The Role of DNA Methylation in Arthropods.

Thesis Submitted for the Degree of
Doctor of Philosophy
at the University of Leicester.

By

Hollie Jade Marshall

Department of Genetics and Genome Biology
School of Biological Sciences
College of Medicine, Biological Sciences and Psychology
August 2019

Abstract

The Role of DNA Methylation in Arthropods.

Hollie Jade Marshall.

Epigenetic mechanisms, such as DNA methylation, are poorly understood in arthropods compared to mammals and plants. Arthropods have been shown to display a variety of DNA methylation profiles across species, making them ideal for understanding the function of DNA methylation outside of a mammalian context. This thesis explores the role of DNA methylation in two arthropod species; the eusocial bumblebee, *Bombus terrestris* and the freshwater crustacean *Daphnia magna*.

Previous research has implicated DNA methylation in caste determination in some social insect species. I have found differentially methylated genes between worker castes of *B. terrestris*, some of which are involved in reproduction. However, there was no direct link with differentially expressed genes. This indicates DNA methylation does not causally affect gene expression differences between castes.

Another possible function of DNA methylation in *B. terrestris* is the regulation of imprinted genes. Imprinted genes are those which display parent-of-origin allele-specific expression. Predictions based on the kinship theory state imprinted genes should exist in *B. terrestris*. I have identified parent-of-origin expression in this species, indicating some support for the kinship theory. However, DNA methylation does not appear to be directly mediating this process.

The final chapter of this thesis identified DNA methylation changes through time in a single resurrected population of *D. magna*. A small number of genes which exhibited DNA methylation changes over time were involved in the production of males, which is usually triggered by environmental change. The data generated in this chapter will be used for novel analyses investigating the adaptive potential of DNA methylation.

This thesis has contributed new knowledge to three fields: caste determination in social insects, imprinted genes in social insects and adaptive epigenetics. Taken as a whole, the studies presented here highlight the need for functional validation and the consideration of genotype in future ecological epigenetic research.

Acknowledgements

A massive thank you to Dr. Eamonn Mallon for being the most awesome supervisor! You have taught me, not only all of the science-y things I have needed, but also so much more. I've been fighting for a career for years and seeing how you balance your career with your family, and put them first, genuinely made me re-think my priorities. Thank you so much for that. On that note, thank you for grounding me when I needed it but also thank you for letting me pursue, pretty much, whatever I wanted (including swanning off to Birmingham for over a year). Also thank you for supporting the fact I needed to work. Whilst we may never be friends (you have too many already), I hope we can be colleagues.

Thank you to Dr. Luisa Orsini for hosting me in Birmingham for the final chapter of my thesis. Thank you for all of the support you offered through out this project, especially when it was going wrong at every turn. Also thank your for securing students for me even though you were on a 'no student year'. I also want to say how much I appreciate the extra opportunities you have given me to really make this project exciting! Finally a huge thank you for managing to wangle a short-term contract for me so I can finish the analyses on this project and hopefully produce some awesome science! It is very much appreciated (no more working at Gala Bingo for me!).

I also want to say thank you to Prof. Tom Wenseleers, without whom, the bulk of this thesis would not have been possible. Thank you for trusting me with your data and samples, I hope they lead to some great publications. Also thank you for hosting me in Leuven for a week and allowing me to stay with you and Beatrice. I hope to cross paths again in the future.

Next I want to thank Dr. Sinead Drea and Dr. Ezio Rosato for providing so much encouragement and excellent feedback during my PRP meetings. They were a pleasure rather than a chore. Also thank you to Dr. Cas Kramer for offering so many public engagement opportunities and for providing dog-related support when it was very much needed! I would also like to thank Michael Jordan for supplying excellent financial

administrative support for the conferences I organised, I will be holding all future institutions to your standard.

A big thank you to all of the members of Lab 219, especially; Dr. Zoe Lonsdale, Dr. Pshtiwan Bebane, Alun Jones, Christian Thomas and Hannah Sampson. A special thank you to Lisa Bedder for helping me with so many obscure tasks, including all of the *E. coli* help which wasn't even for our lab. Another special thank you to Dr. Ben Hunt for helping tighten the differential methylation pipeline and for providing a listening ear. A final big thank you to Boris Berkhout for being an awesome friend (and tidy house-mate). I appreciate all of the statistical help and hopefully our labs will collaborate one day in the future.

Last, but certainly not least, I want to thank Mike. You have put up with so much from me over the last few years. You have; scarified holidays away, helped with my code, read drafts of my work, supported me emotionally and financially, changed your lifestyle to fit in around all of my jobs and definitely taken more than your share of the dog-related chores. You've even agreed to up-root your life to move to Scotland with me! I genuinely couldn't have asked for a better partner throughout all of this, thank you.

Contents

Abstract i

Acknowledgements ii

Collaborative Work Statement ix

List of Tables x

List of Figures xi

Abbreviations xv

1 Introduction 1

1.1 Epigenetic mechanisms 1

1.1.1 Arthropod DNA methylation 2

1.1.2 Thesis rationale 4

1.2 Methylation and social-insect caste determination 5

1.2.1 Caste determination 5

1.2.2 Social-insect methylation 6

1.2.3 Bumblebees as a model system 8

1.2.4 Project aims 10

1.3 Genomic imprinting in social insects 10

1.3.1 Genomic imprinting 10

1.3.2 Theories of genomic imprinting 11

1.3.3 Haig's kinship theory 12

1.3.4 Social insects as an independent test 13

1.3.5 Bumblebees as a model system 14

1.3.6 Project aims 15

1.4 Adaptive methylation in natural populations 16

1.4.1 *Daphnia* as a model system 18

1.4.2 Project aims 20

2 Methylation and gene expression differences between reproductive castes of bumblebee workers. 21

2.1 Abstract 22
2.2 Introduction 23
2.3 Methods 25
2.3.1 Bee husbandry and tissue sampling 25
2.3.2 RNA and DNA extraction and sequencing 27
2.3.3 Differential expression and alternative splicing 29
2.3.4 Differential methylation 30
2.3.5 GO enrichment 31
2.3.6 Comparative analyses 32
2.4 Results 33
2.4.1 Collection of reproductive castes 33
2.4.2 DNA and RNA extraction 34
2.4.3 Genome-wide methylation differences between castes 35
2.4.4 Gene level methylation differences between castes 38
2.4.5 Expression differences between worker reproductive castes . . . 41
2.4.6 Relationship of methylation and differential gene expression . . 48
2.5 Discussion 52

3 Allele-specific methylation in reproductive and sterile bumblebee workers. 58

3.1 Abstract 59
3.2 Introduction 60
3.3 Methods 61
3.3.1 Data generation 61
3.3.2 Identification of allele-specific expression 62
3.3.3 Identification of allele-specific methylation 63
3.3.4 Gene ontology enrichment 64
3.3.5 Comparative analyses 65

3.4 Results . . . 65
3.4.1 Allele specific expression . . . 65
3.4.2 Allele specific methylation . . . 70
3.4.3 Relationship of allele specific expression and methylation . . . 72
3.5 Discussion . . . 74

4 Reciprocal crosses and RNA-seq to explore genomic imprinting in the bumblebee, *Bombus terrestris*. 79
4.1 Abstract . . . 80
4.2 Introduction . . . 81
4.3 Methods . . . 84
4.3.1 Sample collection . . . 84
4.3.2 DNA and RNA extraction and sequencing . . . 86
4.3.3 Generation of alternative reference genomes . . . 86
4.3.4 Identification of parent-of-origin expression . . . 87
4.3.5 Differential expression . . . 88
4.3.6 Gene ontology enrichment . . . 89
4.3.7 Comparative analyses . . . 89
4.4 Results . . . 90
4.4.1 Generation of alternate genomes . . . 90
4.4.2 Parent-of-origin gene expression . . . 91
4.4.3 Differential expression between reproductive castes . . . 94
4.4.4 Overlap of parent-of-origin genes and differentially expressed genes 97
4.4.5 Honeybee homology . . . 98
4.5 Discussion . . . 99

5 Reciprocal crosses to identify parent-of-origin methylation in the bumblebee, *Bombus terrestris*. 104
5.1 Abstract . . . 105
5.2 Introduction . . . 106
5.3 Methods . . . 108
5.3.1 Sample collection . . . 108

5.3.2 DNA extraction and sequencing . . . 110
5.3.3 Differential methylation . . . 110
5.3.4 Generation of alternative reference genomes . . . 111
5.3.5 Identification of parent-of-origin methylation . . . 112
5.3.6 Gene ontology enrichment . . . 114
5.3.7 Comparative analyses . . . 114
5.4 Results . . . 115
5.4.1 DNA extraction and data quality . . . 115
5.4.2 Differential methylation . . . 116
5.4.3 Parent-of-origin methylation . . . 118
5.4.4 Relationship between parent-of-origin methylation and parent-of-origin expression . . . 122
5.5 Discussion . . . 124

6 Variation of DNA methylation in naturally occurring temporal populations of the water flea, *Daphnia magna*, to environmental stressors. 128
6.1 Abstract . . . 129
6.2 Introduction . . . 130
6.3 Methods . . . 133
6.3.1 Sample origin . . . 133
6.3.2 *Daphnia* husbandry and sampling . . . 135
6.3.3 DNA extraction and sequencing . . . 136
6.3.4 Differential methylation . . . 137
6.3.5 Gene ontology enrichment . . . 138
6.4 Results . . . 138
6.4.1 DNA extraction . . . 138
6.4.2 Data quality . . . 139
6.4.3 Genome-wide methylation differences between temporal temporal populations . . . 140
6.4.4 Differentially methylated genes between populations . . . 141
6.4.5 Similarity between differentially methylated genes . . . 143
6.5 Discussion . . . 146

7 Overall discussion **150**

7.1 Summary of results and major findings 150

7.1.1 Methylation and caste determination in *Bombus terrestris* . . . 150

7.1.2 Genomic imprinting in *Bombus terrestris* 151

7.1.3 Adaptive methylation in *Daphnia magna* 153

7.2 Impact on ecological epigenetics as a field 153

7.3 Future work 155

7.3.1 Functional validation 155

7.3.2 Genomic imprinting as a mechanism of plasticity 157

7.3.3 Transgenerational epigenetic adaptation 157

7.4 Conclusions 159

A Appendix: Chapter 2 **160**

A.1 Published paper 160

B Appendix: Chapter 4 **176**

B.1 Additional figures 176

C Appendix: Chapter 5 **179**

C.1 Poor quality sequencing comparison 179

D Appendix: Chapter 6 **181**

D.1 High-hardness COMBO 181

D.2 DNA extraction: optimised protocol 182

Collaborative Work Statement

Chapter 2: Methylation and gene expression differences between reproductive castes of bumblebee workers.

Dr. Eamonn Mallon conceived the study. Dr. Zoë Lonsdale and I carried out the animal husbandry and lab work. I conducted all bioinformatic analyses.

Chapter 3: Allele-specific methylation and gene expression in reproductive and sterile bumblebee workers.

Dr. Eamonn Mallon conceived the study. Dr. Zoë Lonsdale and I carried out the animal husbandry and lab work. I conducted all bioinformatic analyses.

Chapter 4: Reciprocal crosses and RNA-seq to explore genomic imprinting in the bumblebee, *Bombus terrestris*.

Professor Tom Wenseleers and Dr. Eamonn Mallon conceived the study. The reciprocal crosses were carried out by Biobest (Westerlo, Belgium) under supervision of Professor Felix Wäckers. Dr. Jelle van Zweden and Kristof Benaets carried out the behavioural observations and the lab work. I conducted all bioinformatic analyses.

Chapter 5: Reciprocal crosses to identify parent-of-origin methylation in the bumblebee, *Bombus terrestris*.

Dr. Eamonn Mallon, Professor Tom Wenseleers and I conceived the study. The reciprocal crosses were carried out by Biobest (Westerlo, Belgium) under supervision Professor Felix Wäckers. Dr. Jelle van Zweden and Kristof Benaets carried out the behavioural observations. I carried out the lab work and all bioinformatic analyses.

Chapter 6: Variation of methylation in naturally occurring temporal populations of the water flea, *Daphnia magna*, to environmental stressors.

Dr. Luisa Orsini and I conceived the study, with input from Dr. Eamonn Mallon and Dr. Leda Mirbahai. I carried out all animal husbandry, lab work and bioinformatic analyses.

List of Tables

2.1 Mean ovary weight and mean oocyte length. 33

2.2 Summary statistics of the linear models used to check for differences in weighted methylation level between gene sets. 50

3.1 Example of how the counts per SNP were allocated to assumed alleles. 63

3.2 Allelically methylated and allelically expressed genes in both castes. . . 73

5.1 Genes identified as showing parent-of-origin methylation. 120

6.1 Post-hoc stats for weighted methylation differences between temporal populations. 141

6.2 Filtering levels of CpGs throughout the analysis and total number of differentially methylated genes between temporal populations. 142

C.1 Summary statistics of the data generated by Liverpool Genomics and BGI. 180

D.1 Main stock solutions needed to create high-hardness COMBO media for culturing *Daphnia magna*. 181

D.2 Stock solutions required for Animate. 181

D.3 Stock solutions required for the VIM. 182

List of Figures

1.1 Percentage distribution of epigenetics research. 1
1.2 Bisulfite conversion process. 4
1.3 Genetic and epigenetic caste-determination model of *Melipona scutellaris*. 8
1.4 Bumblebee colont life cycle. 9
1.5 Inheritance probabilities of maternal and paternal genes in a bumblebee colony. 15
1.6 *Daphnia* life cycle. 18
1.7 *Daphnia magna* adult female with brood. 19

2.1 In lab colony set up. 26
2.2 Reproductive and sterile ovaries. 27
2.3 Overview of sample preparation for sequencing. 29
2.4 Reproductive and sterile sample statistics. 34
2.5 Agarose gel of DNA. 35
2.6 Genome-wide methylation differences between castes. 37
2.7 Linkage group methylation differences between castes. 38
2.8 Scatter plot of the average weighted methylation level for each caste. . 39
2.9 Hierarchical cluster and permutation results histogram. 40
2.10 Differential expression graphs including sample J8_24. 42
2.11 Differential expression graphs excluding sample J8_24. 43
2.12 An example of a gene which shows differential exon expression. 45
2.13 The relationship between methylation and gene expression between castes. 47
2.14 The relationship between methylation and differential gene/exon expression between castes. 49
2.15 Scatter plot of the difference in the mean weighted methylation level across colonies and UpSet plot showing the number of common genes between analyses. 51

2.16 UpSet plot showing the number of putative orthologs between *A. mellifera* and *B. terrestris*. 52

3.1 Total SNPs per sample and total genes with SNPs present. 66
3.2 Spread of allelic ratios averaged across all colonies and reproductive samples. 67
3.3 Scatter plot of the allelic expression proportion for reproductive and sterile workers. 68
3.4 Unique allelically expressed genes by caste. 68
3.5 Colony variation of allelically expressed genes. 69
3.6 Allelically methylated genes by caste and genomic locations. 71
3.7 Overlap of allele-specific expression and allele-specific methylation. . . . 72
3.8 Allelic expression levels of allelically methylated genes by caste. 74

4.1 Bumblebee inheritance probabilities of the maternal and paternal genome in queen-less conditions. 84
4.2 Graphic display of the family-wise reciprocal crosses carried out. 85
4.3 Overview of the bioinformatic pipeline used to identify genes with parent-of-origin expression. 88
4.4 Component bar plot showing the total number of SNPs called per sample. 90
4.5 Maternal expression proportion by reproductive caste. 92
4.6 Overlapping genes showing parent-of-origin expression in reproductive and sterile workers. 93
4.7 PCA plot for the expression levels of all genes. 94
4.8 Heatmaps showing the 100 most differentially expressed genes between reproductive and sterile workers. 96
4.9 Overlapping genes showing parent-of-origin expression in reproductive and sterile workers with genes showing differential expression in head tissue. 97
4.10 Overlapping genes showing parent-of-origin expression in reproductive and sterile workers of *B. terrestris* and *A. mellifera*. 99

5.1 Graphic display of the family-wise reciprocal crosses carried out. 109

5.2 Overview schematic for identifying allelic methylation differences in the worker offspring. 112
5.3 Agarose gel of DNA extracted from head tissue. 115
5.4 Genome-wide methylation differences between queens, males and reproductive workers. 117
5.5 Component bar chart showing the total number of SNPs called per sample. 119
5.6 Scatter graph of genes which show a weighted methylation difference between worker alleles and the parental weighted methylation difference of each gene. 122
5.7 Scatter graph of genes showing a weighted methylation difference between worker alleles and the proportion of paternal expression for each gene from Chapter 4. 123

6.1 *Daphnia* life cycle. 132
6.2 Location and profile of Lake Ring. 134
6.3 Schematic of lake phases. 135
6.4 Photos of the experimental set-up and juvenile *Daphnia*. 136
6.5 Agarose gel of extracted DNA. 139
6.6 Clustering of samples by CpG methylation. 140
6.7 Weighted methylation for each temporal population. 141
6.8 Common differentially methylated genes between temporal populations. 144
6.9 Weighted methylation by temporal population of common differentially methylated genes. 145
6.10 Treemap of GO terms associated with common differentially methylated genes. 145

B.1 Heatmaps showing the 100 most differentially expressed genes between dominant reproductive workers and sterile workers. 176
B.2 Overlapping genes showing parent-of-origin expression in reproductive and sterile workers with genes showing differential expression in abdomen tissue. 177

B.3 Overlapping genes showing differential expression between reproductive and sterile workers of *B. terrestris* and *A. mellifera*. 178

C.1 M-bias plots showing poor quality sequencing. 180

Abbreviations

ATAC-Seq	Assay for transposase-accessible chromatin sequencing
bp	Base pair
C	Carbon
cDNA	Complementary DNA
ChIP-Seq	Chromatin immunoprecipitation sequencing
CpG	Cytosine base followed by a guanine base
DEE	Differentially expressed exon
DEG	Differentially expressed gene
DNA	Deoxyribonucleic acid
FDR	False discovery rate
GLM	General linear model
GO	Gene ontology
ICR	Imprinting control region
Mb	Megabases
MSC	Methylation status calling
ncRNA	Non-coding RNA
PBS	Phosphate-buffered saline
PCA	Principle component analysis
PCR	Polymerase chain reaction
RNA	Ribonucleic acid
RNAi	RNA interference
SNP	Single nucleotide polymorphism
WGBS	Whole genome bisulfite sequencing
X	Times (number of reads per base)
v.	Version

Chapter 1

Introduction

1.1 Epigenetic mechanisms

Epigenetics refers to changes in gene expression which are not a product of the underlying genetic code. Epigenetic changes can be both inter-generational and trans-generational (Burggren and Crews, 2014). To date the vast majority of epigenetic research has been conducted in relation to disease and mechanistic understanding in humans (Feil and Fraga, 2012, Fig. 1.1). However, recent reviews and special issues of *Molecular Ecology* and *Heredity* have called for a greater understanding of the function of epigenetics in ecology and evolution (Verhoeven *et al.*, 2016; Burggren, 2016; Lind and Spagopoulou, 2018).

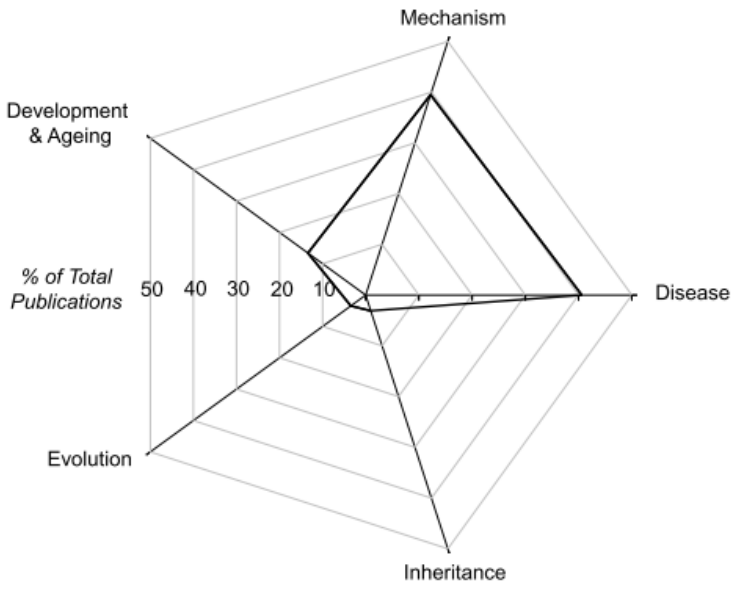


Figure 1.1: Radar diagram showing the percentage of publications in 2016 which refer to epigenetics within a particular research area, figure adapted from Burggren (2016).

Epigenetic mechanisms include: histone modifications, non-coding RNAs and DNA methylation. Histone modifications refer to chemical changes, such as: acetylation, phosphorylation and methylation, which occur on the amino (N)-terminal tails of histones (Bannister and Kouzarides, 2011). Modifications of histones can result in euchromatin, where the chromatin forms an open structure, or heterochromatin where the chromatin is highly condensed, making genes inaccessible and hence decreasing gene expression (Bannister and Kouzarides, 2011). Non-coding RNAs (ncRNAs) are RNA molecules which do not produce a protein, they can affect gene expression via multiple mechanisms, including; RNA-interference and via direction of chromatin-modifying enzymes (Glastad *et al.*, 2015). Whilst more is being understood about these mechanisms, it is DNA methylation which is currently the most studied epigenetic mark (Vogt, 2017).

DNA methylation is the addition of a methyl group to a cytosine nucleotide at the 5' carbon atom. In mammals, methylation primarily occurs in a CpG context (CpG referring to a cytosine base immediately followed by a guanine base), the percentage of CpGs methylated is usually over 70%, with methylation serving to repress gene expression when occurring in promoter regions (Feng *et al.*, 2010). DNA methylation is also observed in other genomic contexts, with centromere methylation thought to be involved in genome stability and the repression of transposable elements (Jones, 2012). Gene body methylation, in mammals, is usually tissue specific and has been linked with cancer (Jones, 2012). DNA methylation is also known to undergo global erasure and re-establishment during embryo development. However, some sites maintain their methylation status, such as those associated with imprinted genes (Messerschmidt *et al.*, 2014, see section 1.3). Whilst much is known about mammalian DNA methylation, and also DNA methylation in plants (reviewed in Zhang *et al.*, 2018), comparatively little is known about the function of DNA methylation in other species groups.

1.1.1 Arthropod DNA methylation

Arthropods are the most species diverse animal phylum and yet little is known about the overall function of DNA methylation within this group (Thomas *et al.*, 2018). Thomas

et al. (2018) recently searched for signals of DNA methylation in 76 arthropod species. They characterised observed/expected CpG content through out each genome. As DNA methylation causes spontaneous deanimation of cytosine nucleotides, a lower than expected CpG density in a given genomic region indicates the presence of DNA methylation. Holometabolous insects tend to show higher CpG observed/expected frequencies indicating lower levels of genome DNA methylation, compared to hemimetabolous insects and non-insect arthropods (Bewick *et al.*, 2016; Thomas *et al.*, 2018; Provataris *et al.*, 2018). Thomas *et al.* (2018) additionally found DNA methylation shows different profiles across arthropod species: holometabolous insects appear to have DNA methylation enriched in exons, Coleoptera and Diptera appear to show very little to no DNA methylation and many other species show methylation enriched in both exons and introns. The variety of methylation profiles across arthropods implies variable functions, making arthropods ideal models for investigating the role of DNA methylation in non-mammalian animals.

Observed/expected CpG density is only a proxy for DNA methylation. However, DNA methylation has been directly identified in species from all four currently extant subphylum of Arthropoda: Hexapoda, Chelicerata, Myriapoda and Crustacea, with insects being explored to the greatest extent (Vogt, 2017). DNA methylation has various proposed roles within arthropods, including: polyphenism in insects, speciation in crustaceans and adaptation in arachnids (Vogt, 2017; Liu *et al.*, 2019). Polyphenisms are an extreme forms of phenotypic plasticity, where more than one distinct phenotype is produced by the same genotype (Colgan *et al.*, 2011). DNA methylation differences have been associated with insect polyphenisms, such as: social insect castes (Lyko *et al.*, 2010; Bonasio *et al.*, 2012) and gregarious and solitary locusts (Falckenhayn *et al.*, 2013). Large differences in genome-wide methylation have also been observed between two recently diverged cray-fish species, *Procambarus virginalis* and *Procambarus fallax* (Gatzmann *et al.*, 2018), suggesting a potential role for DNA methylation in speciation. Finally DNA methylation has been hypothesised to play a role in the adaptive capability of species with low genetic diversity, such as the social spider, *Stegodyphus dumicola* (Liu *et al.*, 2019).

This thesis attempts to further explore the role of DNA methylation in a hexapod

and crustacean species, the primitively eusocial insect, *Bombus terrestris* and the parthenogenic crustacean, *Daphnia magna*. To do this I will use the current gold standard for DNA methylation identification, whole-genome bisulfite sequencing. This method involves treating genomic DNA with bisulfite. Bisulfite treatment causes deanimation of any unmethylated cytosine, resulting in a uracil base, this is then transcribed into a thymine during PCR (Fig. 1.2), any remaining cytosine nucleotides are therefore known to be methylated. The treated DNA can then be sequenced using next-generation sequencing technologies and advances in bioinformatic pipelines allow methylated bases to be identified with confidence.

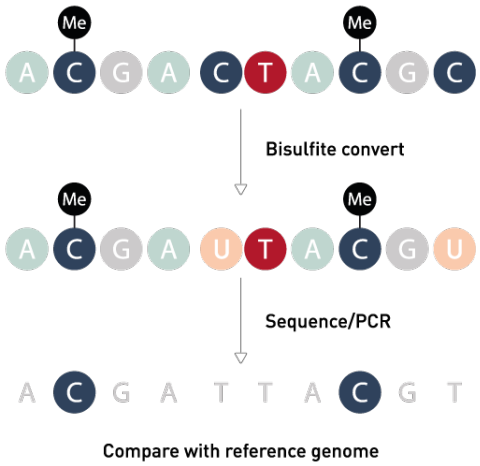


Figure 1.2: The bisulfite chemical causes deanimation of unmethylated cytosine nucleotides, forming uracil. The uracil is then translated into thymine during the PCR process. Final sequencing data contains only cytosines which were methylated in the original sample. Image adapted from: https://www.diagenode.com/en/categories/bisulfite-conversion.

1.1.2 Thesis rationale

The following sections provide more specific background for the three projects of this thesis:

- DNA methylation as a mechanism of caste-determination in the social insect *Bombus terrestris* (Section 1.2, Chapter 2)
- DNA methylation as a mechanism of imprinting genes in the social insect *Bombus*

terrestris (Section 1.3, Chapters 3, 4 and 5)

- DNA methylation as an adaptive mechanism in the crustacean *Daphnia magna* (Section 1.4, Chapter 6).

Whilst I provide a comprehensive introduction, each chapter is written in a 'stand-alone' manuscript style in order to ease later publication. This means there will be some repetition between the the main introduction and the individual chapter introductions.

1.2 Methylation and social-insect caste determination

1.2.1 Caste determination

Phenotypic plasticity is the production of multiple phenotypes from a single genome. It plays a crucial role in the adaptive capabilities of species (Chevin *et al.*, 2010) and is notably observed in social insects. Social insects exhibit, sometimes extreme, morphological and behavioural differences between individuals of a single colony, known as castes. The mechanisms by which species develop differences between castes are diverse; some species use only environmental cues whilst others rely only on inherited changes, with some species falling somewhere in between these two extremes (Matsuura *et al.*, 2018).

Genetic caste determination has been observed in species of *Cataglyphis* and *Pogonomyrmex* ant, this occurs when two distinct genetic lines cross to produce sterile workers, whereas inbreeding within a single line produces reproductive queens (Leniaud *et al.*, 2012; Eyer *et al.*, 2013; Mott *et al.*, 2015). Kuhn *et al.* (2018) have shown one of these species, *Cataglyphis mauritanica*, is capable of producing single-lineage workers as well as hybrid reproductive queens in lab conditions, although the latter was in response to juvenile hormone treatment. This shows that whilst this species exhibits genetic caste-determination, it still maintains some level of phenotypic plasticity within its genome.

Many other species utilise cues from the environment in order to determine caste. For example, the presence of queen pheromone, as well as queen-worker interactions, in *Bombus* species have been shown to reduce the reproductive development of workers (Padilla *et al.*, 2016). In a species of primitively eusocial paper wasp, *Polistes jokahamae*, exposure to short-photoperiods was found to cause a higher production of new queens (Yoshimura and Yamada, 2018). Additionally, nutritional content and food availability have been shown to influence caste determination, for example when honeybee larvae are fed royal jelly they develop into queens rather than workers. (Haydak, 1943).

With the production of new molecular techniques it has recently become possible to begin to explore the epigenetic mechanisms which may underlie caste determination in response to environmental factors. Various epigenetic differences have now been associated with different castes in various species. For example, variation in microRNA expression levels has been identified in both honeybee (Ashby *et al.*, 2016) and bumblebee (Collins *et al.*, 2017) castes. Additionally, histone acetylation has been shown to alter the behaviour of major workers of the ant species *Camponotus floridanus*, making them more similar to the behaviour of minor workers (Simola *et al.*, 2016). However, the most active research in this area has been focused on DNA methylation (Glastad *et al.*, 2015).

1.2.2 Social-insect methylation

DNA methylation has been associated with the switching of worker castes in honeybees (Herb *et al.*, 2012). A major finding was that silencing of the *Dnmt3* gene (involved in methylation establishment) in larvae produced queens rather than workers (Kucharski *et al.*, 2008). DNA methylation has also been linked with alternative splicing differences between castes in two ant species (Bonasio *et al.*, 2012) and is thought to be involved in caste determination in *Copidosoma koehleri*, a species of primitively social wasp (Shaham *et al.*, 2016).

However, it is clear DNA methylation is not a conserved mechanism in Hymenoptera for caste differentiation. No association between caste and methylation has been found

in a number of ant and wasp species (Patalano *et al.*, 2015; Standage *et al.*, 2016). Additionally, the statistical methods of previous next generation sequencing analyses on social insect methylation have been brought into question (Libbrecht *et al.*, 2016).

Whilst DNA methylation differences have been found in some species, the actual role of DNA methylation in caste determination is still unknown. Cardoso-Júnior *et al.* (2017) propose a combined genetic-epigenetic mechanism of caste determination in the stingless bee, *Melipona scutellaris* (Fig. 1.3). Previous work found evidence for a genetic caste-determination system governed by two separate genes (Corona *et al.*, 2016), whereas Cardoso-Júnior *et al.* (2017) found DNA methylation and histone modifications linked to different castes which may be influenced by larval nutrition. This work shows the importance of understanding whether DNA methylation has a causal relationship with changes in gene expression or whether it is a consequence of caste-differences.

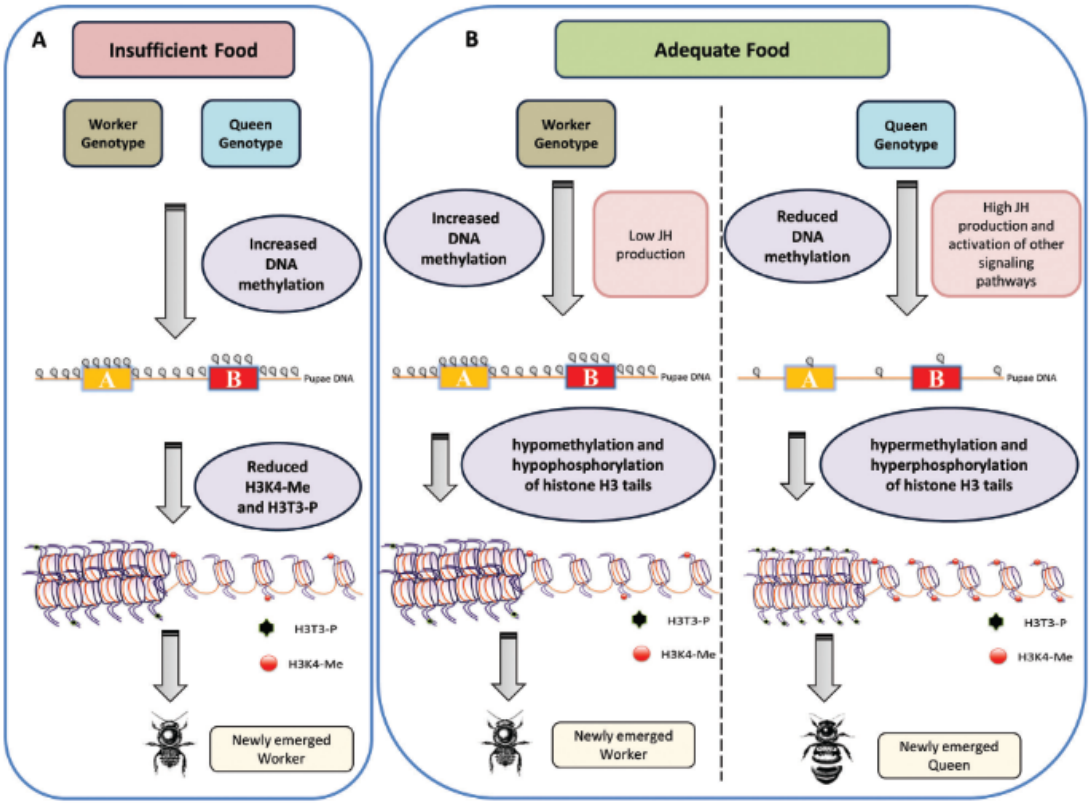


Figure 1.3: (A) Cardoso-Júnior *et al.* (2017) propose low nutrient consumption in the stingless bee, *Melipona scutellaris*, leads to increased DNA methylation which in turn reduces histone modifications, leading to the production of workers, regardless of the underlying genotype. (B) under good nutrient conditions, a queen-genotype is needed to create a decrease in DNA methylation leading to an increase in histone modifications which enable the queen phenotype. Image from Cardoso-Júnior *et al.* (2017).

1.2.3 Bumblebees as a model system

Bumblebees provide an ideal system to further investigate the relationship between gene expression and methylation in social insect caste determination. Firstly, bumblebees are important both economically and environmentally as a pollinator species. They are generalist pollinators and are given keystone species status in some ecosystems (Woodard *et al.*, 2015). *B. terrestris* colonies are annual and are founded by a singly-mated queen in early spring (Fig. 1.4), she will lay diploid eggs resulting in female workers and later switch to male haploid eggs, known as the switching point (Bloch, 1999). A competition phase then occurs between queens and workers, where some workers will become reproductive and produce their own haploid sons (Alaux

et al., 2006), this results in distinct reproductive worker phenotypes within the colony. Throughout this thesis I will refer to individuals with a reproductive or sterile phenotype as distinct worker castes. This deviates from the traditional definition of a caste as these phenotypes are not fixed during development. Instead, some individual workers develop the reproductive phenotype later in life in response to environmental cues.

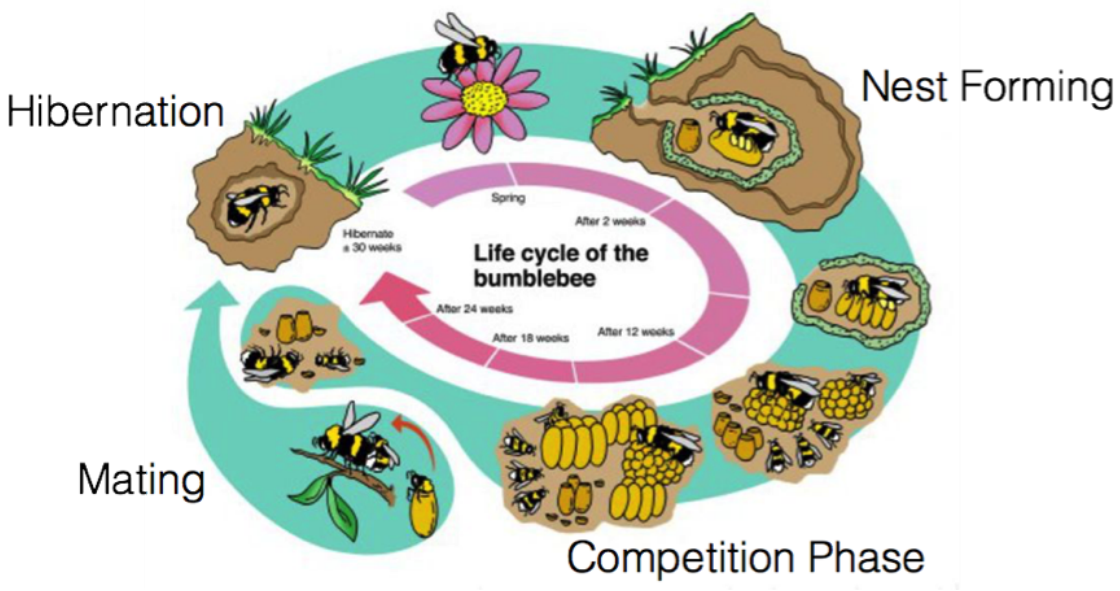


Figure 1.4: Bumblebee life cycle: nests are formed from mated queens emerging from hibernation, they lay female worker destined eggs, once hatched the workers then aid in foraging and brood care. During the competition phase some workers develop functioning ovaries and lay haploid male eggs, the queen will also being to lay haploid male eggs and produce female queen destined larvae. Males and new queens will leave the nest and new queens will be singly mated (i.e. by only one male) before hibernating. Figure adapted from: https://www.natupol.com/why-natupol/our-best-bumblebees/longevity/.

B. terrestris also has a sequenced genome, the genome size is small, 249Mb, allowing large computational analyses to be run in relatively short time periods (Sadd *et al.*, 2015). Sequencing of the genome revealed a methylation system: including two copies of the *DNMT3* gene and a copy of *DNMT1* (needed for the methylation of genes), a copy of *PIWI* (involved in methylation targeting) and a copy of *TET* (involved in methylation removal). Overall CpG methylation levels, are relatively low compared to mammals, with only 0.5-0.6% of all CpG's being methylated (Sadd *et al.*, 2015). Additionally, genes involved in DNA methylation have also been shown to have varying expression levels between queens, workers and drones (Li *et al.*, 2018) and experimental changes

in methylation in *B. terrestris* workers has been shown to alter levels of reproductive behaviour (Amarasinghe *et al.*, 2014). These studies hint to the possibility that DNA methylation may play a role in caste determination in *B. terrestris*.

1.2.4 Project aims

The first results chapter of this thesis, Chapter 2, aims to determine if there is a direct association between reproductive caste determination and DNA methylation in *B. terrestris*. As part of this project, this chapter also aims to characterise the *B. terrestris* methylome and determine the relationship between DNA methylation, gene expression and alternative splicing in this species. If differentially methylated genes are identified between castes which are enriched for differentially expressed or alternatively spliced genes, involved in reproductive processes, this would indicate the potential of DNA methylation as a mechanism of caste determination in *B. terrestris*.

1.3 Genomic imprinting in social insects

1.3.1 Genomic imprinting

Genomic imprinting is the expression of only one allele at a given locus, in a diploid organism, with expression being dependent upon the parental origin of the allele (Barlow and Bartolomei, 2014). Genomic imprinting was first discovered in the 1980's. Mouse embryos formed from a single parent, whilst still having a diploid genome, did not develop normally. Chromosomes from both a male and female parent were needed (McGrath and Solter, 1984). Imprinted genes have primarily been described in placental mammals and flowering plants (Barlow and Bartolomei, 2014). However, the term 'imprinting' was first used to describe elimination of specific parental chromosomes in a species of fly, *Sciara impatiens* (Crouse *et al.*, 1971).

Whilst the mechanisms of chromosomal imprinting in insects remain unknown, DNA methylation has been found to be the primary epigenetic imprinting mark in mammals.

DNA methylation controls gene expression by occurring in imprinting control regions (ICRs) (Delaval and Feil, 2004). Hypermethylation of ICRs can result in either allelic silencing or allelic expression, depending on the mechanism of action (Drewell *et al.*, 2012; Barlow, 2011).

Imprinted genes may be individually silenced by DNA methylation, this occurs when DNA methylation blocks transcription factors from binding to the gene promotor (Drewell *et al.*, 2012). It is also thought DNA methylation may signal the recruitment of histone modifications which result in heterochromatin formation, silencing the expression of all alleles within a region (Barlow, 2011). DNA methylation can also signal the expression of imprinted genes by silencing an 'imprinting control element', such as a long non-coding RNA, which, when expressed, would cause transcriptional silencing of nearby genes (Barlow, 2011). It is also worth noting that most of the currently identified imprinted genes in mammals have some association with DNA methylation. However, there are cases where imprinting has been linked solely with a particular histone modification (Inoue *et al.*, 2017).

1.3.2 Theories of genomic imprinting

Genomic imprinting presents an evolutionary paradox. In diploid organisms having two copies of a particular gene means that if one allele carries a harmful mutation, the other allele can compensate, so function is not lost. However, the expression of only a single allele means this evolutionary advantage is removed (Amarasinghe *et al.*, 2014). Many theories therefore attempt to explain the presence of genomic imprinting, the three most widely accepted theories are: the sexual antagonism theory (Day and Bonduriansky, 2004), the maternal-offspring co-adaptation theory (Wolf and Hager, 2006) and the kinship theory (Haig, 2000).

The sexual antagonism theory is based on gender specific selection pressures, if males and females are under different selection pressures then alleles will have different frequencies in the eggs and sperm, meaning different frequencies of matrigenes (genes from the mother) and patrigenes (genes from the father) in the offspring (Patten *et al.*, 2014). For example if sexual selection favours a particular trait that is only expressed in males

then the maternal allele should be imprinted (silenced in this case) making the phenotype of the male offspring more heritable (Day and Bonduriansky, 2004). However, this theory fails to explain the expression of matrigenes in the testes of mammalian males and the expression of patrigenes in the mammary-glands of females (Patten *et al.*, 2014).

Wolf and Hager (2006) proposed the maternal-offspring co-adaptation theory. This theory predicts imprinting occurs because each allele in the offspring provides a different level of 'fitness interaction' with the mother (Patten *et al.*, 2014). For example, if fitness is increased when there is a high similarity between the mother's genetic make up and the offspring's, then it can be expected the maternal alleles are expressed and the paternal alleles are silenced (Patten *et al.*, 2014). Wolf and Hager (2006) acknowledge the most widely accepted theory for genomic imprinting is that of conflict between maternal and paternal alleles over maternal investment, this principle is the basis of Haig's kinship theory (Haig, 2000).

1.3.3 Haig's kinship theory

Haig's kinship theory is currently the most widely accepted theory for genomic imprinting (Spencer and Clark, 2014). This theory was originally developed in the late 1990's, Haig (1996) suggests that in a polyandrous mating system the genetic relatedness of the offspring is higher for maternally inherited alleles than it is for paternally inherited alleles, this is because offspring may have different fathers. Therefore selection should act on paternally inherited alleles to increase individual resource allocation from the mother, thereby increasing paternal inclusive fitness, whereas maternal alleles should be selected to favour equal resource distribution amongst offspring to maximise maternal inclusive fitness (Wilkins and Haig, 2003). This theory would explain why, in mammals, imprinted genes which express the maternal allele favour a decrease in individual size and imprinted genes which express the paternal allele favour an increase in size (Queller, 2003). This theory also fits with genomic imprinting being prevalent in mammals and flowering plants where the mother provides resources (Queller, 2003). This theory also extends beyond the polyandrous mating system and is thought to be applicable in cases where males provide the offspring care (reversing the theory's

predictions) and in haplodiploid insect systems (Haig, 2000; Queller, 2003).

1.3.4 Social insects as an independent test

Eusocial hymenoptera provide an ideal system to study Haig's kinship theory. For example; colonies of social bees consist of diploid females (queens and workers) and haploid males created from unfertilised eggs. This haplodiploidy results in workers which all share the full paternal genome, when queens are singly mated. In this scenario the kinship theory (Haig, 2000) predicts patrigenes should be under stronger selection for general care-giving compared to matrigenes. However, when queens mate with multiple males, workers are more likely to have higher maternally derived relatedness and the predictions reverse (Queller, 2003).

There has been a recent increase in evidence for the predictions of genomic imprinting in social insects. Firstly, the presence of functional DNA methylation systems (the main mechanism of imprinting in mammals and flowering plants) have been found in multiple species (Glastad *et al.*, 2015). DNA methylation has been traced to the gametes in honeybees and Drewell *et al.* (2014) suggest some of the patterns seen indicate parent specific methylation patterns. Oldroyd *et al.* (2014) found a parent-of-origin effect on ovary size in honeybees concurrent with the kinship theory's predictions. Additionally, paternal effects were observed in care-giving associated behaviours and in sex allocation of offspring in the Argentine ant, *Linepithema humile* (Libbrecht and Keller, 2012; Libbrecht *et al.*, 2011).

More recently, reciprocal crosses and next generation sequencing technologies have been used to identify genes with parent-of-origin expression patterns in honeybees. Kocher *et al.* (2015) and Galbraith *et al.* (2016b) both used RNA-Seq to study parent-of-origin gene expression in hybrid crosses of honeybee sub-species. Kocher *et al.* (2015) found a matrigenic bias in gene expression. However, it was later shown that sub-species incompatibility effects influenced the results obtained (Gibson *et al.*, 2015). Showing some support for the kinship theory, Galbraith *et al.* (2016b) found a greater patrigenic expression in reproductive workers compared to sterile workers, with increased patrigenic expression in the reproductive tissues. However, this study is limited to only one

species and tests only one prediction from the many predictions made in Queller (2003) for how matrigenic/patrigenic expression bias may play a role in social insect colonies.

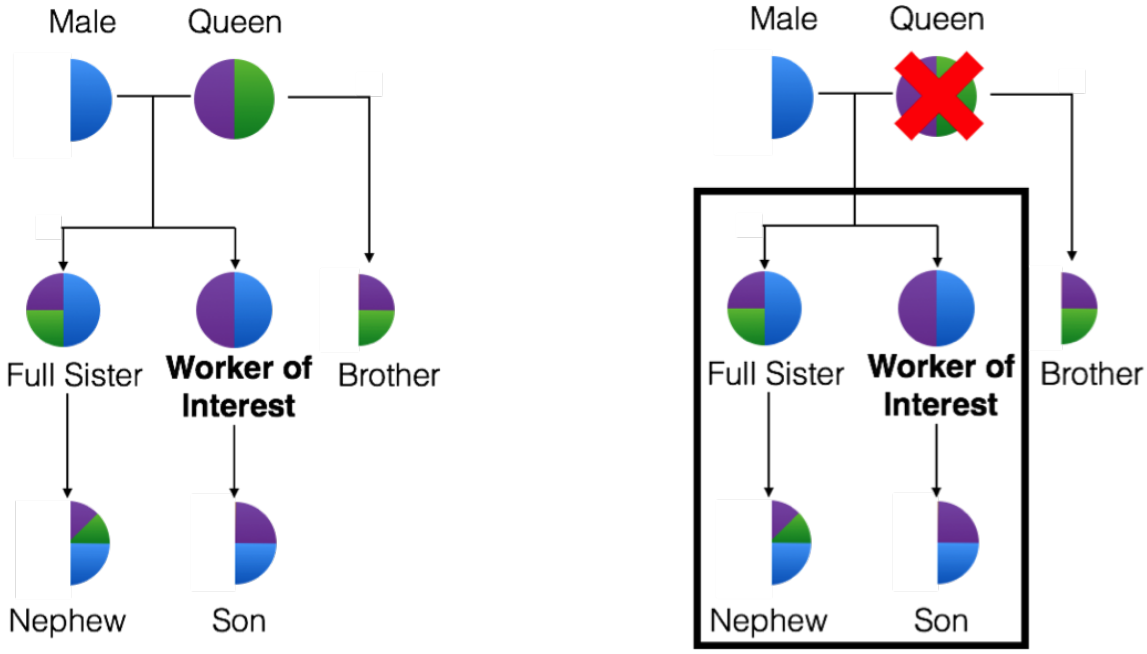
1.3.5 Bumblebees as a model system

Bumblebees provide an ideal model to further test Haig's kinship theory in social insects. As discussed in section 1.2.3, *Bombus terrestris* can be easily reared in the lab and has a small sequenced genome. Additionally, this species has a functional DNA methylation system which may be involved in reproductive caste determination (Amarasinghe *et al.*, 2014), meaning the epigenetic tools which drive imprinting in mammals and plants are present.

Additionally, previous research has identified both allele-specific expression and allele-specific methylation in *B. terrestris*, hinting to the existence of imprinted genes. Using a candidate gene approach, previous research identified allele-specific expression in a gene (ecdysone 20-monooxygenase-like) related to worker reproductive behaviour in *B. terrestis* (Amarasinghe *et al.*, 2015). Additional research has since used RNA-seq data to identify >500 loci showing allele-specific expression throughout the *B. terrestris* genome (Lonsdale *et al.*, 2017). This same study also identified 19 genes displaying allele-specific expression and allele-specific methylation, although this was in a single individual (Lonsdale *et al.*, 2017).

Finally, bumblebees provide a robust test for the kinship theory as predictions regarding worker reproduction are the opposite of those for the honeybee, which previous research has focused on (Galbraith *et al.*, 2016b; Kocher *et al.*, 2015). In bumblebee colonies under queen-right conditions, Queller (2003) predicts patrigenes in any given worker will be selected to favour worker reproduction as there is a 50% chance they will occur in any worker offspring, but a 0% chance they will occur in the queen's male offspring (Fig. 1.5a). Patrigenes in workers should therefore be selected to increase egg laying at the cost of rearing fewer brothers. Matrigenes should be selected to regulate worker reproduction when it is associated with high costs to brothers as these genes are less likely to occur in nephews than they are in brothers.

Under queen-less conditions the predictions are reversed. Matrigenes should now be selected to favour individual worker reproduction as there is a higher likelihood they are present in the individual worker's offspring than in her nephews (Fig. 1.5b). Patrigenes should now not experience selective pressure for reproductive behaviour as it is equally likely they will occur in the offspring of an individual worker or her nephews, meaning sterility and nursing behaviour are just as beneficial as reproductive behaviour.



(a) Queen-right (b) Queen-less

Figure 1.5: Schematic adapted from Drewell *et al.* (2012) showing the inheritance probabilities of the maternal and paternal genome in various offspring in singly-mated bumblebee colonies. (a) Under a queen-right scenario patrigenes should be under selection pressures to increase worker reproduction at the cost of rearing brothers. (b) Under queen-less conditions matrigenes should now experience higher selection pressures for worker reproduction compared to nursing behaviour for nephews.

1.3.6 Project aims

Building on previous research, Chapter 3 in this thesis aims to identify allele-specific expression and allele-specific methylation in both reproductive and sterile *B. terrestris* workers. If genomic imprinting plays a role in worker reproductive behaviour in *B. terrestris*, genes showing allele-specific expression will be enriched for reproductive pro-

cesses. Additionally, if DNA methylation acts as an imprinting mark in *B. terrestris*, a direct association between allele-specific expression and allele-specific methylation will be found.

Chapter 4 then aims to test Haig's kinship theory of genomic imprinting by utilising reciprocal crosses of two *B. terrestris* sub-species, *B. t. audax* and *B. t. dalmatinus*. RNA-seq from reproductive and sterile workers, collected under queen-less conditions, should show higher matrigenic expression bias in genes displaying parent-of-origin allele-specific expression. Additionally, if genomic imprinting plays a direct role in reproductive caste determination, differentially expressed genes between castes will be enriched for genes that also display parent-of-origin allele-specific expression.

Finally, Chapter 5 aims to identify parent-of-origin methylation in reproductive workers, collected under queen-less conditions, from independent reciprocal crosses of *B. t. audax* and *B. t. dalmatinus*. If DNA methylation is an epigenetic imprinting mark in *B. terrestris* then parent-of-origin allele-specific methylation will be identified in numerous genes. Additionally, if DNA methylation directly affects parent-of-origin allele-specific expression in a consistent manner, then there may be overlap with the genes identified in Chapter 4.

1.4 Adaptive methylation in natural populations

Adaptive epigenetics is a relatively new field of research (Verhoeven *et al.*, 2016). When there is limited genetic diversity within a population, it has been suggested selection can act upon phenotypes which are a result of the underlying epigenetic code (Lind and Spagopoulou, 2018). Additionally, the rate of spontaneous epimutations has been estimated to be higher than that of genetic mutations providing increased variation which may enable adaptation (van der Graaf *et al.*, 2015). Epigenetic adaptations can come in the form of: short term temporary responses (epigenetic plasticity), long term permanent responses and heritable permanent responses (epigenetic adaptation) (Weyrich *et al.*, 2015). Research has focused on DNA methylation as it has been suggested that it can provide an additional heritable layer of information upon which

selection and adaptive evolution can act (Richards *et al.*, 2010).

Epigenetic mechanisms underlie various types of phenotypic plasticity, with many studies recording changes in DNA methylation in response to environmental stressors. These studies span a variety of species, for example: *Arabidopsis thaliana* (Dowen *et al.*, 2012), stickleback (Artemov *et al.*, 2017) and corals (Dixon *et al.*, 2018). Additionally, permanent epigenetic differences between locally adapted populations have been identified in: *A. thaliana* (Kooke and Keurentjes, 2015), bats (Liu *et al.*, 2015), oak trees (Platt *et al.*, 2015), chickens (Zhang *et al.*, 2017) and stickleback (Heckwolf *et al.*, 2019).

As well as environmentally induced changes in DNA methylation and stable epimutations contributing to adaptive phenotypes, it is also thought changes in DNA methylation in response to the environment may contribute to later genetic adaptation. The presence of DNA methylation has been associated with an increased rate of C/T SNP substitutions which occur through spontaneous deamination (Flores *et al.*, 2013). Flores *et al.* (2013) propose environmentally induced DNA methylation, that is beneficial in terms of survival and reproduction, will remain present in individuals when the environment is constant. This will lead to an increase in C/T mutations which may facilitate maintenance of the phenotype produced originally by the DNA methylation. However, this particular theory is difficult to test given the long-term nature of the study needed.

Many of the studies mentioned above either focus on a single experimental generation or utilise the 'space-for-time' method, whereby spatially separated populations under different environmental conditions are used as a proxy to try to understand how species adapt to environmental change. However, it is difficult to take all naturally occurring variables into account with this method and so observing adaptation in a single population over time is preferable. Observing adaptation through time often involves long-term studies across multiple generations, of which there are few, see Grant and Grant (2002) as a rare example. Resurrection ecology provides a means of observing temporal adaptation within the same population by utilising dormant life stages such as seeds or eggs from dated sediment cores (Kerfoot *et al.*, 1999), avoiding the long-term nature of such studies.

1.4.1 *Daphnia* as a model system

The freshwater crustacean, *Daphnia magna*, provides an ideal model to study the adaptive ability of DNA methylation in arthropods. It produces a dormant life stage which can be hatched after hundreds of years of dormancy, with the oldest resurrected individual dated to around 700 years old (Frisch *et al.*, 2014), this means the same population can be directly studied through evolutionary time. Additionally, *D. magna* reproduces clonally during its life cycle (Fig. 1.6) and it is easily cultured in the lab, allowing a resurrected 'genotype' to be maintained for many generations. Additionally, each resurrected individual is sexually produced and so provides a unique genetic line (Fig. 1.6). Previous research has found resurrected individuals provide a genetically representative sample of temporal populations obtained from dated sediment cores (Orsini *et al.*, 2016).

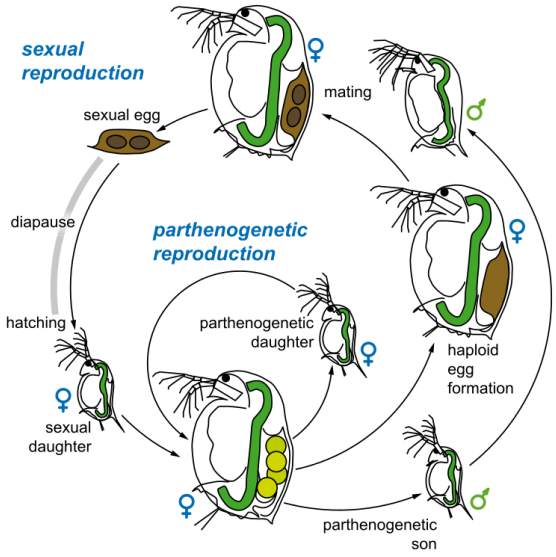


Figure 1.6: *Daphnia* life cycle. *Daphnia* exhibit cyclic parthenogenesis. Under stable environmental conditions females reproduce clonally. Under stressful conditions they produce males and sexual haploid eggs which are fertilised to produce a 'resting' life stage. These sexual eggs will eventually hatch into a genetically distinct female. Image credit: Dita Vizoso, source: http://scienceresourcebox.co.nz/blog/post&post_id=24.

