTRG.21842.4	3.210	MSTRG.27223.1	1.478
MSTRG.45769.13	10.938	MSTRG.11796.97	3.208	MSTRG.24259.1	1.478
MSTRG.19173.20	10.931	MSTRG.8021.2	3.206	MSTRG.16390.1	1.476
MSTRG.31027.2	10.927	MSTRG.39348.1	3.200	MSTRG.13393.2	1.476

MSTRG.396.2	10.916	MSTRG.15553.2	3.199	MSTRG.21887.1	1.476
MSTRG.22846.9	10.909	MSTRG.22884.6	3.193	MSTRG.25935.1	1.475
MSTRG.39364.3	10.903	MSTRG.38899.2	3.193	MSTRG.47157.1	1.475
MSTRG.27622.2	10.891	MSTRG.18196.9	3.191	MSTRG.12850.1	1.473
MSTRG.36.2	10.890	MSTRG.9692.17	3.186	MSTRG.14171.1	1.470
MSTRG.17055.2	10.889	MSTRG.28456.1	3.185	MSTRG.42300.3	1.467
MSTRG.5048.5	10.882	MSTRG.23213.1	3.184	MSTRG.19927.1	1.466
MSTRG.12700.2	10.881	MSTRG.23439.1	3.179	MSTRG.33715.2	1.466
MSTRG.26247.1	10.871	MSTRG.21664.2	3.179	MSTRG.47156.1	1.465
MSTRG.9769.3	10.869	MSTRG.26943.1	3.175	MSTRG.21901.1	1.464
MSTRG.40321.2	10.856	MSTRG.9649.2	3.172	MSTRG.18906.2	1.463
MSTRG.31160.6	10.855	MSTRG.11762.1	3.170	MSTRG.27934.1	1.463
MSTRG.39674.2	10.841	MSTRG.45669.1	3.168	MSTRG.41576.1	1.461
MSTRG.25669.4	10.841	MSTRG.1717.2	3.161	MSTRG.38737.1	1.455
MSTRG.40571.1	10.840	MSTRG.4016.1	3.160	MSTRG.18636.1	1.454
MSTRG.47309.2	10.829	MSTRG.40555.35	3.158	MSTRG.19799.1	1.454
MSTRG.24120.2	10.827	MSTRG.38742.3	3.157	MSTRG.35474.1	1.450
MSTRG.17760.4	10.818	MSTRG.36718.1	3.153	MSTRG.97.1	1.446
MSTRG.45260.2	10.816	MSTRG.20872.1	3.149	MSTRG.10725.1	1.445
MSTRG.29558.2	10.813	MSTRG.21026.2	3.148	MSTRG.25558.1	1.444
MSTRG.28784.5	10.798	MSTRG.10412.1	3.143	MSTRG.32495.1	1.444
MSTRG.9164.4	10.790	MSTRG.40563.23	3.137	MSTRG.38092.1	1.443
MSTRG.45623.2	10.774	MSTRG.31476.2	3.134	MSTRG.45231.1	1.440
MSTRG.21750.2	10.767	MSTRG.47158.5	3.132	MSTRG.18709.2	1.437
MSTRG.22846.7	10.757	MSTRG.31360.1	3.130	MSTRG.22190.1	1.436
MSTRG.12300.5	10.744	MSTRG.40750.4	3.121	MSTRG.44148.1	1.434
MSTRG.24688.3	10.744	MSTRG.32085.2	3.120	MSTRG.17764.3	1.434

MSTRG.27913.2	10.738	MSTRG.8282.1	3.111	MSTRG.19017.1	1.430
MSTRG.18497.2	10.725	MSTRG.47420.3	3.110	MSTRG.7420.1	1.430
MSTRG.29464.3	10.721	MSTRG.107.1	3.108	MSTRG.12540.1	1.428
MSTRG.2843.6	10.721	MSTRG.19309.5	3.108	MSTRG.28926.1	1.427
MSTRG.2566.3	10.698	MSTRG.7592.1	3.103	MSTRG.36076.1	1.425
MSTRG.48760.5	10.696	MSTRG.25249.2	3.102	MSTRG.15609.1	1.424
MSTRG.35979.3	10.694	MSTRG.38166.2	3.100	MSTRG.40984.1	1.421
MSTRG.13506.2	10.688	MSTRG.11796.91	3.095	MSTRG.6138.1	1.421
MSTRG.9724.2	10.684	MSTRG.2270.1	3.092	MSTRG.41640.1	1.420
MSTRG.8625.2	10.680	MSTRG.14995.1	3.089	MSTRG.7309.1	1.419
MSTRG.25316.9	10.672	MSTRG.22309.7	3.087	MSTRG.24039.4	1.418
MSTRG.21240.3	10.665	MSTRG.41852.1	3.080	MSTRG.18044.1	1.417
MSTRG.48080.1	10.663	MSTRG.33214.2	3.079	MSTRG.1459.1	1.416
MSTRG.41125.2	10.657	MSTRG.47466.1	3.073	MSTRG.7332.1	1.415
MSTRG.25264.3	10.656	MSTRG.11796.94	3.064	MSTRG.37776.1	1.415
MSTRG.32895.3	10.653	MSTRG.15139.1	3.059	MSTRG.35443.2	1.413
MSTRG.2093.2	10.651	MSTRG.38011.2	3.056	MSTRG.24167.1	1.413
MSTRG.36093.2	10.647	MSTRG.9296.1	3.053	MSTRG.2252.1	1.411
MSTRG.44190.2	10.639	MSTRG.44887.2	3.051	MSTRG.21173.1	1.409
MSTRG.45972.4	10.619	MSTRG.43462.1	3.051	MSTRG.21032.1	1.408
MSTRG.24657.2	10.598	MSTRG.3662.3	3.047	MSTRG.7941.1	1.407
MSTRG.24231.1	10.596	MSTRG.22718.2	3.042	MSTRG.13746.1	1.407
MSTRG.40523.2	10.591	MSTRG.5602.1	3.041	MSTRG.18526.1	1.405
MSTRG.3938.1	10.589	MSTRG.38196.1	3.026	MSTRG.16677.1	1.405
MSTRG.2922.2	10.585	MSTRG.46024.1	3.019	MSTRG.45166.1	1.404
MSTRG.3396.4	10.581	MSTRG.34610.1	3.005	MSTRG.31511.1	1.404
MSTRG.14850.3	10.574	MSTRG.3778.1	3.004	MSTRG.1404.1	1.403

MSTRG.2697.2	10.572	MSTRG.9312.1	2.993	MSTRG.20313.1	1.402
MSTRG.11209.2	10.566	MSTRG.28829.2	2.991	MSTRG.3148.1	1.401
MSTRG.27109.3	10.565	MSTRG.41969.2	2.986	MSTRG.45017.1	1.399
MSTRG.9888.2	10.562	MSTRG.9911.1	2.984	MSTRG.41986.1	1.396
MSTRG.33281.1	10.561	MSTRG.9691.4	2.982	MSTRG.21536.6	1.395
MSTRG.4951.2	10.561	MSTRG.28708.1	2.981	MSTRG.32776.1	1.395
MSTRG.28745.3	10.557	MSTRG.13865.1	2.965	MSTRG.42810.1	1.386
MSTRG.28645.3	10.550	MSTRG.14850.2	2.962	MSTRG.38137.1	1.385
MSTRG.21453.4	10.529	MSTRG.36851.1	2.960	MSTRG.23652.3	1.382
MSTRG.17318.6	10.525	MSTRG.11784.10	2.959	MSTRG.10480.1	1.381
MSTRG.9533.1	10.523	MSTRG.8848.2	2.958	MSTRG.46492.1	1.379
MSTRG.5155.2	10.517	MSTRG.4001.2	2.956	MSTRG.4211.1	1.379
MSTRG.36707.2	10.515	MSTRG.32447.7	2.955	MSTRG.11895.1	1.379
MSTRG.37577.3	10.502	MSTRG.46623.1	2.952	MSTRG.9555.1	1.378
MSTRG.23401.1	10.488	MSTRG.17680.1	2.945	MSTRG.25091.2	1.378
MSTRG.15661.2	10.488	MSTRG.25512.1	2.936	MSTRG.27163.3	1.377
MSTRG.38670.5	10.486	MSTRG.4014.1	2.932	MSTRG.43156.1	1.377
MSTRG.6072.2	10.485	MSTRG.40480.4	2.919	MSTRG.5143.1	1.376
MSTRG.743.1	10.476	MSTRG.13468.1	2.908	MSTRG.27922.1	1.375
MSTRG.24701.4	10.468	MSTRG.44191.1	2.907	MSTRG.35656.1	1.375
MSTRG.23596.4	10.460	MSTRG.37941.1	2.900	MSTRG.5839.1	1.374
MSTRG.3542.2	10.441	MSTRG.48651.1	2.892	MSTRG.45342.1	1.373
MSTRG.46902.1	10.439	MSTRG.20094.6	2.888	MSTRG.14772.1	1.373
MSTRG.10837.2	10.426	MSTRG.11603.2	2.887	MSTRG.23429.1	1.372
MSTRG.2989.25	10.407	MSTRG.36852.1	2.887	MSTRG.34667.1	1.371
MSTRG.45341.1	10.400	MSTRG.23584.1	2.885	MSTRG.35883.1	1.370
MSTRG.26632.4	10.374	MSTRG.44885.1	2.884	MSTRG.5365.2	1.370

MSTRG.35396.2	10.373	MSTRG.16394.1	2.878	MSTRG.41809.1	1.370
MSTRG.22623.2	10.372	MSTRG.48280.2	2.876	MSTRG.29730.1	1.369
MSTRG.9084.2	10.360	MSTRG.26891.3	2.875	MSTRG.42912.3	1.367
MSTRG.40585.2	10.360	MSTRG.12745.1	2.862	MSTRG.4378.1	1.365
MSTRG.23252.5	10.355	MSTRG.10093.1	2.852	MSTRG.17850.1	1.364
MSTRG.37483.4	10.350	MSTRG.18196.7	2.852	MSTRG.40868.1	1.362
MSTRG.43101.1	10.348	MSTRG.31812.2	2.846	MSTRG.2928.1	1.360
MSTRG.29842.3	10.315	MSTRG.29102.3	2.846	MSTRG.14099.1	1.359
MSTRG.12859.3	10.295	MSTRG.2271.1	2.840	MSTRG.42159.1	1.357
MSTRG.35099.2	10.281	MSTRG.24759.1	2.836	MSTRG.19453.1	1.357
MSTRG.13424.3	10.276	MSTRG.30750.1	2.833	MSTRG.529.3	1.355
MSTRG.17462.3	10.271	MSTRG.7128.5	2.829	MSTRG.28784.4	1.354
MSTRG.22846.5	10.270	MSTRG.24181.1	2.822	MSTRG.34935.1	1.353
MSTRG.20908.4	10.253	MSTRG.20412.1	2.819	MSTRG.8636.1	1.351
MSTRG.2022.2	10.247	MSTRG.20676.2	2.812	MSTRG.32262.1	1.350
MSTRG.27119.4	10.239	MSTRG.6855.3	2.811	MSTRG.37258.1	1.350
MSTRG.23234.6	10.231	MSTRG.34851.1	2.810	MSTRG.12051.1	1.349
MSTRG.9179.2	10.230	MSTRG.1239.1	2.807	MSTRG.38515.1	1.349
MSTRG.6189.2	10.219	MSTRG.38100.1	2.797	MSTRG.1470.1	1.346
MSTRG.45029.15	10.216	MSTRG.37351.1	2.794	MSTRG.6856.1	1.346
MSTRG.6625.2	10.215	MSTRG.14155.1	2.794	MSTRG.41329.5	1.345
MSTRG.38022.2	10.207	MSTRG.11796.96	2.791	MSTRG.41348.1	1.345
MSTRG.19068.4	10.206	MSTRG.31110.1	2.789	MSTRG.6350.1	1.345
MSTRG.21997.2	10.193	MSTRG.16824.1	2.784	MSTRG.47363.1	1.344
MSTRG.6886.2	10.192	MSTRG.44642.1	2.781	MSTRG.11487.1	1.343
MSTRG.29193.3	10.187	MSTRG.46580.1	2.776	MSTRG.2532.1	1.342
MSTRG.2613.2	10.178	MSTRG.11796.93	2.772	MSTRG.9728.1	1.342

MSTRG.30294.1	10.174	MSTRG.21093.1	2.767	MSTRG.25949.1	1.341
MSTRG.20381.9	10.169	MSTRG.34063.2	2.764	MSTRG.31351.3	1.339
MSTRG.1083.2	10.157	MSTRG.30184.1	2.763	MSTRG.16391.1	1.338
MSTRG.20677.3	10.149	MSTRG.38312.4	2.756	MSTRG.44069.1	1.337
MSTRG.16777.2	10.148	MSTRG.32518.1	2.756	MSTRG.13927.2	1.336
MSTRG.4184.2	10.147	MSTRG.25624.1	2.748	MSTRG.34297.1	1.335
MSTRG.45196.2	10.145	MSTRG.29626.1	2.747	MSTRG.658.1	1.332
MSTRG.13769.2	10.144	MSTRG.16098.1	2.745	MSTRG.39429.2	1.332
MSTRG.47283.3	10.143	MSTRG.48405.2	2.744	MSTRG.46792.1	1.331
MSTRG.25377.5	10.137	MSTRG.6942.2	2.740	MSTRG.47864.1	1.330
MSTRG.40555.23	10.128	MSTRG.41225.5	2.740	MSTRG.18907.1	1.329
MSTRG.8105.4	10.125	MSTRG.38267.1	2.734	MSTRG.28889.1	1.328
MSTRG.42632.4	10.110	MSTRG.40601.6	2.733	MSTRG.7912.1	1.327
MSTRG.32045.1	10.077	MSTRG.9691.2	2.731	MSTRG.9344.1	1.327
MSTRG.47254.3	10.067	MSTRG.44981.1	2.729	MSTRG.6018.2	1.325
MSTRG.22626.3	10.060	MSTRG.42404.1	2.727	MSTRG.24732.1	1.325
MSTRG.16180.3	10.037	MSTRG.441.2	2.726	MSTRG.37014.1	1.324
MSTRG.227.2	10.012	MSTRG.36739.2	2.725	MSTRG.43591.1	1.322
MSTRG.37694.2	9.995	MSTRG.18603.1	2.723	MSTRG.24371.5	1.322
MSTRG.12423.2	9.983	MSTRG.25102.1	2.722	MSTRG.24154.1	1.320
MSTRG.18957.4	9.959	MSTRG.45914.3	2.722	MSTRG.9823.1	1.320
MSTRG.10545.2	9.955	MSTRG.34503.2	2.721	MSTRG.32927.1	1.320
MSTRG.33510.3	9.951	MSTRG.37501.1	2.714	MSTRG.6690.1	1.319
MSTRG.39280.3	9.941	MSTRG.31937.3	2.713	MSTRG.30407.1	1.316
MSTRG.42257.2	9.931	MSTRG.6701.1	2.705	MSTRG.41155.1	1.316
MSTRG.46131.4	9.923	MSTRG.21124.1	2.705	MSTRG.17555.1	1.313
MSTRG.20211.2	9.913	MSTRG.5264.1	2.704	MSTRG.25292.2	1.313

MSTRG.37027.2	9.904	MSTRG.17825.3	2.700	MSTRG.36235.6	1.312
MSTRG.5904.1	9.901	MSTRG.32997.1	2.698	MSTRG.7315.4	1.311
MSTRG.6873.1	9.893	MSTRG.9808.1	2.698	MSTRG.5858.1	1.310
MSTRG.39971.2	9.884	MSTRG.20269.1	2.698	MSTRG.20081.1	1.309
MSTRG.9322.8	9.883	MSTRG.28309.1	2.693	MSTRG.1193.1	1.309
MSTRG.445.2	9.880	MSTRG.11802.3	2.688	MSTRG.33557.1	1.308
MSTRG.12472.1	9.872	MSTRG.41478.3	2.688	MSTRG.28912.1	1.305
MSTRG.44654.2	9.871	MSTRG.24813.1	2.687	MSTRG.9968.3	1.303
MSTRG.3958.2	9.869	MSTRG.5353.1	2.685	MSTRG.1256.1	1.302
MSTRG.16864.4	9.867	MSTRG.36011.1	2.684	MSTRG.21089.1	1.300
MSTRG.48026.2	9.863	MSTRG.47423.2	2.684	MSTRG.32062.2	1.300
MSTRG.22382.3	9.843	MSTRG.37050.1	2.676	MSTRG.28183.1	1.299
MSTRG.12558.2	9.842	MSTRG.24578.14	2.673	MSTRG.19097.1	1.298
MSTRG.44703.5	9.824	MSTRG.45655.1	2.672	MSTRG.20380.1	1.295
MSTRG.31952.3	9.815	MSTRG.9669.9	2.669	MSTRG.46277.1	1.295
MSTRG.24657.3	9.809	MSTRG.10541.2	2.664	MSTRG.36460.1	1.293
MSTRG.29705.6	9.780	MSTRG.25558.2	2.661	MSTRG.15184.1	1.293
MSTRG.6520.5	9.743	MSTRG.18634.3	2.661	MSTRG.36066.3	1.292
MSTRG.27525.1	9.723	MSTRG.9550.1	2.661	MSTRG.209.1	1.292
MSTRG.48707.2	9.719	MSTRG.11246.1	2.658	MSTRG.40479.1	1.290
MSTRG.9769.2	9.711	MSTRG.6673.1	2.656	MSTRG.4699.2	1.290
MSTRG.47099.1	9.703	MSTRG.34748.6	2.653	MSTRG.11567.2	1.289
MSTRG.8983.2	9.693	MSTRG.13870.1	2.652	MSTRG.10336.1	1.289
MSTRG.30138.2	9.686	MSTRG.25100.1	2.652	MSTRG.42858.1	1.289
MSTRG.32045.10	9.662	MSTRG.12278.2	2.650	MSTRG.11257.1	1.287
MSTRG.41934.3	9.658	MSTRG.32678.1	2.642	MSTRG.30582.1	1.286
MSTRG.22149.3	9.655	MSTRG.537.2	2.641	MSTRG.16880.1	1.286

MSTRG.35205.9	9.654	MSTRG.26017.1	2.639	MSTRG.47433.1	1.285
MSTRG.36025.5	9.642	MSTRG.11761.1	2.637	MSTRG.6587.2	1.284
MSTRG.28114.7	9.638	MSTRG.17876.1	2.634	MSTRG.26802.1	1.281
MSTRG.29315.2	9.603	MSTRG.48080.16	2.634	MSTRG.25092.1	1.281
MSTRG.31254.3	9.591	MSTRG.34391.6	2.634	MSTRG.22843.2	1.277
MSTRG.43710.2	9.589	MSTRG.9405.1	2.632	MSTRG.15229.1	1.275
MSTRG.37419.2	9.583	MSTRG.11230.1	2.630	MSTRG.35778.1	1.275
MSTRG.17129.3	9.578	MSTRG.6146.1	2.628	MSTRG.1942.1	1.273
MSTRG.18073.2	9.576	MSTRG.47387.1	2.624	MSTRG.15954.1	1.273
MSTRG.31801.2	9.564	MSTRG.31217.4	2.623	MSTRG.42737.1	1.272
MSTRG.34864.2	9.509	MSTRG.21027.7	2.622	MSTRG.27747.1	1.268
MSTRG.43317.1	9.502	MSTRG.45234.1	2.620	MSTRG.14156.2	1.266
MSTRG.19071.2	9.499	MSTRG.15967.3	2.619	MSTRG.28513.1	1.265
MSTRG.20425.4	9.493	MSTRG.22664.2	2.613	MSTRG.13691.1	1.265
MSTRG.23439.2	9.484	MSTRG.24203.1	2.600	MSTRG.10575.14	1.264
MSTRG.14133.3	9.478	MSTRG.46018.6	2.600	MSTRG.14936.1	1.263
MSTRG.34630.3	9.471	MSTRG.11779.2	2.597	MSTRG.6562.1	1.263
MSTRG.5494.3	9.469	MSTRG.13615.2	2.596	MSTRG.7315.5	1.262
MSTRG.39831.4	9.461	MSTRG.40955.2	2.595	MSTRG.4284.2	1.262
MSTRG.2778.2	9.452	MSTRG.21166.1	2.593	MSTRG.14255.1	1.262
MSTRG.8295.2	9.437	MSTRG.48134.3	2.593	MSTRG.20929.1	1.261
MSTRG.4202.2	9.437	MSTRG.44945.1	2.591	MSTRG.44973.7	1.255
MSTRG.21027.4	9.434	MSTRG.17118.2	2.588	MSTRG.4080.1	1.254
MSTRG.43965.2	9.431	MSTRG.17602.2	2.587	MSTRG.953.1	1.254
MSTRG.43992.4	9.423	MSTRG.40546.3	2.587	MSTRG.3060.1	1.253
MSTRG.48738.1	9.409	MSTRG.16348.5	2.586	MSTRG.15507.1	1.250
MSTRG.20157.4	9.405	MSTRG.26536.2	2.583	MSTRG.17844.1	1.249

MSTRG.21390.2	9.396	MSTRG.43280.1	2.577	MSTRG.22837.4	1.249
MSTRG.8882.1	9.393	MSTRG.25626.1	2.574	MSTRG.8691.1	1.248
MSTRG.34778.1	9.367	MSTRG.33733.1	2.572	MSTRG.14510.3	1.246
MSTRG.29191.2	9.361	MSTRG.16294.1	2.572	MSTRG.37937.1	1.246
MSTRG.34257.2	9.353	MSTRG.14807.1	2.559	MSTRG.35753.1	1.245
MSTRG.23675.2	9.344	MSTRG.35605.1	2.550	MSTRG.46853.3	1.245
MSTRG.41478.2	9.326	MSTRG.41782.3	2.548	MSTRG.27903.1	1.245
MSTRG.19349.12	9.323	MSTRG.9692.7	2.547	MSTRG.15353.1	1.245
MSTRG.40546.4	9.309	MSTRG.9910.1	2.547	MSTRG.22867.1	1.244
MSTRG.35774.4	9.305	MSTRG.4700.1	2.542	MSTRG.13405.1	1.244
MSTRG.38670.2	9.300	MSTRG.459.1	2.541	MSTRG.43700.1	1.244
MSTRG.38098.2	9.286	MSTRG.21222.4	2.536	MSTRG.20676.1	1.244
MSTRG.29185.2	9.283	MSTRG.38925.1	2.521	MSTRG.20662.1	1.243
MSTRG.17358.1	9.271	MSTRG.45865.1	2.520	MSTRG.551.1	1.243
MSTRG.43992.3	9.270	MSTRG.41763.1	2.511	MSTRG.23738.1	1.241
MSTRG.16218.2	9.267	MSTRG.46440.2	2.511	MSTRG.39685.1	1.240
MSTRG.7591.10	9.266	MSTRG.9301.1	2.510	MSTRG.43163.2	1.240
MSTRG.21415.10	9.265	MSTRG.34728.3	2.496	MSTRG.6123.1	1.240
MSTRG.25518.1	9.250	MSTRG.41159.1	2.496	MSTRG.12653.1	1.239
MSTRG.28556.4	9.245	MSTRG.29054.1	2.495	MSTRG.34755.4	1.238
MSTRG.25164.2	9.244	MSTRG.25126.1	2.493	MSTRG.4779.1	1.238
MSTRG.13030.4	9.212	MSTRG.47655.1	2.490	MSTRG.21522.1	1.237
MSTRG.32899.2	9.202	MSTRG.21905.1	2.487	MSTRG.14708.1	1.237
MSTRG.41097.3	9.201	MSTRG.2509.2	2.484	MSTRG.1185.1	1.236
MSTRG.3959.1	9.185	MSTRG.1960.1	2.483	MSTRG.27582.1	1.235
MSTRG.27932.1	9.173	MSTRG.30187.1	2.481	MSTRG.44652.2	1.235
MSTRG.20554.1	9.167	MSTRG.23153.1	2.474	MSTRG.32770.1	1.235

MSTRG.38001.2	9.152	MSTRG.26579.2	2.471	MSTRG.38850.1	1.235
MSTRG.34662.3	9.152	MSTRG.5631.2	2.470	MSTRG.15162.1	1.233
MSTRG.22120.4	9.142	MSTRG.204.1	2.470	MSTRG.46705.3	1.232
MSTRG.37767.2	9.126	MSTRG.40563.29	2.464	MSTRG.47827.1	1.229
MSTRG.29954.2	9.104	MSTRG.6550.2	2.450	MSTRG.843.1	1.227
MSTRG.28785.5	9.103	MSTRG.10826.1	2.445	MSTRG.32980.1	1.227
MSTRG.45698.2	9.102	MSTRG.37329.1	2.437	MSTRG.27750.1	1.226
MSTRG.17523.2	9.084	MSTRG.14245.2	2.436	MSTRG.17251.1	1.226
MSTRG.18754.2	9.077	MSTRG.3569.1	2.434	MSTRG.18179.1	1.225
MSTRG.19071.3	9.072	MSTRG.34216.1	2.432	MSTRG.45403.1	1.224
MSTRG.31191.10	9.066	MSTRG.8751.2	2.429	MSTRG.28629.1	1.224
MSTRG.18906.3	9.041	MSTRG.42657.5	2.424	MSTRG.47927.1	1.223
MSTRG.24596.4	9.029	MSTRG.3590.1	2.423	MSTRG.21552.1	1.222
MSTRG.2545.2	9.026	MSTRG.31890.3	2.423	MSTRG.45045.2	1.222
MSTRG.8909.2	9.020	MSTRG.46844.3	2.420	MSTRG.22264.1	1.221
MSTRG.9196.4	9.010	MSTRG.37345.4	2.417	MSTRG.16382.1	1.220
MSTRG.34675.1	9.004	MSTRG.15895.1	2.417	MSTRG.35047.1	1.217
MSTRG.48760.8	8.993	MSTRG.19867.1	2.415	MSTRG.19855.1	1.217
MSTRG.41275.2	8.978	MSTRG.48560.1	2.414	MSTRG.15206.1	1.216
MSTRG.22626.2	8.969	MSTRG.41969.8	2.406	MSTRG.5651.1	1.213
MSTRG.46001.3	8.968	MSTRG.34546.1	2.406	MSTRG.44486.1	1.209
MSTRG.27138.3	8.954	MSTRG.13819.1	2.399	MSTRG.44923.1	1.208
MSTRG.17100.3	8.952	MSTRG.27204.1	2.396	MSTRG.45429.1	1.207
MSTRG.36093.4	8.931	MSTRG.9198.1	2.391	MSTRG.24399.2	1.207
MSTRG.24701.5	8.925	MSTRG.28064.1	2.391	MSTRG.48219.1	1.205
MSTRG.38102.2	8.909	MSTRG.4012.2	2.387	MSTRG.13513.1	1.205
MSTRG.18395.2	8.898	MSTRG.35793.1	2.387	MSTRG.29195.1	1.203

MSTRG.47779.2	8.893	MSTRG.40246.1	2.387	MSTRG.42709.1	1.203
MSTRG.23940.2	8.893	MSTRG.26225.1	2.385	MSTRG.16646.1	1.202
MSTRG.494.3	8.875	MSTRG.23606.2	2.384	MSTRG.3073.1	1.200
MSTRG.16142.2	8.860	MSTRG.28173.4	2.383	MSTRG.38150.1	1.200
MSTRG.36373.4	8.854	MSTRG.9899.1	2.382	MSTRG.43922.1	1.198
MSTRG.45776.3	8.853	MSTRG.37895.4	2.378	MSTRG.10874.4	1.198
MSTRG.7340.3	8.829	MSTRG.6698.1	2.376	MSTRG.1096.1	1.198
MSTRG.17212.3	8.754	MSTRG.9996.1	2.374	MSTRG.1479.1	1.197
MSTRG.30423.2	8.753	MSTRG.25519.1	2.374	MSTRG.5674.1	1.197
MSTRG.45991.3	8.746	MSTRG.6148.1	2.373	MSTRG.1715.1	1.197
MSTRG.42188.2	8.745	MSTRG.48564.1	2.373	MSTRG.7276.2	1.196
MSTRG.728.2	8.736	MSTRG.10702.5	2.373	MSTRG.8177.1	1.196
MSTRG.29585.12	8.728	MSTRG.23422.3	2.373	MSTRG.42811.1	1.196
MSTRG.40074.10	8.716	MSTRG.19959.1	2.365	MSTRG.20816.1	1.196
MSTRG.24044.3	8.704	MSTRG.13288.2	2.363	MSTRG.18084.1	1.195
MSTRG.43193.6	8.699	MSTRG.12836.1	2.360	MSTRG.48591.1	1.195
MSTRG.27649.3	8.689	MSTRG.19913.1	2.357	MSTRG.5681.1	1.195
MSTRG.20286.3	8.672	MSTRG.3402.1	2.348	MSTRG.20745.2	1.193
MSTRG.1323.3	8.666	MSTRG.34074.10	2.346	MSTRG.42802.2	1.192
MSTRG.38442.4	8.635	MSTRG.15546.3	2.342	MSTRG.30840.2	1.192
MSTRG.18036.5	8.628	MSTRG.4542.1	2.339	MSTRG.18127.1	1.191
MSTRG.48080.10	8.616	MSTRG.9164.2	2.338	MSTRG.37177.4	1.191
MSTRG.29420.11	8.614	MSTRG.25854.4	2.338	MSTRG.24979.1	1.190
MSTRG.41118.2	8.601	MSTRG.8631.1	2.334	MSTRG.3208.2	1.190
MSTRG.46018.2	8.601	MSTRG.30345.4	2.334	MSTRG.18341.1	1.189
MSTRG.19666.4	8.599	MSTRG.27372.4	2.334	MSTRG.7369.2	1.188
MSTRG.26901.5	8.590	MSTRG.41579.1	2.333	MSTRG.13740.1	1.187

MSTRG.27525.3	8.582	MSTRG.44419.2	2.325	MSTRG.39147.1	1.186
MSTRG.35887.2	8.521	MSTRG.14253.1	2.325	MSTRG.2134.1	1.186
MSTRG.38117.2	8.513	MSTRG.19310.1	2.324	MSTRG.13098.1	1.185
MSTRG.27647.1	8.512	MSTRG.33356.2	2.324	MSTRG.48333.2	1.184
MSTRG.3632.2	8.482	MSTRG.21299.1	2.323	MSTRG.20381.6	1.183
MSTRG.4807.3	8.465	MSTRG.3951.3	2.323	MSTRG.47136.1	1.182
MSTRG.30341.4	8.456	MSTRG.39848.1	2.321	MSTRG.17651.1	1.182
MSTRG.4382.10	8.427	MSTRG.29521.2	2.318	MSTRG.30449.11	1.182
MSTRG.7026.3	8.392	MSTRG.1205.3	2.314	MSTRG.21682.1	1.181
MSTRG.38156.2	8.369	MSTRG.1671.1	2.311	MSTRG.3004.1	1.181
MSTRG.42632.6	8.321	MSTRG.32779.1	2.309	MSTRG.30449.1	1.180
MSTRG.35668.2	8.319	MSTRG.5851.3	2.309	MSTRG.40596.1	1.180
MSTRG.9288.1	8.283	MSTRG.1542.1	2.309	MSTRG.33428.1	1.180
MSTRG.43512.1	8.282	MSTRG.37940.1	2.307	MSTRG.21518.1	1.179
MSTRG.17049.2	8.252	MSTRG.14246.1	2.302	MSTRG.41756.1	1.178
MSTRG.44920.2	8.234	MSTRG.29708.1	2.301	MSTRG.10409.1	1.178
MSTRG.38056.8	8.223	MSTRG.16840.1	2.296	MSTRG.33198.2	1.178
MSTRG.10850.2	8.204	MSTRG.31111.1	2.289	MSTRG.21871.1	1.177
MSTRG.3199.1	8.201	MSTRG.42868.1	2.288	MSTRG.10332.1	1.177
MSTRG.47822.1	8.182	MSTRG.26536.3	2.286	MSTRG.13216.2	1.177
MSTRG.31661.5	8.167	MSTRG.9692.6	2.284	MSTRG.45220.1	1.177
MSTRG.11030.4	8.161	MSTRG.41969.6	2.283	MSTRG.16280.1	1.177
MSTRG.38545.4	8.155	MSTRG.17098.1	2.282	MSTRG.33184.1	1.177
MSTRG.34161.2	8.138	MSTRG.21092.1	2.280	MSTRG.14256.1	1.176
MSTRG.40020.3	8.126	MSTRG.38312.5	2.280	MSTRG.48304.1	1.176
MSTRG.33805.2	8.125	MSTRG.10882.2	2.278	MSTRG.34947.1	1.175
MSTRG.16450.3	8.098	MSTRG.37261.2	2.277	MSTRG.45238.1	1.175

MSTRG.29946.4	8.095	MSTRG.23154.1	2.277	MSTRG.11867.1	1.175
MSTRG.40371.2	8.012	MSTRG.48297.1	2.275	MSTRG.33412.1	1.174
MSTRG.46511.7	7.993	MSTRG.43558.1	2.273	MSTRG.45584.1	1.174
MSTRG.29167.3	7.960	MSTRG.22178.4	2.271	MSTRG.842.1	1.174
MSTRG.36764.1	7.918	MSTRG.36977.1	2.266	MSTRG.46644.1	1.172
MSTRG.15676.11	7.910	MSTRG.2270.3	2.265	MSTRG.875.4	1.172
MSTRG.39151.4	7.869	MSTRG.31450.5	2.264	MSTRG.14094.1	1.171
MSTRG.1295.1	7.862	MSTRG.25161.1	2.264	MSTRG.22661.1	1.170
MSTRG.45182.1	7.861	MSTRG.36759.1	2.262	MSTRG.20833.1	1.170
MSTRG.35742.3	7.861	MSTRG.8278.1	2.255	MSTRG.46645.1	1.169
MSTRG.18463.3	7.790	MSTRG.45663.1	2.252	MSTRG.45237.1	1.169
MSTRG.31751.7	7.734	MSTRG.24284.2	2.251	MSTRG.46305.1	1.167
MSTRG.9515.2	7.729	MSTRG.33590.1	2.250	MSTRG.47173.1	1.167
MSTRG.8105.5	7.700	MSTRG.32217.2	2.243	MSTRG.32505.1	1.166
MSTRG.7892.2	7.693	MSTRG.4382.3	2.243	MSTRG.30409.1	1.165
MSTRG.29220.13	7.659	MSTRG.44423.1	2.241	MSTRG.41269.4	1.164
MSTRG.24578.15	7.656	MSTRG.45453.3	2.240	MSTRG.8137.1	1.161
MSTRG.40154.1	7.621	MSTRG.2465.1	2.236	MSTRG.6546.1	1.160
MSTRG.48775.1	7.569	MSTRG.3401.1	2.236	MSTRG.740.1	1.158
MSTRG.5275.2	7.546	MSTRG.20677.1	2.235	MSTRG.9542.2	1.158
MSTRG.3877.2	7.510	MSTRG.1345.1	2.234	MSTRG.44745.1	1.156
MSTRG.15007.2	7.492	MSTRG.32517.4	2.234	MSTRG.48103.1	1.156
MSTRG.36547.4	7.483	MSTRG.36207.3	2.233	MSTRG.20908.1	1.155
MSTRG.1918.2	7.431	MSTRG.16499.1	2.231	MSTRG.32715.1	1.153
MSTRG.9221.2	7.387	MSTRG.1914.1	2.231	MSTRG.13941.1	1.151
MSTRG.8217.2	7.382	MSTRG.15405.3	2.227	MSTRG.28268.1	1.151
MSTRG.47870.3	7.377	MSTRG.4384.1	2.223	MSTRG.7324.1	1.151

MSTRG.41576.2	7.354	MSTRG.3570.3	2.221	MSTRG.48090.1	1.151
MSTRG.19299.2	7.343	MSTRG.21030.2	2.221	MSTRG.40609.1	1.150
MSTRG.6931.1	7.315	MSTRG.36744.1	2.215	MSTRG.5069.1	1.150
MSTRG.533.2	7.312	MSTRG.24185.1	2.214	MSTRG.2100.2	1.149
MSTRG.29833.2	7.305	MSTRG.31142.1	2.207	MSTRG.5416.1	1.148
MSTRG.6263.2	7.305	MSTRG.14770.4	2.205	MSTRG.26654.1	1.147
MSTRG.20679.1	7.302	MSTRG.41559.1	2.204	MSTRG.41814.2	1.147
MSTRG.21536.5	7.258	MSTRG.1534.2	2.203	MSTRG.9404.1	1.145
MSTRG.10886.2	7.246	MSTRG.43910.3	2.200	MSTRG.27326.7	1.145
MSTRG.21953.2	7.244	MSTRG.43050.2	2.197	MSTRG.20517.1	1.144
MSTRG.39024.1	7.227	MSTRG.1929.1	2.190	MSTRG.19403.1	1.143
MSTRG.46714.1	7.223	MSTRG.18407.1	2.188	MSTRG.32307.1	1.141
MSTRG.26679.2	7.211	MSTRG.2944.1	2.175	MSTRG.6117.1	1.141
MSTRG.1707.2	7.206	MSTRG.13609.10	2.173	MSTRG.41814.1	1.140
MSTRG.47664.2	7.201	MSTRG.29929.5	2.170	MSTRG.28026.1	1.139
MSTRG.33886.2	7.115	MSTRG.39731.1	2.169	MSTRG.35860.1	1.137
MSTRG.23422.8	7.089	MSTRG.23615.1	2.163	MSTRG.47690.1	1.136
MSTRG.43716.3	7.087	MSTRG.12765.3	2.161	MSTRG.40113.1	1.135
MSTRG.29979.2	7.084	MSTRG.47555.1	2.159	MSTRG.47042.1	1.135
MSTRG.3685.11	7.067	MSTRG.490.1	2.144	MSTRG.24151.4	1.133
MSTRG.42636.1	7.065	MSTRG.20908.3	2.140	MSTRG.29897.1	1.133
MSTRG.28114.3	7.035	MSTRG.25477.10	2.139	MSTRG.43501.1	1.130
MSTRG.15606.1	7.028	MSTRG.26389.2	2.135	MSTRG.11097.1	1.128
MSTRG.13007.2	7.026	MSTRG.40252.1	2.135	MSTRG.566.1	1.127
MSTRG.25126.5	7.024	MSTRG.44567.2	2.134	MSTRG.38379.1	1.127
MSTRG.8468.3	7.023	MSTRG.19931.1	2.130	MSTRG.45671.1	1.125
MSTRG.5909.2	7.006	MSTRG.25640.2	2.129	MSTRG.23479.1	1.124

MSTRG.28025.2	6.994	MSTRG.46839.1	2.128	MSTRG.16652.1	1.122
MSTRG.18737.2	6.989	MSTRG.30535.2	2.124	MSTRG.26172.1	1.121
MSTRG.28716.2	6.980	MSTRG.12704.1	2.122	MSTRG.25339.1	1.120
MSTRG.3321.4	6.964	MSTRG.48562.1	2.120	MSTRG.13319.1	1.119
MSTRG.33969.1	6.932	MSTRG.1897.2	2.119	MSTRG.19993.1	1.118
MSTRG.25327.4	6.921	MSTRG.7667.1	2.119	MSTRG.46137.1	1.118
MSTRG.1194.2	6.912	MSTRG.19309.4	2.117	MSTRG.47172.1	1.117
MSTRG.7862.2	6.887	MSTRG.40645.1	2.117	MSTRG.39940.1	1.117
MSTRG.21772.2	6.863	MSTRG.7496.3	2.116	MSTRG.13396.1	1.115
MSTRG.41352.3	6.863	MSTRG.20167.1	2.116	MSTRG.21856.1	1.114
MSTRG.12291.3	6.835	MSTRG.6700.1	2.111	MSTRG.30816.1	1.114
MSTRG.42597.4	6.802	MSTRG.29111.11	2.104	MSTRG.30115.1	1.113
MSTRG.37602.1	6.800	MSTRG.40066.1	2.103	MSTRG.24503.1	1.113
MSTRG.32732.2	6.796	MSTRG.25162.1	2.101	MSTRG.8869.1	1.112
MSTRG.25965.2	6.782	MSTRG.10354.1	2.100	MSTRG.1464.1	1.110
MSTRG.18251.3	6.771	MSTRG.38561.1	2.100	MSTRG.21470.2	1.110
MSTRG.29688.4	6.765	MSTRG.8393.1	2.099	MSTRG.37374.2	1.110
MSTRG.29055.2	6.759	MSTRG.20745.3	2.098	MSTRG.10256.2	1.109
MSTRG.41392.3	6.745	MSTRG.27567.1	2.098	MSTRG.19984.1	1.107
MSTRG.37326.2	6.736	MSTRG.19204.1	2.096	MSTRG.44417.1	1.107
MSTRG.6637.2	6.735	MSTRG.4071.2	2.095	MSTRG.38366.1	1.107
MSTRG.38553.3	6.713	MSTRG.38151.1	2.090	MSTRG.1911.1	1.106
MSTRG.21568.3	6.679	MSTRG.1084.1	2.090	MSTRG.25964.1	1.105
MSTRG.92.3	6.668	MSTRG.45939.1	2.090	MSTRG.8960.1	1.104
MSTRG.36224.2	6.657	MSTRG.12282.2	2.089	MSTRG.5846.1	1.104
MSTRG.11984.2	6.604	MSTRG.44362.1	2.088	MSTRG.27973.1	1.103
MSTRG.30549.2	6.577	MSTRG.42120.1	2.088	MSTRG.32327.3	1.102

MSTRG.22489.2	6.573	MSTRG.8851.3	2.086	MSTRG.44693.1	1.102
MSTRG.21691.6	6.573	MSTRG.6697.1	2.082	MSTRG.21857.1	1.102
MSTRG.24962.4	6.549	MSTRG.26003.1	2.081	MSTRG.14305.1	1.101
MSTRG.19053.1	6.532	MSTRG.28191.1	2.077	MSTRG.42300.1	1.101
MSTRG.44667.2	6.530	MSTRG.17199.1	2.077	MSTRG.6346.1	1.099
MSTRG.17754.2	6.527	MSTRG.33643.1	2.076	MSTRG.29260.2	1.098
MSTRG.35881.1	6.503	MSTRG.26053.1	2.076	MSTRG.20196.1	1.098
MSTRG.30319.5	6.485	MSTRG.15547.1	2.076	MSTRG.27955.1	1.098
MSTRG.42363.1	6.474	MSTRG.27914.1	2.073	MSTRG.15504.1	1.097
MSTRG.1670.2	6.465	MSTRG.31351.4	2.069	MSTRG.8403.2	1.095
MSTRG.23360.14	6.464	MSTRG.23422.1	2.066	MSTRG.18649.1	1.093
MSTRG.4323.1	6.456	MSTRG.31735.1	2.066	MSTRG.3957.1	1.093
MSTRG.28650.1	6.444	MSTRG.24817.1	2.061	MSTRG.20813.1	1.092
MSTRG.6577.5	6.437	MSTRG.38007.3	2.060	MSTRG.26685.1	1.091
MSTRG.43193.3	6.437	MSTRG.23205.1	2.060	MSTRG.41991.1	1.091
MSTRG.41719.3	6.395	MSTRG.3131.1	2.051	MSTRG.44180.4	1.090
MSTRG.48064.4	6.359	MSTRG.35174.1	2.048	MSTRG.1881.1	1.090
MSTRG.21030.6	6.341	MSTRG.38118.2	2.047	MSTRG.24217.1	1.088
MSTRG.6540.6	6.322	MSTRG.12585.1	2.042	MSTRG.21776.1	1.088
MSTRG.8673.3	6.319	MSTRG.37150.1	2.037	MSTRG.25060.1	1.086
MSTRG.23056.2	6.286	MSTRG.36799.1	2.034	MSTRG.46297.1	1.085
MSTRG.17129.2	6.255	MSTRG.31207.1	2.028	MSTRG.44567.1	1.085
MSTRG.13020.7	6.202	MSTRG.25507.1	2.027	MSTRG.47093.1	1.083
MSTRG.28124.3	6.182	MSTRG.40555.33	2.026	MSTRG.45488.1	1.082
MSTRG.1670.3	6.163	MSTRG.12707.1	2.021	MSTRG.31239.1	1.081
MSTRG.21216.2	6.141	MSTRG.39088.1	2.021	MSTRG.7316.4	1.081
MSTRG.6003.2	6.139	MSTRG.18245.1	2.019	MSTRG.41888.1	1.080

MSTRG.8139.2	6.116	MSTRG.9028.6	2.016	MSTRG.39214.1	1.078
MSTRG.44944.2	6.097	MSTRG.36459.1	2.014	MSTRG.3723.1	1.078
MSTRG.32148.3	6.081	MSTRG.26799.5	2.013	MSTRG.16933.1	1.078
MSTRG.40555.37	6.076	MSTRG.23858.1	2.013	MSTRG.42581.1	1.077
MSTRG.19636.4	6.032	MSTRG.23859.1	2.013	MSTRG.21216.1	1.076
MSTRG.44840.2	6.023	MSTRG.25057.1	2.012	MSTRG.47741.1	1.074
MSTRG.29764.5	6.016	MSTRG.7873.2	2.009	MSTRG.18581.1	1.074
MSTRG.12272.3	6.013	MSTRG.48736.1	2.008	MSTRG.7823.1	1.073
MSTRG.6697.3	5.986	MSTRG.39770.1	2.007	MSTRG.36285.1	1.072
MSTRG.46018.7	5.984	MSTRG.5067.1	1.998	MSTRG.16026.1	1.072
MSTRG.24485.9	5.972	MSTRG.25832.1	1.998	MSTRG.24272.1	1.071
MSTRG.352.1	5.953	MSTRG.22492.1	1.987	MSTRG.46562.1	1.071
MSTRG.18281.4	5.952	MSTRG.29509.5	1.986	MSTRG.27366.1	1.071
MSTRG.46018.5	5.939	MSTRG.40570.1	1.986	MSTRG.18884.1	1.070
MSTRG.9033.2	5.937	MSTRG.14133.1	1.983	MSTRG.2112.1	1.070
MSTRG.9646.1	5.925	MSTRG.36157.1	1.973	MSTRG.31536.1	1.070
MSTRG.45587.6	5.920	MSTRG.24174.1	1.971	MSTRG.25527.1	1.069
MSTRG.11273.2	5.920	MSTRG.33842.4	1.971	MSTRG.27965.1	1.068
MSTRG.5985.2	5.892	MSTRG.31707.1	1.971	MSTRG.38647.1	1.068
MSTRG.9592.5	5.859	MSTRG.7021.1	1.970	MSTRG.21028.2	1.067
MSTRG.15512.2	5.856	MSTRG.25861.1	1.967	MSTRG.46826.1	1.067
MSTRG.16988.3	5.837	MSTRG.41797.1	1.964	MSTRG.15058.1	1.066
MSTRG.13101.13	5.823	MSTRG.5336.3	1.963	MSTRG.13367.2	1.066
MSTRG.35448.2	5.822	MSTRG.29196.1	1.961	MSTRG.457.1	1.065
MSTRG.8881.2	5.815	MSTRG.22311.1	1.960	MSTRG.27326.5	1.063
MSTRG.36422.1	5.804	MSTRG.46141.1	1.960	MSTRG.6084.1	1.063
MSTRG.26196.5	5.785	MSTRG.10124.1	1.959	MSTRG.22511.2	1.062

MSTRG.32888.2	5.776	MSTRG.15952.1	1.954	MSTRG.43173.1	1.062
MSTRG.46184.2	5.762	MSTRG.29102.6	1.954	MSTRG.36853.1	1.061
MSTRG.39326.2	5.740	MSTRG.43163.1	1.952	MSTRG.10721.1	1.061
MSTRG.15311.2	5.726	MSTRG.48010.4	1.950	MSTRG.46281.1	1.061
MSTRG.33283.2	5.707	MSTRG.30419.1	1.947	MSTRG.27167.1	1.061
MSTRG.12565.4	5.649	MSTRG.488.1	1.944	MSTRG.17730.1	1.061
MSTRG.7893.2	5.634	MSTRG.7276.5	1.943	MSTRG.31404.1	1.060
MSTRG.28575.3	5.624	MSTRG.11131.1	1.939	MSTRG.33831.1	1.060
MSTRG.41973.1	5.619	MSTRG.34888.1	1.939	MSTRG.4191.1	1.059
MSTRG.22687.5	5.587	MSTRG.19043.1	1.935	MSTRG.39160.1	1.058
MSTRG.36327.6	5.582	MSTRG.46959.1	1.930	MSTRG.10328.1	1.057
MSTRG.18168.7	5.557	MSTRG.17601.1	1.927	MSTRG.5659.1	1.056
MSTRG.3839.2	5.546	MSTRG.456.1	1.925	MSTRG.965.1	1.056
MSTRG.40927.2	5.531	MSTRG.36720.1	1.924	MSTRG.36214.1	1.055
MSTRG.8267.2	5.527	MSTRG.9692.1	1.922	MSTRG.37163.1	1.055
MSTRG.5868.3	5.505	MSTRG.25093.1	1.922	MSTRG.10450.1	1.053
MSTRG.27372.5	5.493	MSTRG.16393.1	1.922	MSTRG.12467.13	1.051
MSTRG.23433.1	5.490	MSTRG.40270.1	1.921	MSTRG.22695.1	1.050
MSTRG.34995.2	5.481	MSTRG.16229.2	1.919	MSTRG.36836.1	1.049
MSTRG.374.7	5.478	MSTRG.18174.1	1.918	MSTRG.34709.1	1.048
MSTRG.41862.3	5.476	MSTRG.13620.1	1.914	MSTRG.42846.1	1.048
MSTRG.35958.4	5.458	MSTRG.14810.2	1.912	MSTRG.7212.2	1.046
MSTRG.38492.2	5.452	MSTRG.22735.2	1.909	MSTRG.44021.1	1.046
MSTRG.15896.1	5.444	MSTRG.13489.2	1.909	MSTRG.44093.1	1.045
MSTRG.7316.5	5.418	MSTRG.44418.1	1.906	MSTRG.38542.1	1.045
MSTRG.15271.2	5.417	MSTRG.46210.1	1.905	MSTRG.18262.1	1.045
MSTRG.47504.1	5.411	MSTRG.33108.1	1.905	MSTRG.21392.1	1.043

MSTRG.16949.2	5.400	MSTRG.42919.1	1.905	MSTRG.45044.1	1.043
MSTRG.1323.4	5.397	MSTRG.47437.1	1.901	MSTRG.3797.1	1.042
MSTRG.40034.1	5.394	MSTRG.34142.4	1.900	MSTRG.24939.1	1.041
MSTRG.10390.3	5.375	MSTRG.19960.1	1.899	MSTRG.29125.1	1.041
MSTRG.33048.8	5.374	MSTRG.40914.1	1.894	MSTRG.17509.1	1.041
MSTRG.42104.3	5.349	MSTRG.9221.3	1.893	MSTRG.48492.1	1.040
MSTRG.36427.4	5.339	MSTRG.34590.1	1.892	MSTRG.10479.6	1.039
MSTRG.2645.7	5.324	MSTRG.5649.1	1.892	MSTRG.37756.1	1.039
MSTRG.32447.6	5.302	MSTRG.21402.8	1.890	MSTRG.35346.1	1.037
MSTRG.42634.1	5.288	MSTRG.42298.1	1.888	MSTRG.28961.1	1.037
MSTRG.24937.3	5.278	MSTRG.28652.1	1.882	MSTRG.34621.1	1.037
MSTRG.23623.3	5.264	MSTRG.45027.1	1.882	MSTRG.26461.1	1.037
MSTRG.26580.3	5.249	MSTRG.31351.5	1.881	MSTRG.36156.1	1.035
MSTRG.27922.6	5.230	MSTRG.15255.1	1.880	MSTRG.33316.1	1.034
MSTRG.27832.2	5.229	MSTRG.35794.1	1.876	MSTRG.28267.1	1.034
MSTRG.36103.6	5.227	MSTRG.5878.1	1.874	MSTRG.7905.1	1.034
MSTRG.24841.3	5.206	MSTRG.29644.1	1.873	MSTRG.17767.1	1.033
MSTRG.43535.2	5.200	MSTRG.16395.1	1.869	MSTRG.40866.1	1.033
MSTRG.36262.4	5.184	MSTRG.37319.1	1.866	MSTRG.24805.1	1.033
MSTRG.20470.8	5.170	MSTRG.17652.1	1.863	MSTRG.15888.1	1.033
MSTRG.24382.9	5.162	MSTRG.12652.2	1.863	MSTRG.26538.1	1.033
MSTRG.22668.3	5.146	MSTRG.38412.1	1.862	MSTRG.28987.1	1.033
MSTRG.1411.2	5.141	MSTRG.28402.1	1.861	MSTRG.14592.2	1.030
MSTRG.3984.2	5.133	MSTRG.17079.1	1.861	MSTRG.46223.1	1.030
MSTRG.42155.2	5.125	MSTRG.45621.1	1.860	MSTRG.26100.1	1.029
MSTRG.27833.5	5.111	MSTRG.30579.1	1.858	MSTRG.19435.2	1.029
MSTRG.48150.5	5.111	MSTRG.40921.1	1.857	MSTRG.24612.1	1.028

MSTRG.23430.2	5.109	MSTRG.27261.2	1.853	MSTRG.15894.1	1.028
MSTRG.27833.3	5.108	MSTRG.36158.1	1.849	MSTRG.11602.1	1.027
MSTRG.29055.3	5.091	MSTRG.32397.3	1.849	MSTRG.34668.2	1.026
MSTRG.10563.6	5.088	MSTRG.13404.1	1.849	MSTRG.32684.1	1.024
MSTRG.4951.1	5.088	MSTRG.10331.1	1.848	MSTRG.45681.1	1.023
MSTRG.42434.2	5.072	MSTRG.7914.1	1.844	MSTRG.16268.1	1.022
MSTRG.374.6	5.072	MSTRG.9013.1	1.842	MSTRG.6018.3	1.020
MSTRG.39388.4	5.071	MSTRG.13436.1	1.839	MSTRG.46494.1	1.019
MSTRG.11756.3	5.060	MSTRG.9759.5	1.839	MSTRG.45877.1	1.019
MSTRG.39350.2	5.053	MSTRG.10333.2	1.835	MSTRG.32190.1	1.018
MSTRG.36220.2	5.051	MSTRG.5941.3	1.833	MSTRG.46802.1	1.017
MSTRG.6240.2	5.048	MSTRG.28046.1	1.832	MSTRG.21194.1	1.016
MSTRG.14250.1	5.029	MSTRG.5538.1	1.829	MSTRG.37732.2	1.016
MSTRG.23464.4	4.972	MSTRG.29609.1	1.827	MSTRG.16978.1	1.015
MSTRG.46112.2	4.949	MSTRG.41796.1	1.826	MSTRG.45756.1	1.015
MSTRG.12482.2	4.941	MSTRG.6820.1	1.826	MSTRG.46966.2	1.015
MSTRG.11603.3	4.929	MSTRG.40782.1	1.824	MSTRG.42788.1	1.014
MSTRG.16160.1	4.925	MSTRG.17080.1	1.824	MSTRG.23636.1	1.014
MSTRG.6522.2	4.891	MSTRG.15408.2	1.824	MSTRG.12377.1	1.012
MSTRG.27906.3	4.882	MSTRG.4790.3	1.821	MSTRG.6441.1	1.012
MSTRG.36311.2	4.876	MSTRG.20099.1	1.820	MSTRG.12538.1	1.012
MSTRG.32336.4	4.872	MSTRG.6337.1	1.817	MSTRG.18627.1	1.012
MSTRG.30319.3	4.865	MSTRG.14851.4	1.816	MSTRG.38886.1	1.011
MSTRG.10491.1	4.865	MSTRG.6935.1	1.815	MSTRG.37048.1	1.011
MSTRG.40563.3	4.860	MSTRG.14399.1	1.813	MSTRG.39597.1	1.011
MSTRG.10340.3	4.850	MSTRG.11488.1	1.812	MSTRG.32541.1	1.010
MSTRG.15472.4	4.842	MSTRG.27976.1	1.810	MSTRG.32494.1	1.009