D. magna also has a fully functional DNA methylation system, with methylation primarily found in gene bodies and associated with higher gene expression (Kvist *et al.*, 2018). Additionally, single-site CpG methylation levels have been reported between

0.7-1.7% (Kvist *et al.*, 2018; Hearn *et al.*, 2019), which is also similar to some insect species (Bewick *et al.*, 2016), such as *Bombus terrestris* which shows around 0.2% CpG methylation (Chapter 2).

The methylome of *D. magna* has been shown to be responsive to changes in environmental conditions. For example: sex-determination and sexual reproduction are the product of epigenetic changes caused by stressful conditions (Harris *et al.*, 2012), the presence of predators induces epigenetic changes which alter the phenotype (Asselman *et al.*, 2015) and calorie restriction alters genome-wide CpG methylation (Hearn *et al.*, 2019). Transgenerational effects on DNA methylation induced by chemical exposure (Vandegehuchte *et al.*, 2010) and salt stress (Jeremias *et al.*, 2018) have also been documented. Jeremias *et al.* (2018) found that changes in methylation after salt stress persisted until the F3 generation, indicating adaptive epigenetic heritability. When assessing the heritability of DNA methylation changes, that are environmentally induced, it it vital that individuals are examined at least three generations after the removal of the environment in question. This is because the gametes which generate the F2 generation would have been exposed to the test environment (Fig. 1.7).

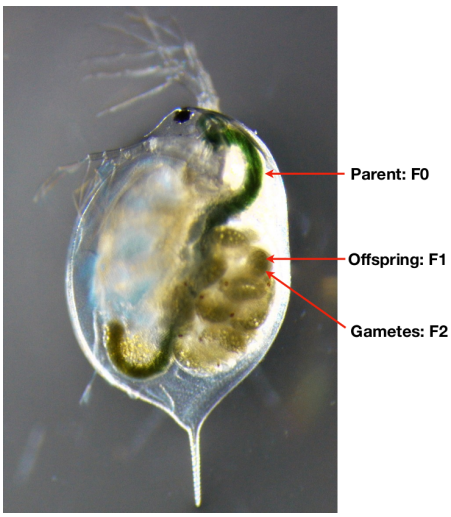


Figure 1.7: Adult female *Daphnia magna* with neonates inside the brood pouch. Exposure of the generation would also result in exposure up to the F2 generation via the germline of the F1.

1.4.2 Project aims

The final results chapter of this thesis, Chapter 6, aims to use resurrection ecology to assess changes in DNA methylation in a naturally occurring temporal population of *Daphnia magna*. The population chosen underwent historical eutrophication and pesticide exposure during two separate time periods. The identification of stable DNA methylation differences in historically exposed sub-populations compared to historically unexposed sub-populations would indicate environmentally induced heritable DNA methylation changes exist in *D. magna*. These differences could indicate an adaptive role for DNA methylation in this species.

Chapter 2

Methylation and gene expression differences between reproductive castes of bumblebee workers.

Hollie Marshall, Zoë Lonsdale and Eamonn Mallon.

Work from this chapter is published in:

Marshall, H., Lonsdale, Z.N. and Mallon, E.B. (2019). Methylation and gene expression differences between reproductive castes of bumblebee workers. *Evolution Letters*. DOI: https://doi.org/10.1002/evl3.129

Appendix A.

2.1 Abstract

Phenotypic plasticity is the production of multiple phenotypes from a single genome and is notably observed in social insects. Multiple epigenetic mechanisms have been associated with social insect plasticity, with DNA methylation being explored to the greatest extent. DNA methylation is thought to play a role in caste determination in *Apis mellifera*, and other social insects, but there is limited knowledge on its role in other bee species. In this study, I analysed whole genome bisulfite sequencing and RNA-seq data sets from head tissue of reproductive and sterile castes of the eusocial bumblebee *Bombus terrestris*. I found that genome-wide methylation in *B. terrestris* is similar to other holometabolous insects and does not differ between reproductive castes. I also found differentially methylated genes between castes, which are enriched for multiple biological processes including reproduction. However, I found no relationship between differential methylation and differential gene expression or differential exon usage between castes. My results also indicate high intercolony variation in methylation. These findings suggest that methylation is associated with caste differences but may serve an alternate function, other than direct caste determination in this species. This study provides the first insights into the nature of a bumblebee caste-specific methylome as well as its interaction with gene expression and caste-specific alternative splicing, providing greater understanding of the role of methylation in phenotypic plasticity within social bee species. Future experimental work is needed to determine the function of methylation and other epigenetic mechanisms in insects.

2.2 Introduction

Phenotypic plasticity is the production of multiple phenotypes from a single genome. It plays a crucial role in the adaptive capabilities of species (Chevin *et al.*, 2010) and is notably observed in social insects. Social insects exhibit sometimes extreme morphological and behavioural differences within a single colony, known as castes. The mechanisms by which species develop differences between castes are diverse; some species use only environmental cues whilst others rely only on inherited changes, with many species falling somewhere in between these two extremes (Matsuura *et al.*, 2018). For example some ant species from the *Pogonomyrmex* genus have purely genetic caste determination (Mott *et al.*, 2015). On the other hand, many ant species undergo caste determination in response to only the environment, indicating their genomes must contain the code for all caste possibilities, with the phenotype potentially determined by epigenetic factors (Bonasio *et al.*, 2012).

Multiple epigenetic mechanisms have been associated with social insect plasticity. Histone modifications have been shown to be involved with plasticity, for example changes in histone acetylation alter the behaviour of major workers of the ant species *Camponotus floridanus*, making them more similar to the behaviour of minor workers (Simola *et al.*, 2016). Variation in microRNA expression levels has been identified in both honeybee (Ashby *et al.*, 2016) and bumblebee (Collins *et al.*, 2017) castes. However, the most active research in this area has been focused on DNA methylation (Glastad *et al.*, 2015).

DNA methylation is the addition of a methyl group to a cytosine nucleotide. In mammals, methylation primarily occurs in a CpG context (CpG referring to a cytosine base immediately followed by a guanine base), the percentage of CpG's methylated is usually over 70%, with methylation serving to repress gene expression when occurring in promoter regions (Feng *et al.*, 2010). However, in insects it is generally found in much lower quantities, ranging from zero methylation in most Diptera species studied, to >2% in Hymenoptera and up to 14% in some species of Blattodea (Provataris *et al.*, 2018). It is also enriched in gene bodies rather than throughout the genome, as in mammals (Fang

et al., 2012; Wang *et al.*, 2013), with a possible role in alternative splicing (Bonasio *et al.*, 2012).

DNA methylation has been associated with the switching of worker castes in honeybees (Herb *et al.*, 2012). A major finding was that silencing of the *Dnmt3* gene (involved in methylation establishment) in larvae produced queens rather than workers (Kucharski *et al.*, 2008). DNA methylation has also been linked with alternative splicing differences between castes in two ant species (Bonasio *et al.*, 2012) and is thought to be involved in caste determination in *Copidosoma koehleri*, a species of primitively social wasp (Shaham *et al.*, 2016). However, it is clear DNA methylation is not a conserved mechanism in Hymenoptera for caste differentiation. No association between caste and methylation has been found in a number of wasp and ant species (Patalano *et al.*, 2015; Standage *et al.*, 2016). Additionally, the statistical methods of previous next generation sequencing analyses on social insect methylation have been brought into question (Libbrecht *et al.*, 2016).

A greater variety of species are needed to begin to understand the role of DNA methylation in social insect caste determination. Here, we assess whole genome methylation differences between reproductive castes of the bumblebee, *Bombus terrestris*, with an aim to investigate the role of methylation in caste determination in this species. Bumblebees are primitively eusocial and are an important pollinator species, both economically and environmentally. They are generalist pollinators and are keystone species in some ecosystems (Woodard *et al.*, 2015). *B. terrestris* colonies are annual and are founded by a singly-mated queen in early spring, she will lay diploid eggs resulting in female workers and later switch to male haploid eggs, known as the switching point (Bloch, 1999). A competition phase then occurs between queens and workers, where some workers will become reproductive and produce their own haploid sons (Alaux *et al.*, 2006), this results in distinct reproductive worker castes within the colony. Multiple recent studies have highlighted *B. terrestris* as an ideal organism to assess methylation as a potential regulatory mechanism for reproductive caste determination (Amarasinghe *et al.*, 2014; Lonsdale *et al.*, 2017; Li *et al.*, 2018).

Methylation regulatory genes were identified in the bumblebee genome and have since

been shown to have varying expression levels between queens, workers and drones (Li *et al.*, 2018). Additionally, genes showing allele-specific methylation and gene expression have been identified and are enriched in reproductive related processes (Lonsdale *et al.*, 2017). Finally, experimental changes in methylation in *B. terrestris* workers has been shown to alter levels of reproductive behaviour (Amarasinghe *et al.*, 2014). Whilst these studies highlight differences in methylation between *B. terrestris* castes it is still unclear where those differences are within the genome and also whether methylation differences are related to changes in gene expression, potentially leading to caste differentiation.

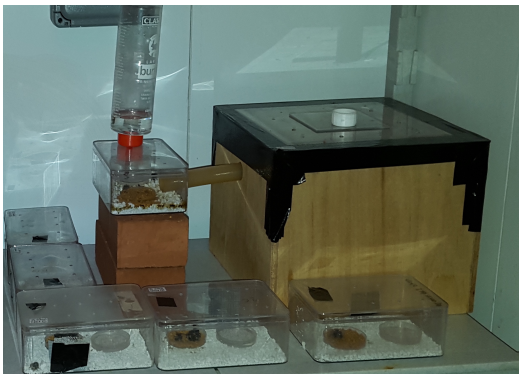
In this study, I compared whole genome bisulfite sequencing data sets from reproductive and sterile worker castes of *B. terrestris*, allowing me to identify differences in methylation at base-pair resolution throughout the genome. I then linked these data with gene expression data for the same individuals to identify a potential relationship between gene expression and methylation regarding reproductive caste determination. Within this study I have also characterised the *B. terrestris* methylome in order to allow comparative analyses between castes. If methylation plays a role in caste determination I would expect to find differentially methylated genes between castes, with functions related to reproduction. I would also expect any differentially methylated genes between castes to be enriched for differentially expressed genes or genes which have different exon usage between castes. Additionally if there is a conserved role for methylation in caste determination in Hymenoptera I would expect to find orthologous genes differentially methylated between *B. terrestris* reproductive castes and *A. mellifera* reproductive castes.

2.3 Methods

2.3.1 Bee husbandry and tissue sampling

Eight *B. terrestris* colonies, from Agralan, UK, were reared in constant red light at 26°C and 60% humidity (Fig. 2.1a). They were fed 50% v/v apiary solution (Meliose-Roquette, France) and pollen (Percie du set, France) *ad libitum*. Callow workers, less

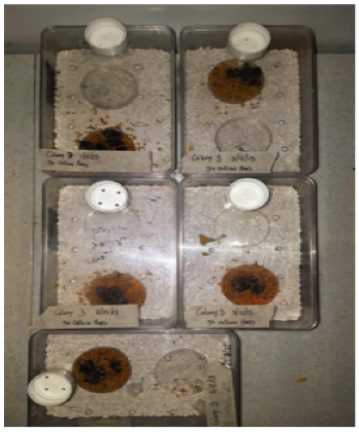
than 24 hours old (Fig. 2.1c), were taken from each colony and placed in small rearing boxes of five individuals (Fig. 2.1d).



(a) Colony Rearing Set-up

(b) View of Developed Colony

(c) Callow Worker

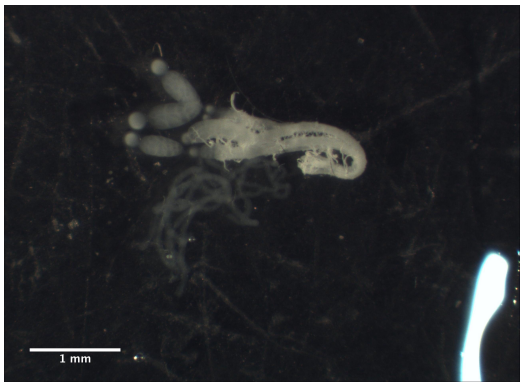


(d) Rearing Boxes

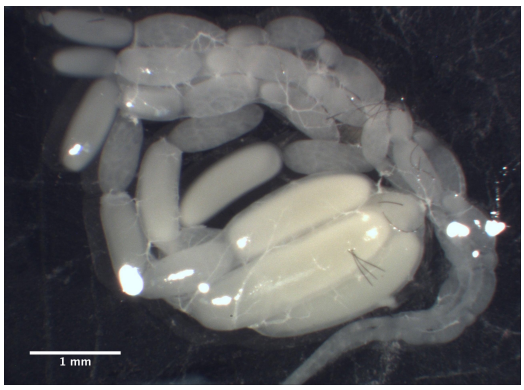
Figure 2.1: (a) Wooden colony box with attached foraging area, containing constant supply of sugar water and a dish of pollen grains. (b) Internal view of the wooden colony box, the queen can be seen at the top right with a yellow distinguishing mark, made by nail polish. (c) Sedated callow worker (individual <24 hours old, distinguished by the grey colouring and wings curled around the abdomen. (d) Rearing boxes containing five individuals, lined with cat litter and supplied with sugar water and pollen in petri dishes.

The worker bees were sacrificed at six days old. For each bee, the head was snap frozen in liquid nitrogen. Through dissection in 1% PBS solution, the reproductive status of each bee was determined and classed as either reproductive, sterile, or intermediate. Workers were classed as having developed ovaries, and therefore reproductive, if the largest oocyte was larger than the trophocyte follicle (Duchateau and Velthuis, 1988). This measurement is tightly correlated with reproductive status (Geva *et al.*, 2005;

Foster *et al.*, 2004). The ovaries of each worker were weighed, and the length of the largest oocyte was measured using ImageJ v.1.50e (Schneider *et al.*, 2012). Worker 'reproductiveness' was classified on a scale from 0-4 based on Duchateau and Velthuis (1988), 0 begin completely sterile (Fig. 2.2a) and 4 having fully developed ovaries (Fig. 2.2b).



(a) Sterile Ovaries.



(b) Reproductive Ovaries.

Figure 2.2: (a) single ovary without developed oocyctes from a sterile worker, reproductive score = 0. (b) single ovary containing developed oocytes from a reproductive worker, reproductive score = 4.

2.3.2 RNA and DNA extraction and sequencing

Three reproductive individuals and three sterile individuals, sampled from the queenless rearing boxes, were selected for RNA and DNA extraction, see Figure 2.3 for an overview. Heads were cut in half (using a lateral incision central between the eyes). Each head half was randomly allocated for either DNA/RNA extraction to avoid left/right hemisphere bias. RNA was extracted using the Sigma-Aldrich GenElute Mammalian Total RNA Miniprep kit and DNA was extracted using the Qiagen DNeasy blood and Tissue kit, individually for each half head per sample, following manufacturers protocols. The extracted RNA was treated with DNase and the extracted DNA was treated with RNase. DNA was pooled per colony and reproductive status, i.e. the three reproductive samples from a single colony were pooled to create one representative reproductive sample for that colony (Fig. 2.3). RNA samples were processed individually. DNA and RNA quality and quantity was determined by Nanodrop and

Qubit® fluorometers. A total of 18 RNA samples (three individuals per reproductive status for each of the three colonies) were sent for 100bp paired-end sequencing and six pooled DNA samples (one sample per reproductive status per colony consisting of three individuals per pool) were sent for 100bp paired-end bisulfite sequencing on a HiSeq 2000 machine (Illumina, Inc.) by BGI Tech Solution Co., Ltd.(Hong Kong). Library preparation was carried out by BGI. A 1% lambda spike was included as an unmethylated control in each whole genome bisulfite sequencing (WGBS) library. Directional bisulfite libraries were prepared by fragmenting genomic DNA to 100-300bp by sonication, DNA-end repair was then carried out along with ligation of methylated sequencing adaptors. The ZYMO EZ DNA Methylation-Gold kit was used for bisulfite treatment with subsequent desaltation, size selection, PCR amplification and final size selection before sequencing. RNA-seq libraries were prepared by using magnetic beads with an Oligo (dT) to enrich for mRNA, the mRNA was then fragmented and cDNA was synthesised using random hexamer priming, size selection and PCR amplification were then carried out prior to sequencing.

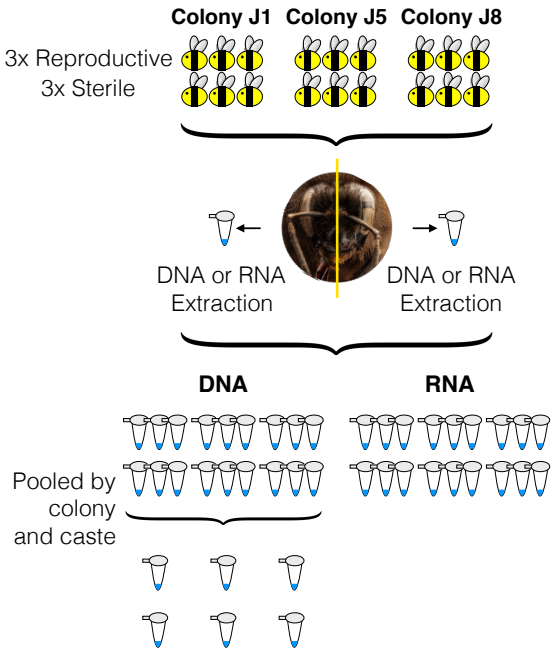


Figure 2.3: Overview of sample preparation for sequencing. Three *Bombus terrestris* reproductive workers and three sterile workers were selected from three colonies (J1, J5 and J8 represent colony names). Half of each head was randomly allocated for RNA/DNA extraction. All 18 RNA samples were sent for RNA-Seq (three of each caste from each colony). DNA samples were pooled by colony and caste creating a representative reproductive and sterile samples per colony.

2.3.3 Differential expression and alternative splicing

Low quality bases were removed from the RNA-Seq libraries using CutAdapt v1.1 (Martin, 2011). Reads were aligned to the reference genome (Bter_1.0, Refseq accession no. GCF_000214255.1 (Sadd *et al.*, 2015)) using STAR v2.5.2 (Dobin *et al.*, 2016) with standard parameters. Reads were counted per gene using HTseq v0.10.0 (Anders *et al.*, 2015). Differential expression analysis was then carried out after count normalisation via a negative binomial generalised linear model implemented by DEseq2 v1.20.0 (Love *et al.*, 2014) in R v.3.4.0 (http://www.R-project.org) with colony and reproductive status as independent variables. Genes were classed as differentially expressed when $q<0.05$ after correction for multiple testing using the Benjamini-Hochberg method (Benjamini and Hochberg, 1995).

Differential exon expression was determined using the DEXseq v1.26.0 R package (An-

ders *et al.*, 2012), briefly this package calculated the ratio of expression of a given exon in a given gene relative to other exons in the same gene for each sample. The relative exon expression per colony was then calculated taking into account dispersion between colonies. A general linear model was then used to test for a difference in the relative proportion of expression of each exon between castes, accounting for sample differences and overall gene expression differences between castes, p-values were corrected for multiple testing using the Benjamini-Hochberg method (Benjamini and Hochberg, 1995) and exons were classed as differentially used between castes when q <0.1. The benefit of this method over general alternative splicing analysis is that specific differentially used exons can be identified between castes allowing the relationship with exonic methylation to be investigated.

2.3.4 Differential methylation

WGBS libraries were aligned to the reference genome (Bter_1.0, Refseq accession no. GCF_000214255.1, (Sadd *et al.*, 2015)) using Bismark v.0.16.1 (Krueger and Andrews, 2011) and bowtie2 v.2.2.6 (Langmead and Salzberg, 2012) with standard parameters. Bismark was also used to extract methylation counts and carry out deduplication. Annotation of the methylation counts with genomic features (from the *B. terrestis* annotation file, Refseq accession no. GCF_000214255.1) was carried out using custom R scripts implementing the sqldf v.0.4.11 library (Grothendieck, 2017). Bisulfite conversion efficiency was calculated by aligning reads to the lambda reference genome (Refseq accession no. GCF_000840245.1) and calculating the single-site methylation level as in Schultz *et al.* (2012).

Prior to differential methylation analysis, coverage outliers (above the 99.9th percentile) were removed along with bases covered by less than 10 reads. The methylation status of each CpG was then determined using the 'methylation status calling' (MSC) procedure, as described in Cheng and Zhu (2014). Briefly, this involves applying a mixed binomial model to each CpG which includes estimation of both the false discovery rate and the non-false discovery rate in order to make a binary methylation call per site. CpG sites were then filtered to remove any site that did not return as methylated in at least

one sample. This functions to reduce the number of tests and hence decreases the required stringency of the later FDR correction applied during differential methylation testing. This is a vital step for species, such as bumblebees, with extremely low genome methylation where the majority of sites show zero methylation in all samples. A logistic regression model was then applied, via the R package methylKit v1.6.1 (Akalin *et al.*, 2012), to determine differentially methylated sites, taking into account colony as a covariate due to high inter-colony variation. A minimum difference of at least 10% methylation and a q-value of <0.05 were required for a single site to be classed as differentially methylated. Genes containing at least one differentially methylated CpG and a minimum weighted methylation difference of 10% across the entire gene were classed as differentially methylated between reproductive castes. Weighted methylation level is determined as the total number of methylated cytosines (C) within a region (i) divided by the total coverage of a region (Equation 2.1), as described in Schultz *et al.* (2012).

$$\sum_{i=1}^{n} C_i / \sum_{i=1}^{n} C_i + T_i \tag{2.1}$$

A permutation test was computed as part of the differential methylation analysis, as seen in previous research (Arsenault *et al.*, 2018; Libbrecht *et al.*, 2016). After removal of positions containing zero methylation for every sample and filtering by coverage, the sample labels for data at each CpG were randomly shuffled 10,000 times. A logistic regression was carried out for each random data set using methylKit.

2.3.5 GO enrichment

Gene ontology terms for *B. terrestris* were taken from a custom database from Bebane *et al.* (2019). GO enrichment analysis was carried out using a hypergeometric test with Benjamini-Hochberg (Benjamini and Hochberg, 1995) multiple-testing correction. GO terms were defined as enriched when q <0.05. GO terms from differentially methylated genes were tested for enrichment against GO terms associated with all methylated

genes. Genes were classed as methylated when the weighted methylation score per gene was greater than zero (Schultz *et al.*, 2012). Additionally the GO terms associated with hypermethylated genes (i.e. genes with higher methylation levels in one condition compared to the other) in either sterile or reproductive workers were tested for enrichment against the GO terms associated with all differentially methylated genes between castes to determined if there are different functions for hypermethylated genes in either sterile or reproductive workers. GO terms for differentially expressed genes and genes containing different exon usage between castes were tested for enrichment against GO terms associated with all genes identified in the RNA-seq data. REVIGO (Supek *et al.*, 2011) was used to obtain the GO descriptions from the GO identification numbers.

2.3.6 Comparative analyses

The hypergeometric test was applied to gene lists from the various analyses to determine if any overlaps were statistically significant. Custom R scripts were used to investigate the relationship between gene expression and methylation. A reciprocal blast between the honeybee (Amel_4.5, Refseq accession no. GCA_000002195.1) and bumblebee genome (Bter_1.0, Refseq accession no. GCA_000214255.1) was carried out using blast+ v2.5.0 (Camacho *et al.*, 2009), where the fasta sequence for each gene of each species was blasted against a custom database containing the fasta sequence for every gene of the opposite species, allowing only one match per gene and a minimum e-value of 1 x10^{-3}. The results were then filtered to ensure only matches that occurred in both directions and to only one gene were used. For example, multiple honeybee genes matched the same bumblebee gene, therefore all of these matches were discarded. This allowed us to construct a database of putative orthologous genes. A custom script was then used to check for overlap between the differentially methylated genes identified here and differentially methylated genes identified in Lyko *et al.* (2010) between honeybee reproductive castes.

All bioinformatic scripts used within this chapter can be found at: `https://zenodo.org/badge/latestdoi/162321404`.

2.4 Results

2.4.1 Collection of reproductive castes

From the eight reared colonies a total of 46 boxes of five callow workers were collected (totalling 230 individuals). The majority of females were classed as either reproductive (ovary score of 3-4) or sterile with only some individuals falling in the intermediate stage (ovary score of 1-2) (Fig. 2.4a). The mean weight of the ovaries along with the mean oocyte length for intermediate and reproductive workers can be found in Table 2.1. Reproductive workers had significantly heavier ovaries than both intermediate and sterile workers and intermediate workers had significantly heavier ovaries than sterile workers (Kruskal-Wallis test: chi-squared = 124.5, df = 2, p <0.000, Wilcoxon rank sum test: sterile and intermediate p <0.000, sterile and reproductive p <0.000 and intermediate and reproductive p <0.000)(Fig. 2.4b). Reproductive workers had significantly longer oocytes than intermediate workers (t-test: t = -10.367, df = 85.815, p <0.000)(Fig. 2.4c). Samples were selected from three colonies, as biological replicates (supplementary 1.0.0).

Table 2.1: Mean ovary weight and mean oocyte length with standard deviation for all samples from each of the three worker reproductive classifications.

Reproductive Status	Mean Ovary Weight (g)	Standard Deviation (g)	Mean Oocyte Length (mm)	Standard Deviation (mm)
Reproductive (score 3-4)	0.0164	+/- 0.01	1.633	+/- 0.39
Intermediate (score 1-2)	0.0075	+/- 0.003	0.981	+/- 0.24
Non-Reproductive (score 0)	0.0026	+/- 0.0019	N/A	N/A

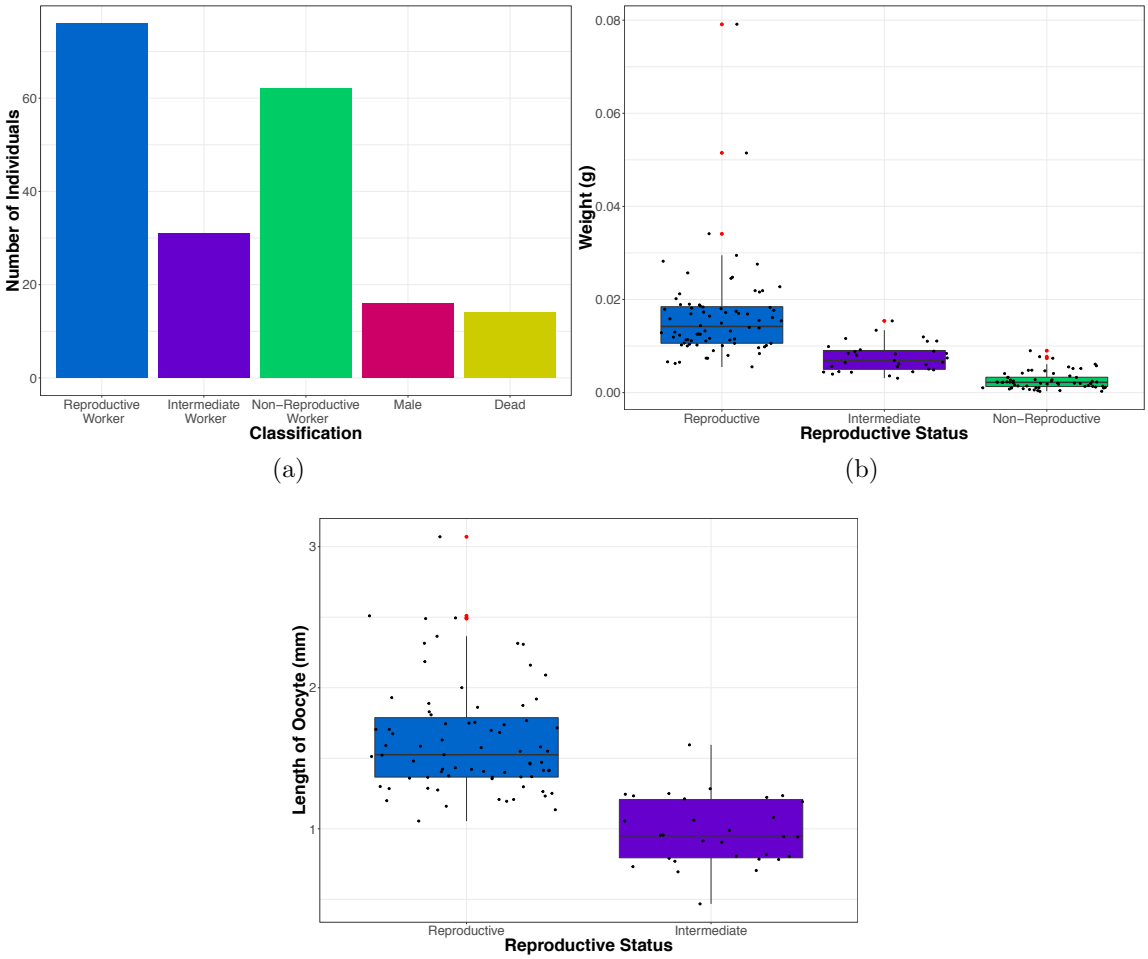


Figure 2.4: (a) Bar plot showing the total number of individual *Bombus terrestris* samples collected per reproductive classification, including any male samples taken by mistake and the number of individuals which died during rearing. (b) Boxplots of the weight of the ovaries collected from workers per each reproductive classification. Each boxplot shows the median along with the 25th and 75th percentile. The whiskers represent 1.5X the interquartile range. Outliers are represented as additional red points. Each offset black point represents an individual sample. Reproductive N = 76, intermediate N = 31 and non-reproductive N = 62. (c) Boxplot of the length of the largest oocyte of reproductive and intermediate workers.

2.4.2 DNA and RNA extraction

DNA extracted from half a head was pooled from three reproductive workers and three sterile workers per colony. This gave more than 1μg for each colony specific sample. Quality scores were all within acceptable ranges for sequencing (supplementary 1.0.1)

and DNA fragment sizes were generally above 10,000bp but with a smear of smaller fragments present (Fig. 2.5). RNA extracted from the second half of the head of each bee also gave acceptable quantity and quality scores for sequencing (supplementary 1.0.2).

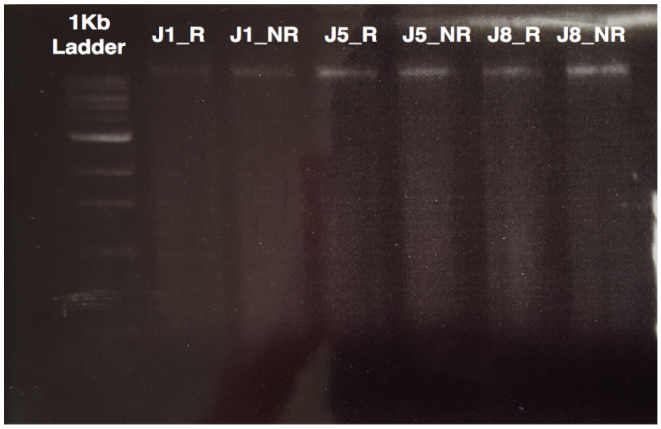


Figure 2.5: 1% agarose gel showing the DNA bands for all *Bombus terrestris* samples. There is a band above 10,000bp for all samples and they all show a smear of smaller fragments.

2.4.3 Genome-wide methylation differences between castes

Up to a maximum of 10bp were trimmed from the start of all reads due to base bias generated by the Illumina sequencing protocol (Krueger *et al.*, 2011). The mean mapping efficiency was 63.6% ± 1.4% (mean ± standard deviation) and the mean coverage was 17.7 ± 0.5 reads per base. The average number of uniquely mapped reads were 27,709,214 ± 753,203. The mean bisulfite conversion efficiency, calculated from the unmethylated lambda spike, was 99.55% ± 0.02%. After accounting for the conversion efficiency there were no methylated cytosines in a non-CpG context. The mean single site methylation level (Schultz *et al.*, 2012) in a CpG context was determined as 0.22% ± 0.07, calculated from the number of methylated cytosines divided by the sum of methylated and unmethylated cytosines and accounting for bisulfite conversion efficiency.

A total of 3,412 genes were classed as methylated, i.e. they had a weighted methylation level greater than the conversion error rate of >0.05 in at least one sample. There

was no significant difference in the overall weighted methylation level of the methylated genes between reproductive and sterile workers (Mann-Whitney U test: W = 5948300, p = 0.117, Fig. 2.6a). GO terms enriched in methylated genes compared to all genes annotated in the genome (q <0.05) include a large variety of biological processes (supplementary 1.0.3). The GO terms: *post-transcriptional regulation of gene expression* (GO:0010608), *histone modification* (GO:0016570) and *chromatin remodelling* (GO:0006338) are enriched as well as terms related to reproductive processes, e.g. *reproduction* (GO:0000003), *gamete generation* (GO:0007276), *oogenesis* (GO:0048477) and *oocyte differentiation* (GO:0009994).

There was no significant difference in the weighted methylation level of any genomic feature (e.g. exon, intron, gene) between reproductive and sterile workers (Two-way ANOVA, interaction between genomic feature and reproductive status; $F_{1,6} = 0.637$, p = 0.701, Fig. 2.6b). I also tested for differences in methylation levels of putative promotors but as promotor regions are currently unannotated for the current bumblebee genomic annotation I feel these results are not reliable (Fig. 2.6b). Irrespective of worker reproductive status we found methylation differences between genomic features (Kruskal-Wallis; chi-squared = 729.35, df = 7, p <0.000). With methylation being significantly enriched in coding regions compared to introns and ncRNAs (supplementary 1.0.6).

I also found no difference in the weighted methylation level across the genome per linkage group between reproductive and sterile workers (Two-way ANOVA, interaction between linkage group and reproductive status; $F_{1,17} = 0.034$, p = 1, Fig. 2.7). Weighted methylation did vary significantly between linkage groups within the genome irrespective of reproductive status (Kruskal-Wallis chi-squared = 131.59, df = 17, p <0.000, supplementary 1.0.6). However, due to the number of unplaced scaffolds these results should be interpreted with care.

Finally, using CpG methylation levels, samples cluster by colony rather than by reproductive caste (Fig. 2.6c and 2.6d). This indicates high inter-colony variation in methylation.

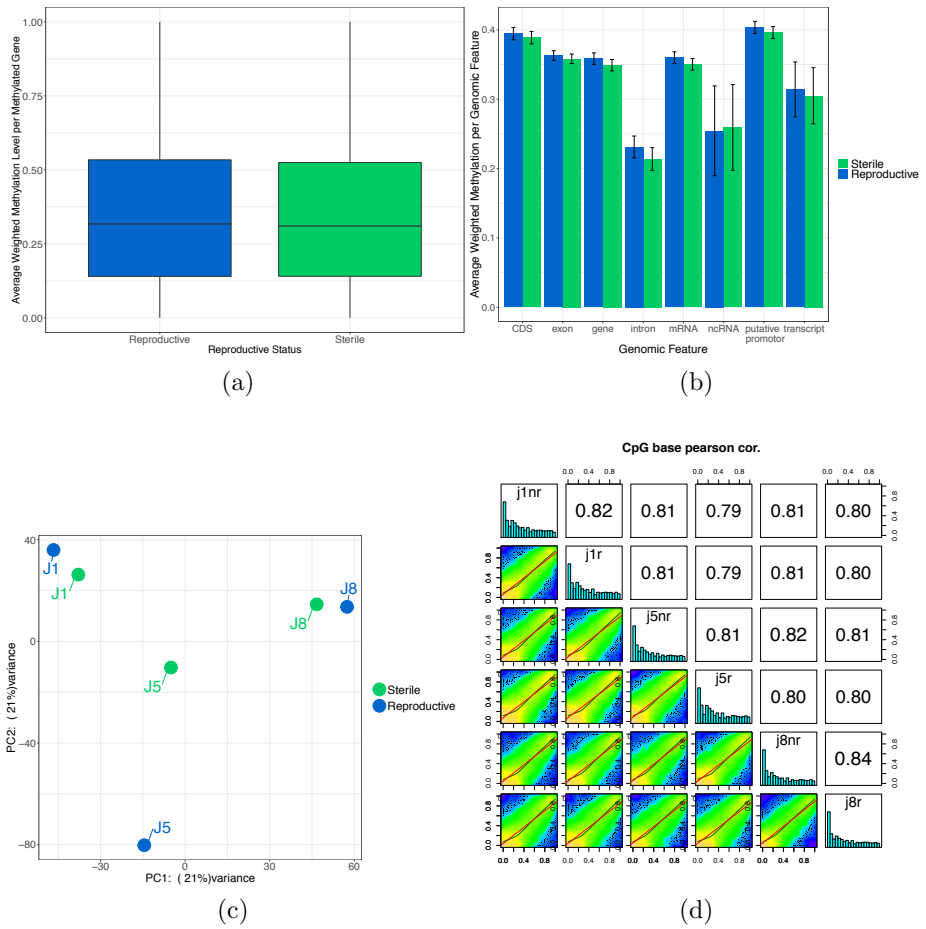


Figure 2.6: (a) Box plot of the mean weighted methylation level of methylated genes (N = 3412) across *Bombus terrestris* colonies for each caste. Each boxplot shows the median along with the 25th and 75th percentile. The whiskers represent 1.5X the interquartile range. Outliers are represented as additional red points. (b) The mean weighted methylation level across colonies for each genomic feature for both reproductive and sterile workers. Error bars are 95% confidence intervals of the mean. This graph includes a putative promotor region, this was defined as 5000bp upstream of each gene annotation. As the current annotation file for *B. terrestris* does not include promotor regions. This result should be viewed with care as some of the 'putative promotor' regions also contain other annotated genomic features such as other genes and coding regions. (c) PCA plot generated by methylKit showing samples cluster by colony using per site CpG methylation. Total CpGs = 28,735,331. (d) Methylation correlation matrix of all samples in a CpG context. The numbers represent the pairwise correlation coefficients. The corresponding scatter plots are fitted with a linear regression (red line) and a polynomial regression, fit using the LOESS method (green line). The internal bar plots show the percentage of methylation per base.

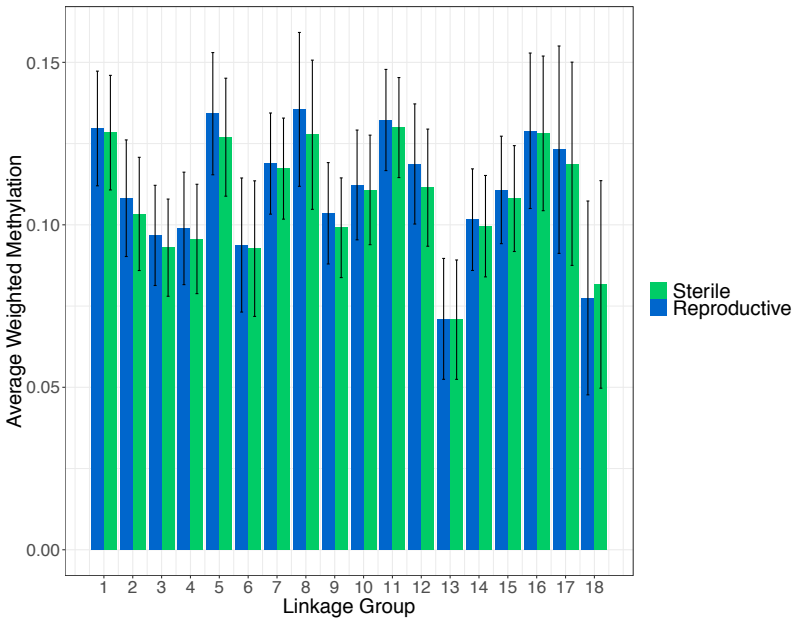


Figure 2.7: The mean weighted methylation level across *Bombus terrestris* colonies for each linkage group defined in the B. terrestris genome Bter_1.0 (NCBI Accession: GCA_000214255.1). Error bars are 95% confidence intervals of the man. This figure should also be viewed with caution as currently there are >5,000 unplaced scaffolds for this genome build which are not included in the figure.

2.4.4 Gene level methylation differences between castes

A total of 4,681,131 CpG sites had a coverage >10 in all six sample data sets, of those 16,194 returned as methylated in at least one sample after running the MSC procedure. A total of 624 of these CpGs were identified as differentially methylated between reproductive castes, 613 of these were located in a total of 478 genes (supplementary 1.0.4). 11 differentially methylated CpGs were located outside of genes, nine of those were within 5000bp upstream or downstream of a gene with no apparent trend in the expression of near-by genes (supplementary 1.0.5). After stringent filtering of these genes to also require each gene to show a minimum weighted methylation difference of 10% we found 111 differentially methylated genes between reproductive and sterile workers (supplementary 1.0.7, Fig. 2.8).

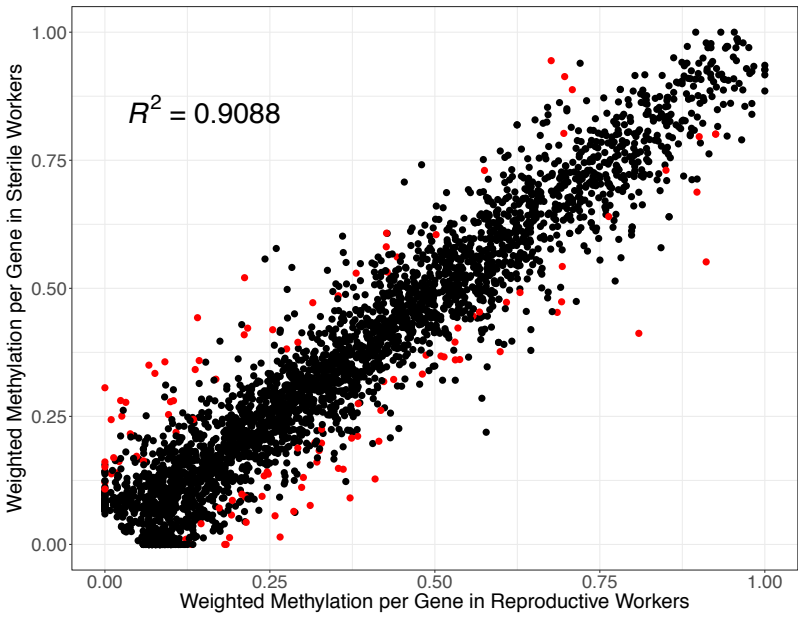


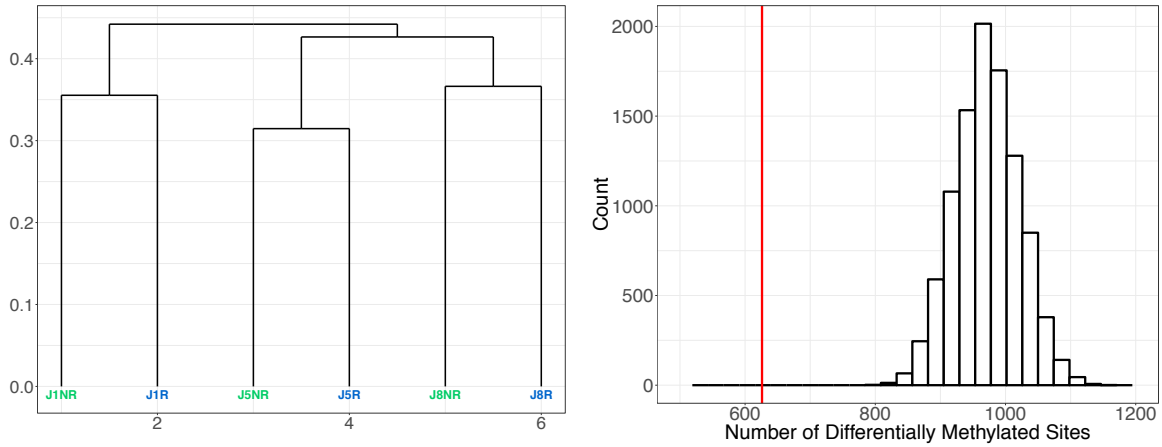
Figure 2.8: Scatter plot of the average weighted methylation level (across *Bombus terrestris* colonies) for reproductive workers against sterile workers. Each dot represents a gene (N = 3412) and each red dot represents a differentially methylated gene (q <0.05 and a minimum gene weighted methylation difference of 10%).

Of the 111 differentially methylated genes, there was no preference for genes to be hypermethylated in either reproductive or sterile workers (Chi-squared goodness of fit, chi-squared = 2.027, df = 1, p = 0.154), with 63 genes hypermethylated in reproductive workers and 48 genes hypermethylated in sterile workers.

GO terms enriched in differentially methylated genes compared to all methylated genes (q <0.05) contained a variety of biological processes (supplementary 1.0.8), amongst these were terms involved with reproduction, including: *meiotic cell cycle* (GO:0051321), *maintenance of oocyte nucleus location involved in oocyte dorsal/ventral axis specification* (GO:0042070), *negative regulation of transcription involved in meiotic cell cycle* (GO:0051038), *female meiosis chromosome segregation* (GO:0016321) and *female germline ring canal stabilisation* (GO:0008335). One of the genes associated with the above GO terms is *eggless* (LOC100647514: *histone-lysine N-methyltransferase eggless*) which shows hypermethylation in sterile workers. This gene contains a Methyl-CpG binding domain which has been associated with histone H3, lysine 9-specific methyltransferase which contributes to repression of transcription (Wakefield *et al.*, 1999).

There were no specific GO terms enriched for either the hypermethylated genes in sterile workers or the hypermethylated genes in reproductive workers compared to all differentially methylated genes as a background.

A valid permutation test was not possible due to the structure within the data caused by colony (Fig. 2.9a). More sites were found to be differentially methylated using the random data as variation between colonies is higher than variation caused by reproductive status. Using this method 'colony' can no longer be taken into account as a consistent covariate and the effect therefore inflates the number of obtained differentially methylated sites (Fig. 2.9b).



(a) (b)

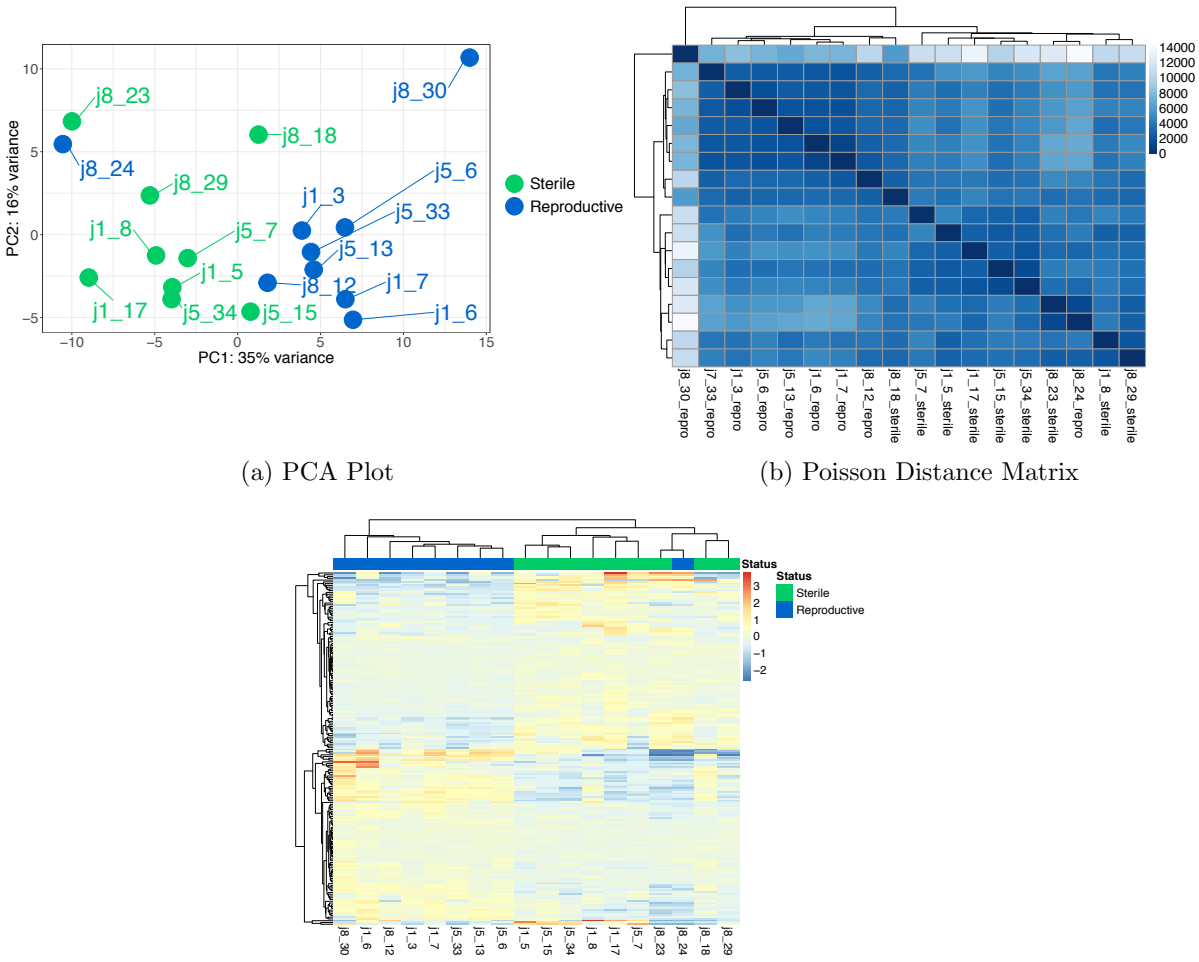
Figure 2.9: (a) Hierarchical cluster based on CpG (N = 28,735,331) methylation correlation distances for all *Bombus terrestris* samples, calculated using the 'ward' method. (b) Histogram of the number of differentially methylated sites obtained from 10,000 permutations. The red line indicates the number of sites observed from the un-shuffled data.

Whilst permutation tests are useful for some data sets, when structure is present in the data they become unreliable, as discussed in Winkler *et al.* (2015). A higher number of replicates would allow label shuffling within confounding factors, maintaining the structure of the data, thus allowing a permutation test.

2.4.5 Expression differences between worker reproductive castes

All reads had 13bp trimmed from the start due to base bias generated by the Illumina protocol (Krueger *et al.*, 2011). The mean percentage of uniquely mapped reads was 89.4% ± 0.8% (mean ± standard deviation). This equated to a mean of 10,115,366 ± 1,849,600 uniquely mapped reads. After running a differential expression analysis with DESeq2, the decision was made to remove one sample from all downstream analysis due to possible mislabelling of reproductive status.

Sample J8_24 was classed as reproductive but clustered with the sterile samples in both a principle component analysis (PCA) and a poisson distance matrix, taking into account expression levels of all genes (Fig. 2.10a and 2.10b). It also clustered with sterile samples in a hierarchical cluster using euclidean distances based on the top 100 differentially expressed genes (Fig. 2.10c). Including this sample led to a decrease in the number of differentially expressed genes identified (110 with sample, 334 without sample). After removal of this sample all other samples clustered by reproductive status (Fig. 2.11a, 2.11b and 2.11c).

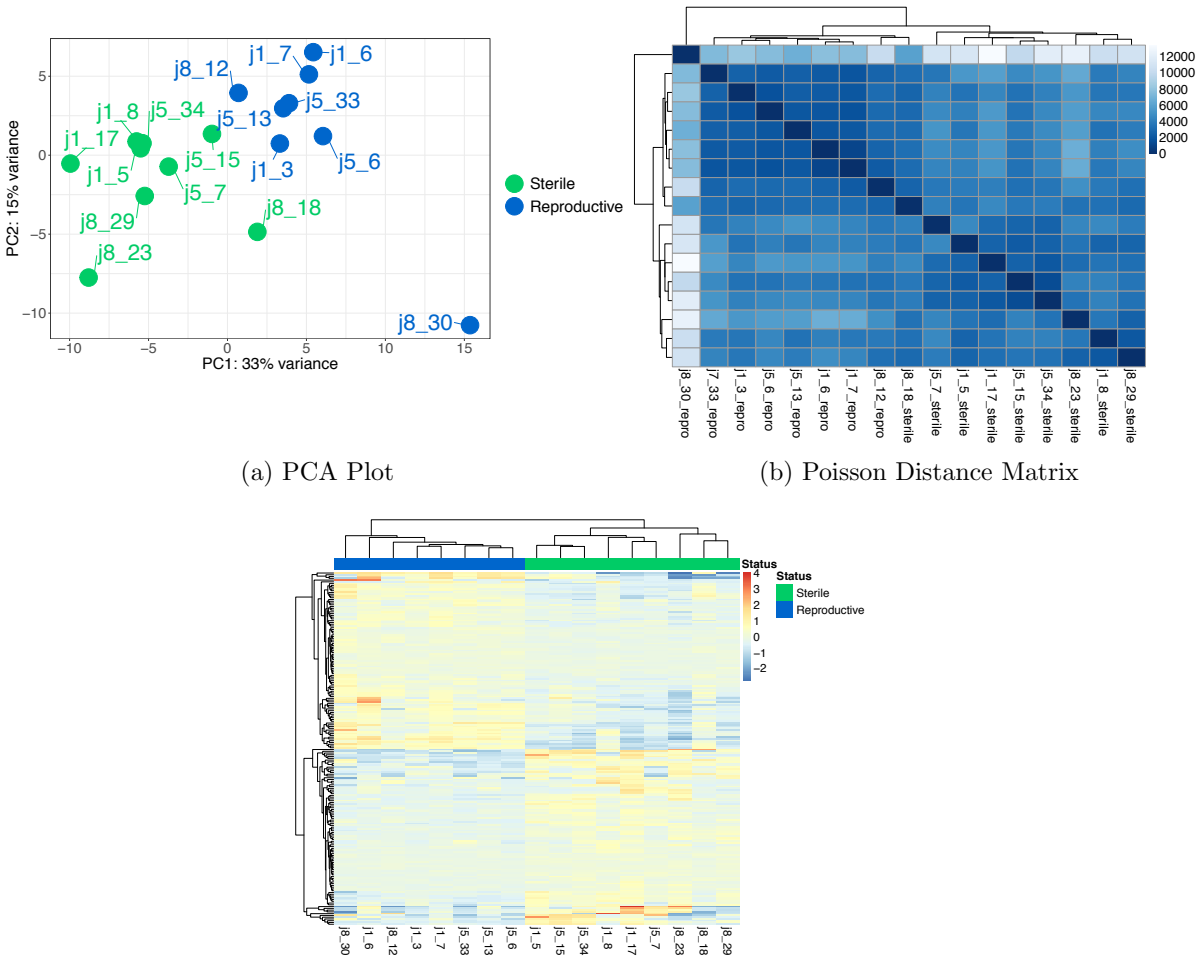


(a) PCA Plot

(b) Poisson Distance Matrix

(c) Elucidean Cluster Heatmap

Figure 2.10: Graphs generated from differential expression analysis using DESeq2 for all *Bombus terrestris* samples. (a) PCA plot showing the different reproductive status' grouped together, based on the expression of all genes (N = 11,732). (b) Poisson measurement of dissimilarity between counts of all genes for each sample compared to every other sample. The lighter colours represent higher dissimilarity with other samples. The dendograms are mirrored and show hierarchical clustering of all samples. (c) Heatmap showing the top 100 differentially expressed genes in reproductive and sterile workers. Red colour indicates over-expression and blue colour indicates under-expression. The top dendogram shows hierarchical clustering by sample based on the counts of the genes shown. The left-hand dendogram shows count similarity between the top 50 over expressed genes in reproductive workers and the top 50 over expressed genes in sterile workers.



(a) PCA Plot

(b) Poisson Distance Matrix

(c) Elucidean Cluster Heatmap

Figure 2.11: Graphs generated from differential expression analysis using DESeq2 for all *Bombus terrestris* samples, excluding J8_24. (a) PCA plot showing the different reproductive status' grouped together, based on the expression of all genes (N = 11,732). (b) Poisson measurement of dissimilarity between counts of all genes for each sample compared to every other sample. The lighter colours represent higher dissimilarity with other samples. The dendograms are mirrored and show hierarchical clustering of all samples. (c) Heatmap showing the top 100 differentially expressed genes in reproductive and sterile workers. Red colour indicates over-expression and blue colour indicates under-expression. The top dendogram shows hierarchical clustering by sample based on the counts of the genes shown. The left-hand dendogram shows count similarity between the top 50 over expressed genes in reproductive workers and the top 50 over expressed genes in sterile workers.

A total of 334 genes were identified as differentially expressed (q <0.05). There was no difference in the number of up-regulated genes in either reproductive or sterile workers (Chi-squared goodness of fit: chi-squared = 0.2994, df = 1, p-value = 0.584), with

172 genes up-regulated in reproductive workers and 162 genes up-regulated in sterile workers.

One of the most up-regulated genes in reproductive workers was vitellogenin (gene ID: LOC100650436, log2 fold-change of 2.92, q = <0.000). Previous work has found up-regulation of this gene in reproductive *B. terrestris* workers is linked to aggressive behaviour rather than directly to ovary development (Amsalem *et al.*, 2014; Lockett *et al.*, 2016). Additionally two genes coding for serine-protease inhibitors were found to be up-regulated in reproductive workers, these proteins have been linked to reproduction in other insect species (Bao *et al.*, 2014).

Enriched GO terms associated with the differentially expressed genes compared to the background of all genes in the RNA-seq data (q <0.05) contained a variety of biological processes (supplementary 1.1.0), including *embryonic process involved in female pregnancy* (GO:0060136) and *positive regulation of oviposition* (GO:1901046). Additionally there were no specific GO terms enriched in up-regulated genes of reproductive workers compared to all differentially expressed genes as the background. However, there were two GO terms enriched for up-regulated genes in sterile workers compared to differentially expressed genes as the background, these were: *cellular lipid metabolic process* (GO:0044255) and *isoprenoid biosynthetic process* (GO:0008299).

A total of 59 genes were identified as having differential exon usage, containing 83 differentially expressed exons between reproductive castes (q <0.1, supplementary 1.1.1, Fig. 2.12). There is no difference in the number of up-regulated exons in reproductive workers compared to sterile workers (Chi-squared goodness of fit: chi-squared = 3.4819, df = 1, p-value = 0.06), with reproductive workers having 33 up-regulated exons and sterile workers having 50 up-regulated exons. The enriched GO terms associated with genes containing differentially used exons compared to the background of all genes in the RNA-seq data (q <0.05) contained a variety of biological processes (supplementary 1.1.2.). However, there were no GO terms with a clear connection to reproductive processes.

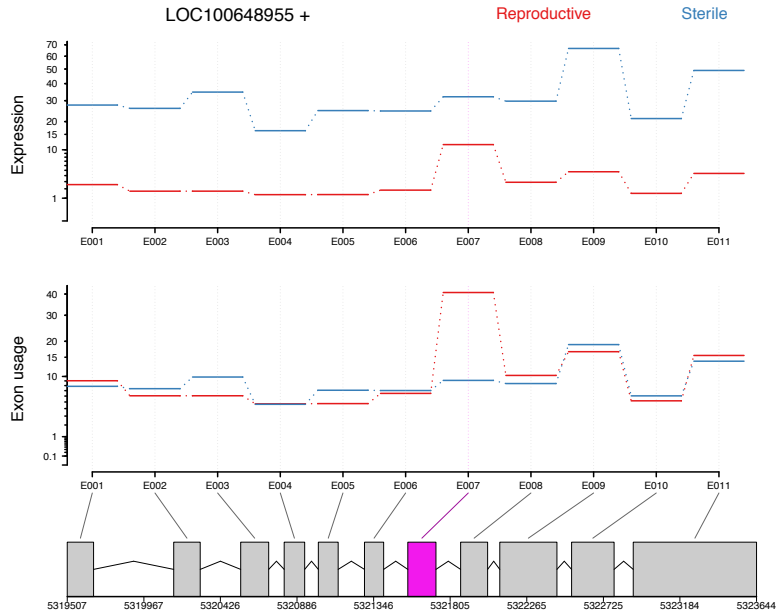


Figure 2.12: An example of a gene which shows differential exon expression in one exon between *Bombus terrestris* reproductive castes. The top section of the plot shows the general expression differences between castes, the second section shows the normalised counts per exon (given expression differences) and the third section highlights the differentially expressed exon in pink. Gene shown: *probable peroxisomal acyl-coenzyme A oxidase 1* (ID: LOC100648955).

Relationship of methylation and gene expression

On an individual gene basis, methylation and reproductive caste have no effect on expression level (Fig. 2.13a and 2.13b, linear mixed effects model with colony as a random factor; methylation: df = 49172, t = -1.295, p = 0.195, reproductive status: df = 49172, t = -0.638, p = 0.524, interaction between methylation and reproductive status: df = 49172, t = 0.112, p = 0.911).

However, gene groups with varying methylation levels show different levels of expression (Kruskal-Wallis; chi-squared = 131.59, df = 17, p <0.000, Fig.2.13c). Specifically genes with no methylation show higher expression than genes classed as lowly methylated but lower expression than genes classed as medium/high in terms of methylation (Dunn's test with Benjamini-Hochberg multiple-testing correction; no methylation vs low methylation: Z = -13.14, p <0.000, no methylation vs medium methylation: Z = 4.5, p <0.000, no methylation vs high methylation: Z = 7.32, p <0.000, Fig. 2.13c).

Reproductive caste still has no effect on gene expression in relation to methylation status when genes are grouped (Two-way ANOVA, interaction between reproductive status and methylation level; $F_{1,3} = 0.017$, $p = 0.99$).

A linear mixed effects model was then applied to assess the relationship between gene expression, methylation and reproductive status for only methylated genes using colony as a random factor. There is a positive relationship between gene expression and methylation in methylated genes with reproductive status having no effect (Fig. 2.13d, methylation: df = 17390, t = 6.154, p <0.000, reproductive status: df = 17390, t = -0.328, p = 0.743, interaction between methylation and reproductive status: df = 17390, t = -0.200, p = 0.842).

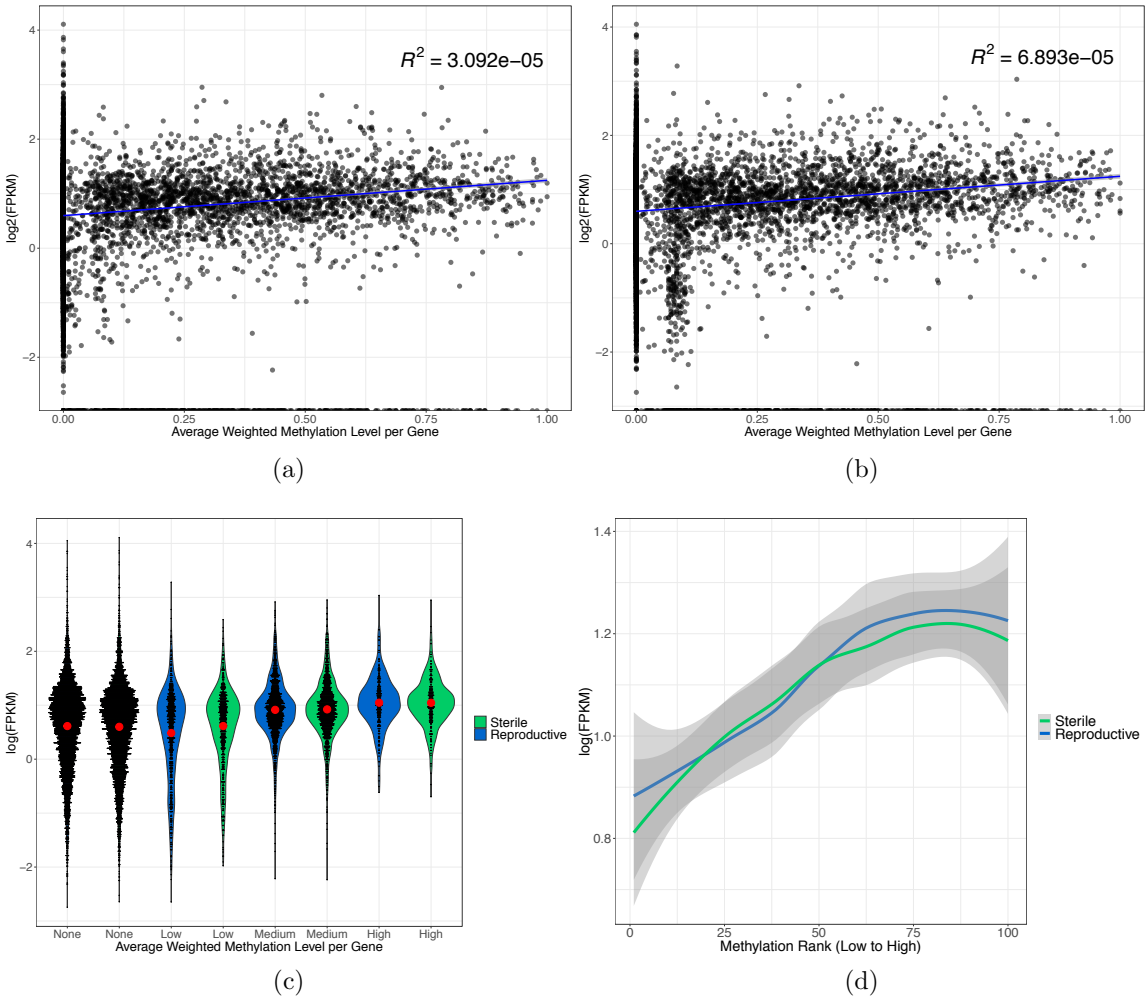


Figure 2.13: (a) and (b) the colony average weighted methylation level for every gene plotted against the log(FPKM) of that gene (N = 8,709) for *Bombus terrestris* sterile workers and reproductive workers respectively. Each black dot represents a single gene. The blue line is a fitted linear regression with the grey shaded area representing 95% confidence intervals. (c) Violin plots showing the distribution of the data via a mirrored density plot, meaning the widest part of the plots represent the most genes. Weighted methylation level per gene per caste, averaged across colonies, was binned into four categories, no methylation (reproductive N = 5,373 and sterile N = 5,474), low (>0 - 0.2, reproductive N = 1,075 and sterile N = 981), medium (0.2 - 0.7, reproductive N = 1,871 and sterile N = 1,883) and high (0.7 - 1, reproductive N = 390 and sterile N = 371), as in Liu *et al.* (2019). The red dot indicates the mean with 95% confidence intervals. Each black dot represents a single gene. (d) Binned methylated genes (N = 3412, 100 being the most highly methylated) based on the mean weighted methylation level across colonies per reproductive caste, plotted against the log(FPKM) expression level per gene. Data were smoothed using the LOESS method, grey areas are 95% confidence intervals.

2.4.6 Relationship of methylation and differential gene expression

Weighted methylation differences between differentially expressed genes and non-differentially expressed genes were assessed along with weighted methylation differences between genes containing differentially expressed exons and genes without differentially expressed exons (Fig. 2.14a and Fig. 2.14b). Differentially expressed genes and genes containing differentially expressed exons between castes show lower methylation than non-differentially expressed genes or genes containing no differentially expressed exons, with reproductive status and the interaction of reproductive status with gene expression type having no effect (Table 2.2, Fig. 2.14a and 2.14b). When weighted methylation is assessed per exon, differentially expressed exons have lower weighted methylation than non-differentially expressed exons (Fig. 2.14c), with reproductive status and the interaction of reproductive status and exon expression having no effect (Table 2.2).

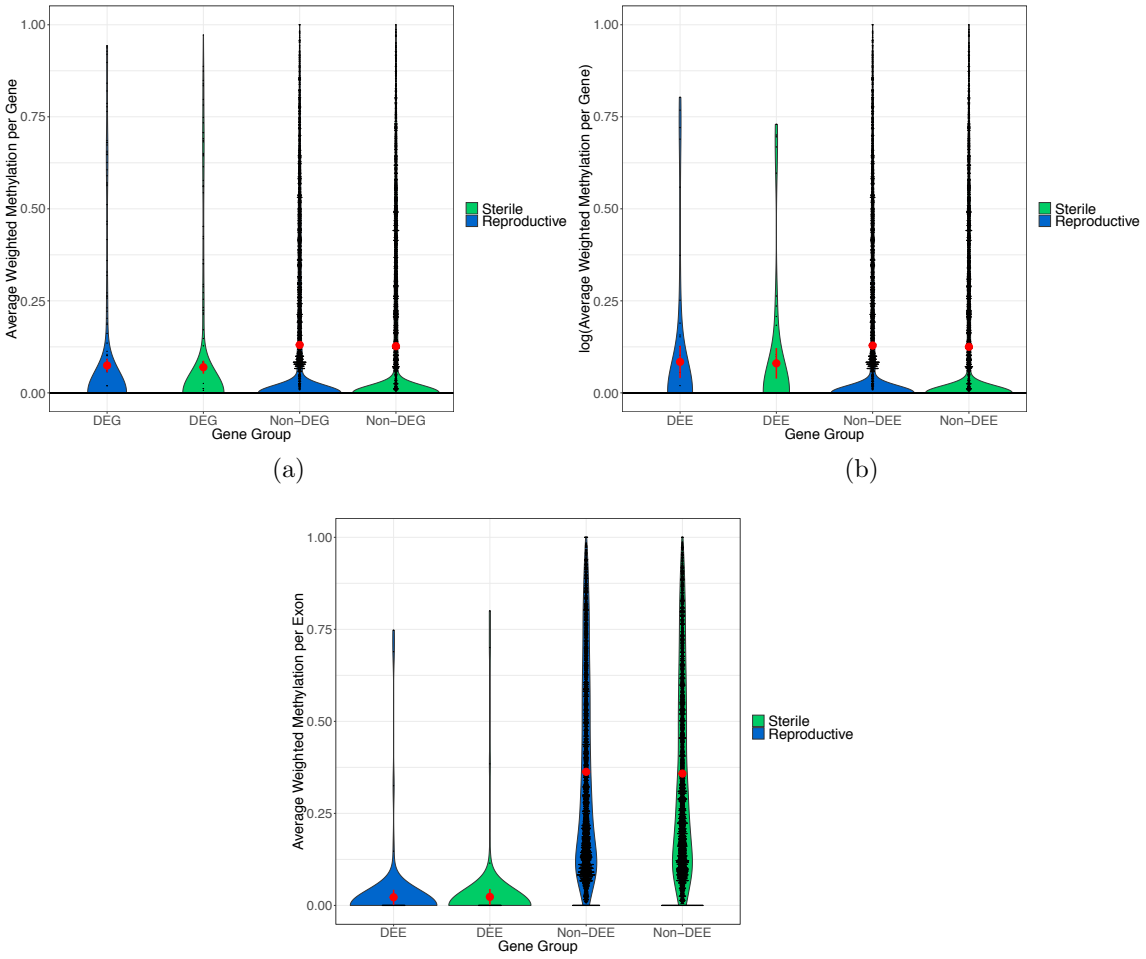
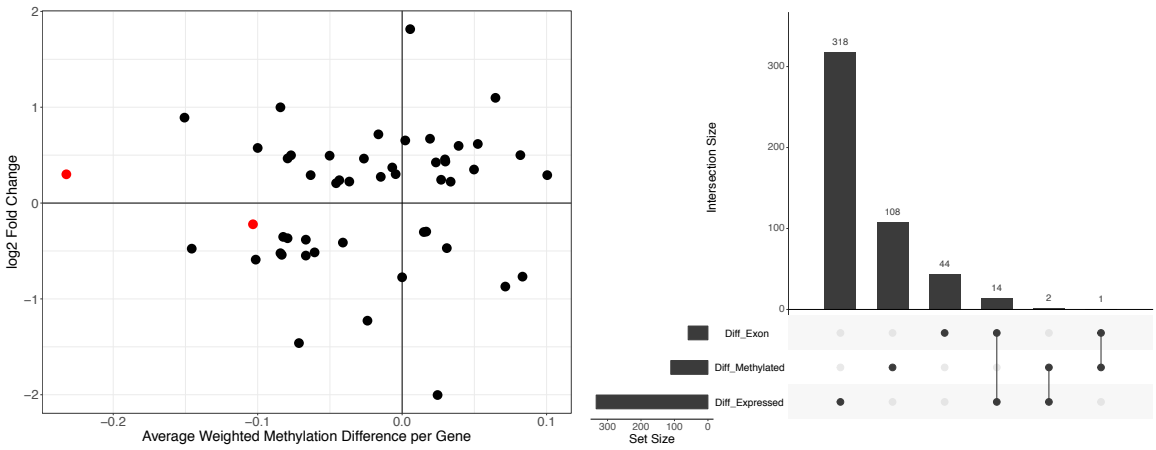


Figure 2.14: (a) Violin plots showing the distribution of the data via a mirrored density plot, meaning the widest part of the plots represent the most genes. The red dots represent the mean of each gene set along with error bars representing 95% confidence intervals of the mean. Each black dot is an individual gene. The mean weighted methylation per gene across *Bombus terrestris* colonies per caste is plotted for either differentially expressed genes (DEG, N = 334) or non-differentially expressed genes (non-DEG, N = 7,911). (b) Violin plots of the mean weighted methylation per gene across colonies per caste is plotted for either genes containing differentially expressed exons (DEE, N = 59) or genes with no differentially expressed exons (non-DEE, N = 8,147). (c) Violin plots of the mean weighted methylation per exon across colonies per caste for differentially expressed exons (DEE, N = 59) and non-differentially expressed exons (non-DEE, N = 3,011). The red dots represent the mean of each gene set along with error bars representing 95% confidence intervals of the mean. Each black dot is an individual exon.

Table 2.2: Summary statistics of the linear models used to check for differences in weighted methylation level between gene sets, taking into account reproductive status. The interaction vs main effects models were tested using the *anova* function in R to assess the interaction effect between gene set and reproductive status. * indicates a significant p-value <0.05.

	Res.Df	RSS	Df	Sum of Sq	F	P
Differentially expressed genes						
Interaction vs main effects model	16487	833.1	-1	-2.98×10^{-4}	5.9×10^{-3}	0.93
DEG vs Non-DEG	N/A	835.14	1	2.04	40.38	<0.000*
Reproductive vs Sterile	N/A	833.15	1	0.049	0.97	0.32
Genes with differentially expressed exons						
Interaction vs main effects model	16409	832.69	-1	-7.93×10^{-6}	2.00×10^{-4}	0.99
DEE vs Non-DEE	N/A	832.92	1	0.23	4.59	0.032*
Reproductive vs Sterile	N/A	832.74	1	0.048	0.95	0.33
Differentially expressed exons						
Interaction vs main effects model	11301	780.36	-1	-1.39×10^{-3}	0.02	0.89
DEE vs Non-DEE	N/A	799.69	1	19.33	279.97	<0.000*
Reproductive vs Sterile	N/A	780.42	1	0.06	0.86	0.35

Of the 334 differentially expressed genes, 50 also showed some level of weighted methylation difference between reproductive and sterile workers (weighted methylation difference >0) (Fig. 2.15a). However, there is no relationship between the level of differential methylation and the level of differential expression for these 50 genes (linear model: $F_{1,\,58} = 0.2717$, $p = 0.604$).



(a) (b)

Figure 2.15: (a) Scatter plot of the difference in the mean weighted methylation level across *Bombus terrestris* colonies between castes plotted against the log2 fold change in expression of differentially expressed genes between castes. Each dot represents a gene, only genes which have a methylation difference >0 are shown (N = 51). The red dots indicate the gene is also differentially methylated. (b) UpSet plot showing the number of common genes between analyses. The set size indicates the number of genes in each category: differentially expressed, differentially methylated or genes containing a differentially expressed exon. The intersection size shows how many genes the corresponding lists, represented by the jointed dots in the lower panel, have in common. A single dot in the lower panel refers to the number of genes unique to each list.

Gene lists were checked for potential overlap from all analyses. There was no significant overlap between differentially methylated genes and differentially expressed genes (two genes, hypergeometric test; p = 0.658, Fig. 2.15b). There was also no significant overlap between differentially methylated genes and genes containing differentially expressed exons (one gene, hypergeometric test; p = 0.12, Fig. 2.15b).

There was a significant overlap of genes found to be differentially expressed with those containing differentially expressed exons, 14 total (hypergeometric test; p <0.000, Fig. 2.15b). All lists of overlapping genes can be found in supplementary 1.1.3.

Honeybee orthologous differentially methylated genes

Custom honeybee and bumblebee putative-ortholog databases were created from 15,314 and 10,339 annotated genes respectively (Amel_4.5 GCA_000002195.1, Bter_1.0

GCA_000214255.1). 9,244 honeybee genes matched at least one bumblebee gene and 7,985 bumblebee genes matched at least one honeybee gene with an e-value of $<1 \times 10^{-3}$. A total of 7,345 genes made the same match in both blast searches. Of these genes 392 matched more than one gene in one or both blasts and were therefore removed. This left a final putative ortholog list of 6,953 genes. 99 of the 111 differentially methylated genes identified here were present in the final putative ortholog list. However, none of them matched the 549 genes identified as differentially methylated between honeybee reproductive castes by Lyko *et al.* (2010) (Fig. 2.16).

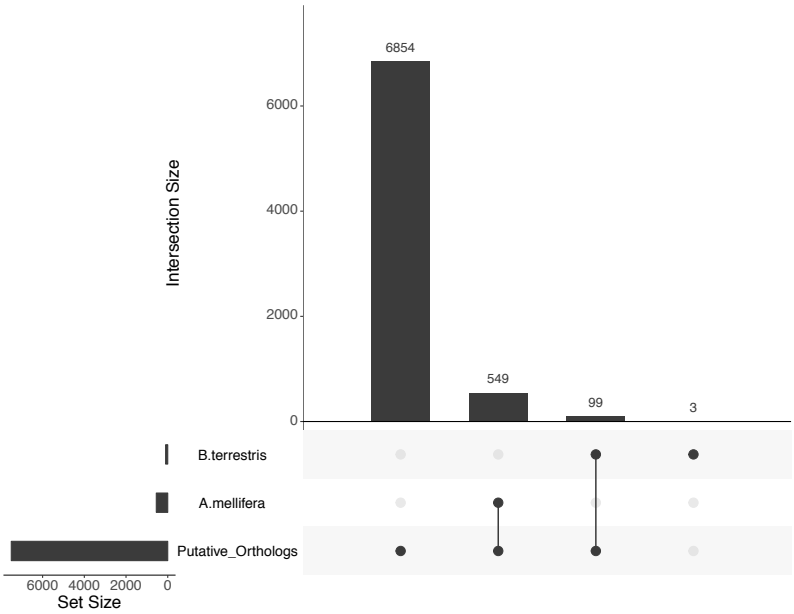


Figure 2.16: UpSet plot showing the number of putative orthologs between *A. mellifera* and *B. terrestris* along with the number of differentially methylated genes identified in Lyko *et al.* (2010) and in this study which are present in the putative ortholog database. The set size indicates the number of genes in each category. The intersection size shows how many genes the corresponding lists, represented by the jointed dots in the lower panel, have in common. A single dot in the lower panel refers to the number of genes unique to each list.

2.5 Discussion

I have used whole genome bisulfite sequencing and gene expression libraries from the same individual *B. terrestris* workers to investigate the role of methylation in caste determination. I found both reproductive and sterile workers show similar methylation

patterns to other holometabolous insects. Methylation also has a similar relationship with gene expression compared to most other holometabolous insects currently studied, with more highly methylated genes showing higher levels of expression and lower levels of methylation being associated with differentially expressed genes. I found no methylation differences on a genomic scale between castes. However, 111 genes were differentially methylated. These were involved in a variety of functions including reproductive related processes. I found no relationship between genes that are differentially expressed, or contain differential exon usage between castes with those that show differential methylation between castes. Finally I also found no common putative orthologous genes differentially methylated between *B. terrestris* and *A. mellifera* reproductive castes.

This is the first data set to accurately quantify methylation at base-pair resolution for *B. terrestris* castes. It confirms low methylation levels throughout the genome as predicted by Sadd *et al.* (2015). These low levels along with enrichment for CpG methylation in coding regions are also seen in many social insect species, including *A. mellifera* (Lyko *et al.*, 2010) and multiple ant species (Bonasio *et al.*, 2012; Libbrecht *et al.*, 2016). These trends are also seen more generally in holometabolous insects (Provataris *et al.*, 2018). However, they are not completely conserved among all holometabolous insects, for example the primitively social wasp species *Polistes dominula* shows 6% CpG methylation (Weiner *et al.*, 2013), and the highly social termite, *Zootermopsis nevadensis*, has exceptionally high methylation levels compared to the majority of insects (Bewick *et al.*, 2016), with 12% CpG methylation, and methylation being just as common in introns as exons (Glastad *et al.*, 2016).

Higher levels of CpG methylation are associated with higher levels of gene expression in both *B. terrestris* reproductive castes. This is also the case in some other social insects, with Figures 2.13a and 2.13d showing almost identical trends to those found in Bonasio *et al.* (2012), Patalano *et al.* (2015) and Libbrecht *et al.* (2016). Additionally other social insect species, show higher methylation in non-differentially expressed genes as we found here, examples include: *Dinoponera quadriceps* (Patalano *et al.*, 2015), *Polistes canadensis* (Patalano *et al.*, 2015), *Zootermopsis nevadensis* (Glastad *et al.*, 2016) and *Cerapachys biroi* (Libbrecht *et al.*, 2016). Higher levels of methylation in more highly

expressed genes and in non-differentially expressed genes is thought to indicate a role for methylation in housekeeping genes in some holometabolous insects (Foret *et al.*, 2009; Lyko *et al.*, 2010; Bonasio *et al.*, 2012; Wang *et al.*, 2013; Provataris *et al.*, 2018). High levels of gene body methylation is also found in highly expressed genes in plants, whilst currently the function is unknown, Zilberman (2017) hypothesises it functions to stabilise expression by reducing histone variants and Bewick and Schmitz (2017) hypothesise it is a byproduct of transposable element silencing.

As well as a similar methylation profile to other social insects, I also predicted that if methylation plays a role in reproductive caste determination we would find differentially methylated genes between castes with reproductive related functions. I found 111 differentially methylated genes which include enriched GO terms for various reproductive related processes, this suggests methylation has some association with the switch between sterility and reproduction in *B. terrestris*. This supports previous work which exposed *B. terrestris* to a chemical which decreases general methylation levels and found workers were more likely to become reproductive (Amarasinghe *et al.*, 2014). However, we did not find a difference in the genome-wide methylation levels of sterile and reproductive workers. It is also worth noting a worker classed as reproductive appeared to show a sterile transcriptional profile and this was included in the pool for the reproductive sample for colony J8. This will have 'diluted' the strength of the methylation profile for this particular sample. It is therefore likely our data contains false negatives, meaning there may be differentially methylated genes between reproductive castes which do not appear in our data set.

Whilst I found differentially methylated genes between castes I found no evidence for a relationship between methylation and gene expression in relation to reproductive and sterile workers. Only a small non-significant number of genes are both differentially methylated and differentially expressed between castes and there is no relationship between the degree of differential methylation and differential expression on a gene level. Previous research using the milkweed bug (*Oncopeltus fasciatus*) found knocking down *Dnmt1*, the gene responsible for DNA methylation maintenance, in ovary tissue with RNAi had no effect on gene expression. However, these individuals could no longer reproduce (Bewick *et al.*, 2019). This suggests methylation may play an alternative

role, rather than direct regulation of gene expression, in reproduction of some insects. Bewick *et al.* (2019) suggest this role may be the regulation of genome stability and/or the regulation of vital cellular processes. The variety of GO terms involved in biological processes we obtained for the differentially methylated genes between castes supports this idea.

Additionally, I observed high inter-colony variation in methylation. However, I did not have sufficient replicates to test for exact differences between colonies. High inter-colony variation could suggest methylation may also play a role in the adaptive abilities of *B. terrestris*. Stable environmentally induced 'epialleles' have been proposed to act as an additional layer of information for which selection can act upon (Flores *et al.*, 2013). However, we currently do not know if *B. terrestris* methylation shows transgenerational inheritance or whether a large proportion is wiped during development, as in mammals (Messerschmidt *et al.*, 2014).

It has also been suggested methylation may regulate alternative splicing, rather than expression in some insects (Glastad *et al.*, 2011). I found no evidence here for the role of exon methylation in exonic expression differences between castes. Previous research using honeybees did find an association between methylation and caste specific alternative splicing. Methylation differences between queens and workers in *A. mellifera* have been associated with caste specific splicing events (Lyko *et al.*, 2010). Additionally a knock-down of *Dnmt3* by RNA interference was found to affect alternative splicing patterns in *A. mellifera*, with decreased methylation levels being directly related to exon skipping and intron retention (Li-Byarlay *et al.*, 2013). However, another social insect species, the primitively social wasp, *Polistes dominula*, has also shown no direct association between methylation and alternative splicing (Standage *et al.*, 2016). However, this species shows extremely low genome methylation and appears to lack the *Dnmt3* gene responsible for *de novo* methylation, suggesting that the link between methylation and alternative splicing in insects is variable.

Exon methylation has been shown to play a role in histone modifications and nucleosome stability in mammals (Jones, 2012; Singer *et al.*, 2015). These modifications have the ability to affect alternative splicing patterns through RNA polymerase accessibility,

meaning whilst changes in DNA methylation may not be observed as directly related to alternative splicing, it's possible these changes have a downstream effect leading to transcriptional changes (Hunt *et al.*, 2013). The analysis of the relationship between methylation and alternative splicing done here could be elaborated on further to include non-caste specific splicing sites and to also potentially identify the role of exon methylation in other epigenetic processes, which may themselves, lead to alternative splicing.

It is also worth noting other epigenetic mechanisms may play a role in caste determination, for example microRNAs have been associated with caste switching in *A. mellifera* (Ashby *et al.*, 2016). Additionally Simola *et al.* (2016) found histone acetylation differences between worker castes of *Camponotus floridanus*. They inhibited histone acetylation and found this caused the major worker caste to behave more like a minor worker. This same species has also been shown to have caste specific methylation profiles (Bonasio *et al.*, 2012). These examples indicate it is likely an interplay between multiple mechanisms that ultimately cause social insect caste differentiation, again supported by the fact we find no association between methylation and caste-specific alternative splicing.

My final prediction was that differentially methylated genes between worker *B. terrestris* castes would be similar to those found to be differentially methylated between *A. mellifera* reproductive castes if methylation was involved in caste determination in Hymenoptera; I did not find any putative orthologues in common. This supports the idea in Bewick *et al.* (2019) that methylation may not directly influence caste determination. However, the differentially methylated gene list obtained for *A. mellifera* used queen samples to represent the reproductive caste (Lyko *et al.*, 2010), whereas here reproductive worker samples were used, this could also explain the lack of agreement.

Considerably more experimental research is needed to better define the relationship between epigenetic processes and caste determination in social insects. Future work should focus on the consequences of experimental methylation removal or addition (Pegoraro *et al.*, 2017), as well as exploring additional epigenetic mechanisms to attempt to identify a full pathway leading to reproductive caste differences. For example, CRISPR

has recently been used to knockout two sex-determining genes in *A. mellifera* causing individuals to change gender (Mcafee *et al.*, 2019). This technology has also been adapted to be able to change the methylation state of a given loci (Vojta *et al.*, 2016), allowing the possibility of exploring the function of methylation in specific genes.

Overall, I have found the *B. terrestris* methylome appears similar to some other holometabolous insects, in terms of overall levels and the relationship with gene expression. I found no genome-wide methylation differences between reproductive castes. However, we did find differentially methylated genes between reproductive castes, with GO terms enriched in many biological processes, including reproduction. These results combined with previous research, (Amarasinghe *et al.*, 2014), indicate an association between methylation and reproductive caste differences in *B. terrestris*. However, it is clear, owing to the lack of consistency between differentially methylated genes and differentially expressed genes, methylation is not directly responsible for the associated changes in gene expression leading to the different reproductive phenotypes in *B. terrestris*. Additionally the lack of similarity between differentially methylated genes between castes in *B. terrestris* and between castes in *A. mellifera* suggest methylation may not directly contribute to caste determination in some Hymenoptera. Future work should focus on the experimental manipulation of epigenetic processes, such as methylation, in social insects in order to clarify functional roles within and across species.

Chapter 3

Allele-specific methylation in reproductive and sterile bumblebee workers.

Hollie Marshall, Zoë Lonsdale and Eamonn Mallon.

3.1 Abstract

Allele-specific expression is when one allele of a gene shows higher levels of expression compared to the other allele, in a diploid organism. Genomic imprinting is an extreme example of this, where some genes exhibit allele-specific expression in a parent-of-origin manner. Recent work has identified potentially imprinted genes in two species of Hymenoptera. However, the molecular mechanism which drives this allelic expression bias remains unknown. In mammals DNA methylation is often associated with imprinted genes. DNA methylation systems have been described in species of Hymenoptera, providing a candidate imprinting mechanism. Using previously generated RNA-Seq and whole genome bisulfite sequencing from reproductive and sterile *B. terrestris* workers I have identified genome-wide allele-specific expression and allele-specific DNA methylation. The majority of genes displaying allele-specific expression are common between reproductive castes and the proportion of allele-specific expression bias generally varies between colonies. This study has also identified allele-specific methylation differences between reproductive castes and found there is no significant overlap of genes showing allele-specific expression and allele-specific methylation. These results indicate that DNA methylation does not drive genome-wide allele-specific expression in this species. It may be that DNA methylation is just one of a number of epigenetic factors acting in *trans* to direct gene expression patterns. The relationship between DNA methylation and open chromatin regions would help to elucidate this relationship. Additionally, only a small number of the genes identified may be 'imprinted' and it may be these genes which are associated with allele-specific DNA methylation. Future work utilising reciprocal crosses to identify parent-of-origin DNA methylation will further clarify the role of DNA methylation in parent-of-origin allele-specific expression.

3.2 Introduction

Allele-specific expression is when one allele of a gene shows higher levels of expression compared to the other allele, in a diploid organism. Unlike genetic dominance, allele-specific expression can be tissue specific and/or caused by epigenetic modifications, independent of the underlying genotype. It has been associated with genomic mechanisms such as X-chromosome inactivation and genomic imprinting, i.e. parent-of-origin allele-specific expression (Knight, 2004). It has been predicted that social insects should display imprinted genes (Queller, 2003) based on assumptions of the kinship theory (Haig, 2000). Recent research has identified parent-of-origin allele-specific expression in honeybees (Galbraith *et al.*, 2016b; Kocher *et al.*, 2015), with one study identifying greater paternal-allele (patrigene) expression bias in reproductive workers compared to sterile workers, as predicted by the kinship theory (Galbraith *et al.*, 2016b). However, the mechanism by which these genes exhibit this expression bias remains unknown.

In mammals and angiosperm plants imprinted genes are often associated with allele-specific DNA methylation (Barlow and Bartolomei, 2014) and occasionally with histone modifications (Inoue *et al.*, 2017). Many social insects have functional DNA methylation systems, including the honeybee (Bewick *et al.*, 2016; Lyko *et al.*, 2010), which also exhibits genes with allele-specific expression. However, the function of DNA methylation in insects remains debated (Glastad *et al.*, 2018).

Various studies have found an association between methylation and gene expression (Glastad *et al.*, 2014; Bonasio *et al.*, 2012; Patalano *et al.*, 2015, Chapter 2), and alternative splicing (Lyko *et al.*, 2010; Glastad *et al.*, 2016) in social insects. However, this is not uniform across all social species (Standage *et al.*, 2016). Additionally, allele-specific expression has been associated with allele-specific methylation in two ant species, *Camponotus floridanus* and *Harpegnathos saltator* (Bonasio *et al.*, 2012). Another study did not find any relationship between allele-specific expression and methylation in a hybrid cross of two non-social wasp species, *Nasonia vitripennis* and *Nasonia giraulti* (Wang *et al.*, 2016). These results support the general hypothesis that imprinted genes exist specifically in social insect species (Queller, 2003) and also suggest that DNA methy-

lation could serve as the imprinting mark.

Bumblebees provide an ideal system to further investigate the relationship between allele-specific methylation and allele-specific expression, specifically with a view of elucidating potential mechanisms involved in genomic imprinting in social insects. Using a candidate gene approach, previous research identified allele-specific expression in a gene (ecdysone 20-monooxygenase-like) related to worker reproductive behaviour in *B. terrestis* (Amarasinghe *et al.*, 2015). Additional research has since used RNA-seq data to identify >500 loci showing allele-specific expression throughout the *B. terrestris* genome (Lonsdale *et al.*, 2017). This same study also identified 19 genes displaying allele-specific expression and allele-specific methylation, although this was in a single individual (Lonsdale *et al.*, 2017).

It is predicted that imprinted genes in *B. terrestris* will specifically have a role regarding worker reproductive behaviour (Queller, 2003). Methylation has been directly associated with reproductive behaviour in *B. terrestris* (Amarasinghe *et al.*, 2014) and recent research has identified differentially methylated genes between reproductive and sterile castes (Chapter 2).

Whole genome bisulfite sequencing and RNA-seq from reproductive and sterile workers, spanning three genetically distinct colonies, were used to investigate allele-specific expression and allele-specific methylation in *B. terrestris*. I hypothesise that if genomic imprinting plays a role in worker reproductive behaviour in *B. terrestris*, genes showing allele-specific expression will be enriched for reproductive processes. Additionally, if DNA methylation acts as an imprinting mark in *B. terrestris*, a direct association between allele-specific expression and allele-specific methylation will be found.

3.3 Methods

3.3.1 Data generation

The data used for this study were generated in Chapter 2, see sections 2.3.1 and 2.3.2.

3.3.2 Identification of allele-specific expression

Data were quality checked using fastqc v.0.11.5 (Andrews, 2010) and trimmed using CutAdapt v1.1 (Martin, 2011). Trimmed data were aligned to the reference genome (Bter_1.0, Refseq accession no. GCF_000214255.1 (Sadd *et al.*, 2015)) using STAR v2.5.2 (Dobin *et al.*, 2016) with standard parameters. SNPs were then called per sample following the 'GATK best practices for SNP calling from RNA-Seq data' pipeline (Auwera, 2014). Briefly this involves assigning read groups and marking duplicate reads using Picard v.2.6.0 (Broad Institute, 2018), removing reads overlapping introns to keep only exonic reads, calling SNPs with a minimum confidence score of 20.0, then filtering SNPs by windows of three within a 35bp region, to keep only those with a Fisher strand value greater than 30.0 and a quality by depth value greater than 2.0 (these filtering steps are considered particularly stringent) (Auwera, 2014). SNPs were then filtered to keep only biallelic SNPs and reads were then counted per SNP using the 'ASEreadcounter' program from GATK.

A custom R script was used to annotate the SNP positions with gene identifiers, SNPs were filtered to remove those with a coverage of less than 10. SNPs were also removed if they had a count of zero for either the alternative or reference SNP as they may have been mis-called by the SNP caller as heterozygous when they are actually homozygous. Two new columns were then created to represent each allele, as it is not possible to tell which SNPs belong to which allele (e.g. a reference SNP at a given position may be accompanied with an alternative SNP on the same allele). The counts for each SNP were then allocated to either 'allele: 1' or 'allele: 2', with the highest counts per SNP allocated to 'allele: 1', Table 3.1. Counts per SNP per allele were then summed over each gene for each reproductive status per colony creating one representative sample per reproductive status per colony.

Table 3.1: Example of how the counts per SNP were allocated to assumed alleles.

Chromosome	SNP	Ref Count	Alt Count	Allele 1	Allele 2
NC_015762.1	265980	11	11	11	11
NC_015762.1	276809	23	25	25	23
NC_015762.1	276870	24	21	24	21
NC_015762.1	277048	36	34	36	34
NC_015762.1	278272	19	23	23	19

As this method is naive to allele specific alternative splicing, stringent filtering was applied throughout. Only genes with counts found in every reproductive status in each colony were considered for allele specific expression analysis. A logistic regression model was then applied with the proportion of allelic expression per gene as the dependent variable and with reproductive status and colony as independent variables, a quasibiomial distribution was applied to account for any overdispersion within the data. P-values were corrected for multiple testing using the Benjimini-Hochberg method (Benjamini and Hochberg, 1995) and genes were classed as showing allele specific expression if the adjusted p-value was <0.05 and the average proportion of allelic expression across colonies was >0.7. This stringent filtering was used to account for the possible mis-allocation of SNPs to the correct alleles and to account for differences in genomic *cis*-effects across colonies.

3.3.3 Identification of allele-specific methylation

Data were quality checked using fastqc v.0.11.5 (Andrews, 2010) and trimmed using CutAdapt v1.1 (Martin, 2011). Trimmed data were aligned to the reference genome (Bter_1.0, Refseq accession no. GCF_000214255.1, (Sadd *et al.*, 2015)) using Bismark v.0.16.1 (Krueger and Andrews, 2011) and bowtie2 v.2.2.6 (Langmead and Salzberg, 2012) with standard parameters. Alignment output files were deduplicated using Bismark v.0.16.1 (Krueger and Andrews, 2011) and sorted and indexed using samtools v.1.3.2 (Li *et al.*, 2009).

Allele-specific methylation was determined using a probabilistic model implemented using the 'amrfinder' program from the MethPipe package v.3.4.2 (Fang *et al.*, 2012). This program scans the genome using a sliding window approach and fits two models

to each interval, one model predicts the methylation levels of each window are the same for both alleles and a second model predicts the methylation levels are different for each allele. The likelihood of the two models is then compared and a false discovery rate corrected p-value is generated per window (Fang *et al.*, 2012). Sample input files were merged by reproductive group in order to increase the coverage per CpG as this method does not take replication into account. Windows were defined as three CpGs with a minimum coverage of 10 reads each. Only regions within the main 18 linkage groups of the *B. terrestris* genome were tested for allele specific methylation as the program is not designed to cope with the number of unplaced scaffolds (5,591) that the current genome build contains. Finally, allelically methylated regions falling within a gene were annotated with the gene identifier using a custom R script.

This method of identifying allelically methylated regions is preferable compared to using SNP data to identify alleles for the data presented here. Firstly, it is difficult to call SNPs reliably from bisulfite data, this is because C/T SNPs and C/T conversions introduced during bisulfite treatment appear the same within the data (Liu *et al.*, 2012). Secondly, as the samples used were pooled females, each sample may contain multiple SNPs at a given locus meaning the coverage produced per SNP would be too low to produce any reliable estimates of allelic methylation.

3.3.4 Gene ontology enrichment

Gene ontology terms for *B. terrestris* were taken from a custom database made in Bebane *et al.* (2019). GO enrichment analysis was carried out using the hypergeometric test with Benjamini-Hochberg (Benjamini and Hochberg, 1995) multiple-testing correction, $q < 0.05$. GO terms from genes showing allele-specific expression were tested for enrichment against a database made from the GO terms of all genes identified in the RNA-Seq data. GO terms from genes showing allele-specific methylation were tested for enrichment against a database made from the GO terms of all genes identified as methylated from the BS-Seq data set. Descriptions of GO terms and treemaps were generated by REVIGO (Supek *et al.*, 2011).

3.3.5 Comparative analyses

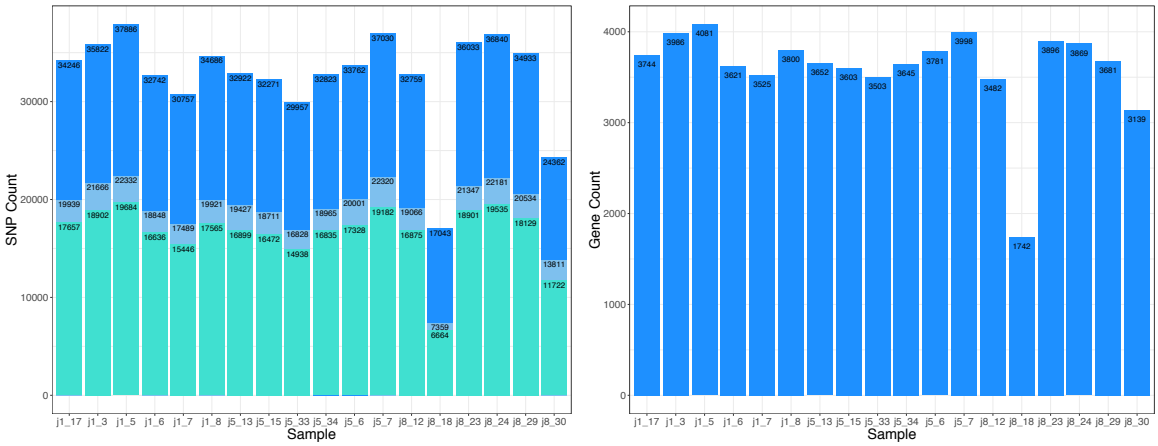
Significant overlap between genes showing allele-specific expression and allele-specific methylation was tested using a hypergeometric test. Overlap plots were generated using the *UpSetR* package in R (Lex *et al.*, 2016). Custom R scripts were used to test for a relationship between allele-specific expression and allelically methylated genes and the interaction of that relationship with reproductive caste.

All bioinformatic scripts used within this chapter can be found at: `http://doi.org/10.5281/zenodo.1974852`.

3.4 Results

3.4.1 Allele specific expression

All reads had 13bp trimmed from the start due to base bias generated by the Illumina protocol (Krueger *et al.*, 2011). The mean number of uniquely mapped reads was 89.4% ± 0.8% (mean ± standard deviation). This equated to a mean of 10,115,366 ± 1,849,600 uniquely mapped reads (supplementary 3.0.0). The average number of heterozygous SNPs called per sample was 32,604 ± 4,983, of which an average of 18,930 ± 3,594 had a coverage greater than 10 and after filtering to remove potentially homozygous SNPs the average final number of SNPs per sample was 16,631 ± 3,135 (Fig. 3.1a). The average number of genes with at least one SNP per sample was 3,597 ± 514 (Fig. 3.1b). Sample J8_24 was removed from all downstream analyses as it was potentially incorrectly labelled, see Chapter 2, section 2.3.5. Sample J8_18 was also removed from all downstream analyses due to the considerably lower number of SNPs obtained. Given that genes must occur in every sample to be used, keeping this sample would have greatly reduced the number of genes available to test. Upon data inspection, it is likely there were considerably less SNPs called in this sample as the sequencing depth was considerably lower than all other samples, with 3,354,181 uniquely mapped reads compared to the mean of >10,000,000, as stated above.



(a) SNP Counts (b) Gene Counts

Figure 3.1: (a) Component bar chart showing the total number of SNPs called per *Bombus terrestris* sample, the number of which have a minimum coverage of 10 and of those which have coverage for both alternate and reference alleles. (b) The number of genes per sample which have at least one SNP present. The sample names represent the unique colony (j1, j5 or j8) and the individual number.

Only genes present in all conditions (colony and reproductive status) were tested for allele-specific expression, this lead to a final conservative list of 2,489 genes (22.6% of all annotated genes in the reference genome Bter_1.0). A total of 98 genes were found to show significant allelic expression bias (adjusted p <0.5 and average allelic expression proportion >0.7) (Fig. 3.2, supplementary 3.0.1).

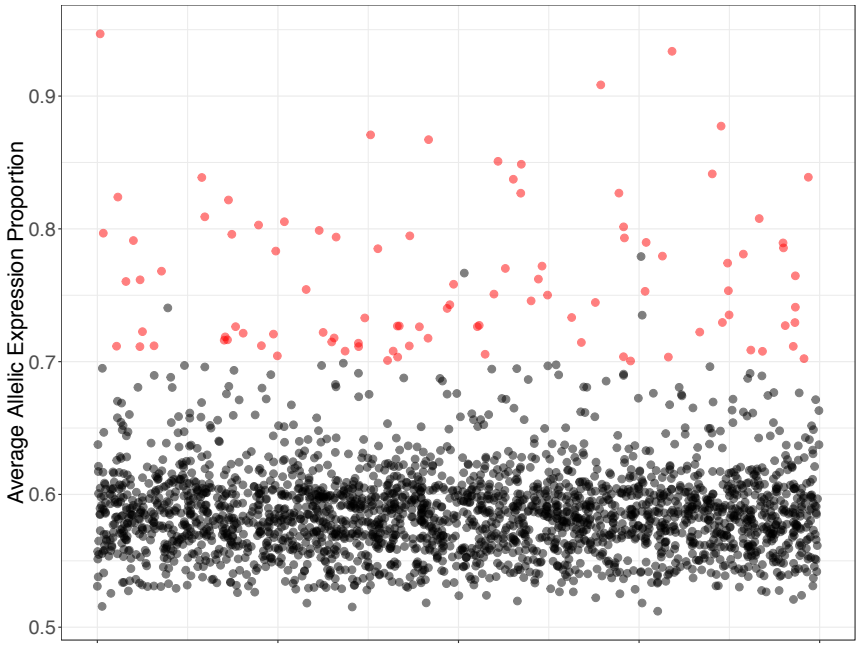
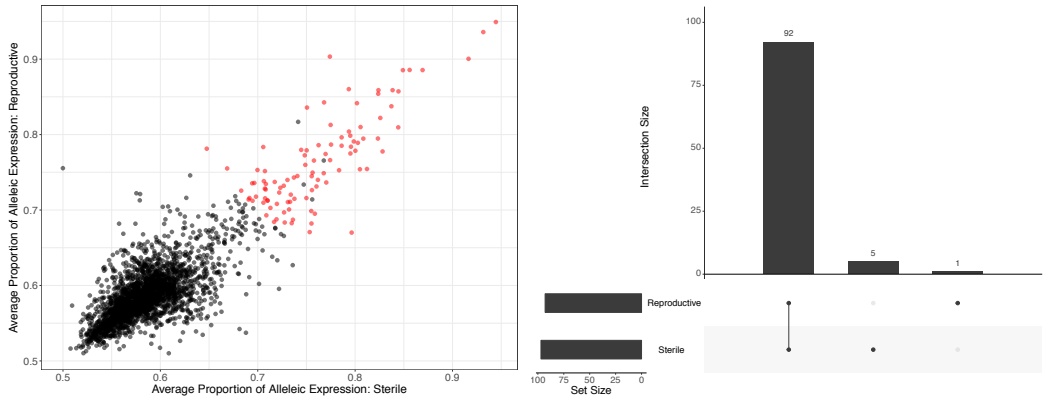


Figure 3.2: Spread of allelic ratios averaged across all *Bombus terrestris* colonies and reproductive samples. Each dot represents a gene (N = 2,489), the red dots show genes showing significant allelic expression bias (adjusted p <0.05 and average allelic expression proportion >0.7).

The genes of reproductive and sterile workers show similar levels of allelic expression (Spearman's rank correlation, S = 790780000, rho = 0.6922959, p <0.000, Fig. 3.3a). Of the 98 genes found to show allele specific expression a significant number are shared between reproductive and sterile workers (hypergeometric test p = <0.000, Fig. 3.3b), with five found only in sterile workers and one found only in reproductive workers, (Fig. 3.4). There is also some variability in allelic expression proportion between colonies (Fig. 3.5).



(a) Scatter Plot (b) UpSet Overlap

Figure 3.3: (a) Scatter plot showing the allelic expression proportion of *Bombus terrestris* sterile workers plotted against the allelic expression proportion of reproductive workers (allelic expression proportion averaged across colonies). Each point is a gene (N = 2,489), the red points indicate genes showing significant allele specific expression (adjusted p-value <0.05 and average allelic expression proportion >0.7). (b) An UpSet plot showing the number of allelically expressed genes shared by reproductive status and the number unique to reproductive or sterile workers. The set size indicates the number of genes in each category. The intersection size shows how many genes the corresponding lists, represented by the jointed dots in the lower panel, have in common. A single dot in the lower panel refers to the number of genes unique to each list.

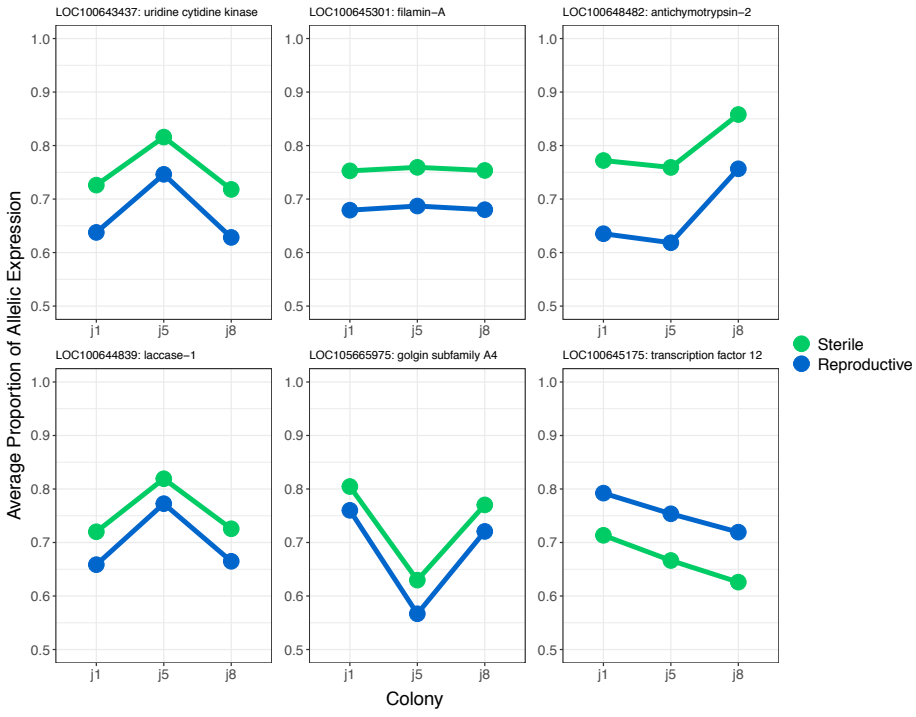


Figure 3.4: The average proportion of allelic expression for genes found to show significant allele specific expression in only sterile or reproductive *Bombus terrestris* workers.

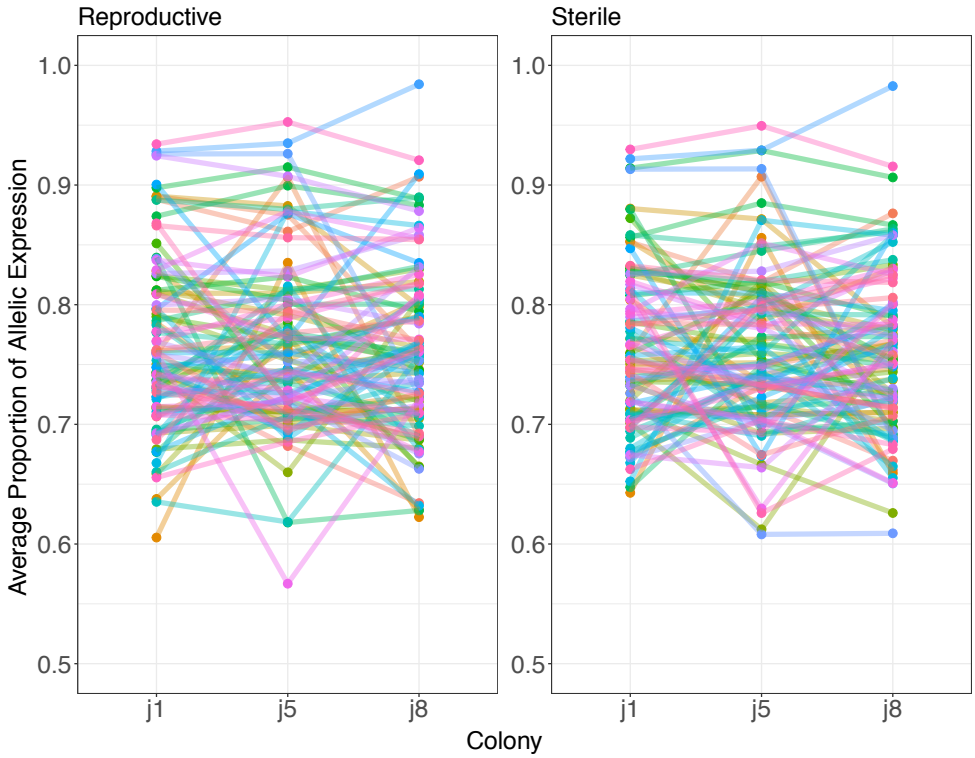


Figure 3.5: The average proportion of allelic expression for reproductive and sterile *Bombus terrestris* workers across each colony. Each colour represents a unique gene (N = 98). Genes shown are those deemed to show significant allele-specific expression (q <0.05 and average proportion of expression bias >0.7).