MSTRG.21110.2	4.841	MSTRG.11780.1	1.809	MSTRG.45778.1	1.009
MSTRG.39454.1	4.807	MSTRG.13473.1	1.809	MSTRG.33660.1	1.009
MSTRG.38969.2	4.795	MSTRG.1982.1	1.809	MSTRG.20033.1	1.008
MSTRG.8735.2	4.769	MSTRG.34852.2	1.807	MSTRG.47269.1	1.007
MSTRG.16974.2	4.768	MSTRG.17801.1	1.802	MSTRG.10411.1	1.006
MSTRG.27833.1	4.767	MSTRG.40121.1	1.801	MSTRG.42859.1	1.006
MSTRG.28273.2	4.761	MSTRG.15161.1	1.799	MSTRG.38650.1	1.006
MSTRG.2349.3	4.761	MSTRG.38411.1	1.799	MSTRG.13624.2	1.005
MSTRG.43663.3	4.749	MSTRG.47678.3	1.799	MSTRG.7786.1	1.005
MSTRG.16495.2	4.729	MSTRG.15087.1	1.799	MSTRG.15290.1	1.005
MSTRG.6203.2	4.728	MSTRG.48647.1	1.798	MSTRG.47437.2	1.004
MSTRG.7492.2	4.725	MSTRG.15256.1	1.798	MSTRG.1711.1	1.003
MSTRG.16289.3	4.720	MSTRG.44978.1	1.798	MSTRG.45880.1	1.002
MSTRG.47729.1	4.712	MSTRG.22623.4	1.796	MSTRG.22245.2	1.000
MSTRG.46490.1	4.692	MSTRG.41762.1	1.796		
MSTRG.45891.2	4.682	MSTRG.48061.1	1.791		

Table S4.5: Downregulated transcripts under chilling conditions in *Corylus avellana* cv Cakildak with iDEP

Transcript ID	log2 FoldChange	Transcript ID	log2 FoldChange	Transcript ID	log2 FoldChange
MSTRG.38679.1	-26.602	MSTRG.2319.1	-2.654	MSTRG.4760.1	-1.672
MSTRG.20762.2	-26.397	MSTRG.28785.3	-2.651	MSTRG.20455.1	-1.671
MSTRG.11584.1	-26.232	MSTRG.33353.1	-2.650	MSTRG.22307.1	-1.670
MSTRG.196.1	-25.744	MSTRG.17621.3	-2.646	MSTRG.32791.1	-1.670
MSTRG.201.6	-25.713	MSTRG.2376.1	-2.640	MSTRG.18575.1	-1.669
MSTRG.2783.1	-25.357	MSTRG.29678.1	-2.639	MSTRG.37459.1	-1.667
MSTRG.6894.1	-25.296	MSTRG.46604.1	-2.638	MSTRG.32158.2	-1.667
MSTRG.11160.4	-24.901	MSTRG.2648.1	-2.637	MSTRG.13369.1	-1.666
MSTRG.37708.7	-24.873	MSTRG.33330.1	-2.636	MSTRG.41111.1	-1.666
MSTRG.30857.2	-24.758	MSTRG.46938.1	-2.634	MSTRG.31863.3	-1.665
MSTRG.25851.2	-24.733	MSTRG.22876.1	-2.633	MSTRG.42901.1	-1.665
MSTRG.37632.9	-24.704	MSTRG.28811.1	-2.629	MSTRG.33154.4	-1.664
MSTRG.32756.1	-24.663	MSTRG.33353.5	-2.629	MSTRG.18292.1	-1.661
MSTRG.18229.2	-24.526	MSTRG.17878.1	-2.628	MSTRG.13600.2	-1.661
MSTRG.26521.2	-24.363	MSTRG.45567.5	-2.626	MSTRG.27717.1	-1.661
MSTRG.12557.8	-24.359	MSTRG.26134.1	-2.624	MSTRG.13579.1	-1.660
MSTRG.33918.2	-24.329	MSTRG.13489.1	-2.624	MSTRG.16187.1	-1.660
MSTRG.3884.7	-24.163	MSTRG.33123.2	-2.624	MSTRG.45561.3	-1.657
MSTRG.7276.4	-23.937	MSTRG.26140.1	-2.618	MSTRG.21044.1	-1.657
MSTRG.48251.1	-23.796	MSTRG.14968.2	-2.618	MSTRG.45455.1	-1.657
MSTRG.42306.7	-23.690	MSTRG.16697.1	-2.615	MSTRG.23321.1	-1.657
MSTRG.46397.2	-23.669	MSTRG.7111.1	-2.614	MSTRG.6203.1	-1.656
MSTRG.26165.1	-23.653	MSTRG.15724.1	-2.609	MSTRG.7297.1	-1.655
MSTRG.10045.2	-23.648	MSTRG.10368.3	-2.607	MSTRG.31237.1	-1.655

MSTRG.21860.4	-23.519	MSTRG.37147.4	-2.604	MSTRG.25203.1	-1.653
MSTRG.14432.1	-23.168	MSTRG.40250.1	-2.602	MSTRG.29023.1	-1.653
MSTRG.3163.5	-23.165	MSTRG.14974.3	-2.601	MSTRG.44778.1	-1.653
MSTRG.15859.2	-23.143	MSTRG.36820.5	-2.601	MSTRG.182.2	-1.653
MSTRG.24200.2	-22.901	MSTRG.48693.1	-2.600	MSTRG.46731.1	-1.653
MSTRG.23637.9	-22.261	MSTRG.3980.1	-2.596	MSTRG.10703.1	-1.652
MSTRG.29420.10	-21.778	MSTRG.4142.1	-2.594	MSTRG.43116.1	-1.652
MSTRG.19687.1	-19.671	MSTRG.46017.1	-2.594	MSTRG.28797.1	-1.651
MSTRG.48817.10	-19.061	MSTRG.29004.1	-2.593	MSTRG.16805.4	-1.651
MSTRG.3925.4	-16.693	MSTRG.47422.2	-2.591	MSTRG.33354.1	-1.648
MSTRG.14446.1	-16.374	MSTRG.17775.1	-2.591	MSTRG.45824.1	-1.648
MSTRG.36123.5	-15.672	MSTRG.12662.1	-2.587	MSTRG.7710.11	-1.648
MSTRG.2480.1	-15.634	MSTRG.27946.1	-2.586	MSTRG.17732.1	-1.647
MSTRG.28069.1	-15.099	MSTRG.41072.1	-2.580	MSTRG.30975.2	-1.646
MSTRG.48602.1	-14.714	MSTRG.6104.5	-2.579	MSTRG.27861.3	-1.646
MSTRG.27958.3	-14.677	MSTRG.33974.1	-2.576	MSTRG.6151.2	-1.645
MSTRG.40667.2	-14.334	MSTRG.33285.2	-2.575	MSTRG.23238.1	-1.645
MSTRG.25304.1	-14.309	MSTRG.18070.1	-2.575	MSTRG.15873.2	-1.642
MSTRG.9775.4	-14.249	MSTRG.42877.1	-2.575	MSTRG.3255.1	-1.642
MSTRG.42306.6	-14.050	MSTRG.10381.2	-2.574	MSTRG.17895.1	-1.639
MSTRG.31365.2	-13.989	MSTRG.19584.2	-2.573	MSTRG.5255.1	-1.638
MSTRG.19388.1	-13.874	MSTRG.5902.1	-2.572	MSTRG.46574.2	-1.637
MSTRG.10538.1	-13.812	MSTRG.38163.1	-2.572	MSTRG.28891.2	-1.637
MSTRG.41288.6	-13.811	MSTRG.34364.2	-2.572	MSTRG.21334.1	-1.636
MSTRG.13266.1	-13.642	MSTRG.12261.1	-2.572	MSTRG.25082.2	-1.636
MSTRG.41606.2	-13.487	MSTRG.17926.1	-2.570	MSTRG.7888.1	-1.636
MSTRG.1075.1	-13.428	MSTRG.43228.1	-2.567	MSTRG.33957.1	-1.635

MSTRG.38363.1	-13.416	MSTRG.3989.2	-2.566	MSTRG.31718.1	-1.633
MSTRG.36044.2	-13.283	MSTRG.7602.1	-2.561	MSTRG.3559.1	-1.633
MSTRG.6115.1	-13.231	MSTRG.2219.3	-2.561	MSTRG.21202.1	-1.633
MSTRG.34197.1	-13.212	MSTRG.16144.1	-2.559	MSTRG.13502.1	-1.631
MSTRG.34252.1	-13.207	MSTRG.22768.2	-2.558	MSTRG.5179.2	-1.631
MSTRG.34148.1	-13.065	MSTRG.31106.1	-2.556	MSTRG.32327.1	-1.630
MSTRG.656.1	-13.001	MSTRG.42547.1	-2.555	MSTRG.27541.1	-1.630
MSTRG.9816.1	-12.898	MSTRG.45265.1	-2.554	MSTRG.46983.2	-1.629
MSTRG.6122.1	-12.894	MSTRG.15179.1	-2.552	MSTRG.41945.1	-1.629
MSTRG.23400.2	-12.876	MSTRG.8694.3	-2.551	MSTRG.37386.1	-1.628
MSTRG.266.2	-12.843	MSTRG.3475.3	-2.550	MSTRG.15599.1	-1.627
MSTRG.35507.1	-12.759	MSTRG.16650.1	-2.550	MSTRG.27360.1	-1.627
MSTRG.39667.1	-12.759	MSTRG.36820.6	-2.550	MSTRG.25614.1	-1.627
MSTRG.28090.2	-12.720	MSTRG.40189.3	-2.550	MSTRG.27948.1	-1.627
MSTRG.26234.5	-12.642	MSTRG.2277.4	-2.549	MSTRG.4529.2	-1.625
MSTRG.26091.3	-12.641	MSTRG.29165.1	-2.548	MSTRG.17410.1	-1.625
MSTRG.14835.2	-12.628	MSTRG.10187.1	-2.546	MSTRG.34691.1	-1.625
MSTRG.2277.1	-12.584	MSTRG.18764.1	-2.545	MSTRG.12443.2	-1.625
MSTRG.32596.5	-12.538	MSTRG.45308.1	-2.544	MSTRG.30493.1	-1.624
MSTRG.13717.1	-12.367	MSTRG.4646.3	-2.542	MSTRG.22149.1	-1.624
MSTRG.2277.13	-12.326	MSTRG.33859.3	-2.540	MSTRG.13559.1	-1.624
MSTRG.27109.4	-12.287	MSTRG.40585.1	-2.534	MSTRG.1980.1	-1.624
MSTRG.5462.1	-12.279	MSTRG.19489.1	-2.533	MSTRG.33421.1	-1.621
MSTRG.4208.1	-12.253	MSTRG.2592.1	-2.533	MSTRG.19664.1	-1.621
MSTRG.31551.2	-12.194	MSTRG.43944.2	-2.529	MSTRG.34826.1	-1.620
MSTRG.42657.9	-12.177	MSTRG.8083.2	-2.526	MSTRG.10921.1	-1.620
MSTRG.21440.1	-12.139	MSTRG.23160.1	-2.523	MSTRG.32834.1	-1.620

MSTRG.24030.1	-12.050	MSTRG.36229.1	-2.522	MSTRG.39708.2	-1.618
MSTRG.27111.2	-12.026	MSTRG.27867.2	-2.516	MSTRG.34694.1	-1.618
MSTRG.42482.1	-11.994	MSTRG.29191.1	-2.515	MSTRG.30656.3	-1.617
MSTRG.48760.2	-11.942	MSTRG.1149.3	-2.508	MSTRG.38238.1	-1.616
MSTRG.33773.2	-11.912	MSTRG.21019.2	-2.505	MSTRG.44536.1	-1.616
MSTRG.16864.15	-11.777	MSTRG.41523.1	-2.503	MSTRG.47083.1	-1.615
MSTRG.12859.2	-11.726	MSTRG.40133.1	-2.503	MSTRG.28621.1	-1.614
MSTRG.22845.2	-11.656	MSTRG.11784.16	-2.501	MSTRG.16725.1	-1.614
MSTRG.5048.1	-11.651	MSTRG.12426.2	-2.499	MSTRG.40097.4	-1.613
MSTRG.19571.2	-11.625	MSTRG.34594.1	-2.497	MSTRG.8343.1	-1.613
MSTRG.17681.1	-11.542	MSTRG.169.1	-2.497	MSTRG.28784.1	-1.611
MSTRG.4007.1	-11.511	MSTRG.21631.1	-2.497	MSTRG.27013.1	-1.610
MSTRG.40415.1	-11.373	MSTRG.44874.1	-2.495	MSTRG.20514.1	-1.609
MSTRG.2693.1	-11.352	MSTRG.20466.1	-2.495	MSTRG.19057.1	-1.608
MSTRG.6873.5	-11.098	MSTRG.44046.1	-2.487	MSTRG.18895.1	-1.608
MSTRG.22811.2	-11.010	MSTRG.2212.1	-2.485	MSTRG.45906.1	-1.607
MSTRG.22859.2	-10.815	MSTRG.29401.1	-2.485	MSTRG.35379.4	-1.607
MSTRG.48758.3	-10.610	MSTRG.35218.1	-2.484	MSTRG.38390.1	-1.606
MSTRG.40097.6	-10.606	MSTRG.45661.1	-2.482	MSTRG.31498.1	-1.604
MSTRG.29231.1	-10.594	MSTRG.37754.1	-2.478	MSTRG.48616.8	-1.604
MSTRG.8798.1	-10.447	MSTRG.33191.1	-2.477	MSTRG.48246.2	-1.603
MSTRG.35723.2	-10.437	MSTRG.13592.1	-2.475	MSTRG.10213.6	-1.603
MSTRG.33757.2	-10.404	MSTRG.7936.1	-2.474	MSTRG.930.1	-1.601
MSTRG.10670.2	-10.403	MSTRG.1195.1	-2.473	MSTRG.12496.1	-1.600
MSTRG.8872.2	-10.340	MSTRG.3554.1	-2.472	MSTRG.32275.1	-1.598
MSTRG.42011.2	-10.055	MSTRG.48732.1	-2.469	MSTRG.29729.1	-1.598
MSTRG.23464.5	-9.937	MSTRG.7710.1	-2.469	MSTRG.2613.1	-1.597

MSTRG.18819.1	-9.819	MSTRG.33353.4	-2.468	MSTRG.46376.1	-1.597
MSTRG.27422.2	-9.736	MSTRG.40932.1	-2.468	MSTRG.15838.1	-1.596
MSTRG.45830.5	-9.729	MSTRG.37947.1	-2.468	MSTRG.23980.1	-1.595
MSTRG.20533.1	-9.629	MSTRG.48134.1	-2.468	MSTRG.5835.1	-1.595
MSTRG.29004.4	-9.620	MSTRG.42343.1	-2.467	MSTRG.5285.1	-1.593
MSTRG.12096.1	-9.615	MSTRG.20381.7	-2.467	MSTRG.10685.6	-1.592
MSTRG.28671.1	-9.600	MSTRG.23841.1	-2.466	MSTRG.26738.1	-1.591
MSTRG.33174.4	-9.564	MSTRG.44749.3	-2.463	MSTRG.40891.1	-1.591
MSTRG.12945.2	-9.448	MSTRG.42730.1	-2.463	MSTRG.25120.4	-1.591
MSTRG.196.5	-9.415	MSTRG.34901.1	-2.463	MSTRG.1761.1	-1.590
MSTRG.29742.1	-9.377	MSTRG.39910.1	-2.460	MSTRG.18741.2	-1.590
MSTRG.14017.2	-9.319	MSTRG.26036.1	-2.459	MSTRG.33031.1	-1.590
MSTRG.32579.1	-9.303	MSTRG.45884.1	-2.459	MSTRG.2565.1	-1.589
MSTRG.39901.2	-9.274	MSTRG.20589.1	-2.459	MSTRG.28784.2	-1.588
MSTRG.31143.1	-9.274	MSTRG.20983.1	-2.458	MSTRG.41885.1	-1.588
MSTRG.18186.1	-9.267	MSTRG.35340.1	-2.453	MSTRG.43143.1	-1.586
MSTRG.32016.2	-9.067	MSTRG.10987.1	-2.452	MSTRG.3591.1	-1.585
MSTRG.44314.1	-9.058	MSTRG.35079.1	-2.450	MSTRG.26394.1	-1.583
MSTRG.5150.2	-9.029	MSTRG.2633.1	-2.447	MSTRG.8909.1	-1.583
MSTRG.1181.1	-8.961	MSTRG.21626.1	-2.447	MSTRG.19363.1	-1.583
MSTRG.40297.4	-8.958	MSTRG.20435.1	-2.441	MSTRG.35611.3	-1.582
MSTRG.40297.5	-8.938	MSTRG.47375.1	-2.431	MSTRG.8815.1	-1.581
MSTRG.33771.1	-8.889	MSTRG.3655.2	-2.429	MSTRG.33174.12	-1.581
MSTRG.29567.2	-8.875	MSTRG.22148.1	-2.426	MSTRG.45074.1	-1.581
MSTRG.46394.10	-8.850	MSTRG.16267.1	-2.424	MSTRG.35860.2	-1.578
MSTRG.43033.1	-8.829	MSTRG.21416.1	-2.423	MSTRG.22992.1	-1.577
MSTRG.3884.9	-8.828	MSTRG.107.3	-2.422	MSTRG.11354.1	-1.575

MSTRG.28570.7	-8.824	MSTRG.6182.15	-2.421	MSTRG.38545.1	-1.574
MSTRG.33679.1	-8.782	MSTRG.29666.1	-2.420	MSTRG.28159.1	-1.572
MSTRG.13786.3	-8.501	MSTRG.29257.1	-2.418	MSTRG.46066.1	-1.571
MSTRG.22166.6	-8.473	MSTRG.10277.1	-2.417	MSTRG.11369.1	-1.571
MSTRG.25327.3	-8.445	MSTRG.27333.2	-2.416	MSTRG.14975.1	-1.570
MSTRG.44753.10	-8.421	MSTRG.34906.1	-2.415	MSTRG.21615.1	-1.570
MSTRG.12012.2	-8.387	MSTRG.2440.1	-2.414	MSTRG.22591.1	-1.569
MSTRG.9209.8	-8.375	MSTRG.23139.1	-2.414	MSTRG.24927.1	-1.569
MSTRG.7310.4	-8.359	MSTRG.4206.1	-2.412	MSTRG.25613.1	-1.568
MSTRG.19655.1	-8.312	MSTRG.7457.1	-2.412	MSTRG.10209.1	-1.563
MSTRG.2350.2	-8.312	MSTRG.38136.1	-2.407	MSTRG.14803.1	-1.562
MSTRG.46707.2	-8.311	MSTRG.13704.1	-2.407	MSTRG.47450.4	-1.559
MSTRG.25656.1	-8.247	MSTRG.45304.1	-2.405	MSTRG.14420.3	-1.558
MSTRG.22778.3	-8.215	MSTRG.9449.1	-2.404	MSTRG.45078.1	-1.558
MSTRG.4437.1	-8.209	MSTRG.10257.1	-2.402	MSTRG.31669.1	-1.556
MSTRG.10222.8	-8.176	MSTRG.928.3	-2.402	MSTRG.503.2	-1.555
MSTRG.8234.1	-8.170	MSTRG.31555.2	-2.400	MSTRG.5155.1	-1.554
MSTRG.5482.1	-8.124	MSTRG.35094.1	-2.400	MSTRG.24876.1	-1.553
MSTRG.30750.2	-8.094	MSTRG.4406.1	-2.399	MSTRG.31061.1	-1.553
MSTRG.34243.1	-7.936	MSTRG.4138.2	-2.399	MSTRG.17530.1	-1.550
MSTRG.11859.2	-7.931	MSTRG.19429.1	-2.394	MSTRG.32267.1	-1.549
MSTRG.25168.1	-7.900	MSTRG.4033.3	-2.393	MSTRG.20368.3	-1.548
MSTRG.28503.1	-7.836	MSTRG.39710.1	-2.392	MSTRG.20340.1	-1.547
MSTRG.304.1	-7.832	MSTRG.20183.1	-2.392	MSTRG.1642.1	-1.547
MSTRG.36953.1	-7.823	MSTRG.10557.6	-2.390	MSTRG.12456.1	-1.546
MSTRG.24634.2	-7.817	MSTRG.27704.1	-2.387	MSTRG.17560.1	-1.546
MSTRG.26899.4	-7.781	MSTRG.22908.2	-2.381	MSTRG.17678.3	-1.545

MSTRG.20536.1	-7.758	MSTRG.14220.1	-2.380	MSTRG.18337.1	-1.545
MSTRG.36302.17	-7.711	MSTRG.1260.1	-2.380	MSTRG.33243.4	-1.544
MSTRG.42597.1	-7.680	MSTRG.29884.1	-2.379	MSTRG.42384.1	-1.544
MSTRG.15998.3	-7.649	MSTRG.42604.1	-2.377	MSTRG.13980.1	-1.544
MSTRG.5561.2	-7.600	MSTRG.1295.2	-2.376	MSTRG.42763.5	-1.543
MSTRG.16831.7	-7.589	MSTRG.31667.1	-2.376	MSTRG.25204.1	-1.543
MSTRG.40505.1	-7.560	MSTRG.39756.1	-2.375	MSTRG.44323.1	-1.540
MSTRG.14982.1	-7.521	MSTRG.41778.1	-2.373	MSTRG.22348.1	-1.538
MSTRG.46913.3	-7.461	MSTRG.26329.1	-2.373	MSTRG.21946.1	-1.537
MSTRG.23230.3	-7.452	MSTRG.21536.2	-2.373	MSTRG.27584.2	-1.535
MSTRG.14194.3	-7.320	MSTRG.10285.1	-2.371	MSTRG.208.1	-1.535
MSTRG.16222.1	-7.297	MSTRG.41080.1	-2.366	MSTRG.13448.1	-1.535
MSTRG.45467.13	-7.284	MSTRG.13743.1	-2.363	MSTRG.32612.1	-1.535
MSTRG.5275.1	-7.213	MSTRG.20491.1	-2.363	MSTRG.22118.1	-1.534
MSTRG.613.1	-7.190	MSTRG.2432.1	-2.362	MSTRG.21861.1	-1.534
MSTRG.26466.3	-7.075	MSTRG.45598.2	-2.361	MSTRG.35251.1	-1.533
MSTRG.21108.1	-7.064	MSTRG.23390.1	-2.359	MSTRG.20906.2	-1.533
MSTRG.41294.1	-6.959	MSTRG.33174.11	-2.356	MSTRG.31368.1	-1.531
MSTRG.36955.1	-6.875	MSTRG.10886.1	-2.354	MSTRG.43401.1	-1.531
MSTRG.39426.3	-6.826	MSTRG.15059.1	-2.353	MSTRG.29376.4	-1.529
MSTRG.302.2	-6.764	MSTRG.1695.3	-2.352	MSTRG.41931.1	-1.528
MSTRG.45455.2	-6.762	MSTRG.14659.1	-2.350	MSTRG.38518.1	-1.527
MSTRG.8366.3	-6.738	MSTRG.10522.1	-2.350	MSTRG.38952.1	-1.527
MSTRG.8796.8	-6.694	MSTRG.23655.1	-2.348	MSTRG.24652.1	-1.526
MSTRG.9679.12	-6.645	MSTRG.26407.1	-2.347	MSTRG.41224.2	-1.525
MSTRG.46170.31	-6.635	MSTRG.27816.1	-2.347	MSTRG.552.1	-1.524
MSTRG.31160.2	-6.511	MSTRG.10220.4	-2.346	MSTRG.14370.1	-1.523

MSTRG.23216.4	-6.461	MSTRG.10569.1	-2.346	MSTRG.43471.1	-1.522
MSTRG.23072.2	-6.458	MSTRG.36066.4	-2.343	MSTRG.554.1	-1.522
MSTRG.16797.1	-6.456	MSTRG.42203.1	-2.342	MSTRG.26713.3	-1.521
MSTRG.32617.2	-6.449	MSTRG.42833.18	-2.341	MSTRG.28015.1	-1.521
MSTRG.8085.2	-6.439	MSTRG.28031.1	-2.341	MSTRG.36044.1	-1.521
MSTRG.23169.2	-6.431	MSTRG.38208.7	-2.341	MSTRG.37863.1	-1.520
MSTRG.28273.1	-6.369	MSTRG.22102.1	-2.341	MSTRG.48683.1	-1.519
MSTRG.23763.4	-6.337	MSTRG.19682.2	-2.340	MSTRG.2599.1	-1.519
MSTRG.10368.1	-6.322	MSTRG.27731.1	-2.338	MSTRG.40973.1	-1.519
MSTRG.31160.5	-6.278	MSTRG.20116.1	-2.337	MSTRG.20642.1	-1.518
MSTRG.28897.3	-6.278	MSTRG.28678.1	-2.336	MSTRG.12246.1	-1.518
MSTRG.48519.6	-6.269	MSTRG.467.1	-2.335	MSTRG.5985.1	-1.517
MSTRG.44531.1	-6.243	MSTRG.32038.1	-2.334	MSTRG.39541.1	-1.517
MSTRG.24308.1	-6.147	MSTRG.30490.3	-2.333	MSTRG.4637.2	-1.516
MSTRG.38934.2	-6.147	MSTRG.27389.1	-2.332	MSTRG.38566.1	-1.516
MSTRG.38492.1	-6.074	MSTRG.40561.3	-2.331	MSTRG.39439.1	-1.514
MSTRG.37188.1	-5.971	MSTRG.33353.3	-2.329	MSTRG.3759.1	-1.511
MSTRG.27200.1	-5.967	MSTRG.17267.1	-2.327	MSTRG.10151.1	-1.510
MSTRG.5303.2	-5.898	MSTRG.38978.1	-2.322	MSTRG.45797.1	-1.510
MSTRG.34108.3	-5.884	MSTRG.14906.2	-2.322	MSTRG.34299.1	-1.508
MSTRG.45504.1	-5.851	MSTRG.42308.6	-2.321	MSTRG.41411.1	-1.508
MSTRG.9204.1	-5.835	MSTRG.43404.1	-2.318	MSTRG.47952.1	-1.507
MSTRG.5193.4	-5.830	MSTRG.41692.1	-2.318	MSTRG.40119.1	-1.507
MSTRG.18911.1	-5.815	MSTRG.13809.2	-2.318	MSTRG.10286.1	-1.506
MSTRG.11010.1	-5.783	MSTRG.8450.1	-2.316	MSTRG.5601.16	-1.504
MSTRG.9061.2	-5.759	MSTRG.38245.1	-2.311	MSTRG.5045.1	-1.501
MSTRG.10370.1	-5.730	MSTRG.30971.1	-2.310	MSTRG.48503.7	-1.501

MSTRG.31079.1	-5.718	MSTRG.38102.1	-2.309	MSTRG.22579.1	-1.500
MSTRG.30949.2	-5.665	MSTRG.43676.2	-2.309	MSTRG.8598.1	-1.497
MSTRG.18751.1	-5.656	MSTRG.14210.1	-2.309	MSTRG.31919.1	-1.496
MSTRG.16133.1	-5.650	MSTRG.27987.1	-2.307	MSTRG.35614.3	-1.495
MSTRG.9078.1	-5.628	MSTRG.29721.2	-2.306	MSTRG.13605.1	-1.495
MSTRG.23169.1	-5.585	MSTRG.27342.1	-2.306	MSTRG.24742.1	-1.494
MSTRG.41329.15	-5.548	MSTRG.39924.1	-2.301	MSTRG.12765.2	-1.494
MSTRG.20588.1	-5.546	MSTRG.5046.1	-2.301	MSTRG.17675.1	-1.492
MSTRG.19766.1	-5.510	MSTRG.295.1	-2.300	MSTRG.16767.1	-1.491
MSTRG.35230.3	-5.494	MSTRG.8760.1	-2.299	MSTRG.48675.1	-1.490
MSTRG.15690.4	-5.477	MSTRG.5316.10	-2.297	MSTRG.30657.3	-1.488
MSTRG.36141.1	-5.450	MSTRG.32952.1	-2.297	MSTRG.36403.1	-1.488
MSTRG.40098.1	-5.449	MSTRG.33269.1	-2.296	MSTRG.9033.1	-1.487
MSTRG.17363.1	-5.421	MSTRG.511.2	-2.296	MSTRG.39674.1	-1.487
MSTRG.16474.6	-5.409	MSTRG.48080.3	-2.295	MSTRG.48052.1	-1.487
MSTRG.43763.1	-5.406	MSTRG.19948.2	-2.295	MSTRG.48678.1	-1.485
MSTRG.32730.2	-5.386	MSTRG.42630.1	-2.289	MSTRG.42718.1	-1.485
MSTRG.43082.7	-5.372	MSTRG.30691.1	-2.288	MSTRG.20456.1	-1.485
MSTRG.22664.3	-5.354	MSTRG.37287.1	-2.281	MSTRG.46669.1	-1.484
MSTRG.20152.2	-5.341	MSTRG.13901.1	-2.277	MSTRG.30134.1	-1.483
MSTRG.27844.2	-5.278	MSTRG.44667.1	-2.277	MSTRG.16474.2	-1.482
MSTRG.17397.2	-5.276	MSTRG.4469.1	-2.276	MSTRG.22176.1	-1.482
MSTRG.33550.2	-5.276	MSTRG.36793.1	-2.276	MSTRG.38742.1	-1.481
MSTRG.24736.2	-5.250	MSTRG.508.4	-2.274	MSTRG.32210.1	-1.481
MSTRG.35565.5	-5.241	MSTRG.5378.1	-2.273	MSTRG.21666.1	-1.480
MSTRG.8413.1	-5.190	MSTRG.31254.5	-2.273	MSTRG.37992.4	-1.479
MSTRG.10292.2	-5.182	MSTRG.4917.1	-2.272	MSTRG.16532.1	-1.478

MSTRG.4985.6	-5.176	MSTRG.40746.3	-2.271	MSTRG.47852.1	-1.478
MSTRG.43766.1	-5.160	MSTRG.36300.1	-2.271	MSTRG.22392.2	-1.478
MSTRG.40097.8	-5.156	MSTRG.14790.2	-2.270	MSTRG.15722.1	-1.478
MSTRG.27252.1	-5.128	MSTRG.16385.2	-2.267	MSTRG.3289.1	-1.478
MSTRG.23912.1	-5.109	MSTRG.36663.1	-2.267	MSTRG.1834.1	-1.478
MSTRG.7892.1	-5.106	MSTRG.34588.1	-2.267	MSTRG.20416.11	-1.477
MSTRG.27502.3	-5.085	MSTRG.7663.1	-2.267	MSTRG.45260.1	-1.477
MSTRG.5941.5	-5.085	MSTRG.24547.1	-2.267	MSTRG.9863.1	-1.477
MSTRG.22678.3	-5.079	MSTRG.4118.1	-2.267	MSTRG.15415.1	-1.476
MSTRG.22309.5	-5.069	MSTRG.11272.1	-2.264	MSTRG.32906.1	-1.476
MSTRG.10062.1	-5.064	MSTRG.18960.1	-2.264	MSTRG.5773.1	-1.476
MSTRG.40789.1	-5.062	MSTRG.6527.2	-2.262	MSTRG.14643.1	-1.476
MSTRG.42350.2	-5.013	MSTRG.41573.1	-2.261	MSTRG.26439.1	-1.475
MSTRG.1233.1	-5.012	MSTRG.7603.1	-2.261	MSTRG.29705.10	-1.475
MSTRG.29315.3	-5.003	MSTRG.2265.1	-2.260	MSTRG.11356.1	-1.474
MSTRG.35509.1	-4.992	MSTRG.46631.1	-2.260	MSTRG.2369.2	-1.474
MSTRG.26379.4	-4.991	MSTRG.45803.1	-2.258	MSTRG.30728.1	-1.472
MSTRG.6762.1	-4.984	MSTRG.21293.2	-2.255	MSTRG.40560.1	-1.472
MSTRG.25120.2	-4.981	MSTRG.18886.1	-2.251	MSTRG.6607.1	-1.471
MSTRG.6918.1	-4.975	MSTRG.45078.2	-2.251	MSTRG.33833.2	-1.471
MSTRG.7581.2	-4.951	MSTRG.35729.5	-2.250	MSTRG.31863.2	-1.470
MSTRG.22046.1	-4.951	MSTRG.4114.1	-2.250	MSTRG.17394.1	-1.470
MSTRG.29954.1	-4.942	MSTRG.17390.1	-2.250	MSTRG.47657.1	-1.469
MSTRG.6839.1	-4.936	MSTRG.28036.1	-2.249	MSTRG.45524.1	-1.468
MSTRG.40297.3	-4.931	MSTRG.29842.2	-2.245	MSTRG.13515.3	-1.468
MSTRG.29184.3	-4.904	MSTRG.26346.1	-2.244	MSTRG.25428.1	-1.465
MSTRG.39151.2	-4.894	MSTRG.34825.1	-2.242	MSTRG.41906.1	-1.464

MSTRG.44841.1	-4.876	MSTRG.27651.1	-2.242	MSTRG.37954.2	-1.464
MSTRG.4320.1	-4.871	MSTRG.15872.2	-2.240	MSTRG.11711.1	-1.464
MSTRG.33933.14	-4.869	MSTRG.15450.1	-2.239	MSTRG.1246.4	-1.463
MSTRG.10045.1	-4.863	MSTRG.15956.1	-2.239	MSTRG.32613.1	-1.463
MSTRG.92.2	-4.855	MSTRG.25823.1	-2.238	MSTRG.28145.1	-1.462
MSTRG.12074.2	-4.847	MSTRG.10545.1	-2.237	MSTRG.31969.1	-1.462
MSTRG.21403.7	-4.819	MSTRG.48026.1	-2.236	MSTRG.33285.1	-1.458
MSTRG.35508.1	-4.801	MSTRG.14725.1	-2.235	MSTRG.4120.1	-1.458
MSTRG.5987.1	-4.800	MSTRG.36678.1	-2.234	MSTRG.26142.1	-1.457
MSTRG.39581.1	-4.799	MSTRG.770.1	-2.233	MSTRG.6289.1	-1.456
MSTRG.40531.5	-4.763	MSTRG.1504.1	-2.231	MSTRG.2005.2	-1.456
MSTRG.2062.1	-4.745	MSTRG.47570.1	-2.229	MSTRG.4075.1	-1.454
MSTRG.44041.1	-4.736	MSTRG.19487.1	-2.228	MSTRG.1640.1	-1.452
MSTRG.23080.2	-4.731	MSTRG.7310.1	-2.227	MSTRG.34230.1	-1.452
MSTRG.27249.1	-4.725	MSTRG.40533.1	-2.227	MSTRG.34211.1	-1.452
MSTRG.35725.1	-4.722	MSTRG.34226.14	-2.226	MSTRG.22884.3	-1.450
MSTRG.33307.3	-4.718	MSTRG.32222.1	-2.224	MSTRG.29102.1	-1.450
MSTRG.7558.1	-4.705	MSTRG.3529.1	-2.223	MSTRG.38147.1	-1.448
MSTRG.33510.2	-4.699	MSTRG.8357.2	-2.221	MSTRG.31169.1	-1.447
MSTRG.32571.1	-4.688	MSTRG.42227.1	-2.219	MSTRG.83.1	-1.446
MSTRG.45467.6	-4.687	MSTRG.39964.2	-2.218	MSTRG.16218.1	-1.445
MSTRG.22002.3	-4.670	MSTRG.511.1	-2.218	MSTRG.26616.4	-1.445
MSTRG.6024.1	-4.652	MSTRG.22658.2	-2.218	MSTRG.4465.1	-1.444
MSTRG.45264.1	-4.634	MSTRG.6040.1	-2.216	MSTRG.30568.1	-1.444
MSTRG.15771.1	-4.629	MSTRG.43616.1	-2.213	MSTRG.38525.1	-1.442
MSTRG.31097.1	-4.619	MSTRG.29635.1	-2.213	MSTRG.32011.1	-1.442
MSTRG.34125.1	-4.617	MSTRG.8708.1	-2.212	MSTRG.45143.1	-1.441

MSTRG.47523.2	-4.616	MSTRG.22482.1	-2.212	MSTRG.6756.1	-1.441
MSTRG.46246.1	-4.602	MSTRG.1696.1	-2.211	MSTRG.8349.1	-1.441
MSTRG.23603.1	-4.597	MSTRG.7710.4	-2.211	MSTRG.1246.2	-1.440
MSTRG.12049.1	-4.596	MSTRG.9711.1	-2.211	MSTRG.37883.1	-1.439
MSTRG.44703.1	-4.589	MSTRG.46394.2	-2.210	MSTRG.15240.1	-1.439
MSTRG.6287.4	-4.565	MSTRG.24281.1	-2.210	MSTRG.37394.1	-1.438
MSTRG.20582.1	-4.564	MSTRG.27372.1	-2.208	MSTRG.48497.1	-1.437
MSTRG.39047.1	-4.557	MSTRG.17880.1	-2.207	MSTRG.12951.1	-1.437
MSTRG.43082.5	-4.539	MSTRG.48696.1	-2.205	MSTRG.5051.1	-1.437
MSTRG.20821.1	-4.537	MSTRG.36079.1	-2.203	MSTRG.47451.1	-1.435
MSTRG.35503.1	-4.537	MSTRG.14027.2	-2.200	MSTRG.30555.1	-1.434
MSTRG.16529.6	-4.526	MSTRG.24739.1	-2.199	MSTRG.31245.1	-1.430
MSTRG.4437.6	-4.519	MSTRG.48635.1	-2.194	MSTRG.10253.9	-1.430
MSTRG.19160.2	-4.509	MSTRG.9236.1	-2.194	MSTRG.36005.1	-1.427
MSTRG.12272.1	-4.507	MSTRG.36473.1	-2.193	MSTRG.26959.2	-1.427
MSTRG.32305.1	-4.502	MSTRG.2626.1	-2.191	MSTRG.10233.1	-1.425
MSTRG.48079.1	-4.501	MSTRG.38344.1	-2.190	MSTRG.41196.1	-1.425
MSTRG.20587.1	-4.500	MSTRG.47522.1	-2.189	MSTRG.12033.2	-1.424
MSTRG.676.1	-4.500	MSTRG.14027.1	-2.187	MSTRG.9285.3	-1.424
MSTRG.16726.1	-4.494	MSTRG.11744.1	-2.186	MSTRG.22559.1	-1.424
MSTRG.1855.1	-4.491	MSTRG.10083.1	-2.185	MSTRG.40649.1	-1.424
MSTRG.10575.26	-4.488	MSTRG.1104.1	-2.185	MSTRG.25164.1	-1.423
MSTRG.47209.1	-4.470	MSTRG.15311.1	-2.183	MSTRG.19716.1	-1.422
MSTRG.23404.1	-4.461	MSTRG.10600.1	-2.182	MSTRG.12443.1	-1.422
MSTRG.5959.1	-4.459	MSTRG.46816.1	-2.178	MSTRG.7349.1	-1.421
MSTRG.494.2	-4.454	MSTRG.27828.1	-2.178	MSTRG.10909.9	-1.421
MSTRG.31795.2	-4.441	MSTRG.36141.2	-2.175	MSTRG.27876.1	-1.421

MSTRG.657.2	-4.436	MSTRG.46393.3	-2.174	MSTRG.33177.1	-1.421
MSTRG.31609.4	-4.435	MSTRG.31898.10	-2.174	MSTRG.6844.1	-1.421
MSTRG.33386.1	-4.434	MSTRG.36103.1	-2.174	MSTRG.10253.22	-1.418
MSTRG.18629.2	-4.416	MSTRG.31287.1	-2.174	MSTRG.28306.1	-1.417
MSTRG.35958.1	-4.411	MSTRG.17513.1	-2.171	MSTRG.32051.1	-1.417
MSTRG.5740.1	-4.405	MSTRG.27827.1	-2.171	MSTRG.10685.3	-1.416
MSTRG.10042.2	-4.387	MSTRG.27947.1	-2.171	MSTRG.27428.1	-1.416
MSTRG.43120.1	-4.380	MSTRG.26361.1	-2.168	MSTRG.20515.1	-1.416
MSTRG.42721.1	-4.368	MSTRG.13091.1	-2.168	MSTRG.38146.1	-1.414
MSTRG.23405.1	-4.364	MSTRG.6602.1	-2.164	MSTRG.44293.1	-1.414
MSTRG.29220.12	-4.358	MSTRG.12660.1	-2.164	MSTRG.47684.1	-1.413
MSTRG.38166.1	-4.337	MSTRG.251.1	-2.164	MSTRG.24103.1	-1.412
MSTRG.6182.19	-4.334	MSTRG.39964.1	-2.163	MSTRG.26843.1	-1.412
MSTRG.41523.6	-4.316	MSTRG.28771.1	-2.161	MSTRG.18812.1	-1.411
MSTRG.11368.2	-4.312	MSTRG.1487.1	-2.161	MSTRG.3444.3	-1.411
MSTRG.16178.1	-4.307	MSTRG.43255.1	-2.161	MSTRG.4870.3	-1.410
MSTRG.6075.2	-4.294	MSTRG.38208.10	-2.159	MSTRG.14366.1	-1.410
MSTRG.31215.1	-4.287	MSTRG.7672.1	-2.159	MSTRG.31759.1	-1.410
MSTRG.33291.1	-4.283	MSTRG.35526.1	-2.157	MSTRG.37483.1	-1.410
MSTRG.16356.2	-4.280	MSTRG.20516.1	-2.155	MSTRG.11796.37	-1.409
MSTRG.26768.2	-4.276	MSTRG.37403.1	-2.155	MSTRG.13371.1	-1.408
MSTRG.37504.1	-4.269	MSTRG.40470.2	-2.152	MSTRG.44546.1	-1.407
MSTRG.30781.1	-4.268	MSTRG.709.1	-2.152	MSTRG.17388.1	-1.406
MSTRG.10045.3	-4.259	MSTRG.977.1	-2.152	MSTRG.39971.1	-1.406
MSTRG.15860.1	-4.254	MSTRG.2989.22	-2.151	MSTRG.39774.1	-1.404
MSTRG.17517.1	-4.251	MSTRG.711.1	-2.147	MSTRG.4116.1	-1.404
MSTRG.15481.1	-4.247	MSTRG.18032.1	-2.147	MSTRG.19295.1	-1.404

MSTRG.12557.5	-4.244	MSTRG.12298.1	-2.146	MSTRG.8717.1	-1.404
MSTRG.48247.7	-4.232	MSTRG.18673.4	-2.143	MSTRG.29020.1	-1.403
MSTRG.28975.1	-4.220	MSTRG.15670.1	-2.141	MSTRG.8516.1	-1.403
MSTRG.27578.1	-4.218	MSTRG.26328.1	-2.140	MSTRG.27622.1	-1.401
MSTRG.27114.4	-4.213	MSTRG.5342.1	-2.138	MSTRG.39280.1	-1.401
MSTRG.32336.1	-4.209	MSTRG.45567.4	-2.136	MSTRG.28969.1	-1.399
MSTRG.508.5	-4.205	MSTRG.13583.1	-2.135	MSTRG.31917.1	-1.399
MSTRG.45473.1	-4.197	MSTRG.7972.2	-2.134	MSTRG.45938.6	-1.398
MSTRG.25354.1	-4.190	MSTRG.6765.1	-2.133	MSTRG.41928.1	-1.397
MSTRG.45851.5	-4.187	MSTRG.9776.1	-2.133	MSTRG.11586.2	-1.397
MSTRG.26753.1	-4.187	MSTRG.44950.1	-2.130	MSTRG.29812.1	-1.396
MSTRG.20603.5	-4.185	MSTRG.34079.1	-2.125	MSTRG.6254.1	-1.396
MSTRG.15811.1	-4.171	MSTRG.27465.1	-2.125	MSTRG.41622.1	-1.394
MSTRG.1352.1	-4.168	MSTRG.27418.1	-2.125	MSTRG.41019.1	-1.394
MSTRG.43142.1	-4.151	MSTRG.1826.1	-2.118	MSTRG.3295.1	-1.394
MSTRG.6186.1	-4.151	MSTRG.18751.3	-2.117	MSTRG.32441.1	-1.394
MSTRG.28104.1	-4.151	MSTRG.40145.1	-2.117	MSTRG.3308.1	-1.392
MSTRG.15415.2	-4.142	MSTRG.42527.2	-2.116	MSTRG.45136.1	-1.392
MSTRG.15385.1	-4.137	MSTRG.22830.1	-2.115	MSTRG.13655.1	-1.392
MSTRG.31788.1	-4.137	MSTRG.44329.1	-2.113	MSTRG.12901.2	-1.391
MSTRG.14948.4	-4.132	MSTRG.11435.1	-2.110	MSTRG.38797.1	-1.391
MSTRG.437.3	-4.132	MSTRG.9707.1	-2.110	MSTRG.1128.2	-1.391
MSTRG.8356.1	-4.125	MSTRG.15668.1	-2.109	MSTRG.18457.1	-1.390
MSTRG.9221.1	-4.116	MSTRG.32013.1	-2.107	MSTRG.8714.1	-1.388
MSTRG.9687.2	-4.111	MSTRG.10644.4	-2.105	MSTRG.14553.1	-1.388
MSTRG.35519.1	-4.097	MSTRG.14796.6	-2.105	MSTRG.16228.1	-1.387
MSTRG.19910.1	-4.090	MSTRG.14016.1	-2.103	MSTRG.24218.1	-1.387

MSTRG.611.1	-4.076	MSTRG.25330.3	-2.103	MSTRG.1375.1	-1.387
MSTRG.5998.2	-4.075	MSTRG.33355.1	-2.102	MSTRG.20275.1	-1.386
MSTRG.18327.8	-4.072	MSTRG.28121.1	-2.101	MSTRG.34301.1	-1.386
MSTRG.32148.1	-4.059	MSTRG.18281.1	-2.101	MSTRG.22483.1	-1.386
MSTRG.5508.1	-4.056	MSTRG.18294.1	-2.101	MSTRG.25884.1	-1.385
MSTRG.33697.1	-4.054	MSTRG.22081.1	-2.098	MSTRG.13631.1	-1.385
MSTRG.24910.1	-4.034	MSTRG.26183.1	-2.098	MSTRG.10454.1	-1.384
MSTRG.46707.3	-4.028	MSTRG.37219.1	-2.097	MSTRG.23520.5	-1.383
MSTRG.31089.1	-4.020	MSTRG.14790.1	-2.096	MSTRG.24407.1	-1.381
MSTRG.675.1	-4.005	MSTRG.31920.1	-2.096	MSTRG.38755.1	-1.379
MSTRG.7930.5	-3.991	MSTRG.33266.1	-2.094	MSTRG.45147.1	-1.378
MSTRG.35190.2	-3.974	MSTRG.13027.3	-2.093	MSTRG.20451.1	-1.378
MSTRG.10061.1	-3.974	MSTRG.14027.4	-2.092	MSTRG.29683.3	-1.375
MSTRG.6015.2	-3.974	MSTRG.15136.1	-2.091	MSTRG.10082.1	-1.374
MSTRG.44940.3	-3.962	MSTRG.2283.6	-2.091	MSTRG.1223.1	-1.373
MSTRG.48760.3	-3.960	MSTRG.19863.1	-2.090	MSTRG.32583.1	-1.371
MSTRG.2479.1	-3.960	MSTRG.40428.2	-2.090	MSTRG.12889.1	-1.371
MSTRG.14685.3	-3.952	MSTRG.14381.1	-2.090	MSTRG.29929.3	-1.371
MSTRG.5179.1	-3.941	MSTRG.35936.1	-2.088	MSTRG.15452.1	-1.371
MSTRG.34909.1	-3.936	MSTRG.23166.1	-2.087	MSTRG.15492.1	-1.370
MSTRG.27592.1	-3.934	MSTRG.45520.1	-2.086	MSTRG.38981.1	-1.370
MSTRG.6839.4	-3.933	MSTRG.45864.1	-2.085	MSTRG.44171.1	-1.370
MSTRG.27007.3	-3.932	MSTRG.19124.2	-2.082	MSTRG.39109.1	-1.369
MSTRG.15508.1	-3.927	MSTRG.895.1	-2.081	MSTRG.27870.1	-1.369
MSTRG.5193.2	-3.917	MSTRG.2264.1	-2.079	MSTRG.24431.1	-1.366
MSTRG.41118.1	-3.913	MSTRG.7137.1	-2.077	MSTRG.19715.1	-1.366
MSTRG.31174.2	-3.910	MSTRG.10085.1	-2.076	MSTRG.3530.2	-1.364

MSTRG.37261.4	-3.903	MSTRG.14978.1	-2.076	MSTRG.47845.2	-1.363
MSTRG.34995.1	-3.903	MSTRG.7980.1	-2.076	MSTRG.8716.1	-1.363
MSTRG.47450.1	-3.903	MSTRG.29709.4	-2.076	MSTRG.45829.1	-1.362
MSTRG.37667.1	-3.895	MSTRG.41616.1	-2.075	MSTRG.32851.1	-1.361
MSTRG.33157.1	-3.894	MSTRG.45616.1	-2.074	MSTRG.47868.1	-1.360
MSTRG.38457.1	-3.891	MSTRG.45529.2	-2.071	MSTRG.29602.2	-1.360
MSTRG.22845.1	-3.886	MSTRG.46394.8	-2.071	MSTRG.40557.2	-1.359
MSTRG.19626.2	-3.878	MSTRG.26901.1	-2.070	MSTRG.16296.1	-1.359
MSTRG.9664.1	-3.878	MSTRG.10692.1	-2.070	MSTRG.48769.1	-1.358
MSTRG.36359.1	-3.876	MSTRG.40146.1	-2.069	MSTRG.39673.1	-1.357
MSTRG.924.1	-3.872	MSTRG.44325.1	-2.069	MSTRG.20239.1	-1.357
MSTRG.34397.4	-3.872	MSTRG.18696.1	-2.069	MSTRG.13698.1	-1.356
MSTRG.26679.1	-3.861	MSTRG.28991.1	-2.069	MSTRG.23965.1	-1.355
MSTRG.31823.5	-3.848	MSTRG.4889.2	-2.069	MSTRG.41079.1	-1.355
MSTRG.30131.1	-3.831	MSTRG.47987.1	-2.069	MSTRG.9099.3	-1.351
MSTRG.24070.1	-3.827	MSTRG.12253.2	-2.067	MSTRG.41197.1	-1.351
MSTRG.3471.1	-3.827	MSTRG.17389.1	-2.066	MSTRG.1694.1	-1.350
MSTRG.4250.4	-3.822	MSTRG.22987.2	-2.065	MSTRG.1804.1	-1.350
MSTRG.27007.1	-3.820	MSTRG.45309.1	-2.064	MSTRG.15509.1	-1.349
MSTRG.20708.4	-3.806	MSTRG.35050.1	-2.062	MSTRG.13855.2	-1.349
MSTRG.21415.7	-3.797	MSTRG.12244.1	-2.062	MSTRG.3765.1	-1.348
MSTRG.28280.2	-3.791	MSTRG.2219.1	-2.062	MSTRG.19630.9	-1.348
MSTRG.40096.1	-3.787	MSTRG.24442.2	-2.060	MSTRG.17488.1	-1.348
MSTRG.42536.2	-3.787	MSTRG.1635.1	-2.059	MSTRG.17828.1	-1.347
MSTRG.44529.1	-3.785	MSTRG.18674.1	-2.056	MSTRG.20218.1	-1.346
MSTRG.39958.1	-3.785	MSTRG.3640.1	-2.055	MSTRG.14263.1	-1.346
MSTRG.36123.2	-3.780	MSTRG.21747.3	-2.055	MSTRG.1262.1	-1.343

MSTRG.1826.2	-3.780	MSTRG.13458.1	-2.050	MSTRG.12822.1	-1.342
MSTRG.5997.1	-3.777	MSTRG.14027.5	-2.048	MSTRG.26377.1	-1.341
MSTRG.36783.1	-3.768	MSTRG.31543.1	-2.047	MSTRG.26959.3	-1.341
MSTRG.36756.1	-3.760	MSTRG.22100.1	-2.047	MSTRG.5396.1	-1.340
MSTRG.20532.1	-3.749	MSTRG.28256.3	-2.045	MSTRG.30566.1	-1.339
MSTRG.31301.3	-3.731	MSTRG.14027.3	-2.044	MSTRG.25120.3	-1.338
MSTRG.33040.2	-3.727	MSTRG.27861.1	-2.044	MSTRG.32511.1	-1.338
MSTRG.31174.6	-3.724	MSTRG.32879.1	-2.044	MSTRG.18456.1	-1.337
MSTRG.2477.1	-3.713	MSTRG.30657.1	-2.043	MSTRG.40557.1	-1.335
MSTRG.6182.5	-3.709	MSTRG.28037.1	-2.043	MSTRG.28135.1	-1.334
MSTRG.38386.2	-3.706	MSTRG.9411.2	-2.037	MSTRG.8083.1	-1.334
MSTRG.2989.7	-3.702	MSTRG.11419.1	-2.035	MSTRG.6290.1	-1.329
MSTRG.31952.1	-3.702	MSTRG.43143.2	-2.034	MSTRG.32785.1	-1.328
MSTRG.24373.1	-3.699	MSTRG.34572.3	-2.034	MSTRG.206.1	-1.328
MSTRG.47615.1	-3.688	MSTRG.20903.3	-2.033	MSTRG.31213.1	-1.328
MSTRG.30482.1	-3.677	MSTRG.41747.4	-2.032	MSTRG.8357.1	-1.327
MSTRG.31340.1	-3.672	MSTRG.37491.2	-2.032	MSTRG.15379.1	-1.326
MSTRG.7943.3	-3.671	MSTRG.34262.1	-2.032	MSTRG.18509.1	-1.326
MSTRG.13380.1	-3.668	MSTRG.7981.1	-2.032	MSTRG.20580.2	-1.326
MSTRG.9047.1	-3.666	MSTRG.7500.1	-2.031	MSTRG.23485.3	-1.325
MSTRG.21132.1	-3.665	MSTRG.25244.1	-2.031	MSTRG.10295.1	-1.325
MSTRG.25264.2	-3.663	MSTRG.39695.1	-2.030	MSTRG.18741.1	-1.323
MSTRG.12712.1	-3.663	MSTRG.9653.2	-2.030	MSTRG.10235.1	-1.322
MSTRG.18281.2	-3.659	MSTRG.24458.1	-2.029	MSTRG.48006.1	-1.320
MSTRG.7668.1	-3.658	MSTRG.38207.1	-2.029	MSTRG.20922.1	-1.320
MSTRG.6182.7	-3.656	MSTRG.30656.2	-2.028	MSTRG.47463.1	-1.319
MSTRG.28973.1	-3.656	MSTRG.34855.1	-2.027	MSTRG.7503.2	-1.319