Enriched GO terms associated with genes showing significant allele specific expression were involved in multiple biological processes, including: *female gamete generation* (GO:0007292), *positive regulation of ovulation* (GO:0060279) and *positive regulation of histone H3-K9 methylation* (GO:0051574), supplementary 3.0.2.

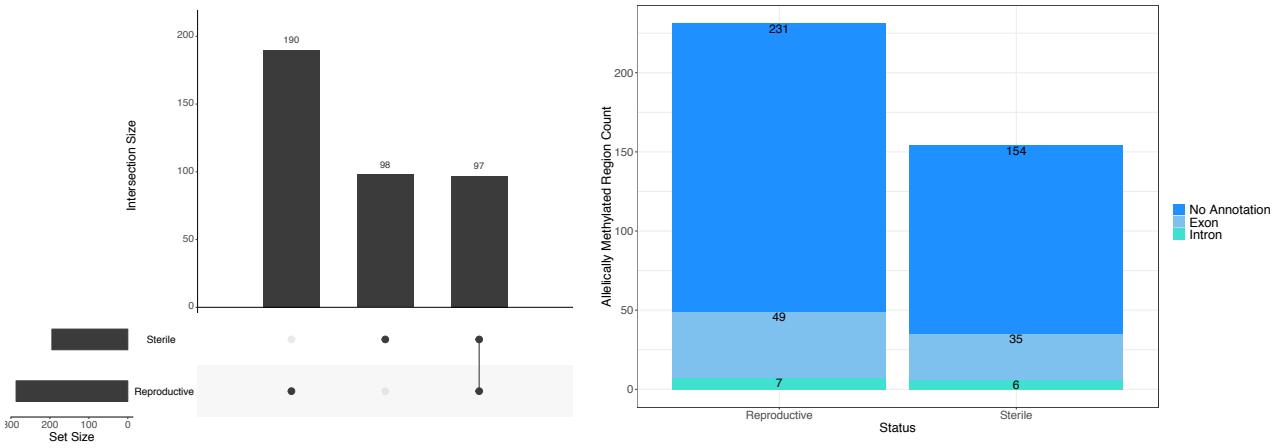
GO terms enriched for the five genes showing allele specific expression in sterile workers also included a variety of biological processes, for example *determination of adult lifespan* (GO:0008340). The GO terms enriched for the single gene showing allele specific expression in reproductive workers included: *ovarian follicle cell development* (GO:0030707) and *female gamete generation* (GO:0007292), supplementary 3.0.2. These results should be interpreted with care as the gene lists are relatively small. However, it is worth noting that the hypergeometric test used to generate the enriched terms has been previously shown to be the most appropriate statistic for gene ontology enrichment for small gene lists (Rivals *et al.*, 2007).

3.4.2 Allele specific methylation

Up to a maximum of 10bp were trimmed from the start of all reads due to base bias generated by the Illumina sequencing protocol (Krueger *et al.*, 2011). The mean mapping efficiency was 63.6% ± 1.4% (mean ± standard deviation) and the mean coverage was 17.7 ± 0.5 reads per base, the average number of uniquely mapped reads were 27,709,214 ± 753,203 (supplementary 3.0.3). 12.79% of genome was not tested for allele-specific methylation as only regions in the main 18 linkage groups of the *B. terrestris* genome (Bter_1.0) could be tested.

Reproductive workers have significantly more allelically methylated regions compared to sterile workers, 303 (supplementary 3.0.4) compared to 201 (supplementary 3.0.5) respectively (Chi-squared goodness of fit; X-squared = 20.643, df = 1, p <0.000). The majority of these regions occur within annotated genes, 26 and 15 allelically methylated regions occur outside of a gene for reproductive and sterile workers respectively.

Most allelically methylated genes are unique to either sterile or reproductive workers. However, there is a significant number of common allelically methylated genes (hypergeometric test p <0.000, Fig. 3.6a). Most allelically methylated regions found within genes do not have additional annotation. However, there are more located in exons compared to introns for both reproductive and sterile castes (Fig. 3.6b).



(a) (b)

Figure 3.6: (a) UpSet plot showing the number of genes with allele specific methylation in just reproductive and sterile *Bombus terrestris* workers, as well as the number of genes in common between both reproductive castes. The set size indicates the number of genes in each category. The intersection size shows how many genes the corresponding lists, represented by the jointed dots in the lower panel, have in common. A single dot in the lower panel refers to the number of genes unique to each list. (b) Component bar plot showing the umber of allelically methylated regions (within genes), found in exons and introns and the number without additional annotation.

Enriched GO terms associated with allelically methylated genes in both castes are involved in a variety of biological processes with many relating to the term *positive regulation of RNA splicing* (GO:0033120). As above, the enriched GO terms associated with allelically methylated genes in just sterile or reproductive workers are also involved in a large number of biological processes. However, the terms *oocyte development* (GO:0048599), *ovarian follicle development* (GO:0001541), *oogenesis stage* (GO:0022605) and other reproductive terms were enriched in allelically methylated genes of reproductive workers. Additionally none of these terms were identified in the GO terms associated with the allelically methylated genes of sterile workers (supplementary 3.0.6).

3.4.3 Relationship of allele specific expression and methylation

There is no significant overlap between genes showing allele specific expression and allele specific methylation (overlap between all conditions; hypergeometric test p = 0.055, overlap between allele specific expression and allele specific methylation in reproductive workers; hypergeometric test p = 0.519, Fig. 3.7). However, six genes were found to show allele specific methylation and expression in both reproductive castes and one gene was found to show allele specific expression in both castes and allele specific methylation in reproductive workers (Table 3.2).

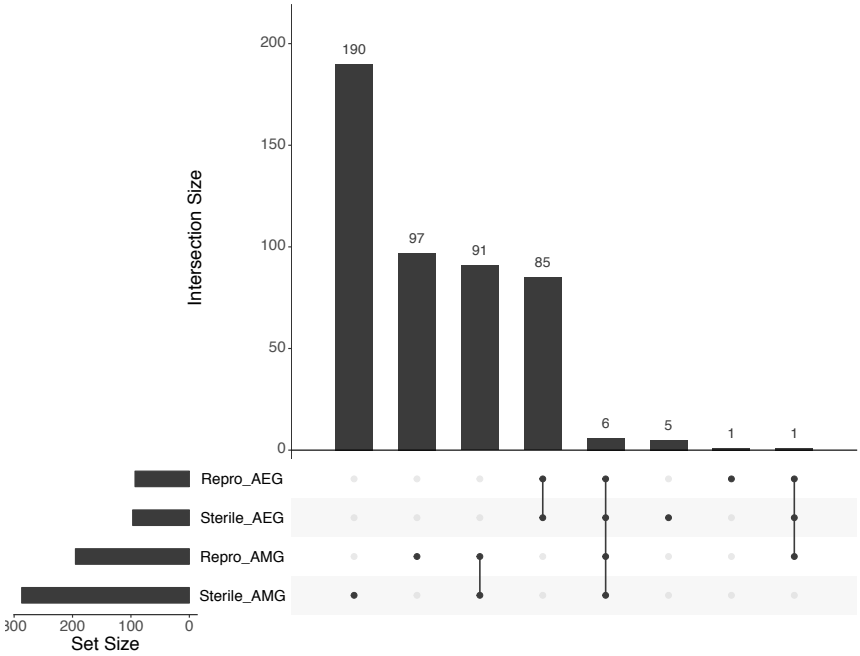


Figure 3.7: (a) UpSet plot showing the overlapping genes identified as allelically methylated and/or allelically expressed in both *Bombus terrestris* castes. The set size indicates the number of genes in each category. The intersection size shows how many genes the corresponding lists, represented by the jointed dots in the lower panel, have in common. A single dot in the lower panel refers to the number of genes unique to each list.

Table 3.2: Genes identified as showing allele specific methylation and expression in both reproductive castes. * this gene does not show allele specific methylation in sterile workers.

Gene ID	**Gene Description**
LOC100643777	40S ribosomal protein S6
LOC100643807	protein Jumonji
LOC100645564	peripheral plasma membrane protein CASK
LOC100651252	ATP-dependent RNA helicase WM6
LOC100652132	importin-11
LOC105666051	uncharacterized
LOC105666711*	tyrosine-protein kinase Btk29A*

The GO terms enriched for the genes found to be allelically methylated and expressed (Table 3.2) compared to the entire genome as background, included multiple biological processes (supplementary 3.0.7). Specifically various reproductive related terms were enriched; *multi-organism reproductive behaviour* (GO:0044705), *female gamete generation* (GO:0007292) and *germ cell development* (GO:0007281).

There is a significant difference in the proportion of allelic expression of genes allelically methylated in either reproductive workers, sterile workers or both (Kruskal-Wallis; chi-squared = 30.103, df = 2, p <0.000). Genes allelically methylated in both castes show on average higher levels of allele specific expression compared to those unique to either reproductive or sterile workers (Dunn test with Benjamin-Hochberg correction; both compared to unique in reproductive workers Z = 5.445, q <0.000, both compared to unique in sterile workers Z = 3.621, q <0.000), Fig. 3.8. Additionally, genes with allele specific methylation unique to reproductive workers show lower levels of allele specific expression compared to genes with allele specific methylation unique to sterile workers (Dunn test with Benjamin-Hochberg correction; reproductive compared to sterile Z = -2.688, q <0.000), Fig. 3.8. Finally, there is no interaction between reproductive caste and allele specific expression proportion on the allelic methylation status of a gene (Anova, interaction vs main effects model, $F^{-2,\ 255} = 0.0114$, p = 0.988), Fig. 3.8.

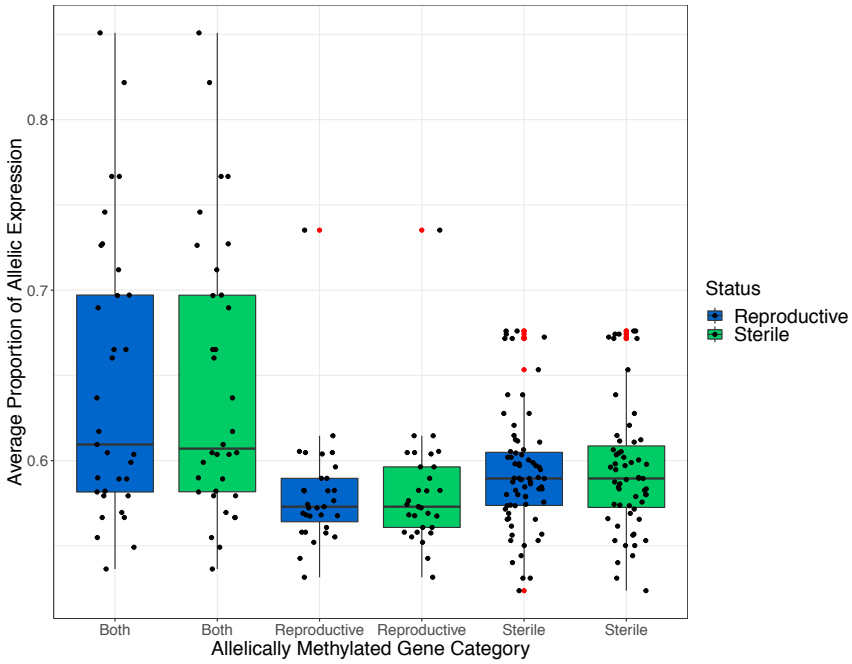


Figure 3.8: Boxplots showing the proportion of allele specific expression in reproductive and sterile *Bombus terrestris* workers for genes identified as allelically methylated in either both castes, just reproductive workers or just sterile workers. Each boxplot shows the median along with the 25th and 75th percentile. The whiskers represent 1.5X the interquartile range. Outliers are represented as additional red points and each gene is represented by a black dot. Allelically methylated in both castes = 33. Allelically methylated genes in reproductive workers = 29 and in sterile workers = 57.

All bioinformatic scripts used within this chapter can be found at: `http://doi.org/10.5281/zenodo.1974852`.

3.5 Discussion

Using whole genome bisulfite sequencing and RNA-seq from reproductive and sterile *B. terrestris* workers from three independent colonies I have identified genome wide allele-specific expression and allele-specific methylation. The majority of genes displaying allele-specific expression are common between reproductive castes and the proportion of allele-specific expression generally varies between colonies. This study has also identified allele-specific methylation differences between reproductive castes and found the majority of allelic-methylation events are located within genes. However, there is no significant overlap of genes showing allele-specific expression and allele-specific methy-

lation. I have also found that genes with common allele-specific methylation between castes show a higher proportion of allelic-expression bias compared to allelically methylated genes unique to either reproductive or sterile workers.

This study has identified 98 genes which show allele-specific expression from a stringent subset of genes covering 22% of all annotated genes within the *B. terrestris* genome. This number is in line with previous research that identified around 500 loci across the whole genome of *B. terrestris* (Lonsdale *et al.*, 2017). Predictions based on the kinship theory suggest if imprinted genes exist in social insects, such as *B. terrestris*, they will be involved in worker reproductive behaviour (Queller, 2003). GO terms enriched for the allelically expressed genes were involved in reproductive processes, additionally the single gene showing allele-specific expression in only reproductive workers is involved in female reproduction. These findings support the idea that if imprinted genes are present in *B. terrestris* some will be involved in worker reproductive behaviour.

The proportion of allelic expression bias differed between colonies and the GO terms enriched for all allelically expressed genes, whilst containing reproductive terms, were varied. This indicates allele-specific expression may be involved in other mechanisms, rather than solely imprinting, and that it plays a diverse role in *B. terrestris*. Previous research identified 61 genes showing allele-specific expression in a cross of two *Nasonia* species, the expression bias in all genes was attributed to *cis*-effects (Wang *et al.*, 2016).There have also been a number of non-imprinted loci found in humans which show allele-specific expression directly associated with *cis*-acting polymorphic sites, such a single nucleotide polymorphisms (SNPs) (Tycko, 2010). Given that each colony used here is genetically distinct, *cis*-effects, such as SNPs, are likely represented in the results. In humans <1% of genes are imprinted but considerably more exhibit allele-specific expression (Tycko, 2010), it is therefore reasonable to assume only a small percentage of the genes identified as showing allele-specific expression in this study may actually be imprinted genes.

Whilst the majority of genes showing allele-specific expression were common between reproductive castes, a large number of genes show allele-specific methylation which are unique to either reproductive or sterile workers. Additionally, there are significantly

more allelically-methylated sites in reproductive workers compared to sterile workers, with allelically methylated genes in reproductive workers enriched for GO terms related to reproduction. These findings support previous research which suggests methylation is associated with worker reproductive behaviour. Amarasinghe *et al.* (2014) found a global erasure of DNA methylation increased reproductive behaviour, Liu *et al.* (2018) found differences in expression in genes responsible for methylation between castes and Chapter 2 found differentially methylated genes between *B. terrestris* castes, some of which were involved in reproductive processes. Numerous other studies have linked methylation to caste differences in various other social insect species, such as: *Apis mellifera* (Lyko *et al.*, 2010; Elango *et al.*, 2009), *Camponotus floridanus* and *Harpegnathos saltator* (Bonasio *et al.*, 2012), *Polistes dominula* (Weiner *et al.*, 2013) and *Zootermopsis nevadensis* (Glastad *et al.*, 2016). The development of experimental techniques to alter DNA methylation, such as CRISPR/Cas (Vojta *et al.*, 2016), will allow for experiments to test the causal effect of DNA methylation and allele-specific methylation on caste determination in social insects.

It is clear from this study that DNA methylation does not play a direct causal role in the production of all allele-specific expression events, with only a small number of genes displaying both allele-specific expression and methylation. This does not rule out the possibility that methylation may act as an imprinting mark, if only a small number of genes are actually imprinted, as in humans (Tycko, 2010). GO terms enriched for the few genes which do show allele-specific methylation and allele-specific expression include reproductive related terms. As theory predicts imprinted genes should affect reproduction in *B. terrestris* (Queller, 2003), the identification of these genes provides the groundwork for future research to further investigate the possibility of parent-of-origin methylation as an imprinting mark.

Additional imprinting marks should not be ruled out as GO terms enriched for genes showing allele-specific methylation included histone modifications. Genes displaying allele-specific methylation may feed into other mechanisms which may, in-turn, drive allele-specific expression, accounting for the lack of direct association. For example, methylation can signal histone modifications which create condensed chromatin, silencing many genes in one region (Barlow, 2011), this process can also occur in an

allele-specific manner (Tycko, 2010).

Whilst only a small number of genes show allele-specific methylation and allele-specific expression, genes showing allele-specific methylation in both reproductive castes had higher allelic expression bias compared to those found only in one caste. One explanation is that allelically methylated genes present in both castes carry out different functions to those identified in a single caste. This is supported by the diverse GO terms obtained for shared and caste-specific allelically methylated genes. In humans, the majority of allele-specific methylation is genotype dependent rather than parentally inherited (Meaburn *et al.*, 2010). Whereas, allele-specific methylation associated with imprinting is known to change at different stages of development (Edwards *et al.*, 2017). It may therefore be that the common allelically methylated genes identified here are linked to genotype (i.e. epialleles) whereas the caste-specific allelically methylated genes may represent imprinting marks.

In order to further understand the role and origin of allele-specific methylation a pipeline is needed which integrates SNP data (generated from genomic DNA), to allow the identification of specific alleles. Using this method rather than the probabilistic models employed here would enable hyper/hypomethylation (i.e. higher or lower methylation in one conditions compared to another) to be associated with allele-specific expression when they occur in tandem. Additionally, this method, with increased biological replication per colony, would facilitate the identification of epialleles, i.e. when allele-specific methylation is driven by genotype. Epialleles have been identified in the honeybee (Wedd *et al.*, 2016) and will be important in the identification of parent-of-origin methylation (Remnant *et al.*, 2016).

Overall, this study provides additional evidence suggesting imprinted genes exist in *B. terrestris* and are related to worker reproductive behaviour as predicted by Queller (2003) and Haig (2000). However, the role of DNA methylation, as a mechanism of potential imprinting, is still unclear. The diverse function of genes showing allele-specific expression and/or allele-specific methylation suggests a varied role for these genomic mechanisms and experimental validation of their function is required. Future research utilising highly related reciprocal crosses, in order to identify the parental

origin of an allele, is needed to discover imprinted genes and to take into account *cis*-effects, such as genotype. These types of crosses can also be used to further investigate DNA methylation as a mechanism of imprinting.

Chapter 4

Reciprocal crosses and RNA-seq to explore genomic imprinting in the bumblebee, *Bombus terrestris*.

Hollie Marshall, Jelle Van Zweden, Kristof Benaets, Felix Wäckers, Tom Wenseleers and Eamonn Mallon.

4.1 Abstract

Genomic imprinting is the expression bias of one allele in a diploid organism, expression being dependent upon which parent the allele was inherited from. Haig's kinship theory predicts that genomic imprinting occurs due to an evolutionary conflict-of-interest between the matrigenes (maternal alleles) and patrigenes (paternal alleles) of an individual. In social insects, it has been suggested that genomic imprinting should be widespread, since relatedness asymmetries within the colony would be expected to lead to many conflicts-of-interest between matrigenes and patrigenes. One recent study identified parent-of-origin gene expression in honeybees and found evidence supporting one prediction of Haig's kinship theory. However very little is known about genomic imprinting in Hymenoptera, and insects in general, and multiple theoretical predictions must be tested to avoid single-study confirmation bias. In the present investigation, I therefore decided to test if parent-of-origin gene expression also occurs in another social bee, the bumblebee *Bombus terrestris*. Four family-wise reciprocal crosses between the subspecies, *B. terrestris audax* and *B. terrestris dalmatinus* were carried out. Whole genome sequencing of the parents and RNA-seq of the offspring allowed the identification of parent-of-origin gene expression. I found equal numbers of maternally and paternally expressed alleles in both reproductive and sterile workers with the majority of genes showing the same expression bias in both castes. There was very little overlap of differentially expressed genes between reproductive worker castes and genes showing parent-of-origin expression. I also found low evolutionary conservation of potentially imprinted genes in Hymenoptera, with only two homologous genes showing parent-of-origin expression in *B. terrestris* and *A. mellifera* suggesting rapid evolution of imprinted genes in this class. Additionally this study highlights the importance of using many species to test multiple predictions in the evaluation of evolutionary theories. Future work exploring epigenetic imprinting mechanisms and the function of genes showing parent-of-origin expression is needed.

4.2 Introduction

Genomic imprinting is the expression of only one allele in a diploid organism, expression being dependent upon which parent the allele was inherited from, i.e. parent of origin-dependent gene expression (Rodrigues and Zilberman, 2015). Multiple evolutionary theories attempt to explain its existence (reviewed in Patten *et al.*, 2014). The most widely accepted explanation is the kinship theory developed by Haig (2000). This theory predicts genomic imprinting arose due to natural selection acting differently on the matrigenes (maternal alleles) and the patrigenes (paternal alleles) of an individual for given processes. For example; in a polyandrous mating system with maternal care, patrigenes are predicted to be subject to selection pressures which increase resource allocation from the mother at the expense of siblings. Matrigenes in this scenario are predicted to be selected for equal resource distribution amongst offspring.

The majority of support for this theory comes from studies based on mammal and flowering plant systems (Patten *et al.*, 2014). However, it has been suggested haplodiploid social insects can provide an ideal system to independently test Haig's kinship theory (Queller, 2003). Colonies of social bees consist of diploid females (queens and workers) and haploid males created from unfertilised eggs. This haplodiploidy results in workers which all share the full paternal genome, when queens are singly mated. In this scenario the kinship theory (Haig, 2000) predicts patrigenes should be under stronger selection for general care-giving compared to matrigenes. However, when queens mate with multiple males, workers are more likely to have higher maternally derived relatedness and the predictions reverse (Queller, 2003).

Genomic imprinting in mammals and plants is mediated via methylation marks in many cases, with higher promotor methylation generally associated with transcriptional silencing of one allele (Scott and Spielman, 2006; Li *et al.*, 2003; Satyaki and Gehring, 2017). Multiple social insects are known to possess fully functional methylation systems (Glastad *et al.*, 2015). Methylation in social insects is enriched in gene bodies with possible implications in alternative splicing (Li-Byarlay, 2016; Lyko *et al.*, 2010) and is associated with highly expressed genes, such as housekeeping genes (Glastad *et al.*,

2011, 2013; Hunt *et al.*, 2010). Whilst displaying some differences and some similarities to both plant and mammal methylation systems (Li-Byarlay, 2016; Feng *et al.*, 2010), methylation in social insects provides a possible mechanism for producing parent-of-origin gene expression.

To date the majority of research exploring parent-of-origin effects in social insects has focused on the behavioural and physiological outputs of genetic crosses and in only two species. In the Argentine ant (*Linepithema humile*) paternal effects were observed in care-giving associated behaviours and in sex allocation of offspring (Libbrecht and Keller, 2012; Libbrecht *et al.*, 2011). Paternal effects on dominance and stinging behaviour have also been observed in crosses of European and Africanized honeybees (Guzman-Novoa *et al.*, 2005). Additionally Oldroyd *et al.* (2014) found a parent-of-origin effect on increased ovary size in honeybees but could not definitively determine which parent this effect was driven by.

More recently, reciprocal crosses and next generation sequencing technologies have been used to identify genes with parent-of-origin expression patterns in honeybees. Kocher *et al.* (2015) and Galbraith *et al.* (2016b) both used RNA-Seq to study parent-of-origin gene expression in hybrid crosses of honeybee sub-species. Kocher *et al.* (2015) found a matrigenic bias in gene expression. However, it was later shown that sub-species incompatibility effects influenced the results obtained (Gibson *et al.*, 2015). Showing some support for the kinship theory, Galbraith *et al.* (2016b) found a greater patrigenic expression in reproductive workers compared to sterile workers, with increased patrigenic expression in the reproductive tissues. However, this study is limited to only one species and tests only one prediction from the many predictions made in Queller (2003) for how matrigenic/patrigenic expression bias may play a role in social insect colonies.

To test the robustness of Haig's kinship theory I present gene expression data of reproductive and sterile workers from reciprocal crosses of sub-species of the eusocial bumblebee, *Bombus terrestris*. This species is naturally singly-mated and as such the reproductive predictions for the presence of matrigenic/patrigenic expression bias are the reverse of those predicted for the naturally multiply-mated honeybee. As in Galbraith *et al.* (2016b) I also test the effect of queen-less conditions. Under queen-less

conditions matrigenes should be selected to favour individual worker reproduction as there is a higher likelihood they are present in the individual worker's offspring than in her nephews (Fig. 4.1). It is equally likely patrigenes will occur in the offspring of an individual worker and her nephews. Therefore, patrigenes should not experience selective pressure for reproductive behaviour or for sterile nursing behaviour as both are just as beneficial.

I have utilised RNA-seq libraries from reproductive workers and sterile workers, as well as whole genome sequencing libraries from both parents, in order to identify parent-of-origin allele specific expression as a test for Haig's kinship theory of genomic imprinting. I predict higher matrigenic expression bias in both reproductive and sterile workers under queen-less conditions. I also predict that genes showing parent-of-origin expression will be enriched for reproductive related processes.

Reproductive and sterile workers were chosen in order to provide a robust test for the kinship theory. Imprinted genes should maintain their expression bias regardless of the current reproductive state of the individual, i.e. higher matrigenic expression compared to patrigenic expression should be present in queen-less workers regardless of whether they have become reproductive or remained sterile. Additionally the use of sterile and reproductive workers allows us to assess differential expression between castes. This means I can investigate if there is a relationship between differentially expressed genes between reproductive castes and genes showing parent-of-origin expression. A high overlap of differentially expressed genes between reproductive castes with genes showing parent-of-origin expression would suggest a role for imprinted genes in reproductive caste determination.

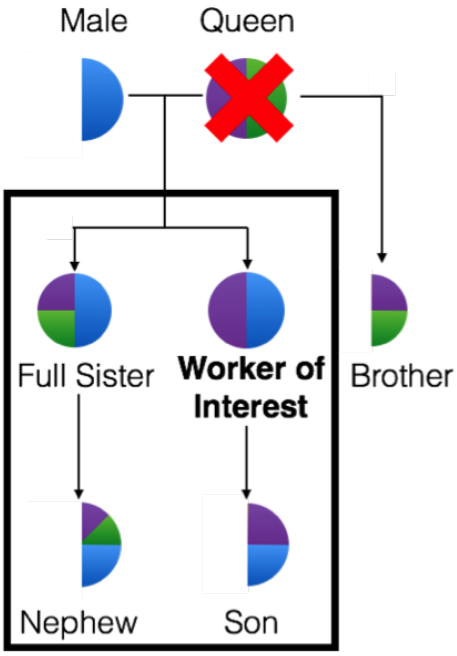


Figure 4.1: Schematic adapted from Drewell *et al.* (2012) showing the inheritance probabilities of the maternal and paternal genome in *Bombus terrestris* under queen-less conditions. Matrigenes should experience higher selection pressures for worker reproduction compared to nursing behaviour for nephews.

4.3 Methods

4.3.1 Sample collection

Reciprocal crosses of *B. terrestris dalmatinus* (native to southern Europe) and *B. terrestris audax* (native to the UK) were carried out by Biobest, Leuven. Reciprocal crosses allow subspecies-of-origin effects (i.e. the effect of genotype) to be disentangled from parent-of-origin effects (Kocher *et al.*, 2015; Galbraith *et al.*, 2016b). In order to obtain enough successful colonies multiple males and females for each cross (Fig. 4.2) were released into cages to mate. Once mating had occurred the male and female were removed. The male was immediately frozen at -80°C and female was placed in cold conditions for eight weeks to induce diapause. Ten matings were carried out for each cross.

Four successful colonies (one of each cross direction) from two 'families' (Fig. 4.2) were

housed at the University of Leuven and kept in 21°C with red light conditions, they were fed *ad libitum* with pollen and a sugar syrup. Callow workers were labelled with numbered disks in order to determine age and allow behaviour to be recorded. Once each colony contained approximately 30 workers the queen was removed. The colonies were then filmed under queen-less conditions for 30mins per day for 14 days in order to score individual behaviour. The following behaviours were used to classify workers: incubating, feeding larvae, inspecting brood cells, building egg cups, ventilation, biting, pushing, egg-laying, egg-eating, foraging, feeding and grooming. Workers were classified based on the frequency of each of the above behaviours as either: sterile foragers, sterile nurses, dominant reproductives or subordinate reproductives (supplementary 4.0.0).

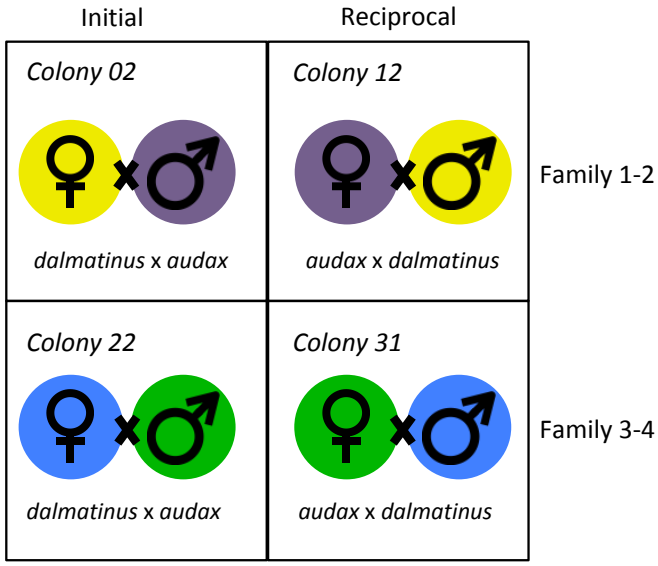


Figure 4.2: Graphic display of the family-wise reciprocal crosses carried out between *Bombus terrestris audax* and *Bombus terrestris dalmatinus*. Each colour refers to related individuals, i.e. the queen from colony 02 is the sister of the male used in colony 12. This design reduces genetic variability between the initial and reciprocal crosses.

Worker reproductive status was confirmed by ovary dissection, ovaries were scored on a 0-4 scale as in Duchateau and Velthuis (1988), entire bodies were then stored at -80°C along with the original queen mothers and male fathers. Workers were selected for sequencing based on their behavioural classification and ovary status. Two of each behavioural type per colony were selected (i.e. two dominant reproductives, two subordinate reproductives, two nurses and two foragers), with the exception of colony 22

(Fig. 4.2) which contained three subordinate reproductives and one dominant reproductive. All sterile and reproductive samples were age matched. This gave a total of 32 samples, eight per colony with four of each reproductive status, reproductive or sterile. See supplementary 4.0.0 for behavioural and ovary scoring per sample.

4.3.2 DNA and RNA extraction and sequencing

DNA was extracted from the mother and father of each colony using the Qiagen DNeasy® Blood & Tissue Kit. Thirty-two workers were selected for RNA sequencing, as described above. The head and abdomen were dissected and RNA extracted separately for each, using the Qiagen RNeasy® Lipid Tissue Kit, giving 64 total RNA samples. The quality of the DNA and RNA extraction were measured by Nanodrop and Qubit® fluorometer. Whole genome parental DNA was sequenced using 91bp paired-end reads and worker RNA was sequenced using 90bp paired-end reads on an Illumina HiSeq 2000 by BGI, China. Lane effects were minimised for the RNA samples by spreading colony and tissue samples across five lanes.

4.3.3 Generation of alternative reference genomes

Whole genome sequencing data was checked using fastqc v.0.11.05 (Andrews, 2010) and adapters and low quality reads were trimmed using Cutadapt v.1.11 (Martin, 2011). Reads were aligned to the bumblebee reference genome (Bter_1.0, Refseq accession no. GCF_000214255.1 (Sadd *et al.*, 2015)) using BWA-mem v.0.7.15 (Li and Durbin, 2009) with standard parameters. SNPs were then called using freebayes v.1.1.0 (Garrison and Marth, 2012) which can account for the difference in ploidy between males and females, a minimum of five reads per SNP were required. Queen SNPs were then filtered so only the homozygous alternative SNPs remained. The subtractbed command from BEDtools v.2.25.0 (Quinlan and Hall, 2010) was then used to create files containing SNPs unique to either the mother/father of each colony. The individual parental SNP files were then used to create alternate reference genomes for each parent using the 'fasta alternate reference maker' command in GATK v.3.6 (McKenna *et al.*, 2010) (Fig. 4.3).

4.3.4 Identification of parent-of-origin expression

RNA-Seq data was quality checked and trimmed as above. STAR v.2.5.2b (Dobin *et al.*, 2016) was used to align worker RNA-seq reads to each of that colony's specific parental genomes with zero mismatches allowed. This ensures any reads containing a SNP will only be matched to the parent that the given allele was inherited from. Alignment files were then filtered using BEDtools v.2.25.0 (Quinlan and Hall, 2010) so only alignments which contain an informative SNP (a unique SNP from either the mother or father) were kept. Reads were counted for the maternal/paternal alignments, also using BEDtools v.2.25.0 (Quinlan and Hall, 2010) and SNP positions were annotated with a gene ID taken from the Bter_1.0 annotation file (Refseq accession no. GCF_000214255.1) using a custom R script (Fig. 4.3). SNPs which had zero maternal reads in at least one sample were removed completely from the analysis to avoid possible inflation of paternal counts. This would occur if the queen position was mis-called as homozygous with the missing allele matching that of the male (Galbraith *et al.*, 2016b).

Genes showing parent-of-origin expression were determined using a logistic regression model in R v.3.4.0 (https://cran.r-project.org). Only genes occurring in both cross directions and in both family combinations, with a minimum of two SNPs per gene were analysed, this left a total of 7,508 genes. If any gene showed zero reads for paternal counts this was changed to 1 to avoid complete separation. A quasibinominal distribution was also used to account for overdispersion within the data. Fixed factors included the direction of the cross, family and reproductive status (reproductive or sterile). Correction for multiple testing was carried out using the Benjamini–Hochberg method (Benjamini and Hochberg, 1995). Genes were determined as showing parent-of-origin expression if the allelic ratio (maternal/paternal) corrected p-value was <0.05 and the parental expression proportion was >0.6.

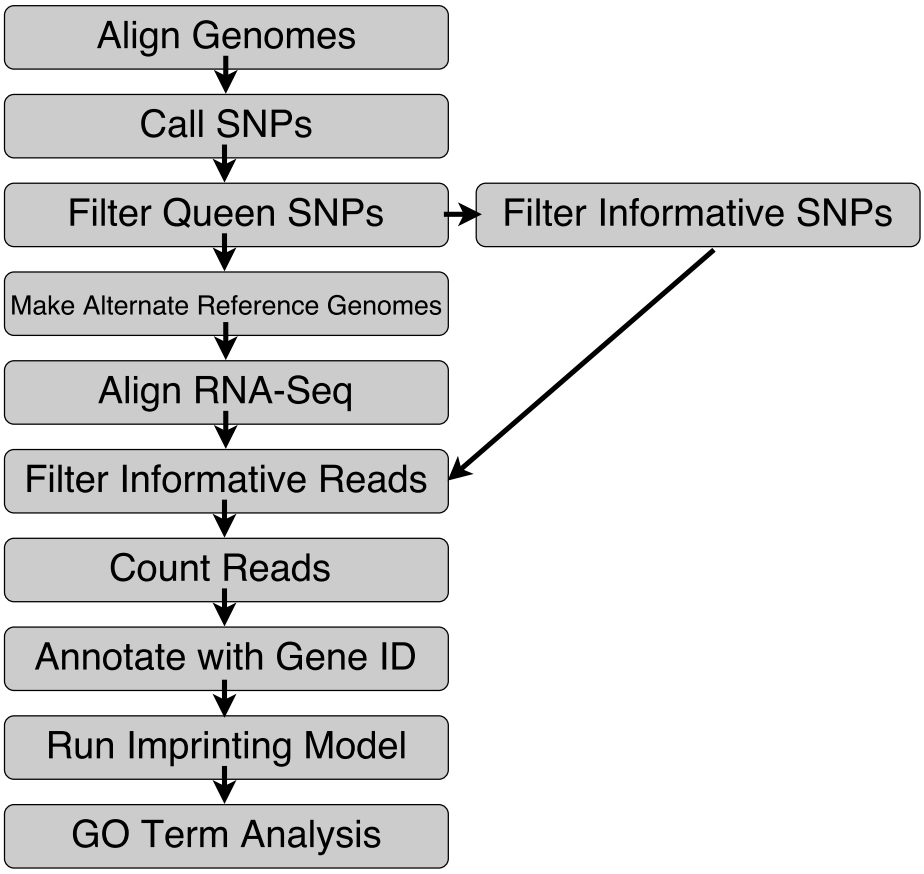


Figure 4.3: Overview of the bioinformatic pipeline used to identify genes with parent-of-origin expression. Informative SNPs refer to those unique to either the mother/father per colony.

4.3.5 Differential expression

All RNA-seq samples were aligned to the reference genome (Bter_1.0, Refseq accession no. GCF_000214255.1 (Sadd *et al.*, 2015)) using STAR v.2.5.2b (Dobin *et al.*, 2016) with standard parameters. HTseq v.0.8.0 (Anders *et al.*, 2013) was then used to count the number of reads per gene for each sample. Differential gene expression between reproductive and sterile workers for head and abdomen samples was assessed using the DESeq2 package v.1.16.1 (Love *et al.*, 2014) in R. DESeq2 allows the incorporation of a general linear model to identify differential expression: family, age, weight, direction of the cross, tissue type and reproductive status were all factors. P-values were corrected for multiple testing using the the Benjamini–Hochberg method (Benjamini and Hochberg, 1995).

4.3.6 Gene ontology enrichment

GO enrichment analysis was carried out using the hypergeometric test with Benjamini-Hochberg (Benjamini and Hochberg, 1995) multiple-testing correction in a custom R script, ($q < 0.05$). This script utilised a previously made GO database for the *B. terrestris* genome, Bter_1.0 (Bebane *et al.*, 2019). GO terms for differentially expressed genes were tested for enrichment against GO terms associated with all genes identified in either the the RNA-seq data from the abdomen or head. Up-regulated genes in either reproductive or sterile workers were tested for GO term enrichment against all differentially expressed genes from the respective tissue type as a background set.

Genes showing parent-of-origin expression were tested for enrichment against GO terms associated with all genes identified in both abdomen and head RNA-Seq data sets. Genes maternally or paternally biased were checked for GO term enrichment against all genes showing parent-of-origin expression as a background set. REVIGO (Supek *et al.*, 2011) was used to obtain the GO descriptions from the GO identification numbers.

4.3.7 Comparative analyses

A hypergeometric test was applied to gene lists from the differential expression analysis and the parent-of-origin expression analysis to identify potential enrichment. *B. terrestis* and *A. mellifera* homologous genes were determined as in Chapter 2 and a custom R script was then used to check for overlap between genes identified as showing parent-of-origin expression here and homologous *A. mellifera* genes identified as showing parent-of-origin expression in Galbraith *et al.* (2016b).

All code from this project is available at:
`https://doi.org/10.5281/zenodo.3235637`.

4.4 Results

4.4.1 Generation of alternate genomes

A maximum of 10 bases were trimmed from the 3' end of each read due to base bias generated by the Illumina protocol (Krueger *et al.*, 2011). The mean mapping percentage of uniquely mapped reads was 98.0% ± 0.3% (mean ± standard deviation). The mean number of uniquely mapped reads was 39,467,171 ± 2,957,976. This gave a mean genome coverage of 14.3 ± 1.1, supplementary 4.0.1.

An average of 967,505 SNPs were called in the male samples and 1,059,559 in the queen samples (Figure 4.4). The total queen SNPs reduced to an average of 441,876 after quality filtering and filtering for homozygous alternative SNPs. There were significantly more unique SNPs found in the male of each colony compared to unique SNPs belonging to the queen of each colony, an average of 675,198 and 150,793 respectively (t-test: t = 12.496, df = 5.5772, p <0.000).

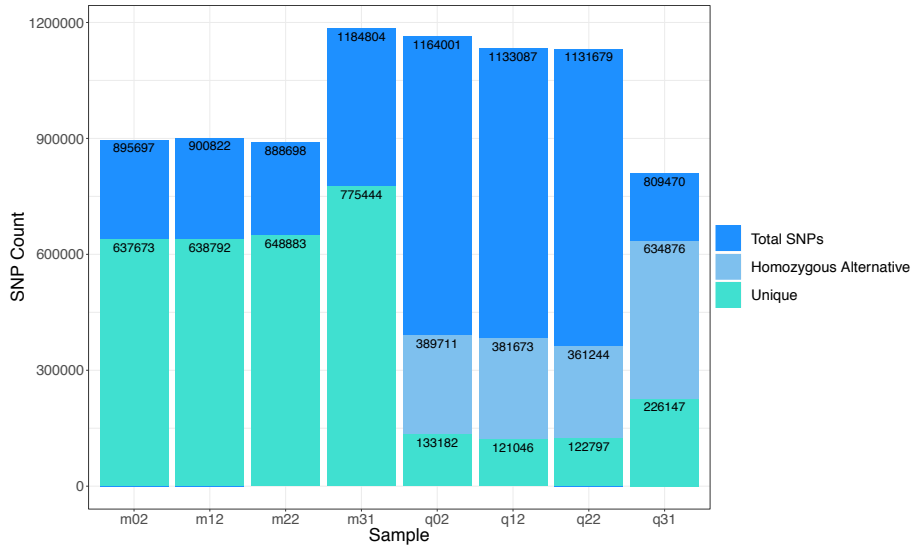


Figure 4.4: Component bar plot showing the total number of SNPs called per sample ('m' representing male and 'q' representing queen), the total number of homozygous alternative SNPs for the queens and the total number of unique SNPs per sample when compared to the corresponding male/queen for that colony.

4.4.2 Parent-of-origin gene expression

Ten bases were trimmed from the 3' end of each worker RNA-seq read due to base bias generated by the Illumina protocol (Krueger *et al.*, 2011). The mean number of uniquely mapped reads to the maternal genomes was 91.31% ± 0.57% (mean ± standard deviation) for the head samples and 91.53% ± 1.86% for the abdomen samples. This equated to a mean of 13,602,926 ± 2,774,040 and 14,181,003 ± 1,303,486 uniquely mapped reads respectively (supplementary 4.0.1). The mean number of uniquely mapped reads to the paternal genomes was 91.50% ± 0.68% (mean ± standard deviation) for the head samples and 91.70% ± 1.83% for the abdomen samples. This equated to a mean of 13,630,611 ± 2,776,779 and 14,208,273 ± 1,307,054 uniquely mapped reads respectively (supplementary 4.0.1).

A total of 10,211 genes had a minimum of two SNPs with at least a coverage of five reads each. Of those, 7,508 genes occurred in every cross, worker-type and tissue type. 700 genes had significant maternal/paternal expression bias in both cross-directions for queen-right workers ($q < 0.05$), and 747 were significant for queen-less workers. The expression bias was averaged across: tissue type, worker type, family and direction of cross to obtain an extremely conservative expression proportion. The significant genes were then filtered to also have an average maternal expression proportion of >0.6 or <0.4 to give a final confident list of genes showing parent-of-origin expression.

Reproductive workers have 163 genes showing significant parent-of-origin expression ($q < 0.05$ and maternal expression proportion >0.6 or <0.4, Fig. 4.5) (supplementary 4.0.2). Sterile workers have 170 genes showing significant parent-of-origin expression ($q < 0.05$ and maternal expression proportion >0.6 or <0.4, Fig. 4.5) (supplementary 4.0.3). There is no difference in the number of genes showing paternal expression bias compared to maternal expression bias in reproductive and sterile workers, assessed independently (chi-squared goodness of fit, queen-right: X-squared = 1.3804, df = 1, p-value = 0.24, queen-less: X-squared = 1.5059, df = 1, p-value = 0.219). There is no significant difference between the number of genes showing maternal expression bias compared to paternal expression bias based on reproductive status (chi-squared test of independence, X-squared = 0, df = 1, p-value = 1). The most extreme expression

bias is seen in the maternally expressed alleles in both reproductive castes, with 17 genes showing a maternal expression proportion of >0.9 in both reproductive and sterile workers (Fig. 4.5). There were no genes showing >0.9 paternal expression bias. Additionally we did not find any genes with sub-species expression bias.

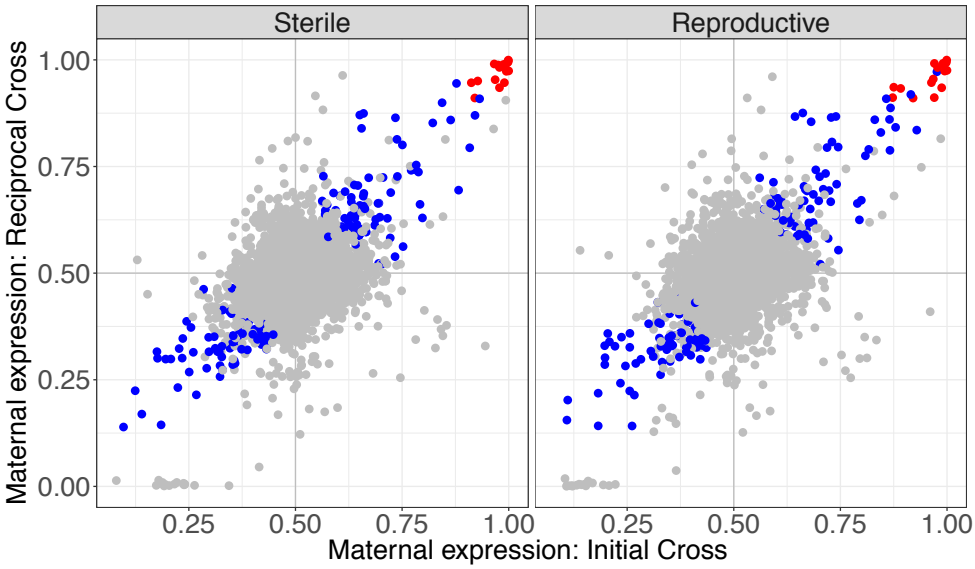


Figure 4.5: Maternal expression proportion by reproductive caste. Each point represents a gene (N = 7,508). Blue points are genes with significant parental expression bias (q <0.05 and expression proportion >0.6). Red points are genes with significant parental expression bias (q <0.05) with the proportion of expression >0.9. The top left quadrant of each plot represents genes with a *B. terrestris audax* expression bis, the bottom right quadrant represents gene with a *B. terrestris dalmatinus* expression bias. The top right represents genes with a maternal expression bias and the bottom left represents genes with a paternal expression bias.

Reproductive and sterile workers share a significant number of genes showing parent-of-origin expression with the same parental bias (Fig. 4.6, maternal expression bias: hypergeometric test, p <0.000, paternal expression bias: hypergeometric test, p <0.000). There were no genes with maternal/paternal bias in one caste which had the opposite bias in the other caste.

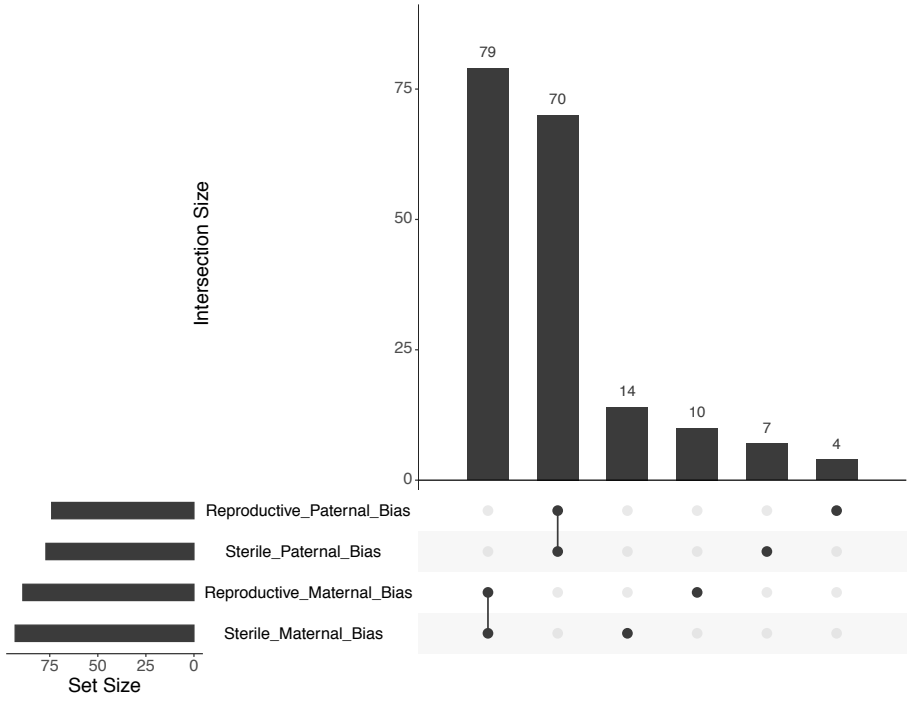


Figure 4.6: Overlapping genes showing parent-of-origin expression in reproductive and sterile workers. The set size indicates the number of genes in each list. The intersection size shows how many genes the corresponding lists, represented by the jointed dots in the lower panel, have in common. A single dot in the lower panel refers to the number of genes unique to each list.

Overall genes showing parent-of-origin expression have enriched GO terms for multiple biological processes (supplementary 4.0.4), specifically the GO terms *negative regulation of reproductive processes* (GO:2000242) and *female germ-line sex determination* (GO:0019099) are enriched. Genes with maternal and paternal bias in both reproductive and sterile workers also have enriched GO terms for multiple biological processes (supplementary 4.0.5). Specifically, paternally expressed genes in both reproductive and sterile workers are enriched for the GO term *behaviour* (GO:0007610).

Enriched GO terms for genes showing parent-of-origin expression in only reproductive or sterile workers were also enriched for various biological processes (supplementary 4.0.6). Including *histone ubiquitination* (GO:0016574) and *histone H2A monoubiquitination* (GO:0035518) in reproductive paternally expressed genes.

4.4.3 Differential expression between reproductive castes

Ten bases were trimmed from the 3' end of each read due to base bias generated by the Illumina protocol (Krueger *et al.*, 2011). The mean number of uniquely mapped reads was 95.29% ± 0.36% (mean ± standard deviation) for the head samples and 94.88% ± 1.77% for the abdomen samples, when samples were mapped to the reference genome Bter_1.0. This equated to a mean of 14,196,707 ± 2,886,920 and 14,701,980 ± 1,358,895 uniquely mapped reads respectively (supplementary 4.0.7).

Tissue type explains the majority of variation within all of the RNA-seq samples, followed by reproductive status, either reproductive or sterile (Fig. 4.7). Following differential expression analysis a total of 3,505 genes were up-regulated in the abdomen of reproductive workers compared to sterile workers and 4,069 genes were down-regulated (q <0.01) (supplementary 4.0.8).

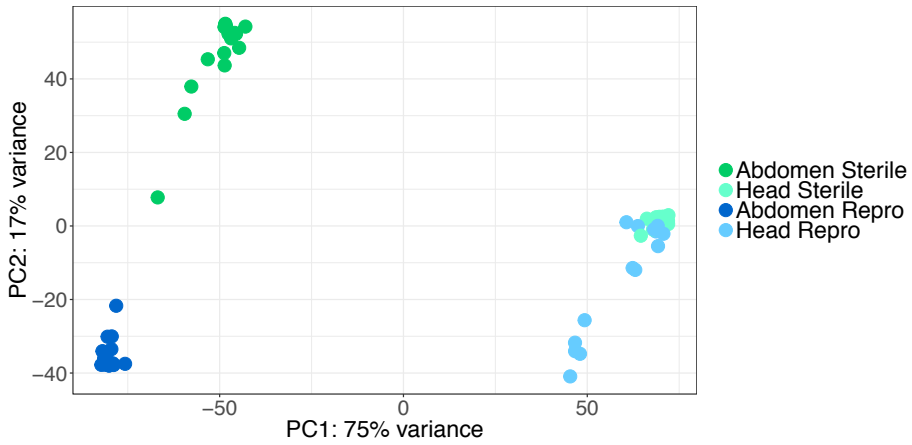


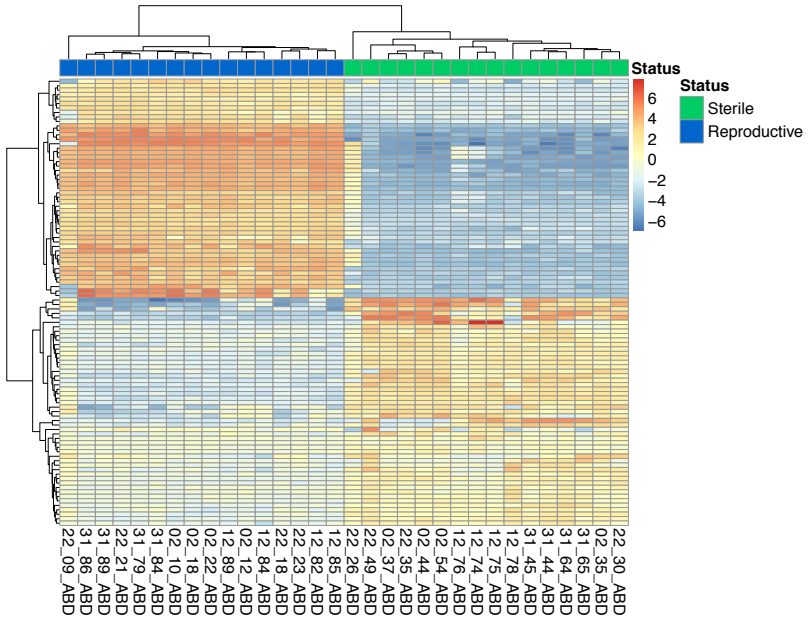
Figure 4.7: PCA plot for the expression levels of all genes (N = 11,087). PCA1 separates samples by tissue type and PCA2 separates samples by reproductive caste.

The enriched GO terms for the differentially expressed genes between reproductive and sterile castes in the abdomen included mostly regulatory processes but also *reproduction*

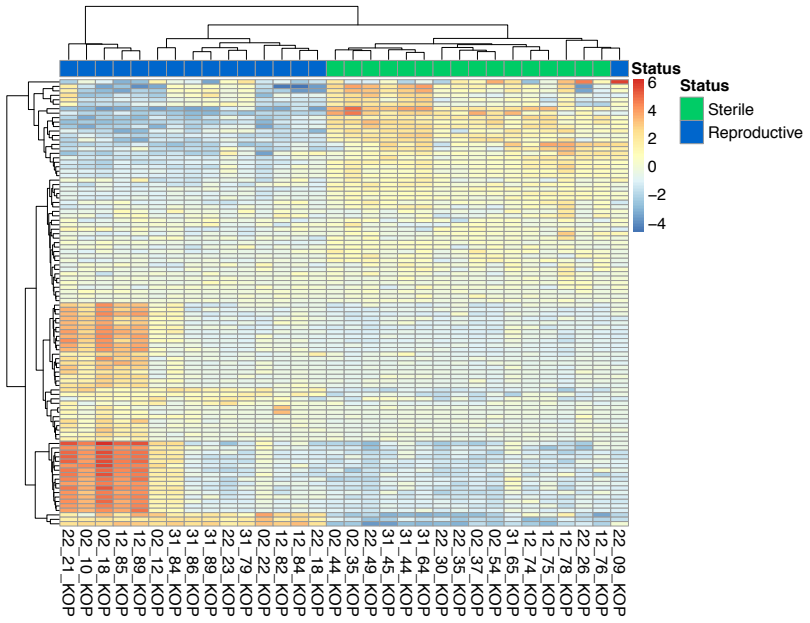
(GO:0000003) (supplementary 4.0.9). Enriched GO terms associated specifically with up-regulated genes in reproductive workers in the abdomen also included: *reproduction* (GO:0000003) and *DNA methylation* (GO:0006306) (supplementary 4.1.0), these terms were not found in the enriched GO terms for genes up-regulated in sterile workers.