MSTRG.10369.1	-3.656	MSTRG.8506.1	-2.026	MSTRG.12742.1	-1.319
MSTRG.18353.4	-3.654	MSTRG.44381.1	-2.026	MSTRG.16488.1	-1.318
MSTRG.47521.3	-3.654	MSTRG.42318.9	-2.024	MSTRG.40471.1	-1.317
MSTRG.11042.1	-3.651	MSTRG.30913.1	-2.024	MSTRG.39989.1	-1.317
MSTRG.22149.2	-3.643	MSTRG.15669.1	-2.024	MSTRG.2545.1	-1.316
MSTRG.48097.1	-3.642	MSTRG.15312.1	-2.024	MSTRG.30323.1	-1.316
MSTRG.33054.2	-3.635	MSTRG.3609.1	-2.023	MSTRG.38051.2	-1.315
MSTRG.16864.14	-3.635	MSTRG.29351.1	-2.023	MSTRG.4265.1	-1.315
MSTRG.9164.3	-3.632	MSTRG.39440.1	-2.023	MSTRG.34895.1	-1.314
MSTRG.30490.5	-3.626	MSTRG.37503.1	-2.020	MSTRG.42381.1	-1.314
MSTRG.43032.1	-3.625	MSTRG.29371.6	-2.020	MSTRG.14225.1	-1.314
MSTRG.34305.1	-3.623	MSTRG.15872.1	-2.019	MSTRG.18813.1	-1.313
MSTRG.31003.1	-3.620	MSTRG.42013.1	-2.019	MSTRG.35853.1	-1.312
MSTRG.6587.1	-3.619	MSTRG.42097.16	-2.018	MSTRG.23332.1	-1.311
MSTRG.46517.1	-3.619	MSTRG.12025.1	-2.016	MSTRG.33254.1	-1.310
MSTRG.25114.1	-3.613	MSTRG.26135.1	-2.016	MSTRG.30365.1	-1.308
MSTRG.26632.1	-3.606	MSTRG.15873.1	-2.016	MSTRG.26584.3	-1.308
MSTRG.38438.1	-3.599	MSTRG.48482.1	-2.013	MSTRG.48124.1	-1.307
MSTRG.2575.1	-3.599	MSTRG.17343.1	-2.012	MSTRG.36975.1	-1.307
MSTRG.34551.1	-3.598	MSTRG.1828.1	-2.011	MSTRG.21807.1	-1.307
MSTRG.43931.1	-3.596	MSTRG.35129.2	-2.010	MSTRG.10206.1	-1.306
MSTRG.29059.1	-3.596	MSTRG.28033.1	-2.010	MSTRG.24460.1	-1.305
MSTRG.43881.2	-3.591	MSTRG.29164.1	-2.008	MSTRG.41920.1	-1.304
MSTRG.17294.1	-3.589	MSTRG.16784.1	-2.006	MSTRG.1554.2	-1.302
MSTRG.33480.1	-3.583	MSTRG.10813.1	-2.006	MSTRG.13092.1	-1.302
MSTRG.25547.1	-3.581	MSTRG.34901.4	-2.006	MSTRG.21972.1	-1.301
MSTRG.45459.1	-3.580	MSTRG.30656.1	-2.005	MSTRG.30366.1	-1.301

MSTRG.4437.2	-3.570	MSTRG.20683.1	-2.004	MSTRG.35611.4	-1.301
MSTRG.28113.3	-3.570	MSTRG.37033.6	-2.003	MSTRG.2018.1	-1.300
MSTRG.14948.5	-3.568	MSTRG.39911.1	-2.002	MSTRG.10253.14	-1.299
MSTRG.17203.4	-3.565	MSTRG.1107.1	-1.999	MSTRG.13653.1	-1.296
MSTRG.10447.11	-3.562	MSTRG.5905.1	-1.998	MSTRG.42802.1	-1.295
MSTRG.18976.1	-3.562	MSTRG.25441.1	-1.998	MSTRG.18251.1	-1.295
MSTRG.32001.1	-3.562	MSTRG.33175.1	-1.997	MSTRG.39343.2	-1.292
MSTRG.25555.5	-3.560	MSTRG.19488.1	-1.994	MSTRG.2212.5	-1.292
MSTRG.21240.2	-3.553	MSTRG.45567.2	-1.992	MSTRG.10463.1	-1.291
MSTRG.29102.5	-3.550	MSTRG.41231.1	-1.991	MSTRG.35611.2	-1.291
MSTRG.22643.1	-3.546	MSTRG.38501.1	-1.990	MSTRG.33679.3	-1.290
MSTRG.35958.2	-3.538	MSTRG.6184.1	-1.989	MSTRG.38243.1	-1.288
MSTRG.48419.1	-3.538	MSTRG.40097.3	-1.989	MSTRG.6253.1	-1.286
MSTRG.45993.1	-3.537	MSTRG.10886.4	-1.986	MSTRG.35611.1	-1.285
MSTRG.27163.2	-3.536	MSTRG.26907.8	-1.985	MSTRG.34005.1	-1.285
MSTRG.45364.1	-3.536	MSTRG.34424.1	-1.984	MSTRG.17853.1	-1.285
MSTRG.39439.2	-3.533	MSTRG.5601.2	-1.983	MSTRG.48102.1	-1.284
MSTRG.13381.1	-3.533	MSTRG.22562.1	-1.983	MSTRG.42308.2	-1.282
MSTRG.40299.1	-3.530	MSTRG.29598.1	-1.983	MSTRG.22291.1	-1.282
MSTRG.31174.3	-3.530	MSTRG.33195.1	-1.981	MSTRG.23712.1	-1.282
MSTRG.7302.1	-3.527	MSTRG.20581.1	-1.981	MSTRG.8762.1	-1.281
MSTRG.16830.1	-3.521	MSTRG.21415.20	-1.979	MSTRG.7434.1	-1.281
MSTRG.41632.1	-3.521	MSTRG.9527.1	-1.977	MSTRG.39710.3	-1.281
MSTRG.20772.1	-3.520	MSTRG.26139.1	-1.976	MSTRG.18705.1	-1.281
MSTRG.24795.1	-3.517	MSTRG.17289.1	-1.974	MSTRG.7604.1	-1.277
MSTRG.24291.1	-3.513	MSTRG.12682.1	-1.974	MSTRG.26527.1	-1.277
MSTRG.23359.11	-3.510	MSTRG.29722.1	-1.973	MSTRG.35392.1	-1.275

MSTRG.18036.1	-3.505	MSTRG.40779.2	-1.973	MSTRG.22988.1	-1.275
MSTRG.4339.1	-3.499	MSTRG.36103.3	-1.970	MSTRG.47228.1	-1.274
MSTRG.44545.1	-3.498	MSTRG.34599.1	-1.970	MSTRG.32310.1	-1.274
MSTRG.39431.1	-3.494	MSTRG.18764.3	-1.968	MSTRG.19701.1	-1.273
MSTRG.12068.3	-3.492	MSTRG.48269.1	-1.968	MSTRG.41439.1	-1.273
MSTRG.4942.2	-3.488	MSTRG.20337.2	-1.966	MSTRG.33918.1	-1.272
MSTRG.38670.3	-3.471	MSTRG.792.1	-1.965	MSTRG.26368.1	-1.272
MSTRG.36820.4	-3.467	MSTRG.18850.1	-1.962	MSTRG.20832.1	-1.271
MSTRG.26065.1	-3.465	MSTRG.24382.7	-1.960	MSTRG.6018.1	-1.270
MSTRG.30615.3	-3.461	MSTRG.29894.1	-1.958	MSTRG.1323.1	-1.270
MSTRG.10685.1	-3.456	MSTRG.17929.1	-1.957	MSTRG.48566.1	-1.269
MSTRG.2820.1	-3.454	MSTRG.37371.1	-1.957	MSTRG.47026.2	-1.269
MSTRG.17771.1	-3.454	MSTRG.7710.6	-1.955	MSTRG.44588.1	-1.269
MSTRG.11405.2	-3.452	MSTRG.48646.1	-1.955	MSTRG.40651.1	-1.268
MSTRG.45467.7	-3.447	MSTRG.41447.1	-1.954	MSTRG.22998.1	-1.266
MSTRG.22985.1	-3.442	MSTRG.12070.1	-1.952	MSTRG.22569.1	-1.264
MSTRG.5720.1	-3.434	MSTRG.8083.4	-1.951	MSTRG.31499.1	-1.263
MSTRG.38837.1	-3.433	MSTRG.39316.1	-1.948	MSTRG.30558.1	-1.263
MSTRG.28913.2	-3.431	MSTRG.4870.4	-1.948	MSTRG.19374.1	-1.263
MSTRG.43186.1	-3.426	MSTRG.24465.1	-1.948	MSTRG.7407.1	-1.262
MSTRG.4433.1	-3.422	MSTRG.21266.1	-1.947	MSTRG.28686.1	-1.260
MSTRG.35751.1	-3.421	MSTRG.5191.8	-1.946	MSTRG.5076.1	-1.260
MSTRG.234.2	-3.420	MSTRG.33889.1	-1.944	MSTRG.12033.1	-1.258
MSTRG.249.7	-3.416	MSTRG.5960.7	-1.944	MSTRG.47918.1	-1.258
MSTRG.18378.1	-3.416	MSTRG.6633.1	-1.943	MSTRG.26480.1	-1.256
MSTRG.31095.1	-3.403	MSTRG.598.1	-1.943	MSTRG.31979.1	-1.255
MSTRG.25172.1	-3.403	MSTRG.18486.1	-1.943	MSTRG.28984.1	-1.255

MSTRG.8708.2	-3.397	MSTRG.30220.1	-1.943	MSTRG.30505.2	-1.255
MSTRG.7078.1	-3.394	MSTRG.25023.1	-1.941	MSTRG.27175.1	-1.253
MSTRG.2416.1	-3.392	MSTRG.4646.4	-1.940	MSTRG.42319.1	-1.253
MSTRG.4985.18	-3.387	MSTRG.16222.2	-1.939	MSTRG.30924.3	-1.252
MSTRG.46693.1	-3.384	MSTRG.36311.1	-1.939	MSTRG.42705.1	-1.252
MSTRG.33958.3	-3.383	MSTRG.31978.1	-1.937	MSTRG.4996.1	-1.251
MSTRG.7950.3	-3.378	MSTRG.26042.1	-1.937	MSTRG.30700.1	-1.250
MSTRG.46932.3	-3.378	MSTRG.23773.7	-1.935	MSTRG.24917.4	-1.248
MSTRG.35527.1	-3.376	MSTRG.38794.2	-1.933	MSTRG.44604.3	-1.246
MSTRG.16937.1	-3.374	MSTRG.42341.1	-1.933	MSTRG.24477.3	-1.244
MSTRG.43517.1	-3.370	MSTRG.23960.1	-1.933	MSTRG.45546.1	-1.244
MSTRG.40191.1	-3.370	MSTRG.8789.1	-1.932	MSTRG.33667.1	-1.242
MSTRG.23230.1	-3.362	MSTRG.32139.1	-1.932	MSTRG.15051.1	-1.242
MSTRG.45420.1	-3.359	MSTRG.36019.2	-1.930	MSTRG.14194.1	-1.242
MSTRG.29859.1	-3.359	MSTRG.8078.1	-1.930	MSTRG.31848.2	-1.241
MSTRG.9199.7	-3.356	MSTRG.32211.1	-1.929	MSTRG.4.1	-1.240
MSTRG.2495.3	-3.349	MSTRG.2236.1	-1.928	MSTRG.44326.1	-1.240
MSTRG.7303.1	-3.347	MSTRG.13129.1	-1.927	MSTRG.38438.3	-1.240
MSTRG.31036.1	-3.343	MSTRG.10912.1	-1.926	MSTRG.33275.1	-1.239
MSTRG.14616.1	-3.343	MSTRG.41485.1	-1.923	MSTRG.35572.1	-1.238
MSTRG.25590.3	-3.340	MSTRG.6143.1	-1.920	MSTRG.22247.1	-1.238
MSTRG.2277.16	-3.340	MSTRG.8855.1	-1.918	MSTRG.30952.1	-1.237
MSTRG.18754.1	-3.336	MSTRG.39184.1	-1.916	MSTRG.17415.1	-1.237
MSTRG.8355.1	-3.336	MSTRG.45569.1	-1.916	MSTRG.25121.1	-1.237
MSTRG.7782.2	-3.328	MSTRG.40816.1	-1.915	MSTRG.33529.1	-1.236
MSTRG.24196.1	-3.326	MSTRG.23205.2	-1.915	MSTRG.29812.3	-1.235
MSTRG.34794.1	-3.324	MSTRG.35934.1	-1.915	MSTRG.48515.1	-1.233

MSTRG.38208.3	-3.324	MSTRG.29951.1	-1.913	MSTRG.29439.1	-1.233
MSTRG.22505.1	-3.324	MSTRG.46652.1	-1.912	MSTRG.25661.1	-1.231
MSTRG.28131.1	-3.319	MSTRG.27807.1	-1.912	MSTRG.41112.1	-1.231
MSTRG.45472.1	-3.314	MSTRG.885.1	-1.912	MSTRG.45380.1	-1.231
MSTRG.27939.1	-3.310	MSTRG.16226.1	-1.909	MSTRG.29817.1	-1.230
MSTRG.6153.1	-3.310	MSTRG.42399.2	-1.907	MSTRG.9721.1	-1.229
MSTRG.5712.1	-3.305	MSTRG.30222.1	-1.907	MSTRG.3279.4	-1.228
MSTRG.19071.1	-3.299	MSTRG.33648.1	-1.906	MSTRG.33732.1	-1.228
MSTRG.19493.1	-3.299	MSTRG.29683.1	-1.904	MSTRG.6749.1	-1.227
MSTRG.39086.1	-3.295	MSTRG.9373.7	-1.903	MSTRG.47320.1	-1.226
MSTRG.31426.1	-3.290	MSTRG.3169.1	-1.902	MSTRG.28783.1	-1.225
MSTRG.24468.1	-3.290	MSTRG.44537.1	-1.901	MSTRG.8398.1	-1.225
MSTRG.17440.1	-3.290	MSTRG.48697.1	-1.900	MSTRG.9395.1	-1.224
MSTRG.22538.1	-3.283	MSTRG.20256.1	-1.899	MSTRG.30864.1	-1.224
MSTRG.25023.2	-3.280	MSTRG.10434.1	-1.899	MSTRG.7360.1	-1.223
MSTRG.16169.2	-3.279	MSTRG.16284.1	-1.899	MSTRG.17935.1	-1.223
MSTRG.41013.2	-3.273	MSTRG.9335.3	-1.899	MSTRG.39818.2	-1.222
MSTRG.46530.1	-3.268	MSTRG.34572.2	-1.898	MSTRG.21415.16	-1.222
MSTRG.42302.1	-3.268	MSTRG.12430.1	-1.897	MSTRG.35336.1	-1.222
MSTRG.23074.1	-3.267	MSTRG.26278.1	-1.897	MSTRG.21334.2	-1.221
MSTRG.29167.1	-3.265	MSTRG.8881.1	-1.897	MSTRG.32944.1	-1.220
MSTRG.28704.1	-3.263	MSTRG.13622.1	-1.895	MSTRG.38276.1	-1.219
MSTRG.36299.1	-3.258	MSTRG.11246.2	-1.895	MSTRG.43882.1	-1.218
MSTRG.6675.1	-3.256	MSTRG.37389.1	-1.894	MSTRG.43143.3	-1.217
MSTRG.36093.1	-3.255	MSTRG.41193.1	-1.893	MSTRG.45519.1	-1.216
MSTRG.12061.1	-3.253	MSTRG.28767.1	-1.893	MSTRG.21950.1	-1.216
MSTRG.18673.3	-3.253	MSTRG.7925.3	-1.892	MSTRG.17436.1	-1.213

MSTRG.26616.2	-3.252	MSTRG.16910.1	-1.891	MSTRG.9024.2	-1.213
MSTRG.33969.2	-3.252	MSTRG.10188.1	-1.889	MSTRG.32085.1	-1.212
MSTRG.11605.4	-3.250	MSTRG.9335.1	-1.889	MSTRG.32762.1	-1.209
MSTRG.41103.1	-3.248	MSTRG.7930.2	-1.887	MSTRG.3951.1	-1.208
MSTRG.6182.4	-3.247	MSTRG.28758.1	-1.886	MSTRG.12786.1	-1.208
MSTRG.6152.1	-3.242	MSTRG.34151.1	-1.886	MSTRG.31340.5	-1.208
MSTRG.24197.1	-3.240	MSTRG.16309.1	-1.886	MSTRG.10449.1	-1.207
MSTRG.6150.12	-3.239	MSTRG.9777.1	-1.885	MSTRG.2053.1	-1.207
MSTRG.11806.1	-3.235	MSTRG.8889.1	-1.885	MSTRG.2054.1	-1.207
MSTRG.24238.3	-3.234	MSTRG.32793.1	-1.885	MSTRG.22350.1	-1.206
MSTRG.37326.1	-3.234	MSTRG.7710.12	-1.884	MSTRG.14177.1	-1.205
MSTRG.10508.1	-3.227	MSTRG.20945.4	-1.882	MSTRG.38477.1	-1.205
MSTRG.47578.1	-3.225	MSTRG.47658.1	-1.882	MSTRG.43572.1	-1.205
MSTRG.29351.5	-3.224	MSTRG.15180.1	-1.877	MSTRG.44756.1	-1.204
MSTRG.35751.2	-3.220	MSTRG.1282.1	-1.876	MSTRG.27430.1	-1.204
MSTRG.24233.1	-3.216	MSTRG.42071.1	-1.874	MSTRG.5834.1	-1.204
MSTRG.31553.4	-3.215	MSTRG.38357.1	-1.870	MSTRG.17606.1	-1.200
MSTRG.10381.1	-3.213	MSTRG.3484.1	-1.868	MSTRG.7348.1	-1.199
MSTRG.16006.1	-3.210	MSTRG.40664.1	-1.868	MSTRG.21574.1	-1.199
MSTRG.972.1	-3.205	MSTRG.30280.2	-1.866	MSTRG.45519.2	-1.199
MSTRG.5511.1	-3.203	MSTRG.45936.1	-1.866	MSTRG.3894.1	-1.198
MSTRG.16428.2	-3.200	MSTRG.28932.1	-1.864	MSTRG.22594.1	-1.198
MSTRG.34562.1	-3.198	MSTRG.8842.1	-1.864	MSTRG.2181.1	-1.196
MSTRG.36103.2	-3.195	MSTRG.40552.1	-1.862	MSTRG.30294.2	-1.196
MSTRG.15685.1	-3.195	MSTRG.16762.1	-1.862	MSTRG.29050.1	-1.195
MSTRG.8556.1	-3.190	MSTRG.29979.1	-1.859	MSTRG.38039.1	-1.194
MSTRG.155.1	-3.187	MSTRG.33174.5	-1.858	MSTRG.18814.1	-1.194

MSTRG.35527.3	-3.184	MSTRG.10602.1	-1.858	MSTRG.25862.1	-1.194
MSTRG.10092.1	-3.183	MSTRG.16428.1	-1.857	MSTRG.29145.1	-1.193
MSTRG.20721.1	-3.183	MSTRG.27797.1	-1.857	MSTRG.36025.4	-1.193
MSTRG.6152.2	-3.175	MSTRG.21942.1	-1.856	MSTRG.9748.1	-1.193
MSTRG.20585.1	-3.175	MSTRG.12785.3	-1.856	MSTRG.10882.1	-1.192
MSTRG.35598.1	-3.162	MSTRG.38051.1	-1.853	MSTRG.6505.2	-1.190
MSTRG.39491.1	-3.158	MSTRG.22478.3	-1.852	MSTRG.30564.1	-1.190
MSTRG.17511.1	-3.156	MSTRG.31595.1	-1.850	MSTRG.47796.2	-1.190
MSTRG.46232.2	-3.154	MSTRG.40856.1	-1.848	MSTRG.12740.4	-1.189
MSTRG.511.4	-3.153	MSTRG.9807.1	-1.847	MSTRG.31314.1	-1.189
MSTRG.10694.1	-3.152	MSTRG.48134.2	-1.846	MSTRG.36396.1	-1.189
MSTRG.40506.1	-3.152	MSTRG.34828.1	-1.845	MSTRG.9524.1	-1.188
MSTRG.30615.2	-3.149	MSTRG.45165.1	-1.845	MSTRG.15489.2	-1.188
MSTRG.28060.1	-3.148	MSTRG.7629.4	-1.841	MSTRG.33120.1	-1.187
MSTRG.39426.1	-3.147	MSTRG.30928.1	-1.840	MSTRG.44294.1	-1.186
MSTRG.8008.2	-3.141	MSTRG.17355.1	-1.840	MSTRG.14793.1	-1.184
MSTRG.8267.1	-3.141	MSTRG.10164.1	-1.838	MSTRG.31490.2	-1.184
MSTRG.36802.1	-3.139	MSTRG.47426.1	-1.838	MSTRG.19163.1	-1.184
MSTRG.10622.1	-3.137	MSTRG.36881.1	-1.837	MSTRG.20307.1	-1.183
MSTRG.35294.2	-3.131	MSTRG.4115.1	-1.836	MSTRG.38817.1	-1.182
MSTRG.39168.1	-3.125	MSTRG.26344.1	-1.836	MSTRG.19833.1	-1.182
MSTRG.11797.3	-3.124	MSTRG.819.1	-1.836	MSTRG.509.1	-1.180
MSTRG.30003.2	-3.122	MSTRG.12838.1	-1.835	MSTRG.30561.6	-1.180
MSTRG.13311.1	-3.120	MSTRG.47633.1	-1.835	MSTRG.4033.2	-1.180
MSTRG.38207.2	-3.112	MSTRG.8295.1	-1.832	MSTRG.17337.1	-1.177
MSTRG.42011.1	-3.110	MSTRG.10475.1	-1.832	MSTRG.15718.1	-1.176
MSTRG.42003.1	-3.108	MSTRG.8180.1	-1.831	MSTRG.48121.1	-1.175

MSTRG.7122.1	-3.106	MSTRG.21211.1	-1.831	MSTRG.26769.1	-1.175
MSTRG.17830.1	-3.106	MSTRG.27326.1	-1.829	MSTRG.5213.1	-1.175
MSTRG.48096.1	-3.105	MSTRG.26282.1	-1.829	MSTRG.15508.2	-1.175
MSTRG.29388.2	-3.104	MSTRG.5025.1	-1.829	MSTRG.14059.1	-1.175
MSTRG.28913.1	-3.102	MSTRG.44022.1	-1.827	MSTRG.2608.1	-1.173
MSTRG.4766.1	-3.097	MSTRG.31553.1	-1.826	MSTRG.5040.1	-1.171
MSTRG.24469.1	-3.081	MSTRG.37350.1	-1.825	MSTRG.21956.1	-1.171
MSTRG.33773.1	-3.075	MSTRG.40042.1	-1.824	MSTRG.46966.1	-1.170
MSTRG.14704.1	-3.068	MSTRG.46489.5	-1.823	MSTRG.27639.1	-1.169
MSTRG.5988.1	-3.068	MSTRG.15225.5	-1.823	MSTRG.45173.1	-1.169
MSTRG.38708.1	-3.066	MSTRG.32031.1	-1.822	MSTRG.10000.1	-1.168
MSTRG.3329.5	-3.065	MSTRG.29535.1	-1.822	MSTRG.11410.1	-1.168
MSTRG.6182.8	-3.063	MSTRG.10685.4	-1.821	MSTRG.43139.1	-1.168
MSTRG.970.1	-3.062	MSTRG.44295.1	-1.819	MSTRG.10453.1	-1.167
MSTRG.11213.1	-3.062	MSTRG.36631.1	-1.819	MSTRG.16838.1	-1.166
MSTRG.20908.2	-3.058	MSTRG.44390.1	-1.817	MSTRG.33127.1	-1.165
MSTRG.42248.1	-3.056	MSTRG.9894.1	-1.815	MSTRG.14770.2	-1.164
MSTRG.11605.6	-3.055	MSTRG.26647.1	-1.815	MSTRG.3520.1	-1.164
MSTRG.7428.1	-3.055	MSTRG.44304.2	-1.814	MSTRG.10208.1	-1.164
MSTRG.29858.1	-3.052	MSTRG.38590.1	-1.813	MSTRG.33682.1	-1.163
MSTRG.13597.1	-3.051	MSTRG.14024.5	-1.813	MSTRG.20920.1	-1.162
MSTRG.33411.1	-3.043	MSTRG.42875.1	-1.812	MSTRG.2051.1	-1.161
MSTRG.25371.1	-3.037	MSTRG.13640.6	-1.812	MSTRG.783.1	-1.160
MSTRG.29268.1	-3.032	MSTRG.7460.1	-1.809	MSTRG.17728.1	-1.159
MSTRG.22927.1	-3.032	MSTRG.32016.1	-1.809	MSTRG.31788.2	-1.157
MSTRG.43000.1	-3.030	MSTRG.27842.1	-1.808	MSTRG.21291.1	-1.157
MSTRG.36585.1	-3.025	MSTRG.27164.1	-1.806	MSTRG.17247.1	-1.155

MSTRG.33936.1	-3.024	MSTRG.10689.1	-1.806	MSTRG.23419.1	-1.155
MSTRG.24199.1	-3.022	MSTRG.18637.2	-1.805	MSTRG.2005.1	-1.155
MSTRG.508.1	-3.020	MSTRG.46037.1	-1.804	MSTRG.45331.1	-1.155
MSTRG.12787.1	-3.017	MSTRG.37454.1	-1.803	MSTRG.4251.1	-1.153
MSTRG.35024.1	-3.016	MSTRG.5960.6	-1.803	MSTRG.19133.1	-1.152
MSTRG.35970.1	-3.016	MSTRG.30657.5	-1.802	MSTRG.28745.1	-1.152
MSTRG.24214.1	-3.014	MSTRG.15553.1	-1.801	MSTRG.434.1	-1.151
MSTRG.40821.1	-3.014	MSTRG.32423.1	-1.799	MSTRG.42836.1	-1.150
MSTRG.12758.2	-3.010	MSTRG.44168.5	-1.797	MSTRG.36847.1	-1.149
MSTRG.26692.2	-3.007	MSTRG.41905.1	-1.797	MSTRG.32266.1	-1.149
MSTRG.21286.2	-3.006	MSTRG.30138.1	-1.797	MSTRG.2657.1	-1.149
MSTRG.12044.1	-3.003	MSTRG.14743.1	-1.797	MSTRG.8243.1	-1.147
MSTRG.48420.1	-3.002	MSTRG.14948.3	-1.796	MSTRG.17437.1	-1.147
MSTRG.19819.1	-3.001	MSTRG.16805.3	-1.795	MSTRG.23560.1	-1.147
MSTRG.39061.1	-2.994	MSTRG.156.1	-1.793	MSTRG.47028.1	-1.146
MSTRG.15073.1	-2.993	MSTRG.30439.1	-1.793	MSTRG.24668.1	-1.146
MSTRG.39116.2	-2.992	MSTRG.2880.1	-1.793	MSTRG.47816.1	-1.146
MSTRG.10041.1	-2.992	MSTRG.8848.1	-1.791	MSTRG.46403.1	-1.145
MSTRG.10690.1	-2.989	MSTRG.46574.1	-1.790	MSTRG.22359.1	-1.145
MSTRG.24462.2	-2.987	MSTRG.18991.1	-1.789	MSTRG.46410.1	-1.145
MSTRG.2407.1	-2.984	MSTRG.696.1	-1.788	MSTRG.30306.1	-1.145
MSTRG.28698.1	-2.983	MSTRG.40653.1	-1.787	MSTRG.11450.2	-1.145
MSTRG.10283.1	-2.981	MSTRG.32037.1	-1.786	MSTRG.47660.1	-1.144
MSTRG.511.3	-2.977	MSTRG.28446.1	-1.786	MSTRG.789.2	-1.144
MSTRG.18284.2	-2.975	MSTRG.26584.5	-1.784	MSTRG.26842.1	-1.142
MSTRG.9316.1	-2.973	MSTRG.37392.1	-1.784	MSTRG.27047.1	-1.142
MSTRG.21842.1	-2.972	MSTRG.32002.1	-1.784	MSTRG.40743.1	-1.141

MSTRG.2226.1	-2.970	MSTRG.24225.1	-1.783	MSTRG.19077.1	-1.140
MSTRG.4392.1	-2.969	MSTRG.39265.1	-1.782	MSTRG.29015.1	-1.139
MSTRG.12300.3	-2.968	MSTRG.5855.1	-1.782	MSTRG.46328.1	-1.139
MSTRG.24657.1	-2.968	MSTRG.13959.1	-1.781	MSTRG.40853.2	-1.139
MSTRG.4038.2	-2.967	MSTRG.18160.1	-1.781	MSTRG.24796.1	-1.138
MSTRG.46232.3	-2.964	MSTRG.31621.1	-1.779	MSTRG.12902.1	-1.136
MSTRG.45571.2	-2.955	MSTRG.41050.1	-1.777	MSTRG.22745.3	-1.135
MSTRG.16388.1	-2.953	MSTRG.1664.1	-1.777	MSTRG.5494.1	-1.134
MSTRG.40979.2	-2.952	MSTRG.24454.1	-1.776	MSTRG.33122.1	-1.134
MSTRG.20945.1	-2.952	MSTRG.32032.1	-1.775	MSTRG.12740.1	-1.133
MSTRG.12758.1	-2.951	MSTRG.28445.1	-1.775	MSTRG.5276.1	-1.131
MSTRG.18911.2	-2.943	MSTRG.36663.2	-1.775	MSTRG.47385.1	-1.130
MSTRG.25908.1	-2.942	MSTRG.1727.1	-1.774	MSTRG.15149.1	-1.126
MSTRG.25442.1	-2.940	MSTRG.29297.1	-1.773	MSTRG.8105.1	-1.126
MSTRG.30783.1	-2.938	MSTRG.24699.1	-1.773	MSTRG.4482.1	-1.126
MSTRG.25682.2	-2.938	MSTRG.28316.2	-1.772	MSTRG.43300.1	-1.125
MSTRG.14001.1	-2.936	MSTRG.37001.1	-1.772	MSTRG.29825.3	-1.125
MSTRG.3586.4	-2.933	MSTRG.22976.1	-1.772	MSTRG.16974.1	-1.124
MSTRG.37345.3	-2.931	MSTRG.20271.1	-1.772	MSTRG.40365.2	-1.124
MSTRG.3639.1	-2.927	MSTRG.3671.1	-1.771	MSTRG.27425.1	-1.124
MSTRG.26066.1	-2.926	MSTRG.35979.1	-1.771	MSTRG.923.10	-1.124
MSTRG.14087.1	-2.921	MSTRG.41961.2	-1.770	MSTRG.46479.1	-1.123
MSTRG.42865.1	-2.918	MSTRG.9448.1	-1.770	MSTRG.47472.2	-1.122
MSTRG.43671.1	-2.916	MSTRG.38356.2	-1.770	MSTRG.12426.5	-1.120
MSTRG.30281.1	-2.914	MSTRG.37450.2	-1.770	MSTRG.30871.1	-1.120
MSTRG.27429.1	-2.913	MSTRG.28158.1	-1.770	MSTRG.19086.1	-1.118
MSTRG.45567.10	-2.912	MSTRG.44578.1	-1.769	MSTRG.35078.1	-1.117

MSTRG.6577.1	-2.912	MSTRG.13676.1	-1.769	MSTRG.21355.1	-1.117
MSTRG.23852.4	-2.911	MSTRG.32411.1	-1.769	MSTRG.15912.1	-1.115
MSTRG.35565.1	-2.905	MSTRG.33174.3	-1.769	MSTRG.35690.3	-1.114
MSTRG.30337.1	-2.903	MSTRG.889.1	-1.768	MSTRG.10819.1	-1.114
MSTRG.508.3	-2.899	MSTRG.32873.1	-1.767	MSTRG.26479.1	-1.114
MSTRG.46231.1	-2.895	MSTRG.1830.1	-1.767	MSTRG.4485.1	-1.113
MSTRG.21043.3	-2.893	MSTRG.8499.1	-1.766	MSTRG.20368.1	-1.111
MSTRG.35752.1	-2.892	MSTRG.16892.1	-1.765	MSTRG.37615.1	-1.111
MSTRG.12074.1	-2.890	MSTRG.7446.1	-1.763	MSTRG.22975.3	-1.110
MSTRG.23232.1	-2.889	MSTRG.41980.1	-1.762	MSTRG.43024.1	-1.110
MSTRG.37611.1	-2.888	MSTRG.6861.4	-1.760	MSTRG.9732.1	-1.110
MSTRG.22591.3	-2.884	MSTRG.35980.1	-1.760	MSTRG.24778.1	-1.109
MSTRG.40450.1	-2.884	MSTRG.26007.1	-1.760	MSTRG.32655.1	-1.107
MSTRG.47664.1	-2.883	MSTRG.17825.1	-1.760	MSTRG.35723.1	-1.103
MSTRG.45563.3	-2.881	MSTRG.1330.1	-1.760	MSTRG.30562.1	-1.102
MSTRG.10621.1	-2.876	MSTRG.40028.1	-1.755	MSTRG.38572.1	-1.101
MSTRG.12828.1	-2.874	MSTRG.46460.1	-1.752	MSTRG.38262.1	-1.101
MSTRG.3427.6	-2.872	MSTRG.32050.1	-1.751	MSTRG.28491.1	-1.099
MSTRG.28778.1	-2.870	MSTRG.28446.2	-1.751	MSTRG.37340.1	-1.099
MSTRG.42010.2	-2.866	MSTRG.40176.1	-1.750	MSTRG.4951.3	-1.099
MSTRG.39355.1	-2.862	MSTRG.10638.1	-1.747	MSTRG.42831.1	-1.098
MSTRG.9656.1	-2.860	MSTRG.48760.1	-1.746	MSTRG.3497.1	-1.097
MSTRG.45567.6	-2.858	MSTRG.40541.1	-1.746	MSTRG.42682.1	-1.096
MSTRG.27841.1	-2.856	MSTRG.10477.1	-1.744	MSTRG.37036.1	-1.096
MSTRG.927.1	-2.852	MSTRG.32593.2	-1.743	MSTRG.3632.1	-1.095
MSTRG.23950.1	-2.851	MSTRG.11784.6	-1.740	MSTRG.8704.1	-1.095
MSTRG.25672.1	-2.847	MSTRG.44613.2	-1.740	MSTRG.36940.1	-1.095

MSTRG.13950.1	-2.847	MSTRG.43722.2	-1.739	MSTRG.27478.1	-1.094
MSTRG.42342.1	-2.846	MSTRG.14024.4	-1.739	MSTRG.27479.1	-1.094
MSTRG.31505.1	-2.840	MSTRG.30877.1	-1.739	MSTRG.30615.1	-1.093
MSTRG.9099.1	-2.838	MSTRG.45766.1	-1.738	MSTRG.34391.1	-1.093
MSTRG.12714.1	-2.834	MSTRG.16481.1	-1.738	MSTRG.31562.1	-1.092
MSTRG.48731.1	-2.832	MSTRG.9599.2	-1.737	MSTRG.45549.1	-1.092
MSTRG.42536.1	-2.831	MSTRG.19890.2	-1.737	MSTRG.29167.2	-1.092
MSTRG.2840.1	-2.830	MSTRG.44895.1	-1.736	MSTRG.15606.2	-1.091
MSTRG.11316.1	-2.829	MSTRG.45970.1	-1.736	MSTRG.30790.1	-1.091
MSTRG.38934.1	-2.828	MSTRG.10878.1	-1.734	MSTRG.19981.1	-1.090
MSTRG.35284.1	-2.823	MSTRG.34527.5	-1.733	MSTRG.38452.1	-1.088
MSTRG.511.6	-2.822	MSTRG.15447.1	-1.733	MSTRG.17266.1	-1.086
MSTRG.48283.2	-2.822	MSTRG.39831.1	-1.733	MSTRG.8179.1	-1.086
MSTRG.41930.1	-2.822	MSTRG.31160.1	-1.732	MSTRG.39050.1	-1.084
MSTRG.24194.2	-2.816	MSTRG.12319.1	-1.732	MSTRG.16182.3	-1.083
MSTRG.37610.1	-2.814	MSTRG.15672.1	-1.732	MSTRG.6770.1	-1.083
MSTRG.17611.1	-2.812	MSTRG.26040.1	-1.732	MSTRG.32213.2	-1.082
MSTRG.38962.1	-2.810	MSTRG.36825.1	-1.731	MSTRG.9525.1	-1.081
MSTRG.15212.1	-2.807	MSTRG.21323.1	-1.730	MSTRG.17529.1	-1.080
MSTRG.16390.3	-2.806	MSTRG.10168.1	-1.729	MSTRG.42845.1	-1.080
MSTRG.9653.1	-2.805	MSTRG.32861.1	-1.729	MSTRG.37369.1	-1.079
MSTRG.31727.1	-2.803	MSTRG.4043.1	-1.728	MSTRG.42435.1	-1.079
MSTRG.30004.1	-2.801	MSTRG.46798.1	-1.727	MSTRG.45461.4	-1.078
MSTRG.8581.1	-2.801	MSTRG.26703.1	-1.726	MSTRG.29266.1	-1.077
MSTRG.41233.1	-2.797	MSTRG.27438.1	-1.725	MSTRG.42963.1	-1.076
MSTRG.28916.1	-2.796	MSTRG.14963.1	-1.724	MSTRG.42186.2	-1.075
MSTRG.31036.2	-2.795	MSTRG.24377.3	-1.724	MSTRG.12906.4	-1.075

MSTRG.42833.6	-2.795	MSTRG.25821.2	-1.723	MSTRG.3918.1	-1.074
MSTRG.33083.1	-2.794	MSTRG.6391.5	-1.723	MSTRG.22824.1	-1.073
MSTRG.28530.1	-2.791	MSTRG.396.1	-1.720	MSTRG.7034.2	-1.072
MSTRG.34997.6	-2.790	MSTRG.1159.1	-1.719	MSTRG.10189.2	-1.072
MSTRG.43615.1	-2.790	MSTRG.36007.1	-1.719	MSTRG.641.1	-1.070
MSTRG.44672.1	-2.782	MSTRG.35613.1	-1.719	MSTRG.34017.1	-1.069
MSTRG.9718.1	-2.782	MSTRG.32174.1	-1.718	MSTRG.37981.1	-1.068
MSTRG.37666.2	-2.777	MSTRG.32123.1	-1.718	MSTRG.40030.1	-1.068
MSTRG.14631.1	-2.776	MSTRG.8599.1	-1.717	MSTRG.35843.5	-1.066
MSTRG.28479.1	-2.771	MSTRG.19487.2	-1.716	MSTRG.8138.1	-1.065
MSTRG.6505.4	-2.771	MSTRG.11888.2	-1.715	MSTRG.27995.10	-1.065
MSTRG.31554.1	-2.768	MSTRG.9123.1	-1.714	MSTRG.45795.1	-1.065
MSTRG.48583.1	-2.765	MSTRG.23557.1	-1.713	MSTRG.22517.1	-1.064
MSTRG.10064.1	-2.761	MSTRG.28043.2	-1.713	MSTRG.3521.1	-1.064
MSTRG.17792.2	-2.760	MSTRG.25934.1	-1.713	MSTRG.4534.1	-1.063
MSTRG.43739.1	-2.758	MSTRG.23258.1	-1.711	MSTRG.12740.3	-1.061
MSTRG.34901.2	-2.756	MSTRG.14024.6	-1.711	MSTRG.44616.1	-1.060
MSTRG.1222.1	-2.756	MSTRG.7497.1	-1.710	MSTRG.17942.1	-1.055
MSTRG.11290.1	-2.752	MSTRG.40189.1	-1.710	MSTRG.10133.1	-1.054
MSTRG.18607.1	-2.752	MSTRG.23448.1	-1.709	MSTRG.7510.1	-1.054
MSTRG.48472.1	-2.751	MSTRG.15872.9	-1.709	MSTRG.12028.1	-1.053
MSTRG.38469.1	-2.751	MSTRG.234.1	-1.708	MSTRG.22880.1	-1.053
MSTRG.38797.6	-2.750	MSTRG.32580.1	-1.708	MSTRG.39376.1	-1.052
MSTRG.10011.2	-2.749	MSTRG.28383.1	-1.707	MSTRG.48565.1	-1.052
MSTRG.44903.3	-2.745	MSTRG.20157.3	-1.706	MSTRG.14459.5	-1.050
MSTRG.24749.1	-2.742	MSTRG.31959.2	-1.705	MSTRG.41937.1	-1.050
MSTRG.7095.1	-2.741	MSTRG.36230.1	-1.705	MSTRG.27220.1	-1.047

MSTRG.17407.1	-2.740	MSTRG.29721.1	-1.705	MSTRG.28970.1	-1.047
MSTRG.13596.1	-2.739	MSTRG.23237.1	-1.704	MSTRG.35179.1	-1.046
MSTRG.47045.3	-2.738	MSTRG.35876.1	-1.704	MSTRG.22747.1	-1.046
MSTRG.2636.2	-2.738	MSTRG.23017.1	-1.704	MSTRG.45534.1	-1.043
MSTRG.26263.2	-2.738	MSTRG.30441.1	-1.704	MSTRG.190.1	-1.043
MSTRG.29485.1	-2.736	MSTRG.16099.1	-1.703	MSTRG.26576.1	-1.043
MSTRG.38244.1	-2.735	MSTRG.21203.1	-1.703	MSTRG.11691.1	-1.042
MSTRG.21936.1	-2.735	MSTRG.34874.2	-1.703	MSTRG.45796.1	-1.041
MSTRG.44824.6	-2.733	MSTRG.2192.1	-1.702	MSTRG.29200.1	-1.041
MSTRG.29872.1	-2.732	MSTRG.18894.1	-1.702	MSTRG.5041.1	-1.041
MSTRG.23632.1	-2.730	MSTRG.29804.2	-1.701	MSTRG.27861.2	-1.040
MSTRG.13030.1	-2.727	MSTRG.17596.1	-1.701	MSTRG.30213.1	-1.040
MSTRG.10498.1	-2.724	MSTRG.39735.1	-1.701	MSTRG.26708.2	-1.040
MSTRG.45571.1	-2.723	MSTRG.8350.1	-1.700	MSTRG.48282.1	-1.039
MSTRG.48859.1	-2.721	MSTRG.38739.1	-1.699	MSTRG.3045.1	-1.039
MSTRG.31043.1	-2.721	MSTRG.34363.1	-1.699	MSTRG.3488.1	-1.038
MSTRG.1534.7	-2.721	MSTRG.16116.1	-1.698	MSTRG.11689.1	-1.037
MSTRG.33311.2	-2.720	MSTRG.520.1	-1.698	MSTRG.38079.1	-1.035
MSTRG.8263.1	-2.715	MSTRG.47123.1	-1.697	MSTRG.20217.3	-1.035
MSTRG.38812.2	-2.706	MSTRG.43344.1	-1.695	MSTRG.11059.2	-1.034
MSTRG.1383.1	-2.706	MSTRG.35500.1	-1.694	MSTRG.5497.1	-1.034
MSTRG.30490.4	-2.705	MSTRG.41447.3	-1.693	MSTRG.15324.1	-1.032
MSTRG.25829.1	-2.703	MSTRG.16488.2	-1.693	MSTRG.39675.1	-1.029
MSTRG.38208.6	-2.699	MSTRG.42756.1	-1.693	MSTRG.24223.1	-1.028
MSTRG.19810.1	-2.699	MSTRG.371.1	-1.692	MSTRG.35194.1	-1.027
MSTRG.34364.1	-2.698	MSTRG.29849.5	-1.692	MSTRG.20464.2	-1.025
MSTRG.35396.1	-2.697	MSTRG.31898.2	-1.691	MSTRG.23034.1	-1.025

MSTRG.43535.1	-2.696	MSTRG.2793.1	-1.689	MSTRG.30251.1	-1.023
MSTRG.42010.1	-2.695	MSTRG.35611.8	-1.688	MSTRG.24928.1	-1.020
MSTRG.38120.1	-2.693	MSTRG.16768.1	-1.688	MSTRG.16099.2	-1.020
MSTRG.35586.6	-2.692	MSTRG.477.3	-1.685	MSTRG.25330.1	-1.020
MSTRG.26651.1	-2.690	MSTRG.44604.4	-1.684	MSTRG.31583.1	-1.019
MSTRG.25671.1	-2.689	MSTRG.15460.1	-1.682	MSTRG.10961.1	-1.019
MSTRG.35528.2	-2.689	MSTRG.2564.1	-1.682	MSTRG.35920.1	-1.019
MSTRG.33805.1	-2.687	MSTRG.16636.4	-1.682	MSTRG.31016.1	-1.018
MSTRG.42593.1	-2.683	MSTRG.42757.1	-1.682	MSTRG.18763.1	-1.017
MSTRG.42004.1	-2.682	MSTRG.19023.1	-1.682	MSTRG.15661.1	-1.015
MSTRG.33479.1	-2.681	MSTRG.15380.1	-1.681	MSTRG.5687.1	-1.015
MSTRG.37808.4	-2.681	MSTRG.19078.1	-1.680	MSTRG.28601.1	-1.013
MSTRG.16984.1	-2.681	MSTRG.3095.1	-1.679	MSTRG.39828.1	-1.010
MSTRG.8399.1	-2.680	MSTRG.31577.1	-1.679	MSTRG.17116.1	-1.009
MSTRG.19225.1	-2.679	MSTRG.29255.1	-1.679	MSTRG.24471.1	-1.007
MSTRG.34901.5	-2.677	MSTRG.22478.1	-1.679	MSTRG.2412.1	-1.007
MSTRG.18726.1	-2.675	MSTRG.11700.1	-1.677	MSTRG.40008.1	-1.007
MSTRG.40652.1	-2.674	MSTRG.33353.2	-1.677	MSTRG.1125.1	-1.007
MSTRG.22819.1	-2.673	MSTRG.38933.1	-1.676	MSTRG.37177.1	-1.007
MSTRG.6660.6	-2.673	MSTRG.35192.1	-1.676	MSTRG.13367.1	-1.006
MSTRG.41094.3	-2.667	MSTRG.35002.1	-1.675	MSTRG.3218.1	-1.005
MSTRG.10561.1	-2.666	MSTRG.6182.1	-1.675	MSTRG.11496.1	-1.005
MSTRG.10563.1	-2.666	MSTRG.31423.1	-1.674	MSTRG.41784.1	-1.004
MSTRG.44018.1	-2.663	MSTRG.42072.1	-1.673	MSTRG.2002.1	-1.002
MSTRG.21177.1	-2.662	MSTRG.7433.1	-1.672	MSTRG.7902.1	-1.002
MSTRG.21719.1	-2.662	MSTRG.15841.1	-1.672	MSTRG.17333.1	-1.001
MSTRG.45394.1	-2.655	MSTRG.46112.1	-1.672	MSTRG.26566.1	-1.000

Table S4.6: Upregulated transcripts under chilling conditions in *Corylus avellana* cv Tombul with iDEP

Transcript ID	log2 FoldChange	Transcript ID	log2 FoldChange	Transcript ID	log2 FoldChange
MSTRG.21026.3	30.544	MSTRG.19070.3	3.364	MSTRG.6528.1	1.588
MSTRG.37633.8	28.915	MSTRG.36157.1	3.356	MSTRG.30419.1	1.588
MSTRG.40917.4	28.525	MSTRG.17876.2	3.353	MSTRG.44692.1	1.588
MSTRG.41358.2	27.882	MSTRG.48707.2	3.353	MSTRG.23705.1	1.588
MSTRG.15019.2	27.849	MSTRG.34610.1	3.348	MSTRG.2237.1	1.588
MSTRG.5213.3	27.690	MSTRG.34852.2	3.348	MSTRG.26288.1	1.588
MSTRG.24181.2	27.417	MSTRG.17075.1	3.343	MSTRG.5447.1	1.587
MSTRG.9042.1	27.218	MSTRG.36871.1	3.343	MSTRG.10702.3	1.587
MSTRG.34324.3	27.117	MSTRG.48061.2	3.339	MSTRG.47056.1	1.586
MSTRG.10525.3	26.875	MSTRG.33113.2	3.332	MSTRG.41950.1	1.586
MSTRG.17294.2	26.605	MSTRG.28811.2	3.332	MSTRG.48848.1	1.584
MSTRG.19270.3	26.577	MSTRG.20289.1	3.329	MSTRG.21536.6	1.584
MSTRG.19149.2	26.527	MSTRG.31584.2	3.326	MSTRG.19855.1	1.581
MSTRG.47541.3	26.426	MSTRG.34697.3	3.325	MSTRG.10331.1	1.579
MSTRG.6893.1	26.424	MSTRG.27031.2	3.319	MSTRG.36076.1	1.577
MSTRG.37128.4	26.256	MSTRG.34802.2	3.316	MSTRG.27480.1	1.577
MSTRG.8925.2	25.960	MSTRG.15536.1	3.313	MSTRG.47106.1	1.577
MSTRG.26241.2	25.918	MSTRG.38887.3	3.312	MSTRG.24322.1	1.576
MSTRG.987.2	25.772	MSTRG.9645.1	3.310	MSTRG.21553.1	1.576
MSTRG.39213.2	25.482	MSTRG.31883.1	3.309	MSTRG.13404.1	1.575
MSTRG.9308.3	25.444	MSTRG.24281.2	3.308	MSTRG.31450.5	1.575
MSTRG.42733.3	25.418	MSTRG.24962.2	3.305	MSTRG.1717.2	1.575
MSTRG.32238.8	25.271	MSTRG.36851.1	3.295	MSTRG.42418.1	1.574
MSTRG.9104.2	25.225	MSTRG.31042.1	3.288	MSTRG.27109.1	1.571

MSTRG.28280.3	25.120	MSTRG.36759.1	3.284	MSTRG.22492.1	1.571
MSTRG.13307.2	25.067	MSTRG.30341.4	3.283	MSTRG.35014.1	1.571
MSTRG.34691.2	24.941	MSTRG.9883.1	3.282	MSTRG.7197.1	1.570
MSTRG.29825.2	24.880	MSTRG.31829.2	3.281	MSTRG.22867.1	1.570
MSTRG.31507.2	24.801	MSTRG.37150.1	3.275	MSTRG.46844.3	1.569
MSTRG.13902.1	24.457	MSTRG.31226.2	3.259	MSTRG.19145.1	1.568
MSTRG.7579.2	24.169	MSTRG.4790.3	3.254	MSTRG.27903.1	1.567
MSTRG.32596.14	23.708	MSTRG.16840.1	3.248	MSTRG.40252.1	1.567
MSTRG.30475.2	23.546	MSTRG.23430.2	3.246	MSTRG.39014.1	1.567
MSTRG.24410.1	23.112	MSTRG.6090.1	3.246	MSTRG.11899.5	1.566
MSTRG.22166.4	17.198	MSTRG.28512.3	3.241	MSTRG.1715.1	1.565
MSTRG.44997.2	16.128	MSTRG.43193.3	3.238	MSTRG.24720.1	1.564
MSTRG.42104.3	16.116	MSTRG.7916.1	3.237	MSTRG.20448.2	1.563
MSTRG.44753.12	16.071	MSTRG.445.2	3.233	MSTRG.18649.1	1.562
MSTRG.27979.3	15.649	MSTRG.38899.2	3.232	MSTRG.1464.1	1.562
MSTRG.14156.2	15.568	MSTRG.41361.1	3.219	MSTRG.22311.1	1.562
MSTRG.1899.1	15.398	MSTRG.21905.1	3.215	MSTRG.12765.3	1.561
MSTRG.37195.2	15.126	MSTRG.7021.1	3.205	MSTRG.25964.1	1.561
MSTRG.4339.2	15.125	MSTRG.14851.3	3.204	MSTRG.2271.1	1.558
MSTRG.12456.2	15.077	MSTRG.25519.1	3.204	MSTRG.23434.5	1.557
MSTRG.1295.5	14.905	MSTRG.15420.2	3.193	MSTRG.5915.1	1.557
MSTRG.17355.4	14.734	MSTRG.34035.1	3.190	MSTRG.7420.1	1.556
MSTRG.33389.2	14.687	MSTRG.23422.3	3.182	MSTRG.2369.1	1.555
MSTRG.42912.3	14.656	MSTRG.12278.2	3.180	MSTRG.24719.1	1.555
MSTRG.20821.3	14.647	MSTRG.17118.2	3.174	MSTRG.8691.1	1.554
MSTRG.23766.2	14.623	MSTRG.1096.1	3.172	MSTRG.13319.1	1.554
MSTRG.35048.4	14.589	MSTRG.30750.1	3.169	MSTRG.20007.1	1.553

MSTRG.23072.4	14.571	MSTRG.42120.1	3.168	MSTRG.11480.1	1.553
MSTRG.39656.2	14.307	MSTRG.45655.1	3.167	MSTRG.40065.3	1.552
MSTRG.15405.3	14.296	MSTRG.40989.1	3.164	MSTRG.41809.1	1.552
MSTRG.32762.3	14.227	MSTRG.45234.1	3.163	MSTRG.47864.1	1.552
MSTRG.17415.3	14.224	MSTRG.5602.1	3.161	MSTRG.13964.1	1.550
MSTRG.41613.2	14.207	MSTRG.22668.3	3.155	MSTRG.36720.1	1.549
MSTRG.31890.4	14.195	MSTRG.47783.1	3.145	MSTRG.24039.4	1.548
MSTRG.27057.2	14.150	MSTRG.31909.2	3.144	MSTRG.31582.1	1.546
MSTRG.25836.3	14.101	MSTRG.29055.3	3.140	MSTRG.6346.1	1.544
MSTRG.22965.6	14.066	MSTRG.46838.2	3.128	MSTRG.32502.1	1.543
MSTRG.42166.2	13.990	MSTRG.33048.8	3.127	MSTRG.15086.1	1.541
MSTRG.40563.13	13.973	MSTRG.46004.1	3.124	MSTRG.27111.1	1.541
MSTRG.10563.6	13.970	MSTRG.48415.2	3.122	MSTRG.17870.5	1.540
MSTRG.26939.4	13.885	MSTRG.27552.1	3.121	MSTRG.3644.1	1.539
MSTRG.47309.2	13.869	MSTRG.13620.1	3.118	MSTRG.40376.1	1.535
MSTRG.30138.4	13.867	MSTRG.46510.1	3.113	MSTRG.4384.1	1.532
MSTRG.38725.6	13.859	MSTRG.9996.1	3.112	MSTRG.42439.2	1.531
MSTRG.47893.3	13.846	MSTRG.32517.4	3.111	MSTRG.19960.1	1.530
MSTRG.28035.1	13.798	MSTRG.9646.1	3.105	MSTRG.31027.1	1.529
MSTRG.21715.2	13.797	MSTRG.48613.1	3.104	MSTRG.46305.1	1.529
MSTRG.13959.2	13.768	MSTRG.22718.2	3.099	MSTRG.47466.1	1.528
MSTRG.8234.5	13.757	MSTRG.24732.1	3.098	MSTRG.18832.1	1.527
MSTRG.2376.2	13.748	MSTRG.36896.4	3.084	MSTRG.46644.1	1.525
MSTRG.22487.3	13.738	MSTRG.29626.1	3.082	MSTRG.2966.1	1.523
MSTRG.6762.2	13.738	MSTRG.34851.1	3.078	MSTRG.21871.1	1.522
MSTRG.24390.2	13.707	MSTRG.441.2	3.077	MSTRG.43315.2	1.522
MSTRG.39491.5	13.700	MSTRG.21027.7	3.074	MSTRG.45338.1	1.522

MSTRG.2335.1	13.690	MSTRG.48118.4	3.072	MSTRG.43992.1	1.521
MSTRG.22965.7	13.660	MSTRG.20618.2	3.066	MSTRG.13098.1	1.518
MSTRG.22569.3	13.627	MSTRG.31479.3	3.064	MSTRG.27665.1	1.518
MSTRG.28672.5	13.597	MSTRG.19913.1	3.064	MSTRG.28723.1	1.517
MSTRG.32016.6	13.512	MSTRG.6820.1	3.063	MSTRG.9669.9	1.516
MSTRG.16690.3	13.496	MSTRG.38925.1	3.058	MSTRG.4628.1	1.515
MSTRG.43868.1	13.483	MSTRG.39731.1	3.048	MSTRG.10884.1	1.515
MSTRG.27418.2	13.422	MSTRG.22594.1	3.045	MSTRG.17522.2	1.515
MSTRG.11784.9	13.421	MSTRG.204.1	3.043	MSTRG.45044.1	1.514
MSTRG.6577.5	13.399	MSTRG.17652.1	3.043	MSTRG.25264.1	1.514
MSTRG.1100.3	13.391	MSTRG.10324.1	3.042	MSTRG.14558.1	1.513
MSTRG.12430.3	13.390	MSTRG.32899.5	3.035	MSTRG.399.1	1.512
MSTRG.44394.3	13.386	MSTRG.33643.1	3.032	MSTRG.47937.1	1.511
MSTRG.43965.6	13.329	MSTRG.35690.2	3.032	MSTRG.10727.1	1.511
MSTRG.2207.3	13.308	MSTRG.32447.7	3.031	MSTRG.10480.1	1.510
MSTRG.36207.6	13.253	MSTRG.27526.1	3.027	MSTRG.47741.1	1.508
MSTRG.46788.2	13.241	MSTRG.40555.35	3.022	MSTRG.27651.2	1.508
MSTRG.13786.5	13.213	MSTRG.10882.2	3.015	MSTRG.11399.1	1.508
MSTRG.6591.1	13.172	MSTRG.43663.3	3.015	MSTRG.41355.2	1.507
MSTRG.31160.6	13.147	MSTRG.15087.1	3.011	MSTRG.48010.1	1.507
MSTRG.40555.37	13.116	MSTRG.35542.1	3.010	MSTRG.4016.1	1.507
MSTRG.18701.5	13.053	MSTRG.8751.2	3.009	MSTRG.45838.1	1.506
MSTRG.28323.3	13.039	MSTRG.29055.1	3.008	MSTRG.18261.2	1.506
MSTRG.39181.4	13.031	MSTRG.29916.2	2.999	MSTRG.2093.1	1.506
MSTRG.17760.4	13.029	MSTRG.37774.2	2.992	MSTRG.13882.1	1.505
MSTRG.36473.3	13.027	MSTRG.23433.1	2.985	MSTRG.16492.1	1.504
MSTRG.21030.7	12.973	MSTRG.21092.1	2.984	MSTRG.28064.1	1.504

MSTRG.599.2	12.965	MSTRG.27162.1	2.979	MSTRG.1883.1	1.504
MSTRG.24336.2	12.945	MSTRG.48367.1	2.979	MSTRG.15697.1	1.503
MSTRG.13592.2	12.945	MSTRG.23623.3	2.975	MSTRG.25461.1	1.503
MSTRG.18039.3	12.916	MSTRG.18446.1	2.970	MSTRG.42163.1	1.503
MSTRG.9908.2	12.905	MSTRG.24203.1	2.964	MSTRG.23728.1	1.502
MSTRG.11632.2	12.879	MSTRG.7893.2	2.963	MSTRG.23429.1	1.502
MSTRG.20660.4	12.845	MSTRG.31937.3	2.963	MSTRG.18907.1	1.502
MSTRG.10769.9	12.843	MSTRG.835.2	2.961	MSTRG.23924.1	1.501
MSTRG.26059.7	12.832	MSTRG.32518.1	2.956	MSTRG.35443.2	1.501
MSTRG.31505.2	12.819	MSTRG.44944.2	2.956	MSTRG.13386.1	1.501
MSTRG.36057.2	12.787	MSTRG.25057.1	2.953	MSTRG.43173.1	1.500
MSTRG.22176.2	12.784	MSTRG.3963.2	2.948	MSTRG.39657.1	1.499
MSTRG.37437.2	12.773	MSTRG.11863.2	2.948	MSTRG.67.1	1.498
MSTRG.38636.2	12.770	MSTRG.10390.3	2.945	MSTRG.48010.2	1.498
MSTRG.12859.3	12.765	MSTRG.21470.2	2.943	MSTRG.32776.1	1.498
MSTRG.47418.6	12.752	MSTRG.48651.1	2.942	MSTRG.11743.1	1.498
MSTRG.437.4	12.737	MSTRG.28437.1	2.922	MSTRG.47269.1	1.496
MSTRG.6930.2	12.722	MSTRG.15311.2	2.921	MSTRG.4605.2	1.494
MSTRG.24048.2	12.694	MSTRG.45224.3	2.919	MSTRG.1193.1	1.494
MSTRG.35049.2	12.663	MSTRG.42636.1	2.916	MSTRG.36156.1	1.494
MSTRG.35668.2	12.638	MSTRG.27832.2	2.911	MSTRG.26154.1	1.493
MSTRG.2071.1	12.626	MSTRG.13328.1	2.911	MSTRG.2025.1	1.491
MSTRG.38797.5	12.600	MSTRG.17768.1	2.908	MSTRG.2805.1	1.490
MSTRG.46271.2	12.593	MSTRG.37345.4	2.902	MSTRG.44693.1	1.489
MSTRG.36585.2	12.574	MSTRG.8403.1	2.899	MSTRG.48560.1	1.489
MSTRG.38109.4	12.558	MSTRG.40782.1	2.893	MSTRG.15170.1	1.488
MSTRG.10580.2	12.558	MSTRG.32779.1	2.891	MSTRG.29817.4	1.487

MSTRG.40537.4	12.542	MSTRG.907.1	2.889	MSTRG.23383.1	1.487
MSTRG.48255.2	12.533	MSTRG.16069.2	2.886	MSTRG.7955.1	1.486
MSTRG.42763.4	12.531	MSTRG.1897.2	2.880	MSTRG.19959.1	1.485
MSTRG.5534.9	12.530	MSTRG.20744.1	2.878	MSTRG.40576.1	1.485
MSTRG.44967.2	12.520	MSTRG.14538.1	2.875	MSTRG.729.1	1.485
MSTRG.4951.1	12.514	MSTRG.3317.15	2.870	MSTRG.26247.1	1.484
MSTRG.4178.1	12.491	MSTRG.5838.1	2.870	MSTRG.4080.1	1.483
MSTRG.35194.2	12.489	MSTRG.24817.1	2.866	MSTRG.10644.1	1.482
MSTRG.41392.3	12.487	MSTRG.12423.2	2.862	MSTRG.7285.1	1.482
MSTRG.21861.2	12.477	MSTRG.20745.1	2.860	MSTRG.11780.1	1.481
MSTRG.45401.2	12.475	MSTRG.20458.1	2.854	MSTRG.24036.1	1.479
MSTRG.29395.2	12.458	MSTRG.47870.3	2.853	MSTRG.29685.1	1.478
MSTRG.27913.2	12.451	MSTRG.25161.1	2.852	MSTRG.1216.1	1.478
MSTRG.92.3	12.444	MSTRG.47387.1	2.852	MSTRG.30409.1	1.477
MSTRG.13797.2	12.417	MSTRG.41989.1	2.852	MSTRG.43163.2	1.476
MSTRG.33856.3	12.416	MSTRG.13068.1	2.851	MSTRG.32777.1	1.476
MSTRG.42248.4	12.395	MSTRG.43600.1	2.851	MSTRG.44652.2	1.474
MSTRG.41294.4	12.389	MSTRG.25162.1	2.850	MSTRG.40069.5	1.473
MSTRG.48760.8	12.370	MSTRG.39326.2	2.848	MSTRG.34586.1	1.472
MSTRG.12565.4	12.330	MSTRG.23400.1	2.847	MSTRG.44245.3	1.472
MSTRG.7581.4	12.317	MSTRG.4749.1	2.844	MSTRG.37998.1	1.472
MSTRG.47779.2	12.284	MSTRG.7914.1	2.842	MSTRG.43988.1	1.470
MSTRG.21536.5	12.275	MSTRG.27326.5	2.835	MSTRG.24151.1	1.469
MSTRG.10602.3	12.274	MSTRG.38312.4	2.833	MSTRG.6178.2	1.469
MSTRG.41719.4	12.271	MSTRG.18245.1	2.831	MSTRG.5651.1	1.469
MSTRG.498.2	12.266	MSTRG.14155.1	2.828	MSTRG.11796.93	1.468
MSTRG.13030.4	12.265	MSTRG.40750.4	2.827	MSTRG.28046.1	1.468

MSTRG.18737.2	12.223	MSTRG.39769.1	2.826	MSTRG.45115.1	1.467
MSTRG.819.4	12.184	MSTRG.9626.3	2.825	MSTRG.15353.1	1.467
MSTRG.2545.3	12.175	MSTRG.20677.1	2.817	MSTRG.27979.7	1.467
MSTRG.22166.7	12.172	MSTRG.30611.4	2.817	MSTRG.9924.1	1.467
MSTRG.21647.4	12.171	MSTRG.12745.1	2.813	MSTRG.20610.1	1.465
MSTRG.33969.1	12.158	MSTRG.48647.1	2.805	MSTRG.17814.1	1.464
MSTRG.18174.1	12.149	MSTRG.123.1	2.805	MSTRG.32463.2	1.464
MSTRG.5960.4	12.147	MSTRG.43783.1	2.802	MSTRG.12387.1	1.464
MSTRG.28544.2	12.140	MSTRG.7128.5	2.801	MSTRG.29882.1	1.463
MSTRG.26802.2	12.136	MSTRG.30576.1	2.799	MSTRG.6018.2	1.462
MSTRG.27200.3	12.131	MSTRG.30341.3	2.797	MSTRG.3401.1	1.462
MSTRG.22054.2	12.113	MSTRG.10756.1	2.794	MSTRG.37014.1	1.462
MSTRG.34450.2	12.108	MSTRG.11148.6	2.791	MSTRG.29282.1	1.461
MSTRG.45563.4	12.086	MSTRG.5288.3	2.784	MSTRG.27750.1	1.461
MSTRG.35099.2	12.085	MSTRG.45587.6	2.782	MSTRG.16382.2	1.459
MSTRG.33679.4	12.082	MSTRG.13819.1	2.781	MSTRG.6697.2	1.459
MSTRG.29234.2	12.070	MSTRG.11796.96	2.779	MSTRG.27163.3	1.458
MSTRG.29558.2	12.061	MSTRG.42634.1	2.778	MSTRG.21880.5	1.456
MSTRG.13424.3	12.032	MSTRG.46429.3	2.773	MSTRG.41269.4	1.455
MSTRG.6625.2	12.025	MSTRG.22683.1	2.771	MSTRG.24158.1	1.454
MSTRG.3938.1	12.009	MSTRG.47158.5	2.770	MSTRG.28513.1	1.452
MSTRG.47822.1	12.008	MSTRG.40555.33	2.769	MSTRG.41782.3	1.451
MSTRG.22489.2	11.998	MSTRG.28518.1	2.768	MSTRG.12957.1	1.450
MSTRG.4365.2	11.996	MSTRG.38647.1	2.767	MSTRG.31735.1	1.446
MSTRG.37027.2	11.996	MSTRG.36327.6	2.764	MSTRG.47042.1	1.446
MSTRG.25477.10	11.986	MSTRG.12838.6	2.760	MSTRG.6536.2	1.446
MSTRG.2002.2	11.986	MSTRG.14488.3	2.758	MSTRG.5264.1	1.445

MSTRG.10837.2	11.967	MSTRG.2094.1	2.756	MSTRG.13941.1	1.445
MSTRG.31143.2	11.959	MSTRG.27261.2	2.755	MSTRG.37258.1	1.442
MSTRG.12272.4	11.927	MSTRG.29102.6	2.751	MSTRG.32824.1	1.442
MSTRG.17621.4	11.922	MSTRG.11246.1	2.745	MSTRG.26979.1	1.442
MSTRG.3642.2	11.906	MSTRG.9692.4	2.743	MSTRG.18550.1	1.441
MSTRG.2671.2	11.893	MSTRG.35604.1	2.742	MSTRG.40378.1	1.441
MSTRG.37694.4	11.875	MSTRG.34590.1	2.729	MSTRG.27965.1	1.441
MSTRG.27119.4	11.871	MSTRG.32145.4	2.724	MSTRG.41824.1	1.438
MSTRG.22846.7	11.870	MSTRG.24963.1	2.723	MSTRG.9968.3	1.437
MSTRG.22846.9	11.868	MSTRG.2059.16	2.721	MSTRG.16978.1	1.437
MSTRG.11632.4	11.863	MSTRG.41159.1	2.719	MSTRG.9229.2	1.437
MSTRG.40523.2	11.858	MSTRG.1084.1	2.717	MSTRG.33660.1	1.436
MSTRG.32888.2	11.855	MSTRG.42919.1	2.714	MSTRG.19804.1	1.436
MSTRG.3172.2	11.854	MSTRG.26225.1	2.709	MSTRG.28270.1	1.436
MSTRG.31191.10	11.836	MSTRG.18906.2	2.709	MSTRG.17844.1	1.435
MSTRG.47826.2	11.835	MSTRG.31707.1	2.707	MSTRG.9405.1	1.434
MSTRG.2626.2	11.830	MSTRG.14995.1	2.704	MSTRG.42633.1	1.433
MSTRG.42682.2	11.822	MSTRG.44642.1	2.701	MSTRG.38850.1	1.432
MSTRG.27109.3	11.805	MSTRG.23423.14	2.700	MSTRG.36387.1	1.430
MSTRG.42434.2	11.799	MSTRG.9296.1	2.697	MSTRG.41640.1	1.429
MSTRG.40371.2	11.795	MSTRG.32719.1	2.697	MSTRG.24151.4	1.428
MSTRG.9158.2	11.787	MSTRG.10245.2	2.691	MSTRG.7419.1	1.426
MSTRG.16697.6	11.787	MSTRG.48280.2	2.686	MSTRG.24663.1	1.426
MSTRG.16180.3	11.785	MSTRG.33842.4	2.682	MSTRG.31511.1	1.425
MSTRG.20381.9	11.783	MSTRG.36977.1	2.682	MSTRG.45266.1	1.424
MSTRG.18395.2	11.775	MSTRG.537.2	2.679	MSTRG.45045.2	1.424
MSTRG.15661.2	11.774	MSTRG.37501.1	2.674	MSTRG.26325.1	1.423

MSTRG.24657.2	11.768	MSTRG.22735.2	2.669	MSTRG.11761.1	1.423
MSTRG.38492.6	11.765	MSTRG.7333.3	2.666	MSTRG.22803.2	1.423
MSTRG.25316.9	11.760	MSTRG.10253.2	2.665	MSTRG.25861.1	1.422
MSTRG.13393.2	11.753	MSTRG.21093.1	2.663	MSTRG.18561.3	1.422
MSTRG.39795.5	11.739	MSTRG.40563.3	2.663	MSTRG.42455.3	1.420
MSTRG.27429.4	11.732	MSTRG.16988.4	2.659	MSTRG.7922.1	1.419
MSTRG.33321.2	11.721	MSTRG.27914.1	2.658	MSTRG.1529.1	1.419
MSTRG.17055.2	11.718	MSTRG.29667.3	2.658	MSTRG.10018.1	1.418
MSTRG.3819.2	11.706	MSTRG.28556.1	2.658	MSTRG.33058.1	1.415
MSTRG.35887.2	11.701	MSTRG.41167.1	2.651	MSTRG.14708.1	1.414
MSTRG.2626.3	11.698	MSTRG.29420.11	2.650	MSTRG.42859.1	1.414
MSTRG.33510.3	11.681	MSTRG.26017.1	2.649	MSTRG.11568.1	1.414
MSTRG.29929.2	11.675	MSTRG.37732.2	2.648	MSTRG.6856.1	1.412
MSTRG.48080.1	11.670	MSTRG.38267.1	2.647	MSTRG.658.1	1.410
MSTRG.11209.2	11.666	MSTRG.38056.2	2.646	MSTRG.45900.1	1.410
MSTRG.14022.2	11.651	MSTRG.13383.1	2.645	MSTRG.27177.2	1.410
MSTRG.20676.2	11.640	MSTRG.37776.1	2.645	MSTRG.39503.1	1.410
MSTRG.34662.3	11.638	MSTRG.25284.1	2.637	MSTRG.20739.1	1.410
MSTRG.1194.2	11.614	MSTRG.34057.1	2.637	MSTRG.14099.1	1.409
MSTRG.9003.3	11.610	MSTRG.44688.1	2.635	MSTRG.14256.1	1.409
MSTRG.396.2	11.604	MSTRG.688.2	2.634	MSTRG.15230.1	1.408
MSTRG.4951.2	11.601	MSTRG.459.1	2.634	MSTRG.18526.1	1.406
MSTRG.28808.1	11.594	MSTRG.25102.1	2.625	MSTRG.3208.2	1.406
MSTRG.41982.5	11.585	MSTRG.13762.1	2.624	MSTRG.21066.1	1.406
MSTRG.21453.4	11.580	MSTRG.39348.1	2.620	MSTRG.17552.1	1.404
MSTRG.2843.6	11.578	MSTRG.20745.3	2.618	MSTRG.198.1	1.404
MSTRG.27.2	11.577	MSTRG.1982.1	2.617	MSTRG.32327.3	1.404

MSTRG.33317.4	11.574	MSTRG.16832.1	2.616	MSTRG.42350.1	1.403
MSTRG.10413.4	11.565	MSTRG.12597.1	2.613	MSTRG.36623.1	1.403
MSTRG.24382.8	11.556	MSTRG.27257.1	2.609	MSTRG.34142.4	1.403
MSTRG.34675.1	11.553	MSTRG.47504.1	2.607	MSTRG.12372.1	1.403
MSTRG.35979.3	11.539	MSTRG.24890.1	2.604	MSTRG.27223.1	1.403
MSTRG.46542.1	11.527	MSTRG.33356.2	2.603	MSTRG.28277.1	1.402
MSTRG.2545.2	11.521	MSTRG.20381.5	2.601	MSTRG.11784.10	1.401
MSTRG.17462.3	11.517	MSTRG.31373.1	2.601	MSTRG.31720.1	1.401
MSTRG.23596.4	11.507	MSTRG.38566.3	2.599	MSTRG.32062.2	1.401
MSTRG.28645.3	11.500	MSTRG.40927.2	2.595	MSTRG.36782.1	1.401
MSTRG.36.2	11.491	MSTRG.15246.1	2.593	MSTRG.21208.1	1.401
MSTRG.26849.2	11.446	MSTRG.20744.2	2.592	MSTRG.4012.3	1.399
MSTRG.20157.4	11.436	MSTRG.24371.5	2.589	MSTRG.45267.1	1.399
MSTRG.45260.2	11.429	MSTRG.44318.1	2.584	MSTRG.23422.1	1.398
MSTRG.5407.1	11.412	MSTRG.8521.20	2.581	MSTRG.2112.1	1.397
MSTRG.18957.4	11.403	MSTRG.31890.3	2.579	MSTRG.4547.1	1.397
MSTRG.24120.2	11.392	MSTRG.42302.2	2.579	MSTRG.11645.2	1.396
MSTRG.23247.7	11.376	MSTRG.7912.1	2.578	MSTRG.14629.1	1.395
MSTRG.40585.2	11.354	MSTRG.5353.1	2.577	MSTRG.8636.1	1.394
MSTRG.3839.2	11.353	MSTRG.23647.1	2.575	MSTRG.14255.1	1.394
MSTRG.29464.3	11.351	MSTRG.38742.3	2.574	MSTRG.37677.1	1.394
MSTRG.6189.2	11.350	MSTRG.39429.2	2.572	MSTRG.20176.1	1.393
MSTRG.1083.2	11.345	MSTRG.22778.2	2.572	MSTRG.41756.1	1.393
MSTRG.13515.2	11.327	MSTRG.10124.1	2.566	MSTRG.11901.1	1.393
MSTRG.32293.5	11.321	MSTRG.37838.1	2.564	MSTRG.32826.1	1.392
MSTRG.5868.3	11.302	MSTRG.41969.2	2.564	MSTRG.41983.1	1.391
MSTRG.29764.5	11.297	MSTRG.46719.1	2.564	MSTRG.17509.1	1.391

MSTRG.5071.2	11.250	MSTRG.17761.1	2.562	MSTRG.11097.1	1.391
MSTRG.43401.2	11.247	MSTRG.9551.1	2.560	MSTRG.16162.3	1.390
MSTRG.24657.3	11.230	MSTRG.28737.1	2.559	MSTRG.4699.2	1.387
MSTRG.2509.2	11.206	MSTRG.15139.1	2.558	MSTRG.16391.1	1.386
MSTRG.30138.2	11.180	MSTRG.27372.4	2.556	MSTRG.17082.1	1.386
MSTRG.3396.4	11.168	MSTRG.36870.1	2.556	MSTRG.28987.1	1.383
MSTRG.44837.1	11.157	MSTRG.26943.1	2.555	MSTRG.566.1	1.382
MSTRG.28745.3	11.153	MSTRG.15829.1	2.555	MSTRG.25190.1	1.382
MSTRG.21027.4	11.149	MSTRG.44567.2	2.553	MSTRG.12848.1	1.380
MSTRG.13020.5	11.146	MSTRG.45198.1	2.551	MSTRG.12702.1	1.379
MSTRG.9028.6	11.140	MSTRG.20099.1	2.544	MSTRG.32397.3	1.376
MSTRG.27138.3	11.138	MSTRG.13870.1	2.543	MSTRG.26802.1	1.376
MSTRG.22622.4	11.115	MSTRG.29699.3	2.543	MSTRG.47515.1	1.374
MSTRG.19810.2	11.113	MSTRG.13889.1	2.542	MSTRG.5917.1	1.373
MSTRG.42412.2	11.104	MSTRG.40955.2	2.539	MSTRG.15032.1	1.373
MSTRG.9196.4	11.098	MSTRG.43910.3	2.537	MSTRG.43700.1	1.372
MSTRG.11719.2	11.090	MSTRG.23434.1	2.535	MSTRG.45403.1	1.371
MSTRG.16474.7	11.086	MSTRG.16018.1	2.532	MSTRG.40642.1	1.371
MSTRG.11477.2	11.072	MSTRG.37607.1	2.530	MSTRG.40008.2	1.369
MSTRG.14133.3	11.070	MSTRG.17371.1	2.526	MSTRG.39325.1	1.369
MSTRG.5631.2	11.060	MSTRG.41986.1	2.526	MSTRG.7953.2	1.369
MSTRG.31801.2	11.054	MSTRG.23439.2	2.524	MSTRG.16278.1	1.368
MSTRG.34864.2	11.036	MSTRG.24394.1	2.523	MSTRG.44898.1	1.368
MSTRG.11030.4	11.025	MSTRG.20745.2	2.522	MSTRG.41403.2	1.367
MSTRG.872.3	11.016	MSTRG.24486.1	2.517	MSTRG.28736.1	1.367
MSTRG.35565.4	10.998	MSTRG.8882.3	2.517	MSTRG.37163.1	1.367
MSTRG.18906.3	10.972	MSTRG.13623.1	2.517	MSTRG.38138.1	1.366

MSTRG.36262.4	10.968	MSTRG.22968.3	2.513	MSTRG.22511.2	1.366
MSTRG.32895.3	10.961	MSTRG.39503.2	2.513	MSTRG.30611.1	1.364
MSTRG.43710.2	10.954	MSTRG.9228.2	2.511	MSTRG.7276.2	1.363
MSTRG.43965.2	10.949	MSTRG.31619.1	2.504	MSTRG.41264.1	1.362
MSTRG.743.1	10.933	MSTRG.4778.1	2.502	MSTRG.17940.1	1.362
MSTRG.21390.2	10.923	MSTRG.8294.1	2.502	MSTRG.40618.1	1.362
MSTRG.4075.2	10.870	MSTRG.16495.2	2.494	MSTRG.46623.1	1.361
MSTRG.23401.1	10.866	MSTRG.9692.6	2.493	MSTRG.14504.2	1.361
MSTRG.34778.1	10.861	MSTRG.14171.1	2.492	MSTRG.21488.1	1.361
MSTRG.37411.5	10.853	MSTRG.35615.1	2.492	MSTRG.14177.2	1.357
MSTRG.3958.2	10.851	MSTRG.8530.8	2.488	MSTRG.5594.1	1.357
MSTRG.37767.2	10.839	MSTRG.28553.1	2.484	MSTRG.45990.1	1.355
MSTRG.2989.25	10.837	MSTRG.42220.1	2.480	MSTRG.12681.1	1.354
MSTRG.728.4	10.835	MSTRG.40921.1	2.479	MSTRG.31892.1	1.354
MSTRG.4807.3	10.833	MSTRG.38001.2	2.478	MSTRG.38196.1	1.354
MSTRG.8105.5	10.807	MSTRG.45089.1	2.477	MSTRG.11230.1	1.353
MSTRG.374.7	10.799	MSTRG.25792.1	2.476	MSTRG.1304.1	1.353
MSTRG.36025.1	10.784	MSTRG.21166.1	2.474	MSTRG.34133.7	1.353
MSTRG.38383.6	10.778	MSTRG.3790.1	2.474	MSTRG.23057.1	1.353
MSTRG.21240.3	10.748	MSTRG.36427.4	2.472	MSTRG.35399.1	1.352
MSTRG.32341.4	10.739	MSTRG.6214.1	2.468	MSTRG.8100.1	1.351
MSTRG.9533.1	10.726	MSTRG.42222.1	2.468	MSTRG.42262.1	1.351
MSTRG.24596.4	10.721	MSTRG.9692.17	2.466	MSTRG.24317.1	1.351
MSTRG.41097.3	10.718	MSTRG.10720.1	2.463	MSTRG.45702.1	1.350
MSTRG.46018.2	10.716	MSTRG.16348.5	2.462	MSTRG.32541.1	1.349
MSTRG.8625.2	10.709	MSTRG.23448.2	2.462	MSTRG.22313.1	1.349
MSTRG.4154.3	10.688	MSTRG.46018.6	2.459	MSTRG.11144.1	1.349

MSTRG.44654.2	10.677	MSTRG.35544.1	2.459	MSTRG.27163.4	1.348
MSTRG.19071.3	10.673	MSTRG.11796.95	2.459	MSTRG.25036.1	1.348
MSTRG.38022.2	10.660	MSTRG.1239.1	2.458	MSTRG.16266.1	1.347
MSTRG.10541.2	10.647	MSTRG.21026.2	2.456	MSTRG.14305.1	1.347
MSTRG.17688.2	10.631	MSTRG.728.1	2.455	MSTRG.4014.1	1.347
MSTRG.34687.2	10.597	MSTRG.12704.1	2.455	MSTRG.13716.1	1.346
MSTRG.13506.2	10.596	MSTRG.45429.1	2.453	MSTRG.21015.1	1.346
MSTRG.37577.5	10.593	MSTRG.29652.2	2.449	MSTRG.46645.1	1.345
MSTRG.3321.4	10.584	MSTRG.29713.1	2.447	MSTRG.42037.1	1.345
MSTRG.9033.2	10.575	MSTRG.6855.3	2.447	MSTRG.17540.1	1.345
MSTRG.38670.2	10.545	MSTRG.22264.1	2.444	MSTRG.23738.1	1.344
MSTRG.4202.2	10.513	MSTRG.14246.1	2.441	MSTRG.16485.1	1.343
MSTRG.12558.2	10.496	MSTRG.21889.1	2.439	MSTRG.12051.1	1.341
MSTRG.42257.2	10.492	MSTRG.4012.2	2.439	MSTRG.9013.1	1.341
MSTRG.27704.2	10.467	MSTRG.37801.1	2.439	MSTRG.13740.1	1.341
MSTRG.38670.5	10.459	MSTRG.10934.2	2.439	MSTRG.19931.1	1.339
MSTRG.41420.3	10.427	MSTRG.45580.1	2.438	MSTRG.8722.1	1.338
MSTRG.11796.33	10.422	MSTRG.6701.1	2.438	MSTRG.7698.5	1.337
MSTRG.19666.4	10.420	MSTRG.37602.1	2.437	MSTRG.32981.1	1.336
MSTRG.29705.6	10.417	MSTRG.15690.3	2.436	MSTRG.17793.1	1.334
MSTRG.17318.6	10.414	MSTRG.6203.2	2.433	MSTRG.21064.1	1.334
MSTRG.36025.5	10.413	MSTRG.9477.1	2.433	MSTRG.41814.2	1.333
MSTRG.34257.2	10.402	MSTRG.43086.1	2.430	MSTRG.38424.1	1.333
MSTRG.37694.2	10.397	MSTRG.47744.1	2.429	MSTRG.39038.1	1.333
MSTRG.26923.1	10.385	MSTRG.48718.1	2.426	MSTRG.16382.1	1.332
MSTRG.4699.4	10.378	MSTRG.17680.1	2.420	MSTRG.17468.1	1.332
MSTRG.32942.3	10.373	MSTRG.6546.2	2.417	MSTRG.33827.1	1.331

MSTRG.39471.2	10.360	MSTRG.30187.1	2.417	MSTRG.34697.1	1.330
MSTRG.21997.2	10.344	MSTRG.6752.3	2.412	MSTRG.35648.2	1.330
MSTRG.25264.3	10.342	MSTRG.9692.2	2.411	MSTRG.11867.1	1.330
MSTRG.42428.3	10.329	MSTRG.17601.1	2.405	MSTRG.36407.3	1.329
MSTRG.37483.2	10.324	MSTRG.41225.5	2.404	MSTRG.46141.1	1.329
MSTRG.14850.5	10.323	MSTRG.35605.1	2.403	MSTRG.12377.1	1.328
MSTRG.38117.2	10.322	MSTRG.32617.1	2.402	MSTRG.28784.4	1.327
MSTRG.9769.3	10.309	MSTRG.10354.1	2.402	MSTRG.9929.1	1.327
MSTRG.38156.2	10.285	MSTRG.27867.1	2.402	MSTRG.44951.1	1.327
MSTRG.13007.2	10.280	MSTRG.45579.1	2.400	MSTRG.37073.1	1.327
MSTRG.352.1	10.271	MSTRG.39388.4	2.400	MSTRG.7401.2	1.327
MSTRG.44703.5	10.256	MSTRG.37774.1	2.394	MSTRG.15055.1	1.326
MSTRG.29842.3	10.251	MSTRG.31110.1	2.394	MSTRG.45389.1	1.325
MSTRG.35197.6	10.219	MSTRG.13886.1	2.390	MSTRG.33004.1	1.325
MSTRG.39280.3	10.216	MSTRG.36799.1	2.390	MSTRG.25417.3	1.323
MSTRG.48503.3	10.197	MSTRG.17790.1	2.389	MSTRG.25626.1	1.323
MSTRG.36025.2	10.174	MSTRG.17720.1	2.388	MSTRG.33064.1	1.323
MSTRG.39971.2	10.164	MSTRG.39770.1	2.385	MSTRG.46491.1	1.322
MSTRG.42923.2	10.158	MSTRG.45418.2	2.384	MSTRG.23153.1	1.321
MSTRG.23763.7	10.150	MSTRG.8631.1	2.384	MSTRG.40943.1	1.320
MSTRG.39971.3	10.118	MSTRG.21691.6	2.383	MSTRG.23098.1	1.319
MSTRG.8105.4	10.118	MSTRG.34788.1	2.374	MSTRG.42298.1	1.318
MSTRG.32045.10	10.117	MSTRG.37941.1	2.372	MSTRG.24151.2	1.318
MSTRG.27922.6	10.115	MSTRG.28652.1	2.371	MSTRG.39637.1	1.317
MSTRG.29946.3	10.114	MSTRG.11756.3	2.362	MSTRG.28463.1	1.316
MSTRG.48226.2	10.108	MSTRG.37177.4	2.361	MSTRG.14592.2	1.316
MSTRG.27422.3	10.068	MSTRG.28514.1	2.359	MSTRG.15278.1	1.315

MSTRG.29315.2	10.066	MSTRG.23729.1	2.355	MSTRG.45488.1	1.315
MSTRG.15625.2	10.066	MSTRG.15065.1	2.354	MSTRG.9924.8	1.314
MSTRG.9322.8	10.059	MSTRG.41580.1	2.351	MSTRG.17653.1	1.314
MSTRG.46515.3	10.050	MSTRG.30535.2	2.341	MSTRG.43053.1	1.312
MSTRG.41125.2	10.019	MSTRG.39848.1	2.340	MSTRG.42045.1	1.311
MSTRG.27622.2	10.007	MSTRG.35648.1	2.339	MSTRG.21872.1	1.311
MSTRG.19349.12	10.002	MSTRG.46112.2	2.333	MSTRG.33662.1	1.311
MSTRG.728.5	9.989	MSTRG.37050.1	2.330	MSTRG.5769.4	1.310
MSTRG.32899.2	9.976	MSTRG.38100.1	2.326	MSTRG.48205.1	1.308
MSTRG.35205.9	9.968	MSTRG.551.1	2.326	MSTRG.4775.1	1.306
MSTRG.2613.2	9.964	MSTRG.38411.1	2.325	MSTRG.17764.3	1.306
MSTRG.11663.1	9.960	MSTRG.38007.3	2.322	MSTRG.46706.1	1.304
MSTRG.6072.2	9.950	MSTRG.9691.2	2.320	MSTRG.44973.5	1.304
MSTRG.13287.2	9.913	MSTRG.5067.1	2.317	MSTRG.28271.1	1.303
MSTRG.28382.1	9.882	MSTRG.24048.4	2.316	MSTRG.38263.1	1.303
MSTRG.40321.2	9.849	MSTRG.36852.1	2.315	MSTRG.27754.1	1.303
MSTRG.15639.2	9.816	MSTRG.12331.1	2.313	MSTRG.26803.1	1.303
MSTRG.2906.2	9.802	MSTRG.22626.3	2.312	MSTRG.40089.2	1.301
MSTRG.37577.3	9.795	MSTRG.37674.3	2.311	MSTRG.33606.2	1.301
MSTRG.38102.2	9.787	MSTRG.7915.1	2.304	MSTRG.48404.1	1.299
MSTRG.18463.3	9.756	MSTRG.29196.1	2.302	MSTRG.32922.1	1.299
MSTRG.32517.3	9.715	MSTRG.48297.1	2.302	MSTRG.13660.1	1.298
MSTRG.6666.2	9.713	MSTRG.11802.5	2.300	MSTRG.15291.1	1.296
MSTRG.3959.1	9.684	MSTRG.47423.2	2.298	MSTRG.41883.1	1.296
MSTRG.17129.3	9.628	MSTRG.34889.1	2.296	MSTRG.28386.1	1.295
MSTRG.30475.5	9.606	MSTRG.16677.1	2.292	MSTRG.25527.1	1.295
MSTRG.8641.1	9.597	MSTRG.1989.1	2.291	MSTRG.44180.4	1.294

MSTRG.48775.1	9.595	MSTRG.1990.1	2.291	MSTRG.39214.1	1.293
MSTRG.34527.2	9.590	MSTRG.3855.6	2.290	MSTRG.10575.14	1.293
MSTRG.36093.4	9.583	MSTRG.29509.5	2.288	MSTRG.3971.1	1.293
MSTRG.24044.3	9.576	MSTRG.40570.1	2.288	MSTRG.43014.1	1.293
MSTRG.48760.5	9.555	MSTRG.16933.1	2.287	MSTRG.3402.1	1.292
MSTRG.35774.4	9.510	MSTRG.16229.2	2.286	MSTRG.32495.1	1.292
MSTRG.45192.2	9.491	MSTRG.6697.3	2.283	MSTRG.10269.1	1.292
MSTRG.6263.2	9.447	MSTRG.25339.1	2.280	MSTRG.39409.1	1.291
MSTRG.25449.1	9.406	MSTRG.34063.2	2.280	MSTRG.17251.3	1.291
MSTRG.36103.6	9.401	MSTRG.44982.1	2.279	MSTRG.95.1	1.291
MSTRG.16450.3	9.380	MSTRG.21887.1	2.276	MSTRG.5003.1	1.290
MSTRG.39849.2	9.376	MSTRG.28066.1	2.272	MSTRG.6690.1	1.288
MSTRG.32517.1	9.352	MSTRG.38906.1	2.270	MSTRG.5466.1	1.288
MSTRG.3988.4	9.288	MSTRG.38303.2	2.270	MSTRG.4641.1	1.288
MSTRG.15158.2	9.285	MSTRG.23164.1	2.265	MSTRG.5391.3	1.288
MSTRG.19594.1	9.276	MSTRG.6003.2	2.264	MSTRG.26461.1	1.285
MSTRG.36739.2	9.266	MSTRG.39040.2	2.264	MSTRG.27755.1	1.285
MSTRG.34297.1	9.250	MSTRG.35240.1	2.261	MSTRG.4505.1	1.285
MSTRG.23679.2	9.246	MSTRG.9074.4	2.258	MSTRG.7600.1	1.284
MSTRG.45029.15	9.246	MSTRG.8393.1	2.257	MSTRG.14403.1	1.284
MSTRG.3974.1	9.245	MSTRG.45939.1	2.257	MSTRG.38582.1	1.283
MSTRG.37419.2	9.222	MSTRG.15547.1	2.256	MSTRG.34133.1	1.283
MSTRG.8981.2	9.176	MSTRG.6207.2	2.256	MSTRG.38522.1	1.282
MSTRG.41118.2	9.132	MSTRG.9692.7	2.254	MSTRG.21032.1	1.282
MSTRG.24160.1	9.082	MSTRG.30840.2	2.253	MSTRG.42709.1	1.282
MSTRG.48061.8	9.077	MSTRG.47678.3	2.251	MSTRG.32621.1	1.281
MSTRG.44731.1	9.072	MSTRG.25093.1	2.251	MSTRG.46108.1	1.281

MSTRG.38969.2	9.061	MSTRG.25100.2	2.250	MSTRG.10318.1	1.280
MSTRG.29710.1	9.004	MSTRG.16194.1	2.250	MSTRG.45014.3	1.280
MSTRG.26790.1	8.990	MSTRG.41973.1	2.248	MSTRG.13742.1	1.280
MSTRG.33940.5	8.942	MSTRG.40121.1	2.248	MSTRG.47655.1	1.278
MSTRG.9484.2	8.882	MSTRG.46397.1	2.247	MSTRG.15609.1	1.278
MSTRG.6522.2	8.877	MSTRG.19309.4	2.244	MSTRG.15206.1	1.278
MSTRG.22120.4	8.842	MSTRG.39504.1	2.244	MSTRG.10732.1	1.278
MSTRG.36547.4	8.821	MSTRG.20008.1	2.243	MSTRG.14338.3	1.278
MSTRG.29193.3	8.807	MSTRG.31897.1	2.243	MSTRG.8692.1	1.274
MSTRG.1295.3	8.804	MSTRG.11796.91	2.243	MSTRG.35047.1	1.274
MSTRG.29954.2	8.796	MSTRG.23163.1	2.241	MSTRG.864.1	1.273
MSTRG.42272.3	8.771	MSTRG.9692.1	2.240	MSTRG.1960.1	1.273
MSTRG.22976.2	8.753	MSTRG.37789.2	2.239	MSTRG.47648.2	1.272
MSTRG.25517.1	8.711	MSTRG.9478.1	2.238	MSTRG.2944.1	1.270
MSTRG.23940.2	8.679	MSTRG.44887.2	2.238	MSTRG.20094.6	1.270
MSTRG.29979.2	8.671	MSTRG.9031.5	2.237	MSTRG.41814.1	1.269
MSTRG.728.2	8.665	MSTRG.40248.1	2.234	MSTRG.21518.1	1.268
MSTRG.7862.2	8.647	MSTRG.34031.1	2.234	MSTRG.9229.1	1.267
MSTRG.17049.2	8.619	MSTRG.14154.2	2.230	MSTRG.2791.1	1.267
MSTRG.27372.3	8.571	MSTRG.46902.1	2.228	MSTRG.29730.1	1.265
MSTRG.18309.2	8.570	MSTRG.3569.1	2.226	MSTRG.15409.1	1.265
MSTRG.20380.2	8.547	MSTRG.23205.1	2.225	MSTRG.18044.1	1.265
MSTRG.17870.9	8.526	MSTRG.19706.1	2.225	MSTRG.29171.1	1.263
MSTRG.31952.3	8.512	MSTRG.36013.1	2.222	MSTRG.36535.1	1.263
MSTRG.33886.2	8.510	MSTRG.16369.2	2.221	MSTRG.5836.2	1.263
MSTRG.47420.2	8.509	MSTRG.11796.97	2.221	MSTRG.40154.1	1.262
MSTRG.8295.2	8.498	MSTRG.47611.1	2.220	MSTRG.25387.1	1.262

MSTRG.26901.5	8.493	MSTRG.40984.1	2.220	MSTRG.23451.3	1.261
MSTRG.38918.1	8.474	MSTRG.46183.1	2.219	MSTRG.16998.1	1.261
MSTRG.27531.2	8.467	MSTRG.12101.1	2.218	MSTRG.8419.1	1.261
MSTRG.28145.2	8.465	MSTRG.8725.1	2.218	MSTRG.12808.1	1.260
MSTRG.41576.2	8.422	MSTRG.11719.1	2.217	MSTRG.15676.11	1.260
MSTRG.7340.3	8.403	MSTRG.9569.1	2.216	MSTRG.29717.2	1.258
MSTRG.9897.2	8.398	MSTRG.35153.2	2.211	MSTRG.16499.1	1.258
MSTRG.19299.2	8.389	MSTRG.16265.2	2.210	MSTRG.10468.1	1.257
MSTRG.18754.2	8.389	MSTRG.46018.5	2.205	MSTRG.8841.1	1.255
MSTRG.40074.10	8.387	MSTRG.23584.1	2.202	MSTRG.4731.1	1.255
MSTRG.35396.2	8.380	MSTRG.37326.2	2.201	MSTRG.33200.1	1.255
MSTRG.17523.2	8.321	MSTRG.44417.1	2.200	MSTRG.33892.1	1.255
MSTRG.45776.3	8.266	MSTRG.10754.1	2.199	MSTRG.38094.1	1.254
MSTRG.28227.1	8.236	MSTRG.16294.1	2.199	MSTRG.20100.1	1.254
MSTRG.9724.2	8.200	MSTRG.14772.1	2.196	MSTRG.20381.6	1.254
MSTRG.23056.2	8.159	MSTRG.2252.1	2.196	MSTRG.37627.1	1.252
MSTRG.17754.2	8.129	MSTRG.26655.1	2.191	MSTRG.38699.1	1.252
MSTRG.9769.2	8.063	MSTRG.24095.1	2.191	MSTRG.26324.1	1.252
MSTRG.43535.2	8.007	MSTRG.7521.1	2.190	MSTRG.6614.1	1.250
MSTRG.34630.3	7.962	MSTRG.1020.1	2.189	MSTRG.26984.1	1.249
MSTRG.20470.2	7.930	MSTRG.14249.1	2.189	MSTRG.20908.3	1.249
MSTRG.30423.2	7.900	MSTRG.5649.1	2.189	MSTRG.44362.2	1.248
MSTRG.46758.3	7.825	MSTRG.13615.2	2.188	MSTRG.29195.1	1.248
MSTRG.29167.3	7.815	MSTRG.10702.5	2.187	MSTRG.20913.1	1.247
MSTRG.3088.1	7.812	MSTRG.22664.2	2.186	MSTRG.43501.1	1.247
MSTRG.23754.1	7.801	MSTRG.25832.1	2.186	MSTRG.21212.1	1.246
MSTRG.24964.2	7.788	MSTRG.17358.1	2.184	MSTRG.46297.1	1.246

MSTRG.37570.1	7.767	MSTRG.15895.1	2.183	MSTRG.8940.1	1.245
MSTRG.20470.12	7.751	MSTRG.3979.2	2.182	MSTRG.13528.1	1.245
MSTRG.42597.4	7.711	MSTRG.42868.1	2.180	MSTRG.28926.1	1.245
MSTRG.47254.3	7.702	MSTRG.14851.5	2.179	MSTRG.37002.1	1.244
MSTRG.40546.4	7.694	MSTRG.1286.1	2.178	MSTRG.38300.1	1.244
MSTRG.11784.19	7.666	MSTRG.1285.1	2.178	MSTRG.44567.1	1.244
MSTRG.23234.6	7.664	MSTRG.18580.1	2.177	MSTRG.19213.1	1.243
MSTRG.22299.1	7.649	MSTRG.24241.1	2.175	MSTRG.11221.2	1.243
MSTRG.29946.4	7.631	MSTRG.31111.1	2.175	MSTRG.39926.4	1.240
MSTRG.23252.5	7.615	MSTRG.18603.1	2.170	MSTRG.21299.1	1.239
MSTRG.9164.4	7.599	MSTRG.12282.2	2.168	MSTRG.3797.1	1.238
MSTRG.21530.3	7.548	MSTRG.38412.1	2.168	MSTRG.2928.1	1.238
MSTRG.20211.2	7.538	MSTRG.1727.2	2.164	MSTRG.7873.2	1.238
MSTRG.22505.3	7.527	MSTRG.456.1	2.159	MSTRG.46266.5	1.237
MSTRG.17129.2	7.524	MSTRG.48564.1	2.158	MSTRG.27366.1	1.237
MSTRG.8673.3	7.485	MSTRG.24813.1	2.157	MSTRG.30120.1	1.236
MSTRG.1707.2	7.463	MSTRG.21892.1	2.156	MSTRG.46492.1	1.236
MSTRG.27358.1	7.449	MSTRG.824.2	2.153	MSTRG.22511.1	1.234
MSTRG.4585.2	7.445	MSTRG.40066.1	2.151	MSTRG.37211.1	1.232
MSTRG.22687.5	7.400	MSTRG.20381.11	2.151	MSTRG.19122.1	1.231
MSTRG.16356.3	7.302	MSTRG.40563.27	2.148	MSTRG.14594.1	1.229
MSTRG.10850.2	7.292	MSTRG.3131.1	2.143	MSTRG.38137.1	1.228
MSTRG.1670.2	7.277	MSTRG.41897.1	2.140	MSTRG.6123.1	1.225
MSTRG.30294.1	7.274	MSTRG.40802.1	2.140	MSTRG.3230.1	1.225
MSTRG.6807.3	7.271	MSTRG.25507.1	2.139	MSTRG.15162.1	1.224
MSTRG.41950.2	7.256	MSTRG.3948.1	2.136	MSTRG.40868.1	1.224
MSTRG.45891.2	7.233	MSTRG.28616.1	2.135	MSTRG.38092.1	1.224

MSTRG.2645.7	7.233	MSTRG.36011.1	2.134	MSTRG.28912.1	1.224
MSTRG.8468.3	7.230	MSTRG.15071.2	2.131	MSTRG.19643.1	1.223
MSTRG.30549.2	7.187	MSTRG.48756.1	2.131	MSTRG.5191.7	1.223
MSTRG.35881.1	7.174	MSTRG.4001.2	2.130	MSTRG.41808.1	1.223
MSTRG.16180.2	7.157	MSTRG.694.1	2.128	MSTRG.24260.1	1.222
MSTRG.43193.6	7.136	MSTRG.21467.1	2.128	MSTRG.47827.1	1.222
MSTRG.47420.3	7.085	MSTRG.24183.1	2.126	MSTRG.39055.1	1.222
MSTRG.17422.1	7.074	MSTRG.10412.1	2.122	MSTRG.24259.1	1.219
MSTRG.48738.1	7.020	MSTRG.6350.1	2.122	MSTRG.27345.1	1.219
MSTRG.14331.1	6.998	MSTRG.490.1	2.122	MSTRG.20380.1	1.218
MSTRG.1323.3	6.997	MSTRG.29929.5	2.121	MSTRG.41796.1	1.218
MSTRG.46131.4	6.978	MSTRG.6550.2	2.120	MSTRG.803.1	1.217
MSTRG.44667.2	6.963	MSTRG.5858.1	2.120	MSTRG.47173.1	1.214
MSTRG.41934.3	6.962	MSTRG.23599.1	2.119	MSTRG.16292.1	1.213
MSTRG.8267.2	6.925	MSTRG.19853.1	2.119	MSTRG.2942.1	1.213
MSTRG.4700.1	6.917	MSTRG.19310.1	2.118	MSTRG.23154.1	1.213
MSTRG.6873.1	6.901	MSTRG.42295.1	2.115	MSTRG.15649.3	1.212
MSTRG.3199.1	6.891	MSTRG.29232.1	2.114	MSTRG.44362.1	1.212
MSTRG.16142.2	6.887	MSTRG.19799.1	2.113	MSTRG.14458.1	1.212
MSTRG.22846.5	6.884	MSTRG.15255.1	2.113	MSTRG.45606.1	1.211
MSTRG.18281.4	6.882	MSTRG.28383.2	2.112	MSTRG.11475.1	1.211
MSTRG.6931.1	6.869	MSTRG.35860.1	2.110	MSTRG.39076.1	1.209
MSTRG.17212.3	6.866	MSTRG.34289.2	2.108	MSTRG.492.1	1.208
MSTRG.374.6	6.838	MSTRG.23055.1	2.106	MSTRG.697.1	1.208
MSTRG.9020.1	6.819	MSTRG.10108.1	2.105	MSTRG.36708.1	1.207
MSTRG.5904.1	6.803	MSTRG.11829.1	2.104	MSTRG.20818.1	1.207
MSTRG.29585.12	6.796	MSTRG.9344.1	2.104	MSTRG.38886.1	1.206

MSTRG.835.4	6.784	MSTRG.45091.1	2.100	MSTRG.6935.1	1.206
MSTRG.38553.3	6.744	MSTRG.34049.1	2.097	MSTRG.15692.1	1.205
MSTRG.41275.2	6.742	MSTRG.23816.1	2.096	MSTRG.115.3	1.204
MSTRG.25965.2	6.738	MSTRG.37044.2	2.096	MSTRG.48219.1	1.203
MSTRG.40571.1	6.723	MSTRG.14133.1	2.096	MSTRG.47172.1	1.203
MSTRG.42632.6	6.717	MSTRG.17825.3	2.095	MSTRG.11395.1	1.200
MSTRG.27795.1	6.624	MSTRG.41593.3	2.091	MSTRG.4542.1	1.199
MSTRG.46184.2	6.620	MSTRG.17850.1	2.091	MSTRG.26690.1	1.199
MSTRG.3884.3	6.617	MSTRG.23439.1	2.090	MSTRG.19256.1	1.199
MSTRG.1430.1	6.546	MSTRG.15171.1	2.086	MSTRG.46681.1	1.198
MSTRG.23612.2	6.515	MSTRG.7520.1	2.085	MSTRG.9502.1	1.198
MSTRG.1628.5	6.483	MSTRG.6240.2	2.084	MSTRG.4085.1	1.198
MSTRG.38442.4	6.472	MSTRG.34667.1	2.083	MSTRG.20282.1	1.197
MSTRG.41083.2	6.458	MSTRG.34748.6	2.081	MSTRG.48128.1	1.197
MSTRG.44684.3	6.438	MSTRG.11796.94	2.079	MSTRG.44278.1	1.195
MSTRG.26037.1	6.428	MSTRG.27934.1	2.077	MSTRG.7951.2	1.195
MSTRG.36123.1	6.409	MSTRG.40178.1	2.074	MSTRG.343.1	1.195
MSTRG.46018.7	6.382	MSTRG.21856.1	2.072	MSTRG.20662.1	1.195
MSTRG.21216.2	6.379	MSTRG.11258.2	2.072	MSTRG.39054.1	1.194
MSTRG.41719.3	6.356	MSTRG.31863.1	2.070	MSTRG.20033.1	1.193
MSTRG.8881.2	6.334	MSTRG.39881.2	2.069	MSTRG.31929.1	1.193
MSTRG.11273.2	6.319	MSTRG.18177.1	2.068	MSTRG.36673.2	1.192
MSTRG.11564.2	6.296	MSTRG.31897.2	2.066	MSTRG.21216.1	1.191
MSTRG.17894.1	6.285	MSTRG.24570.1	2.066	MSTRG.44574.1	1.191
MSTRG.42188.2	6.265	MSTRG.28897.7	2.065	MSTRG.29260.2	1.191
MSTRG.48519.10	6.256	MSTRG.4380.1	2.065	MSTRG.5941.3	1.190
MSTRG.18036.5	6.254	MSTRG.36025.3	2.063	MSTRG.1460.1	1.189

MSTRG.43512.1	6.254	MSTRG.12091.1	2.063	MSTRG.26059.1	1.188
MSTRG.35133.4	6.240	MSTRG.14059.2	2.063	MSTRG.17028.1	1.188
MSTRG.26446.4	6.233	MSTRG.45487.2	2.062	MSTRG.42788.1	1.188
MSTRG.39151.4	6.233	MSTRG.6942.2	2.061	MSTRG.36389.1	1.188
MSTRG.8735.2	6.224	MSTRG.32439.1	2.061	MSTRG.39144.1	1.188
MSTRG.6562.3	6.191	MSTRG.35980.4	2.055	MSTRG.11681.1	1.188
MSTRG.11603.3	6.177	MSTRG.6146.1	2.054	MSTRG.33360.1	1.187
MSTRG.37959.2	6.171	MSTRG.23702.2	2.053	MSTRG.31019.1	1.186
MSTRG.35294.3	6.169	MSTRG.14262.1	2.050	MSTRG.9107.1	1.186
MSTRG.28025.2	6.157	MSTRG.7183.1	2.049	MSTRG.32217.1	1.185
MSTRG.37295.3	6.151	MSTRG.10888.2	2.044	MSTRG.21522.1	1.182
MSTRG.46511.7	6.143	MSTRG.10349.1	2.044	MSTRG.46234.1	1.181
MSTRG.5155.2	6.115	MSTRG.16936.1	2.043	MSTRG.19497.1	1.181
MSTRG.29135.5	6.104	MSTRG.21562.2	2.043	MSTRG.11905.1	1.181
MSTRG.36107.2	6.094	MSTRG.28829.2	2.042	MSTRG.35793.1	1.180
MSTRG.15007.2	6.089	MSTRG.2993.3	2.040	MSTRG.13409.1	1.180
MSTRG.13512.2	6.070	MSTRG.8960.1	2.037	MSTRG.12850.1	1.180
MSTRG.23766.1	6.046	MSTRG.47927.1	2.036	MSTRG.22245.2	1.180
MSTRG.494.3	6.040	MSTRG.9164.2	2.034	MSTRG.44973.6	1.179
MSTRG.36311.3	6.028	MSTRG.13746.1	2.032	MSTRG.20313.1	1.179
MSTRG.17876.1	6.027	MSTRG.43595.1	2.031	MSTRG.42159.1	1.178
MSTRG.29572.1	5.994	MSTRG.3590.1	2.030	MSTRG.41823.1	1.178
MSTRG.48026.2	5.976	MSTRG.34234.1	2.028	MSTRG.44899.1	1.178
MSTRG.20470.8	5.957	MSTRG.6222.1	2.028	MSTRG.37212.1	1.176
MSTRG.2376.3	5.943	MSTRG.45669.1	2.027	MSTRG.1797.1	1.176
MSTRG.1323.4	5.933	MSTRG.39940.1	2.025	MSTRG.12540.1	1.175
MSTRG.9221.2	5.923	MSTRG.44923.1	2.025	MSTRG.46024.1	1.174