Considerably fewer genes were differentially expressed in the head samples; 86 up-regulated genes in reproductive compared to sterile workers and 41 down-regulated genes ($q < 0.01$) (supplementary 4.1.1). The majority of the GO terms associated with these differentially expressed genes involved biosynthetic processes (supplementary 4.1.2). Up-regulated genes in the head tissue of reproductive workers also included *reproduction* (GO:0000003) whereas the up-regulated genes in the head tissue of sterile workers consisted of mostly metabolic processes (supplementary 4.1.2).

A heatmap of the top 100 differentially expressed genes in the abdomen clearly shows a segregation of reproductive and sterile workers (Figure 4.8a). However, the same heatmap for the head samples shows that reproductive workers form two clusters, one more closely related to sterile workers than the other. One reproductive individual also clusters within the sterile samples (Figure 4.8b). Re-running the analysis taking into account dominant and subordinate reproductive status (supplementary Fig. B.1) shows five of the seven dominant reproductive samples form the over expressed group shown in Figure 4.8b.



(a) Abdomen



(b) Head

Figure 4.8: Heatmaps showing the 100 most differentially expressed genes between reproductive and sterile workers for (a) the abdomen and (b) the head. The top dendogram shows hierarchical clustering by sample based on the counts of the genes shown. The left-hand dendogram shows count similarity between the top 50 over expressed genes in reproductive workers and the top 50 over expressed genes in sterile workers. The red colour indiciates over expression and the blue colour indiciates under expression. Sample names along the bottom refer to the colony of origin, the individual and the tissue type; ABD = abdomen and KOP = head. Red indicates up-regulation and blue indicates down-regulation.

4.4.4 Overlap of parent-of-origin genes and differentially expressed genes

Genes showing maternal parent-of-origin expression are enriched for genes which are also differentially expressed in head tissue (Fig. 4.9, hypergeometric test, p = 0.004). Specifically *Serine Protease Inhibitor 3/4* (LOC100652301) shows maternal expression bias in both reproductive and sterile workers and is up-regulated in the head tissue of reproductive workers.

Genes with paternal parent-of-origin expression do not significantly overlap with differentially expressed genes (Fig. 4.9, hypergeometric test, p = 0.148). There is also no significant overlap between genes showing parent-of-origin expression bias and differential expression in the abdomen (supplementary Fig. B.2, hypergeometric test, p = 0.996).

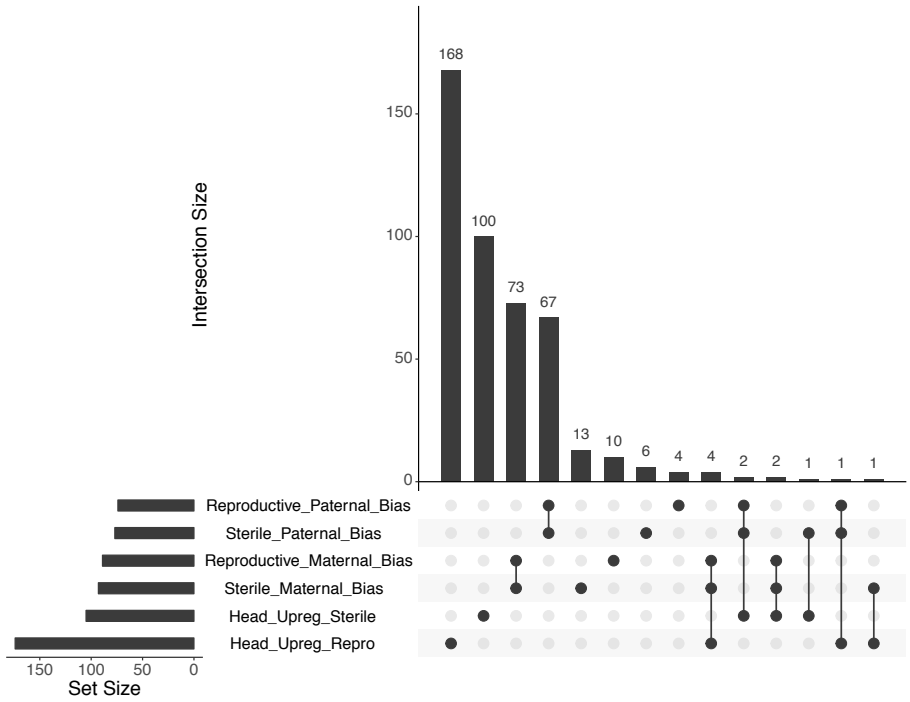


Figure 4.9: Overlapping genes showing parent-of-origin expression in reproductive and sterile workers with genes showing differential expression in head tissue. The set size indicates the number of genes in each category. The intersection size shows how many genes the corresponding lists, represented by the jointed dots in the lower panel, have in common. A single dot in the lower panel refers to the number of genes unique to each list. 7/103 genes showing maternal bias are also differentially expressed in the head.

4.4.5 Honeybee homology

A custom homology database was made between *A. mellifera* and *B. terrestris*, as in Chapter 2, containing 6,539 genes. Here 68% of differentially expressed abdominal genes were identified within the database, 43% of differentially expressed head genes and 46% of genes showing parent-of-origin expression bias (supplementary 4.1.6). Gene lists were obtained from Galbraith *et al.* (2016b), the homology database contained 38% of the differentially expressed genes identified between honeybee reproductive worker castes and 53% of the genes found to show parent-of-origin expression bias (supplementary 4.1.6).

There was no significant overlap between the genes identified as showing parent-of-origin expression between both studies (hypergeometric $p = 0.64$), with only two genes overlapping (Fig. 4.10). One of which is uncharacterised in both species (honeybee id: LOC552195, bumblebee id: LOC100648162) and the second is a serine protease inhibitor (honeybee id: LOC411889, bumblebee id: LOC100644680). The serine protease inhibitor shows paternal expression bias in honeybees and maternal bias in both bumblebee reproductive and sterile castes. It is not differentially expressed in the honeybee but it shows up-regulation in the abdomen tissue of reproductive bumblebee workers compared to sterile workers.

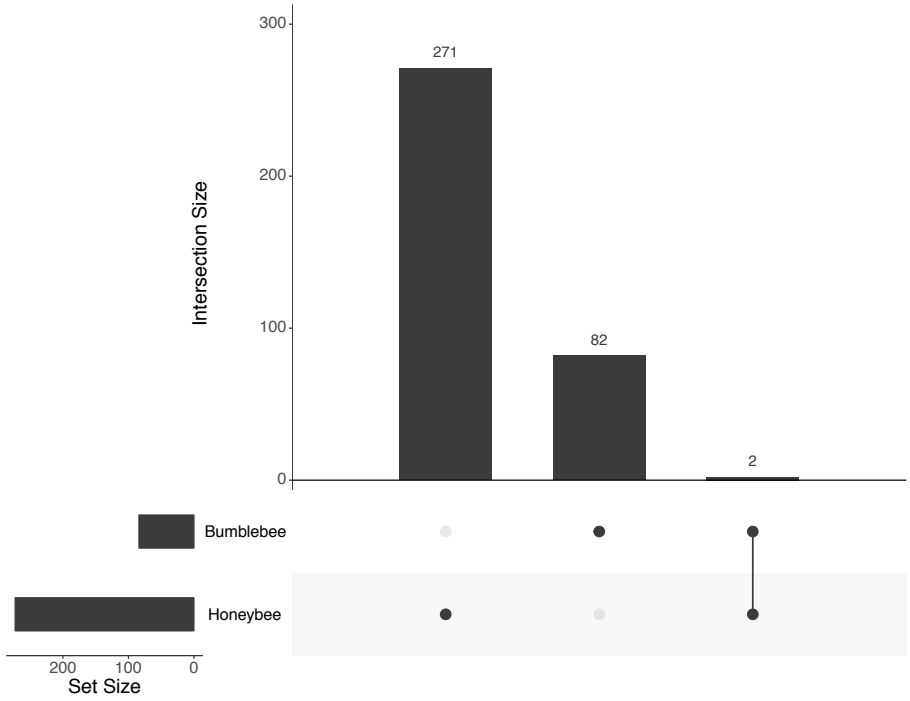


Figure 4.10: Overlapping genes showing parent-of-origin expression in reproductive and sterile workers of *B. terrestris* and *A. mellifera* (genes identified in Galbraith *et al.* (2016a)). The set size indicates the number of genes in each category. The intersection size shows how many genes the corresponding lists, represented by the jointed dots in the lower panel, have in common. A single dot in the lower panel refers to the number of genes unique to each list.

There was also no significant overlap between differentially expressed genes identified in head tissue and abdomen tissue between *B. terrestris* reproductive castes with those identified as differentially expressed between reproductive castes of *A. mellifera* from Galbraith *et al.* (2016a) (supplementary Fig. B.3, head: hypergeometric p = 1, abdomen hypergeometric p = 1).

4.5 Discussion

Using parental genome sequencing and offspring RNA-seq I have identified genes showing parent-of-origin expression in a eusocial bumblebee species. I predicted higher matrigenic expression bias in queen-less workers, in genes related to reproductive functions, following the predictions of Haig's kinship theory (Queller, 2003; Haig, 2000).

There was no difference in the number of genes showing maternal or paternal expression bias in either reproductive or sterile workers. However, genes showing the highest proportion of expression bias were all maternally expressed in both castes. Additionally, reproductive related GO terms were enriched in both maternally and paternally expressed genes along with multiple other biological processes.

These results provide some support for Haig's kinship theory; I find the most highly biased genes are maternally expressed and genes showing parent-of-origin expression are related to reproductive processes. Galbraith *et al.* (2016b) found overall patrigenic expression bias in reproductive and sterile workers from a reciprocal cross of honeybee sub-species, with significantly more patrigenic expression bias in reproductive workers compared to sterile workers, supporting Haig's kinship theory. Whilst, I do not find an overall maternal expression bias, the difference in the signal obtained between species highlights the importance of using multiple species to test various predictions when evaluating evolutionary theory.

I do not find any direct association between parent-of-origin expression and reproductive status. However, I did find different genes involved in histone modifications to be paternally expressed in reproductive workers. Histone modifications have been identified as an imprinting mark in plants (Rodrigues and Zilberman, 2015) and thought to be involved in imprinting maintenance in mammals (Delaval and Feil, 2004). Additionally histone modifications can alter gene expression by affecting gene accessibility via chromatin (Bannister and Kouzarides, 2011). Chromatin modifications have been associated with parent-of-origin expression in the fruit fly *Drosophilia melanogaster* (Joanis and Lloyd, 2002). Additionally Galbraith *et al.* (2016b) also found genes involved in histone modifications showing parent-of-origin expression in the honeybee *A. mellifera*. My results hint to the possibility that parent-of-origin expression affects epigenetic mechanisms, which may in turn influence reproductive related genes. This is purely speculative and provides a potential avenue for future research to pursue.

As in Galbraith *et al.* (2016b) I also found no significant overlap of paternally expressed genes with differentially expressed genes between reproductive and sterile workers. However, I did find a significant overlap with maternally expressed genes and genes differen-

tially expressed in head tissue between reproductive and sterile castes. This significant overlap should be interpreted cautiously as only seven of the 103 unique maternally biased genes were differentially expressed in head tissue between reproductive castes. The lack of overlap of differentially expressed genes with paternally expressed genes and the small overlap with maternally expressed genes suggests parent-of-origin expression may not directly influence reproductive status in bumblebee workers.

One of the overlapping genes found to be differentially expressed in head tissue between reproductive castes which also shows maternal expression bias is a serine protease inhibitor. One of the two homologous genes identified as showing parent-of-origin expression in this study and in honeybees from Galbraith *et al.* (2016b) was also a serine protease inhibitor. Serine proteases (also know as serpins) have been shown to be involved in insect immunity in various species including: the silkworm *Bombyx mori* (Zou *et al.*, 2009), another species of silk producing moth *Antheraea pernyi* (Yu *et al.*, 2017) and the mosquito *Anopheles gambiae* (Gorman and Paskewitz, 2001). They also have functions involved with venom production in two parasitoid wasp species: *Pteromalus puparum* (Yang *et al.*, 2017) and *Nasonia vitripennis* (Qian *et al.*, 2015).

Most recently a kazal-type serine protease inhibitor has been directly linked to oocyte development in the desert locust *Schistocerca gregaria* (Guo *et al.*, 2019). A knock-down of the protein producing gene *Greglin* by RNAi caused extreme effects on reproduction, including: diminished oocyte production and maturation, a decline in the number of eggs produced and hatching success (Guo *et al.*, 2019). Future work identifying the function of serine protease inhibitors in social insects is needed to better understand the function of parent-of-origin expression of these genes in both *B. terrestris* and *A. mellifera*.

As mentioned, only two genes were found in common between those found in Galbraith *et al.* (2016b) as showing parent-of-origin gene expression in the honeybee *A. mellifera* and those identified here in *B. terrestris*. Galbraith *et al.* (2016b) used ovaries and fat bodies as their tissues samples whereas I selected to test whole head and whole abdomen samples for strong signals of expression bias. Some imprinted genes in mammals are known to be tissue specific, such as *GBR10* which has been found to be maternally

expressed in brain and muscle tissue but not in growth plate cartilage (McCann *et al.*, 2001). Tissue specificity could account for the lack of concordance in parentally expressed genes found between *B. terrestris* and *A. mellifera*. Additionally a large proportion of genes identified in both studies were not present in the homology database created. This suggests the function of potentially imprinted genes in Hymenoptera is not strictly conserved.

The lack of conservation between genes showing parent-of-origin expression in *A. mellifera* and *B. terrestris* suggests imprinted genes have evolved rapidly in Hymenoptera. Imprinted genes in mammals show much more consistency across species, with mice and humans reportedly sharing around 50 imprinted genes out of around 150 and 100 characterised in each respectively (Babak *et al.*, 2015). Additionally, domestic cattle and pigs have been shown to share 14 imprinted genes out of 26 and 18 respectively (Tian, 2013). However, imprinted genes in plants generally show less conservation, with one study reporting 14% of maternally expressed genes and 29% of paternally expressed genes in *Capsella rubella* show the same imprinting status in *Arabidopsis thaliana*, even though both species belong to the same family, Brassicaceae (Hatorangan *et al.*, 2016). Hatorangan *et al.* (2016) suggest the lack of consistency between species could be the result of a historical shift in mating-systems. Given the differences in mating-systems between honeybees and bumblebees, and that variable predictions from the kinship theory apply to each species, rapid evolution of imprinted genes in Hymenoptera is a feasible explanation for the lack of consistency in potentially imprinted genes identified here and in Galbraith *et al.* (2016b).

Whilst I present some correlative evidence for parentally expressed genes being associated with reproduction, the GO terms associated with both maternally and paternally expressed genes are diverse. It has been suggested imprinted genes can function as a mechanism for plasticity, allowing gene regulation to change depending on environmental conditions by activating the silenced allele and increasing dosage of that gene (Radford *et al.*, 2011). Social insects display, sometimes extreme, phenotypic plasticity, where multiple discrete phenotypes (castes) can arise from a single genome within a colony. In some species this is genetically determined (Mott *et al.*, 2015). However, there is growing evidence epigenetic factors may play a role in caste determination in

some species (Lyko *et al.*, 2010; Bonasio *et al.*, 2012, Chapter 2). Matsuura *et al.* (2018) modelled a genomic imprinting mediated caste determination system in the termite *Reticulitermes speratus* and found this better explained the influence of parental phenotype on offspring than a purely genetic model. Given the diversity of genes found here showing both maternal and paternal expression bias I believe, along with Matsuura *et al.* (2018), that further experimental investigation into the role of genomic imprinting in caste determination in social insects is needed.

The identification of genes showing parent-of-origin expression in this study lays the ground work for future research to identify potential epigenetic mechanisms of allele specific expression in social insects. Genes showing allele specific expression and methylation have been previously identified in *B. terrestris* (Lonsdale *et al.*, 2017), and genes involved in the reproductive process have been shown to be differentially methylated between reproductive castes (Chapter 2). It is known methylation is the mechanism of some imprinted genes in mammals and plants (Scott and Spielman, 2006) and so investigation of parent-of-origin methylation in *B. terrestris* may be fruitful.

This is the first study to identify parent-of-origin gene expression in a eusocial bumblebee species. I found the most highly biased genes show maternal expression bias, and parentally biased genes in general in this species may be involved in worker reproduction, as predicted by Haig's kinship theory. This discovery is in line with previous work using honeybees and highlights the vital importance of using multiple species to test multiple predictions in the evaluation of evolutionary theories. Additionally, the lack of consistency between potentially imprinted genes in *B. terrestris* and *A. mellifera* suggests rapid evolution of imprinted genes in these species. Finally, the results of this study create a base for many future avenues of research including: gene function analysis of serine protease inhibitors in Hymenoptera, epigenetic mechanisms of imprinting in insects and imprinted genes as a mechanism for plasticity and caste determination.

Chapter 5

Reciprocal crosses to identify parent-of-origin methylation in the bumblebee, *Bombus terrestris*.

Hollie Marshall, Jelle Van Zweden, Annaleen Van Geystelen, Kristof Benaets, Felix Wäckers, Eamonn Mallon and Tom Wenseleers.

5.1 Abstract

Genomic imprinting is defined as parent-of-origin allele-specific expression. In order for genes to be expressed in this manner an 'imprinting' mark must be present to distinguish the parental alleles within the genome. In mammals and flowering plants imprinted genes are primarily associated with DNA methylation. Genes exhibiting parent-of-origin expression have recently been identified in two species of Hymenoptera; *Apis mellifera* and *Bombus terrestris*. Additionally, DNA methylation systems have been described in these species and previous work has shown a small number of genes in *B. terrestis* show allele-specific expression and allele-specific DNA methylation. However, whether DNA methylation can be transmitted in a parent-of-origin manner, making it a potential imprinting mark, is still unknown. Utilising whole genome bisulfite sequencing of parents and offspring from reciprocal crosses of two subspecies (*B. terrestris audax* and *B. terrestris dalmatinus*) I have identified parent-of-origin CpG methylation in *B. terrestris* reproductive workers. Genes containing parent-of-origin DNA methylation marks were not consistent with those previously described as showing parent-of-origin expression. This suggests DNA methylation may not be directly responsible for altering gene expression of potentially imprinted genes. It is possible an interplay of epigenomic mechanisms, acting in both *cis* and *trans*, are what drive parent-of-origin expression. Future work exploring the relationship between parent-of-origin DNA methylation and open chromatin regions will further elucidate the molecular mechanisms of imprinted genes in insects.

5.2 Introduction

Genomic imprinting is defined as parent-of-origin allele-specific expression (Rodrigues and Zilberman, 2015). In order for genes to be expressed in this manner an 'imprinting' mark must be present to distinguish the parental alleles within the genome. In mammals and flowering plants imprinted genes are primarily associated with DNA methylation in areas of the genome known as imprinting control regions (ICRs) (Barlow and Bartolomei, 2014). The presence of DNA methylation, as an imprinting mark, has been associated with both allelic silencing as well as allelic expression (Drewell *et al.*, 2012; Barlow, 2011).

DNA methylation can serve to repress expression of a individual allele by preventing a transcription factor from binding to a promoter region (Drewell *et al.*, 2012). It is also thought DNA methylation may signal the recruitment of histone modifications which result in heterochromatin formation, silencing the expression of all alleles within a region (Barlow, 2011). DNA methylation can also enable allele-specific expression of imprinted genes by silencing an 'imprinting control element', such as a long non-coding RNA, which, when expressed, would cause transcriptional silencing of nearby genes (Barlow, 2011). It is also worth noting whilst most identified imprinted genes in mammals have some association with methylation there are cases where imprinting has been observed independently of methylation and instead associated solely with a particular histone modification (Inoue *et al.*, 2017).

Whilst parent-of-origin expression and the underlying epigenetic marks are well documented in mammals and flowering plants, it is only recently that genes exhibiting parent-of-origin expression in insects have been identified (Galbraith *et al.*, 2016a, Chapter 4). Previous studies had only found sub-species specific allelic expression (Wang *et al.*, 2016), and the results of one study (Kocher *et al.*, 2015) were later found to be driven by sub-species incompatibilities (Gibson *et al.*, 2015). However, imprinted chromosomes or chromosome regions have been identified in multiple insect species, including *Drosophilia melanogaster* (Anaka *et al.*, 2009), with various species exhibiting paternal genome elimination, where only the maternal chromosomes of a male are

passed on to the subsequent offspring (Hodson *et al.*, 2017). Given the lack of research into parent-of-origin gene expression in insects, little is known about the potential epigenetic mechanisms driving the imprinting of parental alleles. DNA methylation has recently been shown to exist in all orders of insects, except for Diptera (Bewick *et al.*, 2016), it is therefore possible DNA methylation may also play a role in genomic imprinting in insects, as seen in mammals and flowering plants.

Insect DNA methylation, like mammalian methylation, is generally found in a CpG context (referring to a cytosine base immediately followed by a guanine base) (Glastad *et al.*, 2014). It is found in lower levels, with <1% - 14% of CpGs being methylated, compared to mammals where around 70% of CpG sites are methylated (Bewick *et al.*, 2016; Feng *et al.*, 2010). Additionally DNA methylation in insects is generally located in gene bodies and associated with more highly expressed genes, such as housekeeping genes (Provataris *et al.*, 2018; Elango *et al.*, 2009; Foret *et al.*, 2009).

The function of DNA methylation in insects is largely unknown and thought to be variable based on the range of overall levels between classes (Provataris *et al.*, 2018). Both insect species known to show parent-of-origin gene expression belong to the order: Hymenoptera (Galbraith *et al.*, 2016b, Chapter 4). In Hymenoptera, DNA methylation has been associated with caste differentiation in various species, for example: *Apis mellifera* (Lyko *et al.*, 2010), *Bombus terrestris* (Chapter 2), *Zootermopsis nevadensis* (Glastad *et al.*, 2016) and *Camponotus floridanus* (Bonasio *et al.*, 2012). Although no association between the level of sociality of a species and the level of DNA methylation has been found (Weiner *et al.*, 2013; Glastad *et al.*, 2017). The leading theory for the evolution of genomic imprinting, Haig's kinship theory (Haig, 2000), predicts social insects should display imprinted genes. It has also been thought genomic imprinting in social insects could contribute to caste differentiation (Matsuura *et al.*, 2018).

Here, I identify parent-of-origin methylation marks in the eusocial bumblebee *Bombus terrestris*, to investigate the hypothesis that DNA methylation can also act as an epigenetic mark for genomic imprinting in social insects. *B. terrestris* is the ideal model species to explore this hypothesis; it has previously been shown to exhibit parent-of-origin gene expression of both maternally derived and paternally derived alleles (Chap-

ter 4), *B. terrestris* possess a fully functional methylation system (Liu *et al.*, 2018; Amarasinghe *et al.*, 2014, Chapter 2) and it displays allele-specific methylation at multiple loci throughout the genome (Lonsdale *et al.*, 2017, Chapter 3). This study will determine if some of these allele-specific DNA methylation events which exist in *B. terrestris* are determined in a parent-of-origin manner. Combined with previously generated parent-of-origin gene expression data (Chapter 4) this study may provide the first evidence for a molecular imprinting mechanism in Hymenoptera.

I have generated whole genome bisulfite sequencing (WGBS) libraries from the parents and pooled worker offspring of two family-wise reciprocal crosses. Male *B. terrestris* are haploid meaning every worker daughter inherits the same copy of the paternal genome, whilst queens are diploid meaning there are two possible maternal alleles that can be present in the offspring. SNPs unique to the father and homozygous SNPs unique to the queen mother have been used to identify the parental origin of alleles within the offspring genome, allowing parent-of-origin methylation to be identified. Utilising WGBS I have also identified methylation differences between queens and males and established if these methylation differences are maintained in the parental alleles of the offspring. Finally, taking advantage of the previously generated parent-of-origin allele-specific expression data set from Chapter 4 I have searched for a link between parent-of-origin methylation and parent-of-origin expression in *B. terrestris*, exploring the potential role of DNA methylation in genomic imprinting in insects.

5.3 Methods

5.3.1 Sample collection

The samples used in this chapter are from the same experiment as those used in Chapter 4. However, different colonies were selected. Ideally I would have used the same colonies for the exploration of parent-of-origin expression and methylation. However, the gene expression data were already generated before the collaboration between labs was established, see page iii.

Reciprocal crosses of *B.terrestris dalmatinus* (native to southern Europe) and *B.terrestris audax* (native to the UK) were carried out by Biobest, Leuven. Four successful colonies (one of each cross direction) from two 'families' (Fig. 5.1) were housed at the University of Leuven and kept in 21°C with red light conditions, they were fed *ad libitum* with pollen and a sugar syrup. Callow workers were tagged in order to determine age.

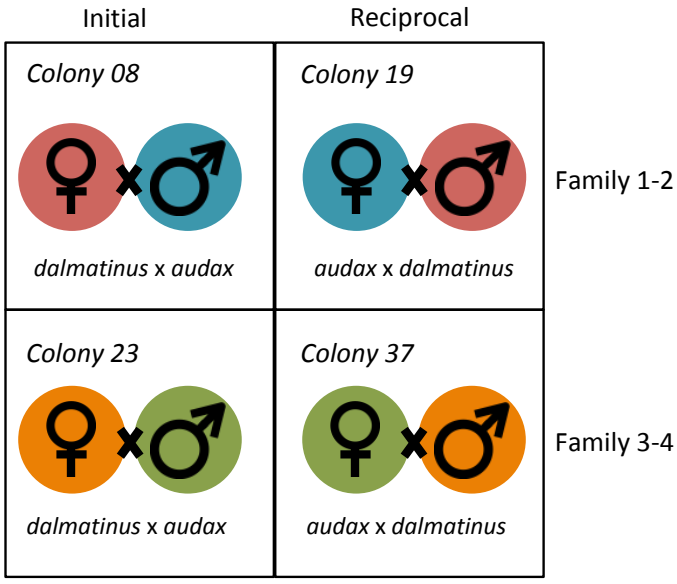


Figure 5.1: Graphic display of the family-wise reciprocal crosses carried out between *Bombus terrestris audax* and *Bombus terrestris dalmatinus*. Each colour refers to related individuals, i.e. the queen from colony 08 is the sister of the male used in colony 19. This design reduces genetic variability between the initial and reciprocal crosses.

Worker reproductive status was confirmed by ovary dissection, ovaries were scored on a 0-4 scale as in Duchateau and Velthuis (1988), entire bodies were then stored at -80°C along with the original queen mothers and male fathers. Three reproductive workers, aged 16-17days, were selected from queen-less conditions from each of the crosses (supplementary 5.0.0).

5.3.2 DNA extraction and sequencing

DNA was extracted from whole heads of the mother and father of each colony as well as from 12 reproductive workers (three per colony) using the Qiagen DNeasy® Blood & Tissue Kit following the manufacturers protocol. Reproductive workers were chosen to reduce the variation between samples as sterile and reproductive worker castes show different methylation profiles (Chapter 2). Each sample was treated with RNAse. DNA from the three reproductive samples per colony were pooled to produce one representative offspring sample per colony. DNA quantity and quality were determined by Nanodrop and Qubit® fluorometers as well as via gel electrophoresis.

DNA samples were originally sent to the Centre for Genomic Research at the University of Liverpool for whole genome bisulfite sequencing, using paired-end libraries (2 x 150bp) across two lanes of an Illumina HiSeq 4000 platform with 40% phiX inclusion. However, data received were of extremely poor quality (Appendix C). There was enough DNA to re-sequence the samples and therefore samples were sent, by the University of Liverpool, to BGI Tech Solution Co., Ltd.(Hong Kong) for sequencing using the same method. The method consists of; DNA fragmentation to 100-300bp by sonication, purification using the Qiagen MiniElute PCR Purification Kit, incubation at 20°C with an end repair mix, 3' adenine addition and ligation of methylated adapters, purification of 300-400bp fragments with Qiagen QIAquick Gel Extraction Kit, bisulfite treatment with the Zymo Methylation-Gold kit, PCR and a final size selection of 350-400bp fragments using the Qiagen QIAquick Gel Extraction Kit. A 1% lambda DNA spike was included in all libraries in order to assess bisulfite conversion efficiency, as the lambda genome is known to be unmethylated.

5.3.3 Differential methylation

Sequencing data were checked using fastqc v.0.11.5 (Andrews, 2010) and poor quality bases were trimmed using cutadapt v.1.11 (Martin, 2011). Libraries were then aligned to the reference genome (Bter_1.0, Refseq accession no. GCF_000214255.1, (Sadd *et al.*, 2015)) using Bismark v.0.16.1 (Krueger and Andrews, 2011) and bowtie2 v.2.2.6 (Lang-

mead and Salzberg, 2012) with standard parameters. Bismark was also used to extract methylation calls and carry out deduplication. Coverage outliers (above the 99.9th percentile) were removed along with bases covered by less than 10 reads. The methylation status of each CpG was then determined, using the 'methylation status calling' (MSC) procedure, as described in Cheng and Zhu (2014). CpG sites were then filtered to remove any site that did not return as methylated in at least one sample.

Differential methylation was assessed at the CpG level in pair-wise comparisons (queen-male, queen-worker, male-worker) using the R package *methylKit* (Akalin *et al.*, 2012). A logistic regression model was applied to each comparison. For differential methylation between workers and queens/males the model included subspecies (*B. t. audax*, *B. t. dalmatinus* or mixed; for the worker) and colony as covariates. For differential methylation between males and queens the model covariates were subspecies and family. The inclusion of colony or family as a covariate allows the relatedness between workers and parents or workers and parental siblings to be taken into account.

For a CpG to be differentially methylated a minimum difference of at least 10% methylation and a q-value of <0.05 were required. Genes were determined as differentially methylated genes if they contained at least one differentially methylated CpG and had an overall weighted methylation difference of $>10\%$. Weighted methylation level is determined as the total number of methylated cytosines (C) within a region (i) divided by the total coverage of a region (Equation 5.1), as described in Schultz *et al.* (2012).

$$\sum_{i=1}^{n} C_i / \sum_{i=1}^{n} C_i + T_i \tag{5.1}$$

5.3.4 Generation of alternative reference genomes

Data were aligned and deduplicated as in section 5.3.3. SNPs were then called from the parental bisulfite-genomes using a high-stringency SNP caller designed for bisulfite treated data, Bis-SNP v.1.0.0 (Liu *et al.*, 2012). In order to use Bis-SNP, the alignment output files (.bam) were sorted and indexed using samtools v.1.3.2 (Li *et al.*, 2009) and

read group data was added using picard v.2.6.0 (Broad Institute, 2018).

After quality filtering, queen SNPs were then filtered so only the homozygous alternative SNPs remained. Males SNPs were also filtered to remove any potentially mis-labelled heterozygous SNPs, this can occur as Bis-SNP cannot take ploidy into account. The *subtractbed* command from BEDtools v.2.25.0 (Quinlan and Hall, 2010) was then used to create files containing SNPs unique to either the mother/father of each colony. The individual parental SNP files were then used to create alternate reference genomes (Fig. 5.2) for each parent using the *fasta alternate reference maker* command in GATK v.3.6 (McKenna *et al.*, 2010).

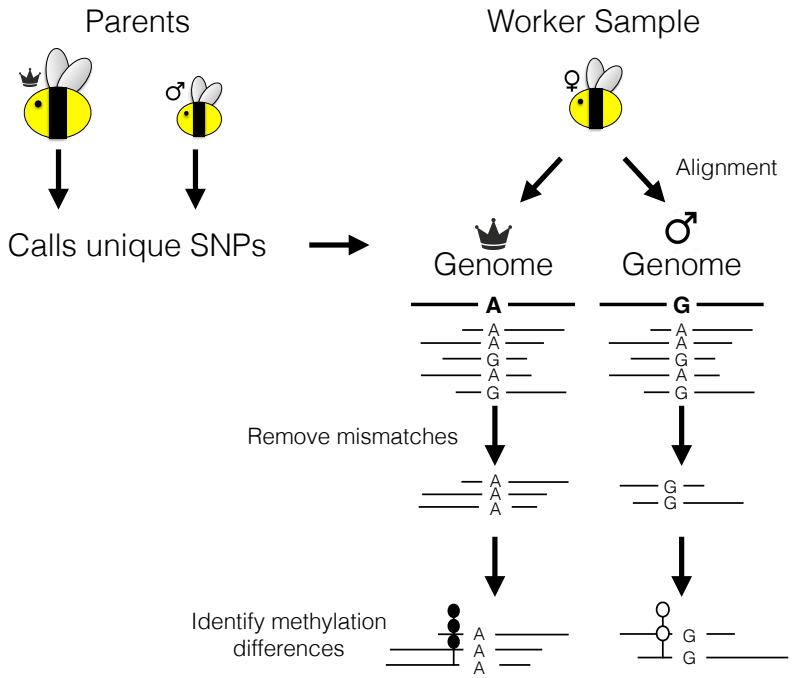


Figure 5.2: Overview schematic for identifying allelic methylation differences in the worker offspring. SNPs unique to either the mother or father are used to create phased reference genomes. The worker daughter sample is then aligned to both genomes and reads are filtered to keep only those with no bisulfite related mismatches. Methylation differences between the alleles can then be assessed and compared to the parental methylation levels of that gene.

5.3.5 Identification of parent-of-origin methylation

WGBS libraries of the pooled workers were aligned to their parent-specific phased genomes using Bismark v0.18.1 (Krueger and Andrews, 2011). The *–non_bs_mm* option

was implemented during alignment which reports the number of non-bisulfite related mismatches per read. Alignment files were then filtered to keep only reads with zero non-bisulfite related mismatches. This makes sure only reads matching the unique parental allele are kept per alignment (Fig. 5.2), giving a set of reads unique to each parental allele. Alignment files were then deduplicated using Bismark v0.18.1 (Krueger and Andrews, 2011), and sorted using samtools v.1.3.2 (Li *et al.*, 2009).

CpG sites per allelic read set were then filtered on a minimum coverage of 10 and coverage outliers (above 99.9th percentile) were removed, additionally only CpGs found in all allelic read sets were kept. The methylation status of each CpG was then determined, using the 'methylation status calling' (MSC) procedure, described in Cheng and Zhu (2014). CpG sites were then filtered to remove any site that did not return as methylated in at least one allelic read set.

A differential methylation analysis was then carried out between the allelic read sets (maternal alleles vs paternal alleles) using a logistic regression model implemented by methylKit (Akalin *et al.*, 2012) with Benjamini-Hochberg correction for multiple testing (Benjamini and Hochberg, 1995). CpGs were classed as showing parent-of-origin methylation if there was a minimum of 5% methylation difference between the allelic read sets and a q-value <0.05.

The general linear model (*glm*) applied in Chapter 4 to identify genes showing parent-of-origin expression is not appropriate for identifying parent-of-origin methylation. Expression data per SNP is count based and so a proportion of maternal/paternal expression can be generated per SNP per gene and the *glm* designed can be applied. However, methylation data is already proportional in nature, i.e. a single methylation site consists of the proportion of methylation reads and unmethylated reads and so these data cannot be modelled using this previous approach.

To identify the relationship between the methylation level of the alleles in the offspring and the methylation level of the genes in the parents the mean weighted methylation level of each gene was calculated using Equation. 5.1. The weighted methylation level per gene/allele was calculated for the workers, queens and males and then a mean was taken across each set. This gave a methylation level for each gene for queens /

males / maternal worker alleles and paternal worker alleles. The methylation difference between worker alleles was calculated as the paternal allelic methylation level minus the maternal allelic methylation level. The difference in methylation level between genes in queens and males was calculated as the male gene methylation level minus the queen gene methylation level. The parental methylation difference was then plotted against the worker allelic difference to identify genes which show high methylation in the parents and in the inherited parental allele, determining whether methylation level of a gene in the parent is maintained in the parental allele of the offspring.

5.3.6 Gene ontology enrichment

Gene ontology (GO) terms for *B. terrestris* were taken from a custom database made in Bebane *et al.* (2019). GO enrichment analysis was carried out using the hypergeometric test with Benjamini-Hochberg (Benjamini and Hochberg, 1995) multiple-testing correction, $q < 0.05$. GO terms from differentially methylated genes between queens and males and GO terms for genes identified as containing a differentially methylated CpG between alleles in workers were tested against a GO term database made from the GO terms associated with all methylated genes. Genes were determined as methylated if they had a mean weighted methylation level greater than the bisulfite conversion error rate of >0.05 in either queens, males or workers. REVIGO (Supek *et al.*, 2011) was used to generate GO descriptions from the GO ids.

5.3.7 Comparative analyses

Genes identified as showing parent-of-origin expression from Chapter 4 and genes which are differentially methylated between worker reproductive castes from Chapter 2 were checked for overlap with genes found here to contain a parent-of-origin methylated CpG using a hypergeometric test.

To identify trends between parent-of-origin expression and parent-of-origin methylation the allelic weighted methylation difference was determined as the male allelic methylation level - the queen allelic methylation level. The paternal expression proportion

was then plotted for each gene that shows some methylation difference between worker alleles.

All bioinformatic scripts used within this chapter can be found at: `https://doi.org/10.5281/zenodo.3235646`.

5.4 Results

5.4.1 DNA extraction and data quality

DNA extracted from whole head tissue of all queens, males and reproductive workers gave suitable quantities for sequencing (supplementary 5.0.1). DNA generally showed little degradation across samples, except for three of the four male samples (Fig. 5.3).

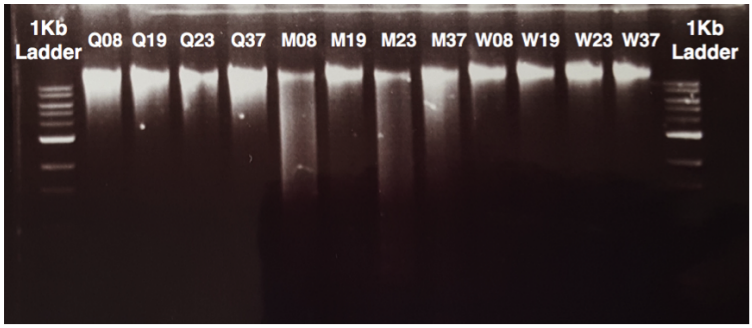
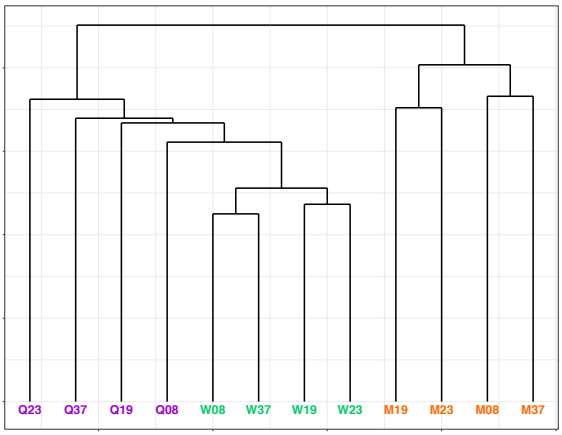


Figure 5.3: 2% agarose gel of DNA extracted from head tissue with 1Kb ladders in lanes 1 and 14. 'Q' refers to the queen samples, 'M' refers to the male samples and 'W' refers to the pooled worker samples, the corresponding numbers refer to the colony of origin. Some degradation can be seen in the samples: M08, M23 and M37.

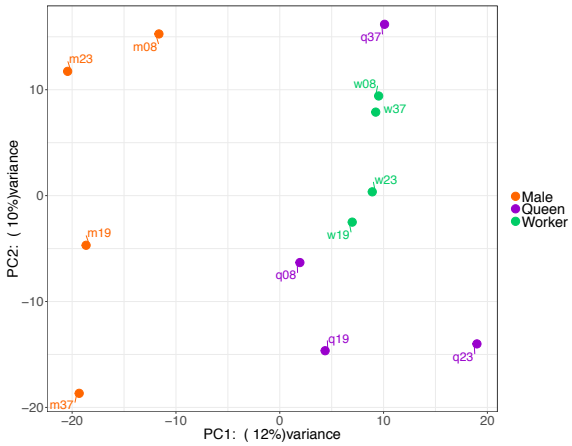
An average of 60.1% ± 3.0% (mean ± standard deviation) of the data received from BGI aligned uniquely to the reference genome, after removal of PCR duplicates the final genome coverage was 13.9X ± 1.6X (supplementary 5.0.2). The bisulfite conversion efficiency, determined by the lambda spike, was 99.5%. After correcting methylation levels for an error rate of 0.05% methylation was only detected in a CpG context with an average single-site level of 0.25% ± 0.05% (supplementary 5.0.3).

5.4.2 Differential methylation

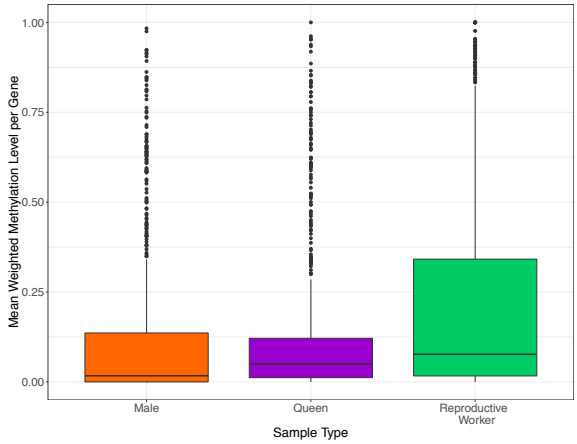
Bumblebee workers, queens and males show different CpG methylation profiles, with males clustering away from the two female castes (Fig. 5.4a and 5.4b). The levels of weighted methylation across all methylated genes differ significantly between sample type (Kruskal-Wallis test, chi-squared = 10011, df = 3, p <0.000, (Fig. 5.4c). The average weighted methylation per gene in males is 0.129 ± 0.222 (mean ± standard deviation), in queens is 0.139 ± 0.221 and in reproductive workers is 0.213 ± 0.267. Reproductive workers have significantly higher levels of CpG methylation per gene compared to males and queens (Dunn test with Benjamini-Hochberg correction, compared to males: Z = -10.33, q <0.000, compared to queens: Z = -5.36, q <0.000). Queens also have higher CpG methylation per gene compared to males (Dunn test with Benjamini-Hochberg correction, Z = -4.35, q <0.000).



(a) Dendogram



(b) PCA Plot



(c) Boxplot of Weighted Methylation per Gene

Figure 5.4: (a) Hierarchical cluster based on methylation correlation distances calculated using the 'ward' method, showing samples cluster by gender (total CpGs = 28,735,33). (b) PCA plot showing samples cluster primarily by gender but with much more spread in the queens and males (total CpGs = 28,735,33). (c) Boxplots showing the varying weighted methylation levels across genes which have >0 weighted methylation in all three castes, N = 2,663. Each boxplot shows the median along with the 25th and 75th percentile. The whiskers represent 1.5X the interquartile range. Outliers are represented as additional black points.

There were no differentially methylated CpG sites found between workers and males and between workers and queens. A total of 703 CpGs were differentially methylated between queens and males, of these 660 were found to be contained within a gene, with 412 unique genes showing differential methylation (supplementary 5.0.4). Of these 344 genes also had a weighted methylation difference of at least 10% between queens and males and were classed as differentially methylated genes (supplementary 5.0.5).

There were significantly more genes hypermethylated (i.e. with higher methylation) in queens compared to males (chi-squared goodness of fit; X-squared = 5.1279, df = 1, p = 0.023). With queens showing 193 hypermethylated genes and males showing 151 hypermethylated genes.

Enriched GO terms for the differentially methylated genes included a variety of biological processes (supplementary 5.0.5), specifically '*spermatogenesis*' (GO:0007283), '*dosage compensation by inactivation of X chromosome*' (GO:0009048) and '*chromosome organisation*' (GO:0051276) were enriched.

Enriched GO terms specifically associated with hypermethylated genes in males included mostly developmental processes (supplementary 5.0.7). Enriched GO terms specifically associated with hypermethylated genes in queens included mostly biosynthetic processes (supplementary 5.0.7).

5.4.3 Parent-of-origin methylation

SNPs were called from the parental methylation data, an average of 21,688 ± 9,143 (mean ± standard deviation) unique homozygous alternative SNPs were identified in the queen which were not present in the corresponding male sample and an average of 42,152 ± 4,000 unique SNPs were identified in the male sample which were not present in the corresponding queen sample (Fig. 5.5).

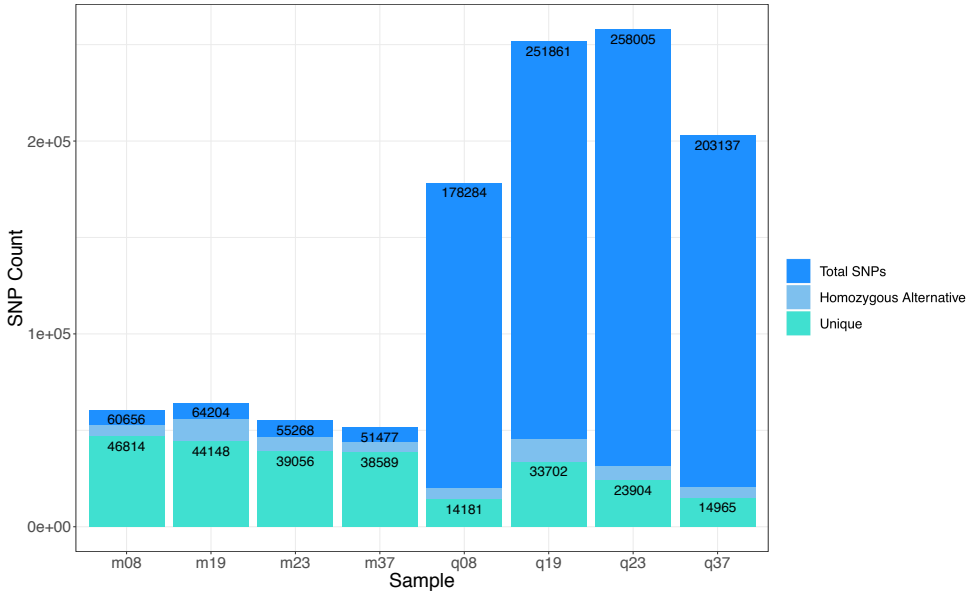


Figure 5.5: Component bar chart showing the total number of SNPs called per sample after quality filtering and, of those, the number which are unique per sample.

Alignment rates of the worker samples to their parentally phased genomes were slightly higher than to the standard reference genome, with similar alignment rates found between the father's (62.1% ± 1.9%) and mother's (62.0% ± 1.9%) phased genome. This increased coverage to 14.1X ± 0.4X (supplementary 5.0.8).

Of the allelic read sets (reads aligning to either the maternal or paternal genome) an average of 21.5% ± 0.6% were removed as they contained a non-bisulfite mismatch, this reduced the average coverage to 11.1X ± 0.4X. The average number of CpGs per allelic read set with coverage >10 was 3,788,483 ± 868,658. However, of these, only 434,717 CpGs were identified in every allelic read set. After calling the methylation status of each CpG in each allelic read set, using the MSC procedure, and filtering so only CpGs remained that were methylated in at least one allelic read set, only 6,157 CpGs were subjected to a differential methylation test between maternal/paternal alleles to identify parent-of-origin CpG methylation.

11 CpGs showed consistent parent-of-origin allele-specific methylation across all reciprocal crosses (q <0.05 and a minimum difference of 5%). Ten of these are located in genes and of those, 9 are located in exons, Table 5.1.

Table 5.1: Genes identified as showing parent-of-origin methylation. Allele refers to the hypermethylated allele.

Scaffold	**CpG**	**p-value**	**q-value**	**Methylation Difference (%)**	**Allele**	**Gene ID**	**Gene Name**	**Genomic Feature**
NC_015775.1	7967701	0.476	0.002	-6.39	queen	LOC100651896	eukaryotic translation initiation factor 3 subunit A	exon
NW_003565564.1	2211	0.234	0.002	-6.73	queen	LOC100643266	chromatin-remodeling complex ATPase chain Iswi	exon
NW_003565564.1	2302	0.432	0.002	5.74	male	LOC100643266	chromatin-remodeling complex ATPase chain Iswi	exon
NW_003565564.1	2372	0.337	0.002	-6.02	queen	LOC100643266	chromatin-remodeling complex ATPase chain Iswi	exon
NW_003565564.1	2375	0.401	0.002	-5.45	queen	LOC100643266	chromatin-remodeling complex ATPase chain Iswi	exon
NC_015779.1	2134019	0.396	0.002	-7.61	queen	LOC100650940	uncharacterized	exon
NC_015768.1	17499062	0.433	0.002	7.55	male	LOC100644967	small G protein signaling modulator 3 homolog	exon
NC_015764.1	9590490	0.497	0.002	6.00	male	LOC100644008	uncharacterized	exon
NC_015766.1	7785652	0.442	0.002	-6.98	queen	LOC100648553	protein kinase C	exon
NW_003565443.1	99114	0.364	0.002	-8.04	queen	LOC100645270	DENN domain-containing protein 5A	intron
NW_003565443.1	99114	0.364	0.002	-8.04	queen	LOC105666746	uncharacterized	intron
NW_003565435.1	579314	0.508	0.002	-5.46	queen	N/A	N/A	N/A

The genes identified as containing a CpG showing parent-of-origin methylation had various enriched GO terms including: *response to ecdysone* (GO:0037076) and *ecdysone receptor-mediated signaling pathway* (GO:0035076), supplementary 5.0.9.

The weighted methylation levels of each of the parental alleles within the worker were calculated along with the weighted methylation level of each gene within the parents. A linear model was fitted with the worker allelic methylation difference (male allele - queen allele) as the independent variable to test for the effect of parental methylation differences on allelic methylation levels in the offspring. There was no significant effect of parental methylation difference (male gene - queen gene) on worker allelic methylation difference ($F_{1,\,70} = 1.618$, p-value = 0.207). No significant correlation was found between parental methylation difference and worker allelic methylation difference (Fig. 5.6), a positive correlation of one would indicate methylation in the parental genes is maintained in the parental alleles in the offspring.

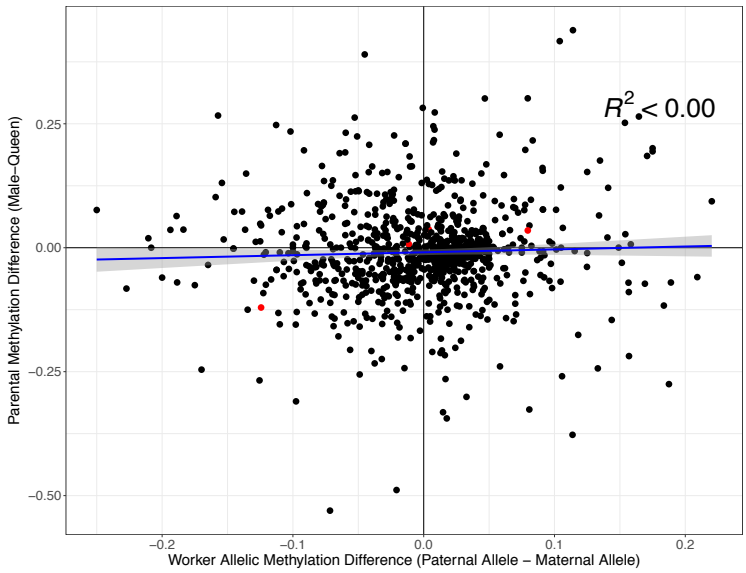


Figure 5.6: Scatter graph of genes which show a weighted methylation difference between worker alleles and the parental weighted methylation difference of each gene. Each point represents a single gene, N = 986. The red points show genes which also contain a significant differentially methylated CpG between alleles. The blue line shows a fitted linear regression with grey areas indicating 95% confidence intervals. Genes in the top right quadrant show higher methylation in the male inherited allele and higher methylation levels in the male gene compared to the queen gene. Genes in the bottom right quadrant show higher methylation in the male inherited allele and higher methylation levels in the queen gene compared to the male gene. Genes in the bottom left quadrant show higher methylation in the queen inherited allele and higher methylation levels in the queen gene compared to the male gene. Genes in the top left quadrant show higher methylation in the queen inherited allele and higher methylation levels in the male gene compared to the queen gene.

5.4.4 Relationship between parent-of-origin methylation and parent-of-origin expression

None of the genes containing a significant differentially methylated CpG between maternal / paternal alleles also show significant parent-of-origin expression from Chapter 4. A linear model was fitted with the worker allelic methylation difference as the independent variable to test for the effect of parent-of-origin expression. There was no significant effect of expression (paternal expression proportion) on worker allelic methylation difference ($F_{1,60} = 0.2828$, P-value = 0.596). No significant correlation was found between paternal expression proportion and worker allelic methylation difference (Fig.

5.7), a positive correlation of one would indicate higher paternal allelic methylation is linked to higher paternal expression.

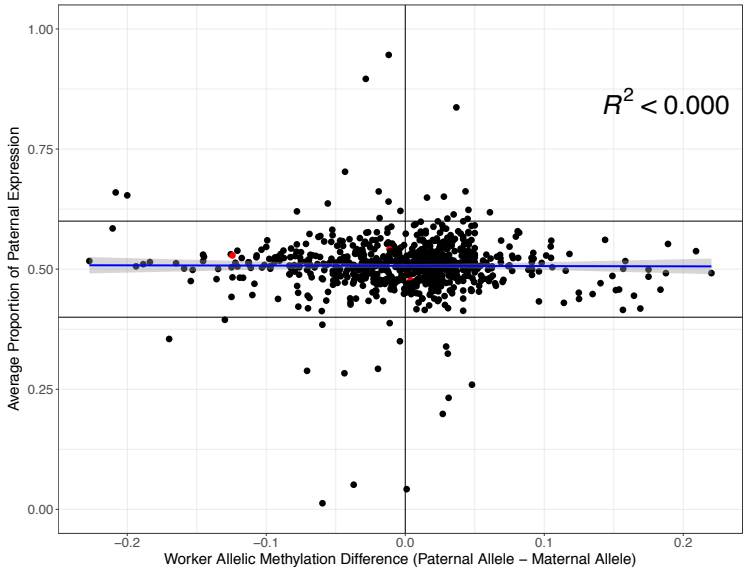


Figure 5.7: Scatter graph of genes showing a weighted methylation difference between worker alleles and the proportion of paternal expression for each gene from Chapter 4. Each point represents a single gene, N = 805. The red points show genes which also contain a significant differentially methylated CpG. The horizontal lines show the minimum proportion of expression required for calling a gene as showing parental-expression bias, i.e. >0.6 and <0.4. The blue line shows a fitted linear regression with grey areas indicating 95% confidence intervals. Genes in the top right quadrant show higher methylation in the male inherited allele and higher expression of the paternally inherited allele. Genes in the bottom right quadrant show higher methylation in the male inherited allele and higher expression of the maternally inherited allele. Genes in the bottom left quadrant would show higher methylation in the queen inherited allele and higher expression of the maternally inherited allele. Genes in the top left quadrant show higher methylation in the queen inherited allele and higher expression of the paternally inherited allele.

There was no significant overlap between genes containing a differentially methylated CpG between worker alleles and genes which are also differentially methylated between worker reproductive castes from Chapter 2 (hypergeometric test, p = 0.06). The only common gene was *small G protein signaling modulator 3 homolog* (LOC100644967) which shows paternal allele hypermethylation of a CpG and is also hypermethylated in reproductive workers compared to sterile workers but is not differentially expressed between worker castes. Additionally none of the genes identified here containing a parent-of-origin methylated CpG also show allele-specific methylation in a previous

data-set from Chapter 3.

5.5 Discussion

Using whole genome bisulfite sequencing I have identified specific CpGs showing consistent parent-of-origin methylation across two sets of reciprocal crosses. I have additionally identified methylation differences between queens and males and determined there is no relationship between the parental methylation of a gene and allele-specific methylation in reproductive worker offspring. Finally I found no allelic-methylation differences in genes previously shown to exhibit parent-of-origin expression. These results do not support the hypothesis that *cis*-acting DNA methylation is the imprinting mark for genes with parent-of-origin expression. It may be that *trans*-acting DNA methylation may interact with other epigenomic mechanisms, such as histone modifications, to produce parent-of-origin expression. It may also be that other molecular mechanisms, such as non-coding RNAs, play a role.