MSTRG.39695.2	5.886	MSTRG.21890.1	2.025	MSTRG.46676.1	1.173
MSTRG.32148.3	5.867	MSTRG.32021.1	2.025	MSTRG.3198.1	1.173
MSTRG.20425.4	5.865	MSTRG.16280.1	2.024	MSTRG.11567.2	1.173
MSTRG.25886.2	5.849	MSTRG.1470.1	2.024	MSTRG.6527.1	1.172
MSTRG.8909.2	5.820	MSTRG.34102.1	2.023	MSTRG.8230.1	1.172
MSTRG.18368.4	5.795	MSTRG.8278.1	2.023	MSTRG.45756.1	1.172
MSTRG.36207.3	5.756	MSTRG.24256.2	2.021	MSTRG.1305.1	1.172
MSTRG.44840.2	5.752	MSTRG.19204.1	2.020	MSTRG.14662.1	1.171
MSTRG.16098.1	5.749	MSTRG.10529.1	2.020	MSTRG.34860.1	1.171
MSTRG.23766.3	5.743	MSTRG.37374.2	2.018	MSTRG.45027.1	1.170
MSTRG.25327.4	5.730	MSTRG.11762.1	2.014	MSTRG.36148.1	1.169
MSTRG.35958.4	5.716	MSTRG.36093.2	2.013	MSTRG.31234.2	1.169
MSTRG.10642.1	5.705	MSTRG.3148.1	2.009	MSTRG.40628.2	1.169
MSTRG.26580.3	5.694	MSTRG.13865.1	2.009	MSTRG.38650.1	1.169
MSTRG.40909.1	5.685	MSTRG.44945.1	2.008	MSTRG.493.1	1.168
MSTRG.40341.4	5.673	MSTRG.1929.1	2.005	MSTRG.30964.1	1.168
MSTRG.15351.1	5.666	MSTRG.45342.1	2.003	MSTRG.34795.1	1.167
MSTRG.20243.2	5.649	MSTRG.29708.1	2.003	MSTRG.23161.1	1.167
MSTRG.34995.2	5.642	MSTRG.38412.2	2.003	MSTRG.7212.2	1.167
MSTRG.15350.2	5.639	MSTRG.9582.1	2.000	MSTRG.21072.1	1.166
MSTRG.20833.2	5.632	MSTRG.9583.1	2.000	MSTRG.40065.1	1.166
MSTRG.15350.1	5.618	MSTRG.34888.1	1.999	MSTRG.36186.2	1.166
MSTRG.30319.5	5.610	MSTRG.1795.1	1.995	MSTRG.8636.2	1.165
MSTRG.1670.3	5.578	MSTRG.2109.4	1.995	MSTRG.14887.1	1.165
MSTRG.46131.3	5.553	MSTRG.1901.1	1.994	MSTRG.9542.1	1.164
MSTRG.25518.1	5.549	MSTRG.12092.1	1.991	MSTRG.7332.1	1.164
MSTRG.32336.4	5.543	MSTRG.46206.1	1.991	MSTRG.46482.1	1.163

MSTRG.12700.2	5.541	MSTRG.28349.1	1.990	MSTRG.1048.1	1.163
MSTRG.2778.2	5.535	MSTRG.40985.1	1.988	MSTRG.39496.1	1.162
MSTRG.20514.2	5.517	MSTRG.22535.1	1.988	MSTRG.7918.1	1.162
MSTRG.38149.4	5.496	MSTRG.18196.9	1.988	MSTRG.24590.1	1.161
MSTRG.18997.1	5.486	MSTRG.7276.5	1.986	MSTRG.17938.1	1.161
MSTRG.17059.2	5.485	MSTRG.5679.2	1.983	MSTRG.18627.1	1.159
MSTRG.33283.2	5.484	MSTRG.41323.1	1.982	MSTRG.4069.1	1.158
MSTRG.39931.3	5.459	MSTRG.43336.3	1.980	MSTRG.48074.8	1.157
MSTRG.7492.2	5.434	MSTRG.5696.1	1.970	MSTRG.43035.3	1.157
MSTRG.21030.6	5.421	MSTRG.41762.1	1.969	MSTRG.1404.1	1.156
MSTRG.27906.3	5.373	MSTRG.38312.5	1.968	MSTRG.20871.1	1.156
MSTRG.8848.2	5.367	MSTRG.33226.1	1.967	MSTRG.457.1	1.156
MSTRG.31751.7	5.365	MSTRG.47044.1	1.965	MSTRG.33717.1	1.156
MSTRG.28575.3	5.360	MSTRG.31601.3	1.962	MSTRG.15194.1	1.155
MSTRG.5048.5	5.357	MSTRG.9301.1	1.961	MSTRG.15229.1	1.155
MSTRG.45972.4	5.351	MSTRG.32262.1	1.960	MSTRG.10400.1	1.155
MSTRG.46021.3	5.332	MSTRG.8023.1	1.960	MSTRG.43922.1	1.154
MSTRG.37592.2	5.329	MSTRG.15952.1	1.958	MSTRG.34101.1	1.154
MSTRG.1411.2	5.328	MSTRG.32732.2	1.954	MSTRG.38737.1	1.153
MSTRG.9592.5	5.290	MSTRG.2100.2	1.953	MSTRG.45436.1	1.153
MSTRG.25669.4	5.288	MSTRG.43558.1	1.952	MSTRG.11220.1	1.153
MSTRG.27525.3	5.287	MSTRG.11131.1	1.952	MSTRG.10404.3	1.153
MSTRG.22316.3	5.280	MSTRG.40914.1	1.952	MSTRG.9392.1	1.153
MSTRG.26679.2	5.277	MSTRG.26003.1	1.951	MSTRG.4273.1	1.152
MSTRG.48080.10	5.275	MSTRG.31599.1	1.946	MSTRG.17121.1	1.152
MSTRG.47281.3	5.265	MSTRG.30112.1	1.944	MSTRG.22777.1	1.151
MSTRG.24391.1	5.261	MSTRG.953.1	1.942	MSTRG.32690.1	1.151

MSTRG.2422.3	5.260	MSTRG.40270.1	1.941	MSTRG.40783.1	1.151
MSTRG.20677.3	5.259	MSTRG.2532.1	1.939	MSTRG.27924.1	1.151
MSTRG.24962.4	5.240	MSTRG.21028.2	1.938	MSTRG.14669.1	1.149
MSTRG.8407.1	5.234	MSTRG.28456.1	1.936	MSTRG.8047.1	1.148
MSTRG.31734.1	5.215	MSTRG.47795.1	1.934	MSTRG.45272.1	1.148
MSTRG.31541.1	5.183	MSTRG.33715.2	1.932	MSTRG.29881.1	1.148
MSTRG.20412.1	5.160	MSTRG.17602.2	1.931	MSTRG.40065.5	1.148
MSTRG.41603.1	5.149	MSTRG.37303.1	1.930	MSTRG.19810.3	1.147
MSTRG.2093.2	5.148	MSTRG.8196.1	1.929	MSTRG.25435.1	1.147
MSTRG.1190.3	5.146	MSTRG.12585.1	1.923	MSTRG.26187.1	1.147
MSTRG.34182.4	5.144	MSTRG.22286.1	1.922	MSTRG.3709.1	1.146
MSTRG.9924.5	5.129	MSTRG.40236.1	1.921	MSTRG.23085.1	1.145
MSTRG.24382.9	5.123	MSTRG.7309.1	1.919	MSTRG.17737.1	1.145
MSTRG.21110.2	5.120	MSTRG.32022.1	1.918	MSTRG.23690.1	1.144
MSTRG.40246.1	5.113	MSTRG.24185.1	1.917	MSTRG.1666.1	1.144
MSTRG.23649.2	5.104	MSTRG.7333.2	1.917	MSTRG.46618.1	1.144
MSTRG.39024.1	5.085	MSTRG.41521.1	1.915	MSTRG.24252.1	1.143
MSTRG.22846.4	5.073	MSTRG.8545.1	1.915	MSTRG.48216.1	1.142
MSTRG.31920.2	5.068	MSTRG.17858.1	1.915	MSTRG.4071.2	1.142
MSTRG.1295.1	5.057	MSTRG.16487.1	1.914	MSTRG.21857.1	1.142
MSTRG.5494.3	5.041	MSTRG.29702.4	1.913	MSTRG.20250.1	1.140
MSTRG.15623.1	5.031	MSTRG.44987.1	1.912	MSTRG.27047.2	1.140
MSTRG.44418.1	5.030	MSTRG.22719.1	1.912	MSTRG.11779.2	1.140
MSTRG.6887.1	5.023	MSTRG.33108.1	1.911	MSTRG.22609.1	1.139
MSTRG.16864.4	5.023	MSTRG.20559.1	1.911	MSTRG.1151.1	1.138
MSTRG.22547.2	5.013	MSTRG.7651.1	1.910	MSTRG.23636.1	1.137
MSTRG.23560.2	5.013	MSTRG.35882.1	1.908	MSTRG.21156.1	1.137

MSTRG.27833.5	5.012	MSTRG.26536.3	1.905	MSTRG.14271.2	1.136
MSTRG.36669.12	5.011	MSTRG.1627.8	1.901	MSTRG.5607.1	1.135
MSTRG.41083.3	4.994	MSTRG.5674.1	1.901	MSTRG.7316.4	1.135
MSTRG.47729.1	4.983	MSTRG.11443.1	1.901	MSTRG.4068.2	1.134
MSTRG.4055.1	4.979	MSTRG.12707.1	1.900	MSTRG.21901.1	1.134
MSTRG.34238.3	4.967	MSTRG.16393.1	1.898	MSTRG.33428.1	1.134
MSTRG.9285.4	4.958	MSTRG.2697.2	1.898	MSTRG.41772.1	1.133
MSTRG.21108.3	4.956	MSTRG.36220.2	1.897	MSTRG.39147.1	1.132
MSTRG.16160.1	4.952	MSTRG.6337.1	1.897	MSTRG.17064.1	1.132
MSTRG.38056.8	4.949	MSTRG.41554.1	1.896	MSTRG.16880.1	1.130
MSTRG.39963.2	4.941	MSTRG.27432.1	1.895	MSTRG.9542.2	1.130
MSTRG.16797.3	4.940	MSTRG.29644.1	1.893	MSTRG.18950.1	1.129
MSTRG.15408.2	4.939	MSTRG.42632.1	1.888	MSTRG.27260.1	1.129
MSTRG.3894.2	4.920	MSTRG.14245.2	1.887	MSTRG.15470.1	1.129
MSTRG.41862.3	4.912	MSTRG.31217.4	1.886	MSTRG.41789.1	1.128
MSTRG.41593.4	4.902	MSTRG.12652.2	1.885	MSTRG.13624.2	1.128
MSTRG.16289.3	4.899	MSTRG.22779.1	1.882	MSTRG.26728.1	1.126
MSTRG.23390.2	4.879	MSTRG.10411.1	1.881	MSTRG.25756.1	1.125
MSTRG.8783.1	4.872	MSTRG.23213.1	1.878	MSTRG.12462.1	1.124
MSTRG.47283.3	4.871	MSTRG.25558.2	1.875	MSTRG.11878.1	1.123
MSTRG.18196.7	4.856	MSTRG.36718.2	1.875	MSTRG.31351.4	1.123
MSTRG.18251.3	4.850	MSTRG.2736.1	1.875	MSTRG.13942.1	1.123
MSTRG.48409.3	4.848	MSTRG.26799.1	1.874	MSTRG.33653.1	1.123
MSTRG.19867.1	4.841	MSTRG.5164.1	1.873	MSTRG.9852.1	1.123
MSTRG.27833.2	4.838	MSTRG.26799.5	1.872	MSTRG.20135.1	1.122
MSTRG.16824.1	4.817	MSTRG.44953.1	1.872	MSTRG.44973.4	1.122
MSTRG.25920.3	4.813	MSTRG.10522.2	1.871	MSTRG.20676.1	1.122

MSTRG.24937.3	4.800	MSTRG.6562.1	1.869	MSTRG.25153.2	1.121
MSTRG.24917.3	4.791	MSTRG.25791.1	1.869	MSTRG.45681.1	1.121
MSTRG.27372.5	4.787	MSTRG.34666.1	1.866	MSTRG.10171.1	1.119
MSTRG.7842.1	4.776	MSTRG.9519.1	1.866	MSTRG.45752.1	1.118
MSTRG.31027.2	4.775	MSTRG.16498.1	1.866	MSTRG.34809.1	1.118
MSTRG.15967.5	4.774	MSTRG.45453.3	1.866	MSTRG.7698.7	1.118
MSTRG.27550.1	4.757	MSTRG.31413.1	1.865	MSTRG.3572.1	1.118
MSTRG.44944.1	4.748	MSTRG.1459.1	1.861	MSTRG.32273.7	1.117
MSTRG.40768.1	4.744	MSTRG.17029.1	1.859	MSTRG.31495.2	1.116
MSTRG.1875.1	4.729	MSTRG.42822.1	1.858	MSTRG.10336.1	1.116
MSTRG.42155.2	4.724	MSTRG.3004.1	1.857	MSTRG.31158.1	1.116
MSTRG.28845.2	4.723	MSTRG.25558.1	1.857	MSTRG.44658.1	1.114
MSTRG.42657.6	4.716	MSTRG.41762.2	1.856	MSTRG.5069.1	1.114
MSTRG.13468.1	4.716	MSTRG.42858.1	1.855	MSTRG.17735.1	1.113
MSTRG.37134.4	4.694	MSTRG.14851.4	1.854	MSTRG.12467.13	1.113
MSTRG.27833.1	4.681	MSTRG.28191.1	1.853	MSTRG.35704.1	1.113
MSTRG.47418.5	4.674	MSTRG.46277.1	1.851	MSTRG.6084.1	1.113
MSTRG.27449.2	4.663	MSTRG.17118.1	1.851	MSTRG.875.4	1.112
MSTRG.17021.4	4.653	MSTRG.2134.1	1.851	MSTRG.3060.1	1.112
MSTRG.24759.1	4.651	MSTRG.44973.7	1.849	MSTRG.29054.1	1.111
MSTRG.12272.3	4.650	MSTRG.240.2	1.848	MSTRG.22615.1	1.111
MSTRG.25270.1	4.617	MSTRG.8137.1	1.848	MSTRG.90.1	1.111
MSTRG.8682.4	4.615	MSTRG.1345.1	1.848	MSTRG.10332.1	1.110
MSTRG.40513.1	4.575	MSTRG.12968.1	1.847	MSTRG.30816.2	1.110
MSTRG.13020.7	4.569	MSTRG.21682.1	1.847	MSTRG.32494.1	1.110
MSTRG.29611.3	4.562	MSTRG.31777.1	1.846	MSTRG.39669.1	1.110
MSTRG.16988.3	4.558	MSTRG.26799.3	1.844	MSTRG.40113.1	1.109

MSTRG.39088.1	4.545	MSTRG.16394.1	1.840	MSTRG.1942.1	1.108
MSTRG.21793.4	4.537	MSTRG.22149.3	1.839	MSTRG.42632.4	1.107
MSTRG.5191.5	4.533	MSTRG.21552.3	1.839	MSTRG.43180.1	1.107
MSTRG.5275.2	4.531	MSTRG.12836.1	1.838	MSTRG.19017.1	1.107
MSTRG.11141.3	4.519	MSTRG.22377.3	1.836	MSTRG.27326.7	1.106
MSTRG.16824.6	4.516	MSTRG.22884.6	1.836	MSTRG.10479.4	1.106
MSTRG.32999.3	4.495	MSTRG.22681.2	1.835	MSTRG.33435.1	1.104
MSTRG.32449.2	4.490	MSTRG.46210.1	1.835	MSTRG.45078.6	1.104
MSTRG.45698.2	4.482	MSTRG.9221.3	1.832	MSTRG.26540.1	1.104
MSTRG.6637.2	4.479	MSTRG.9728.1	1.832	MSTRG.24979.1	1.103
MSTRG.28124.3	4.478	MSTRG.7496.3	1.832	MSTRG.8177.1	1.103
MSTRG.5909.2	4.477	MSTRG.42417.1	1.832	MSTRG.47437.1	1.102
MSTRG.25512.1	4.475	MSTRG.11488.1	1.827	MSTRG.45880.1	1.101
MSTRG.29055.2	4.461	MSTRG.1895.1	1.827	MSTRG.23172.1	1.101
MSTRG.7592.1	4.454	MSTRG.6546.1	1.825	MSTRG.11574.1	1.101
MSTRG.30579.1	4.445	MSTRG.20872.1	1.824	MSTRG.9308.4	1.101
MSTRG.21972.2	4.443	MSTRG.14145.2	1.823	MSTRG.28237.1	1.100
MSTRG.6816.2	4.433	MSTRG.16439.1	1.822	MSTRG.16437.1	1.100
MSTRG.13721.5	4.433	MSTRG.38907.1	1.820	MSTRG.8502.1	1.099
MSTRG.34161.2	4.429	MSTRG.26917.3	1.819	MSTRG.6673.1	1.099
MSTRG.31661.5	4.418	MSTRG.26976.1	1.819	MSTRG.8738.1	1.098
MSTRG.34503.2	4.404	MSTRG.26799.2	1.819	MSTRG.43910.1	1.098
MSTRG.43462.1	4.403	MSTRG.14650.1	1.817	MSTRG.38949.1	1.098
MSTRG.8139.2	4.400	MSTRG.7872.2	1.816	MSTRG.48591.1	1.097
MSTRG.41755.2	4.393	MSTRG.7941.1	1.816	MSTRG.22190.1	1.097
MSTRG.2571.4	4.388	MSTRG.48736.1	1.814	MSTRG.36446.1	1.097
MSTRG.42318.4	4.382	MSTRG.15553.2	1.814	MSTRG.3651.1	1.097

MSTRG.35432.1	4.377	MSTRG.25272.1	1.814	MSTRG.43919.1	1.096
MSTRG.32447.6	4.377	MSTRG.1143.1	1.810	MSTRG.22942.2	1.096
MSTRG.11863.1	4.374	MSTRG.5878.1	1.809	MSTRG.12087.1	1.096
MSTRG.29191.2	4.371	MSTRG.22681.1	1.808	MSTRG.19678.1	1.095
MSTRG.536.2	4.356	MSTRG.32003.8	1.807	MSTRG.6433.1	1.094
MSTRG.47420.1	4.350	MSTRG.4131.1	1.805	MSTRG.25757.1	1.093
MSTRG.47413.1	4.341	MSTRG.12225.1	1.802	MSTRG.28630.1	1.093
MSTRG.42752.3	4.340	MSTRG.31207.1	1.802	MSTRG.9404.1	1.093
MSTRG.9312.1	4.339	MSTRG.1227.3	1.802	MSTRG.29586.1	1.093
MSTRG.32213.1	4.339	MSTRG.12820.1	1.798	MSTRG.18884.1	1.093
MSTRG.19071.2	4.338	MSTRG.28851.1	1.798	MSTRG.42811.1	1.092
MSTRG.27833.3	4.303	MSTRG.3991.11	1.797	MSTRG.18068.1	1.091
MSTRG.16974.2	4.286	MSTRG.36913.1	1.795	MSTRG.42143.1	1.090
MSTRG.29185.2	4.275	MSTRG.579.1	1.794	MSTRG.28761.1	1.090
MSTRG.36127.2	4.273	MSTRG.41000.1	1.794	MSTRG.40609.1	1.089
MSTRG.29351.3	4.270	MSTRG.27910.1	1.792	MSTRG.32912.1	1.089
MSTRG.33805.2	4.259	MSTRG.27034.1	1.792	MSTRG.5681.1	1.088
MSTRG.15690.1	4.255	MSTRG.39883.1	1.791	MSTRG.46580.1	1.088
MSTRG.26053.1	4.247	MSTRG.1534.2	1.786	MSTRG.15058.1	1.088
MSTRG.19064.3	4.245	MSTRG.43163.1	1.782	MSTRG.35883.1	1.088
MSTRG.17304.1	4.242	MSTRG.14488.6	1.780	MSTRG.48105.1	1.088
MSTRG.33281.1	4.241	MSTRG.37294.2	1.780	MSTRG.16895.1	1.087
MSTRG.2100.4	4.240	MSTRG.36362.1	1.779	MSTRG.45621.1	1.086
MSTRG.29833.2	4.234	MSTRG.45572.1	1.777	MSTRG.41263.1	1.084
MSTRG.3114.2	4.222	MSTRG.32217.2	1.777	MSTRG.39497.1	1.084
MSTRG.24231.1	4.211	MSTRG.18341.1	1.775	MSTRG.16263.2	1.082
MSTRG.45351.1	4.195	MSTRG.7315.3	1.775	MSTRG.24151.3	1.082

MSTRG.41773.2	4.186	MSTRG.45238.1	1.773	MSTRG.31239.1	1.081
MSTRG.24841.3	4.184	MSTRG.29521.2	1.771	MSTRG.3969.1	1.081
MSTRG.22382.3	4.175	MSTRG.46203.1	1.770	MSTRG.10272.1	1.081
MSTRG.27832.1	4.175	MSTRG.4779.1	1.767	MSTRG.26101.1	1.080
MSTRG.47425.1	4.154	MSTRG.43119.1	1.763	MSTRG.15290.1	1.080
MSTRG.4184.2	4.142	MSTRG.21089.1	1.762	MSTRG.31394.1	1.080
MSTRG.28939.3	4.137	MSTRG.48819.1	1.759	MSTRG.35983.1	1.080
MSTRG.21992.2	4.127	MSTRG.41958.3	1.759	MSTRG.20139.1	1.080
MSTRG.25516.1	4.102	MSTRG.15919.2	1.759	MSTRG.9439.1	1.080
MSTRG.33957.2	4.102	MSTRG.1205.3	1.758	MSTRG.29248.1	1.079
MSTRG.3077.1	4.101	MSTRG.11802.3	1.758	MSTRG.23105.1	1.078
MSTRG.27833.4	4.087	MSTRG.36066.3	1.758	MSTRG.24287.1	1.077
MSTRG.14884.1	4.087	MSTRG.45991.2	1.757	MSTRG.35138.1	1.077
MSTRG.47139.2	4.075	MSTRG.45991.3	1.755	MSTRG.10437.3	1.076
MSTRG.7843.1	4.062	MSTRG.1487.2	1.755	MSTRG.29260.1	1.076
MSTRG.42384.3	4.057	MSTRG.31030.1	1.754	MSTRG.19097.1	1.076
MSTRG.33214.2	4.050	MSTRG.33683.1	1.754	MSTRG.20778.2	1.075
MSTRG.47555.1	4.047	MSTRG.29609.1	1.752	MSTRG.22695.1	1.075
MSTRG.23432.1	4.045	MSTRG.2270.1	1.752	MSTRG.47107.1	1.074
MSTRG.14017.1	4.044	MSTRG.21970.2	1.751	MSTRG.7929.1	1.072
MSTRG.36707.2	4.035	MSTRG.25434.1	1.749	MSTRG.36378.1	1.072
MSTRG.16218.2	4.033	MSTRG.41763.1	1.748	MSTRG.13763.1	1.072
MSTRG.13636.2	4.029	MSTRG.18905.1	1.747	MSTRG.20283.1	1.072
MSTRG.3632.2	4.024	MSTRG.15184.1	1.747	MSTRG.9630.1	1.071
MSTRG.14922.2	4.024	MSTRG.37531.1	1.745	MSTRG.13164.1	1.071
MSTRG.40397.6	4.021	MSTRG.11603.2	1.745	MSTRG.9050.1	1.071
MSTRG.12465.8	4.020	MSTRG.36388.1	1.744	MSTRG.41877.1	1.070

MSTRG.1804.2	4.011	MSTRG.19453.1	1.741	MSTRG.12381.1	1.070
MSTRG.32286.3	4.006	MSTRG.37329.1	1.740	MSTRG.18116.1	1.070
MSTRG.39350.2	4.004	MSTRG.46839.1	1.737	MSTRG.40601.6	1.068
MSTRG.40569.1	3.995	MSTRG.37457.1	1.736	MSTRG.11099.1	1.068
MSTRG.32997.1	3.993	MSTRG.10333.2	1.735	MSTRG.48090.1	1.067
MSTRG.47615.2	3.990	MSTRG.45914.3	1.734	MSTRG.15894.1	1.067
MSTRG.36459.1	3.989	MSTRG.22165.1	1.733	MSTRG.31206.1	1.066
MSTRG.36311.2	3.981	MSTRG.10970.2	1.733	MSTRG.5001.1	1.066
MSTRG.9515.2	3.974	MSTRG.16395.1	1.731	MSTRG.25811.1	1.066
MSTRG.3286.2	3.971	MSTRG.35448.2	1.729	MSTRG.14879.1	1.065
MSTRG.42867.2	3.970	MSTRG.27758.1	1.727	MSTRG.44973.3	1.065
MSTRG.25296.1	3.968	MSTRG.44996.1	1.726	MSTRG.28276.1	1.064
MSTRG.41240.4	3.955	MSTRG.20286.3	1.725	MSTRG.37596.1	1.064
MSTRG.30184.1	3.949	MSTRG.44419.2	1.724	MSTRG.9844.1	1.064
MSTRG.36718.1	3.944	MSTRG.9214.1	1.724	MSTRG.45912.2	1.063
MSTRG.40421.1	3.944	MSTRG.15472.4	1.723	MSTRG.31932.1	1.063
MSTRG.47653.2	3.941	MSTRG.48737.1	1.723	MSTRG.13217.1	1.063
MSTRG.37632.8	3.934	MSTRG.12653.1	1.720	MSTRG.19435.1	1.061
MSTRG.29359.1	3.932	MSTRG.3988.7	1.720	MSTRG.26538.1	1.060
MSTRG.25640.2	3.931	MSTRG.34216.1	1.720	MSTRG.29699.1	1.060
MSTRG.38545.4	3.926	MSTRG.6018.3	1.719	MSTRG.27674.1	1.060
MSTRG.31476.2	3.921	MSTRG.16390.1	1.716	MSTRG.4747.1	1.059
MSTRG.25249.2	3.919	MSTRG.19712.1	1.715	MSTRG.46494.1	1.059
MSTRG.24485.9	3.918	MSTRG.7823.1	1.712	MSTRG.44069.1	1.058
MSTRG.26016.1	3.901	MSTRG.32684.1	1.712	MSTRG.33980.1	1.058
MSTRG.42439.1	3.896	MSTRG.26569.1	1.709	MSTRG.9968.1	1.057
MSTRG.3951.3	3.888	MSTRG.9696.1	1.709	MSTRG.19993.1	1.056

MSTRG.47418.2	3.885	MSTRG.23923.1	1.705	MSTRG.36384.1	1.055
MSTRG.45075.2	3.882	MSTRG.38150.1	1.705	MSTRG.44175.1	1.054
MSTRG.36631.2	3.876	MSTRG.31509.1	1.705	MSTRG.27039.1	1.054
MSTRG.3542.2	3.870	MSTRG.19801.1	1.705	MSTRG.22685.1	1.054
MSTRG.1918.2	3.869	MSTRG.2100.3	1.704	MSTRG.11246.3	1.054
MSTRG.2270.3	3.861	MSTRG.43385.1	1.704	MSTRG.27935.1	1.054
MSTRG.747.1	3.861	MSTRG.43485.7	1.703	MSTRG.18179.1	1.053
MSTRG.20876.1	3.852	MSTRG.11802.6	1.703	MSTRG.16997.1	1.053
MSTRG.28784.5	3.849	MSTRG.23308.1	1.702	MSTRG.35961.1	1.053
MSTRG.9808.1	3.842	MSTRG.10648.1	1.700	MSTRG.10858.1	1.052
MSTRG.18283.1	3.841	MSTRG.24167.1	1.700	MSTRG.43085.1	1.051
MSTRG.33748.2	3.839	MSTRG.14004.1	1.699	MSTRG.28786.1	1.051
MSTRG.533.2	3.833	MSTRG.132.1	1.697	MSTRG.28026.1	1.051
MSTRG.30345.4	3.831	MSTRG.13436.1	1.695	MSTRG.44508.1	1.050
MSTRG.27525.1	3.807	MSTRG.13750.1	1.692	MSTRG.19167.1	1.050
MSTRG.8282.1	3.807	MSTRG.48562.1	1.692	MSTRG.41604.1	1.050
MSTRG.24281.4	3.802	MSTRG.18332.1	1.692	MSTRG.41547.1	1.049
MSTRG.35174.1	3.802	MSTRG.14810.2	1.691	MSTRG.46405.1	1.049
MSTRG.25377.5	3.801	MSTRG.41735.1	1.688	MSTRG.35212.1	1.049
MSTRG.12679.1	3.798	MSTRG.28735.1	1.686	MSTRG.10256.2	1.049
MSTRG.27932.1	3.793	MSTRG.46705.3	1.685	MSTRG.29249.1	1.048
MSTRG.31812.2	3.788	MSTRG.23615.1	1.685	MSTRG.2735.1	1.048
MSTRG.23464.4	3.788	MSTRG.488.1	1.684	MSTRG.19418.2	1.047
MSTRG.25100.1	3.785	MSTRG.20675.1	1.684	MSTRG.36215.1	1.047
MSTRG.28264.1	3.780	MSTRG.13288.2	1.683	MSTRG.34973.1	1.046
MSTRG.37774.4	3.780	MSTRG.44878.2	1.678	MSTRG.33104.1	1.046
MSTRG.10348.3	3.768	MSTRG.23652.1	1.677	MSTRG.564.1	1.046

MSTRG.44180.5	3.767	MSTRG.40866.1	1.675	MSTRG.4606.1	1.045
MSTRG.41852.1	3.766	MSTRG.45224.6	1.673	MSTRG.33076.1	1.045
MSTRG.39971.6	3.764	MSTRG.17311.1	1.672	MSTRG.4652.1	1.043
MSTRG.44981.1	3.764	MSTRG.45237.1	1.671	MSTRG.28793.1	1.043
MSTRG.36744.1	3.763	MSTRG.41473.1	1.670	MSTRG.48416.1	1.042
MSTRG.42740.3	3.761	MSTRG.27243.1	1.670	MSTRG.3493.1	1.042
MSTRG.6148.1	3.751	MSTRG.9847.2	1.669	MSTRG.14867.1	1.042
MSTRG.22960.2	3.741	MSTRG.34758.1	1.669	MSTRG.46735.1	1.041
MSTRG.10934.3	3.740	MSTRG.14158.3	1.666	MSTRG.15888.1	1.040
MSTRG.31314.2	3.735	MSTRG.5621.1	1.665	MSTRG.31404.1	1.040
MSTRG.9728.2	3.734	MSTRG.10093.1	1.665	MSTRG.23037.1	1.039
MSTRG.10245.3	3.732	MSTRG.19886.1	1.665	MSTRG.47826.1	1.039
MSTRG.36587.1	3.727	MSTRG.354.1	1.665	MSTRG.10450.1	1.039
MSTRG.44191.1	3.722	MSTRG.17199.1	1.661	MSTRG.35341.2	1.038
MSTRG.38398.3	3.717	MSTRG.6338.1	1.660	MSTRG.16646.1	1.037
MSTRG.26196.5	3.717	MSTRG.43050.2	1.660	MSTRG.33629.1	1.037
MSTRG.40563.28	3.717	MSTRG.20842.1	1.660	MSTRG.32917.1	1.035
MSTRG.38553.2	3.714	MSTRG.7192.2	1.659	MSTRG.38774.4	1.035
MSTRG.35716.3	3.713	MSTRG.17252.6	1.659	MSTRG.36040.2	1.035
MSTRG.46999.1	3.712	MSTRG.46440.2	1.658	MSTRG.24272.1	1.034
MSTRG.33414.6	3.711	MSTRG.45778.1	1.656	MSTRG.27567.1	1.034
MSTRG.22626.2	3.710	MSTRG.5299.1	1.656	MSTRG.10480.2	1.033
MSTRG.28716.2	3.707	MSTRG.18407.1	1.653	MSTRG.34668.2	1.032
MSTRG.3964.1	3.705	MSTRG.3570.3	1.652	MSTRG.41252.2	1.031
MSTRG.29606.1	3.703	MSTRG.28889.1	1.651	MSTRG.478.1	1.031
MSTRG.48168.1	3.701	MSTRG.32924.1	1.651	MSTRG.5909.1	1.031
MSTRG.41782.4	3.696	MSTRG.14399.1	1.650	MSTRG.38019.2	1.030

MSTRG.4312.2	3.663	MSTRG.42887.1	1.650	MSTRG.7438.1	1.026
MSTRG.22490.1	3.650	MSTRG.32727.1	1.648	MSTRG.27210.1	1.026
MSTRG.39686.1	3.647	MSTRG.14906.1	1.647	MSTRG.16410.1	1.026
MSTRG.29050.2	3.644	MSTRG.22424.1	1.646	MSTRG.15693.1	1.025
MSTRG.17077.1	3.643	MSTRG.13521.1	1.644	MSTRG.6088.1	1.025
MSTRG.25100.3	3.639	MSTRG.26579.2	1.644	MSTRG.23171.1	1.024
MSTRG.15606.1	3.635	MSTRG.41204.2	1.644	MSTRG.33542.1	1.024
MSTRG.39454.5	3.623	MSTRG.9054.1	1.643	MSTRG.26685.1	1.024
MSTRG.33892.2	3.623	MSTRG.22680.3	1.643	MSTRG.6280.1	1.024
MSTRG.42369.1	3.620	MSTRG.21173.1	1.642	MSTRG.4068.1	1.024
MSTRG.12730.3	3.613	MSTRG.11357.2	1.639	MSTRG.37940.1	1.023
MSTRG.32678.1	3.606	MSTRG.35651.1	1.639	MSTRG.45663.1	1.022
MSTRG.40555.62	3.605	MSTRG.26427.1	1.638	MSTRG.45015.1	1.021
MSTRG.13101.28	3.603	MSTRG.40563.23	1.637	MSTRG.6697.1	1.021
MSTRG.15760.1	3.601	MSTRG.21552.1	1.637	MSTRG.10707.1	1.021
MSTRG.39454.1	3.601	MSTRG.4663.1	1.637	MSTRG.35054.1	1.021
MSTRG.29715.1	3.600	MSTRG.13367.2	1.636	MSTRG.22104.1	1.021
MSTRG.29671.1	3.598	MSTRG.13431.1	1.633	MSTRG.43096.8	1.020
MSTRG.42657.5	3.593	MSTRG.33190.1	1.633	MSTRG.27261.1	1.020
MSTRG.29835.2	3.588	MSTRG.4382.3	1.632	MSTRG.28309.1	1.020
MSTRG.42456.1	3.588	MSTRG.46985.1	1.631	MSTRG.17715.1	1.020
MSTRG.16867.1	3.583	MSTRG.42809.2	1.631	MSTRG.41613.1	1.019
MSTRG.4091.3	3.570	MSTRG.22244.3	1.630	MSTRG.11789.1	1.019
MSTRG.24284.2	3.555	MSTRG.23479.1	1.630	MSTRG.29206.1	1.018
MSTRG.41931.2	3.550	MSTRG.18942.3	1.629	MSTRG.21363.1	1.018
MSTRG.16823.3	3.547	MSTRG.27240.1	1.627	MSTRG.32668.1	1.017
MSTRG.19309.5	3.541	MSTRG.37351.1	1.626	MSTRG.34053.1	1.017

MSTRG.35823.1	3.531	MSTRG.43035.4	1.626	MSTRG.33338.1	1.017
MSTRG.15544.1	3.509	MSTRG.25091.2	1.624	MSTRG.26536.1	1.017
MSTRG.32085.2	3.497	MSTRG.10466.1	1.623	MSTRG.3073.1	1.017
MSTRG.92.1	3.495	MSTRG.46959.1	1.622	MSTRG.46103.1	1.016
MSTRG.48009.8	3.493	MSTRG.44148.1	1.621	MSTRG.17665.2	1.016
MSTRG.40568.2	3.492	MSTRG.43320.1	1.620	MSTRG.44075.1	1.015
MSTRG.32702.1	3.492	MSTRG.17651.1	1.619	MSTRG.7698.3	1.015
MSTRG.41960.1	3.489	MSTRG.35517.1	1.619	MSTRG.11126.1	1.014
MSTRG.20167.1	3.488	MSTRG.40745.1	1.619	MSTRG.41559.1	1.013
MSTRG.37895.4	3.484	MSTRG.34728.3	1.617	MSTRG.5908.1	1.012
MSTRG.36422.1	3.479	MSTRG.24281.3	1.615	MSTRG.39237.1	1.011
MSTRG.33984.1	3.478	MSTRG.1881.1	1.615	MSTRG.46966.2	1.011
MSTRG.21789.1	3.476	MSTRG.11895.1	1.615	MSTRG.9842.1	1.011
MSTRG.19992.1	3.470	MSTRG.14245.1	1.613	MSTRG.42300.3	1.010
MSTRG.24627.2	3.463	MSTRG.28578.1	1.613	MSTRG.33332.1	1.010
MSTRG.15967.3	3.461	MSTRG.9924.10	1.611	MSTRG.41275.1	1.009
MSTRG.40480.4	3.459	MSTRG.46792.1	1.611	MSTRG.47156.1	1.009
MSTRG.38151.1	3.459	MSTRG.15364.1	1.610	MSTRG.33557.1	1.008
MSTRG.21415.10	3.457	MSTRG.868.1	1.609	MSTRG.18546.1	1.007
MSTRG.40563.29	3.452	MSTRG.10725.1	1.607	MSTRG.2344.1	1.006
MSTRG.42733.2	3.449	MSTRG.34467.2	1.605	MSTRG.2664.1	1.006
MSTRG.42000.2	3.446	MSTRG.8139.4	1.605	MSTRG.6136.1	1.005
MSTRG.7184.1	3.445	MSTRG.11357.1	1.604	MSTRG.43238.1	1.005
MSTRG.42944.3	3.443	MSTRG.10886.2	1.603	MSTRG.20778.1	1.004
MSTRG.37442.1	3.440	MSTRG.23379.1	1.602	MSTRG.20524.1	1.003
MSTRG.10253.21	3.438	MSTRG.1312.1	1.601	MSTRG.45775.1	1.003
MSTRG.1914.1	3.434	MSTRG.107.1	1.599	MSTRG.16582.1	1.003

MSTRG.38920.1	3.426	MSTRG.17875.1	1.599	MSTRG.35778.1	1.003
MSTRG.10575.23	3.417	MSTRG.31886.1	1.599	MSTRG.8473.1	1.003
MSTRG.37469.5	3.412	MSTRG.22675.1	1.599	MSTRG.36535.2	1.003
MSTRG.38015.1	3.406	MSTRG.13432.1	1.596	MSTRG.29283.1	1.002
MSTRG.21568.4	3.386	MSTRG.17801.1	1.594	MSTRG.42708.1	1.002
MSTRG.15262.1	3.380	MSTRG.14253.1	1.594	MSTRG.42404.1	1.002
MSTRG.26891.3	3.376	MSTRG.7164.1	1.593	MSTRG.28732.1	1.002
MSTRG.28090.1	3.371	MSTRG.210.1	1.593	MSTRG.34672.1	1.001
MSTRG.22309.7	3.370	MSTRG.25624.1	1.592	MSTRG.16026.1	1.001
MSTRG.8783.3	3.367	MSTRG.7954.1	1.591	MSTRG.16132.1	1.000
MSTRG.38919.1	3.365	MSTRG.11713.1	1.590	MSTRG.7556.1	1.000

Table S4.7: Downregulated transcripts under chilling conditions in *Corylus avellana* cv Tombul with iDEP

Transcript ID	log2 FoldChange	Transcript ID	log2 FoldChange	Transcript ID	log2 FoldChange
MSTRG.6894.1	-44.129	MSTRG.10164.1	-2.660	MSTRG.30799.1	-1.642
MSTRG.37708.7	-42.508	MSTRG.44018.1	-2.658	MSTRG.23332.1	-1.641
MSTRG.26165.1	-41.961	MSTRG.6182.8	-2.654	MSTRG.33626.1	-1.640
MSTRG.30857.2	-41.874	MSTRG.15447.2	-2.647	MSTRG.35611.3	-1.640
MSTRG.11160.4	-40.279	MSTRG.36756.1	-2.647	MSTRG.2312.1	-1.639
MSTRG.15859.2	-39.852	MSTRG.12020.1	-2.646	MSTRG.31978.1	-1.639
MSTRG.7276.4	-38.959	MSTRG.42721.1	-2.646	MSTRG.30924.3	-1.638
MSTRG.32756.1	-38.950	MSTRG.48732.1	-2.646	MSTRG.29550.1	-1.637
MSTRG.42306.7	-37.712	MSTRG.23912.1	-2.646	MSTRG.38797.6	-1.637
MSTRG.46397.2	-36.543	MSTRG.32861.1	-2.645	MSTRG.10206.1	-1.637
MSTRG.12557.8	-35.741	MSTRG.45459.1	-2.645	MSTRG.435.1	-1.637
MSTRG.3163.5	-35.145	MSTRG.31301.3	-2.643	MSTRG.48420.1	-1.637
MSTRG.10045.2	-34.274	MSTRG.12951.1	-2.641	MSTRG.23390.1	-1.637
MSTRG.24200.2	-33.620	MSTRG.32665.2	-2.641	MSTRG.23950.1	-1.637
MSTRG.14432.1	-32.734	MSTRG.41447.3	-2.639	MSTRG.17488.1	-1.637
MSTRG.11584.1	-31.386	MSTRG.20152.2	-2.639	MSTRG.27939.1	-1.635
MSTRG.25996.3	-30.190	MSTRG.29401.1	-2.638	MSTRG.17926.1	-1.634
MSTRG.14274.1	-29.482	MSTRG.1727.1	-2.637	MSTRG.19202.1	-1.634
MSTRG.10720.2	-28.686	MSTRG.21747.3	-2.637	MSTRG.32583.1	-1.634
MSTRG.10245.5	-28.518	MSTRG.15111.2	-2.634	MSTRG.42759.1	-1.633
MSTRG.18246.4	-27.436	MSTRG.32158.2	-2.632	MSTRG.13653.1	-1.633
MSTRG.11605.5	-27.374	MSTRG.47426.1	-2.632	MSTRG.29266.1	-1.632
MSTRG.27665.2	-27.158	MSTRG.17270.1	-2.631	MSTRG.35528.2	-1.632
MSTRG.18648.1	-26.497	MSTRG.39546.1	-2.629	MSTRG.7604.1	-1.631

MSTRG.22579.2	-26.368	MSTRG.29388.2	-2.627	MSTRG.11888.2	-1.630
MSTRG.40802.2	-26.302	MSTRG.44529.1	-2.625	MSTRG.47658.1	-1.630
MSTRG.23009.6	-26.186	MSTRG.31036.1	-2.625	MSTRG.46731.1	-1.630
MSTRG.29969.2	-26.171	MSTRG.35586.6	-2.624	MSTRG.15460.1	-1.629
MSTRG.7333.4	-26.113	MSTRG.18814.1	-2.623	MSTRG.21415.20	-1.628
MSTRG.21796.3	-25.904	MSTRG.23980.1	-2.623	MSTRG.15312.1	-1.627
MSTRG.38486.1	-25.610	MSTRG.1670.1	-2.622	MSTRG.10986.1	-1.627
MSTRG.31777.2	-25.342	MSTRG.15073.1	-2.621	MSTRG.42831.1	-1.626
MSTRG.25954.1	-24.198	MSTRG.45455.2	-2.621	MSTRG.10909.9	-1.626
MSTRG.17917.17	-19.746	MSTRG.19630.8	-2.621	MSTRG.21204.3	-1.626
MSTRG.17917.13	-17.853	MSTRG.1104.1	-2.619	MSTRG.22987.2	-1.625
MSTRG.37343.31	-16.937	MSTRG.4327.1	-2.619	MSTRG.30210.1	-1.625
MSTRG.28361.6	-16.794	MSTRG.29083.1	-2.616	MSTRG.5720.1	-1.625
MSTRG.44753.10	-16.523	MSTRG.31554.1	-2.615	MSTRG.27541.1	-1.625
MSTRG.14446.1	-16.265	MSTRG.30505.2	-2.614	MSTRG.22538.1	-1.623
MSTRG.30371.4	-15.592	MSTRG.46394.8	-2.612	MSTRG.19584.2	-1.623
MSTRG.5415.5	-15.530	MSTRG.35752.1	-2.611	MSTRG.37261.4	-1.622
MSTRG.15481.1	-15.348	MSTRG.34555.1	-2.608	MSTRG.9866.4	-1.622
MSTRG.9775.4	-15.347	MSTRG.5959.1	-2.608	MSTRG.7349.1	-1.622
MSTRG.6869.6	-15.328	MSTRG.40428.2	-2.608	MSTRG.22350.1	-1.619
MSTRG.8234.1	-15.302	MSTRG.3559.1	-2.606	MSTRG.42072.1	-1.618
MSTRG.48817.10	-15.224	MSTRG.9164.3	-2.605	MSTRG.32834.1	-1.617
MSTRG.42900.3	-15.033	MSTRG.31254.5	-2.602	MSTRG.12033.2	-1.616
MSTRG.45938.6	-14.828	MSTRG.25798.1	-2.602	MSTRG.13406.14	-1.615
MSTRG.29013.1	-14.701	MSTRG.43931.1	-2.600	MSTRG.48503.7	-1.614
MSTRG.34170.2	-14.497	MSTRG.44304.2	-2.599	MSTRG.25821.2	-1.614
MSTRG.21953.2	-14.448	MSTRG.8343.1	-2.596	MSTRG.22744.1	-1.613

MSTRG.1075.1	-14.437	MSTRG.12261.1	-2.593	MSTRG.12740.1	-1.613
MSTRG.19388.1	-14.169	MSTRG.5384.1	-2.593	MSTRG.35611.1	-1.612
MSTRG.24027.1	-14.145	MSTRG.30913.1	-2.590	MSTRG.10475.1	-1.612
MSTRG.3884.9	-14.115	MSTRG.34226.14	-2.589	MSTRG.26837.12	-1.610
MSTRG.23212.2	-14.025	MSTRG.29897.1	-2.588	MSTRG.22569.1	-1.609
MSTRG.26853.9	-14.024	MSTRG.46231.1	-2.585	MSTRG.39439.1	-1.608
MSTRG.27958.3	-13.998	MSTRG.28158.1	-2.584	MSTRG.48419.1	-1.607
MSTRG.28069.1	-13.865	MSTRG.2265.1	-2.584	MSTRG.16116.1	-1.607
MSTRG.16289.4	-13.858	MSTRG.7932.1	-2.580	MSTRG.45906.1	-1.606
MSTRG.31177.3	-13.797	MSTRG.48026.1	-2.580	MSTRG.11419.1	-1.605
MSTRG.4208.1	-13.729	MSTRG.7672.1	-2.579	MSTRG.32174.1	-1.605
MSTRG.25449.3	-13.704	MSTRG.23485.3	-2.578	MSTRG.1195.1	-1.605
MSTRG.5074.2	-13.655	MSTRG.45473.1	-2.578	MSTRG.6586.1	-1.603
MSTRG.41288.9	-13.646	MSTRG.29485.1	-2.577	MSTRG.31245.1	-1.603
MSTRG.23315.2	-13.601	MSTRG.35613.1	-2.574	MSTRG.42254.1	-1.602
MSTRG.22811.2	-13.585	MSTRG.28811.1	-2.569	MSTRG.34301.1	-1.598
MSTRG.48602.1	-13.571	MSTRG.38717.1	-2.568	MSTRG.10987.1	-1.598
MSTRG.11784.17	-13.568	MSTRG.4653.1	-2.568	MSTRG.2181.1	-1.597
MSTRG.34148.1	-13.543	MSTRG.28194.2	-2.563	MSTRG.38708.1	-1.597
MSTRG.32447.8	-13.480	MSTRG.7457.1	-2.562	MSTRG.11356.1	-1.597
MSTRG.24308.1	-13.450	MSTRG.9230.9	-2.561	MSTRG.38242.1	-1.596
MSTRG.23400.2	-13.428	MSTRG.17055.1	-2.560	MSTRG.8350.1	-1.596
MSTRG.23212.3	-13.417	MSTRG.35285.1	-2.558	MSTRG.17268.1	-1.595
MSTRG.25304.1	-13.400	MSTRG.20945.4	-2.557	MSTRG.4206.1	-1.595
MSTRG.23698.1	-13.382	MSTRG.24442.2	-2.556	MSTRG.47195.2	-1.594
MSTRG.20708.3	-13.369	MSTRG.33174.11	-2.555	MSTRG.12596.3	-1.594
MSTRG.21818.10	-13.361	MSTRG.25354.1	-2.554	MSTRG.30560.1	-1.594

MSTRG.10538.1	-13.356	MSTRG.36396.1	-2.551	MSTRG.48616.8	-1.592
MSTRG.5581.3	-13.236	MSTRG.35503.1	-2.550	MSTRG.45598.2	-1.592
MSTRG.7591.2	-13.230	MSTRG.1222.1	-2.549	MSTRG.37389.1	-1.590
MSTRG.34586.3	-13.207	MSTRG.4465.1	-2.549	MSTRG.36825.1	-1.590
MSTRG.21235.6	-13.032	MSTRG.14360.1	-2.547	MSTRG.11343.1	-1.589
MSTRG.17657.8	-13.010	MSTRG.10621.1	-2.543	MSTRG.21626.1	-1.589
MSTRG.39667.1	-12.980	MSTRG.42248.1	-2.542	MSTRG.39047.1	-1.587
MSTRG.25682.2	-12.886	MSTRG.11605.4	-2.540	MSTRG.42718.1	-1.587
MSTRG.31777.3	-12.877	MSTRG.31499.1	-2.539	MSTRG.17415.1	-1.586
MSTRG.33174.21	-12.844	MSTRG.2407.1	-2.539	MSTRG.23931.1	-1.586
MSTRG.23464.5	-12.833	MSTRG.40506.1	-2.537	MSTRG.4870.4	-1.585
MSTRG.28090.2	-12.825	MSTRG.26361.1	-2.536	MSTRG.1635.1	-1.584
MSTRG.8085.2	-12.816	MSTRG.17775.1	-2.536	MSTRG.18705.1	-1.584
MSTRG.20061.7	-12.792	MSTRG.40450.1	-2.533	MSTRG.41875.1	-1.583
MSTRG.44600.2	-12.786	MSTRG.46394.2	-2.532	MSTRG.38356.2	-1.582
MSTRG.24578.15	-12.753	MSTRG.30220.1	-2.530	MSTRG.15872.1	-1.582
MSTRG.33174.4	-12.747	MSTRG.10689.1	-2.530	MSTRG.18741.2	-1.581
MSTRG.11281.1	-12.747	MSTRG.970.1	-2.529	MSTRG.783.1	-1.581
MSTRG.34533.4	-12.737	MSTRG.13792.1	-2.528	MSTRG.18637.2	-1.580
MSTRG.42306.6	-12.719	MSTRG.5046.1	-2.526	MSTRG.31788.2	-1.580
MSTRG.37632.15	-12.718	MSTRG.22830.3	-2.525	MSTRG.45824.1	-1.579
MSTRG.48758.3	-12.715	MSTRG.14975.1	-2.525	MSTRG.40146.1	-1.579
MSTRG.6873.5	-12.652	MSTRG.20945.5	-2.520	MSTRG.11784.18	-1.577
MSTRG.40236.2	-12.622	MSTRG.18629.2	-2.520	MSTRG.17935.1	-1.576
MSTRG.3327.3	-12.558	MSTRG.11560.4	-2.518	MSTRG.9575.1	-1.573
MSTRG.31551.2	-12.492	MSTRG.36359.1	-2.517	MSTRG.14210.1	-1.573
MSTRG.45769.8	-12.458	MSTRG.38812.1	-2.517	MSTRG.36229.1	-1.572

MSTRG.8872.2	-12.434	MSTRG.48080.4	-2.516	MSTRG.35567.1	-1.572
MSTRG.39471.1	-12.430	MSTRG.6871.1	-2.516	MSTRG.19225.1	-1.572
MSTRG.12096.1	-12.368	MSTRG.22830.1	-2.515	MSTRG.39710.3	-1.571
MSTRG.2671.3	-12.366	MSTRG.8581.1	-2.515	MSTRG.1603.1	-1.571
MSTRG.928.3	-12.355	MSTRG.45769.4	-2.514	MSTRG.28037.1	-1.570
MSTRG.12012.2	-12.346	MSTRG.30138.1	-2.514	MSTRG.18912.1	-1.570
MSTRG.39723.4	-12.345	MSTRG.295.1	-2.513	MSTRG.598.1	-1.569
MSTRG.22778.3	-12.323	MSTRG.31003.1	-2.512	MSTRG.32952.1	-1.569
MSTRG.27357.4	-12.305	MSTRG.2319.1	-2.510	MSTRG.17880.1	-1.568
MSTRG.7710.4	-12.297	MSTRG.32952.3	-2.509	MSTRG.39968.2	-1.568
MSTRG.7128.3	-12.293	MSTRG.972.1	-2.509	MSTRG.22291.1	-1.567
MSTRG.29688.2	-12.290	MSTRG.29014.1	-2.508	MSTRG.38952.1	-1.567
MSTRG.26036.1	-12.268	MSTRG.14790.2	-2.505	MSTRG.3427.6	-1.567
MSTRG.14017.2	-12.212	MSTRG.4870.3	-2.505	MSTRG.8349.1	-1.563
MSTRG.6122.1	-12.198	MSTRG.2636.2	-2.502	MSTRG.45593.1	-1.562
MSTRG.24340.2	-12.175	MSTRG.19948.2	-2.501	MSTRG.10032.1	-1.561
MSTRG.11006.1	-12.162	MSTRG.40299.1	-2.501	MSTRG.22992.1	-1.561
MSTRG.2277.4	-12.158	MSTRG.23230.1	-2.498	MSTRG.2018.1	-1.561
MSTRG.33958.3	-12.157	MSTRG.20983.1	-2.498	MSTRG.930.1	-1.560
MSTRG.13382.1	-12.153	MSTRG.45567.4	-2.497	MSTRG.19964.9	-1.560
MSTRG.34108.3	-12.129	MSTRG.46707.3	-2.495	MSTRG.11586.2	-1.560
MSTRG.12450.4	-12.124	MSTRG.18509.1	-2.493	MSTRG.10878.1	-1.559
MSTRG.12450.5	-12.097	MSTRG.31314.1	-2.490	MSTRG.35614.3	-1.559
MSTRG.39590.1	-12.026	MSTRG.1149.3	-2.490	MSTRG.12785.3	-1.558
MSTRG.19910.1	-12.001	MSTRG.26842.1	-2.489	MSTRG.27360.1	-1.558
MSTRG.43082.1	-11.986	MSTRG.42011.1	-2.488	MSTRG.28412.1	-1.558
MSTRG.43971.3	-11.982	MSTRG.23074.1	-2.486	MSTRG.10235.1	-1.554

MSTRG.7712.1	-11.979	MSTRG.17573.3	-2.486	MSTRG.20642.1	-1.554
MSTRG.6115.1	-11.973	MSTRG.29164.1	-2.485	MSTRG.33773.1	-1.553
MSTRG.40667.2	-11.973	MSTRG.28975.1	-2.483	MSTRG.3591.1	-1.553
MSTRG.13045.2	-11.971	MSTRG.36678.1	-2.479	MSTRG.20455.1	-1.552
MSTRG.26899.4	-11.943	MSTRG.40122.1	-2.478	MSTRG.5826.1	-1.551
MSTRG.14670.2	-11.940	MSTRG.9157.6	-2.478	MSTRG.16830.1	-1.551
MSTRG.30515.2	-11.935	MSTRG.33254.1	-2.477	MSTRG.47028.1	-1.549
MSTRG.42657.9	-11.927	MSTRG.41485.1	-2.476	MSTRG.14027.1	-1.548
MSTRG.35507.1	-11.890	MSTRG.17884.1	-2.475	MSTRG.20116.1	-1.547
MSTRG.26091.3	-11.875	MSTRG.8516.1	-2.472	MSTRG.21574.1	-1.547
MSTRG.32579.1	-11.865	MSTRG.28121.1	-2.471	MSTRG.27704.1	-1.546
MSTRG.12074.2	-11.818	MSTRG.5750.9	-2.471	MSTRG.45165.1	-1.546
MSTRG.27111.2	-11.752	MSTRG.20532.1	-2.470	MSTRG.24390.4	-1.544
MSTRG.45074.1	-11.742	MSTRG.28131.1	-2.470	MSTRG.35509.1	-1.542
MSTRG.15998.3	-11.699	MSTRG.41523.6	-2.470	MSTRG.48769.1	-1.541
MSTRG.41288.6	-11.689	MSTRG.47852.1	-2.468	MSTRG.8506.1	-1.539
MSTRG.26264.3	-11.680	MSTRG.33269.1	-2.465	MSTRG.35536.1	-1.537
MSTRG.44389.2	-11.680	MSTRG.38208.3	-2.464	MSTRG.39933.1	-1.536
MSTRG.8725.2	-11.624	MSTRG.31555.2	-2.462	MSTRG.3095.1	-1.535
MSTRG.196.5	-11.622	MSTRG.31556.1	-2.459	MSTRG.35508.1	-1.535
MSTRG.15849.8	-11.598	MSTRG.18764.3	-2.457	MSTRG.35936.1	-1.534
MSTRG.1872.1	-11.598	MSTRG.10694.1	-2.457	MSTRG.40653.1	-1.533
MSTRG.3685.11	-11.586	MSTRG.44749.3	-2.456	MSTRG.18783.1	-1.533
MSTRG.13717.1	-11.583	MSTRG.37981.1	-2.455	MSTRG.48282.1	-1.533
MSTRG.43033.1	-11.532	MSTRG.6633.1	-2.454	MSTRG.2376.1	-1.532
MSTRG.27305.2	-11.460	MSTRG.42593.1	-2.453	MSTRG.3308.1	-1.532
MSTRG.37033.6	-11.405	MSTRG.46273.2	-2.452	MSTRG.44639.2	-1.532

MSTRG.8268.1	-11.393	MSTRG.38933.1	-2.448	MSTRG.10213.6	-1.532
MSTRG.16527.1	-11.378	MSTRG.30490.3	-2.445	MSTRG.22678.5	-1.531
MSTRG.17397.2	-11.314	MSTRG.31406.2	-2.441	MSTRG.22745.1	-1.531
MSTRG.32031.1	-11.253	MSTRG.31061.1	-2.440	MSTRG.24454.1	-1.529
MSTRG.20597.1	-11.175	MSTRG.37188.1	-2.439	MSTRG.36079.1	-1.528
MSTRG.24346.1	-11.151	MSTRG.37450.2	-2.439	MSTRG.19488.1	-1.527
MSTRG.26379.4	-11.143	MSTRG.7446.1	-2.437	MSTRG.44171.1	-1.527
MSTRG.26391.4	-11.131	MSTRG.2212.1	-2.437	MSTRG.6417.1	-1.526
MSTRG.19339.2	-11.042	MSTRG.37954.2	-2.432	MSTRG.35611.2	-1.526
MSTRG.22859.2	-11.041	MSTRG.40552.1	-2.430	MSTRG.40979.2	-1.526
MSTRG.29004.4	-10.984	MSTRG.15179.1	-2.429	MSTRG.13548.1	-1.526
MSTRG.30384.1	-10.934	MSTRG.11806.1	-2.429	MSTRG.35611.4	-1.525
MSTRG.33771.1	-10.930	MSTRG.37492.1	-2.428	MSTRG.27389.1	-1.524
MSTRG.20533.1	-10.925	MSTRG.29165.1	-2.427	MSTRG.14576.10	-1.524
MSTRG.28006.1	-10.891	MSTRG.44326.1	-2.426	MSTRG.552.1	-1.523
MSTRG.17681.1	-10.804	MSTRG.7911.2	-2.426	MSTRG.35691.1	-1.522
MSTRG.21403.7	-10.709	MSTRG.28490.1	-2.425	MSTRG.35723.1	-1.522
MSTRG.48251.1	-10.688	MSTRG.33007.2	-2.425	MSTRG.20271.1	-1.522
MSTRG.8938.1	-10.680	MSTRG.511.3	-2.423	MSTRG.43143.1	-1.520
MSTRG.29742.1	-10.674	MSTRG.48731.1	-2.422	MSTRG.41961.1	-1.520
MSTRG.22845.2	-10.659	MSTRG.22976.1	-2.421	MSTRG.9123.1	-1.520
MSTRG.27417.1	-10.633	MSTRG.7936.1	-2.418	MSTRG.39964.2	-1.518
MSTRG.39061.1	-10.628	MSTRG.6153.1	-2.415	MSTRG.8015.1	-1.518
MSTRG.47594.1	-10.622	MSTRG.13596.1	-2.413	MSTRG.30895.1	-1.517
MSTRG.10111.1	-10.579	MSTRG.38457.1	-2.413	MSTRG.36663.2	-1.517
MSTRG.33773.2	-10.545	MSTRG.46932.3	-2.412	MSTRG.39440.1	-1.517
MSTRG.29735.4	-10.513	MSTRG.554.1	-2.412	MSTRG.19636.5	-1.516

MSTRG.3925.5	-10.408	MSTRG.29729.1	-2.411	MSTRG.22483.1	-1.516
MSTRG.45566.2	-10.355	MSTRG.31667.1	-2.410	MSTRG.14368.1	-1.515
MSTRG.656.1	-10.340	MSTRG.31969.1	-2.410	MSTRG.38051.2	-1.514
MSTRG.10045.1	-10.335	MSTRG.14725.1	-2.409	MSTRG.22975.2	-1.514
MSTRG.47987.1	-10.327	MSTRG.15380.1	-2.409	MSTRG.19715.1	-1.511
MSTRG.16864.15	-10.319	MSTRG.9653.1	-2.408	MSTRG.9448.1	-1.509
MSTRG.28060.2	-10.276	MSTRG.10011.2	-2.406	MSTRG.7972.2	-1.509
MSTRG.266.2	-10.254	MSTRG.47522.1	-2.403	MSTRG.34691.1	-1.509
MSTRG.8806.1	-10.062	MSTRG.19626.2	-2.399	MSTRG.10477.1	-1.508
MSTRG.21789.2	-10.060	MSTRG.32037.1	-2.398	MSTRG.47029.1	-1.508
MSTRG.25900.1	-10.015	MSTRG.11435.1	-2.396	MSTRG.43401.1	-1.508
MSTRG.10370.1	-10.010	MSTRG.41905.1	-2.393	MSTRG.5025.1	-1.508
MSTRG.33933.14	-9.908	MSTRG.10187.1	-2.393	MSTRG.206.1	-1.506
MSTRG.42482.1	-9.858	MSTRG.4120.1	-2.392	MSTRG.11744.1	-1.505
MSTRG.13101.18	-9.851	MSTRG.39673.1	-2.392	MSTRG.23977.1	-1.505
MSTRG.8796.8	-9.826	MSTRG.42830.1	-2.390	MSTRG.45394.1	-1.504
MSTRG.2277.1	-9.775	MSTRG.36473.1	-2.389	MSTRG.503.2	-1.503
MSTRG.26391.3	-9.736	MSTRG.28767.1	-2.387	MSTRG.27870.1	-1.503
MSTRG.4007.1	-9.731	MSTRG.34855.1	-2.387	MSTRG.39192.3	-1.503
MSTRG.37444.1	-9.661	MSTRG.40585.1	-2.380	MSTRG.39735.1	-1.503
MSTRG.39151.2	-9.590	MSTRG.30783.1	-2.379	MSTRG.47026.2	-1.503
MSTRG.27114.4	-9.580	MSTRG.32793.1	-2.379	MSTRG.21946.1	-1.502
MSTRG.23216.4	-9.559	MSTRG.22805.1	-2.374	MSTRG.29155.1	-1.501
MSTRG.25656.1	-9.466	MSTRG.8789.1	-2.373	MSTRG.17675.1	-1.500
MSTRG.15308.1	-9.391	MSTRG.8050.1	-2.370	MSTRG.31131.1	-1.498
MSTRG.29231.1	-9.388	MSTRG.43739.1	-2.369	MSTRG.15672.1	-1.498
MSTRG.14835.2	-9.343	MSTRG.42343.1	-2.368	MSTRG.38386.1	-1.498

MSTRG.20191.2	-9.335	MSTRG.1260.1	-2.368	MSTRG.28451.1	-1.497
MSTRG.9816.1	-9.265	MSTRG.21536.2	-2.365	MSTRG.12035.1	-1.496
MSTRG.27200.1	-9.218	MSTRG.26083.3	-2.365	MSTRG.19716.1	-1.495
MSTRG.45851.6	-9.133	MSTRG.17703.1	-2.364	MSTRG.47379.1	-1.495
MSTRG.47521.3	-9.115	MSTRG.31089.1	-2.361	MSTRG.13369.1	-1.494
MSTRG.15941.2	-8.994	MSTRG.38120.1	-2.360	MSTRG.46403.1	-1.493
MSTRG.32016.2	-8.981	MSTRG.1222.2	-2.360	MSTRG.45549.1	-1.493
MSTRG.13786.3	-8.901	MSTRG.39924.1	-2.358	MSTRG.18607.1	-1.492
MSTRG.39912.1	-8.854	MSTRG.15956.1	-2.358	MSTRG.19163.1	-1.492
MSTRG.16514.1	-8.801	MSTRG.2432.1	-2.358	MSTRG.21796.2	-1.491
MSTRG.41294.1	-8.764	MSTRG.45567.2	-2.355	MSTRG.11450.5	-1.489
MSTRG.40841.2	-8.725	MSTRG.20683.1	-2.354	MSTRG.4282.1	-1.488
MSTRG.34063.1	-8.491	MSTRG.5255.1	-2.352	MSTRG.12742.1	-1.488
MSTRG.25073.2	-8.351	MSTRG.9527.1	-2.351	MSTRG.10545.1	-1.487
MSTRG.18368.2	-8.235	MSTRG.48503.1	-2.351	MSTRG.44604.4	-1.487
MSTRG.5340.2	-8.221	MSTRG.44305.1	-2.349	MSTRG.43286.1	-1.487
MSTRG.33757.2	-8.159	MSTRG.9628.1	-2.349	MSTRG.17929.1	-1.486
MSTRG.5482.1	-8.030	MSTRG.5316.10	-2.348	MSTRG.7710.11	-1.486
MSTRG.16931.5	-8.005	MSTRG.21323.1	-2.346	MSTRG.23965.1	-1.485
MSTRG.12679.2	-7.985	MSTRG.35309.1	-2.346	MSTRG.41692.1	-1.484
MSTRG.11010.1	-7.985	MSTRG.38344.1	-2.346	MSTRG.20482.1	-1.483
MSTRG.18650.1	-7.952	MSTRG.13622.1	-2.345	MSTRG.28797.1	-1.483
MSTRG.33377.3	-7.946	MSTRG.28605.5	-2.344	MSTRG.38518.1	-1.482
MSTRG.10222.8	-7.839	MSTRG.8737.1	-2.343	MSTRG.45936.1	-1.482
MSTRG.27306.1	-7.788	MSTRG.16222.2	-2.343	MSTRG.8842.1	-1.481
MSTRG.31711.2	-7.531	MSTRG.39695.1	-2.341	MSTRG.30033.3	-1.480
MSTRG.43491.1	-7.501	MSTRG.23175.1	-2.339	MSTRG.40008.1	-1.480

MSTRG.29294.3	-7.493	MSTRG.11059.1	-2.335	MSTRG.43446.1	-1.479
MSTRG.18052.2	-7.406	MSTRG.7078.1	-2.334	MSTRG.10000.1	-1.479
MSTRG.30986.1	-7.374	MSTRG.27649.8	-2.333	MSTRG.45078.1	-1.478
MSTRG.42597.1	-7.277	MSTRG.13355.1	-2.332	MSTRG.35392.1	-1.478
MSTRG.16921.17	-7.275	MSTRG.33243.4	-2.332	MSTRG.33031.1	-1.477
MSTRG.19630.9	-7.228	MSTRG.10220.4	-2.332	MSTRG.37001.1	-1.476
MSTRG.20437.3	-7.205	MSTRG.39541.1	-2.331	MSTRG.28036.1	-1.476
MSTRG.301.2	-7.178	MSTRG.17878.1	-2.330	MSTRG.10921.1	-1.474
MSTRG.27422.2	-7.169	MSTRG.29268.1	-2.330	MSTRG.47846.8	-1.473
MSTRG.23359.11	-7.143	MSTRG.26768.2	-2.328	MSTRG.2440.1	-1.472
MSTRG.8454.2	-7.116	MSTRG.47450.1	-2.328	MSTRG.3289.1	-1.472
MSTRG.6861.4	-7.060	MSTRG.46394.3	-2.328	MSTRG.43261.13	-1.471
MSTRG.33174.18	-7.036	MSTRG.45797.1	-2.326	MSTRG.16218.1	-1.468
MSTRG.48760.2	-6.999	MSTRG.6607.1	-2.325	MSTRG.28491.1	-1.468
MSTRG.28273.1	-6.968	MSTRG.27342.1	-2.325	MSTRG.1100.1	-1.468
MSTRG.4807.17	-6.931	MSTRG.34252.1	-2.322	MSTRG.5905.2	-1.464
MSTRG.39491.2	-6.918	MSTRG.4529.2	-2.319	MSTRG.46652.1	-1.463
MSTRG.34197.1	-6.903	MSTRG.37287.1	-2.317	MSTRG.45563.3	-1.462
MSTRG.33510.2	-6.869	MSTRG.14024.4	-2.317	MSTRG.38983.1	-1.462
MSTRG.27578.1	-6.821	MSTRG.36103.2	-2.317	MSTRG.12182.6	-1.460
MSTRG.4884.3	-6.784	MSTRG.36330.1	-2.315	MSTRG.1827.7	-1.460
MSTRG.9883.3	-6.768	MSTRG.29872.1	-2.315	MSTRG.22579.1	-1.460
MSTRG.39674.3	-6.765	MSTRG.28784.1	-2.314	MSTRG.32002.1	-1.459
MSTRG.16726.1	-6.749	MSTRG.6152.1	-2.314	MSTRG.15872.9	-1.459
MSTRG.3925.4	-6.742	MSTRG.4339.1	-2.309	MSTRG.10685.3	-1.458
MSTRG.12272.1	-6.740	MSTRG.6184.1	-2.309	MSTRG.39818.2	-1.458
MSTRG.18168.5	-6.711	MSTRG.5179.2	-2.305	MSTRG.38357.1	-1.458

MSTRG.10064.1	-6.706	MSTRG.24739.1	-2.304	MSTRG.28784.2	-1.458
MSTRG.437.3	-6.703	MSTRG.9669.10	-2.302	MSTRG.32580.1	-1.457
MSTRG.20491.2	-6.658	MSTRG.40816.1	-2.302	MSTRG.7500.1	-1.456
MSTRG.48339.1	-6.625	MSTRG.4115.1	-2.300	MSTRG.27445.1	-1.455
MSTRG.31160.2	-6.609	MSTRG.3169.1	-2.300	MSTRG.36896.3	-1.453
MSTRG.19964.10	-6.604	MSTRG.12828.1	-2.299	MSTRG.42751.1	-1.452
MSTRG.9679.12	-6.556	MSTRG.5041.1	-2.299	MSTRG.44897.1	-1.452
MSTRG.34443.2	-6.455	MSTRG.21240.2	-2.298	MSTRG.25718.1	-1.452
MSTRG.16253.5	-6.453	MSTRG.4406.1	-2.297	MSTRG.25120.4	-1.451
MSTRG.22851.2	-6.452	MSTRG.32665.1	-2.297	MSTRG.32038.1	-1.450
MSTRG.33723.4	-6.446	MSTRG.6421.1	-2.294	MSTRG.17386.1	-1.447
MSTRG.36820.6	-6.439	MSTRG.2626.1	-2.294	MSTRG.30790.1	-1.447
MSTRG.273.2	-6.404	MSTRG.40176.1	-2.293	MSTRG.41616.1	-1.447
MSTRG.25327.3	-6.370	MSTRG.1504.1	-2.291	MSTRG.39703.1	-1.445
MSTRG.2082.1	-6.362	MSTRG.6152.2	-2.290	MSTRG.25053.3	-1.445
MSTRG.31160.5	-6.361	MSTRG.35979.1	-2.287	MSTRG.27013.1	-1.445
MSTRG.46170.31	-6.358	MSTRG.8267.1	-2.286	MSTRG.22294.1	-1.444
MSTRG.37402.4	-6.352	MSTRG.11605.6	-2.286	MSTRG.42655.1	-1.444
MSTRG.26863.1	-6.282	MSTRG.13704.1	-2.285	MSTRG.26713.3	-1.444
MSTRG.34910.3	-6.251	MSTRG.27007.1	-2.283	MSTRG.5601.16	-1.443
MSTRG.36783.1	-6.214	MSTRG.40250.1	-2.282	MSTRG.8499.1	-1.442
MSTRG.12712.1	-6.208	MSTRG.48646.1	-2.281	MSTRG.5497.1	-1.442
MSTRG.657.2	-6.114	MSTRG.5179.1	-2.280	MSTRG.5396.1	-1.441
MSTRG.27410.1	-6.101	MSTRG.34901.4	-2.278	MSTRG.6378.1	-1.441
MSTRG.15603.2	-6.099	MSTRG.26665.1	-2.278	MSTRG.39316.1	-1.441
MSTRG.36953.1	-6.078	MSTRG.2575.1	-2.276	MSTRG.29619.1	-1.440
MSTRG.9592.6	-6.075	MSTRG.8356.1	-2.276	MSTRG.36044.1	-1.440

MSTRG.35690.1	-6.068	MSTRG.9199.7	-2.275	MSTRG.33910.1	-1.439
MSTRG.23169.1	-6.046	MSTRG.26751.1	-2.274	MSTRG.31920.1	-1.439
MSTRG.38812.2	-6.032	MSTRG.48697.1	-2.274	MSTRG.47493.1	-1.439
MSTRG.8703.2	-5.972	MSTRG.9335.3	-2.274	MSTRG.1695.3	-1.439
MSTRG.22309.5	-5.954	MSTRG.8599.1	-2.273	MSTRG.12456.1	-1.439
MSTRG.7581.2	-5.941	MSTRG.36802.1	-2.273	MSTRG.11450.2	-1.438
MSTRG.92.2	-5.934	MSTRG.8269.1	-2.269	MSTRG.17530.1	-1.437
MSTRG.45571.2	-5.924	MSTRG.511.1	-2.268	MSTRG.45308.1	-1.436
MSTRG.32001.1	-5.907	MSTRG.22100.1	-2.266	MSTRG.509.1	-1.436
MSTRG.34562.1	-5.875	MSTRG.10690.1	-2.265	MSTRG.8889.1	-1.435
MSTRG.39910.1	-5.845	MSTRG.17355.1	-2.265	MSTRG.30975.2	-1.435
MSTRG.32596.5	-5.820	MSTRG.27946.1	-2.263	MSTRG.8083.4	-1.432
MSTRG.41553.10	-5.811	MSTRG.44329.1	-2.260	MSTRG.8357.2	-1.431
MSTRG.26632.1	-5.798	MSTRG.17513.1	-2.259	MSTRG.8783.2	-1.431
MSTRG.15811.1	-5.790	MSTRG.27622.1	-2.259	MSTRG.28043.2	-1.430
MSTRG.22166.6	-5.787	MSTRG.16390.3	-2.258	MSTRG.23742.1	-1.429
MSTRG.45966.5	-5.780	MSTRG.4530.1	-2.256	MSTRG.46018.13	-1.429
MSTRG.36080.1	-5.722	MSTRG.33389.1	-2.255	MSTRG.10592.1	-1.429
MSTRG.30539.7	-5.682	MSTRG.22884.3	-2.254	MSTRG.38525.1	-1.427
MSTRG.23990.1	-5.673	MSTRG.30281.1	-2.252	MSTRG.22348.1	-1.427
MSTRG.24736.2	-5.645	MSTRG.42391.1	-2.250	MSTRG.473.3	-1.426
MSTRG.28503.1	-5.619	MSTRG.33007.3	-2.249	MSTRG.10151.1	-1.424
MSTRG.17511.1	-5.594	MSTRG.24634.2	-2.247	MSTRG.6357.2	-1.424
MSTRG.9221.1	-5.590	MSTRG.10692.1	-2.247	MSTRG.43469.1	-1.423
MSTRG.24943.2	-5.556	MSTRG.6236.1	-2.247	MSTRG.33120.1	-1.423
MSTRG.48760.3	-5.549	MSTRG.13266.1	-2.246	MSTRG.15415.1	-1.422
MSTRG.19810.1	-5.542	MSTRG.26407.1	-2.245	MSTRG.32327.1	-1.421

MSTRG.22664.3	-5.539	MSTRG.19078.1	-2.245	MSTRG.18457.1	-1.420
MSTRG.26466.3	-5.532	MSTRG.29020.1	-2.245	MSTRG.33667.1	-1.419
MSTRG.30949.2	-5.514	MSTRG.16385.2	-2.243	MSTRG.48269.1	-1.418
MSTRG.7892.1	-5.506	MSTRG.41094.3	-2.242	MSTRG.37454.1	-1.418
MSTRG.24722.2	-5.499	MSTRG.33174.3	-2.242	MSTRG.43842.7	-1.417
MSTRG.19506.1	-5.485	MSTRG.41224.2	-2.242	MSTRG.47660.1	-1.416
MSTRG.33311.2	-5.471	MSTRG.22479.2	-2.242	MSTRG.41906.1	-1.415
MSTRG.15859.1	-5.456	MSTRG.12787.1	-2.242	MSTRG.9599.2	-1.415
MSTRG.15860.1	-5.451	MSTRG.28973.1	-2.240	MSTRG.23139.1	-1.415
MSTRG.30490.4	-5.416	MSTRG.15379.1	-2.239	MSTRG.14225.1	-1.414
MSTRG.32617.2	-5.403	MSTRG.611.1	-2.238	MSTRG.26647.1	-1.411
MSTRG.9078.1	-5.371	MSTRG.46669.1	-2.238	MSTRG.33912.1	-1.410
MSTRG.16178.1	-5.359	MSTRG.20629.1	-2.235	MSTRG.9863.1	-1.409
MSTRG.27844.2	-5.358	MSTRG.2226.1	-2.233	MSTRG.29602.2	-1.409
MSTRG.43479.1	-5.358	MSTRG.26899.1	-2.233	MSTRG.24927.1	-1.408
MSTRG.5193.4	-5.357	MSTRG.16529.6	-2.231	MSTRG.12131.1	-1.408
MSTRG.14948.4	-5.348	MSTRG.28698.1	-2.229	MSTRG.23144.1	-1.408
MSTRG.9204.1	-5.343	MSTRG.16309.1	-2.228	MSTRG.24225.1	-1.408
MSTRG.20582.1	-5.338	MSTRG.17754.1	-2.227	MSTRG.42877.1	-1.408
MSTRG.30031.3	-5.313	MSTRG.3989.2	-2.226	MSTRG.44293.1	-1.407
MSTRG.45480.1	-5.291	MSTRG.30285.4	-2.225	MSTRG.11155.1	-1.404
MSTRG.33040.2	-5.260	MSTRG.38670.3	-2.224	MSTRG.21044.1	-1.403
MSTRG.28280.2	-5.214	MSTRG.18160.1	-2.224	MSTRG.27047.1	-1.402
MSTRG.9164.1	-5.208	MSTRG.46604.1	-2.223	MSTRG.10084.1	-1.402
MSTRG.15663.7	-5.202	MSTRG.29709.4	-2.223	MSTRG.3521.1	-1.402
MSTRG.494.2	-5.195	MSTRG.36123.5	-2.220	MSTRG.14643.1	-1.401
MSTRG.23763.8	-5.184	MSTRG.15670.1	-2.219	MSTRG.32050.1	-1.399

MSTRG.10368.1	-5.175	MSTRG.43766.1	-2.219	MSTRG.29683.1	-1.399
MSTRG.13055.1	-5.156	MSTRG.28479.1	-2.218	MSTRG.19057.1	-1.399
MSTRG.31215.1	-5.154	MSTRG.25330.3	-2.217	MSTRG.28195.1	-1.398
MSTRG.24336.3	-5.153	MSTRG.27807.1	-2.216	MSTRG.7798.1	-1.397
MSTRG.11608.2	-5.137	MSTRG.24749.1	-2.214	MSTRG.47083.1	-1.397
MSTRG.2422.1	-5.135	MSTRG.35999.1	-2.214	MSTRG.22355.1	-1.397
MSTRG.8556.1	-5.133	MSTRG.10557.6	-2.214	MSTRG.18886.1	-1.397
MSTRG.27987.1	-5.102	MSTRG.21266.1	-2.213	MSTRG.22908.1	-1.396
MSTRG.39550.8	-5.060	MSTRG.33353.3	-2.203	MSTRG.13492.1	-1.396
MSTRG.16474.6	-5.060	MSTRG.38742.1	-2.202	MSTRG.22975.3	-1.395
MSTRG.19462.2	-5.053	MSTRG.24917.4	-2.199	MSTRG.6846.1	-1.395
MSTRG.24373.1	-5.050	MSTRG.16650.1	-2.199	MSTRG.13367.1	-1.394
MSTRG.38438.1	-5.050	MSTRG.20792.1	-2.198	MSTRG.45795.1	-1.394
MSTRG.28113.3	-5.040	MSTRG.48283.2	-2.197	MSTRG.36490.1	-1.393
MSTRG.12074.1	-5.039	MSTRG.14027.5	-2.197	MSTRG.20887.1	-1.391
MSTRG.40505.1	-5.039	MSTRG.10295.1	-2.195	MSTRG.19363.1	-1.391
MSTRG.40097.6	-4.991	MSTRG.33353.5	-2.195	MSTRG.22988.1	-1.390
MSTRG.1352.1	-4.988	MSTRG.42318.9	-2.193	MSTRG.20628.1	-1.390
MSTRG.8882.1	-4.987	MSTRG.28015.1	-2.193	MSTRG.36019.2	-1.390
MSTRG.26059.4	-4.961	MSTRG.8914.2	-2.192	MSTRG.29535.1	-1.389
MSTRG.508.5	-4.943	MSTRG.34305.1	-2.191	MSTRG.16428.1	-1.389
MSTRG.42112.1	-4.928	MSTRG.41930.1	-2.191	MSTRG.1262.1	-1.389
MSTRG.21574.2	-4.917	MSTRG.15724.1	-2.188	MSTRG.22176.1	-1.388
MSTRG.11796.13	-4.909	MSTRG.11290.1	-2.188	MSTRG.26584.3	-1.388
MSTRG.45504.1	-4.908	MSTRG.42989.1	-2.188	MSTRG.37094.1	-1.388
MSTRG.17642.1	-4.908	MSTRG.36331.1	-2.187	MSTRG.29812.1	-1.388
MSTRG.16169.2	-4.899	MSTRG.19495.1	-2.185	MSTRG.7977.1	-1.387

MSTRG.36955.1	-4.892	MSTRG.7930.5	-2.184	MSTRG.40042.1	-1.387
MSTRG.31609.4	-4.882	MSTRG.32032.1	-2.183	MSTRG.22880.1	-1.386
MSTRG.28605.4	-4.872	MSTRG.27465.1	-2.183	MSTRG.10913.1	-1.384
MSTRG.30657.4	-4.869	MSTRG.22481.1	-2.182	MSTRG.40557.2	-1.384
MSTRG.30004.1	-4.868	MSTRG.29297.1	-2.182	MSTRG.13502.1	-1.383
MSTRG.5988.1	-4.863	MSTRG.1534.7	-2.181	MSTRG.26007.1	-1.381
MSTRG.27109.4	-4.859	MSTRG.22480.1	-2.181	MSTRG.38739.1	-1.379
MSTRG.40789.1	-4.859	MSTRG.24194.2	-2.180	MSTRG.41231.1	-1.379
MSTRG.8413.1	-4.852	MSTRG.47450.4	-2.180	MSTRG.396.1	-1.379
MSTRG.4437.2	-4.846	MSTRG.16784.1	-2.178	MSTRG.28184.1	-1.379
MSTRG.21568.3	-4.831	MSTRG.5601.2	-2.175	MSTRG.14194.1	-1.378
MSTRG.41329.15	-4.827	MSTRG.34289.1	-2.174	MSTRG.3894.1	-1.377
MSTRG.6762.1	-4.824	MSTRG.31898.2	-2.173	MSTRG.42963.1	-1.377
MSTRG.508.4	-4.817	MSTRG.24458.1	-2.168	MSTRG.15599.1	-1.376
MSTRG.21043.3	-4.813	MSTRG.36066.4	-2.168	MSTRG.36311.1	-1.376
MSTRG.30319.3	-4.796	MSTRG.42527.2	-2.168	MSTRG.4265.1	-1.375
MSTRG.48760.1	-4.785	MSTRG.14001.1	-2.168	MSTRG.48696.1	-1.375
MSTRG.36224.2	-4.778	MSTRG.18337.1	-2.165	MSTRG.25023.1	-1.375
MSTRG.27714.1	-4.776	MSTRG.41750.4	-2.164	MSTRG.3559.2	-1.374
MSTRG.40098.1	-4.773	MSTRG.35050.1	-2.164	MSTRG.31595.1	-1.374
MSTRG.5987.1	-4.766	MSTRG.4766.1	-2.164	MSTRG.15782.1	-1.374
MSTRG.13030.1	-4.754	MSTRG.10381.1	-2.163	MSTRG.44639.1	-1.372
MSTRG.16797.1	-4.743	MSTRG.36631.1	-2.162	MSTRG.32123.1	-1.372
MSTRG.39491.1	-4.741	MSTRG.17828.1	-2.161	MSTRG.17389.1	-1.372
MSTRG.16133.1	-4.740	MSTRG.12889.1	-2.161	MSTRG.6249.1	-1.371
MSTRG.3586.4	-4.737	MSTRG.28932.1	-2.160	MSTRG.3980.1	-1.371
MSTRG.7668.1	-4.698	MSTRG.27584.2	-2.160	MSTRG.1375.1	-1.370

MSTRG.29905.3	-4.696	MSTRG.34364.1	-2.158	MSTRG.14027.4	-1.370
MSTRG.12061.1	-4.694	MSTRG.21631.1	-2.157	MSTRG.38276.1	-1.370
MSTRG.46893.3	-4.689	MSTRG.38590.1	-2.157	MSTRG.43944.2	-1.369
MSTRG.11796.11	-4.674	MSTRG.23960.1	-2.156	MSTRG.23170.1	-1.369
MSTRG.29220.13	-4.668	MSTRG.48246.2	-2.154	MSTRG.42757.1	-1.369
MSTRG.5850.2	-4.668	MSTRG.1696.1	-2.153	MSTRG.44289.1	-1.369
MSTRG.12758.2	-4.668	MSTRG.23841.1	-2.153	MSTRG.20708.6	-1.368
MSTRG.18911.1	-4.660	MSTRG.5514.1	-2.152	MSTRG.3632.1	-1.368
MSTRG.19160.2	-4.655	MSTRG.19124.2	-2.152	MSTRG.41197.1	-1.368
MSTRG.22004.2	-4.654	MSTRG.34572.2	-2.151	MSTRG.30294.2	-1.367
MSTRG.11853.4	-4.652	MSTRG.10912.1	-2.150	MSTRG.10082.1	-1.367
MSTRG.17573.1	-4.649	MSTRG.46574.2	-2.149	MSTRG.33154.4	-1.365
MSTRG.613.1	-4.639	MSTRG.15434.4	-2.148	MSTRG.45519.1	-1.364
MSTRG.35251.1	-4.636	MSTRG.42010.2	-2.148	MSTRG.11805.2	-1.363
MSTRG.44824.6	-4.626	MSTRG.45970.1	-2.147	MSTRG.5040.1	-1.363
MSTRG.2480.1	-4.608	MSTRG.42010.1	-2.144	MSTRG.26439.1	-1.363
MSTRG.23550.3	-4.604	MSTRG.21440.1	-2.144	MSTRG.19086.1	-1.363
MSTRG.33679.1	-4.597	MSTRG.26081.1	-2.144	MSTRG.39596.1	-1.363
MSTRG.15685.1	-4.580	MSTRG.16144.1	-2.144	MSTRG.947.1	-1.363
MSTRG.30984.4	-4.575	MSTRG.107.3	-2.143	MSTRG.4043.1	-1.362
MSTRG.41606.2	-4.571	MSTRG.33480.1	-2.141	MSTRG.39343.2	-1.361
MSTRG.22360.2	-4.567	MSTRG.12253.2	-2.140	MSTRG.46112.1	-1.359
MSTRG.40531.5	-4.566	MSTRG.9718.1	-2.140	MSTRG.36005.1	-1.358
MSTRG.44022.1	-4.559	MSTRG.27861.1	-2.140	MSTRG.2340.2	-1.356
MSTRG.25555.5	-4.558	MSTRG.14803.1	-2.139	MSTRG.11796.81	-1.356
MSTRG.10744.2	-4.543	MSTRG.45766.1	-2.138	MSTRG.27717.1	-1.356
MSTRG.44041.1	-4.527	MSTRG.35611.8	-2.138	MSTRG.5773.1	-1.356

MSTRG.19023.1	-4.515	MSTRG.22927.1	-2.137	MSTRG.45034.2	-1.355
MSTRG.7012.4	-4.514	MSTRG.4531.1	-2.137	MSTRG.19961.1	-1.355
MSTRG.12068.3	-4.502	MSTRG.25823.1	-2.136	MSTRG.21019.2	-1.354
MSTRG.6070.1	-4.490	MSTRG.46017.1	-2.133	MSTRG.3639.1	-1.354
MSTRG.234.2	-4.489	MSTRG.29167.2	-2.133	MSTRG.472.1	-1.352
MSTRG.32221.1	-4.484	MSTRG.25672.1	-2.130	MSTRG.47364.2	-1.352
MSTRG.30781.1	-4.482	MSTRG.3444.3	-2.130	MSTRG.7217.1	-1.352
MSTRG.16864.14	-4.475	MSTRG.33174.12	-2.129	MSTRG.3295.1	-1.351
MSTRG.10041.1	-4.470	MSTRG.8355.1	-2.129	MSTRG.13311.1	-1.350
MSTRG.41412.1	-4.467	MSTRG.47851.1	-2.128	MSTRG.37177.2	-1.350
MSTRG.35565.5	-4.464	MSTRG.17407.1	-2.125	MSTRG.8574.1	-1.350
MSTRG.12113.1	-4.462	MSTRG.33411.1	-2.124	MSTRG.255.1	-1.350
MSTRG.38363.1	-4.462	MSTRG.33355.1	-2.124	MSTRG.29439.1	-1.348
MSTRG.6577.1	-4.444	MSTRG.26401.1	-2.122	MSTRG.13091.1	-1.348
MSTRG.24214.1	-4.439	MSTRG.26282.1	-2.121	MSTRG.21416.1	-1.347
MSTRG.18327.1	-4.427	MSTRG.39265.1	-2.118	MSTRG.39831.1	-1.346
MSTRG.4365.1	-4.421	MSTRG.9656.1	-2.117	MSTRG.44578.1	-1.346
MSTRG.9793.3	-4.413	MSTRG.3279.4	-2.117	MSTRG.1415.1	-1.345
MSTRG.6587.1	-4.406	MSTRG.30439.1	-2.115	MSTRG.1416.1	-1.345
MSTRG.10909.1	-4.402	MSTRG.18687.1	-2.115	MSTRG.6770.1	-1.345
MSTRG.42912.1	-4.401	MSTRG.1223.1	-2.115	MSTRG.9322.9	-1.345
MSTRG.47615.1	-4.401	MSTRG.2880.1	-2.113	MSTRG.7111.1	-1.345
MSTRG.12903.1	-4.389	MSTRG.27731.1	-2.112	MSTRG.31863.2	-1.345
MSTRG.43517.1	-4.373	MSTRG.18850.2	-2.111	MSTRG.2545.1	-1.343
MSTRG.45616.1	-4.369	MSTRG.789.2	-2.110	MSTRG.24876.1	-1.343
MSTRG.14194.3	-4.363	MSTRG.28916.1	-2.109	MSTRG.3497.1	-1.342
MSTRG.5193.2	-4.361	MSTRG.18850.1	-2.108	MSTRG.30568.1	-1.342

MSTRG.48134.2	-4.345	MSTRG.4142.1	-2.108	MSTRG.43722.2	-1.342
MSTRG.17318.5	-4.336	MSTRG.42630.1	-2.108	MSTRG.21861.1	-1.341
MSTRG.34997.6	-4.323	MSTRG.31490.2	-2.108	MSTRG.21202.1	-1.341
MSTRG.38163.1	-4.322	MSTRG.38102.1	-2.106	MSTRG.890.1	-1.340
MSTRG.26065.1	-4.321	MSTRG.21648.1	-2.106	MSTRG.234.1	-1.340
MSTRG.31505.1	-4.321	MSTRG.47451.1	-2.106	MSTRG.9024.2	-1.338
MSTRG.10447.11	-4.321	MSTRG.11796.66	-2.104	MSTRG.19950.1	-1.335
MSTRG.13640.6	-4.316	MSTRG.13959.1	-2.103	MSTRG.6175.1	-1.335
MSTRG.5150.2	-4.300	MSTRG.35729.1	-2.100	MSTRG.14370.1	-1.334
MSTRG.39958.1	-4.298	MSTRG.1588.5	-2.099	MSTRG.1246.2	-1.333
MSTRG.23909.2	-4.296	MSTRG.44778.1	-2.098	MSTRG.30555.1	-1.333
MSTRG.27972.1	-4.291	MSTRG.29683.3	-2.096	MSTRG.26959.2	-1.332
MSTRG.42302.1	-4.288	MSTRG.44821.5	-2.095	MSTRG.2212.5	-1.330
MSTRG.48519.6	-4.284	MSTRG.756.3	-2.095	MSTRG.21746.1	-1.330
MSTRG.45851.5	-4.282	MSTRG.30691.1	-2.095	MSTRG.35238.1	-1.329
MSTRG.14983.2	-4.274	MSTRG.45884.1	-2.091	MSTRG.5561.1	-1.329
MSTRG.41553.7	-4.274	MSTRG.8598.1	-2.091	MSTRG.34303.1	-1.328
MSTRG.4250.4	-4.273	MSTRG.42319.1	-2.088	MSTRG.4996.1	-1.326
MSTRG.37345.3	-4.255	MSTRG.37326.1	-2.088	MSTRG.23560.1	-1.326
MSTRG.35230.3	-4.247	MSTRG.26769.1	-2.087	MSTRG.34901.1	-1.326
MSTRG.508.1	-4.243	MSTRG.10685.4	-2.087	MSTRG.1479.2	-1.325
MSTRG.22591.3	-4.242	MSTRG.27861.3	-2.086	MSTRG.7407.1	-1.324
MSTRG.19682.2	-4.237	MSTRG.6391.5	-2.083	MSTRG.23321.1	-1.324
MSTRG.35596.1	-4.237	MSTRG.6150.12	-2.083	MSTRG.57.2	-1.324
MSTRG.40097.8	-4.222	MSTRG.21291.1	-2.082	MSTRG.39168.3	-1.324
MSTRG.6391.2	-4.219	MSTRG.34424.1	-2.082	MSTRG.30512.1	-1.323
MSTRG.45567.7	-4.208	MSTRG.39086.1	-2.081	MSTRG.31043.1	-1.322

MSTRG.31952.1	-4.202	MSTRG.41103.1	-2.080	MSTRG.47552.1	-1.320
MSTRG.41778.1	-4.192	MSTRG.9707.1	-2.079	MSTRG.20337.2	-1.319
MSTRG.6187.1	-4.187	MSTRG.9653.2	-2.079	MSTRG.32441.1	-1.319
MSTRG.15649.1	-4.184	MSTRG.32762.1	-2.078	MSTRG.9179.1	-1.317
MSTRG.33386.1	-4.169	MSTRG.25590.3	-2.077	MSTRG.4075.1	-1.315
MSTRG.18281.2	-4.167	MSTRG.5958.1	-2.076	MSTRG.47228.1	-1.315
MSTRG.30003.2	-4.165	MSTRG.4138.2	-2.072	MSTRG.41885.1	-1.314
MSTRG.45264.1	-4.164	MSTRG.44325.1	-2.071	MSTRG.13655.1	-1.313
MSTRG.21108.1	-4.163	MSTRG.44168.5	-2.070	MSTRG.11688.1	-1.313
MSTRG.7005.1	-4.162	MSTRG.38342.1	-2.069	MSTRG.169.1	-1.312
MSTRG.30721.1	-4.161	MSTRG.18032.1	-2.069	MSTRG.4917.1	-1.311
MSTRG.30722.1	-4.161	MSTRG.7980.1	-2.066	MSTRG.1393.1	-1.311
MSTRG.43763.1	-4.159	MSTRG.26679.1	-2.066	MSTRG.31378.1	-1.310
MSTRG.22908.2	-4.145	MSTRG.12662.1	-2.064	MSTRG.34532.1	-1.310
MSTRG.33307.3	-4.143	MSTRG.18673.4	-2.064	MSTRG.15606.2	-1.309
MSTRG.10807.1	-4.139	MSTRG.31213.1	-2.063	MSTRG.13604.2	-1.309
MSTRG.19054.1	-4.128	MSTRG.47329.1	-2.061	MSTRG.38414.1	-1.309
MSTRG.31174.2	-4.127	MSTRG.20514.1	-2.061	MSTRG.18895.1	-1.309
MSTRG.709.1	-4.125	MSTRG.8450.1	-2.061	MSTRG.45829.1	-1.308
MSTRG.46913.3	-4.117	MSTRG.48096.1	-2.056	MSTRG.30566.1	-1.304
MSTRG.41269.2	-4.115	MSTRG.20708.4	-2.055	MSTRG.38433.1	-1.303
MSTRG.36289.1	-4.108	MSTRG.16006.1	-2.051	MSTRG.20456.1	-1.302
MSTRG.6660.6	-4.108	MSTRG.5462.1	-2.051	MSTRG.13825.1	-1.301
MSTRG.10886.4	-4.107	MSTRG.24218.1	-2.049	MSTRG.30912.1	-1.301
MSTRG.6186.1	-4.107	MSTRG.30928.1	-2.047	MSTRG.8762.1	-1.300
MSTRG.12758.1	-4.103	MSTRG.10283.1	-2.046	MSTRG.48683.1	-1.300
MSTRG.38934.2	-4.075	MSTRG.13950.1	-2.046	MSTRG.10961.1	-1.299

MSTRG.17294.1	-4.067	MSTRG.43882.1	-2.046	MSTRG.43404.1	-1.299
MSTRG.29351.1	-4.049	MSTRG.16974.1	-2.044	MSTRG.48693.1	-1.298
MSTRG.36299.1	-4.046	MSTRG.33354.1	-2.043	MSTRG.32151.1	-1.298
MSTRG.45567.5	-4.045	MSTRG.37666.2	-2.042	MSTRG.16488.1	-1.297
MSTRG.28104.1	-4.035	MSTRG.29678.1	-2.041	MSTRG.23093.1	-1.297
MSTRG.18327.8	-4.035	MSTRG.47045.3	-2.039	MSTRG.30285.1	-1.297
MSTRG.24657.1	-4.033	MSTRG.28758.1	-2.038	MSTRG.40746.3	-1.296
MSTRG.36820.5	-4.025	MSTRG.33353.2	-2.037	MSTRG.696.1	-1.296
MSTRG.2461.1	-4.023	MSTRG.885.1	-2.037	MSTRG.41112.1	-1.296
MSTRG.6918.1	-4.022	MSTRG.29721.1	-2.036	MSTRG.897.1	-1.295
MSTRG.11797.3	-4.022	MSTRG.872.1	-2.035	MSTRG.11920.1	-1.295
MSTRG.47209.1	-4.016	MSTRG.792.1	-2.033	MSTRG.16908.1	-1.293
MSTRG.47664.1	-4.007	MSTRG.31036.2	-2.032	MSTRG.16481.1	-1.292
MSTRG.24910.1	-4.006	MSTRG.28984.1	-2.031	MSTRG.32593.2	-1.291
MSTRG.5404.1	-4.000	MSTRG.190.1	-2.030	MSTRG.16187.1	-1.291
MSTRG.29849.5	-3.999	MSTRG.3529.1	-2.030	MSTRG.45173.1	-1.290
MSTRG.33054.2	-3.999	MSTRG.15450.1	-2.029	MSTRG.45331.1	-1.289
MSTRG.23405.1	-3.998	MSTRG.20217.3	-2.028	MSTRG.847.1	-1.289
MSTRG.24238.3	-3.983	MSTRG.5855.1	-2.027	MSTRG.22081.1	-1.289
MSTRG.29315.3	-3.979	MSTRG.10042.2	-2.027	MSTRG.29884.1	-1.288
MSTRG.46409.2	-3.975	MSTRG.25661.1	-2.026	MSTRG.43553.1	-1.286
MSTRG.30130.1	-3.973	MSTRG.520.1	-2.025	MSTRG.18751.3	-1.286
MSTRG.46500.5	-3.972	MSTRG.466.1	-2.025	MSTRG.6839.4	-1.285
MSTRG.32305.1	-3.968	MSTRG.37403.1	-2.025	MSTRG.756.7	-1.284
MSTRG.675.1	-3.957	MSTRG.29969.3	-2.024	MSTRG.12033.1	-1.283
MSTRG.27777.6	-3.946	MSTRG.33648.1	-2.022	MSTRG.20183.1	-1.282
MSTRG.44467.1	-3.939	MSTRG.12430.1	-2.022	MSTRG.10878.2	-1.281

MSTRG.33859.3	-3.936	MSTRG.3530.2	-2.022	MSTRG.14459.5	-1.281
MSTRG.13381.1	-3.933	MSTRG.29722.1	-2.021	MSTRG.27523.1	-1.281
MSTRG.21530.1	-3.931	MSTRG.33175.1	-2.020	MSTRG.48496.1	-1.279
MSTRG.26837.2	-3.924	MSTRG.26692.2	-2.018	MSTRG.33119.1	-1.278
MSTRG.10369.1	-3.922	MSTRG.924.1	-2.018	MSTRG.22745.3	-1.278
MSTRG.36300.1	-3.919	MSTRG.42802.1	-2.018	MSTRG.2192.1	-1.278
MSTRG.4942.2	-3.917	MSTRG.7663.1	-2.018	MSTRG.32013.1	-1.277
MSTRG.23404.1	-3.915	MSTRG.45534.1	-2.017	MSTRG.2693.1	-1.277
MSTRG.43032.1	-3.912	MSTRG.38195.3	-2.017	MSTRG.7137.1	-1.276
MSTRG.5561.2	-3.908	MSTRG.6253.1	-2.016	MSTRG.23448.1	-1.275
MSTRG.9285.3	-3.906	MSTRG.25884.1	-2.016	MSTRG.9190.1	-1.275
MSTRG.16831.7	-3.904	MSTRG.5494.1	-2.016	MSTRG.11784.2	-1.275
MSTRG.29102.5	-3.897	MSTRG.4448.3	-2.010	MSTRG.5834.1	-1.274
MSTRG.3000.3	-3.895	MSTRG.46668.1	-2.007	MSTRG.40030.1	-1.273
MSTRG.6104.5	-3.893	MSTRG.14553.1	-2.006	MSTRG.34391.3	-1.271
MSTRG.22678.3	-3.889	MSTRG.45304.1	-2.006	MSTRG.16474.2	-1.271
MSTRG.39710.1	-3.887	MSTRG.13515.3	-2.005	MSTRG.18456.1	-1.269
MSTRG.44936.2	-3.878	MSTRG.28778.1	-2.005	MSTRG.29273.1	-1.268
MSTRG.33291.1	-3.877	MSTRG.28060.1	-2.004	MSTRG.4889.2	-1.267
MSTRG.41118.1	-3.853	MSTRG.11316.1	-2.000	MSTRG.30323.1	-1.266
MSTRG.4985.18	-3.849	MSTRG.48497.1	-1.998	MSTRG.42097.1	-1.265
MSTRG.31788.1	-3.847	MSTRG.19374.1	-1.998	MSTRG.7497.1	-1.265
MSTRG.45264.5	-3.846	MSTRG.17785.2	-1.996	MSTRG.46066.1	-1.264
MSTRG.35597.1	-3.844	MSTRG.46393.3	-1.995	MSTRG.4497.1	-1.264
MSTRG.4320.1	-3.841	MSTRG.39708.2	-1.995	MSTRG.10813.1	-1.264
MSTRG.46368.1	-3.837	MSTRG.2219.1	-1.995	MSTRG.32612.1	-1.264
MSTRG.42935.2	-3.834	MSTRG.4775.2	-1.995	MSTRG.1534.5	-1.264

MSTRG.8000.4	-3.833	MSTRG.2613.1	-1.993	MSTRG.20307.1	-1.264
MSTRG.37491.6	-3.829	MSTRG.26040.1	-1.993	MSTRG.31583.1	-1.263
MSTRG.11710.2	-3.814	MSTRG.24465.1	-1.991	MSTRG.43224.1	-1.262
MSTRG.9536.11	-3.810	MSTRG.36975.1	-1.989	MSTRG.11354.1	-1.261
MSTRG.34243.1	-3.810	MSTRG.10277.1	-1.989	MSTRG.48515.1	-1.261
MSTRG.20491.1	-3.805	MSTRG.14381.1	-1.989	MSTRG.15492.1	-1.260
MSTRG.7152.3	-3.803	MSTRG.39184.1	-1.986	MSTRG.12901.2	-1.260
MSTRG.42730.1	-3.800	MSTRG.46489.5	-1.985	MSTRG.9395.1	-1.260
MSTRG.27163.2	-3.794	MSTRG.29929.3	-1.984	MSTRG.31379.1	-1.260
MSTRG.18960.1	-3.793	MSTRG.37472.3	-1.982	MSTRG.32613.1	-1.260
MSTRG.12557.5	-3.787	MSTRG.17267.1	-1.981	MSTRG.35129.2	-1.259
MSTRG.34588.1	-3.783	MSTRG.14420.2	-1.981	MSTRG.7765.1	-1.258
MSTRG.39168.1	-3.782	MSTRG.6602.1	-1.979	MSTRG.208.1	-1.258
MSTRG.27854.1	-3.781	MSTRG.30134.1	-1.979	MSTRG.10703.1	-1.257
MSTRG.20491.3	-3.770	MSTRG.9449.1	-1.979	MSTRG.33889.1	-1.256
MSTRG.7076.1	-3.768	MSTRG.22830.12	-1.978	MSTRG.182.2	-1.256
MSTRG.6765.1	-3.764	MSTRG.33833.2	-1.978	MSTRG.7127.1	-1.255
MSTRG.13380.1	-3.758	MSTRG.10819.1	-1.978	MSTRG.36663.1	-1.254
MSTRG.24771.1	-3.753	MSTRG.22479.1	-1.974	MSTRG.15873.1	-1.254
MSTRG.34226.1	-3.752	MSTRG.9316.1	-1.974	MSTRG.47678.1	-1.254
MSTRG.32336.1	-3.752	MSTRG.11564.1	-1.974	MSTRG.45143.1	-1.252
MSTRG.26329.1	-3.750	MSTRG.23034.1	-1.973	MSTRG.48329.6	-1.252
MSTRG.5960.6	-3.747	MSTRG.18294.1	-1.970	MSTRG.3520.1	-1.252
MSTRG.44940.3	-3.746	MSTRG.38051.1	-1.970	MSTRG.12028.1	-1.251
MSTRG.37491.2	-3.732	MSTRG.4116.1	-1.968	MSTRG.29255.1	-1.250
MSTRG.25114.1	-3.731	MSTRG.10208.1	-1.968	MSTRG.35783.1	-1.250
MSTRG.13458.1	-3.725	MSTRG.31959.2	-1.967	MSTRG.6290.1	-1.250

MSTRG.20603.5	-3.721	MSTRG.43471.1	-1.967	MSTRG.7645.1	-1.249
MSTRG.10381.2	-3.721	MSTRG.17728.1	-1.966	MSTRG.40119.1	-1.248
MSTRG.39911.1	-3.714	MSTRG.37863.1	-1.966	MSTRG.26142.1	-1.248
MSTRG.3163.1	-3.708	MSTRG.155.1	-1.963	MSTRG.27430.1	-1.248
MSTRG.38207.2	-3.702	MSTRG.32791.1	-1.961	MSTRG.47463.1	-1.248
MSTRG.8675.4	-3.694	MSTRG.22119.1	-1.961	MSTRG.7252.1	-1.247
MSTRG.12859.2	-3.689	MSTRG.25428.1	-1.960	MSTRG.35379.4	-1.247
MSTRG.5997.1	-3.687	MSTRG.14963.1	-1.958	MSTRG.44997.1	-1.247
MSTRG.31174.6	-3.678	MSTRG.12244.1	-1.958	MSTRG.20708.7	-1.246
MSTRG.12300.3	-3.671	MSTRG.9033.1	-1.956	MSTRG.10011.3	-1.246
MSTRG.18754.1	-3.664	MSTRG.29812.3	-1.954	MSTRG.28159.1	-1.245
MSTRG.47375.1	-3.660	MSTRG.24469.1	-1.953	MSTRG.28256.3	-1.243
MSTRG.46983.1	-3.659	MSTRG.29705.10	-1.952	MSTRG.31571.1	-1.243
MSTRG.45571.1	-3.658	MSTRG.25172.1	-1.951	MSTRG.1717.1	-1.242
MSTRG.23655.1	-3.655	MSTRG.35980.1	-1.950	MSTRG.48280.1	-1.242
MSTRG.44841.1	-3.655	MSTRG.47570.1	-1.949	MSTRG.29145.1	-1.242
MSTRG.5960.7	-3.654	MSTRG.27841.1	-1.949	MSTRG.5688.1	-1.241
MSTRG.15180.1	-3.651	MSTRG.24654.1	-1.949	MSTRG.7710.1	-1.240
MSTRG.23632.1	-3.648	MSTRG.16099.2	-1.949	MSTRG.21851.1	-1.239
MSTRG.8366.3	-3.638	MSTRG.22398.1	-1.946	MSTRG.2648.1	-1.239
MSTRG.29351.5	-3.632	MSTRG.28704.1	-1.946	MSTRG.8138.1	-1.239
MSTRG.8694.3	-3.630	MSTRG.1834.1	-1.945	MSTRG.42071.1	-1.239
MSTRG.30657.3	-3.630	MSTRG.48583.1	-1.945	MSTRG.7710.6	-1.238
MSTRG.41872.4	-3.628	MSTRG.11691.1	-1.943	MSTRG.12004.1	-1.238
MSTRG.26328.1	-3.628	MSTRG.37667.1	-1.943	MSTRG.24669.1	-1.238
MSTRG.10368.3	-3.604	MSTRG.14978.1	-1.942	MSTRG.42638.1	-1.237
MSTRG.26901.1	-3.600	MSTRG.34901.2	-1.941	MSTRG.40557.1	-1.237