Eight genes have been identified containing at least one CpG site which exhibits parent-of-origin methylation. However, none of these eight genes also show parent-of-origin expression, as identified in Chapter 4. The genes containing a parent-of-origin methylated CpG had enriched GO terms relating to the ecdysone pathway. Ecdysone is a chemical involved in the ovary activation of reproductive workers (Geva *et al.*, 2005), and multiple genes involved in this pathway have been shown to exhibit allele-specific expression in a previous study using *B. terrestris* workers (Amarasinghe *et al.*, 2015). These findings suggest that if methylation plays any role in parent-of-origin expression, it is an indirect role. This is supported by the identification of a gene involved in chromatin remodelling, which contained CpGs with parent-of-origin methylation, all in exonic regions. Condensed chromatin, or heterochromatin, results in the silencing of genes and has been associated with imprinted genes in mammals (Voon *et al.*, 2015). It has also been shown that, in some species, methylation can influence ncRNAs, which proceed to silence genes in other regions of the chromosome (Barlow, 2011). If this process was occurring in *B. terrestris*, it would explain the lack of consistency between

allelic-methylation and allelic-expression.

The lack of consistency between genes showing parent-of-origin expression from Chapter 4 and parent-of-origin methylation may also be due to the use of independent reciprocal crosses and individuals. It has been previously shown that methylation can vary dramatically between biological replicates (colonies) of the same sub-species of *B. terrestris* (Chapter 2). It may therefore also be possible parent-of-origin methylation and expression may be linked but the genes affected are not conserved across the species. This idea does not support the kinship theory (Haig, 2000) of genomic imprinting, that predicts imprinted genes should be involved in the same functions across individuals within a species. Additionally the lack of overlap of genes with parent-of-origin methylation and differentially methylated genes between reproductive castes from Chapter 2 and lack of overlap with genes showing general allele-specific methylation from Chapter 3 also casts doubt on the kinship theories predictions for imprinted genes in bumblebees. However, these results do support the notion that methylation may offer a dynamic mechanism of plasticity, by being highly variable across colonies and between individuals, as discussed in Chapter 2.

Additionally it is worth noting the analyses done here do not take into account all *cis*-effects (the effect of genotype). Whilst *cis*-effects have been minimised in this study, by the stringent determination of parent-of-origin methylated CpGs (i.e. using individuals from all crosses as replicates within the logistic regression model, and additionally using crosses from closely related individuals), it is still possible *cis*-effects exist within the data. Previous research has found the sequence of an allele can determine the methylation status of a CpG, either by a substitution of a cytosine base with another base or by a long-distance method (Remnant *et al.*, 2016), such as chromatin modification or recruitment/expulsion of DNA binding proteins (Tycko, 2010). More specifically Wedd *et al.* (2016) found polymorphic differences in the *AmLAM* gene in *A. mellifera* were strongly correlated with the overall methylation level of the gene. Re-generation of these data using independent replicates of the reciprocal crosses used here, along with parental and offspring whole genome sequencing, to identify SNPs, would allow for a greater understanding of the role of genotype.

This work can also be improved by increasing the coverage obtained during sequencing. Previous research has suggested coverage as low as 12X can allow for allelic bias in the read sets (Remnant *et al.*, 2016), where one allele shows greater coverage than the other. The logistic regression model used here relies heavily on coverage, with the average coverage per base being approximately 11X. Whilst stringent filtering ensured minimum false positives, it is likely our data contains many false negatives owed to the lack of coverage per base. In order to obtain a more reliable picture of the relationship of parent-of-origin methylation and parent-of-origin gene expression, ideally, this experiment would be repeated using data from the same reciprocal crosses with sequencing carried out to a greater depth.

In order to identify the relationship between parent-of-origin methylation and parental methylation of a gene, methylation differences between queens and males were determined. As this is the first data set to examine methylation at base-pair resolution for *B. terrestris* queens and males, genome methylation patterns were assessed. Reproductive workers and queens show a similar CpG methylation pattern compared to males, this is also the case in some other social insects, such as the fire ant, *Solenopsis invicta* (Glastad *et al.*, 2014). However, this pattern is not uniform across social insects; Bonasio *et al.* (2012) found queens had less methylation compared to males and workers in two species of ant, *Camponotus floridanus* and *Harpegnathos saltator*. Additionally castes of the termite, *Zootermopsis nevadensis*, cluster together with gender nested within clusters, when whole genome methylation patterns are assessed (Glastad *et al.*, 2016). Finally the honeybee *A. mellifera* appears to show more genomic methylation in queens compared to workers (Lyko *et al.*, 2010), indicating social insects have varying methylation differences between castes.

Differentially methylated genes between queens and males were involved in a variety of processes including spermatogenesis, dosage compensation and chromosome organisation. This suggests methylation may play an active role in the generation of the male phenotype. Experimental work to alter methylation in specific genes/regions, by using the CRISPR-cas9 system, as described in Vojta *et al.* (2016), could aid better understanding of the role of methylation in haplodiploid systems. There were no differentially methylated sites between workers and queens/males, this is likely due to the

high level of relatedness between samples, which was taken into account as a covariate within the model. As mentioned previously high inter-colony variation in methylation exists in *B. terrestris* (Chapter 2). Methylation differences between castes and genders could be better assessed using samples designed specifically for this question.

The methylation differences identified between parents were not reflected in the parental alleles of the offspring. This indicates methylation may be wiped and re-established during development, as is seen in mammals (Messerschmidt *et al.*, 2014). Previous research using *A. mellifera* found extreme differences in methylation between eggs, sperm and males (Drewell *et al.*, 2014), with males showing less overall methylation compared to the gametes. Drewell *et al.* (2014) suggest these patterns indicate a series of gains and losses of methylation during development. This would account for the lack of consistency observed here between parental genes and offspring alleles. Future research investigating methylation dynamics throughout development, including adults and gametes is needed.

Overall this study is the first to identify consistent CpG sites showing parent-of-origin methylation in *B. terrestris*. I found no relationship between parent-of-origin methylation and parent-of-origin expression, this indicates methylation is not the imprinting mark driving parent-specific allelic expression. However, numerous limitations of this study may also have influenced these results, such as: *cis*-effects, epigenetic variation between colonies and low genome coverage. Nevertheless, this study has still provided a basis for future work into: the role of methylation in dosage compensation in males and investigations exploring the dynamic nature of methylation during development.

Chapter 6

Variation of DNA methylation in naturally occurring temporal populations of the water flea, *Daphnia magna*, to environmental stressors.

Hollie Marshall, Eamonn Mallon, Leda Mirbahai and Luisa Orsini.

6.1 Abstract

Species employ a variety of mechanisms in order to cope with environmental change, such as: migration, tolerance and adaptation in the form of phenotypic plasticity and/or genetic adaptation. The new field of adaptive epigenetics suggests DNA methylation can provide an additional layer of information upon which selection and adaptive evolution can act. Previous studies exploring the possibility of adaptive epigenetics have utilised a space-for-time design due to the long term nature of multi-generational studies. However, these types of studies are confounded by uncontrolled environmental differences. In this study I overcome these issues by utilising resurrection ecology to study epigenomic changes through evolutionary time. Individual *Daphnia magna* from four historical time periods of a lake with documented environmental change were resurrected. Whole genome bisulfite sequencing of the clonal offspring was carried out in order to identify temporal sub-population differences in DNA methylation. I have found that the temporal sub-populations which experienced eutrophication and high levels of pesticide exposure have less methylation compared to temporal sub-populations under less stressful conditions. I have additionally identified differentially methylated genes between temporal sub-populations. Some of these genes are involved in the production of males, which is a known stress response in this species. These results show DNA methylation can change at the population level through evolutionary time, possibly in response to environmental chance. These finding lays the groundwork for future experiments to determine how DNA methylation may provide an adaptive phenotype.

6.2 Introduction

Anthropogenic impacts on the natural environment are increasing in line with human population growth (Rosenzweig *et al.*, 2008). Of particular concern are freshwater ecosystems, due to the high biodiversity they harbour and their use as a freshwater resource for people. Severe eutrophication and pesticide exposure due to agricultural run-off and pollution are thought to be the next biggest threats to freshwater ecosystems, after destruction due to land-use change (Gopal, 2005). Species employ a variety of mechanisms in order to cope with environmental change, such as: migration, tolerance and adaptation in the form of phenotypic plasticity and/or genetic adaptation.

Adaptive epigenetics is a relatively new field of research (Verhoeven *et al.*, 2016). Epigenetic adaptations can come in the form of: short term temporary responses (epigenetic plasticity), long term permanent responses and heritable permanent responses (epigenetic adaptation) (Weyrich *et al.*, 2015). Research has focused on DNA methylation as it has been suggested that it can provide an additional layer of information upon which selection and adaptive evolution can act (Richards *et al.*, 2010).

In mammals, DNA methylation undergoes a cycle of erasure and reprogramming during development (Messerschmidt *et al.*, 2014). This has questioned the heritability of adaptive epigenetic marks. However, imprinted genes display heritable epigenetic marks which are specific to the parent from which they were inherited from (Barlow and Bartolomei, 2014). These marks escape the general reprogramming cycle, showing the possibility of heritable epigenetics. Additionally, some DNA methylation is caused by the underlying genetic code, these loci are known as epialleles (Meaburn *et al.*, 2010). Epialleles can also be considered heritable epigenetic marks as they are later re-established after developmental erasure.

It is thought changes in DNA methylation in response to the environment may contribute to later genetic adaptation. The presence of DNA methylation has been associated with an increased rate of C/T SNP substitutions which occur through spontaneous deamination (Flores *et al.*, 2013). Flores *et al.* (2013) propose environmentally induced DNA methylation, that is beneficial in terms of survival and reproduction, will remain

present in individuals when the environment is constant. This will lead to an increase in C/T mutations which may facilitate maintenance of the phenotype produced originally by the DNA methylation. Whilst this particular theory is difficult to test, given the long-term nature of the type of study needed, there are multiple other studies detailing short term plastic changes in DNA methylation in response to environmental stressors. These studies span a variety of species, for example: *Arabidopsis thaliana* (Dowen *et al.*, 2012), stickleback (Artemov *et al.*, 2017) and corals (Dixon *et al.*, 2018). Additionally, permanent epigenetic differences between locally adapted populations have also been identified in: *A. thaliana* (Kooke and Keurentjes, 2015), bats (Liu *et al.*, 2015), oak trees (Platt *et al.*, 2015), chickens (Zhang *et al.*, 2017) and stickleback (Heckwolf *et al.*, 2019).

Many of the studies mentioned above either focus on a single experimental generation or utilise the 'space-for-time' method, whereby spatially separated populations under different environmental conditions are used as a proxy to try to understand how species adapt to environmental change. However, it is difficult to take all naturally occurring variables into account with this method and so observing adaptation in a single population over time is preferable. Observing adaptation through time often involves long-term studies across multiple generations, of which there are few, see Grant and Grant (2002) as a rare example. Resurrection ecology provides a means of observing temporal adaptation within the same population by utilising dormant life stages such as seeds or eggs from dated sediment cores (Kerfoot *et al.*, 1999), avoiding the long-term nature of such studies.

The freshwater crustacean, *Daphnia magna*, produces a dormant life stage which can be hatched after hundreds of years of dormancy, with the oldest resurrected individual dated to around 700 years old (Frisch *et al.*, 2014). *D. magna* provide an ideal study system to explore the potential role of epigenetic adaptation in response to anthropogenic stressors. Firstly, *D. magna* reproduces clonally during its life cycle (Fig. 6.1) and it is easily cultured in the lab, allowing a particular 'genotype' (i.e. a line of genetically identical offspring from a resurrected individual) to be maintained. Additionally, each resurrected individual is sexually produced and so provides a unique genetic line (Fig. 6.1). Previous research has found resurrected individuals provide a genetically

representative sample of temporal populations (i.e. a population of individuals sampled from a given time period) obtained from dated sediment cores (Orsini *et al.*, 2016).

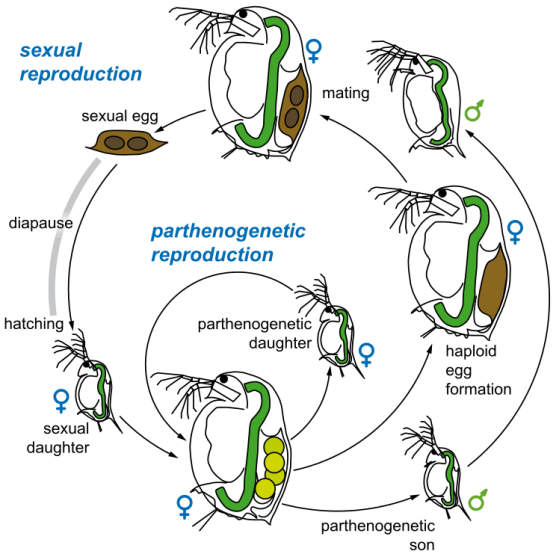


Figure 6.1: *Daphnia magna* life cycle. *Daphnia* exhibit cyclic parthenogenesis. Under stable environmental conditions females reproduce clonally. Under stressful conditions they produce males and sexual haploid eggs which are fertilised to produce a 'resting' life stage. These sexual eggs will eventually hatch into a genetically distinct female. Image credit: Dita Vizoso, source: http://scienceresourcebox.co.nz/blog/post&post_id=24.

D. magna also has a fully functional DNA methylation system, with methylation primarily found in gene bodies and associated with higher gene expression (Kvist *et al.*, 2018). Additionally, single-site CpG methylation levels have been reported between 0.7-1.7% (Kvist *et al.*, 2018; Hearn *et al.*, 2019), which is also similar to some insect species (Bewick *et al.*, 2016), such as *Bombus terrestris* which shows around 0.7% CpG methylation (Chapter 2).

The methylome of *D. magna* has been shown to be responsive to changes in environmental conditions. For example: sex-determination and sexual reproduction are the product of epigenetic changes caused by stressful conditions (Harris *et al.*, 2012), the presence of predators induces epigenetic changes which alter the phenotype (Asselman *et al.*, 2015) and calorie restriction alters genome-wide CpG methylation (Hearn *et al.*, 2019). Transgenerational effects on DNA methylation induced by chemical exposure (Vandegehuchte *et al.*, 2010) and salt stress (Jeremias *et al.*, 2018) have also been documented. Jeremias *et al.* (2018) found that changes in methylation after salt stress

persisted until the F3 generation, indicating adaptive epigenetic heritability. These studies show the potential of *D. magna* as a model organism for adaptive epigenetic research.

The study presented here will utilise whole-genome bisulfite sequencing and resurrection ecology to identify stable epigenetic changes in 40 genotypes from a temporal population of *D. magna*. Each temporal sub-population (i.e. a population of individuals sampled from a given time period from the same spatial population) was historically exposed to different anthropogenic stressors. I hypothesise differences in DNA methylation between sub-populations which historically experienced anthropogenic stress and those which did not experience anthropogenic stress. This is the first study, to my knowledge, to combine the power of resurrection ecology and the benefits of *D. magna* as a epigenetic model organism to identify potential adaptive epigenetic changes in DNA methylation, through time, in response to environmental stress in a natural population.

6.3 Methods

6.3.1 Sample origin

Individual genotypes used in this study originate from sediment cores taken from Lake Ring in Mid Jutland, Denmark (55°57'51.83" North, 9°35'46.87" East, Fig. 6.2).

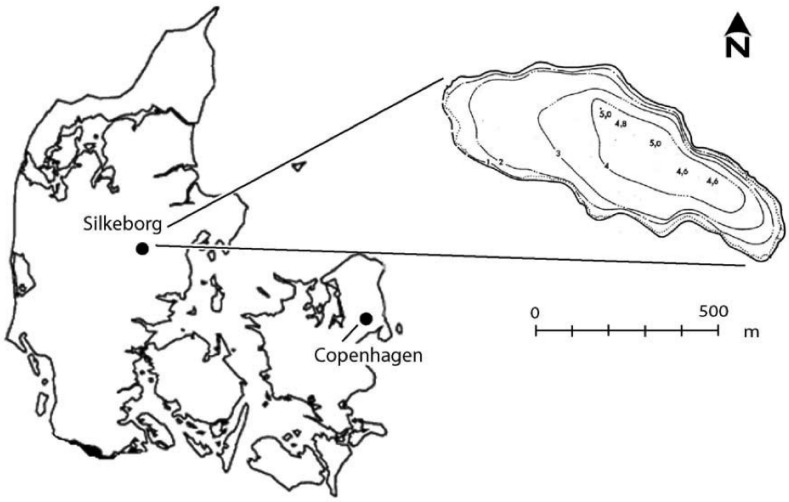


Figure 6.2: Image adapted from Berg *et al.* (1994) and Michels (2007), location of Lake Ring in Denmark and a depth profile in meters.

This lake has a well characterised history; in the 1950s eutrophication occurred due to sewage inflow from a nearby town, this was diverted towards the end of the 1970s (Berg *et al.*, 1994). During the 1980s agricultural land-use increased causing pesticide contamination within the lake (Cuenca Cambronero *et al.*, 2018). Additionally, an invertebrate predation study was carried out in the lake during 1989-1990 where the lake was stocked with white fish (Berg *et al.*, 1994) and was then observed to partially recover from eutrophic conditions post-1989 (Michels, 2007). These well documented periods allow the lake to be split into four distinct phases (Fig. 6.5).

Isolated ephippia (dormant sexual eggs) were hatched from each of the phases from radiometric-dated sediment cores taken from the lake, as described in Cuenca Cambronero *et al.* (2018). Previous research has generated whole genome and transcriptome sequencing for individuals from the all lake phases (unpublished, Orsini Lab, University of Birmingham). The same genotypes were selected for this study. They consist of 11 genotypes from the recovery phase, 10 from the pesticide phase, 9 from the eutrophic phase and 10 genotypes from the pristine phase (Fig. 6.3 and supplementary 6.0.0). Previous work has found that 10 genotypes are sufficient to provide a representative sample of the genetic diversity within a population of *D. magna* (Orsini *et al.*, 2016).

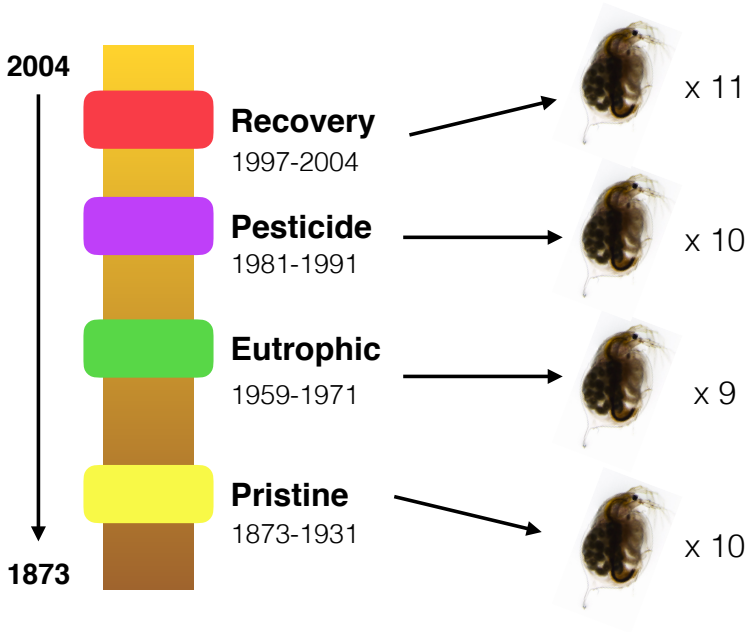


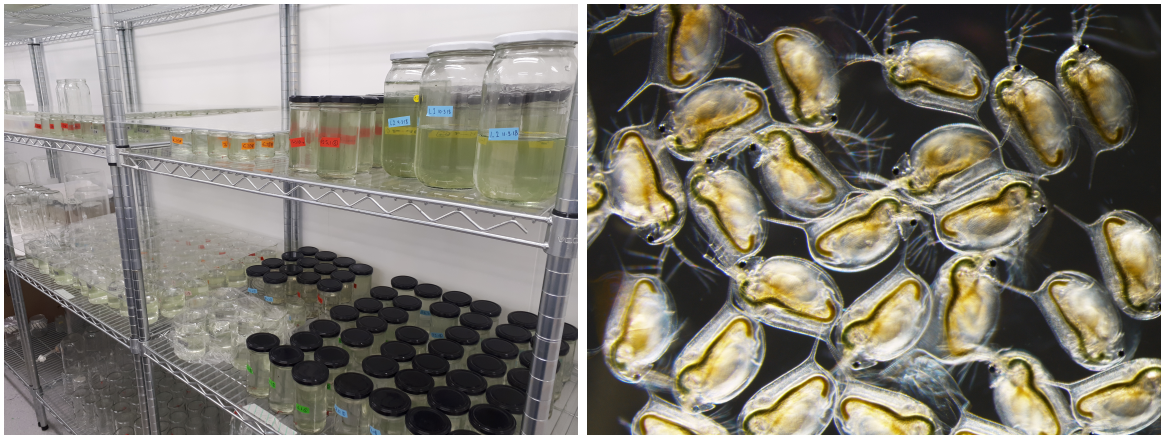
Figure 6.3: Nine to eleven *Daphnia magna* genotypes were selected as temporal subpopulation replicates from the four phases of Lake Ring. Dates show are exact date ranges for the specific genotypes selected, as dated from the sediment cores taken from Lake Ring.

6.3.2 *Daphnia* husbandry and sampling

The original resurrected genotypes were hatched in 2014, as described in Cuenca Cambronero *et al.* (2018). Clonal lines have since been maintained in lab conditions, consisting of: bore-hole water, 10°C, *ad libitum Chlorella vulgaris* algae (0.8mg C/L) and a light:dark regime of 16:8hrs. Individuals from all 40 genotypes were cultured in control conditions for a minimum of two generations prior to sample collection in order to reduce maternal effects from previous culturing in the 10°C stock room. Conditions consisted of: 20°C, *ad libitum Chlorella vulgaris* algae (0.8mg C/L) and a light:dark regime of 16:8hrs. Samples were maintained in high-hardness COMBO medium (Appendix D.1) through out the experiment and the medium was changed three times per week.

After two generations of acclimation, three to five individuals were placed in 250ml jars (Fig. 6.4a). Neonates <24hrs produced from the 3rd-10th brood were cultured

in a new 1L jar (Fig. 6.4a) until they reached four days old (pre-ovary development). The sex and developmental stage of each individual was determined using a dissecting microscope and groups of 20 individuals per genotype (Fig. 6.4b) were flash frozen in liquid nitrogen between 9am-1pm. A strict time period was applied to control for any potential circadian effects on methylation (Pegoraro *et al.*, 2016). A total of 100-200 individuals were used for DNA extraction in order to obtain enough DNA for sequencing. The number of individuals varies per sample as it was not possible to count the number of *Daphnia* per sample and stay within the 9am-1pm time window.



(a) (b)

Figure 6.4: (a) experimental set-up, black lidded jars are the 250ml jars containing the experimental *Daphnia magna* mothers and the white lidded jars are the 1L jars containing the juveniles. (b) a typical sample of healthy 4-day old juvenile female *D. magna*.

6.3.3 DNA extraction and sequencing

Tissue lysis was carried out using a 2025 Geno/Grinder® (SPEX SamplePrep). The Epicenter MasterPure™ Complete DNA and RNA Purification Kit was used following a modified protocol (Appendix D.2) to extract genomic DNA from 100-200 four day old females, per genotype. DNA quantity was assessed using a Qubit® fluorometer and quality was visualised using a 1% agarose gel. Sample preparation took place in the UoB Environmental Omics Sequencing Facility. All DNA samples were sent to BGI Tech Solution Co., Ltd.(Hong Kong) for bisulfite library preparation and sequencing. Directional bisulfite libraries were prepared by fragmenting genomic DNA to 100-300bp

by sonication, DNA-end repair was then carried out along with ligation of methylated sequencing adaptors. The ZYMO EZ DNA Methylation-Gold kit was used for bisulfite treatment with subsequent desaltation, size selection, PCR amplification and final size selection before sequencing. RNA-seq libraries were prepared by using magnetic beads with an Oligo (dT) to enrich for mRNA, the mRNA was then fragmented and cDNA was synthesised using random hexamer priming, size selection and PCR amplification were then carried out prior to sequencing. A 1% unmethylated lambda spike was included in each sample in order to assess later bisulfite conversion rates. Samples were then sequenced across six lanes (along with 30 other *Daphnia* samples from a related project) on an Illumina HiSeq 4000 using 150bp paired-end reads.

6.3.4 Differential methylation

Data quality were checked using fastqc v.0.11.5 (Andrews, 2010) and trimmed using CutAdapt v1.1 (Martin, 2011). Trimmed data were aligned to the reference assembly (daphmag2.4, GenBank accession: GCA_001632505.1) using Bismark v.0.16.1 (Krueger and Andrews, 2011) and bowtie2 v.2.2.6 (Langmead and Salzberg, 2012) with default parameters. Alignment output files were deduplicated using Bismark v.0.16.1 (Krueger and Andrews, 2011) and sorted and indexed using samtools v.1.3.2 (Li *et al.*, 2009).

The R package *methylKit* (Akalin *et al.*, 2012) was used to determine differentially methylated CpG sites between temporal populations. In order to determine how the methylation profile changes across time to given environmental stressors, sequential pair-wise comparisons were used. For each data pair, coverage outliers (above the 99.9th percentile) were removed along with bases covered by less than 10 reads. The methylation status of each CpG was then determined, using the 'methylation status calling' (MSC) procedure, as described in Cheng and Zhu (2014). CpG sites were then filtered to remove any site that did not return as methylated in at least one sample per comparison. A logistic regression model was then applied to the remaining CpG sites with Benjamini-Hochberg multiple testing correction (Benjamini and Hochberg, 1995). Sites were determined as differentially methylated between temporal populations if they exhibited a minimum difference of at least 10% and a q-value of <0.05.

Genes were determined as differentially methylated genes if they contained at least one differentially methylated CpG and had an overall weighted methylation difference of >10%. Weighted methylation level was determined as the total number of methylated cytosines (C) within a region (i), divided by the total coverage of a region (Equation 6.1), as described in Schultz *et al.* (2012).

$$\sum_{i=1}^{n} C_i / \sum_{i=1}^{n} C_i + T_i \tag{6.1}$$

6.3.5 Gene ontology enrichment

Gene ontology (GO) terms for *D. magna* were obtained from `http://arthropods.eugenes.org/EvidentialGene/daphnia/daphnia_magna/Genes/function/cddrps-dapmaevg14.gotab2`. GO enrichment analysis was carried out using the hypergeometric test with Benjamini-Hochberg (Benjamini and Hochberg, 1995) multiple-testing correction, q <0.05. GO terms associated with differentially methylated genes between temporal population were assessed for enrichment against GO terms associated with all methylated genes within the *D. magna* assembly. Genes were classed as methylated if they had a mean weighted methylation level greater than the bisulfite conversion error rate of >0.05 in at least one temporal population. REVIGO was used for GO term visualisation (Supek *et al.*, 2011).

All bioinformatic scripts used within this chapter can be found at: `https://doi.org/10.5281/zenodo.3235644`.

6.4 Results

6.4.1 DNA extraction

DNA extracted from 100-200 four-day old *D. magna* gave a suitable quantity for whole genome bisulfite sequencing (supplementary 6.0.1). All DNA samples showed some level

of degradation. However, they all also had a band >10,000bp and so met the minimum requirements for sequencing.

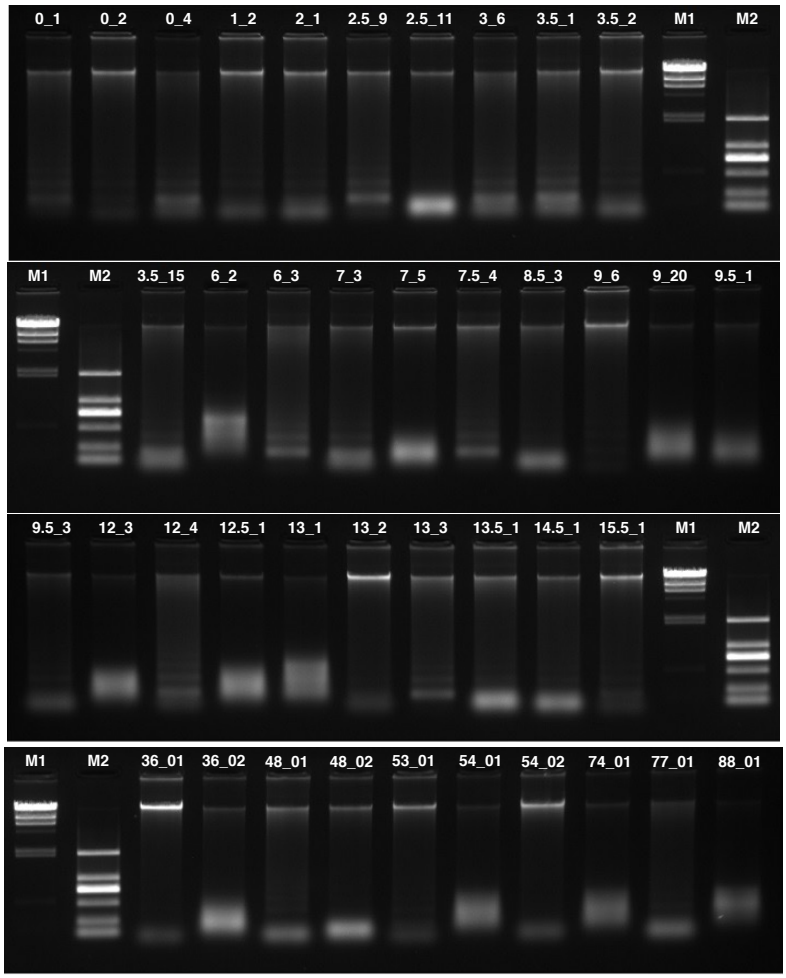


Figure 6.5: 1% agarose gel of all extracted *Daphnia magna* samples with ladders M1 and M2. Each sample label refers to the unique genotype.

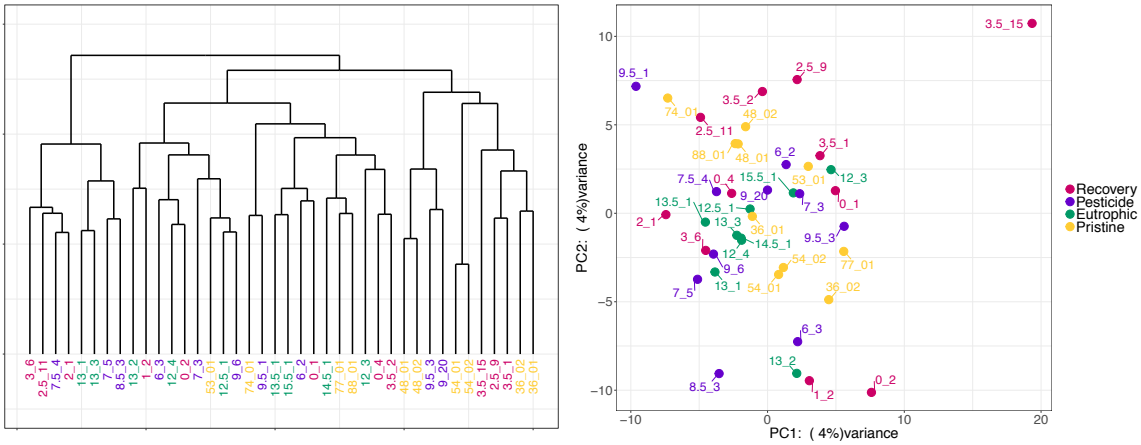
6.4.2 Data quality

The average alignment rate to the daphmag2.4 reference genome was 48.1% ± 2.67% (mean ± standard deviation), which corresponds to 8,715,797 ± 1,301,722 uniquely mapped reads. The average PCR duplication rate was 25.87% ± 2.02%. After removal of PCR duplicates the final coverage was 12.9X ± 1.8X (supplementary 6.0.2). From alignment to the lambda genome, the bisulfite conversion efficiency was determined as 99.6% ± 0.14%. Using this error rate methylation was only identified in a CpG

context, with an average single-site methylation level of 0.5% ± 0.11% across all samples (supplementary 6.0.2).

6.4.3 Genome-wide methylation differences between temporal temporal populations

Temporal populations do not cluster when CpG methylation is plotted (Fig. 6.6a). However, a PCA plot using the same data shows the genotype; 3.5_15, clusters away from all other samples (Fig. 6.6b). The single-site methylation level for this genotype is also more than double the mean of all samples, 1.1% compared to 0.5% respectively (supplementary 6.0.2).



(a) (b)

Figure 6.6: (a) Hierarchical cluster based on methylation correlation distances of all CpG sites methylated in at least one *Daphnia magna* sample (N = 3,938), calculated using the 'ward' method. (b) PCA plot generated using all CpG sites methylated in at least one sample.

There is a significant difference in the weighted methylation level of methylated genes across temporal populations (Kruskal-Wallis: chi-squared = 38036, df = 2, p <0.000, Fig. 6.7). The eutrophic and pesticide populations have a lower weighted methylation level across methylated genes compared to the pristine and the recovery populations (Table 6.1). However, there is no difference between the recovery and the pristine population, or between the pesticide and eutrophic population (Table 6.1).

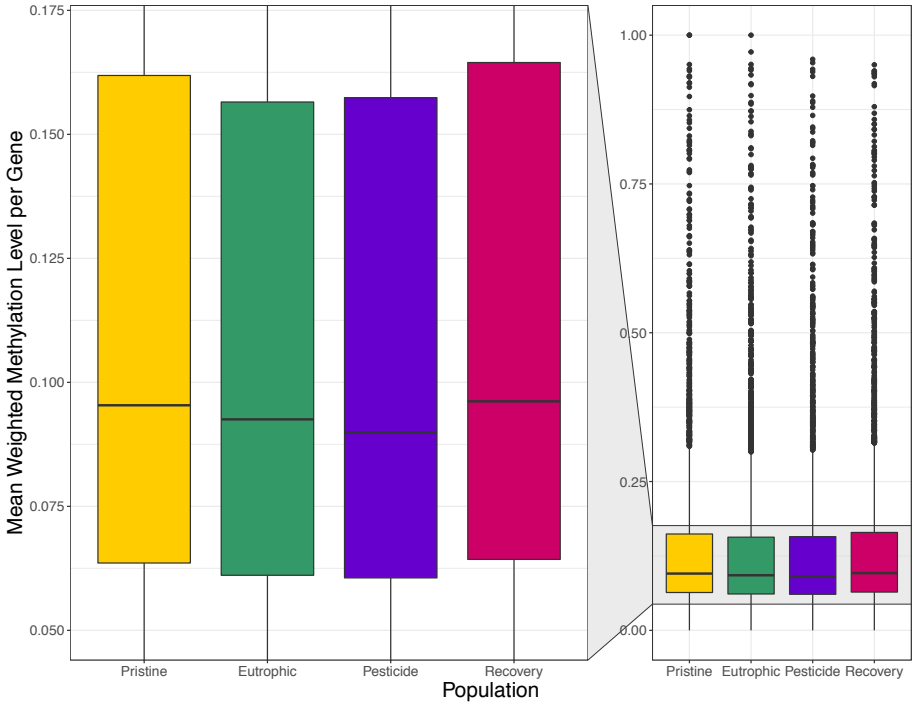


Figure 6.7: Right: boxplot showing the weighted methylation level of methylated genes (N= 3,563) for all temporal sub-populations of *Daphnia magna*. Each boxplot shows the median along with the 25th and 75th percentile. The whiskers represent 1.5X the interquartile range. Outliers are represented as additional black points. Left: an enlarged view of the interquartile range.

Table 6.1: Dunn's test post-hoc comparisons of weighted methylation level across all methylated genes between populations. P-values have been adjusted for multiple testing using the Benjamini-Hochberg method (Benjamini and Hochberg, 1995). * indicates a significant p-value <0.05.

Comparison	**Z**	**Adjusted p-value**
eutrophic - pesticide	0.9495285	0.411
eutrophic - pristine	-2.1803658	0.043*
pesticide - pristine	-3.1296273	0.005*
eutrophic - recovery	-3.0935671	0.003*
pesticide - recovery	-4.0430289	0.000*
pristine - recovery	-0.9124847	0.362

6.4.4 Differentially methylated genes between populations

The majority of differentially methylated CpGs between populations were located within a gene (Table 6.2, supplementary 6.0.3 - 6.0.5). Genes containing at least one

differentially methylated CpG were filtered to provide a list of differentially methylated genes which also have a weighted methylation difference of >10% (Table 6.2, supplementary 6.0.6 - 6.0.8). Only sequential pair-wise comparisons were carried out to identify DNA methylation differences through time. Future research could pose new hypotheses based on specific environmental differences between sub-populations which would then require other sub-population comparisons.

Table 6.2: Table showing the number of CpGs tested for differential methylation between populations after filtering on coverage and to ensure each CpG is methylated in at least one sample. The number of differentially methylated genes between populations and the number found within a gene and outside of a gene are also shown. The filtered genes column refers to the number of genes with at least one differentially methylated CpG and a weighted methylation difference >10%.

Comparison	**CpGs tested**	**Differentially methylated CpGs**	**Located within a gene**	**Located outside of a gene**	**Filtered genes**
Pristine vs Eutrophic	1,970	194	164	30	79
Eutrophic vs Pesticide	1,970	191	160	31	71
Pesticide vs Recovery	2,612	299	268	31	115

The pristine population has significantly more hypermethylated genes (i.e. genes with higher methylation) compared to the eutrophic population, 55 and 24 respectively (Chi-squared goodness of fit: X-squared = 12.165, df = 1, p <0.000). The pesticide population also has more hypermethylated genes compared to the eutrophic population, 48 and 23 respectively (Chi-squared goodness of fit: X-squared = 8.8028, df = 1, p = 0.003). Finally, the recovery population has more hypermethylated genes compared to the pesticide population, 75 and 40 respectively (Chi-squared goodness of fit: X-squared = 10.652, df = 1, p = 0.001).

3,563 genes had a weighted methylation level greater than the bisulfite conversion error rate of 0.05%. Of these, 2,561 had annotated gene ontology terms. There were only 26 genes from the 76 differentially methylated genes between the pristine and eutrophic populations that had annotated GO terms. Significantly enriched GO terms for these genes compared to all methylated genes included a variety of terms (supplementary 6.0.9), such as *oogenesis* (GO:0048477) and *mRNA 3'-end processing* (GO:0031124).

Of the 71 differentially methylated genes found between the eutrophic and the pesti-

cide population, 26 had annotated GO terms. As above, enriched GO terms included a variety of biological processes (supplementary 6.1.0), such as *oocyte development* (GO:0048599) and *stem cell differentiation* (GO:0048863).

There were slightly more differentially methylated genes between the pesticide and the recovery population, that were annotated with gene ontology terms, 40/115. These were also diverse but were significantly enriched for processes relating to DNA repair and protein modifications (supplementary 6.1.1), including *histone H2A K63-linked deubiquitination* (GO:0070537).

6.4.5 Similarity between differentially methylated genes

There are 205 unique genes differentially methylated across temporal populations. Almost half of these are unique to the differentially methylated genes found between the pesticide and the recovery population (Fig. 6.8). There is a significant overlap of differentially methylated genes between the eutrophic/pesticide comparison and the pristine/eutrophic comparison (hypergeometric test, $p < 0.000$, Fig. 6.8, supplementary 6.1.2). Within these overlapping genes 21/36 are hypomethylated in the eutrophic population compared to both the pristine and the pesticide populations, 11 are hypermethylated in the eutrophic population compared both to the pristine and the pesticide populations and four are variable.

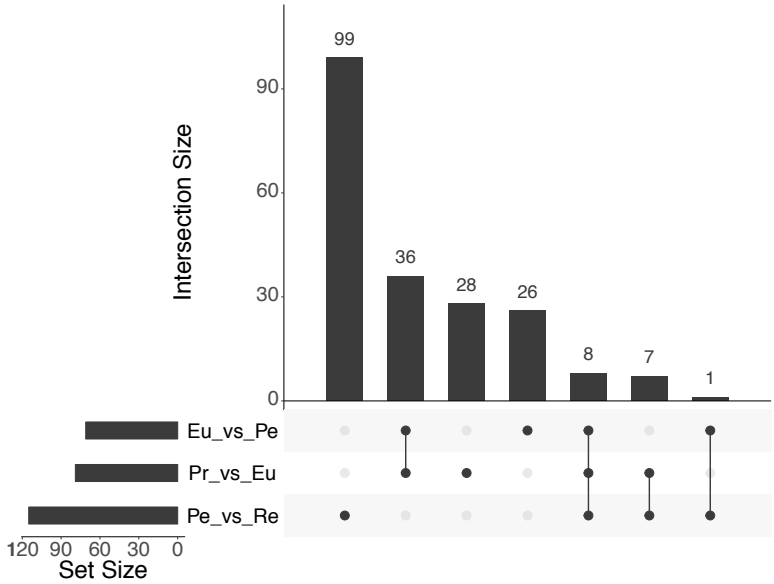


Figure 6.8: UpSet plot showing the number of common differentially methylated genes between *Daphnia magna* sub-population comparisons. Eu = eutrophic, Pe = pesticide, Pr = pristine and Re = recovery. The set size indicates the number of genes in each category. The intersection size shows how many genes the corresponding lists, represented by the jointed dots in the lower panel, have in common. A single dot in the lower panel refers to the number of genes unique to each list.

There are eight genes which are differentially methylated in every comparison across temporal populations (Fig. 6.8, supplementary 6.1.2). There is no apparent trend in the methylation changes for these genes across evolutionary time (Fig. 6.9). Additionally, these genes have some GO terms associated with the generation of males (Fig. 6.10).

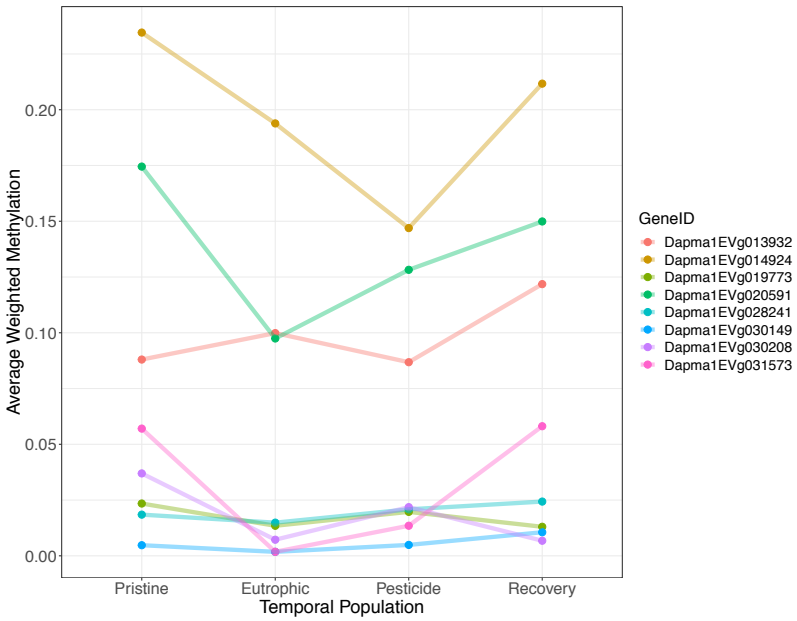


Figure 6.9: The average weighted methylation for each temporal sub-population of *Daphnia magna* for the eight genes which are differentially methylated in every comparison.

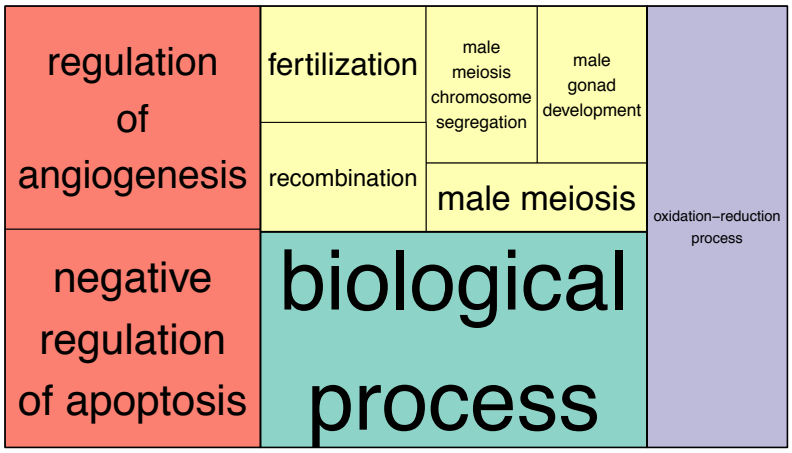


Figure 6.10: Treemap showing GO terms associated with the eight genes which are common amongst all differential methylation comparisons between each *Daphnia magna* sub-popualtion comparison. Each rectangle represents a cluster of related terms, with linked clusters indicated by colour. The size of the rectangle represents uniqueness within each cluster.

6.5 Discussion

This study is the first to identify stable methylation changes in naturally occurring temporal populations of *D. magna*. Using whole genome bisulfite sequencing I have found temporal populations are generally homogeneous in terms of their CpG methylation profiles. However, populations previously exposed to anthropogenic stressors have lower methylation levels in methylated genes compared to unexposed populations. I have also identified differentially methylated genes between temporal populations and found genes which exhibit changes in methylation over evolutionary time.

The single-site methylation level identified here is slightly lower than previously reported for this species, 0.5% compared to 0.7-1.7% (Jeremias *et al.*, 2018; Kvist *et al.*, 2018; Hearn *et al.*, 2019). However, these previous studies have all used a single lab-standard genotype. Here, all sample levels range from 0.4-0.6% except for the genotype; 3.5_15 (from the recovery population) which has a single-site methylation level of 1.1% and clusters away from all other samples in a PCA analysis. This particular genotype was also observed to have much larger broods throughout the experiment, although no numerical data were collected. Previous research using *D. magna* has also identified different phenotypic responses to chemical exposure in five different standard lab genotypes (Baird *et al.*, 1991). This new finding of large methylation differences amongst individuals, along with previous work showing different responses to stressors across genotypes, confirms the importance of using multiple genotypes within an experiment in order to draw population/species level conclusions.

When the methylation level of only methylated genes is assessed, the eutrophic and pesticide populations have lower methylation levels compared to the pristine and recovery populations. Some previous work has found no difference in global methylation levels when the same genotype is exposed to environmental stress (Jeremias *et al.*, 2018; Hearn *et al.*, 2019). However, Vandegehuchte *et al.* (2009) found a decrease in global methylation in *D. magna* after zinc exposure which persisted for one additional generation. As these individuals were maintained in control conditions, the differences in methylation levels observed are likely due to inherited methylation differences, rather

than as a response to the culturing environment. However, it is worth noting that populations/genotypes may respond differently to control conditions (Baird *et al.*, 1991). The conditions used here are likely to be more similar to those experienced by the pristine population, and novel to the other temporal populations. Whilst the clonal lines used in this study have been maintained for many generations within the lab, future work could attempt to replicate the natural environment experienced by each population to examine if the methylome responds differently to historical conditions compared to control culturing conditions.

As well as a difference in the methylation level of methylated genes, there are numerous differentially methylated genes between temporal populations. Differentially methylated genes between the pristine and eutrophic population and between the eutrophic and pesticide population are enriched for GO terms related to reproduction, amongst other terms. It has been well documented that exposure to environmental stressors in *D. magna* affects both fecundity and reproductive timing (e.g. Brown and Yan, 2015; Blinova *et al.*, 2017; Saebelfeld *et al.*, 2017; Sarapultseva *et al.*, 2019). Specifically, Cuenca Cambronero *et al.* (2018) identified fitness responses to environmental stressors, with the same genotypes used here, from the: recovery, pesticide and eutrophic phases. They found temperature and food availability affected fecundity in all three populations and exposure to the pesticide, Carbaryl, caused higher fecundity specifically in the eutrophic population. The identification of potentially permanent methylation changes related to reproduction in *D. magna*, suggests historical exposure to anthropogenic stressors may affect subsequent generations, even after the removal of the stressor. Experimental manipulation of DNA methylation in the eutrophic population, for example via new methods capitalising of the CRISPR/cas system (Vojta *et al.*, 2016), could help to elucidate the relationship between methylation, reproduction and environmental stressors.

The differentially methylated genes identified between the pesticide and recovery population were enriched for multiple GO terms, including GO terms related to histone modifications. DNA methylation has previously been found to signal the recruitment of histone modifications in other species, these modifications can silence genes within a whole genomic region via heterochromatin formation (Barlow, 2011). As DNA methy-

lation is so low in *D. magna*, this epigenetic pathway may provide a mechanism by which DNA methylation can alter the gene expression of multiple genes in response to environmental change. The identification of open chromatin regions via ATAC-seq (Buenrostro *et al.*, 2015) would allow the determination of associations between heterochromatin and DNA methylation.

Whilst enriched GO terms for differentially methylated genes were identified, not all genes within the current daphmag2.4 genome annotation have GO terms assigned. A re-analysis of this data in light of further functional annotation will provide more insight into the role of the differentially methylated genes between temporal populations.

There is a significant overlap in the differentially methylated genes between the eutrophic population and the pristine/pesticide population. The majority of these genes are hypomethylated in the eutrophic population in both comparisons. Previous work has identified large changes in population genetic structure in a population of *Daphnia pulicaria*, in response to historical eutrophication (Frisch *et al.*, 2014). Other work, using the same genotypes as in this study, also found significant differences in the neutral genetic structure between the eutrophic, pesticide and recovery populations (Orsini *et al.*, 2016). This may indicate *D. magna*, in this population, may be using a combination of genetic adaptation and potentially changes in DNA methylation as a means of altering gene expression to cope with environmental stressors. Previous work has associated hypomethylated CpGs with down-regulation of differentially expressed genes, when two genotypes were subjected to various stressors (Kvist *et al.*, 2018). The transcriptomes of the genotypes used here have been generated in a previous study (unpublished, Orsini Lab, University of Birmingham). The identification of the expression patterns exhibited by the hypomethylated genes in the eutrophic population compared to the pristine/pesticide population would elucidate the effect of methylation on the phenotype in this population over time.

Finally, there were eight genes found to be differentially methylated across temporal populations. Whilst there is no apparent trend in the methylation of these genes over time, they are enriched for processes related to sexual reproduction and the creation of males. *Daphnia* reproduce sexually when environmental conditions become

unfavourable (Hebert, 1978). Epigenetic mechanisms, induced by environmental signals, are thought to be the trigger for a change in gene expression of the *doublesex* gene, which leads to male production (LeBlanc and Medlock, 2015). Functional annotation and experimental validation are required to determine if one/some of the genes identified here may play a role in this pathway.

Overall this study has identified methylation differences between temporal populations of *D. magna* which were exposed to different historical conditions. Differentially methylated genes are involved in fitness related traits such as reproduction and the production of males. These differences suggest environmentally induced epigenetic changes, as a consequence of anthropogenic impact, may be heritable in this species, either in the form of epialleles or via direct heritability. Additionally, the varying levels of methylation across individual genotypes highlights the importance of using multiple clonal lines in future studies. Finally, this study lays the groundwork for future experimental validation of the role of DNA methylation in adaptation in this species.

Chapter 7

Overall discussion

7.1 Summary of results and major findings

7.1.1 Methylation and caste determination in *Bombus terrestris*

In Chapter 2 whole genome bisulfite sequencing and RNA-seq from reproductive and sterile *B. terrestris* workers were used to investigate the role of DNA methylation in reproductive caste determination. In order to achieve this I characterised caste specific *B. terrestris* methylomes for the first time. I found they are similar to other holometabolous insects with more highly methylated genes showing higher levels of expression and lower levels of methylation being associated with differentially expressed genes. I found no methylation differences on a genome-wide scale between reproductive castes. However, 111 genes were differentially methylated. These were involved in a variety of functions including reproductive related processes. I found no relationship between genes that are differentially expressed, or contain differential exon usage between castes with those that show differential methylation between castes. Finally I also found no common putative orthologous genes differentially methylated between *B. terrestris* and *A. mellifera* reproductive castes.

This Chapter provides the first insights into the nature of a bumblebee caste-specific methylome as well as its interaction with gene expression and caste-specific alternative splicing, providing greater understanding of the role of methylation in phenotypic plasticity within social bee species. Specifically, DNA methylation does not appear to directly mediate worker reproductive behaviour via changes in gene expression in

B. terrestris. However, given the methylation differences in reproductive genes it may still have an elusive role in reproductive behaviour or be a product of reproductive development.

7.1.2 Genomic imprinting in *Bombus terrestris*

Utilising the data generated in Chapter 2, in Chapter 3 I have identified genome wide allele-specific expression and allele-specific methylation. The majority of genes displaying allele-specific expression are common between reproductive castes and the proportion of allele-specific expression generally varies between colonies. This study has also identified allele-specific methylation differences between reproductive castes and found the majority of allelic-methylation events are located within genes. However, there is no significant overlap of genes showing allele-specific expression and allele-specific methylation. Although, genes with common allele-specific methylation between castes show a higher proportion of allelic-expression bias compared to allelically methylated genes unique to either reproductive or sterile workers.

This Chapter is the first to identify differences in allele-specific expression and allele-specific DNA methylation between reproductive worker castes of *B. terrestris*. There is no significant association between alleleically expressed and alleleically methylated genes indicating *cis*-acting DNA methylation may only play a role in allele-specific expression in a small number of cases. Due to the high amount of allele-specific DNA methylation it may serve to alter gene expression in *trans* and/or by interacting with other epigenetic marks such as histone modifications.

Chapter 4 used parental genome sequencing and offspring RNA-seq to identify genes showing parent-of-origin expression in *B. terrestris*. I predicted higher matrigenic expression bias in queen-less workers, in genes related to reproductive functions, following the predictions of Haig's kinship theory (Queller, 2003; Haig, 2000). There was no difference in the number of genes showing maternal or paternal expression bias in either reproductive or sterile workers. However, genes showing the highest proportion of expression bias were all maternally expressed in both castes. Additionally, reproductive related GO terms were enriched in both maternally and paternally expressed genes

along with multiple other biological processes. Maternally expressed genes also showed significant overlap with differentially expressed genes between reproductive and sterile workers in head tissue. However, there was no significant overlap between genes identified as potentially imprinted in *B. terrestris* and those identified from previous research in *A. mellifera.*

The work from Chapter 4 is the first to identify parent-of-origin expression in *B. terrestris*. Higher maternal expression in queen-less workers is consistent with the predictions of the kinship theory. Additionally, some genes found to show parent-of-origin expression are involved in reproductive related processes, which is also consistent with the kinship theory. However, give the lack of association between genes with parent-of-origin expression and differential expression between castes, potentially-imprinted genes may have additional functions beyond those predicted by the kinship theory. These functions may include adaptation via the regulation of gene expression. However, this hypothesis requires further study.

After the identification allele-specific methylation in Chapter 3 and parent-of-origin expression in Chapter 4, Chapter 5 identified a small number of CpGs which show parent-of-origin allele-specific methylation. In this chapter I have additionally identified differentially methylated genes between queens and males which are enriched for GO terms related to spermatogenesis and chromosome organisation. I have also determined there is no strict relationship between the parental methylation of a gene and allele-specific methylation in reproductive worker offspring. Finally I found no allelic-methylation differences in genes previously shown to exhibit parent-of-origin expression.

To my knowledge, Chapter 5 provides the first evidence for gene-level parent-of-origin DNA methylation in any insect. Due to the lack of association between parent-of-origin DNA methylation and parent-of-origin expression it is clear *cis*-acting DNA methylation is not an imprinting mark in *B. terrestris*. However, as is the case in some imprinted mammalian genes, DNA methylation may be acting in *trans* by altering chromatin accessibility via additional epigenetic marks.

7.1.3 Adaptive methylation in *Daphnia magna*

The final chapter of this thesis, Chapter 6, is the first study to identify stable methylation changes in naturally occurring temporal populations of *D. magna*. Using whole genome bisulfite sequencing I have found temporal populations are generally homogeneous in terms of their CpG methylation profiles. However, populations previously exposed to anthropogenic stressors have lower methylation levels in methylated genes compared to unexposed populations. I have also identified differentially methylated genes between temporal populations and found genes which exhibit changes in methylation over evolutionary time. A small subset of genes which change between each temporal population also have GO terms related to the production of males.