MSTRG.33157.1	-3.595	MSTRG.14793.1	-1.940	MSTRG.28383.1	-1.236
MSTRG.37553.1	-3.590	MSTRG.8760.1	-1.940	MSTRG.14940.1	-1.235
MSTRG.28857.2	-3.586	MSTRG.10602.1	-1.939	MSTRG.30788.1	-1.235
MSTRG.14974.3	-3.582	MSTRG.42227.1	-1.938	MSTRG.23017.1	-1.234
MSTRG.45467.7	-3.580	MSTRG.6015.2	-1.936	MSTRG.31718.1	-1.233
MSTRG.20944.1	-3.579	MSTRG.9453.1	-1.936	MSTRG.21616.1	-1.232
MSTRG.35751.1	-3.578	MSTRG.10214.1	-1.936	MSTRG.20719.1	-1.231
MSTRG.477.3	-3.574	MSTRG.2533.1	-1.934	MSTRG.12765.2	-1.231
MSTRG.14948.5	-3.573	MSTRG.14027.2	-1.934	MSTRG.12838.1	-1.230
MSTRG.29131.2	-3.568	MSTRG.31898.10	-1.933	MSTRG.4956.1	-1.229
MSTRG.7503.2	-3.567	MSTRG.26907.8	-1.933	MSTRG.12906.4	-1.229
MSTRG.27252.1	-3.561	MSTRG.6839.1	-1.931	MSTRG.38147.1	-1.228
MSTRG.38492.1	-3.561	MSTRG.33861.1	-1.931	MSTRG.41495.1	-1.227
MSTRG.27007.3	-3.551	MSTRG.24547.1	-1.930	MSTRG.10434.1	-1.225
MSTRG.8881.1	-3.546	MSTRG.17247.1	-1.930	MSTRG.28145.1	-1.223
MSTRG.41747.4	-3.545	MSTRG.20218.1	-1.929	MSTRG.26368.1	-1.223
MSTRG.39431.1	-3.539	MSTRG.33353.4	-1.929	MSTRG.12906.1	-1.223
MSTRG.10644.4	-3.535	MSTRG.42341.1	-1.928	MSTRG.13201.1	-1.222
MSTRG.25442.1	-3.534	MSTRG.19491.1	-1.928	MSTRG.13371.1	-1.222
MSTRG.5053.1	-3.532	MSTRG.508.3	-1.928	MSTRG.25244.1	-1.221
MSTRG.6675.1	-3.530	MSTRG.10685.6	-1.926	MSTRG.18991.1	-1.221
MSTRG.16725.1	-3.524	MSTRG.29951.1	-1.923	MSTRG.6967.1	-1.220
MSTRG.31079.1	-3.521	MSTRG.29257.1	-1.921	MSTRG.41486.1	-1.220
MSTRG.42097.16	-3.520	MSTRG.14792.1	-1.921	MSTRG.18431.1	-1.220
MSTRG.43096.6	-3.517	MSTRG.31553.1	-1.919	MSTRG.4038.2	-1.219
MSTRG.770.1	-3.514	MSTRG.14027.3	-1.919	MSTRG.38003.1	-1.219
MSTRG.38386.2	-3.513	MSTRG.32873.1	-1.919	MSTRG.4251.1	-1.218

MSTRG.22658.2	-3.513	MSTRG.14612.5	-1.918	MSTRG.30337.1	-1.218
MSTRG.23072.2	-3.507	MSTRG.33210.1	-1.918	MSTRG.1159.1	-1.217
MSTRG.40779.2	-3.507	MSTRG.35860.2	-1.918	MSTRG.11621.1	-1.217
MSTRG.28913.2	-3.505	MSTRG.17792.2	-1.916	MSTRG.1080.1	-1.216
MSTRG.29979.1	-3.504	MSTRG.12443.2	-1.916	MSTRG.13181.1	-1.216
MSTRG.11042.1	-3.503	MSTRG.38797.1	-1.914	MSTRG.14568.2	-1.216
MSTRG.31269.2	-3.502	MSTRG.42604.1	-1.914	MSTRG.18741.1	-1.216
MSTRG.511.6	-3.497	MSTRG.15933.1	-1.914	MSTRG.26377.1	-1.215
MSTRG.30131.1	-3.485	MSTRG.17706.1	-1.914	MSTRG.14915.1	-1.215
MSTRG.29858.1	-3.481	MSTRG.18674.1	-1.913	MSTRG.29721.2	-1.214
MSTRG.40097.5	-3.479	MSTRG.14616.1	-1.912	MSTRG.33118.1	-1.214
MSTRG.47422.2	-3.479	MSTRG.47846.6	-1.912	MSTRG.28445.1	-1.214
MSTRG.10085.1	-3.478	MSTRG.40664.1	-1.912	MSTRG.41750.3	-1.214
MSTRG.29167.1	-3.468	MSTRG.8127.1	-1.911	MSTRG.15447.1	-1.213
MSTRG.4893.1	-3.461	MSTRG.10285.1	-1.911	MSTRG.1804.1	-1.213
MSTRG.16428.2	-3.456	MSTRG.27828.1	-1.910	MSTRG.28446.1	-1.212
MSTRG.38208.6	-3.453	MSTRG.27827.1	-1.910	MSTRG.46745.1	-1.211
MSTRG.35751.2	-3.447	MSTRG.9411.1	-1.909	MSTRG.46460.1	-1.211
MSTRG.38545.3	-3.444	MSTRG.14168.1	-1.909	MSTRG.43120.1	-1.210
MSTRG.20416.11	-3.440	MSTRG.40743.1	-1.909	MSTRG.47952.1	-1.209
MSTRG.40652.1	-3.437	MSTRG.27654.1	-1.908	MSTRG.39280.1	-1.208
MSTRG.10061.1	-3.437	MSTRG.3475.3	-1.908	MSTRG.34230.1	-1.208
MSTRG.13592.1	-3.432	MSTRG.16984.1	-1.908	MSTRG.31759.1	-1.206
MSTRG.12010.1	-3.431	MSTRG.12132.1	-1.907	MSTRG.38981.1	-1.204
MSTRG.29017.1	-3.431	MSTRG.30339.1	-1.906	MSTRG.10522.1	-1.202
MSTRG.23852.4	-3.422	MSTRG.32955.1	-1.905	MSTRG.24460.1	-1.201
MSTRG.26066.1	-3.421	MSTRG.30490.5	-1.902	MSTRG.3671.1	-1.199

MSTRG.47541.1	-3.419	MSTRG.2416.1	-1.901	MSTRG.38977.1	-1.199
MSTRG.23232.1	-3.413	MSTRG.35024.1	-1.900	MSTRG.83.1	-1.199
MSTRG.39426.3	-3.411	MSTRG.46574.1	-1.899	MSTRG.7774.1	-1.199
MSTRG.34409.1	-3.406	MSTRG.14087.1	-1.898	MSTRG.24103.1	-1.198
MSTRG.24382.7	-3.392	MSTRG.20466.1	-1.897	MSTRG.31562.1	-1.197
MSTRG.37469.1	-3.387	MSTRG.29567.3	-1.896	MSTRG.28398.1	-1.196
MSTRG.36960.2	-3.385	MSTRG.15311.1	-1.895	MSTRG.39053.1	-1.196
MSTRG.40096.1	-3.380	MSTRG.16892.1	-1.894	MSTRG.25120.3	-1.195
MSTRG.4646.1	-3.380	MSTRG.1246.4	-1.893	MSTRG.43139.1	-1.195
MSTRG.46530.1	-3.378	MSTRG.12660.1	-1.892	MSTRG.35179.1	-1.194
MSTRG.40434.3	-3.369	MSTRG.12070.1	-1.890	MSTRG.42901.1	-1.194
MSTRG.29735.1	-3.368	MSTRG.33330.1	-1.890	MSTRG.27333.2	-1.194
MSTRG.11984.2	-3.359	MSTRG.25829.1	-1.890	MSTRG.30365.1	-1.194
MSTRG.46517.1	-3.359	MSTRG.41183.4	-1.889	MSTRG.25613.1	-1.193
MSTRG.35527.1	-3.358	MSTRG.15872.2	-1.889	MSTRG.30354.1	-1.192
MSTRG.43082.7	-3.355	MSTRG.28785.3	-1.888	MSTRG.26042.1	-1.192
MSTRG.48079.1	-3.352	MSTRG.21211.1	-1.888	MSTRG.38039.1	-1.188
MSTRG.41573.1	-3.351	MSTRG.43616.1	-1.887	MSTRG.17786.1	-1.187
MSTRG.7710.2	-3.350	MSTRG.31553.4	-1.887	MSTRG.39777.1	-1.186
MSTRG.5712.1	-3.349	MSTRG.1640.1	-1.886	MSTRG.10832.1	-1.186
MSTRG.22819.1	-3.349	MSTRG.41013.2	-1.885	MSTRG.44168.1	-1.184
MSTRG.4648.1	-3.346	MSTRG.43255.1	-1.885	MSTRG.32944.1	-1.183
MSTRG.46693.1	-3.344	MSTRG.32423.1	-1.885	MSTRG.17995.1	-1.183
MSTRG.35284.1	-3.339	MSTRG.10685.1	-1.885	MSTRG.18486.1	-1.183
MSTRG.46915.1	-3.336	MSTRG.23419.1	-1.884	MSTRG.30432.1	-1.182
MSTRG.30222.1	-3.330	MSTRG.25671.1	-1.884	MSTRG.19441.1	-1.182
MSTRG.40097.4	-3.327	MSTRG.10188.1	-1.884	MSTRG.12426.5	-1.182

MSTRG.22387.1	-3.322	MSTRG.15722.1	-1.883	MSTRG.26479.1	-1.181
MSTRG.29859.1	-3.319	MSTRG.33915.1	-1.883	MSTRG.30251.1	-1.180
MSTRG.8708.1	-3.318	MSTRG.46479.1	-1.882	MSTRG.29082.1	-1.180
MSTRG.43082.5	-3.312	MSTRG.26651.1	-1.881	MSTRG.28314.1	-1.180
MSTRG.36585.1	-3.306	MSTRG.7981.1	-1.881	MSTRG.29817.1	-1.178
MSTRG.10575.26	-3.299	MSTRG.22478.3	-1.880	MSTRG.9379.1	-1.178
MSTRG.37808.4	-3.294	MSTRG.17203.4	-1.877	MSTRG.37219.1	-1.177
MSTRG.23991.21	-3.284	MSTRG.46809.9	-1.877	MSTRG.9721.1	-1.177
MSTRG.8213.2	-3.283	MSTRG.25397.1	-1.875	MSTRG.18794.3	-1.176
MSTRG.15415.2	-3.281	MSTRG.31742.1	-1.874	MSTRG.29220.12	-1.175
MSTRG.38978.1	-3.280	MSTRG.19490.1	-1.873	MSTRG.30562.1	-1.175
MSTRG.10769.7	-3.278	MSTRG.3655.2	-1.873	MSTRG.11272.1	-1.175
MSTRG.33550.2	-3.278	MSTRG.42536.2	-1.872	MSTRG.37287.2	-1.174
MSTRG.20772.1	-3.276	MSTRG.7396.1	-1.872	MSTRG.37371.1	-1.173
MSTRG.27249.1	-3.275	MSTRG.2264.1	-1.870	MSTRG.18281.1	-1.173
MSTRG.15771.1	-3.272	MSTRG.2945.2	-1.870	MSTRG.41244.1	-1.172
MSTRG.14420.3	-3.271	MSTRG.15279.2	-1.869	MSTRG.25824.1	-1.172
MSTRG.41632.1	-3.268	MSTRG.42308.2	-1.869	MSTRG.41938.1	-1.171
MSTRG.37945.1	-3.268	MSTRG.27418.1	-1.868	MSTRG.47636.1	-1.170
MSTRG.23773.7	-3.267	MSTRG.36238.1	-1.867	MSTRG.7277.1	-1.170
MSTRG.24535.1	-3.263	MSTRG.676.1	-1.866	MSTRG.4118.1	-1.170
MSTRG.8083.2	-3.262	MSTRG.37567.1	-1.866	MSTRG.8435.1	-1.168
MSTRG.20381.7	-3.262	MSTRG.30347.1	-1.865	MSTRG.17390.1	-1.167
MSTRG.19160.3	-3.261	MSTRG.1330.1	-1.864	MSTRG.26587.2	-1.166
MSTRG.42342.1	-3.260	MSTRG.17771.1	-1.863	MSTRG.19962.1	-1.165
MSTRG.30280.2	-3.260	MSTRG.15841.1	-1.862	MSTRG.16615.1	-1.164
MSTRG.37483.1	-3.256	MSTRG.44323.1	-1.862	MSTRG.7710.12	-1.162

MSTRG.24468.1	-3.248	MSTRG.36474.1	-1.861	MSTRG.32310.1	-1.162
MSTRG.30657.1	-3.248	MSTRG.32571.1	-1.859	MSTRG.1694.1	-1.162
MSTRG.45467.6	-3.241	MSTRG.33174.5	-1.859	MSTRG.38929.1	-1.162
MSTRG.4002.1	-3.235	MSTRG.47385.1	-1.859	MSTRG.8295.1	-1.161
MSTRG.29004.1	-3.233	MSTRG.8179.1	-1.859	MSTRG.32246.1	-1.160
MSTRG.22597.1	-3.225	MSTRG.26344.1	-1.858	MSTRG.11736.1	-1.160
MSTRG.22845.1	-3.222	MSTRG.42060.2	-1.858	MSTRG.22860.1	-1.159
MSTRG.43116.1	-3.219	MSTRG.31106.2	-1.858	MSTRG.44170.1	-1.158
MSTRG.6182.5	-3.213	MSTRG.12426.2	-1.857	MSTRG.6505.2	-1.158
MSTRG.9664.1	-3.210	MSTRG.42875.1	-1.857	MSTRG.44756.1	-1.158
MSTRG.16697.1	-3.208	MSTRG.5740.1	-1.856	MSTRG.28745.1	-1.158
MSTRG.31174.3	-3.204	MSTRG.8708.2	-1.856	MSTRG.12136.1	-1.156
MSTRG.35598.1	-3.204	MSTRG.46798.1	-1.855	MSTRG.35002.1	-1.156
MSTRG.44314.1	-3.203	MSTRG.8399.1	-1.852	MSTRG.16636.4	-1.155
MSTRG.14906.2	-3.200	MSTRG.4117.1	-1.851	MSTRG.26098.1	-1.155
MSTRG.43142.1	-3.199	MSTRG.47320.1	-1.849	MSTRG.35934.1	-1.154
MSTRG.2062.1	-3.197	MSTRG.22636.1	-1.849	MSTRG.33285.1	-1.154
MSTRG.11711.1	-3.197	MSTRG.6254.1	-1.849	MSTRG.10454.1	-1.154
MSTRG.24233.1	-3.196	MSTRG.37558.1	-1.848	MSTRG.37147.4	-1.153
MSTRG.45567.10	-3.192	MSTRG.24431.1	-1.848	MSTRG.17833.1	-1.152
MSTRG.25371.1	-3.185	MSTRG.42547.1	-1.848	MSTRG.27425.1	-1.152
MSTRG.17621.3	-3.184	MSTRG.757.2	-1.847	MSTRG.38452.1	-1.152
MSTRG.46232.3	-3.178	MSTRG.15838.1	-1.847	MSTRG.48102.1	-1.150
MSTRG.43535.1	-3.177	MSTRG.36230.2	-1.846	MSTRG.24653.1	-1.150
MSTRG.29825.1	-3.176	MSTRG.30615.2	-1.846	MSTRG.47496.1	-1.150
MSTRG.27651.1	-3.175	MSTRG.22148.1	-1.846	MSTRG.732.1	-1.149
MSTRG.36141.1	-3.172	MSTRG.5985.1	-1.845	MSTRG.39999.1	-1.148

MSTRG.6182.1	-3.171	MSTRG.16668.1	-1.845	MSTRG.23557.1	-1.147
MSTRG.6505.4	-3.164	MSTRG.31727.1	-1.844	MSTRG.8078.1	-1.146
MSTRG.12298.1	-3.163	MSTRG.24778.1	-1.843	MSTRG.9687.1	-1.146
MSTRG.23763.4	-3.163	MSTRG.31308.1	-1.843	MSTRG.17942.1	-1.145
MSTRG.39353.2	-3.161	MSTRG.13559.1	-1.842	MSTRG.29276.2	-1.145
MSTRG.10569.1	-3.159	MSTRG.4435.1	-1.839	MSTRG.42502.1	-1.144
MSTRG.34125.1	-3.159	MSTRG.36103.1	-1.839	MSTRG.17337.1	-1.143
MSTRG.18976.1	-3.153	MSTRG.30700.1	-1.839	MSTRG.41439.1	-1.142
MSTRG.11784.16	-3.153	MSTRG.41193.1	-1.838	MSTRG.27220.1	-1.141
MSTRG.48651.2	-3.152	MSTRG.34391.1	-1.838	MSTRG.21203.1	-1.140
MSTRG.18036.1	-3.143	MSTRG.819.1	-1.837	MSTRG.5835.1	-1.140
MSTRG.17606.1	-3.140	MSTRG.22478.1	-1.837	MSTRG.7460.1	-1.140
MSTRG.24196.1	-3.139	MSTRG.43143.2	-1.835	MSTRG.44381.1	-1.139
MSTRG.35599.1	-3.135	MSTRG.14024.6	-1.835	MSTRG.22149.1	-1.139
MSTRG.31426.1	-3.134	MSTRG.39674.1	-1.834	MSTRG.7434.1	-1.139
MSTRG.19071.1	-3.133	MSTRG.18673.3	-1.833	MSTRG.23166.1	-1.138
MSTRG.40097.3	-3.133	MSTRG.30728.1	-1.833	MSTRG.21555.1	-1.138
MSTRG.30656.3	-3.129	MSTRG.8105.1	-1.832	MSTRG.1487.1	-1.137
MSTRG.16356.2	-3.127	MSTRG.17732.1	-1.832	MSTRG.23160.1	-1.135
MSTRG.34358.1	-3.123	MSTRG.43572.1	-1.831	MSTRG.34551.1	-1.133
MSTRG.21842.1	-3.116	MSTRG.6391.7	-1.830	MSTRG.6789.3	-1.132
MSTRG.12108.1	-3.113	MSTRG.35094.1	-1.829	MSTRG.48288.1	-1.130
MSTRG.26768.1	-3.112	MSTRG.39708.4	-1.829	MSTRG.8363.2	-1.130
MSTRG.35218.1	-3.111	MSTRG.47796.2	-1.829	MSTRG.37340.1	-1.130
MSTRG.4646.4	-3.102	MSTRG.21615.1	-1.829	MSTRG.39786.1	-1.130
MSTRG.12253.1	-3.098	MSTRG.32148.1	-1.828	MSTRG.31577.1	-1.129
MSTRG.1295.2	-3.097	MSTRG.18813.1	-1.827	MSTRG.8740.2	-1.128

MSTRG.6182.19	-3.096	MSTRG.15669.1	-1.826	MSTRG.24742.1	-1.127
MSTRG.45265.1	-3.094	MSTRG.4760.1	-1.825	MSTRG.8005.1	-1.126
MSTRG.17830.1	-3.093	MSTRG.7888.1	-1.825	MSTRG.42763.5	-1.126
MSTRG.22482.1	-3.087	MSTRG.21355.1	-1.824	MSTRG.39971.1	-1.124
MSTRG.40470.2	-3.085	MSTRG.43470.1	-1.823	MSTRG.24377.3	-1.124
MSTRG.35799.1	-3.083	MSTRG.42756.1	-1.822	MSTRG.3951.1	-1.124
MSTRG.20908.2	-3.079	MSTRG.5905.1	-1.821	MSTRG.28991.1	-1.121
MSTRG.21293.2	-3.079	MSTRG.35572.1	-1.820	MSTRG.12860.1	-1.120
MSTRG.39591.1	-3.078	MSTRG.13649.1	-1.819	MSTRG.24477.3	-1.119
MSTRG.30657.5	-3.077	MSTRG.40932.1	-1.819	MSTRG.36103.3	-1.119
MSTRG.6151.2	-3.073	MSTRG.16910.1	-1.817	MSTRG.2153.1	-1.118
MSTRG.48080.3	-3.071	MSTRG.333.1	-1.816	MSTRG.16182.3	-1.118
MSTRG.38492.2	-3.070	MSTRG.44295.1	-1.814	MSTRG.37615.1	-1.117
MSTRG.40297.5	-3.065	MSTRG.5025.2	-1.814	MSTRG.46376.1	-1.117
MSTRG.35500.1	-3.064	MSTRG.29023.1	-1.813	MSTRG.13809.2	-1.117
MSTRG.45567.6	-3.061	MSTRG.32655.1	-1.813	MSTRG.1826.1	-1.117
MSTRG.45364.1	-3.061	MSTRG.10253.14	-1.813	MSTRG.48482.1	-1.117
MSTRG.35729.5	-3.051	MSTRG.6648.1	-1.812	MSTRG.12183.1	-1.117
MSTRG.3471.1	-3.047	MSTRG.18631.1	-1.811	MSTRG.10750.1	-1.115
MSTRG.25168.1	-3.047	MSTRG.48097.1	-1.810	MSTRG.14729.1	-1.115
MSTRG.5511.1	-3.046	MSTRG.28031.1	-1.810	MSTRG.40887.1	-1.114
MSTRG.19636.3	-3.043	MSTRG.18726.1	-1.810	MSTRG.25614.1	-1.114
MSTRG.7095.1	-3.042	MSTRG.32011.1	-1.810	MSTRG.4033.2	-1.113
MSTRG.42833.18	-3.036	MSTRG.41945.1	-1.810	MSTRG.29190.1	-1.113
MSTRG.10563.1	-3.035	MSTRG.5191.8	-1.809	MSTRG.26692.1	-1.113
MSTRG.5508.1	-3.035	MSTRG.14263.1	-1.808	MSTRG.38146.1	-1.111
MSTRG.34473.1	-3.035	MSTRG.5515.1	-1.808	MSTRG.2575.2	-1.111

MSTRG.41111.1	-3.034	MSTRG.2351.1	-1.807	MSTRG.40974.1	-1.110
MSTRG.34901.5	-3.034	MSTRG.10247.1	-1.805	MSTRG.47845.1	-1.110
MSTRG.40133.1	-3.021	MSTRG.12443.1	-1.805	MSTRG.39216.2	-1.109
MSTRG.895.1	-3.019	MSTRG.10233.1	-1.802	MSTRG.40028.1	-1.108
MSTRG.371.1	-3.018	MSTRG.2592.1	-1.800	MSTRG.40271.1	-1.108
MSTRG.30493.1	-3.015	MSTRG.31863.3	-1.799	MSTRG.10134.1	-1.107
MSTRG.7558.1	-3.010	MSTRG.10021.1	-1.799	MSTRG.45519.2	-1.107
MSTRG.25908.1	-3.009	MSTRG.31160.1	-1.799	MSTRG.14796.1	-1.107
MSTRG.48134.1	-3.006	MSTRG.33732.1	-1.798	MSTRG.38477.1	-1.106
MSTRG.42381.1	-3.005	MSTRG.33177.1	-1.795	MSTRG.43143.3	-1.106
MSTRG.38208.7	-3.004	MSTRG.34572.3	-1.795	MSTRG.14059.1	-1.106
MSTRG.7428.1	-3.001	MSTRG.48566.1	-1.795	MSTRG.25205.1	-1.105
MSTRG.11410.1	-3.000	MSTRG.29842.2	-1.795	MSTRG.9963.1	-1.105
MSTRG.37503.1	-2.999	MSTRG.27164.1	-1.794	MSTRG.40471.1	-1.105
MSTRG.28897.3	-2.998	MSTRG.1282.1	-1.792	MSTRG.641.1	-1.104
MSTRG.20945.1	-2.991	MSTRG.10764.1	-1.792	MSTRG.22824.1	-1.103
MSTRG.35294.2	-2.989	MSTRG.11796.37	-1.792	MSTRG.5342.1	-1.103
MSTRG.30546.2	-2.989	MSTRG.33510.1	-1.791	MSTRG.24070.1	-1.103
MSTRG.10092.1	-2.989	MSTRG.45309.1	-1.791	MSTRG.41928.1	-1.102
MSTRG.31287.1	-2.979	MSTRG.12246.1	-1.789	MSTRG.28002.1	-1.102
MSTRG.40189.3	-2.978	MSTRG.42705.1	-1.789	MSTRG.32837.1	-1.102
MSTRG.46232.2	-2.977	MSTRG.20581.1	-1.788	MSTRG.26359.1	-1.101
MSTRG.25796.1	-2.975	MSTRG.5378.1	-1.788	MSTRG.16099.1	-1.101
MSTRG.47523.2	-2.974	MSTRG.26584.5	-1.788	MSTRG.10614.1	-1.100
MSTRG.24197.1	-2.973	MSTRG.33899.1	-1.785	MSTRG.26721.1	-1.100
MSTRG.19819.1	-2.971	MSTRG.23237.1	-1.784	MSTRG.22747.1	-1.097
MSTRG.20256.1	-2.969	MSTRG.16228.1	-1.784	MSTRG.10771.1	-1.097

MSTRG.1383.1	-2.965	MSTRG.27861.2	-1.784	MSTRG.44895.1	-1.097
MSTRG.14047.2	-2.965	MSTRG.20451.1	-1.784	MSTRG.21956.1	-1.097
MSTRG.39355.1	-2.959	MSTRG.31621.1	-1.784	MSTRG.21535.1	-1.096
MSTRG.36093.1	-2.958	MSTRG.33647.1	-1.783	MSTRG.12740.2	-1.096
MSTRG.28771.1	-2.957	MSTRG.46983.2	-1.782	MSTRG.7348.1	-1.096
MSTRG.15508.1	-2.955	MSTRG.31143.1	-1.780	MSTRG.15212.1	-1.095
MSTRG.6182.15	-2.954	MSTRG.34151.1	-1.779	MSTRG.19077.1	-1.095
MSTRG.4392.1	-2.954	MSTRG.29598.1	-1.779	MSTRG.37386.1	-1.094
MSTRG.41072.1	-2.953	MSTRG.13489.1	-1.778	MSTRG.6987.1	-1.094
MSTRG.2219.3	-2.953	MSTRG.34005.1	-1.777	MSTRG.1128.2	-1.093
MSTRG.38166.1	-2.951	MSTRG.7930.2	-1.777	MSTRG.35843.5	-1.093
MSTRG.249.7	-2.949	MSTRG.30615.3	-1.774	MSTRG.18453.1	-1.092
MSTRG.26843.1	-2.947	MSTRG.12482.1	-1.774	MSTRG.46410.1	-1.092
MSTRG.27429.1	-2.947	MSTRG.33957.1	-1.774	MSTRG.14732.1	-1.092
MSTRG.45529.2	-2.944	MSTRG.13676.1	-1.773	MSTRG.44604.3	-1.091
MSTRG.889.1	-2.944	MSTRG.21936.1	-1.772	MSTRG.11523.1	-1.091
MSTRG.9236.1	-2.942	MSTRG.44400.3	-1.771	MSTRG.5651.2	-1.091
MSTRG.23991.25	-2.940	MSTRG.20368.1	-1.769	MSTRG.19687.2	-1.090
MSTRG.4985.6	-2.937	MSTRG.20906.2	-1.768	MSTRG.13448.1	-1.090
MSTRG.20217.2	-2.936	MSTRG.45424.1	-1.768	MSTRG.41079.1	-1.089
MSTRG.33285.5	-2.936	MSTRG.41080.1	-1.768	MSTRG.12902.1	-1.089
MSTRG.46707.2	-2.932	MSTRG.41931.1	-1.767	MSTRG.20.1	-1.087
MSTRG.16805.3	-2.931	MSTRG.21415.16	-1.766	MSTRG.40973.1	-1.087
MSTRG.44390.1	-2.931	MSTRG.14024.5	-1.765	MSTRG.3255.1	-1.085
MSTRG.42833.6	-2.930	MSTRG.25441.1	-1.764	MSTRG.35908.1	-1.085
MSTRG.19053.1	-2.929	MSTRG.43228.1	-1.763	MSTRG.6203.1	-1.084
MSTRG.34909.1	-2.918	MSTRG.1910.1	-1.761	MSTRG.48678.1	-1.084

MSTRG.434.1	-2.918	MSTRG.27979.5	-1.760	MSTRG.47684.1	-1.083
MSTRG.10083.1	-2.913	MSTRG.31340.5	-1.759	MSTRG.41241.1	-1.083
MSTRG.5998.2	-2.912	MSTRG.33529.1	-1.758	MSTRG.28970.1	-1.082
MSTRG.30656.1	-2.907	MSTRG.23205.2	-1.758	MSTRG.11496.1	-1.082
MSTRG.18764.1	-2.903	MSTRG.47493.2	-1.755	MSTRG.4637.2	-1.082
MSTRG.43109.1	-2.902	MSTRG.28891.2	-1.754	MSTRG.11793.1	-1.081
MSTRG.18911.2	-2.900	MSTRG.4033.3	-1.752	MSTRG.43000.1	-1.081
MSTRG.46938.1	-2.898	MSTRG.6847.1	-1.749	MSTRG.28446.2	-1.079
MSTRG.43227.1	-2.898	MSTRG.20516.1	-1.748	MSTRG.27855.1	-1.078
MSTRG.15570.2	-2.897	MSTRG.9711.1	-1.748	MSTRG.10189.2	-1.077
MSTRG.38245.1	-2.893	MSTRG.40145.1	-1.747	MSTRG.43828.1	-1.077
MSTRG.40191.1	-2.893	MSTRG.9777.1	-1.747	MSTRG.31490.3	-1.077
MSTRG.45078.2	-2.892	MSTRG.30441.1	-1.743	MSTRG.43300.1	-1.074
MSTRG.17440.1	-2.882	MSTRG.19963.1	-1.743	MSTRG.16105.1	-1.074
MSTRG.2989.22	-2.880	MSTRG.32879.1	-1.743	MSTRG.4784.1	-1.073
MSTRG.15240.1	-2.878	MSTRG.941.1	-1.742	MSTRG.37369.1	-1.072
MSTRG.35723.2	-2.878	MSTRG.3427.7	-1.741	MSTRG.19356.1	-1.072
MSTRG.8263.1	-2.878	MSTRG.42974.1	-1.741	MSTRG.12682.1	-1.071
MSTRG.20585.1	-2.876	MSTRG.44663.1	-1.741	MSTRG.17116.1	-1.069
MSTRG.4646.3	-2.871	MSTRG.30561.6	-1.739	MSTRG.14659.1	-1.069
MSTRG.34794.1	-2.867	MSTRG.37206.4	-1.739	MSTRG.13631.1	-1.068
MSTRG.1233.1	-2.867	MSTRG.20340.1	-1.738	MSTRG.41109.1	-1.067
MSTRG.30656.2	-2.866	MSTRG.40856.1	-1.738	MSTRG.22359.1	-1.067
MSTRG.511.4	-2.865	MSTRG.34874.2	-1.737	MSTRG.5045.1	-1.067
MSTRG.34324.1	-2.863	MSTRG.3609.1	-1.737	MSTRG.25121.1	-1.066
MSTRG.30611.5	-2.863	MSTRG.18894.1	-1.736	MSTRG.9807.1	-1.065
MSTRG.14982.1	-2.862	MSTRG.41196.1	-1.736	MSTRG.21110.1	-1.064

MSTRG.5902.1	-2.861	MSTRG.8848.1	-1.735	MSTRG.7297.1	-1.062
MSTRG.38934.1	-2.860	MSTRG.37392.1	-1.734	MSTRG.24421.1	-1.061
MSTRG.38244.1	-2.860	MSTRG.17388.1	-1.733	MSTRG.21916.1	-1.061
MSTRG.42850.2	-2.854	MSTRG.32029.1	-1.732	MSTRG.13516.1	-1.061
MSTRG.31106.1	-2.851	MSTRG.41784.1	-1.732	MSTRG.26183.1	-1.061
MSTRG.1246.6	-2.850	MSTRG.38501.1	-1.732	MSTRG.5155.1	-1.060
MSTRG.13597.1	-2.848	MSTRG.29050.1	-1.731	MSTRG.15051.1	-1.060
MSTRG.14704.1	-2.848	MSTRG.9099.1	-1.731	MSTRG.39856.1	-1.059
MSTRG.39964.1	-2.847	MSTRG.37036.1	-1.731	MSTRG.37245.1	-1.058
MSTRG.28530.1	-2.847	MSTRG.1980.1	-1.730	MSTRG.1008.1	-1.057
MSTRG.25120.2	-2.846	MSTRG.19890.2	-1.728	MSTRG.29538.2	-1.057
MSTRG.10561.1	-2.843	MSTRG.10253.22	-1.727	MSTRG.29869.1	-1.057
MSTRG.12049.1	-2.842	MSTRG.27867.2	-1.725	MSTRG.21972.1	-1.057
MSTRG.29191.1	-2.835	MSTRG.38262.1	-1.725	MSTRG.7629.4	-1.056
MSTRG.14016.1	-2.834	MSTRG.14275.2	-1.724	MSTRG.30724.1	-1.056
MSTRG.7122.1	-2.834	MSTRG.45818.2	-1.724	MSTRG.35194.1	-1.056
MSTRG.44703.1	-2.831	MSTRG.15668.1	-1.723	MSTRG.24044.1	-1.055
MSTRG.31365.2	-2.824	MSTRG.14948.3	-1.722	MSTRG.32211.1	-1.055
MSTRG.33679.3	-2.817	MSTRG.45950.2	-1.720	MSTRG.22677.1	-1.054
MSTRG.22985.1	-2.816	MSTRG.14968.2	-1.720	MSTRG.22527.1	-1.054
MSTRG.29666.1	-2.813	MSTRG.38469.1	-1.719	MSTRG.15149.1	-1.054
MSTRG.36820.4	-2.810	MSTRG.39931.1	-1.719	MSTRG.5851.1	-1.053
MSTRG.35343.1	-2.806	MSTRG.7310.1	-1.719	MSTRG.11577.1	-1.053
MSTRG.44672.1	-2.804	MSTRG.31237.1	-1.719	MSTRG.1568.1	-1.053
MSTRG.2479.1	-2.802	MSTRG.42729.1	-1.715	MSTRG.47816.1	-1.053
MSTRG.38208.10	-2.801	MSTRG.18763.1	-1.715	MSTRG.48675.1	-1.051
MSTRG.15059.1	-2.799	MSTRG.11796.80	-1.715	MSTRG.8716.1	-1.050

MSTRG.29371.6	-2.799	MSTRG.40189.1	-1.714	MSTRG.48125.1	-1.050
MSTRG.708.13	-2.798	MSTRG.31368.1	-1.714	MSTRG.41019.1	-1.050
MSTRG.6024.1	-2.798	MSTRG.15390.1	-1.712	MSTRG.4267.1	-1.048
MSTRG.9047.1	-2.796	MSTRG.21942.1	-1.711	MSTRG.48121.1	-1.048
MSTRG.17611.1	-2.795	MSTRG.17486.1	-1.709	MSTRG.44588.1	-1.047
MSTRG.24462.2	-2.794	MSTRG.10209.1	-1.709	MSTRG.13033.1	-1.047
MSTRG.26738.1	-2.791	MSTRG.8082.1	-1.709	MSTRG.17333.1	-1.047
MSTRG.24199.1	-2.791	MSTRG.10498.1	-1.708	MSTRG.27808.1	-1.047
MSTRG.16226.1	-2.789	MSTRG.2565.1	-1.708	MSTRG.20849.1	-1.046
MSTRG.43186.1	-2.789	MSTRG.2599.1	-1.706	MSTRG.19664.1	-1.046
MSTRG.21666.1	-2.789	MSTRG.31979.1	-1.704	MSTRG.28867.1	-1.045
MSTRG.33123.2	-2.782	MSTRG.8717.1	-1.704	MSTRG.16532.1	-1.045
MSTRG.42536.1	-2.781	MSTRG.34906.1	-1.703	MSTRG.45796.1	-1.045
MSTRG.11405.2	-2.781	MSTRG.40533.1	-1.701	MSTRG.15931.1	-1.045
MSTRG.42865.1	-2.780	MSTRG.42384.1	-1.700	MSTRG.5684.1	-1.044
MSTRG.41447.1	-2.777	MSTRG.2005.1	-1.699	MSTRG.19438.1	-1.044
MSTRG.38962.1	-2.775	MSTRG.16284.1	-1.698	MSTRG.2680.1	-1.042
MSTRG.37947.1	-2.775	MSTRG.47845.2	-1.698	MSTRG.34299.1	-1.041
MSTRG.8357.1	-2.773	MSTRG.8431.1	-1.698	MSTRG.30871.1	-1.040
MSTRG.45803.1	-2.772	MSTRG.27428.1	-1.696	MSTRG.32145.1	-1.040
MSTRG.22149.2	-2.771	MSTRG.2564.1	-1.696	MSTRG.18696.1	-1.040
MSTRG.48052.1	-2.771	MSTRG.39675.1	-1.694	MSTRG.29575.1	-1.039
MSTRG.44394.5	-2.769	MSTRG.26278.1	-1.693	MSTRG.16424.1	-1.039
MSTRG.6182.4	-2.768	MSTRG.28316.2	-1.693	MSTRG.13702.1	-1.037
MSTRG.2477.1	-2.762	MSTRG.34038.1	-1.693	MSTRG.18430.1	-1.037
MSTRG.34299.2	-2.760	MSTRG.13743.1	-1.690	MSTRG.15718.1	-1.037
MSTRG.6505.1	-2.757	MSTRG.27531.1	-1.690	MSTRG.31280.1	-1.036

MSTRG.16388.1	-2.749	MSTRG.13980.1	-1.690	MSTRG.35546.2	-1.035
MSTRG.33936.1	-2.749	MSTRG.26480.1	-1.689	MSTRG.31325.1	-1.034
MSTRG.5213.1	-2.747	MSTRG.19487.2	-1.688	MSTRG.42206.1	-1.034
MSTRG.37779.1	-2.747	MSTRG.24048.1	-1.688	MSTRG.39711.1	-1.033
MSTRG.11213.1	-2.746	MSTRG.18251.1	-1.688	MSTRG.29555.2	-1.033
MSTRG.511.2	-2.744	MSTRG.30558.1	-1.687	MSTRG.17895.1	-1.033
MSTRG.24795.1	-2.744	MSTRG.15410.1	-1.686	MSTRG.36721.1	-1.031
MSTRG.11784.6	-2.742	MSTRG.1554.2	-1.685	MSTRG.41920.1	-1.030
MSTRG.7303.1	-2.742	MSTRG.36354.1	-1.685	MSTRG.19493.1	-1.029
MSTRG.1855.1	-2.741	MSTRG.14743.1	-1.684	MSTRG.18452.1	-1.028
MSTRG.29059.1	-2.741	MSTRG.48324.2	-1.683	MSTRG.9732.1	-1.028
MSTRG.44667.1	-2.735	MSTRG.29234.1	-1.683	MSTRG.35183.1	-1.028
MSTRG.21177.1	-2.733	MSTRG.41980.1	-1.682	MSTRG.20832.1	-1.027
MSTRG.26139.1	-2.730	MSTRG.17289.1	-1.681	MSTRG.33083.1	-1.027
MSTRG.37504.1	-2.730	MSTRG.20368.3	-1.681	MSTRG.26749.1	-1.027
MSTRG.17560.1	-2.728	MSTRG.2022.1	-1.681	MSTRG.21807.1	-1.026
MSTRG.35519.1	-2.727	MSTRG.27175.1	-1.679	MSTRG.13855.2	-1.026
MSTRG.46816.1	-2.726	MSTRG.40561.3	-1.679	MSTRG.10882.1	-1.026
MSTRG.34594.1	-2.725	MSTRG.6668.1	-1.678	MSTRG.20303.1	-1.026
MSTRG.1826.2	-2.722	MSTRG.28194.1	-1.678	MSTRG.3765.1	-1.026
MSTRG.7943.3	-2.722	MSTRG.26576.1	-1.678	MSTRG.14366.1	-1.026
MSTRG.28913.1	-2.719	MSTRG.22374.2	-1.677	MSTRG.26712.1	-1.025
MSTRG.35958.1	-2.717	MSTRG.37459.1	-1.677	MSTRG.31301.1	-1.024
MSTRG.35958.2	-2.717	MSTRG.23238.1	-1.676	MSTRG.20589.1	-1.023
MSTRG.26753.1	-2.713	MSTRG.31498.1	-1.675	MSTRG.17529.1	-1.023
MSTRG.9411.2	-2.710	MSTRG.17410.1	-1.674	MSTRG.45864.1	-1.023
MSTRG.15136.1	-2.709	MSTRG.1323.1	-1.673	MSTRG.7378.1	-1.022

MSTRG.6143.1	-2.708	MSTRG.9776.1	-1.671	MSTRG.13806.1	-1.021
MSTRG.35591.1	-2.708	MSTRG.30877.1	-1.671	MSTRG.30564.1	-1.021
MSTRG.35527.3	-2.708	MSTRG.43752.1	-1.671	MSTRG.27948.1	-1.021
MSTRG.48472.1	-2.707	MSTRG.27438.1	-1.671	MSTRG.6647.5	-1.021
MSTRG.156.1	-2.706	MSTRG.13129.1	-1.670	MSTRG.12740.3	-1.021
MSTRG.7302.1	-2.706	MSTRG.4534.1	-1.670	MSTRG.1830.1	-1.020
MSTRG.4433.1	-2.705	MSTRG.28055.3	-1.668	MSTRG.2696.1	-1.019
MSTRG.21132.1	-2.703	MSTRG.48635.1	-1.668	MSTRG.39376.1	-1.019
MSTRG.10622.1	-2.702	MSTRG.7674.1	-1.668	MSTRG.4000.1	-1.018
MSTRG.45260.1	-2.701	MSTRG.22118.1	-1.667	MSTRG.12135.1	-1.017
MSTRG.6040.1	-2.699	MSTRG.29184.3	-1.667	MSTRG.10257.1	-1.016
MSTRG.31169.1	-2.697	MSTRG.17596.1	-1.667	MSTRG.35853.1	-1.015
MSTRG.42308.6	-2.696	MSTRG.29635.1	-1.665	MSTRG.4134.1	-1.014
MSTRG.10886.1	-2.696	MSTRG.18292.1	-1.664	MSTRG.16767.1	-1.014
MSTRG.33285.2	-2.695	MSTRG.27842.1	-1.663	MSTRG.32051.1	-1.014
MSTRG.29955.1	-2.693	MSTRG.43874.1	-1.661	MSTRG.284.1	-1.013
MSTRG.2989.7	-2.693	MSTRG.47918.1	-1.660	MSTRG.23520.5	-1.013
MSTRG.20588.1	-2.693	MSTRG.12496.1	-1.660	MSTRG.37987.1	-1.012
MSTRG.14631.1	-2.690	MSTRG.28033.1	-1.656	MSTRG.2184.1	-1.012
MSTRG.27305.1	-2.689	MSTRG.35724.1	-1.656	MSTRG.17853.1	-1.011
MSTRG.25547.1	-2.688	MSTRG.17678.3	-1.655	MSTRG.34895.1	-1.011
MSTRG.11986.1	-2.686	MSTRG.29113.1	-1.655	MSTRG.10638.1	-1.011
MSTRG.22002.3	-2.686	MSTRG.35690.3	-1.654	MSTRG.8909.1	-1.011
MSTRG.38136.1	-2.685	MSTRG.45136.1	-1.653	MSTRG.35526.1	-1.011
MSTRG.20721.1	-2.685	MSTRG.29969.4	-1.652	MSTRG.19828.1	-1.011
MSTRG.5259.1	-2.684	MSTRG.26346.1	-1.651	MSTRG.12142.1	-1.010
MSTRG.45661.1	-2.684	MSTRG.711.1	-1.651	MSTRG.5051.1	-1.009

MSTRG.251.1	-2.679	MSTRG.22562.1	-1.650	MSTRG.34617.2	-1.009
MSTRG.35565.1	-2.677	MSTRG.27592.1	-1.648	MSTRG.22876.1	-1.008
MSTRG.17756.1	-2.675	MSTRG.20580.2	-1.648	MSTRG.35192.1	-1.008
MSTRG.12044.1	-2.675	MSTRG.37992.4	-1.648	MSTRG.26566.1	-1.006
MSTRG.30971.1	-2.673	MSTRG.45546.1	-1.646	MSTRG.31423.1	-1.005
MSTRG.31898.1	-2.672	MSTRG.30496.1	-1.646	MSTRG.27160.1	-1.004
MSTRG.38207.1	-2.671	MSTRG.18812.1	-1.646	MSTRG.923.10	-1.002
MSTRG.8855.1	-2.671	MSTRG.47447.2	-1.645	MSTRG.5984.1	-1.002
MSTRG.12025.1	-2.671	MSTRG.44903.3	-1.645	MSTRG.27326.1	-1.002
MSTRG.38785.1	-2.664	MSTRG.33266.1	-1.644	MSTRG.6749.1	-1.002
MSTRG.20945.2	-2.664	MSTRG.29413.1	-1.643	MSTRG.27876.1	-1.002
MSTRG.14790.1	-2.664	MSTRG.32275.1	-1.643	MSTRG.40651.1	-1.001
MSTRG.23606.2	-2.662	MSTRG.11787.13	-1.643	MSTRG.43676.2	-1.000

Table S4.8: Differentially expressed transcripts under chilling conditions between *Corylus avellana* cv Cakildak and cv Tombul with iDEP

Upregulated		**Downregulated**			
Transcript ID	**log2 FoldChange**	**Transcript ID**	**log2 FoldChange**	**Transcript ID**	**log2 FoldChange**
MSTRG.25996.3	28.393	MSTRG.196.1	-24.497	MSTRG.7950.3	-1.901
MSTRG.14274.1	27.014	MSTRG.201.6	-23.715	MSTRG.47578.1	-1.900
MSTRG.10245.5	26.403	MSTRG.2783.1	-22.728	MSTRG.38925.1	-1.788
MSTRG.11605.5	25.576	MSTRG.38679.1	-22.561	MSTRG.24749.1	-1.763
MSTRG.27665.2	25.551	MSTRG.19687.1	-22.337	MSTRG.30281.1	-1.758
MSTRG.18648.1	25.012	MSTRG.25851.2	-22.245	MSTRG.30615.2	-1.742
MSTRG.7333.4	24.926	MSTRG.18229.2	-22.030	MSTRG.12253.2	-1.724
MSTRG.18246.4	24.238	MSTRG.26521.2	-22.016	MSTRG.46021.3	-1.723
MSTRG.22579.2	23.874	MSTRG.20762.2	-22.009	MSTRG.16784.1	-1.669
MSTRG.40802.2	23.798	MSTRG.33918.2	-21.753	MSTRG.41961.2	-1.656
MSTRG.38486.1	23.662	MSTRG.29420.10	-21.583	MSTRG.19867.1	-1.650
MSTRG.31777.2	23.652	MSTRG.23637.9	-20.976	MSTRG.20157.3	-1.634
MSTRG.21796.3	23.624	MSTRG.3884.7	-20.767	MSTRG.30790.1	-1.527
MSTRG.25954.1	22.806	MSTRG.37632.9	-19.928	MSTRG.22987.2	-1.442
MSTRG.23009.6	22.547	MSTRG.21860.4	-18.657	MSTRG.3542.2	-1.425
MSTRG.29969.2	22.095	MSTRG.48251.1	-14.672	MSTRG.46511.7	-1.416
MSTRG.10720.2	18.130	MSTRG.36123.5	-14.245	MSTRG.31042.1	-1.404
MSTRG.45938.6	12.818	MSTRG.34252.1	-13.277	MSTRG.26959.2	-1.368
MSTRG.25682.2	10.900	MSTRG.31365.2	-11.333	MSTRG.5051.1	-1.349
MSTRG.7712.1	10.386	MSTRG.26234.5	-11.318	MSTRG.45455.1	-1.339
MSTRG.45074.1	10.196	MSTRG.13266.1	-10.983	MSTRG.23160.1	-1.339
MSTRG.24340.2	10.016	MSTRG.302.2	-10.947	MSTRG.37838.1	-1.300

MSTRG.26036.1	9.818	MSTRG.27305.1	-10.678	MSTRG.31106.2	-1.246
MSTRG.7710.4	9.697	MSTRG.3925.4	-10.626	MSTRG.21415.20	-1.200
MSTRG.1872.1	9.576	MSTRG.35723.2	-10.531	MSTRG.23816.1	-1.167
MSTRG.7591.2	9.390	MSTRG.24030.1	-10.301	MSTRG.20116.1	-1.122
MSTRG.2277.4	9.339	MSTRG.5462.1	-10.224	MSTRG.36230.1	-1.120
MSTRG.15481.1	9.184	MSTRG.10670.2	-10.025	MSTRG.13901.1	-1.096
MSTRG.47987.1	9.104	MSTRG.45467.13	-9.874	MSTRG.45394.1	-1.079
MSTRG.33958.3	9.081	MSTRG.42011.2	-9.860		
MSTRG.928.3	9.025	MSTRG.15447.2	-9.739		
MSTRG.3327.3	9.020	MSTRG.40297.4	-9.705		
MSTRG.16527.1	9.020	MSTRG.5048.1	-9.676		
MSTRG.24346.1	8.942	MSTRG.20603.5	-9.421		
MSTRG.37033.6	8.861	MSTRG.36044.2	-9.404		
MSTRG.8268.1	8.724	MSTRG.31079.1	-9.387		
MSTRG.21953.2	8.574	MSTRG.2480.1	-9.334		
MSTRG.3685.11	8.397	MSTRG.1181.1	-9.316		
MSTRG.19910.1	8.236	MSTRG.2277.13	-9.248		
MSTRG.21818.10	8.159	MSTRG.2693.1	-9.228		
MSTRG.20191.2	8.011	MSTRG.26837.2	-9.220		
MSTRG.21403.7	7.969	MSTRG.40415.1	-9.209		
MSTRG.39061.1	7.781	MSTRG.34937.1	-9.129		
MSTRG.13382.1	7.712	MSTRG.12859.2	-9.057		
MSTRG.26391.3	7.612	MSTRG.41606.2	-8.945		
MSTRG.24308.1	7.600	MSTRG.38363.1	-8.889		
MSTRG.32031.1	7.461	MSTRG.30721.1	-8.869		
MSTRG.43082.1	7.368	MSTRG.30722.1	-8.869		
MSTRG.7128.3	6.987	MSTRG.5053.1	-8.832		

MSTRG.39912.1	6.517	MSTRG.44585.8	-8.780
MSTRG.8234.1	6.489	MSTRG.4893.1	-8.730
MSTRG.18650.1	6.387	MSTRG.21440.1	-8.641
MSTRG.33933.14	6.231	MSTRG.44314.1	-8.622
MSTRG.5340.2	6.065	MSTRG.23991.21	-8.613
MSTRG.18052.2	5.894	MSTRG.6871.1	-8.554
MSTRG.19630.9	5.892	MSTRG.18186.1	-8.540
MSTRG.30986.1	5.667	MSTRG.12020.1	-8.469
MSTRG.25073.2	5.027	MSTRG.8366.3	-8.252
MSTRG.8703.2	4.812	MSTRG.27109.4	-7.975
MSTRG.38812.2	4.422	MSTRG.19462.2	-7.951
MSTRG.34443.2	4.139	MSTRG.45473.1	-7.937
MSTRG.17511.1	4.054	MSTRG.18819.1	-7.920
MSTRG.39151.2	3.592	MSTRG.12049.1	-7.878
MSTRG.48760.1	3.364	MSTRG.7310.12	-7.738
MSTRG.35251.1	3.265	MSTRG.4437.1	-7.697
MSTRG.11010.1	3.135	MSTRG.5150.2	-7.502
MSTRG.27832.2	3.008	MSTRG.45830.5	-7.331
MSTRG.44022.1	2.932	MSTRG.39591.1	-7.293
MSTRG.30490.4	2.930	MSTRG.16831.7	-7.166
MSTRG.19023.1	2.889	MSTRG.31143.1	-7.166
MSTRG.7152.3	2.816	MSTRG.34125.1	-7.162
MSTRG.27987.1	2.786	MSTRG.40297.5	-7.098
MSTRG.48061.8	2.650	MSTRG.40097.6	-6.874
MSTRG.31505.1	2.627	MSTRG.5404.1	-6.833
MSTRG.23359.11	2.477	MSTRG.16224.1	-6.830
MSTRG.26923.1	2.473	MSTRG.5303.2	-6.083

MSTRG.44940.3	2.425	MSTRG.19655.1	-6.016
MSTRG.31619.1	2.370	MSTRG.18368.2	-5.960
MSTRG.6151.2	2.319	MSTRG.17573.3	-5.881
MSTRG.14420.3	2.299	MSTRG.20536.1	-5.818
MSTRG.31734.1	2.285	MSTRG.24634.2	-5.654
MSTRG.40563.23	2.253	MSTRG.22851.2	-5.523
MSTRG.11719.2	2.186	MSTRG.20152.2	-5.351
MSTRG.13030.1	2.044	MSTRG.6182.19	-5.265
MSTRG.7503.2	2.013	MSTRG.36289.1	-5.250
MSTRG.23439.1	2.010	MSTRG.33679.1	-5.098
MSTRG.45453.3	1.997	MSTRG.45455.2	-4.794
MSTRG.19706.1	1.984	MSTRG.44531.1	-4.767
MSTRG.3163.1	1.927	MSTRG.6861.4	-4.701
MSTRG.43109.1	1.926	MSTRG.46707.2	-4.538
MSTRG.29004.1	1.856	MSTRG.40297.3	-4.461
MSTRG.6697.3	1.836	MSTRG.35309.1	-4.419
MSTRG.21093.1	1.827	MSTRG.17363.1	-4.292
MSTRG.13458.1	1.827	MSTRG.23912.1	-4.063
MSTRG.45661.1	1.819	MSTRG.30382.1	-4.029
MSTRG.15180.1	1.800	MSTRG.6839.4	-3.982
MSTRG.17665.2	1.701	MSTRG.34243.1	-3.866
MSTRG.17756.1	1.677	MSTRG.7012.4	-3.787
MSTRG.14016.1	1.671	MSTRG.37188.1	-3.769
MSTRG.36851.1	1.669	MSTRG.29220.12	-3.704
MSTRG.35343.1	1.652	MSTRG.29954.1	-3.524
MSTRG.16226.1	1.599	MSTRG.31097.1	-3.413
MSTRG.47420.1	1.564	MSTRG.39546.1	-3.086

MSTRG.48732.1	1.558	MSTRG.7782.2	-2.825
MSTRG.45260.1	1.516	MSTRG.4433.1	-2.814
MSTRG.17606.1	1.511	MSTRG.22166.6	-2.806
MSTRG.48061.1	1.508	MSTRG.30924.3	-2.705
MSTRG.39541.1	1.498	MSTRG.20588.1	-2.693
MSTRG.37774.1	1.495	MSTRG.30579.1	-2.660
MSTRG.27552.1	1.481	MSTRG.27939.1	-2.635
MSTRG.37776.1	1.402	MSTRG.48760.8	-2.631
MSTRG.13288.2	1.379	MSTRG.26407.1	-2.629
MSTRG.36718.1	1.354	MSTRG.25908.1	-2.595
MSTRG.9221.1	1.346	MSTRG.40299.1	-2.573
MSTRG.46938.1	1.320	MSTRG.6839.1	-2.547
MSTRG.19819.1	1.304	MSTRG.43120.1	-2.472
MSTRG.45567.6	1.276	MSTRG.11796.37	-2.427
MSTRG.16697.6	1.263	MSTRG.35190.2	-2.408
MSTRG.43535.1	1.256	MSTRG.15111.2	-2.357
MSTRG.40133.1	1.200	MSTRG.6015.2	-2.339
MSTRG.15255.1	1.197	MSTRG.29184.3	-2.333
MSTRG.30149.1	1.189	MSTRG.30615.3	-2.287
MSTRG.40743.1	1.182	MSTRG.37504.1	-2.270
MSTRG.46816.1	1.182	MSTRG.15240.1	-2.199
MSTRG.21208.1	1.177	MSTRG.10042.2	-2.197
MSTRG.16974.1	1.145	MSTRG.28437.1	-2.190
MSTRG.11796.95	1.128	MSTRG.46479.1	-2.157
MSTRG.30134.1	1.079	MSTRG.48707.2	-2.148
MSTRG.8848.1	1.070	MSTRG.23773.7	-2.109
MSTRG.41183.4	1.049	MSTRG.9807.1	-2.067

MSTRG.15139.1	1.041	MSTRG.29485.1	-2.066
MSTRG.32981.1	1.040	MSTRG.11744.1	-2.066
MSTRG.20517.1	1.031	MSTRG.17488.1	-2.050
MSTRG.9692.7	1.019	MSTRG.24070.1	-1.959
MSTRG.41580.1	1.002	MSTRG.20642.1	-1.948

Table S4.9: Differentially expressed transcripts under control conditions between *Corylus avellana* cv Cakildak and cv Tombul with iDEP

Upregulated		**Downregulated**			
Transcript ID	**log2 FoldChange**	**Transcript ID**	**log2 FoldChange**	**Transcript ID**	**log2 FoldChange**
MSTRG.41358.2	26.606	MSTRG.19068.1	-26.532	MSTRG.24917.4	-1.293
MSTRG.21026.3	26.470	MSTRG.24960.10	-26.270	MSTRG.14553.1	-1.290
MSTRG.15019.2	26.234	MSTRG.4504.7	-25.070	MSTRG.26738.1	-1.284
MSTRG.40917.4	26.045	MSTRG.21027.3	-24.986	MSTRG.9807.1	-1.284
MSTRG.30475.2	25.976	MSTRG.18109.2	-24.789	MSTRG.947.1	-1.279
MSTRG.17294.2	25.595	MSTRG.29607.2	-24.590	MSTRG.29055.3	-1.277
MSTRG.34324.3	25.560	MSTRG.23455.2	-24.456	MSTRG.14253.1	-1.277
MSTRG.6893.1	25.547	MSTRG.27264.2	-23.994	MSTRG.31314.1	-1.277
MSTRG.5213.3	25.482	MSTRG.46200.1	-23.971	MSTRG.17935.1	-1.274
MSTRG.32596.14	25.302	MSTRG.16116.2	-23.822	MSTRG.4071.2	-1.274
MSTRG.19270.3	25.296	MSTRG.19068.2	-23.521	MSTRG.26959.2	-1.273
MSTRG.47541.3	25.277	MSTRG.31177.1	-23.497	MSTRG.20580.2	-1.272
MSTRG.24181.2	25.261	MSTRG.12565.1	-23.444	MSTRG.20708.6	-1.270
MSTRG.987.2	25.110	MSTRG.34788.6	-23.413	MSTRG.11230.1	-1.269
MSTRG.8925.2	25.030	MSTRG.2524.1	-23.340	MSTRG.19636.5	-1.265
MSTRG.37633.8	24.858	MSTRG.35565.3	-23.193	MSTRG.17268.1	-1.264
MSTRG.26241.2	24.760	MSTRG.17903.3	-23.161	MSTRG.26842.1	-1.262
MSTRG.7579.2	24.735	MSTRG.44005.5	-23.124	MSTRG.23430.2	-1.254
MSTRG.24410.1	24.733	MSTRG.27578.5	-23.108	MSTRG.24390.4	-1.252
MSTRG.42733.3	24.631	MSTRG.17917.17	-18.417	MSTRG.38925.1	-1.251
MSTRG.34691.2	24.619	MSTRG.17917.13	-16.523	MSTRG.9899.1	-1.237
MSTRG.9104.2	24.580	MSTRG.37343.31	-15.608	MSTRG.29969.4	-1.231

MSTRG.29825.2	24.475	MSTRG.28361.6	-15.465	MSTRG.42831.1	-1.229
MSTRG.32238.8	24.463	MSTRG.30371.4	-14.262	MSTRG.38053.1	-1.228
MSTRG.13902.1	24.410	MSTRG.8882.1	-14.237	MSTRG.18052.2	-1.223
MSTRG.37128.4	24.406	MSTRG.5415.5	-14.201	MSTRG.1603.1	-1.210
MSTRG.39213.2	24.402	MSTRG.33377.3	-14.029	MSTRG.31351.6	-1.208
MSTRG.9308.3	24.188	MSTRG.6869.6	-13.999	MSTRG.3771.1	-1.207
MSTRG.10525.3	23.846	MSTRG.42900.3	-13.704	MSTRG.16099.2	-1.202
MSTRG.9042.1	23.845	MSTRG.29013.1	-13.372	MSTRG.435.1	-1.202
MSTRG.28280.3	23.770	MSTRG.13101.18	-13.271	MSTRG.30407.1	-1.190
MSTRG.13307.2	23.621	MSTRG.21953.2	-13.118	MSTRG.14194.1	-1.187
MSTRG.19149.2	23.587	MSTRG.36289.1	-13.064	MSTRG.19962.1	-1.182
MSTRG.31507.2	23.400	MSTRG.28785.5	-12.884	MSTRG.9478.1	-1.163
MSTRG.17355.4	15.943	MSTRG.18368.2	-12.871	MSTRG.47437.1	-1.163
MSTRG.14156.2	14.595	MSTRG.24027.1	-12.815	MSTRG.45621.1	-1.159
MSTRG.6930.2	14.066	MSTRG.23212.2	-12.695	MSTRG.13489.2	-1.153
MSTRG.2335.1	13.816	MSTRG.26853.9	-12.694	MSTRG.11076.1	-1.152
MSTRG.42912.3	13.349	MSTRG.16289.4	-12.529	MSTRG.42536.1	-1.149
MSTRG.40563.13	13.312	MSTRG.31177.3	-12.468	MSTRG.47195.2	-1.147
MSTRG.38636.2	13.293	MSTRG.25449.3	-12.375	MSTRG.30441.1	-1.146
MSTRG.24048.2	13.020	MSTRG.5074.2	-12.325	MSTRG.36235.1	-1.146
MSTRG.47418.6	12.931	MSTRG.23315.2	-12.271	MSTRG.21355.1	-1.140
MSTRG.2207.3	12.891	MSTRG.2478.1	-12.245	MSTRG.47645.1	-1.140
MSTRG.23766.2	12.882	MSTRG.11784.17	-12.239	MSTRG.8726.1	-1.135
MSTRG.43868.1	12.767	MSTRG.48098.2	-12.171	MSTRG.33980.1	-1.135
MSTRG.39181.4	12.729	MSTRG.23212.3	-12.087	MSTRG.7446.1	-1.133
MSTRG.15405.3	12.177	MSTRG.22851.2	-12.081	MSTRG.757.2	-1.132
MSTRG.2671.2	11.851	MSTRG.23698.1	-12.052	MSTRG.31351.2	-1.119

MSTRG.9003.3	11.836	MSTRG.27305.1	-12.043	MSTRG.25464.1	-1.110
MSTRG.39795.5	11.725	MSTRG.20708.3	-12.039	MSTRG.23153.1	-1.110
MSTRG.46542.1	11.620	MSTRG.47450.3	-11.997	MSTRG.36722.1	-1.108
MSTRG.44967.2	11.544	MSTRG.45966.5	-11.974	MSTRG.27523.1	-1.107
MSTRG.38797.5	11.424	MSTRG.5581.3	-11.906	MSTRG.3723.1	-1.107
MSTRG.14022.2	11.249	MSTRG.23434.1	-11.896	MSTRG.44663.1	-1.104
MSTRG.27200.3	11.115	MSTRG.34586.3	-11.877	MSTRG.21746.1	-1.103
MSTRG.18701.5	10.934	MSTRG.26837.2	-11.820	MSTRG.39151.2	-1.103
MSTRG.2071.1	10.846	MSTRG.21568.3	-11.758	MSTRG.38862.1	-1.091
MSTRG.1899.1	10.843	MSTRG.30319.3	-11.727	MSTRG.2340.2	-1.090
MSTRG.25477.10	10.824	MSTRG.30721.1	-11.706	MSTRG.31301.1	-1.090
MSTRG.44837.1	10.802	MSTRG.30722.1	-11.706	MSTRG.4796.1	-1.084
MSTRG.5534.9	10.796	MSTRG.19462.2	-11.680	MSTRG.7873.2	-1.084
MSTRG.20470.2	10.610	MSTRG.17657.8	-11.680	MSTRG.4014.1	-1.072
MSTRG.27422.3	10.579	MSTRG.31777.3	-11.547	MSTRG.17665.2	-1.071
MSTRG.5631.2	10.347	MSTRG.16921.17	-11.543	MSTRG.21402.8	-1.070
MSTRG.19594.1	10.299	MSTRG.33174.21	-11.515	MSTRG.17715.1	-1.069
MSTRG.13393.2	10.272	MSTRG.39674.3	-11.509	MSTRG.25682.1	-1.063
MSTRG.35049.2	10.259	MSTRG.20061.7	-11.462	MSTRG.47029.1	-1.062
MSTRG.41982.5	10.085	MSTRG.44600.2	-11.457	MSTRG.23154.1	-1.062
MSTRG.28808.1	10.044	MSTRG.24578.15	-11.423	MSTRG.28456.1	-1.061
MSTRG.26059.7	10.043	MSTRG.11281.1	-11.418	MSTRG.15279.1	-1.060
MSTRG.11784.9	10.002	MSTRG.34063.1	-11.415	MSTRG.30505.2	-1.058
MSTRG.29395.2	9.951	MSTRG.34533.4	-11.407	MSTRG.27567.1	-1.052
MSTRG.36585.2	9.935	MSTRG.7012.4	-11.402	MSTRG.39856.1	-1.051
MSTRG.13797.2	9.891	MSTRG.37632.15	-11.388	MSTRG.14915.1	-1.050
MSTRG.11632.2	9.888	MSTRG.5750.7	-11.353	MSTRG.1670.1	-1.048

MSTRG.42412.2	9.873	MSTRG.40236.2	-11.293	MSTRG.14936.1	-1.048
MSTRG.23247.7	9.858	MSTRG.11984.2	-11.292	MSTRG.13568.1	-1.047
MSTRG.41420.3	9.628	MSTRG.22377.3	-11.258	MSTRG.31169.1	-1.046
MSTRG.4365.2	9.583	MSTRG.2216.3	-11.177	MSTRG.13201.1	-1.043
MSTRG.22176.2	9.582	MSTRG.30657.7	-11.118	MSTRG.1910.1	-1.039
MSTRG.17870.9	9.564	MSTRG.39471.1	-11.100	MSTRG.4000.1	-1.033
MSTRG.18174.1	9.557	MSTRG.27651.2	-11.098	MSTRG.32032.1	-1.029
MSTRG.25449.1	9.555	MSTRG.29220.13	-11.089	MSTRG.13217.1	-1.028
MSTRG.38383.6	9.545	MSTRG.15447.2	-11.063	MSTRG.31499.1	-1.024
MSTRG.22622.4	9.497	MSTRG.5053.1	-11.040	MSTRG.11796.94	-1.024
MSTRG.48503.3	9.409	MSTRG.27357.4	-10.975	MSTRG.12742.1	-1.024
MSTRG.4154.3	9.230	MSTRG.38361.2	-10.964	MSTRG.42536.7	-1.016
MSTRG.498.2	9.180	MSTRG.29688.2	-10.961	MSTRG.21299.1	-1.015
MSTRG.22054.2	9.165	MSTRG.36302.16	-10.927	MSTRG.5416.1	-1.012
MSTRG.10563.6	9.067	MSTRG.4893.1	-10.867	MSTRG.15161.1	-1.012
MSTRG.4178.1	9.038	MSTRG.11006.1	-10.832	MSTRG.41796.1	-1.009
MSTRG.5407.1	9.018	MSTRG.12450.4	-10.794	MSTRG.19961.1	-1.008
MSTRG.25836.3	9.015	MSTRG.12450.5	-10.767	MSTRG.22987.2	-1.002
MSTRG.48226.2	9.010	MSTRG.34443.4	-10.736		
MSTRG.14850.5	9.008	MSTRG.44585.8	-10.719		
MSTRG.20676.2	8.992	MSTRG.29702.4	-10.719		
MSTRG.4699.4	8.967	MSTRG.39590.1	-10.697		
MSTRG.6591.1	8.852	MSTRG.43971.3	-10.652		
MSTRG.39471.2	8.819	MSTRG.37402.4	-10.650		
MSTRG.10541.2	8.819	MSTRG.13045.2	-10.642		
MSTRG.34297.1	8.789	MSTRG.23991.21	-10.573		
MSTRG.36025.1	8.714	MSTRG.36224.2	-10.513		

MSTRG.4075.2	8.699	MSTRG.14922.2	-10.488
MSTRG.27704.2	8.693	MSTRG.16253.5	-10.466
MSTRG.8641.1	8.681	MSTRG.43336.3	-10.417
MSTRG.19810.2	8.637	MSTRG.33191.3	-10.346
MSTRG.39971.3	8.616	MSTRG.21235.6	-10.307
MSTRG.34527.2	8.604	MSTRG.15849.8	-10.269
MSTRG.17688.2	8.594	MSTRG.3685.11	-10.256
MSTRG.42104.3	8.489	MSTRG.43315.2	-10.251
MSTRG.2509.2	8.459	MSTRG.27306.1	-10.221
MSTRG.3642.2	8.356	MSTRG.46018.3	-10.199
MSTRG.45192.2	8.333	MSTRG.21562.2	-10.185
MSTRG.11663.1	8.289	MSTRG.34937.1	-10.181
MSTRG.9028.6	8.225	MSTRG.26389.3	-10.155
MSTRG.2376.3	8.107	MSTRG.17573.3	-10.148
MSTRG.15625.2	8.001	MSTRG.32349.2	-10.126
MSTRG.37570.1	7.931	MSTRG.14213.2	-10.117
MSTRG.46515.3	7.863	MSTRG.9793.3	-10.093
MSTRG.27.2	7.832	MSTRG.14511.3	-10.069
MSTRG.728.5	7.809	MSTRG.17873.2	-10.034
MSTRG.36739.2	7.769	MSTRG.19418.2	-10.025
MSTRG.11784.19	7.715	MSTRG.42867.2	-10.024
MSTRG.2906.2	7.665	MSTRG.6861.4	-10.001
MSTRG.6666.2	7.652	MSTRG.34467.2	-9.976
MSTRG.36025.2	7.614	MSTRG.13748.2	-9.921
MSTRG.11796.33	7.564	MSTRG.19053.1	-9.917
MSTRG.15158.2	7.555	MSTRG.12679.2	-9.872
MSTRG.38918.1	7.545	MSTRG.17573.1	-9.808

MSTRG.3974.1	7.477	MSTRG.12020.1	-9.791
MSTRG.728.4	7.453	MSTRG.6871.1	-9.746
MSTRG.40555.37	7.326	MSTRG.19339.2	-9.712
MSTRG.44731.1	7.300	MSTRG.21750.2	-9.695
MSTRG.23754.1	7.231	MSTRG.12773.2	-9.676
MSTRG.33940.5	7.226	MSTRG.10530.2	-9.666
MSTRG.20380.2	7.181	MSTRG.7953.2	-9.654
MSTRG.22299.1	7.146	MSTRG.36547.3	-9.641
MSTRG.47420.2	6.998	MSTRG.24962.2	-9.578
MSTRG.26790.1	6.994	MSTRG.23360.14	-9.538
MSTRG.6577.5	6.904	MSTRG.43405.1	-9.528
MSTRG.6807.3	6.832	MSTRG.35002.2	-9.528
MSTRG.8981.2	6.805	MSTRG.30149.1	-9.526
MSTRG.16180.2	6.771	MSTRG.41079.2	-9.517
MSTRG.18309.2	6.559	MSTRG.5404.1	-9.509
MSTRG.27922.6	6.545	MSTRG.45480.1	-9.497
MSTRG.3988.4	6.498	MSTRG.39364.3	-9.455
MSTRG.28382.1	6.488	MSTRG.13811.8	-9.451
MSTRG.29135.5	6.485	MSTRG.25999.2	-9.447
MSTRG.4951.1	6.441	MSTRG.2697.2	-9.438
MSTRG.28227.1	6.407	MSTRG.33317.5	-9.404
MSTRG.36103.6	6.339	MSTRG.29817.4	-9.381
MSTRG.11477.2	6.311	MSTRG.42632.4	-9.300
MSTRG.46758.3	6.304	MSTRG.11260.3	-9.286
MSTRG.41392.3	6.220	MSTRG.10111.1	-9.249
MSTRG.26037.1	6.205	MSTRG.23909.2	-9.220
MSTRG.20470.12	6.197	MSTRG.37457.1	-9.198

MSTRG.13287.2	6.194	MSTRG.7310.12	-9.178
MSTRG.4585.2	6.149	MSTRG.22626.3	-9.135
MSTRG.23766.3	6.106	MSTRG.18073.2	-9.119
MSTRG.42434.2	6.103	MSTRG.3437.3	-9.109
MSTRG.40909.1	6.040	MSTRG.29667.1	-9.079
MSTRG.29710.1	6.019	MSTRG.22846.12	-9.053
MSTRG.25517.1	6.017	MSTRG.14850.3	-9.027
MSTRG.31734.1	5.970	MSTRG.40841.2	-9.021
MSTRG.374.7	5.840	MSTRG.13769.2	-9.018
MSTRG.36107.2	5.825	MSTRG.29876.2	-8.977
MSTRG.4700.1	5.721	MSTRG.41288.9	-8.968
MSTRG.9484.2	5.702	MSTRG.20603.5	-8.957
MSTRG.18737.2	5.679	MSTRG.36093.2	-8.941
MSTRG.28145.2	5.665	MSTRG.11787.16	-8.934
MSTRG.47420.1	5.636	MSTRG.43388.2	-8.892
MSTRG.92.3	5.608	MSTRG.26247.1	-8.871
MSTRG.3839.2	5.583	MSTRG.43101.1	-8.848
MSTRG.22489.2	5.575	MSTRG.688.2	-8.843
MSTRG.32888.2	5.567	MSTRG.19068.4	-8.829
MSTRG.47413.1	5.478	MSTRG.37956.3	-8.818
MSTRG.13721.5	5.429	MSTRG.27972.1	-8.782
MSTRG.37592.2	5.293	MSTRG.45769.13	-8.760
MSTRG.1190.3	5.250	MSTRG.45623.2	-8.738
MSTRG.21536.5	5.042	MSTRG.32327.4	-8.683
MSTRG.47425.1	4.995	MSTRG.37494.5	-8.641
MSTRG.36262.4	4.987	MSTRG.10545.2	-8.619
MSTRG.47418.5	4.982	MSTRG.18942.7	-8.611

MSTRG.13101.28	4.969	MSTRG.45341.1	-8.601
MSTRG.1875.1	4.964	MSTRG.39674.2	-8.580
MSTRG.32517.3	4.959	MSTRG.20618.2	-8.574
MSTRG.3884.3	4.909	MSTRG.36631.2	-8.573
MSTRG.18997.1	4.763	MSTRG.9592.6	-8.561
MSTRG.23766.1	4.742	MSTRG.48009.8	-8.529
MSTRG.22846.4	4.720	MSTRG.46902.1	-8.516
MSTRG.11141.3	4.525	MSTRG.48707.2	-8.514
MSTRG.12465.1	4.484	MSTRG.22623.2	-8.477
MSTRG.47418.2	4.477	MSTRG.227.2	-8.471
MSTRG.13636.2	4.472	MSTRG.42013.2	-8.424
MSTRG.27531.2	4.466	MSTRG.14670.2	-8.411
MSTRG.37295.3	4.458	MSTRG.6187.1	-8.391
MSTRG.31226.2	4.448	MSTRG.32045.1	-8.368
MSTRG.27552.1	4.394	MSTRG.15225.10	-8.355
MSTRG.46131.3	4.371	MSTRG.41439.2	-8.354
MSTRG.45351.1	4.361	MSTRG.39723.2	-8.326
MSTRG.17894.1	4.340	MSTRG.28114.7	-8.313
MSTRG.40563.28	4.246	MSTRG.42733.2	-8.291
MSTRG.9033.2	4.177	MSTRG.12423.2	-8.286
MSTRG.22594.1	4.092	MSTRG.38492.2	-8.286
MSTRG.33969.1	4.085	MSTRG.9888.2	-8.264
MSTRG.48168.1	3.980	MSTRG.23702.2	-8.231
MSTRG.34697.3	3.898	MSTRG.9084.2	-8.222
MSTRG.9285.4	3.885	MSTRG.44190.2	-8.218
MSTRG.27449.2	3.866	MSTRG.36983.2	-8.214
MSTRG.15408.2	3.857	MSTRG.27749.2	-8.145

MSTRG.1194.2	3.843	MSTRG.16777.2	-8.092
MSTRG.48859.1	3.819	MSTRG.24701.4	-8.081
MSTRG.44418.1	3.793	MSTRG.39963.2	-8.066
MSTRG.31920.2	3.790	MSTRG.3542.2	-7.996
MSTRG.21530.3	3.759	MSTRG.12472.1	-7.948
MSTRG.17304.1	3.741	MSTRG.41593.4	-7.941
MSTRG.31314.2	3.719	MSTRG.20286.3	-7.914
MSTRG.14331.1	3.674	MSTRG.39831.4	-7.902
MSTRG.39426.3	3.665	MSTRG.40563.24	-7.890
MSTRG.15760.1	3.576	MSTRG.47574.3	-7.870
MSTRG.26016.1	3.564	MSTRG.27844.3	-7.839
MSTRG.35508.1	3.562	MSTRG.24688.3	-7.832
MSTRG.28897.3	3.552	MSTRG.45991.3	-7.770
MSTRG.37774.4	3.530	MSTRG.41655.4	-7.754
MSTRG.35509.1	3.519	MSTRG.18497.2	-7.738
MSTRG.41603.1	3.517	MSTRG.26632.4	-7.732
MSTRG.36459.1	3.490	MSTRG.47099.1	-7.716
MSTRG.12679.1	3.486	MSTRG.40555.23	-7.707
MSTRG.22316.3	3.453	MSTRG.21415.10	-7.531
MSTRG.9883.1	3.431	MSTRG.2566.3	-7.490
MSTRG.17422.1	3.401	MSTRG.24701.5	-7.438
MSTRG.7184.1	3.394	MSTRG.7005.1	-7.396
MSTRG.48848.1	3.376	MSTRG.19173.20	-7.341
MSTRG.907.1	3.359	MSTRG.46001.3	-7.341
MSTRG.45089.1	3.340	MSTRG.27777.6	-7.325
MSTRG.48519.10	3.309	MSTRG.10348.3	-7.325
MSTRG.41361.1	3.291	MSTRG.2022.2	-7.312

MSTRG.14835.2	3.291	MSTRG.9179.2	-7.297
MSTRG.48819.1	3.285	MSTRG.36373.4	-7.253
MSTRG.4312.2	3.280	MSTRG.31027.2	-7.249
MSTRG.21108.3	3.264	MSTRG.18368.4	-7.249
MSTRG.37789.2	3.199	MSTRG.23439.2	-7.210
MSTRG.17021.4	3.156	MSTRG.38001.2	-7.197
MSTRG.48613.1	3.150	MSTRG.31079.1	-7.190
MSTRG.20876.1	3.106	MSTRG.37483.4	-7.102
MSTRG.45091.1	3.105	MSTRG.43317.1	-7.085
MSTRG.39426.1	3.084	MSTRG.445.2	-7.079
MSTRG.46021.3	3.071	MSTRG.19506.1	-7.068
MSTRG.42220.1	3.049	MSTRG.29351.3	-7.058
MSTRG.16098.1	3.011	MSTRG.41755.2	-7.050
MSTRG.21216.2	2.992	MSTRG.27647.1	-7.039
MSTRG.35690.2	2.989	MSTRG.20908.4	-6.995
MSTRG.25168.1	2.978	MSTRG.48409.3	-6.995
MSTRG.9551.1	2.972	MSTRG.43992.3	-6.958
MSTRG.835.2	2.948	MSTRG.12300.5	-6.958
MSTRG.36207.3	2.867	MSTRG.43992.4	-6.939
MSTRG.42222.1	2.861	MSTRG.26863.1	-6.905
MSTRG.7132.2	2.861	MSTRG.40154.1	-6.839
MSTRG.17761.1	2.857	MSTRG.6886.2	-6.818
MSTRG.33892.2	2.853	MSTRG.45851.6	-6.795
MSTRG.10934.2	2.838	MSTRG.22149.3	-6.785
MSTRG.46183.1	2.837	MSTRG.16356.3	-6.776
MSTRG.48756.1	2.820	MSTRG.39591.1	-6.761
MSTRG.20412.1	2.792	MSTRG.6520.5	-6.750

MSTRG.29715.1	2.778	MSTRG.23675.2	-6.716
MSTRG.8848.2	2.771	MSTRG.302.2	-6.604
MSTRG.31479.3	2.763	MSTRG.31254.3	-6.592
MSTRG.3855.6	2.752	MSTRG.4184.2	-6.590
MSTRG.39047.1	2.742	MSTRG.29191.2	-6.559
MSTRG.9228.2	2.702	MSTRG.25377.5	-6.554
MSTRG.5288.3	2.684	MSTRG.40020.3	-6.550
MSTRG.656.1	2.667	MSTRG.11853.4	-6.540
MSTRG.42456.1	2.649	MSTRG.40571.1	-6.516
MSTRG.44940.3	2.640	MSTRG.28784.5	-6.516
MSTRG.28090.1	2.638	MSTRG.17100.3	-6.478
MSTRG.37776.1	2.632	MSTRG.2922.2	-6.464
MSTRG.26394.1	2.615	MSTRG.44684.3	-6.460
MSTRG.1855.1	2.615	MSTRG.45196.2	-6.438
MSTRG.29713.1	2.613	MSTRG.38098.2	-6.383
MSTRG.31909.2	2.598	MSTRG.20554.1	-6.324
MSTRG.266.2	2.595	MSTRG.45473.1	-6.318
MSTRG.27249.1	2.580	MSTRG.24231.1	-6.307
MSTRG.14017.1	2.559	MSTRG.36707.2	-6.284
MSTRG.6207.2	2.532	MSTRG.17358.1	-6.282
MSTRG.41580.1	2.495	MSTRG.15676.11	-6.256
MSTRG.38457.1	2.488	MSTRG.30031.3	-6.188
MSTRG.43783.1	2.479	MSTRG.35309.1	-6.170
MSTRG.15536.1	2.479	MSTRG.27932.1	-6.153
MSTRG.19992.1	2.470	MSTRG.42912.1	-6.140
MSTRG.41735.1	2.466	MSTRG.12049.1	-6.124
MSTRG.3790.1	2.460	MSTRG.7026.3	-6.113

MSTRG.46429.3	2.448	MSTRG.48339.1	-6.036
MSTRG.39040.2	2.446	MSTRG.46714.1	-6.027
MSTRG.25172.1	2.433	MSTRG.36311.3	-5.995
MSTRG.132.1	2.423	MSTRG.41478.2	-5.994
MSTRG.12225.1	2.419	MSTRG.22547.2	-5.867
MSTRG.24256.2	2.391	MSTRG.5048.5	-5.839
MSTRG.7183.1	2.376	MSTRG.7892.2	-5.812
MSTRG.40667.2	2.366	MSTRG.45972.4	-5.754
MSTRG.27257.1	2.360	MSTRG.42363.1	-5.739
MSTRG.23485.1	2.349	MSTRG.7591.10	-5.734
MSTRG.28518.1	2.348	MSTRG.30611.5	-5.718
MSTRG.23404.1	2.334	MSTRG.2093.2	-5.710
MSTRG.38920.1	2.330	MSTRG.35742.3	-5.706
MSTRG.38919.1	2.330	MSTRG.34125.1	-5.704
MSTRG.30611.4	2.317	MSTRG.16218.2	-5.653
MSTRG.43142.1	2.303	MSTRG.30384.1	-5.644
MSTRG.37774.1	2.302	MSTRG.12700.2	-5.642
MSTRG.27252.1	2.276	MSTRG.20677.3	-5.616
MSTRG.27326.5	2.268	MSTRG.21772.2	-5.610
MSTRG.14538.1	2.267	MSTRG.32732.2	-5.593
MSTRG.24486.1	2.261	MSTRG.20243.2	-5.546
MSTRG.5508.1	2.256	MSTRG.6562.3	-5.517
MSTRG.37801.1	2.252	MSTRG.12291.3	-5.459
MSTRG.35823.1	2.193	MSTRG.44920.2	-5.452
MSTRG.23729.1	2.191	MSTRG.37602.1	-5.445
MSTRG.39503.1	2.182	MSTRG.43479.1	-5.428
MSTRG.35519.1	2.173	MSTRG.11986.1	-5.427

MSTRG.23163.1	2.161	MSTRG.35294.3	-5.407
MSTRG.10756.1	2.158	MSTRG.27525.1	-5.392
MSTRG.36718.1	2.145	MSTRG.47664.2	-5.387
MSTRG.17371.1	2.145	MSTRG.27114.4	-5.361
MSTRG.46206.1	2.142	MSTRG.42395.4	-5.354
MSTRG.42482.1	2.142	MSTRG.16224.1	-5.258
MSTRG.22778.2	2.130	MSTRG.45467.13	-5.234
MSTRG.42927.1	2.127	MSTRG.8366.3	-5.151
MSTRG.13762.1	2.108	MSTRG.30341.4	-5.132
MSTRG.28270.1	2.103	MSTRG.1295.3	-5.086
MSTRG.16194.1	2.102	MSTRG.38545.3	-5.082
MSTRG.11829.1	2.094	MSTRG.3632.2	-5.070
MSTRG.48061.2	2.084	MSTRG.21691.6	-5.058
MSTRG.12597.1	2.078	MSTRG.39581.1	-4.983
MSTRG.23308.1	2.077	MSTRG.22976.2	-4.957
MSTRG.5179.1	2.072	MSTRG.5985.2	-4.904
MSTRG.11719.1	2.067	MSTRG.6003.2	-4.872
MSTRG.16936.1	2.065	MSTRG.11796.11	-4.869
MSTRG.5621.1	2.063	MSTRG.38545.4	-4.848
MSTRG.44046.1	2.062	MSTRG.35597.1	-4.842
MSTRG.28271.1	2.058	MSTRG.4323.1	-4.812
MSTRG.1285.1	2.056	MSTRG.23606.2	-4.810
MSTRG.45429.1	2.050	MSTRG.6540.6	-4.723
MSTRG.38837.1	2.018	MSTRG.28605.4	-4.710
MSTRG.6222.1	2.017	MSTRG.23422.8	-4.645
MSTRG.42536.2	2.008	MSTRG.30539.7	-4.614
MSTRG.12465.8	2.007	MSTRG.29688.4	-4.547

MSTRG.36851.1	2.004	MSTRG.39546.1	-4.530
MSTRG.4167.2	1.996	MSTRG.5155.2	-4.502
MSTRG.36362.1	1.993	MSTRG.8000.4	-4.498
MSTRG.26569.1	1.987	MSTRG.9164.4	-4.396
MSTRG.32022.1	1.985	MSTRG.46368.1	-4.386
MSTRG.22002.3	1.982	MSTRG.46018.5	-4.377
MSTRG.12092.1	1.974	MSTRG.10886.2	-4.358
MSTRG.37261.4	1.974	MSTRG.30382.1	-4.329
MSTRG.17771.1	1.973	MSTRG.12113.1	-4.306
MSTRG.45418.2	1.945	MSTRG.28114.3	-4.224
MSTRG.39503.2	1.930	MSTRG.47870.3	-4.223
MSTRG.6090.1	1.923	MSTRG.29420.11	-4.214
MSTRG.34586.1	1.911	MSTRG.42636.1	-4.176
MSTRG.20745.2	1.905	MSTRG.20425.4	-4.090
MSTRG.46838.2	1.894	MSTRG.37326.2	-4.078
MSTRG.43766.1	1.894	MSTRG.39024.1	-4.072
MSTRG.38949.1	1.892	MSTRG.43716.3	-4.037
MSTRG.27550.1	1.891	MSTRG.6182.19	-4.026
MSTRG.45579.1	1.889	MSTRG.35690.1	-4.010
MSTRG.10754.1	1.885	MSTRG.29897.1	-3.993
MSTRG.38398.3	1.881	MSTRG.9646.1	-3.962
MSTRG.46719.1	1.879	MSTRG.40034.1	-3.913
MSTRG.43595.1	1.877	MSTRG.15111.2	-3.884
MSTRG.40642.1	1.877	MSTRG.22626.2	-3.875
MSTRG.38887.3	1.873	MSTRG.8909.2	-3.864
MSTRG.17792.2	1.868	MSTRG.15311.2	-3.837
MSTRG.23383.1	1.863	MSTRG.15896.1	-3.835

MSTRG.35542.1	1.861	MSTRG.37945.1	-3.819
MSTRG.21470.2	1.846	MSTRG.533.2	-3.763
MSTRG.16348.5	1.828	MSTRG.14983.2	-3.748
MSTRG.35174.1	1.826	MSTRG.9724.2	-3.697
MSTRG.676.1	1.815	MSTRG.12482.2	-3.664
MSTRG.39756.1	1.813	MSTRG.18729.1	-3.661
MSTRG.37895.4	1.809	MSTRG.10340.3	-3.650
MSTRG.37002.1	1.807	MSTRG.15240.1	-3.638
MSTRG.7922.1	1.792	MSTRG.2349.3	-3.630
MSTRG.3427.6	1.785	MSTRG.9515.2	-3.626
MSTRG.45338.1	1.784	MSTRG.16495.2	-3.619
MSTRG.32021.1	1.774	MSTRG.28716.2	-3.587
MSTRG.35615.1	1.774	MSTRG.47504.1	-3.582
MSTRG.579.1	1.768	MSTRG.16949.2	-3.564
MSTRG.21887.1	1.765	MSTRG.30285.4	-3.532
MSTRG.26799.3	1.761	MSTRG.25518.1	-3.519
MSTRG.2648.1	1.761	MSTRG.29833.2	-3.518
MSTRG.2270.3	1.747	MSTRG.38195.3	-3.478
MSTRG.27240.1	1.737	MSTRG.15606.1	-3.471
MSTRG.24795.1	1.733	MSTRG.42633.1	-3.457
MSTRG.17875.1	1.729	MSTRG.23773.7	-3.441
MSTRG.37732.2	1.724	MSTRG.46809.9	-3.437
MSTRG.21093.1	1.724	MSTRG.20721.1	-3.433
MSTRG.17858.1	1.721	MSTRG.23763.8	-3.433
MSTRG.34758.1	1.715	MSTRG.34161.2	-3.430
MSTRG.33330.1	1.715	MSTRG.43193.3	-3.415
MSTRG.25640.2	1.714	MSTRG.1295.1	-3.411

MSTRG.45891.1	1.707	MSTRG.20792.1	-3.377
MSTRG.20008.1	1.706	MSTRG.5259.1	-3.367
MSTRG.6918.1	1.706	MSTRG.39388.4	-3.356
MSTRG.7916.1	1.699	MSTRG.37469.1	-3.333
MSTRG.22779.1	1.698	MSTRG.37947.1	-3.306
MSTRG.2479.1	1.692	MSTRG.42730.1	-3.306
MSTRG.16933.1	1.688	MSTRG.12253.1	-3.303
MSTRG.24720.1	1.675	MSTRG.7893.2	-3.296
MSTRG.25354.1	1.668	MSTRG.42634.1	-3.209
MSTRG.22244.3	1.668	MSTRG.2351.1	-3.178
MSTRG.210.1	1.666	MSTRG.24963.1	-3.154
MSTRG.42887.1	1.659	MSTRG.494.3	-3.145
MSTRG.17118.1	1.650	MSTRG.34289.1	-3.144
MSTRG.16018.1	1.645	MSTRG.4365.1	-3.134
MSTRG.38907.1	1.644	MSTRG.4327.1	-3.132
MSTRG.11713.1	1.634	MSTRG.9382.3	-3.128
MSTRG.29232.1	1.632	MSTRG.47851.1	-3.119
MSTRG.44417.1	1.628	MSTRG.8051.1	-3.104
MSTRG.45453.3	1.623	MSTRG.32665.2	-3.104
MSTRG.15919.2	1.621	MSTRG.4653.1	-3.101
MSTRG.46676.1	1.619	MSTRG.30924.3	-3.091
MSTRG.35648.2	1.618	MSTRG.45590.1	-3.090
MSTRG.45661.1	1.616	MSTRG.36220.2	-3.085
MSTRG.27243.1	1.614	MSTRG.46500.5	-3.068
MSTRG.29282.1	1.606	MSTRG.28437.1	-3.001
MSTRG.25190.1	1.605	MSTRG.35723.2	-2.972
MSTRG.14616.1	1.599	MSTRG.29371.6	-2.969

MSTRG.9335.1	1.594	MSTRG.13101.13	-2.940
MSTRG.8403.1	1.591	MSTRG.46479.1	-2.916
MSTRG.5769.4	1.588	MSTRG.27714.1	-2.900
MSTRG.42318.4	1.583	MSTRG.11796.80	-2.877
MSTRG.35651.1	1.579	MSTRG.15472.4	-2.837
MSTRG.26263.2	1.579	MSTRG.4531.1	-2.826
MSTRG.34788.1	1.574	MSTRG.11796.37	-2.810
MSTRG.8751.2	1.574	MSTRG.27034.1	-2.804
MSTRG.46397.1	1.558	MSTRG.21204.3	-2.800
MSTRG.1143.1	1.558	MSTRG.9582.1	-2.791
MSTRG.10466.1	1.555	MSTRG.9583.1	-2.791
MSTRG.1151.1	1.546	MSTRG.11756.3	-2.782
MSTRG.39429.2	1.544	MSTRG.1588.5	-2.776
MSTRG.14867.1	1.542	MSTRG.39192.3	-2.774
MSTRG.41521.1	1.540	MSTRG.5150.2	-2.772
MSTRG.34697.1	1.538	MSTRG.22830.3	-2.771
MSTRG.1096.1	1.538	MSTRG.44314.1	-2.767
MSTRG.47783.1	1.538	MSTRG.40248.1	-2.741
MSTRG.19493.1	1.537	MSTRG.40097.4	-2.729
MSTRG.34102.1	1.534	MSTRG.1227.3	-2.728
MSTRG.20842.1	1.532	MSTRG.20458.1	-2.725
MSTRG.13950.1	1.530	MSTRG.35599.1	-2.722
MSTRG.23164.1	1.528	MSTRG.17212.3	-2.718
MSTRG.40236.1	1.528	MSTRG.46112.2	-2.714
MSTRG.24547.1	1.523	MSTRG.44944.2	-2.700
MSTRG.21856.1	1.521	MSTRG.19810.1	-2.700
MSTRG.48693.1	1.514	MSTRG.25908.1	-2.662

MSTRG.20589.1	1.510	MSTRG.10886.4	-2.651
MSTRG.33226.1	1.500	MSTRG.6240.2	-2.650
MSTRG.10522.2	1.500	MSTRG.44493.3	-2.629
MSTRG.9852.1	1.497	MSTRG.8722.1	-2.618
MSTRG.14558.1	1.496	MSTRG.40927.2	-2.615
MSTRG.22678.3	1.495	MSTRG.23433.1	-2.585
MSTRG.45702.1	1.491	MSTRG.35448.2	-2.576
MSTRG.7192.2	1.490	MSTRG.37472.3	-2.576
MSTRG.33083.1	1.486	MSTRG.22811.2	-2.569
MSTRG.11395.1	1.486	MSTRG.31106.2	-2.567
MSTRG.39637.1	1.483	MSTRG.10909.1	-2.536
MSTRG.44973.5	1.481	MSTRG.26407.1	-2.528
MSTRG.23728.1	1.475	MSTRG.28897.7	-2.513
MSTRG.16830.1	1.473	MSTRG.23213.1	-2.509
MSTRG.13311.1	1.465	MSTRG.9645.1	-2.477
MSTRG.40065.3	1.463	MSTRG.6203.2	-2.453
MSTRG.38708.1	1.457	MSTRG.30895.1	-2.443
MSTRG.15364.1	1.457	MSTRG.35285.1	-2.437
MSTRG.28778.1	1.454	MSTRG.14576.10	-2.426
MSTRG.13328.1	1.449	MSTRG.6765.1	-2.415
MSTRG.44693.1	1.446	MSTRG.8737.1	-2.410
MSTRG.18832.1	1.445	MSTRG.48503.1	-2.398
MSTRG.48731.1	1.445	MSTRG.34252.1	-2.393
MSTRG.38699.1	1.442	MSTRG.17703.1	-2.372
MSTRG.31892.1	1.441	MSTRG.47852.1	-2.367
MSTRG.12682.1	1.437	MSTRG.21842.4	-2.362
MSTRG.12091.1	1.437	MSTRG.12951.1	-2.359

MSTRG.14158.3	1.436	MSTRG.48324.2	-2.357
MSTRG.44973.7	1.435	MSTRG.17488.1	-2.339
MSTRG.31019.1	1.435	MSTRG.44390.1	-2.322
MSTRG.31777.1	1.430	MSTRG.22398.1	-2.321
MSTRG.15255.1	1.429	MSTRG.37954.2	-2.320
MSTRG.5915.1	1.426	MSTRG.19682.2	-2.280
MSTRG.13942.1	1.425	MSTRG.29102.3	-2.280
MSTRG.32824.1	1.417	MSTRG.4016.1	-2.280
MSTRG.13149.1	1.414	MSTRG.9911.1	-2.275
MSTRG.35399.1	1.410	MSTRG.6697.2	-2.271
MSTRG.35526.1	1.407	MSTRG.38208.6	-2.270
MSTRG.30409.1	1.406	MSTRG.28055.3	-2.258
MSTRG.5447.1	1.404	MSTRG.1487.2	-2.253
MSTRG.28349.1	1.403	MSTRG.44885.1	-2.247
MSTRG.12968.1	1.403	MSTRG.41478.3	-2.247
MSTRG.13750.1	1.399	MSTRG.38208.10	-2.244
MSTRG.29206.1	1.399	MSTRG.43663.3	-2.244
MSTRG.9502.1	1.397	MSTRG.1727.2	-2.227
MSTRG.16677.1	1.396	MSTRG.31541.6	-2.220
MSTRG.27592.1	1.392	MSTRG.39910.1	-2.218
MSTRG.44692.1	1.391	MSTRG.41473.1	-2.213
MSTRG.24569.1	1.389	MSTRG.18251.3	-2.209
MSTRG.15692.1	1.389	MSTRG.34432.1	-2.204
MSTRG.14659.1	1.388	MSTRG.5905.2	-2.201
MSTRG.38670.3	1.381	MSTRG.20416.11	-2.192
MSTRG.48732.1	1.381	MSTRG.17486.1	-2.189
MSTRG.683.1	1.374	MSTRG.32536.4	-2.187

MSTRG.30337.1	1.374	MSTRG.11711.1	-2.186
MSTRG.41824.1	1.359	MSTRG.22884.6	-2.185
MSTRG.7602.1	1.355	MSTRG.23434.6	-2.185
MSTRG.17926.1	1.355	MSTRG.24095.1	-2.173
MSTRG.31027.1	1.351	MSTRG.3559.2	-2.164
MSTRG.5164.1	1.349	MSTRG.33007.3	-2.159
MSTRG.3980.1	1.347	MSTRG.42974.1	-2.157
MSTRG.39940.1	1.346	MSTRG.11784.16	-2.157
MSTRG.32327.3	1.345	MSTRG.25272.1	-2.146
MSTRG.42306.6	1.336	MSTRG.43032.1	-2.133
MSTRG.19819.1	1.334	MSTRG.1323.3	-2.116
MSTRG.19804.1	1.332	MSTRG.42632.1	-2.114
MSTRG.13583.1	1.331	MSTRG.16832.1	-2.109
MSTRG.8940.1	1.331	MSTRG.42319.1	-2.100
MSTRG.19810.3	1.330	MSTRG.4433.1	-2.097
MSTRG.10648.1	1.330	MSTRG.36427.4	-2.079
MSTRG.46618.1	1.330	MSTRG.5213.1	-2.079
MSTRG.41523.1	1.324	MSTRG.10390.3	-2.077
MSTRG.9509.1	1.321	MSTRG.24048.4	-2.076
MSTRG.45115.1	1.320	MSTRG.6668.1	-2.069
MSTRG.22535.1	1.319	MSTRG.42404.1	-2.059
MSTRG.26288.1	1.318	MSTRG.15390.1	-2.051
MSTRG.40628.2	1.315	MSTRG.48651.2	-2.041
MSTRG.37674.3	1.313	MSTRG.34409.1	-2.033
MSTRG.6752.3	1.311	MSTRG.41875.1	-2.031
MSTRG.42919.1	1.310	MSTRG.39151.4	-2.026
MSTRG.47107.1	1.303	MSTRG.38303.2	-2.008

MSTRG.44567.2	1.302	MSTRG.47379.1	-2.003
MSTRG.46681.1	1.300	MSTRG.40189.3	-1.999
MSTRG.43944.2	1.298	MSTRG.13649.1	-1.995
MSTRG.32439.1	1.297	MSTRG.31742.1	-1.994
MSTRG.4131.1	1.297	MSTRG.20642.1	-1.984
MSTRG.25461.1	1.296	MSTRG.11779.2	-1.976
MSTRG.8725.1	1.294	MSTRG.28309.1	-1.970
MSTRG.19678.1	1.289	MSTRG.32031.1	-1.970
MSTRG.25264.1	1.286	MSTRG.12131.1	-1.967
MSTRG.33191.1	1.283	MSTRG.19491.1	-1.965
MSTRG.9924.10	1.279	MSTRG.8139.2	-1.963
MSTRG.39014.1	1.278	MSTRG.31556.1	-1.950
MSTRG.32517.4	1.277	MSTRG.47466.1	-1.943
MSTRG.399.1	1.277	MSTRG.38812.1	-1.937
MSTRG.35024.1	1.273	MSTRG.11802.3	-1.926
MSTRG.41809.1	1.262	MSTRG.20719.1	-1.924
MSTRG.42822.1	1.258	MSTRG.20217.3	-1.918
MSTRG.24281.1	1.257	MSTRG.29969.3	-1.911
MSTRG.15184.1	1.251	MSTRG.29485.1	-1.908
MSTRG.31373.1	1.251	MSTRG.19490.1	-1.906
MSTRG.39409.1	1.250	MSTRG.6673.1	-1.896
MSTRG.27480.1	1.249	MSTRG.1717.2	-1.891
MSTRG.11480.1	1.248	MSTRG.30790.1	-1.882
MSTRG.7555.1	1.246	MSTRG.4012.3	-1.881
MSTRG.15450.1	1.245	MSTRG.6697.3	-1.866
MSTRG.27816.1	1.244	MSTRG.18687.1	-1.865
MSTRG.10644.1	1.242	MSTRG.6236.1	-1.855

MSTRG.34795.1	1.241	MSTRG.10032.1	-1.841
MSTRG.10498.1	1.235	MSTRG.16784.1	-1.841
MSTRG.34101.1	1.233	MSTRG.40176.1	-1.834
MSTRG.9107.1	1.227	MSTRG.5514.1	-1.832
MSTRG.5720.1	1.226	MSTRG.48405.2	-1.811
MSTRG.23923.1	1.226	MSTRG.11784.10	-1.808
MSTRG.27177.2	1.223	MSTRG.22668.3	-1.807
MSTRG.2532.1	1.219	MSTRG.47493.2	-1.800
MSTRG.21072.1	1.217	MSTRG.12253.2	-1.797
MSTRG.41986.1	1.217	MSTRG.16499.1	-1.785
MSTRG.29004.1	1.216	MSTRG.30928.1	-1.779
MSTRG.5696.1	1.212	MSTRG.2270.1	-1.760
MSTRG.33190.1	1.211	MSTRG.20094.6	-1.758
MSTRG.22876.1	1.207	MSTRG.20739.1	-1.752
MSTRG.23924.1	1.205	MSTRG.16725.1	-1.752
MSTRG.9711.1	1.204	MSTRG.43116.1	-1.751
MSTRG.44652.2	1.200	MSTRG.35980.4	-1.749
MSTRG.10522.1	1.196	MSTRG.33733.1	-1.742
MSTRG.28991.1	1.196	MSTRG.15553.2	-1.740
MSTRG.31619.1	1.195	MSTRG.25126.1	-1.730
MSTRG.12820.1	1.189	MSTRG.18574.1	-1.726
MSTRG.11144.1	1.186	MSTRG.17560.1	-1.714
MSTRG.46985.1	1.185	MSTRG.31351.4	-1.705
MSTRG.35014.1	1.184	MSTRG.34802.2	-1.704
MSTRG.18068.1	1.182	MSTRG.26843.1	-1.697
MSTRG.1312.1	1.182	MSTRG.25798.1	-1.693
MSTRG.39769.1	1.181	MSTRG.31042.1	-1.685

MSTRG.20610.1	1.173	MSTRG.22830.12	-1.682
MSTRG.25791.1	1.172	MSTRG.14729.1	-1.681
MSTRG.13098.1	1.172	MSTRG.31061.1	-1.681
MSTRG.8356.1	1.164	MSTRG.9221.2	-1.679
MSTRG.16393.1	1.159	MSTRG.47493.1	-1.679
MSTRG.39054.1	1.157	MSTRG.34546.1	-1.678
MSTRG.26728.1	1.155	MSTRG.20269.1	-1.677
MSTRG.13027.3	1.151	MSTRG.1671.1	-1.677
MSTRG.48602.1	1.149	MSTRG.22726.1	-1.676
MSTRG.40065.5	1.149	MSTRG.45571.1	-1.675
MSTRG.34057.1	1.149	MSTRG.14975.1	-1.669
MSTRG.15697.1	1.147	MSTRG.14770.4	-1.658
MSTRG.8010.2	1.145	MSTRG.38011.2	-1.646
MSTRG.21880.5	1.143	MSTRG.30210.1	-1.628
MSTRG.12372.1	1.143	MSTRG.5025.2	-1.618
MSTRG.41554.1	1.139	MSTRG.11343.1	-1.608
MSTRG.35528.2	1.139	MSTRG.11258.2	-1.606
MSTRG.45238.1	1.139	MSTRG.30493.1	-1.605
MSTRG.11357.2	1.137	MSTRG.12906.1	-1.602
MSTRG.19122.1	1.136	MSTRG.23912.1	-1.599
MSTRG.22609.1	1.135	MSTRG.46024.1	-1.598
MSTRG.6402.1	1.134	MSTRG.32791.1	-1.597
MSTRG.35240.1	1.133	MSTRG.24048.1	-1.593
MSTRG.67.1	1.128	MSTRG.20629.1	-1.586
MSTRG.8848.1	1.126	MSTRG.11603.2	-1.573
MSTRG.16998.1	1.123	MSTRG.20491.1	-1.570
MSTRG.17343.1	1.121	MSTRG.434.1	-1.567

MSTRG.6203.1	1.120	MSTRG.40955.2	-1.563
MSTRG.20745.1	1.118	MSTRG.42391.1	-1.559
MSTRG.12462.1	1.118	MSTRG.21323.1	-1.557
MSTRG.19712.1	1.110	MSTRG.29849.5	-1.549
MSTRG.11878.1	1.109	MSTRG.7798.1	-1.547
MSTRG.40985.1	1.107	MSTRG.23438.1	-1.542
MSTRG.48419.1	1.107	MSTRG.36186.2	-1.540
MSTRG.17552.1	1.106	MSTRG.2942.1	-1.539
MSTRG.10277.1	1.103	MSTRG.23655.1	-1.538
MSTRG.14220.1	1.102	MSTRG.13865.1	-1.533
MSTRG.26007.1	1.101	MSTRG.4465.1	-1.522
MSTRG.34809.1	1.098	MSTRG.8050.1	-1.510
MSTRG.1048.1	1.098	MSTRG.34074.10	-1.510
MSTRG.25434.1	1.096	MSTRG.41969.6	-1.509
MSTRG.42045.1	1.095	MSTRG.35793.1	-1.497
MSTRG.16439.1	1.095	MSTRG.22623.4	-1.491
MSTRG.13280.2	1.094	MSTRG.25397.1	-1.490
MSTRG.12244.1	1.094	MSTRG.4542.1	-1.481
MSTRG.198.1	1.092	MSTRG.45865.1	-1.481
MSTRG.15693.1	1.091	MSTRG.13393.4	-1.472
MSTRG.42597.1	1.090	MSTRG.31142.1	-1.472
MSTRG.15171.1	1.089	MSTRG.5041.1	-1.462
MSTRG.32922.1	1.088	MSTRG.22975.3	-1.458
MSTRG.17540.1	1.086	MSTRG.12132.1	-1.450
MSTRG.31897.1	1.084	MSTRG.43874.1	-1.448
MSTRG.37211.1	1.083	MSTRG.21892.1	-1.440
MSTRG.15447.1	1.083	MSTRG.17410.1	-1.435

MSTRG.12653.1	1.082	MSTRG.22975.2	-1.431
MSTRG.8960.1	1.082	MSTRG.39265.1	-1.425
MSTRG.22511.1	1.081	MSTRG.30033.3	-1.422
MSTRG.48128.1	1.081	MSTRG.30512.1	-1.421
MSTRG.16474.6	1.079	MSTRG.46018.13	-1.416
MSTRG.42262.1	1.078	MSTRG.33626.1	-1.414
MSTRG.15470.1	1.077	MSTRG.26837.12	-1.414
MSTRG.7137.1	1.074	MSTRG.42295.1	-1.410
MSTRG.45567.6	1.073	MSTRG.35794.1	-1.403
MSTRG.14458.1	1.073	MSTRG.33915.1	-1.401
MSTRG.42163.1	1.067	MSTRG.29825.1	-1.396
MSTRG.9229.1	1.066	MSTRG.42502.1	-1.394
MSTRG.1797.1	1.058	MSTRG.17270.1	-1.394
MSTRG.2805.1	1.058	MSTRG.7217.1	-1.394
MSTRG.45884.1	1.056	MSTRG.36783.1	-1.391
MSTRG.46938.1	1.056	MSTRG.34391.6	-1.390
MSTRG.41323.1	1.055	MSTRG.11744.1	-1.385
MSTRG.7600.1	1.053	MSTRG.37094.1	-1.381
MSTRG.24377.3	1.052	MSTRG.15782.1	-1.378
MSTRG.48420.1	1.052	MSTRG.17386.1	-1.372
MSTRG.18261.2	1.043	MSTRG.42254.1	-1.370
MSTRG.7556.1	1.042	MSTRG.4646.4	-1.370
MSTRG.18712.1	1.042	MSTRG.32029.1	-1.363
MSTRG.29586.1	1.041	MSTRG.10592.1	-1.360
MSTRG.18294.1	1.040	MSTRG.29113.1	-1.356
MSTRG.9308.4	1.038	MSTRG.2575.2	-1.354
MSTRG.16485.1	1.034	MSTRG.37261.2	-1.354

MSTRG.44923.1	1.034	MSTRG.12025.1	-1.351
MSTRG.34133.7	1.032	MSTRG.30220.1	-1.350
MSTRG.18550.1	1.032	MSTRG.5851.3	-1.340
MSTRG.7918.1	1.029	MSTRG.38058.1	-1.338
MSTRG.47044.1	1.027	MSTRG.6839.4	-1.334
MSTRG.29884.1	1.025	MSTRG.47450.4	-1.333
MSTRG.9968.1	1.023	MSTRG.2533.1	-1.332
MSTRG.21028.2	1.022	MSTRG.43261.13	-1.332
MSTRG.11634.1	1.022	MSTRG.44897.1	-1.330
MSTRG.14177.2	1.022	MSTRG.472.1	-1.328
MSTRG.5905.1	1.018	MSTRG.44419.2	-1.327
MSTRG.17468.1	1.016	MSTRG.34005.1	-1.322
MSTRG.1828.1	1.014	MSTRG.11802.6	-1.319
MSTRG.25339.1	1.013	MSTRG.5601.16	-1.308
MSTRG.20381.1	1.005	MSTRG.42097.1	-1.308
MSTRG.21216.1	1.003	MSTRG.14793.1	-1.301
MSTRG.33653.1	1.002	MSTRG.38977.1	-1.299