It has been hypothesised DNA methylation may provide an additional layer of information for selection to act upon. The results of this study support this idea. Primarily, the identification of differentially methylated genes involved in male production (a stress response) which correspond to changes in environmental conditions. The results from this Chapter provide the groundwork for future adaptive epigenetic work in *Daphnia magna*.

7.2 Impact on ecological epigenetics as a field

Whilst each results chapter within this thesis has specific implications for the related research field, as detailed in each individual discussion, the overarching discoveries of this work have wider implications for the field of ecological epigenetics.

The overall aim of this thesis was to identify potential roles of DNA methylation in two arthropod species. Given the variety of methylation profiles observed across arthropods, it is likely DNA methylation serves different purposes between species (Thomas *et al.*, 2018). The differences in DNA methylation between reproductive castes of *B. terrestris* suggests a potential role for DNA methylation in caste determination in this species. The influence of DNA methylation on imprinted genes in *B. terrestris* remains unclear. Additionally, differences in DNA methylation over evolutionary time in a sin-

gle population of *D. magna* have been documented, hinting to the adaptive potential of DNA methylation.

It has been suggested DNA methylation plays a role in maintaining the expression of housekeeping genes in arthropods (Gatzmann *et al.*, 2018; Provataris *et al.*, 2018). Sarda *et al.* (2012) found high sequence conservation in highly methylated genes between various invertebrate species. The presence of DNA methylation in highly conserved coding regions in arthropods is in conflict with the high rate of cytosine-thymine mutations generated by DNA methylation through spontaneous deanimation. It may be that the benefits of transcriptional stability in housekeeping genes outweigh the costs of a higher cytosine-thymine mutation rate. Alternatively, Park *et al.* (2011) found genes with higher DNA methylation in *Nasonia* species have lower overall mutation rates than those with less DNA methylation, suggesting DNA methylation may serve to protect the sequence from non-CpG mutations.

Whilst the highly methylated genes identified in *B. terrestris* in Chapter 2 also show high expression levels, genes with varying levels of methylation in both *B. terrestris* and *D. magna* have been found to be enriched for GO terms related to a variety of processes throughout this thesis. Dixon *et al.* (2018) believe gene-body methylation may be involved in balancing the expression levels of housekeeping genes with more plastic environmentally-responsive genes, suggesting variable roles for DNA methylation. In mammals, DNA methylation in different genomic contexts has different functions, and even within the same context may serve to: repress or up-regulate transcription, provide genomic stability or interact with other epigenetic modifications (Gutierrez-Arcelus *et al.*, 2013). Even though methylation levels are exceptionally low in some arthropod species, such as those studied here, the focus should not be on classifying a single function for DNA methylation in these species, such as the stability of housekeeping genes. Instead we should consider multiple context-dependent functions of DNA methylation.

This is also true for the function of imprinted genes, whilst parent-of-origin gene expression was identified for the first time in *B. terrestris* in this thesis, in a manner predicted by the kinship theory (Queller, 2003), multiple gene functions arose within the GO enrichment analysis. Imprinted genes currently characterised in mammals are

mostly involved in growth and behavioural traits, also supporting the kinship theory (Haig, 2000; Tycko and Morison, 2002). However, imprinting in mammals has still been found to affect a greater variety of biological pathways (Tycko and Morison, 2002), indicating other potential roles. As discussed below, in section 7.3.1, functional validation of individual imprinted or methylated genes will provide more accurate assessments of function.

Finally, variation in DNA methylation has been documented for the first time between genetically distinct *B. terrestris* colonies and between temporal sub-populations of *D. magna*. These findings shows the importance of accounting for genetic variation when attempting to assess differences in methylation profiles between non-isogenic individuals. Lea *et al.* (2017) highlight the importance of considering genetic relatedness in ecological methylation data sets. Associations of DNA methylation with, for example, a climate gradient, in a space-for-time study, may be confounded by genetic variation along the same transect (Lea *et al.*, 2017). Given the call for further research into the role of epigenetics within ecology and evolution the discovery of high methylation variation between replicates highlights the importance of considering genetic factors in future ecological epigenetic studies.

7.3 Future work

7.3.1 Functional validation

In order to understand the direct role of DNA methylation in any arthropod species, functional validation is needed. It is currently possible to alter genome-wide DNA methylation in arthropods via application of the chemical 5-aza-2'-deoxycytidine (Amarasinghe *et al.*, 2014; Cook *et al.*, 2019). This chemical irreversibly binds to DNMT enzymes which are responsible for DNA methylation maintenance (Christman, 2002). Whilst this causes a general loss in DNA methylation over time, not all loci are affected (Cook *et al.*, 2019). Additionally, modifying DNA methylation globally may provide some clues to function, e.g. *B. terrestris* workers were more likely to become reproduc-

tive after treatment (Amarasinghe *et al.*, 2014). However, this method does not assess the direct function of DNA methylation on a gene level.

More recently the CRISPR-Cas9 technology has been modified to allow the methylation or de-methylation of specific sites (Vojta *et al.*, 2016). This has currently been trialled *in vitro* in mammalian cells and *in vivo* in mice, where a Dnmt3a enzyme (involved in methylation establishment) or a Tet1 enzyme (involved in methylation removal) have been used to change methylation at specific sites within the genome (Liu *et al.*, 2016). CRISPR technology has already been successful in a number of insect species, including: *Drosophila melanogaster* (Bassett and Liu, 2014), *Tribolium castaneum* (Gilles *et al.*, 2015), *Bombyx mori* (Liu *et al.*, 2014), *Nasonia vitripennis* (Li *et al.*, 2017) and *Apis mellifera* (Kohno *et al.*, 2016). The application of CRISPR-Cas9 to modify DNA methylation on a per gene basis in arthropods would allow direct phenotypic responses to be observed, providing considerable insight into the function of DNA methylation in individual species on a gene level.

Modifying specific CpG sites would also allow for a greater mechanistic understanding of the cellular pathways potentially influenced by DNA methylation. As discussed throughout this thesis, histone modifications and chromatin arrangement may interact with DNA methylation to provide a phenotype. Utilising techniques such as ChIP-Seq (chromatin immunoprecipitation sequencing) and ATAC-Seq (assay for transposase-accessible chromatin sequencing), alongside RNA-Seq, would allow the molecular affects of changes in DNA methylation to be observed. ChIP-Seq involves using immunoprecipitation to enrich for DNA fragments associated with particular histone modifications (Blecher-Gonen *et al.*, 2013). However, this technique can be costly when multiple histone modifications are targets of interest. ATAC-Seq provides a more general assessment of the chromatin structure, sequencing adapters are ligated into any open chromatin regions allowing sequencing of only accessible DNA (Buenrostro *et al.*, 2015). Combining various epigenomic data sets with RNA-Seq from the same individuals would allow for a greater understanding of the epigenomic pathways which contribute to phenotype.

7.3.2 Genomic imprinting as a mechanism of plasticity

Radford *et al.* (2011) have proposed imprinted genes could act as a mechanism of plasticity by regulating gene expression in response to environmental change. Some imprinted genes have been shown to exhibit monoallelic expression (expression of a single allele) in only some tissue types and during only specific developmental phases (Charalambous *et al.*, 2003), showing the plastic potential of imprinted genes. Additionally, Matsuura *et al.* (2018) propose imprinted genes play a role in caste-determination in termites based on the influence of parental phenotypes on offspring caste-fate. The identification of parent-of-origin expression differences under differing experimental conditions would allow the role of imprinted genes in plasticity to be further understood. Ideally this work would use isogenic lines in order to minimise the effects of genotype.

Additionally, in order to assess the effects of genotype more thoroughly in the data generated in Chapter 5 (parent-of-origin methylation in *B. terrestris*), an improved experiment is recommended. The presence of cytosine SNPs may influence the methylation status of a given CpG (Wedd *et al.*, 2016), these SNPs cannot be easily or confidently identified in bisulfite treated DNA as cytosines are converted to thymine during the process (Liu *et al.*, 2012). To improve on the design of Chapter 5, whole genome sequencing of the parents may be carried out to identify a full complement of SNPs, this would allow for more confident identification of alleles in the offspring and allow the relationship of methylation and genotype to be determined.

7.3.3 Transgenerational epigenetic adaptation

In order to understand the role of DNA methylation in arthropod adaptation it is important to understand the developmental processes underlying DNA methylation heritability. In mammals DNA methylation is almost entirely wiped and re-established during development (Messerschmidt *et al.*, 2014). Drewell *et al.* (2014) examined genome-wide methylation differences between *A. mellifera* eggs, males and sperm. They found reduced levels of DNA methylation in adult males compared to both eggs and sperm and higher levels of methylation in eggs compared to sperm. Additionally, Kay *et al.*

(2018) found higher expression levels of *Dnmt3* in embryos of the ant, *Solenopsis invicta*, compared to instar developmental stages and adults. These results combined suggest DNA methylation likely undergoes a dynamic fluctuation during development in hymenoptera, as seen in mammals. However, given the identification of parent-of-origin methylated CpGs in Chapter 5, a small number of sites may also escape global erasure, as also observed in mammals. Considering the diverse methylation profiles of species within the Arthropoda phylum, differences in genome-wide methylation, in more developmental stages, as well as gametes, are needed for many other species in order to further clarify this process.

The direct heritability of DNA methylation may only be limited to a small number of sites in some species. However, DNA methylation linked to the underlying genomic code provides a means of direct transmission of many epigenetic marks between generations. Chapter 6 in this thesis begins to explore a data set which may shed light on the heritability of DNA methylation in a crustacean species and may also help determine how much of the methylome is linked to genotype. I plan to expand on the analysis done in Chapter 6 by identifying different SNP positions between genotypes, using previously generated whole-genome data. I will then be able to carry out a quantitative trait locus analysis, integrating previously generated RNA-seq from the same genotypes. This type of analysis has previously been carried out by Lu *et al.* (2019), they identified associations between SNPs, DNA methylation and gene expression in human blood cells. Further exploring the relationship between genotype, epigenotype and phenotype will allow greater understanding of the function of DNA methylation across arthropod species.

Additionally, the nature of the data produced from whole-genome bisulfite sequencing lends itself to population genetic analyses. As individual genomic positions may be methylated or unmethylated they can be treated as single methylation polymorphisms (SMPs). Geoghegan and Spencer (2012) have adapted traditional population genetic models to allow for epigenetic considerations. The application of these models to population epigenomic data, as generated in Chapter 6, may allow new insights into the direct effects of selection on epigenetic loci. These examples highlight how the application of techniques and methods from various other disciplines and fields may help

progress ecological epigenetic research.

7.4 Conclusions

The work in this thesis has made various new contributions to the field of ecological epigenetics. Briefly I have: characterised caste-specific bumblebee methylomes, identifying no direct causal relationship with caste-determination via the regulation of gene expression. This highlights the importance of understanding the full molecular pathways involved in phenotype production. I have identified parent-of-origin gene expression in *B. terrestris*, which provides support for the kinship theory of genomic imprinting and contributes the first genome-wide evidence of imprinted genes in this species. Parent-of-origin methylation was also identified in a small number of genes, indicating imprinted genes in insects may be regulated by a different process, compared to mammals. Allele-specific methylation throughout has not been associated with allele-specific gene expression, additionally indicating a potential role for other epigenetic marks in the process of generating allele-specific expression / imprinted genes. Using *D. magna* I have identified temporal DNA methylation fluctuations in a single population, potentially in response to environmental stress. This provides the first evidence for DNA methylation changes through evolutionary time in a single population. With the application of analyses from other research fields these data may aid our understanding of the adaptive potential of DNA methylation. Overall the results of this thesis highlight the need for functional validation within the field of ecological epigenetics, along with improved bioinformatic pipelines which consider the impact of genotype on DNA methylation.

Appendix A

Appendix: Chapter 2

A.1 Published paper

Work from Chapter 2 is published in:

Marshall, H., Lonsdale, Z.N. and Mallon, E.B. (2019). Methylation and gene expression differences between reproductive castes of bumblebee workers. *Evolution Letters*. DOI: https://doi.org/10.1002/evl3.129

LETTER

doi:10.1002/evl3.129

Methylation and gene expression differences between reproductive and sterile bumblebee workers

Hollie Marshall,[1,2] Zoë N. Lonsdale,[1] and Eamonn B. Mallon[1]

[1]*Department of Genetics and Genome Biology, The University of Leicester, Leicester, United Kingdom*

[2]*E-mail: hollie_marshall@hotmail.co.uk*

Received January 21, 2019

Accepted July 12, 2019

Phenotypic plasticity is the production of multiple phenotypes from a single genome and is notably observed in social insects. Multiple epigenetic mechanisms have been associated with social insect plasticity, with DNA methylation being explored to the greatest extent. DNA methylation is thought to play a role in caste determination in *Apis mellifera*, and other social insects, but there is limited knowledge on its role in other bee species. In this study, we analyzed whole genome bisulfite sequencing and RNA-seq data sets from head tissue of reproductive and sterile castes of the eusocial bumblebee *Bombus terrestris*. We found that genome-wide methylation in *B. terrestris* is similar to other holometabolous insects and does not differ between reproductive castes. We did, however, find differentially methylated genes between castes, which are enriched for multiple biological processes including reproduction. However, we found no relationship between differential methylation and differential gene expression or differential exon usage between castes. Our results also indicate high intercolony variation in methylation. These findings suggest that methylation is associated with caste differences but may serve an alternate function, other than direct caste determination in this species. This study provides the first insights into the nature of a bumblebee caste-specific methylome as well as its interaction with gene expression and caste-specific alternative splicing, providing greater understanding of the role of methylation in phenotypic plasticity within social bee species. Future experimental work is needed to determine the function of methylation and other epigenetic mechanisms in insects.

KEY WORDS: Bombus, bumblebee, expression, hymenoptera, methylation.

Impact Summary

Social insects, such as ants, termites, bees, and wasps, can produce individuals with extreme physical and behavioral differences within the same colony known as castes (e.g., workers/soldiers/queens). These individuals have similar genomes and many studies have associated epigenetic mechanisms with the differences observed. Epigenetic modifications are changes that affect how genes are expressed without changing the underlying DNA code. Here, we investigated differences in DNA methylation (a well-researched modified base) between different reproductive castes of the bumblebee, *Bombus terrestris*, an economically and environmentally important pollinator species. We found that *B. terrestris* has a similar methylation profile to other holometabolous insect species in terms of the distribution of methylation throughout the genome and the relationship between methylation and gene expression. Genes that have differences in methylation between reproductive castes are involved in multiple biological processes, including reproduction, suggesting methylation may hold multiple functions in this species. These differentially methylated genes are also different to differentially methylated

© 2019 The Author(s). *Evolution Letters* published by Wiley Periodicals, Inc. on behalf of Society for the Study of Evolution (SSE) and European Society for Evolutionary Biology (ESEB).
This is an open access article under the terms of the Creative Commons Attribution License, which permits use, distribution and reproduction in any medium, provided the original work is properly cited.

genes identified between honeybee reproductive castes, again suggesting methylation may have a variable function. These findings provide a greater understanding of the role of methylation in caste determination in social insect species.

Phenotypic plasticity is the production of multiple phenotypes from a single genome. It plays a crucial role in the adaptive capabilities of species (Chevin et al. 2010) and is notably observed in social insects. Social insects exhibit sometimes extreme morphological and behavioral differences within a single colony, known as castes. The mechanisms by which species develop differences between castes are diverse; some species use only environmental cues, whereas others rely only on inherited changes, with many species falling somewhere in between these two extremes (Matsuura et al. 2018). For example, some ant species from the *Pogonomyrmex* genus have purely genetic caste determination (Mott et al. 2015). On the other hand, many ant species undergo caste determination in response to only the environment, indicating their genomes must contain the code for all caste possibilities, with the phenotype potentially determined by epigenetic factors (Bonasio et al. 2012).

Multiple epigenetic mechanisms have been associated with social insect plasticity. Histone modifications have been shown to be involved with plasticity, for example changes in histone acetylation alter the behavior of major workers of the ant species *Camponotus floridanus*, making them more similar to the behavior of minor workers (Simola et al. 2016). Variation in microRNA expression levels has been identified in both honeybee (Ashby et al. 2016) and bumblebee (Collins et al. 2017) castes. However, the most active research in this area has been focused on DNA methylation (Glastad et al. 2015).

DNA methylation is the addition of a methyl group to a cytosine nucleotide. In mammals, methylation primarily occurs in a CpG context (CpG referring to a cytosine base immediately followed by a guanine base); the percentage of CpGs methylated is usually over 70%, with methylation serving to repress gene expression when occurring in promoter regions (Feng et al. 2010). However, in insects, it is generally found in much lower quantities, ranging from zero methylation in most Diptera species studied to $>2\%$ in Hymenoptera and up to 14% in some species of Blattodea (Provataris et al. 2018). It is also enriched in gene bodies rather than throughout the genome, as in mammals (Fang et al. 2012; Wang et al. 2013), with a possible role in alternative splicing (Bonasio et al. 2012).

DNA methylation has been associated with the switching of worker castes in honeybees (Herb et al. 2012). A major finding was that silencing of the *Dnmt3* gene (involved in methylation establishment) in larvae produced queens rather than workers (Kucharski et al. 2008). DNA methylation has also been linked with alternative splicing differences between castes in two ant species (Bonasio et al. 2012) and is thought to be involved in caste determination in *Copidosoma koehleri*, a species of primitively social wasp (Shaham et al. 2016). However, it is clear DNA methylation is not a conserved mechanism in Hymenoptera for caste differentiation. No association between caste and methylation has been found in a number of wasp and ant species (Patalano et al. 2015; Standage et al. 2016). Additionally, the statistical methods of previous next generation sequencing analyses on social insect methylation have been brought into question (Libbrecht et al. 2016).

A greater variety of species are needed to begin to understand the role of DNA methylation in social insect caste determination. Here, we assess whole genome methylation differences between reproductive castes of the bumblebee, *Bombus terrestris*, with an aim to investigate the role of methylation in caste determination in this species. Bumblebees are primitively eusocial and are an important pollinator species, both economically and environmentally. They are generalist pollinators and are keystone species in some ecosystems (Woodard et al. 2015). *Bombus terrestris* colonies are annual and are founded by a singly mated queen in early spring; she will lay diploid eggs resulting in female workers and later switch to male haploid eggs, known as the switching point (Bloch 1999). A competition phase then occurs between queens and workers, where some workers will become reproductive and produce their own haploid sons (Alaux et al. 2006); this results in distinct reproductive worker castes within the colony. Multiple recent studies have highlighted *B. terrestris* as an ideal organism to assess methylation as a potential regulatory mechanism for reproductive caste determination (Amarasinghe et al. 2014; Lonsdale et al. 2017; Li et al. 2018).

Methylation regulatory genes were identified in the bumblebee genome and have since been shown to have varying expression levels between queens, workers and drones (Li et al. 2018). Additionally, genes showing allele-specific methylation and gene expression have been identified and are enriched in reproductive-related processes (Lonsdale et al. 2017). Finally, experimental changes in methylation in *B. terrestris* workers has been shown to alter levels of reproductive behavior (Amarasinghe et al. 2014). Although these studies highlight differences in methylation between *B. terrestris* castes, it is still unclear where those differences are within the genome and also whether methylation differences are related to changes in gene expression, potentially leading to caste differentiation.

In this study, we compared whole genome bisulfite sequencing (WGBS) data sets from reproductive and sterile worker castes of *B. terrestris*, allowing us to identify differences in methylation

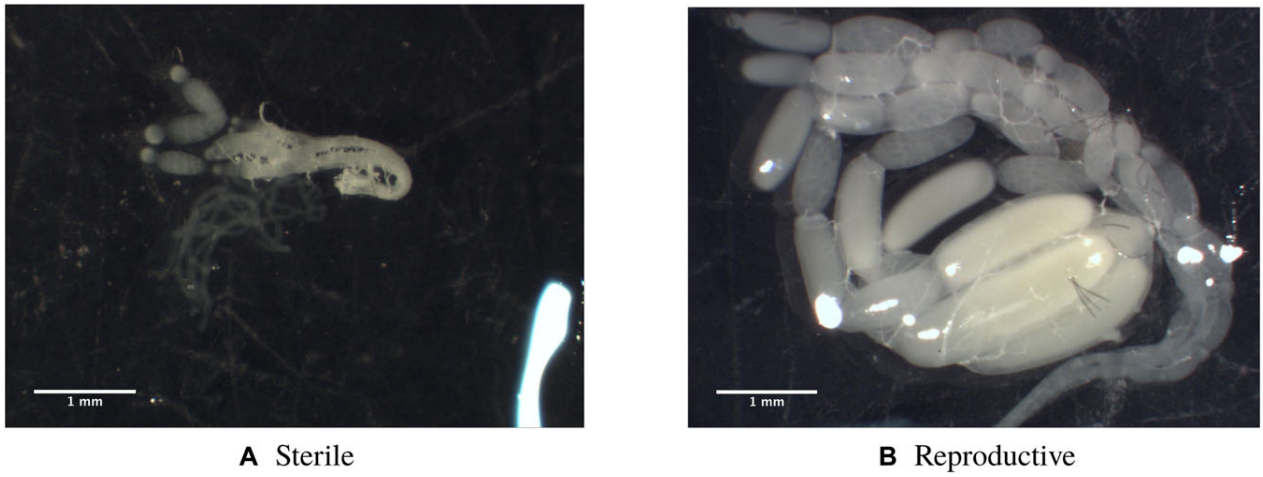


Figure 1. **(A) one half of a pair of ovaries from a sterile bumblebee worker, with a score of 0. (B) One half of a pair of ovaries from a reproductive bumblebee worker, with a score of 4. Scores generated following Duchateau and Velthuis (1988).**

at base-pair resolution throughout the genome. We then linked these data with gene expression data for the same individuals to identify a potential relationship between gene expression and methylation regarding reproductive caste determination. Within this study, we have also characterized the *B. terrestris* methylome to allow comparative analyses between castes. If methylation plays a role in caste determination, we would expect to find differentially methylated genes between castes, with functions related to reproduction. We would also expect any differentially methylated genes between castes to be enriched for differentially expressed genes or genes which have different exon usage between castes. Additionally, if there is a conserved role for methylation in caste determination in Hymenoptera, we would expect to find orthologous genes differentially methylated between *B. terrestris* reproductive castes and *Apis mellifera* reproductive castes.

Methods

BEE HUSBANDRY AND TISSUE SAMPLING

Three *B. terrestris* colonies, from Agralan, UK, were reared in constant red light at 26°C and 60% humidity. They were fed 50% v/v apiary solution (Meliose-Roquette, France) and pollen (Percie du set, France) ad libitum. Callow workers, less than 24 hours old, were taken from each colony and placed in small rearing boxes of five individuals.

The worker bees were sacrificed at six days old. For each bee, the head was snap frozen in liquid nitrogen. Through dissection in 1% PBS solution, the reproductive status of each bee was determined and classed as either reproductive, sterile, or intermediate. Workers were classed as having developed ovaries, and therefore reproductive, if the largest oocyte was larger than the trophocyte follicle (Duchateau and Velthuis 1988). This measurement is tightly correlated with reproductive status (Foster et al. 2004; Geva et al. 2005). The ovaries of each worker were weighed, and the length of the largest oocyte was measured using ImageJ version 1.50e (Schneider et al. 2012) (Supporting Information 1.0.0). Worker "reproductiveness" was classified on a scale from 0 to 4 based on Duchateau and Velthuis (1988), 0 begin completely sterile (Fig. 1A) and 4 having fully developed ovaries (Fig. 1B).

RNA AND DNA EXTRACTION AND SEQUENCING

Three reproductive individuals and three sterile individuals from each of the three colonies were selected for RNA and DNA extraction (see Fig. 2 for an overview). Heads were cut in half (using a lateral incision central between the eyes). Each head half was randomly allocated for either DNA/RNA extraction to avoid left/right hemisphere bias. RNA was extracted using the Sigma-Aldrich GenElute Mammalian Total RNA Miniprep kit and DNA was extracted using the Qiagen DNeasy blood and Tissue kit, individually for each half head per sample, following manufacturers protocols. The extracted RNA was treated with DNase and the extracted DNA was treated with RNase. DNA was pooled per colony and reproductive status, that is, the three reproductive samples from a single colony were pooled to create one representative reproductive sample for that colony (Fig. 2). RNA samples were processed individually. DNA and RNA quality and quantity were determined by Nanodrop and Qubit® fluorometers (Supporting Information 1.0.1 and 1.0.2). A total of 18 RNA samples (three individuals per reproductive status for each of the three colonies) were sent for 100 bp paired-end sequencing and six pooled DNA samples (one sample per reproductive status per colony consisting of three individuals per pool) were sent for 100 bp paired-end bisulfite sequencing on a HiSeq 2000 machine (Illumina, Inc.) by BGI Tech Solution Co., Ltd.(Hong Kong). Library preparation

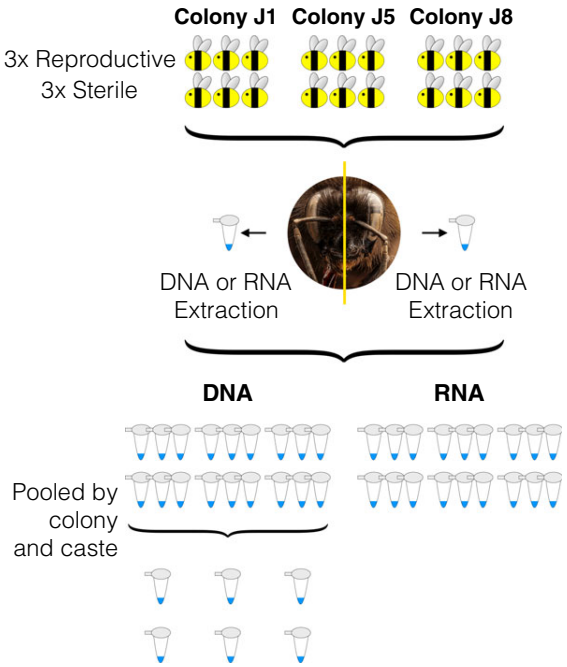


Figure 2. **Overview of sample preparation for sequencing. Three reproductive workers and three sterile workers were selected from three colonies (J1, J5 and J8 represent colony names). Half of each head was randomly allocated for RNA/DNA extraction. All 18 RNA samples were sent for RNA-Seq (three of each caste from each colony). DNA samples were pooled by colony and caste creating a representative reproductive and sterile sample per colony.**

was carried out by BGI using their standard directional WGBS pipeline. A 1% lambda spike was included as an unmethylated control in each WGBS library.

DIFFERENTIAL EXPRESSION AND ALTERNATIVE SPLICING

Low-quality bases were removed from the RNA-Seq libraries using CutAdapt version 1.1 (Martin 2011). Reads were aligned to the reference genome (Bter_1.0, Refseq accession no. GCF_000214255.1; Sadd et al. 2015) using STAR version 2.5.2 (Dobin et al. 2016) with standard parameters. Reads were counted per gene using HTseq version 0.10.0 (Anders et al. 2015). A differential expression analysis was then carried out after count normalization via a negative binomial generalized linear model (GLM) implemented by DEseq2 version 1.20.0 (Love et al. 2014) in R version 3.4.0 (http://www.R-project.org) with colony and reproductive status as independent variables. Genes were classed as differentially expressed when $q < 0.05$ after correction for multiple testing using the Benjamini–Hochberg method (Benjamini and Hochberg 1995).

Differential exon expression was determined using the DEXseq version 1.26.0 R package (Anders et al. 2012); briefly this package calculated the ratio of expression of a given exon in a given gene relative to other exons in the same gene for each sample. The relative exon expression per colony was then calculated taking into account dispersion between colonies. A GLM was then used to test for a difference in the relative proportion of expression of each exon between castes, accounting for sample differences and overall gene expression differences between castes; *P*-values were corrected for multiple testing using the Benjimini–Hochberg method (Benjamini and Hochberg 1995) and exons were classed as differentially used between castes when $q < 0.1$. The benefit of this method over general alternative splicing analysis is that specific differentially used exons can be identified between castes allowing the relationship with exonic methylation to be investigated.

DIFFERENTIAL METHYLATION

BS-seq libraries were aligned to the reference genome (Bter_1.0, Refseq accession no. GCF_000214255.1; Sadd et al. 2015) using Bismark version 0.16.1 (Krueger and Andrews 2011) and bowtie2 version 2.2.6 (Langmead and Salzberg 2012) with standard parameters. Bismark was also used to extract methylation counts and carry out deduplication. Annotation of the methylation counts with genomic features (from the *B. terrestis* annotation file, Refseq accession no. GCF_000214255.1) was carried out using custom R scripts implementing the sqldf version 0.4.11 library (Grothendieck 2017). Bisulfite conversion efficiency was calculated by aligning reads to the lambda reference genome (Refseq accession no. GCF_000840245.1) and calculating the single-site methylation level, as in Schultz et al. (2012).

Prior to differential methylation analysis, coverage outliers (above the 99.9th percentile) were removed along with bases covered by less than 10 reads. The methylation status of each CpG was then determined using the "methylation status calling" (MSC) procedure, as described in Cheng and Zhu (2014). Briefly, this involves applying a mixed binomial model to each CpG, which includes estimation of both the false discovery rate (FDR) and the non-false discovery rate to make a binary methylation call per site. CpG sites were then filtered to remove any site that did not return as methylated in at least one sample. This functions to reduce the number of tests and hence decreases the required stringency of the later FDR correction applied during differential methylation testing. This is a vital step for species, such as bumblebees, with extremely low genome methylation where the majority of sites show zero methylation in all samples. A logistic regression model was then applied via the R package methylKit version 1.6.1 (Akalin et al. 2012) to determine differentially methylated sites, taking into account colony as a covariate due to high inter-colony variation (see Supporting Information 2.0). A minimum difference of at least 10% methylation and a *q*-value of <0.05 were required for a single site to be classed as differentially

methylated. Genes containing at least one differentially methylated CpG and a minimum weighted methylation difference (Schultz et al. 2012) of 10% across the entire gene were classed as differentially methylated between reproductive castes.

We chose not to include a permutation test as part of the differential methylation analysis, as has been seen in previous research (Libbrecht et al. 2016; Arsenault et al. 2018), although it is included in our Supporting Information data. There is structure present in our data due to high methylation variation between colony replicates. When structure is present within data, permutation tests do not produce reliable outcomes, as discussed in Winkler et al. (2015). A higher number of replicates would allow label shuffling within confounding factors, maintaining the structure of the data, thus allowing a valid permutation test (see Supporting Information 2.0).

GENE ONTOLOGY ANALYSIS

Gene ontology (GO) terms for *B. terrestris* were taken from a custom database made in Bebane et al. (2019). GO enrichment analysis was carried out using a hypergeometric test with Benjamini–Hochberg multiple-testing correction (Benjamini and Hochberg 1995). GO terms were defined as enriched when $q < 0.05$. GO terms from differentially methylated genes were tested for enrichment against GO terms associated with all methylated genes. Genes were classed as methylated when the weighted methylation score per gene was greater than zero (Schultz et al. 2012). Additionally, the GO terms associated with hypermethylated genes in either sterile or reproductive workers were tested for enrichment against the GO terms associated with all differentially methylated genes between castes to determine if there are different functions for hypermethylated genes in either sterile or reproductive workers. GO terms for differentially expressed genes and genes containing different exon usage between castes were tested for enrichment against GO terms associated with all genes identified in the RNA-seq data. REVIGO (Supek et al. 2011) was used to obtain the GO descriptions from the GO identification numbers.

COMPARATIVE ANALYSES

The hypergeometric test was applied to gene lists from the various analyses to determine if any overlaps were statistically significant. Custom R scripts were used to investigate the relationship between gene expression and methylation. A reciprocal blast between the honeybee (Amel_4.5, Refseq accession no. GCA_000002195.1) and bumblebee genome (Bter_1.0, Refseq accession no. GCA_000214255.1) was carried out using blast+ version 2.5.0 (Camacho et al. 2009), where the fasta sequence for each gene of each species was blasted against a custom database containing the fasta sequence for every gene of the opposite species, allowing only one match per gene and a minimum *e*-value of 1×10^{-3}. Gene matches were then filtered to ensure only matches that occurred in both directions and to the same gene were kept. For example, multiple honeybee genes matched the same bumblebee gene, therefore all of these matches were discarded. This allowed us to construct a database of putative orthologous genes. A custom script was then used to check for overlap between the differentially methylated genes identified here and differentially methylated genes identified in Lyko et al. (2010) between honeybee reproductive castes.

Results

GENOME-WIDE METHYLATION DIFFERENCES BETWEEN CASTES

Up to a maximum of 10 bp were trimmed from the start of all reads due to base bias generated by the Illumina sequencing protocol (Krueger et al. 2011). The mean mapping efficiency was 63.6 ± 1.4% (mean ± SD) and the mean coverage was 17.7 ± 0.5 reads per base; the average number of uniquely mapped reads was 27,709,214 ± 753,203. The mean bisulfite conversion efficiency, calculated from the unmethylated lambda spike, was 99.55 ± 0.02%. After accounting for the conversion efficiency, there were no methylated cytosines in a non-CpG context. The mean single site methylation level (Schultz et al. 2012) in a CpG context was determined as 0.22 ± 0.07%, calculated from the number of methylated cytosines divided by the sum of methylated and unmethylated cytosines and accounting for bisulfite conversion efficiency.

A total of 3412 genes were classed as methylated, that is, they had a weighted methylation level >0 in at least one sample. There was no significant difference in the overall weighted methylation level of the methylated genes between reproductive and sterile workers (Mann–Whitney *U* test: $W = 5{,}948{,}300$, $P = 0.1172$, Fig. 3A). GO terms enriched in methylated genes compared to all genes annotated in the genome ($q < 0.05$) include a large variety of biological processes (Supporitng Information 1.0.5). Specifically, *posttranscriptional regulation of gene expression* (GO:0010608) and *histone modification* (GO:0016570) are enriched as well as terms related to reproductive processes, for example, *reproduction* (GO:0000003) and *oogenesis* (GO:0048477).

There was no significant difference in the weighted methylation level of all genomic features between reproductive and sterile workers (two-way analysis of variance [ANOVA], interaction between genomic feature and reproductive status; $F_{1,6} = 0.637$, $P = 0.701$, Fig. 3B), we also tested for differences in methylation levels of putative promotors but as promotor regions are currently unannotated for the current genomic annotation we feel these results are not reliable (Supporting Information 2.1, Fig. S3a). Irrespective of worker reproductive status, we found methylation differences between genomic features (Kruskal–Wallis; chi-squared = 729.35, df = 7, $P < 2.2 \times 10^{-16}$), with methylation being

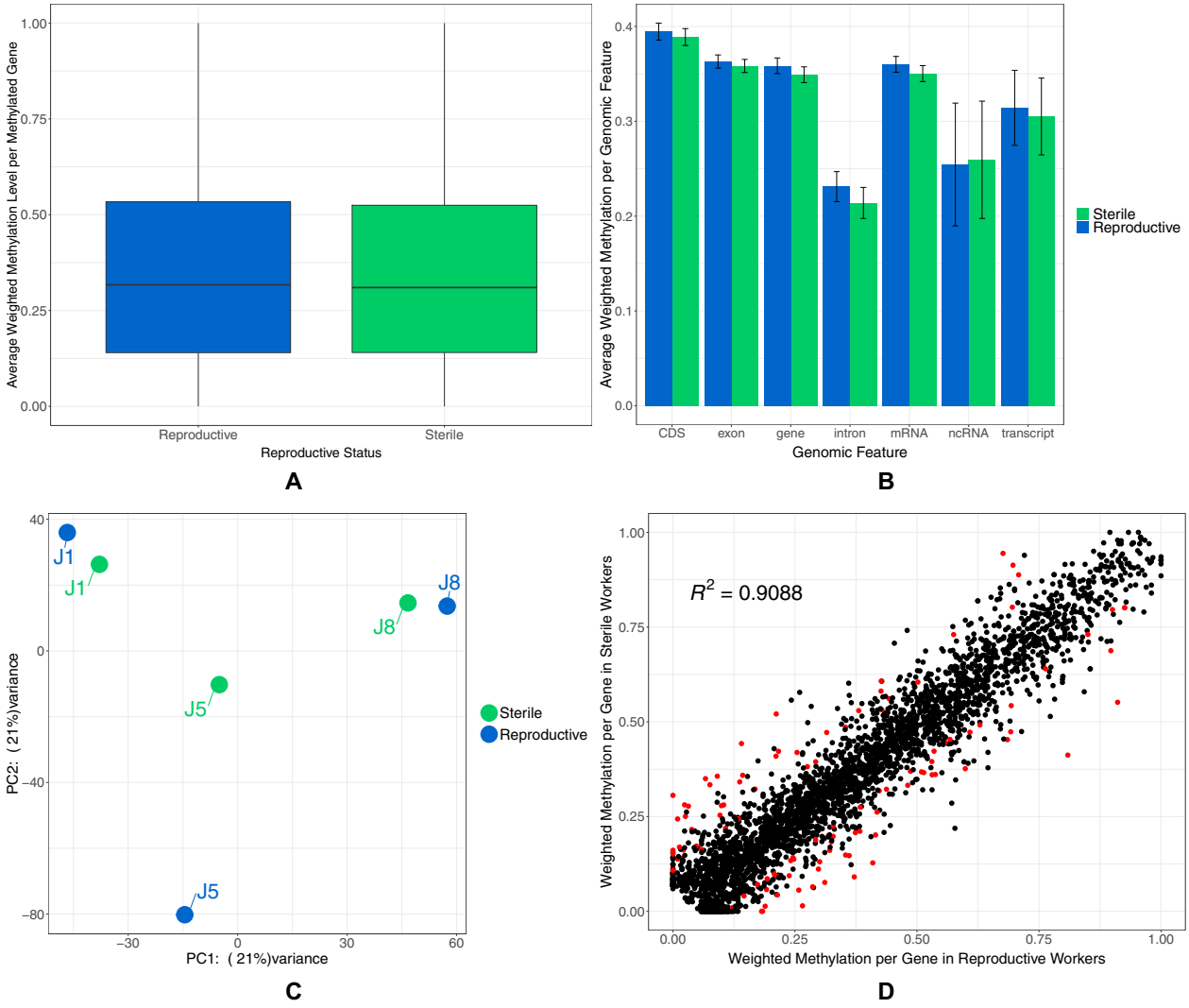


Figure 3. **(A) Box plot of the mean weighted methylation level of methylated genes (n = 3412) across colonies for each caste. (B) The mean weighted methylation level across colonies for each genomic feature for both reproductive and sterile workers. Error bars are 95% confidence intervals of the mean. (C) PCA plot generated by methylKit showing samples cluster by colony using per site CpG methylation. (D) Scatter plot of the average weighted methylation level (across colonies) for reproductive workers against sterile workers. Each dot represents a gene and each red dot represents a differentially methylated gene (q < 0.05 and a minimum gene weighted methylation difference of 10%).**

significantly enriched in coding regions compared to introns and ncRNAs (Supporting Information 1.0.6).

We also found no difference in the weighted methylation level across the genome per linkage group between reproductive and sterile workers (two-way ANOVA, interaction between linkage group and reproductive status; $F_{1,17} = 0.034$, $P = 1.0$, Supporting Information 2.1, Fig. S3b). Weighted methylation did vary significantly between linkage groups within the genome irrespective of reproductive status (Kruskal–Wallis chi-squared = 131.59, df = 17, $P < 2.2 \times 10^{-16}$, Supporting Information 1.0.6), however due to the number of unplaced scaffolds these results should be interpreted with care.

Finally, using CpG methylation levels, samples cluster by colony rather than by reproductive caste (Fig. 3C). This indicates high intercolony variation in methylation.

GENE LEVEL METHYLATION DIFFERENCES BETWEEN CASTES

A total of 4,681,131 CpG sites had a coverage >10 in all six sample data sets, of those 16,194 returned as methylated in at least one sample after running the MSC procedure. A total of 624 of these CpGs were identified as differentially methylated between reproductive castes, 613 of these were located in a total of 478 genes (Supporting Information 1.0.4). Note that 11 differentially

methylated CpGs were located outside of genes, nine of those were within 5000 bp upstream or downstream of a gene with no apparent trend in the expression of near-by genes (Supporting Information 1.0.5). 111 genes contained a differentially methylated CpG and also had a weighted methylation difference of 10% between reproductive and sterile workers (Supporting Information 1.0.7, Fig. 3D).

Of the 111 differentially methylated genes, there was no preference for genes to be hypermethylated in either reproductive or sterile workers (chi-squared goodness of fit, X-squared = 2.027, df = 1, $P = 0.1545$), with 63 genes hypermethylated in reproductive workers and 48 genes hypermethylated in sterile workers.

GO terms enriched in differentially methylated genes compared to all methylated genes ($q < 0.05$) contained a variety of biological processes (Supporting Information 1.0.8), among these processes were terms involved with reproduction, including *meiotic cell cycle* (GO:0051321) and *female germline ring canal stabilization* (GO:0008335). One of the genes associated with the above GO terms is *eggless* (LOC100647514), which shows hypermethylation in sterile workers. This gene contains a Methyl-CpG binding domain, which has been associated with histone H3, lysine 9-specific methyltransferase that contributes to repression of transcription (Wakefield et al. 1999).

There were no specific GO terms enriched for either the hypermethylated genes in sterile workers or the hypermethylated genes in reproductive workers compared to all differentially methylated genes as a background.

EXPRESSION DIFFERENCES BETWEEN CASTES

All reads had 13 bp trimmed from the start due to base bias generated by the Illumina protocol (Krueger et al. 2011). The mean percentage of uniquely mapped reads was 89.4 ± 0.8% (mean ± SD). This equated to a mean of 10,115,366 ± 1,849,600 uniquely mapped reads. After running a differential expression analysis with DESeq2, the decision was made to remove one sample from all downstream analysis due to possible mislabeling of reproductive status (Supporting Information 2.2).

Samples cluster by reproductive status when the expression of all genes is assessed (Fig. 4A). A total of 334 genes were identified as differentially expressed ($q < 0.05$, Fig. 4B). There was no difference in the number of upregulated genes in either reproductive or sterile workers (chi-squared goodness of fit: X-squared = 0.2994, df = 1, $P = 0.5843$), with 172 genes upregulated in reproductive workers and 162 genes upregulated in sterile workers.

One of the most upregulated genes in reproductive workers was vitellogenin (gene ID: LOC100650436, log2 fold-change of 2.92, $q = 4.85 \times 10^{-6}$). Previous work has found upregulation of this gene in reproductive *B. terrestris* workers is linked to aggressive behavior rather than directly to ovary development (Amsalem et al. 2014). Additionally, two genes coding for serine-protease inhibitors were found to be upregulated in reproductive workers; these proteins have been linked to reproduction in other insect species (Bao et al. 2014).

Enriched GO terms associated with the differentially expressed genes compared to the background of all genes in the RNA-seq data ($q < 0.05$) contained a variety of biological processes, including reproductive-related terms (Supporting Information 1.1.0). Additionally, there were no specific GO terms enriched in upregulated genes of reproductive workers compared to all differentially expressed genes as the background. However, there were two GO terms enriched for upregulated genes in sterile workers compared to differentially expressed genes as the background, these were as follows: *cellular lipid metabolic process* (GO:0044255) and *isoprenoid biosynthetic process* (GO:0008299).

A total of 59 genes were identified as having differential exon usage, containing 83 differentially expressed exons between reproductive castes ($q < 0.1$, Supporting Information 1.1.1, see example Fig. 4C). There is no difference in the number of upregulated exons in reproductive workers compared to sterile workers (chi-squared goodness of fit: X-squared = 3.4819, df = 1, $P = 0.06204$), with reproductive workers having 33 upregulated exons and sterile workers having 50 upregulated exons. The enriched GO terms associated with genes containing differentially used exons compared to the background of all genes in the RNA-seq data ($q < 0.05$) contained a variety of biological processes (Supporting Information 1.1.2), however there were no GO terms with a clear connection to reproductive processes.

RELATIONSHIP OF METHYLATION AND GENE EXPRESSION

On an individual gene basis, methylation and reproductive caste have no effect on expression level (Fig. 5A and 5B, linear mixed effects model with colony as a random factor; methylation: df = 49172, $t = -1.295$, $P = 0.195$, reproductive status: df = 49172, $t = -0.638$, $P = 0.524$, interaction between methylation and reproductive status: df = 49172, $t = 0.112$, $P = 0.911$).

However, gene groups with varying methylation levels show different levels of expression (Kruskal–Wallis; chi-squared = 131.59, df = 17, $P < 2.2 \times 10^{-16}$; Fig. 5C). Specifically genes with no methylation show higher expression than genes classed as lowly methylated but lower expression than genes classed as medium/high in terms of methylation (Dunn's test with Benjamini–Hochberg multiple-testing correction; no methylation vs. low methylation: $Z = -13.14$, $P = 4.09 \times 10^{-39}$, no methylation vs. medium methylation: $Z = 4.5$, $P = 6.82 \times 10^{-6}$, no methylation vs. high methylation: $Z = 7.32$, $P = 3.86 \times 10^{-13}$; Fig. 5C). Reproductive caste still has no effect on gene expression in relation to methylation status when genes are grouped

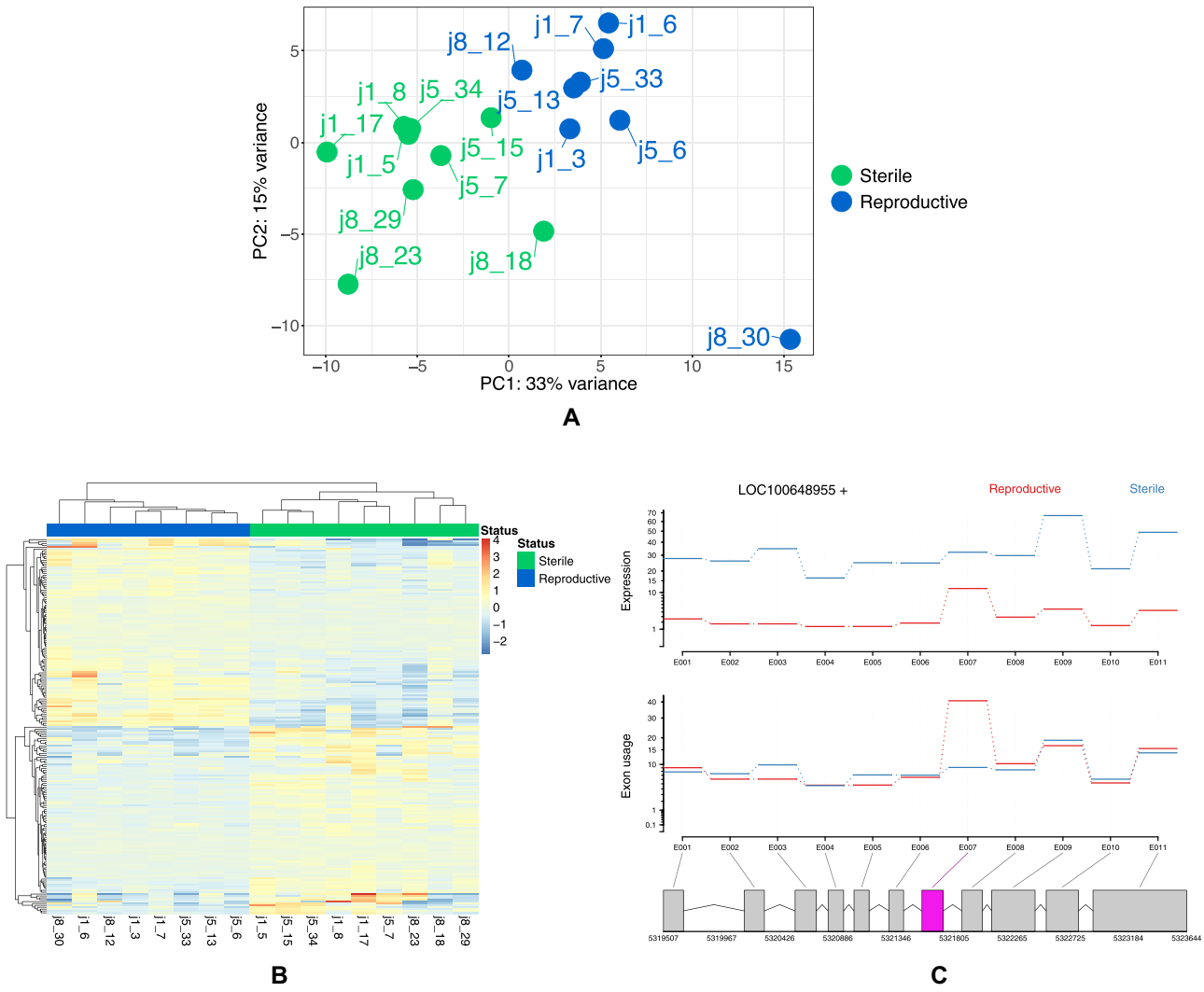


Figure 4. **(A) PCA plot showing samples cluster by caste for gene expression, the first half of each label represents the colony name and the second half is the individual identification number. (B) Heatmap showing the 100 top differentially expressed genes between reproductive castes, samples cluster by reproductive status. Sample names are shown at the bottom of the plot. (C) An example of a gene that shows differential exon expression in one exon between reproductive castes. The top section of the plot shows the general expression differences between castes, the second section shows the normalized counts per exon (given expression differences) and the third section highlights the differentially expressed exon in pink. Gene shown: *probable peroxisomal acyl-coenzyme A oxidase 1* (ID: LOC100648955).**

(two-way ANOVA, interaction between reproductive status and methylation level; $F_{1,3} = 0.017$, $P = 0.99$).

A linear mixed effects model was then applied to assess the relationship between gene expression, methylation, and reproductive status for only methylated genes using colony as a random factor. There is a positive relationship between gene expression and methylation in methylated genes with reproductive status having no effect (Fig. 5D, methylation: df = 17,390, $t = 6.154$, $P = 7.72 \times 10^{-10}$, reproductive status: df = 17,390, $t = -0.328$, $P = 0.743$, interaction between methylation and reproductive status: df = 17,390, $t = -0.200$, $P = 0.842$).

RELATIONSHIP OF METHYLATION AND DIFFERENTIAL GENE EXPRESSION

Weighted methylation differences between differentially expressed genes and nondifferentially expressed genes were assessed along with weighted methylation differences between genes containing differentially expressed exons and genes without differentially expressed exons (Fig. 6A and 6B). Differentially expressed genes and genes containing differentially expressed exons between castes show lower methylation than nondifferentially expressed genes or genes containing no differentially expressed exons, with reproductive status and the interaction of

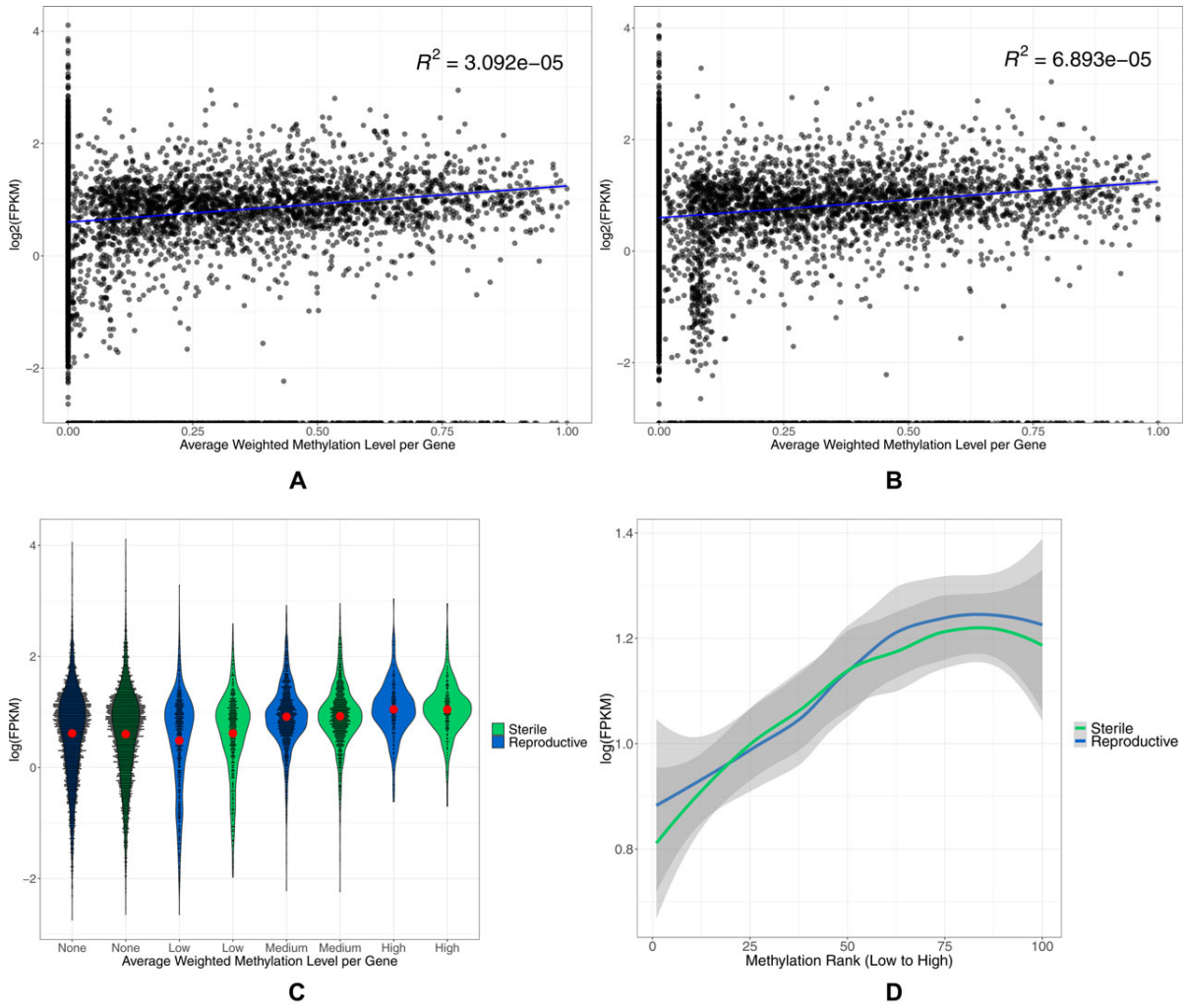


Figure 5. **(A and B) The colony average weighted methylation level for every gene plotted against the log(FPKM) of that gene for sterile workers and reproductive workers, respectively. Each black dot represents a single gene. The blue line is a fitted linear regression with the gray shaded area representing 95% confidence intervals. (C) Violin plots showing the distribution of the data via a mirrored density plot, meaning the widest part of the plots represent the most genes. Weighted methylation level per gene per caste, averaged across colonies, was binned into four categories, no methylation, low (>0–0.2), medium (0.2–0.7), and high (0.7–1), as in Liu et al. (2019). The red dot indicates the mean with 95% confidence intervals. Each black dot represents a single gene. (D) Binned methylated genes (n = 3412, 100 being the most highly methylated) based on the mean weighted methylation level across colonies per reproductive caste, plotted against the log(FPKM) expression level per gene. Data were smoothed using the LOESS method, and gray areas are 95% confidence intervals.**

reproductive status with gene expression type having no effect (Table 1, Fig. 6A and 6B). When weighted methylation is assessed per exon, differentially expressed exons have lower weighted methylation than nondifferentially expressed exons (Fig. 6C), with reproductive status and the interaction of reproductive status and exon expression having no effect (Table 1).

Of the 334 differentially expressed genes, 50 also showed some level of weighted methylation difference between reproductive and sterile workers (weighted methylation difference >0) (Fig. 6D). However, there is no relationship between the level of differential methylation and the level of differential expression for these 50 genes (linear model: $F_{1,58} = 0.2717$, $P = 0.6046$).

Gene lists were checked for potential overlap from all analyses. There was no significant overlap between differentially methylated genes and differentially expressed genes (two genes, hypergeometric test; $P = 0.658$, Fig. 7A). There was also no significant overlap between differentially methylated genes and genes containing differentially expressed exons (one gene, hypergeometric test; $P = 0.12$; Fig. 7A).

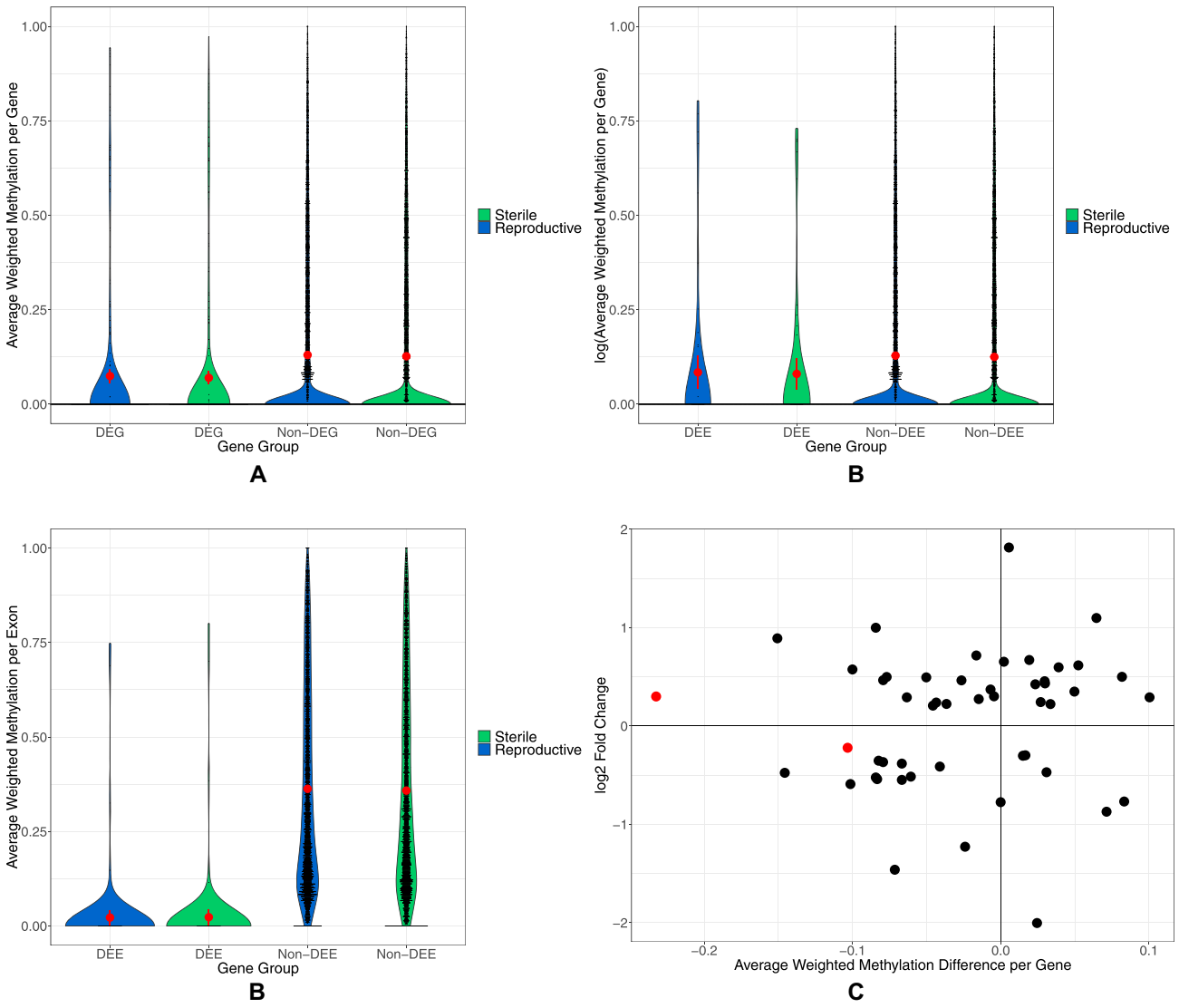


Figure 6. **(A) Violin plots showing the distribution of the data via a mirrored density plot, meaning the widest part of the plots represent the most genes. The red dots represent the mean of each gene set along with error bars representing 95% confidence intervals of the mean. Each black dot is an individual gene. The mean weighted methylation per gene across colonies per caste is plotted for either differentially expressed genes (DEG) or nondifferentially expressed genes (non-DEG). (B) Violin plots of the mean weighted methylation per gene across colonies per caste is plotted for either genes containing differentially expressed exons (DEE) or genes with non-differentially expressed exons (non-DEE). (C) Violin plots of the mean weighted methylation per exon across colonies per caste for DEE and non-DEE. The red dots represent the mean of each exon set along with error bars representing 95% confidence intervals of the mean. Each black dot is an individual exon. (D) Scatter plot of the difference in the mean weighted methylation level across colonies between castes plotted against the log2 fold change in expression of differentially expressed genes between castes. Each dot represents a gene; only genes which have a methylation difference >0 are shown. The red dots indicate that the gene is also differentially methylated.**

There was a significant overlap of genes found to be differentially expressed with those containing differentially expressed exons, 14 total (hypergeometric test; $P = 1.44 \times 10^{-10}$; Fig. 7A). All lists of overlapping genes can be found in Supporting Information 1.1.3.

HONEYBEE ORTHOLOGOUS DIFFERENTIALLY METHYLATED GENES

Custom honeybee and bumblebee putative ortholog databases were created from 15,314 and 10,339 annotated genes, respectively (Amel_4.5 GCA_000002195.1, Bter_1.0

Table 1. Summary statistics of the linear models used to check for differences in weighted methylation level between gene sets by taking into account reproductive status.

	Res. Df	RSS	Df	Sum of square	F	*P*
Differentially expressed genes						
Interaction vs. main effects model	16487	833.1	−1	-2.98×10^{-4}	5.9×10^{-3}	0.93
DEG vs. non-DEG	N/A	835.14	1	2.04	40.38	2.147×10^{-10}*
Reproductive vs. sterile	N/A	833.15	1	0.049	0.97	0.32
Genes with differentially expressed exons						
Interaction vs. main effects model	16409	832.69	−1	-7.93×10^{-6}	2.00×10^{-4}	0.99
DEE vs. non-DEE	N/A	832.92	1	0.23	4.59	0.032*
Reproductive vs. sterile	N/A	832.74	1	0.048	0.95	0.33
Differentially expressed exons						
Interaction vs. main effects model	11301	780.36	−1	-1.39×10^{-3}	0.02	0.89
DEE vs. non-DEE	N/A	799.69	1	19.33	279.97	$<2.00 \times 10^{-16}$*
Reproductive vs. sterile	N/A	780.42	1	0.06	0.86	0.35

*A significant *P*-value <0.05. DEG, differentially expressed genes; DEE, differentially expressed exons. The interaction versus main effects models were tested using the *anova* function in R to assess the interaction effect between gene set and reproductive status.

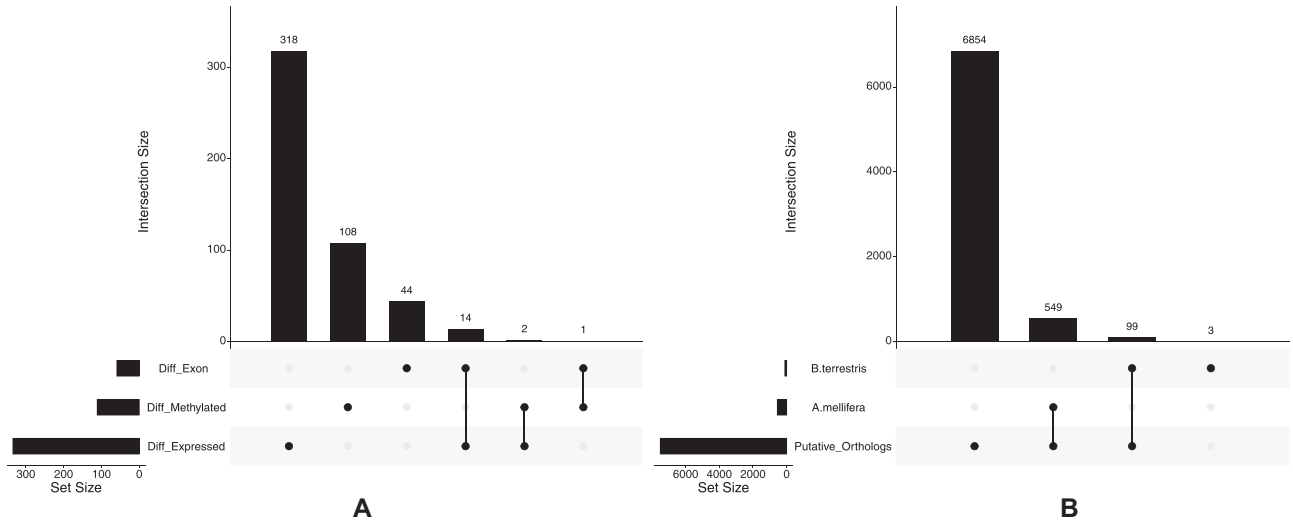


Figure 7. (A) UpSet plot showing the number of common genes between analyses. The set size indicates the number of genes in each category; differentially expressed, differentially methylated or genes containing a differentially expressed exon. The intersection size indicates the number of genes either unique to each set or the number common between sets. A single dot in the lower panel indicates the number of genes unique to the corresponding set and joining dots indicate the number of genes in common between the corresponding sets. (B) UpSet plot showing the number of putative orthologs between *A. mellifera* and *B. terrestris* along with the number of differentially methylated genes identified in Lyko et al. (2010) and in this study which are present in the putative ortholog database.

GCA_000214255.1). Note that 9,244 honeybee genes matched at least one bumblebee gene and 7,985 bumblebee genes matched at least one honeybee gene with an *e*-value of $<1 \times 10^{-3}$. A total of 7,345 genes made the same match in both blast searches. Of these genes, 392 matched more than one gene in one or both blasts and were therefore removed. This left a final putative ortholog list of 6,953 genes. A total of 99 of the 111 differentially methylated genes identified here were present in the final putative ortholog list, however none of them matched the 549 genes identified as differentially methylated between honeybee reproductive castes by Lyko et al. (2010) (Fig. 7B).

Discussion

We have used whole genome bisulfite sequencing and gene expression libraries from the same individual *B. terrestris* workers to investigate the role of methylation in caste determination. We found both reproductive and sterile workers show similar

methylation patterns to other holometabolous insects. Methylation also has a similar relationship with gene expression compared to most other holometabolous insects currently studied, with more highly methylated genes showing higher levels of expression and lower levels of methylation being associated with differentially expressed genes. We found no methylation differences on a genomic scale between castes, however 111 genes were differentially methylated. These were involved in a variety of functions including reproductive related processes. We found no relationship between genes that are differentially expressed, or contain differential exon usage between castes with those that show differential methylation between castes. Finally, we also found no common putative orthologous genes differentially methylated between *B. terrestris* and *A. mellifera* reproductive castes.

This is the first data set to accurately quantify methylation at base-pair resolution for *B. terrestris* castes. It confirms low methylation levels throughout the genome as predicted by Sadd et al. (2015). These low levels along with enrichment for CpG methylation in coding regions are also seen in many social insect species, including *A. mellifera* (Lyko et al. 2010) and multiple ant species (Bonasio et al. 2012; Libbrecht et al. 2016). These trends are also seen more generally in holometabolous insects (Provataris et al. 2018). However, they are not completely conserved among all holometabolous insects, for example the primitively social wasp species *Polistes dominula* shows 6% CpG methylation (Weiner et al. 2013), and the highly social termite, *Zootermopsis nevadensis*, has exceptionally high methylation levels compared to the majority of insects (Bewick et al. 2017), with 12% CpG methylation, and methylation being just as common in introns as exons (Glastad et al. 2016).

Higher levels of CpG methylation are associated with higher levels of gene expression in both *B. terrestris* reproductive castes. This is also the case in some other social insects, with Figure 5A and 5D showing almost identical trends to those found in Bonasio et al. (2012), Patalano et al. (2015), and Libbrecht et al. (2016). Additionally, other social insect species show higher methylation in nondifferentially expressed genes as we found here, for example *Dinoponera quadriceps* (Patalano et al. 2015), *Polistes canadensis* (Patalano et al. 2015), *Zootermopsis nevadensis* (Glastad et al. 2016), and *Cerapachys biroi* (Libbrecht et al. 2016). Higher levels of methylation in more highly expressed genes and in nondifferentially expressed genes is thought to indicate a role for methylation in housekeeping genes in some holometabolous insects (Foret et al. 2009; Lyko et al. 2010; Bonasio et al. 2012; Wang et al. 2013; Provataris et al. 2018). High levels of gene body methylation is also found in highly expressed genes in plants; while currently the function is unknown, Zilberman (2017) hypothesizes that it functions to stabilize expression by reducing histone variants and Bewick and Schmitz (2017) hypothesize that it is a by-product of transposable element silencing.

We predicted that if methylation plays a role in reproductive caste determination, we would find differentially methylated genes between castes with reproductive related functions. We found 111 differentially methylated genes that include enriched GO terms for various reproductive-related processes; this suggests methylation has some association with the switch between sterility and reproduction in *B. terrestris*. This supports previous work that exposed *B. terrestris* to a chemical that decreases general methylation levels and found workers were more likely to become reproductive (Amarasinghe et al. 2014), however we did not find a difference in the genome-wide methylation levels of sterile and reproductive workers. It is also worth noting a worker classed as reproductive appeared to show a sterile transcriptional profile and this was included in the pool for the reproductive sample for colony J8. This will have "diluted" the strength of the methylation profile for this particular sample. It is therefore likely our data contain false negatives, meaning there may be differentially methylated genes between reproductive castes that do not appear in our data set.

Although we found differentially methylated genes between castes, we found no evidence for a relationship between methylation and gene expression in relation to reproductive and sterile workers. Only a small nonsignificant number of genes are both differentially methylated and differentially expressed between castes and there is no relationship between the degree of differential methylation and differential expression on a gene level. Previous research using the milkweed bug (*Oncopeltus fasciatus*) found knocking down *Dnmt1*, the gene responsible for DNA methylation maintenance, in ovary tissue with RNAi had no effect on gene expression, however these individuals could no longer reproduce (Bewick et al. 2019). This suggests methylation may play an alternative role, rather than direct regulation of gene expression, in reproduction of some insects. Bewick et al. (2019) suggest this role may be the regulation of genome stability and/or the regulation of vital cellular processes. The variety of GO terms involved in biological processes we obtained for the differentially methylated genes between castes supports this idea.

Additionally, we observed high intercolony variation in methylation, however we did not have sufficient replicates to test for exact differences between colonies. High intercolony variation could suggest that methylation may also play a role in the adaptive abilities of *B. terrestris*. Stable environmentally induced "epialleles" have been proposed to act as an additional layer of information for which selection can act upon (Flores et al. 2013). However, we currently do not know if *B. terrestris* methylation shows transgenerational inheritance or whether a large proportion is wiped during development, as in mammals (Messerschmidt et al. 2014).

It has also been suggested methylation may regulate alternative splicing, rather than expression in some insects (Glastad et al.

2011). We found no evidence here for the role of exon methylation in exonic expression differences between castes. Previous research using honeybees however did find an association between methylation and caste specific alternative splicing. Methylation differences between queens and workers in *A. mellifera* have been associated with caste-specific splicing events (Lyko et al. 2010). Additionally, a knock-down of *Dnmt3* by RNA interference was found to affect alternative splicing patterns in *A. mellifera*, with decreased methylation levels being directly related to exon skipping and intron retention (Li-Byarlay et al. 2013). However, another social insect species, the primitively social wasp, *Polistes dominula*, has also shown no direct association between methylation and alternative splicing (Standage et al. 2016), however this species shows extremely low genome methylation and appears to lack the *Dnmt3* gene responsible for de novo methylation, suggesting that the link between methylation and alternative splicing in insects is variable.

Exon methylation has been shown to play a role in histone modifications and nucleosome stability in mammals (Jones 2012; Singer et al. 2015). These modifications have the ability to affect alternative splicing patterns through RNA polymerase accessibility, meaning while changes in DNA methylation may not be observed as directly related to alternative splicing, it is possible these changes have a downstream effect leading to transcriptional changes (Hunt et al. 2013). The analysis of the relationship between methylation and alternative splicing done here could be elaborated on further to include noncaste specific splicing sites and to also potentially identify the role of exon methylation in other epigenetic processes, which may themselves lead to alternative splicing.

It is also worth noting other epigenetic mechanisms may play a role in caste determination, for example microRNAs have been associated with caste switching in *A. mellifera* (Ashby et al. 2016). Additionally, Simola et al. (2016) found histone acetylation differences between worker castes of *Camponotus floridanus*. They inhibited histone acetylation and found this caused the major worker caste to behave more like a minor worker. This same species has also been shown to have caste specific methylation profiles (Bonasio et al. 2012). These examples indicate that it is likely an interplay between multiple mechanisms that ultimately cause social insect caste differentiation, again supported by the fact we find no association between methylation and caste-specific alternative splicing.

Our final prediction was that differentially methylated genes between worker *B. terrestris* castes would be similar to those found to be differentially methylated between *A. mellifera* reproductive castes if methylation was involved in caste determination in Hymenoptera; we did not find any putative orthologous in common. This supports the idea in Bewick et al. (2019) that methylation may not directly influence caste determination. However, the differentially methylated gene list obtained for *A. mellifera* used queen samples to represent the reproductive caste (Lyko et al. 2010), whereas here reproductive worker samples were used; this could also explain the lack of agreement.

Considerably more experimental research is needed to better define the relationship between epigenetic processes and caste determination in social insects. Future work should focus on the consequences of experimental methylation removal or addition (Pegoraro et al. 2017), as well as exploring additional epigenetic mechanisms to attempt to identify a full pathway leading to reproductive caste differences. For example, CRISPR has recently been used to knockout two sex-determining genes in *A. mellifera* causing individuals to change gender (Mcafee et al. 2019). This technology has also been adapted to be able to change the methylation state of a given loci (Vojta et al. 2016), allowing the possibility of exploring the function of methylation in specific genes.

Overall, we have found that the *B. terrestris* methylome appears similar to some other holometabolous insects in terms of overall levels and the relationship with gene expression. We found no genome-wide methylation differences between reproductive castes, however we did find differentially methylated genes between reproductive castes, with GO terms enriched in many biological processes including reproduction. These results combined with previous research (Amarasinghe et al. 2014) indicate an association between methylation and reproductive caste differences in *B. terrestris*. However, it is clear, owing to the lack of consistency between differentially methylated genes and differentially expressed genes, methylation is not directly responsible for the associated changes in gene expression leading to the different reproductive phenotypes in *B. terrestris*. Additionally, the lack of similarity between differentially methylated genes between castes in *B. terrestris* and between castes in *A. mellifera* suggests that methylation may not directly contribute to caste determination in some Hymenoptera. Future work should focus on the experimental manipulation of epigenetic processes, such as methylation, in social insects to clarify functional roles within and across species.

AUTHOR CONTRIBUTIONS

EBM conceived the study. HM and ZNL conducted the experiment. HM analyzed the data and wrote the initial manuscript. All authors contributed to and reviewed the final manuscript.

ACKNOWLEDGMENTS

Thank you to Dr. Ben Hunt and Boris Berkhout for important advice and discussion regarding data analysis. Thank you to Dr. Ezio Rosato for providing valuable discussion. Thank you to the reviewers for helpful comments and suggestions. This research used the ALICE2 High Performance Computing Facility at the University of Leicester. HM was supported by a NERC CENTA DTP studentship. ZNL was supported by a BBSRC MIBTP DTP studentship. EBM was funded by NERC grant NE/N010019/1. The authors declare no conflict of interests.

DATA ARCHIVING

Data have been deposited in GenBank under NCBI BioProject: PRJNA533306. All code will also be made available at: https://doi.org/10.5281/zenodo.2394171.

LITERATURE CITED

Akalin, A., M. Kormaksson, S. Li, F. E. Garrett-bakelman, M. E. Figueroa, A. Melnick, et al. 2012. methylKit: A comprehensive R package for the analysis of genome-wide DNA methylation profiles. Genome Biol. 13. https://doi.org/10.1186/gb-2012-13-10-r87.

Alaux, C., P. Jaisson, and A. Hefetz. 2006. Regulation of worker reproduction in bumblebees (*Bombus terrestris*): Workers eavesdrop on a queen signal. Behav. Ecol. Sociobiol. 60:439–446.

Amarasinghe, H. E., C. I. Clayton, and E. B. Mallon. 2014. Methylation and worker reproduction in the bumble-bee (*Bombus terrestris*). Proc. R. Soc. B Biol. Sci. 281. https://doi.org/10.1098/rspb.2013.2502.

Amsalem, E., O. Malka, C. Grozinger, and A. Hefetz. 2014. Exploring the role of juvenile hormone and vitellogenin in reproduction and social behavior in bumble bees. BMC Evol. Biol. 14:45.

Anders, S., A. Reyes, and W. Huber. 2012. Detecting differential usage of exons from RNA-seq data. Genome Res. 22:2008–2017.

Anders, S., P. T. Pyl, and W. Huber. 2015. HTSeq-A Python framework to work with high-throughput sequencing data. Bioinformatics 31:166–169.

Arsenault, S. V., B. G. Hunt, and S. M. Rehan. 2018. The effect of maternal care on gene expression and DNA methylation in a subsocial bee. Nat. Commun. 9. https://doi.org/10.1038/s41467-018-05903-0.

Ashby, R., S. Forêt, I. Searle, and R. Maleszka. 2016. MicroRNAs in honey bee caste determination. Sci. Rep. 6. https://doi.org/10.1038/srep18794.

Bao, Y. Y., X. Qin, B. Yu, L. B. Chen, Z. C. Wang, and C. X. Zhang. 2014. Genomic insights into the serine protease gene family and expression profile analysis in the planthopper, *Nilaparvata lugens*. BMC Genomics 15. https://doi.org/10.1186/1471-2164-15-507.

Bebane, P., B. J. Hunt, M. Pegoraro, A. Jones, H. Marshall, E. Rosato, et al. 2019. The effects of the neonicotinoid imidacloprid on gene expression and DNA methylation in the buff-tailed bumblebee *Bombus terrestris*. Proc. R. Soc. B 286:20190718.

Benjamini, Y., and Y. Hochberg. 1995. Controlling the false discovery rate: A practical and powerful approach to multiple testing. J. R. Statist. Soc. 57:289–300.

Bewick, A. J., and R. J. Schmitz. 2017. Gene body DNA methylation in plants. Curr. Opin. Plant Biol. 36:103–110.

Bewick, A. J., K. J. Vogel, A. J. Moore, and R. J. Schmitz. 2017. Evolution of DNA methylation across insects. Mol. Biol. Evol. 34:654–665.

Bewick, A. J., Z. Sanchez, E. C. McKinney, A. J. Moore, P. J. Moore, and R. J. Schmitz. 2019. Dnmt1 is essential for egg production and embryo viability in the large milkweed bug, *Oncopeltus fasciatus*. Epigenetics Chromatin 12:1–14.

Bloch, G. 1999. Regulation of queen-worker conflict in bumble-bee (*Bombus terrestris*) colonies. Proc. R. Soc. Lond. B 266:2465–2469.

Bonasio, R., Q. Li, J. Lian, N. S. Mutti, L. Jin, H. Zhao, et al. 2012. Genome-wide and caste-specific DNA methylomes of the ants *Camponotus floridanus* and *Harpegnathos saltator*. Curr. Biol. 22:1755–1764.

Camacho, C., G. Coulouris, V. Avagyan, N. Ma, J. Papadopoulos, K. Bealer, et al. 2009. BLAST+: Architecture and applications. BMC Bioinformatics 10:1–9.

Cheng, L., and Y. Zhu. 2014. A classification approach for DNA methylation profiling with bisulfite next-generation sequencing data. Bioinformatics 30:172–179.

Chevin, L.-M., R. Lande, and G. M. Mace. 2010. Adaptation, plasticity, and extinction in a changing environment: Towards a predictive theory. PLoS Biol. 8:e1000357.

Collins, D. H., I. Mohorianu, M. Beckers, V. Moulton, T. Dalmay, and A. F. Bourke. 2017. MicroRNAs associated with caste determination and differentiation in a primitively eusocial insect. Sci. Rep. 7. https://doi.org/10.1038/srep45674.

Dobin, A., T. R. Gingeras, and C. Spring. 2016. Mapping RNA-seq Reads with STAR Alexander. Curr. Protoc. Bioinformatics 51:1–11.

Duchateau, M. J. and H. H. W. Velthuis. 1988. Development and reproductive strategies in *Bombus terrestris* colonies. Behaviour 107:186–207.

Fang, F., E. Hodges, A. Molaro, M. Dean, G. J. Hannon, and A. D. Smith. 2012. Genomic landscape of human allele-specific DNA methylation. Proc. Natl. Acad. Sci. 109:7332–7337.

Feng, S., S. J. Cokus, X. Zhang, P.-Y. Chen, M. Bostick, M. G. Goll, et al. 2010. Conservation and divergence of methylation patterning in plants and animals. Proc. Natl. Acad. Sci. 107:8689–8694.

Flores, K. B., F. Wolschin, and G. V. Amdam. 2013. The role of methylation of DNA in environmental adaptation. Integr. Comp. Biol. 53:359–372.

Foret, S., R. Kucharski, Y. Pittelkow, G. A. Lockett, and R. Maleszka. 2009. Epigenetic regulation of the honey bee transcriptome: Unravelling the nature of methylated genes. BMC Genomics 10:472.

Foster, R. L., A. Brunskill, D. Verdirame, and S. O'Donnell. 2004. Reproductive physiology, dominance interactions, and division of labour among bumble bee workers. Physiol. Entomol. 29:327–334.

Geva, S., K. Hartfelder, and G. Bloch. 2005. Reproductive division of labor, dominance, and ecdysteroid levels in hemolymph and ovary of the bumble bee *Bombus terrestris*. J. Insect Physiol. 51:811–823.

Glastad, K. M., B. G. Hunt, S. V. Yi, and M. A. Goodisman. 2011. DNA methylation in insects: On the brink of the epigenomic era. Insect Mol Biol 20:553–565.

Glastad, K. M., L. M. Chau, and M. A. Goodisman. 2015. Epigenetics in social insects. Pp. 227–269 *in* Physiology, behavior, genomics of social insects. 1 ed. Vol. 48. Elsevier Ltd, Amsterdam, The Netherlands.

Glastad, K. M., K. Gokhale, J. Liebig, and M. A. D. Goodisman. 2016. The caste- and sex-specific DNA methylome of the termite *Zootermopsis nevadensis*. Sci. Rep. 6. https://doi.org/10.1038/srep37110.

Grothendieck, G. 2017. sqldf: Manipulate R Data Frames Using SQL R package. Available at: https://cran.r-project.org/package=sqldf.

Herb, B. R., F. Wolschin, K. D. Hansen, M. J. Aryee, B. Langmead, R. Irizarry, et al. 2012. Reversible switching between epigenetic states in honeybee behavioral subcastes. Nat. Neurosci. 15:1371–1373.

Hunt, B. G., K. M. Glastad, S. V. Yi, and M. A. D. Goodisman. 2013. The function of intragenic DNA methylation: Insights from insect epigenomes. Integr. Comp. Biol. 53:319–328.

A Jones, P.. 2012. Functions of DNA methylation: Islands, start sites, gene bodies and beyond. Nat. Rev. Genet. 13:484–492.

Krueger, F., and S. R. Andrews. 2011. Bismark: A flexible aligner and methylation caller for Bisulfite-Seq applications. Bioinformatics 27:1571–1572.

Krueger, F., S. R. Andrews, and C. S. Osborne. 2011. Large scale loss of data in low-diversity illumina sequencing libraries can be recovered by deferred cluster calling. PLoS ONE 6:4–10.

Kucharski, R., J. Maleszka, S. Foret, and R. Maleszka. 2008. Nutritional control of reproductive status in honeybees via DNA methylation. Science 319:1827–1830.

Langmead, B., and S. L. Salzberg. 2012. Fast gapped-read alignment with Bowtie 2. Nat. Methods 9:357–359.

Li, B., L. Hou, D. Zhu, X. Xu, S. An, and X. Wang. 2018. Identification and caste-dependent expression patterns of DNA methylation associated genes in *Bombus terrestris*. Sci. Rep. 8. https://doi.org/10.1038/s41598-018-20831-1.

Li-Byarlay, H., Y. Li, H. Stroud, S. Feng, T. C. Newman, M. Kaneda, et al. 2013. RNA interference knockdown of DNA methyl-transferase 3 affects gene alternative splicing in the honey bee. Proc. Natl. Acad. Sci. 110:12750–12755.

Libbrecht, R., P. R. Oxley, L. Keller, and D. J. C. Kronauer. 2016. Robust DNA methylation in the clonal raider ant brain. Curr. Biol. 26:1–5.

Liu, S., A. Aageaard, J. Bechsgaard, and T. Bilde. 2019. DNA methylation patterns in the social spider, *Stegodyphus dumicola*. Genes 10:137.

Lonsdale, Z., K. Lee, M. Kiriakidu, H. Amarasinghe, D. Nathanael, C. J. O'Connor, et al. 2017. Allele specific expression and methylation in the bumblebee, *Bombus terrestris*. PeerJ 5:e3798.

Love, M. I., W. Huber, and S. Anders. 2014. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. Genome Biol. 15:550.

Lyko, F., S. Foret, R. Kucharski, S. Wolf, C. Falckenhayn, and R. Maleszka. 2010. The honey bee epigenomes: Differential methylation of brain DNA in queens and workers. PLoS Biol. 8. https://doi.org/10.1371/journal.pbio.1000506.

Martin, M. 2011. Cutadapt removes adapter sequences from high-throughput sequencing reads. EMBnet.journal 17:10.

Matsuura, K., N. Mizumoto, K. Kobayashi, T. Nozaki, T. Fujita, T. Yashiro, et al. 2018. A genomic imprinting model of termite caste determination: Not genetic but epigenetic inheritance influences offspring caste fate. The Am. Nat. 191:677–690.

Mcafee, A., J. S. Pettis, D. R. Tarpy, and L. J. Foster. 2019. *Feminizer* and *doublesex* knock-outs cause honey bees to switch sexes. PLoS Biol. 17:e3000256.

Messerschmidt, D. M., B. B. Knowles, and D. Solter. 2014. DNA methylation dynamics during epigenetic reprogramming in the germline and preimplantation embryos. Genes Dev. 28:812–828.

Mott, B. M., J. Gadau, and K. E. Anderson. 2015. Phylogeography of *Pogonomyrmex barbatus* and *P*. rugosus harvester ants with genetic and environmental caste determination. Ecol. Evol. 5:2798–2826.

Patalano, S., A. Vlasova, C. Wyatt, P. Ewels, F. Camara, P. G. Ferreira, et al. 2015. Molecular signatures of plastic phenotypes in two eusocial insect species with simple societies. Proc. Natl. Acad. Sci. 112:13970–13975.

Pegoraro, M., H. Marshall, Z. N. Lonsdale, and E. B. Mallon. 2017. Do social insects support Haig's kin theory for the evolution of genomic imprinting? Epigenetics 12:725–742.

Provataris, P., K. Meusemann, O. Niehuis, S. Grath, and B. Misof. 2018. Signatures of DNA methylation across insects suggest reduced DNA methylation levels in holometabola. Genome Biol. Evol. 10:1185–1197.

Sadd, B. M., S. M. Barribeau, G. Bloch, D. C. de Graaf, P. Dearden, C. G. Elsik, et al. 2015. The genomes of two key bumblebee species with primitive eusocial organization. Genome Biol. 16:76.

Schneider, C. A., W. S. Rasband, and K. W. Eliceiri. 2012. NIH Image to ImageJ: 25 Years of image analysis. Nat. Methods 9:671–675.

Schultz, M. D., R. J. Schmitz, and J. R. Ecker. 2012. 'Leveling' the playing field for analyses of single-base resolution DNA methylomes. Trends Genet. 28:583–585.

Shaham, R., R. Ben-Shlomo, U. Motro, and T. Keasar. 2016. Genome methylation patterns across castes and generations in a parasitoid wasp. Ecol. Evol. 6:7943–7953.

Simola, D. F., R. J. Graham, C. M. Brady, B. L. Enzmann, C. Desplan, A. Ray, et al. 2016. Epigenetic (re)programming of caste-specific behavior in the ant *Camponotus floridanus*. Science 351. https://doi.org/10.1126/science.aac6633.

Singer, M., I. Kosti, L. Pachter, and Y. Mandel-Gutfreund. 2015. A diverse epigenetic landscape at human exons with implication for expression. Nucleic Acids Res. 43:3498–3508.

Standage, D. S., A. J. Berens, K. M. Glastad, A. J. Severin, V. P. Brendel, and A. L. Toth. 2016. Genome, transcriptome, and methylome sequencing of a primitively eusocial wasp reveal a greatly reduced DNA methylation system in a social insect. Mol. Ecol. 25:1769–1784.

Supek, F., M. Bošnjak, N. Škunca, and T. Šmuc. 2011. REVIGO summarizes and visualizes long lists of gene ontology terms. PLoS ONE 6:e21800.

Vojta, A., P. Dobrinic, V. Tadic, L. Bockor, P. Korac, B. Julg, et al. 2016. Repurposing the CRISPR-Cas9 system for targeted DNA methylation. Nucleic Acids Res. 44:5615–5628.

Wakefield, R. I., B. O. Smith, X. Nan, A. Free, A. Soteriou, D. Uhrin, et al. 1999. The solution structure of the domain from MeCP2 that binds to methylated DNA. J. Mol. Biol. 291:1055–1065.

Wang, X., D. Wheeler, A. Avery, A. Rago, J. H. Choi, J. K. Colbourne, et al. 2013. Function and evolution of DNA methylation in *Nasonia vitripennis*. PLoS Genet. 9:e1003872.

Weiner, S. A., D. A. Galbraith, D. C. Adams, N. Valenzuela, F. B. Noll, C. M. Grozinger, et al. 2013. A survey of DNA methylation across social insect species, life stages, and castes reveals abundant and caste-associated methylation in a primitively social wasp. Naturwissenschaften 100:795–799.

Winkler, A. M., M. A. Webster, D. Vidaurre, T. E. Nichols, and S. M. Smith. 2015. Multi-level block permutation. NeuroImage 123:253–268.

Woodard, S. H., J. D. Lozier, D. Goulson, P. H. Williams, J. P. Strange, and S. Jha. 2015. Molecular tools and bumble bees: Revealing hidden details of ecology and evolution in a model system. Mol. Ecol. 24:2916–2936.

Zilberman, D. 2017. An evolutionary case for functional gene body methylation in plants and animals. Genome Biol. 18:17–19.

Associate Editor: Z. Gompert

Supporting Information

Additional supporting information may be found online in the Supporting Information section at the end of the article.

Figure S1. Histogram of the number of differentially methylated sites obtained from 10,000 permutations.
Figure S2. (a) PCA plot showing samples cluster more closely by colony than by reproductive status.
Figure S3. (a) The mean weighted methylation level across colonies for each genomic feature for both reproductive and sterile workers.
Figure S4. Graphs generated from differential expression analysis using DESEQ2 for all samples.
Figure S5. Graphs generated from differential expression analysis using DESEQ2 for all samples, excluding J8_24.

Appendix B

Appendix: Chapter 4

B.1 Additional figures

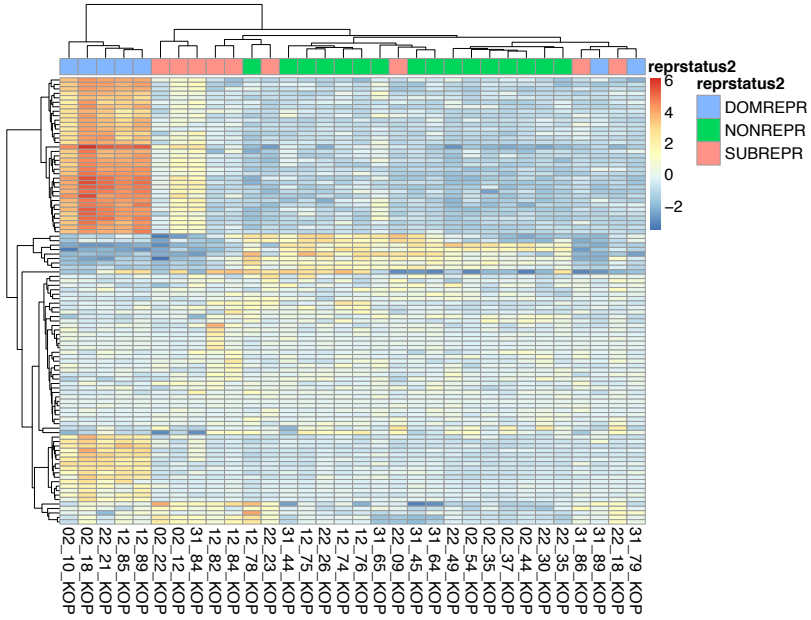


Figure B.1: Heatmaps showing the 100 most differentially expressed genes between dominant reproductive workers and sterile workers, with subordinate reproductive workers also shown. Sample names along the bottom refer to the colony of origin, the individual and the tissue type and KOP = head. Red indicates up-regulation and blue indicates down-regulation.

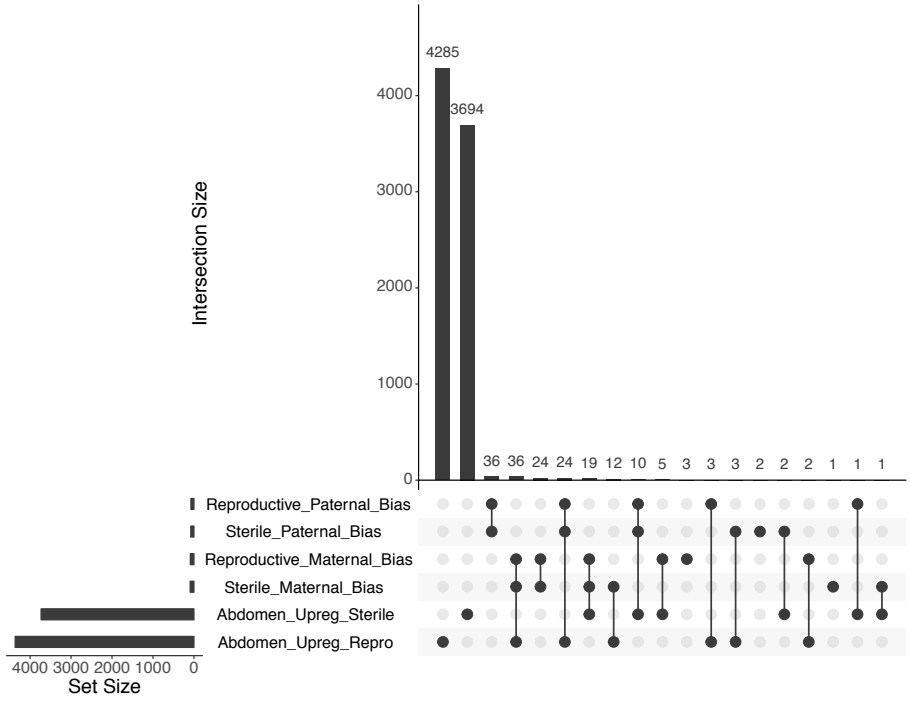


Figure B.2: Overlapping genes showing parent-of-origin expression in reproductive (queen-right) and sterile (queen-less) workers with genes showing differential expression in abdomen tissue. The set size indicates the number of genes in each list. The intersection size shows how many genes the corresponding lists have in common. A single dot refers to the number of genes unique to each list.

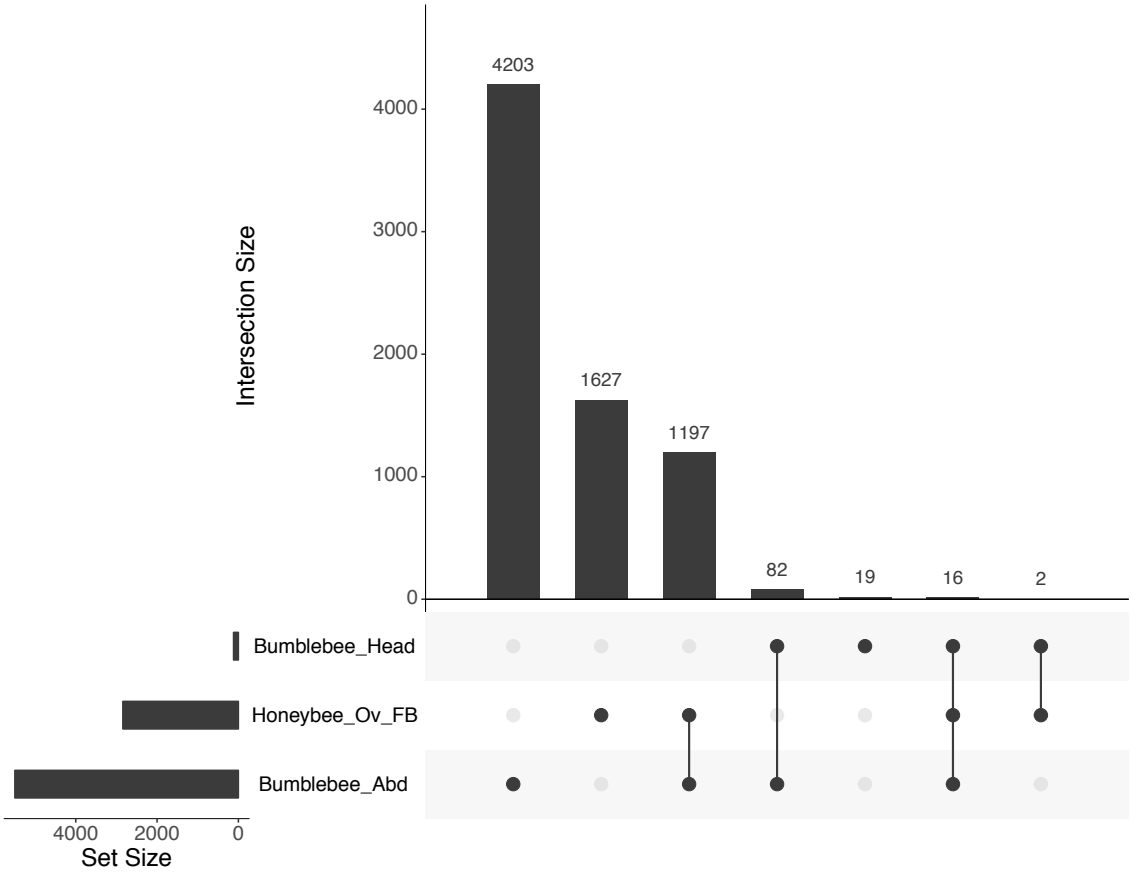


Figure B.3: Overlapping genes showing differential expression between reproductive (queen-right) and sterile (queen-less) workers of *B. terrestris* head and abdomen tissue and *A. mellifera* ovary/fatbody tissue (genes identified in Galbraith *et al.* (2016a)). The set size indicates the number of genes in each list. The intersection size shows how many genes the corresponding lists have in common. A single dot refers to the number of genes unique to each list.

Appendix C

Appendix: Chapter 5

C.1 Poor quality sequencing comparison

All samples were originally sequenced by Liverpool Genomics. The data received were of too poor quality to obtain any reliable results. The first attempt at sequencing produced considerable methylation-bias within the reads (Fig. C.1). This is where a cytosine is more likely to be called as 'methylated' if it occurs in a certain position within a given read. This bias decreased upon the second attempt at sequencing by Liverpool Genomics. However, the reads still contained considerable bias. The final data set used, generated from BGI, had very little bias (Fig. C.1). As well as the removal of an unacceptable level of false positives within the data, BGI also provided slightly more data with greater mapping and less duplication, Table C.1.

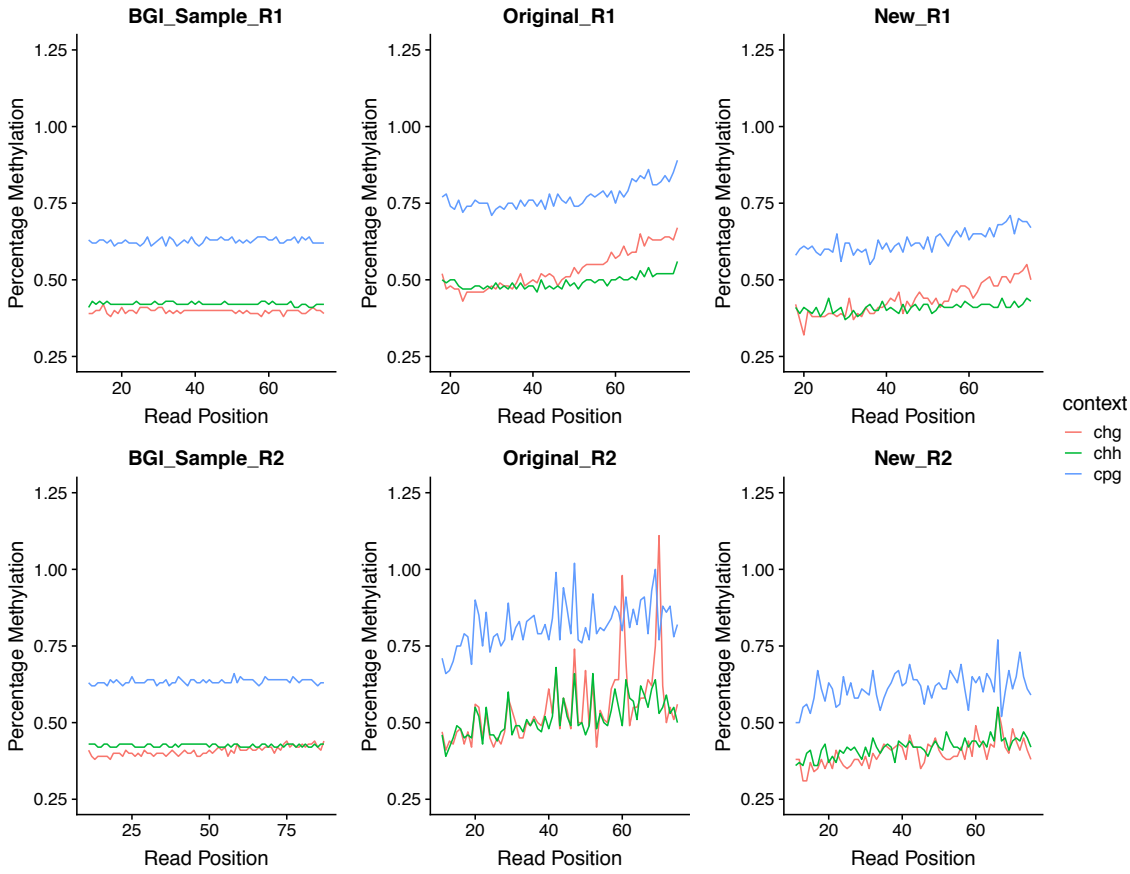


Figure C.1: M-bias plots for sample W08 (pooled worker sample from colony 08). M-bias plots show the average percentage of methylated bases per read position. Read 1 and read 2 are shown separately. All reads have been pre-trimmed to remove 3' base bias. 'Original' refers to the first round of sequencing generated by Liverpool Genomics. 'New' refers to the second round of sequencing carried out by Liverpool Genomics. 'BGI' refers to the sequencing carried out by BGI.

Table C.1: Summary statistics of the data generated by Liverpool Genomics and BGI. All statistics are a mean across all samples.

	Liverpool	**BGI**
Total Reads	30166644	30391345
Unique Mapping (%)	56	60
Total Mapped Reads	16810138	18194268
Duplicated Reads (%)	45	34
Final Reads	9278762	11897611
Original Data Remaining (%)	30	40
Genome Coverage	9.7	12.44

Appendix D

Appendix: Chapter 6

D.1 High-hardness COMBO

Protocol for creating the high-hardness culturing medium, modified from the University of Birmingham, School of Biosciences, Daphnia Facility, Standard Operating Procedure version 1.

Table D.1: Main stock solutions needed to create high-hardness COMBO media for culturing *Daphnia magna*.

Component Number	**Compound**	**Chemical Formula**	**Concentration (g/L)**
1	Calcium chloride dihydrate	$CaCl_2.2H_2O$	110.28
2	Magnesium sulphate heptahydrate	$MgSO_4.7H_2O$	113.5
3	Potassium phosphate dibasic	K_2HPO_4	1.742
4	Sodium nitrate	$NaNO_3$	17.0
5	Sodium metasilicate nonahydrate	$Na_2SiO_3.9H_2O$	13.267
6	Boric acid	H_3BO_3	24.0
7	Potassium chloride	KCl	5.96
8	Sodium bicarbonate	$NaHCO_3$	63.0
9	Sodium selenite	$NaSeO_3$	40μg/L

Table D.2: Stock solutions required for Animate. All stock solutions are to be dispensed into 1.5ml aliquots in Eppendorf tubes and stored at -20°C.

Component Number	**Compound**	**Chemical Formula**	**Concentration (g/L)**
10	Lithium chloride	LiCl	31
11	Rubidium chloride	RbCl	7.0
12	Strontium chloride hexahydrate	$SrCl_2.6H_2O$	15
13	Sodium bromide	NaBr	1.6
14	Potassium iodide	KI	0.33

To prepare the Animate stock solution add 1ml of each of stock solutions **10** to **14** to approximately 500ml of dH_2O and adjust the volume to 1 litre. The Animate stock solution should be stored at approximately 5°C prior to use.

Table D.3: Stock solutions required for the VIM. All stock solutions are to be dispensed into 1.5ml aliquots in Eppendorf tubes and stored at -20°C. Additionally, the B12 should be covered with foil to avoid light exposure.

Component Number	**Compound**	**Preparation**
15	Biotin (d-biotin)	10mg into 96ml of dH_2O
16	B12 (cyanocobalamin)	10mg into 89ml of dH_2O

To prepare the vitamin solution, remove one aliquot of Biotin and B12 from the freezer and allow to defrost. To a 50ml volumetric flask, add 30ml of dH_2O, 0.5ml biotin, 0.5ml B12 and 10mg of Thiamine HCl. Adjust the volume to 50ml with dH_2O then transfer the whole volume to a Duran bottle covered with foil to shield from light and store at approximately 5°C for up to a maximum of 1 week.

To prepare 4L of high-hardness COMBO, add 4ml of stock solutions **1** to **7**, 8ml of stock solution **8** and 200μl of stock solution **9** to 3.5L of dH_2O then adjust the volume to 4 litres. Aerate the medium for approximately 24 hours then adjust the pH to 7.6 – 7.8 prior to the addition of 4ml of Animate and 2ml of VIM stock solutions.

D.2 DNA extraction: optimised protocol

Protocol optimised using the Epicenter MasterPure^{TM} Complete DNA and RNA Purification Kit by Dr. Leda Mirbahai.

Reagents:

- 70% Ethanol (On ice)
- Isopropanol (On ice)
- RNase A (1mg/ml)

- Proteinase K (50μg/μl)
- MPC Protein precipitation buffer (from kit)
- 1x Lysis buffer (from kit)
- Liquid nitrogen

Additional equipment:

- Heating block at 37°C
- Heating block at 65°C
- Centrifuge at 4°C

Protocol:

1. Add 300μl of the lysis buffer and 1μl of proteinase K to a tube of around 20 4-day old *Daphnia*.
2. Carry out tissue lysis using a Geno/Grinder®: 30seconds at 1750rpm.
3. Transfer the tube to a heating block set at 65°C, and incubate for 15 minutes. Invert the tube three times during this time.
4. Cool the samples to 37°C.
5. Add 4μl of 1mg/ml RNase A.
6. Place the tube on heating block at 37°C for 30 minutes.
7. Place on ice for five minutes.
8. Add 175μl of MPC protein reagent and mix well by pipetting it up and down several times.
9. Centrifuge at 4°C for 10 minutes at 10,000g.
10. Transfer the supernatant to a clean tube.
11. Add 500μl of ice cold isopropanol and mix well by pipetting.
12. Centrifuge at 4°C for 10 minutes at 10,000g.

13. Remove and discard the supernatant, the DNA should now be a visible pellet.
14. Add 500μl of ice cold 70% ethanol.
15. Invert the tube once without disturbing the pellet.
16. Centrifuge at 4°C for 10 minutes at 10,000g.
17. Discard the liquid.
18. Add 500μl of ice cold 70% ethanol.
19. Invert the tube once without disturbing the pellet.
20. Centrifuge at 4°C for 10 minutes at 10,000g.
21. Remove all liquid (use a 10μl pipette to remove as much as possible).
22. Leave the tubes on a bench with the lids open to dry for 30 minutes.
23. Add 30μl of RNase/DNase free water, dissolve and quantify.

References

Akalin, A., Kormaksson, M., Li, S., Garrett-bakelman, F. E., Figueroa, M. E., Melnick, A., and Mason, C. E. 2012. methylKit: a comprehensive R package for the analysis of genome-wide DNA methylation profiles. *Genome Biology*, 13(R87).

Alaux, C., Jaisson, P., and Hefetz, A. 2006. Regulation of worker reproduction in bumblebees (*Bombus terrestris*): workers eavesdrop on a queen signal. *Behavioral Ecology and Sociobiology*, 60(3): 439–446.

Amarasinghe, H. E., Clayton, C. I., and Mallon, E. B. 2014. Methylation and worker reproduction in the bumble-bee (*Bombus terrestris*). *Proceedings of the Royal Society B: Biological Sciences*, 281(20132502).

Amarasinghe, H. E., Toghill, B. J., and Mallon, E. B. 2015. Allele specific expression in worker reproduction genes in the bumblebee *Bombus terrestris*. *PeerJ*, page 3:e1079.

Amsalem, E., Malka, O., Grozinger, C., and Hefetz, A. 2014. Exploring the role of juvenile hormone and vitellogenin in reproduction and social behavior in bumble bees. *BMC Evolutionary Biology*, 14(1): 45.

Anaka, M., Lynn, A., McGinn, P., and Lloyd, V. K. 2009. Genomic imprinting in Drosophila has properties of both mammalian and insect imprinting. *Development Genes and Evolution*, 219(2): 59–66.

Anders, S., Reyes, A., and Huber, W. 2012. Detecting differential usage of exons from RNA-seq data. *Genome Research*, 22(10): 2008–2017.

Anders, S., McCarthy, D. J., Chen, Y., Okoniewski, M., Smyth, G. K., Huber, W., and Robinson, M. D. 2013. Count-based differential expression analysis of RNA sequencing data using R and Bioconductor. *Nature Protocols*, 8(9): 1765–1786.

Anders, S., Pyl, P. T., and Huber, W. 2015. HTSeq-A Python framework to work with high-throughput sequencing data. *Bioinformatics*, 31(2): 166–169.

Andrews, S. 2010. Babraham Bioinformatics - FastQC A

Quality Control tool for High Throughput Sequence Data. *http://www.bioinformatics.babraham.ac.uk/projects/fastqc/*.

Arsenault, S. V., Hunt, B. G., and Rehan, S. M. 2018. The effect of maternal care on gene expression and DNA methylation in a subsocial bee. *Nature Communications*, 9(3468).

Artemov, A. V., Mugue, N. S., Rastorguev, S. M., Zhenilo, S., Mazur, A. M., Tsygankova, S. V., Boulygina, E. S., Kaplun, D., Nedoluzhko, A. V., Medvedeva, Y. A., and Prokhortchouk, E. B. 2017. Genome-Wide DNA Methylation Profiling Reveals Epigenetic Adaptation of Stickleback to Marine and Freshwater Conditions. *Molecular biology and evolution*, 34(9): 2203–2213.

Ashby, R., Forêt, S., Searle, I., and Maleszka, R. 2016. MicroRNAs in Honey Bee Caste Determination. *Scientific Reports*, 6(18794).

Asselman, J., De Coninck, D. I., Vandegehuchte, M. B., Jansen, M., Decaestecker, E., De Meester, L., Vanden Bussche, J., Vanhaecke, L., Janssen, C. R., and De Schamphelaere, K. A. 2015. Global cytosine methylation in *Daphnia magna* depends on genotype, environment, and their interaction. *Environmental Toxicology and Chemistry*, 34(5): 1056–1061.

Auwera, G. 2014. The GATK Best Practices for variant calling on RNAseq, in full detail — GATK-Forum. *https://gatkforums.broadinstitute.org/gatk/discussion/3892/the-gatk-best-practices-for-variant-calling-on-rnaseq-in-full-detail*.

Babak, T., Deveale, B., Tsang, E. K., Zhou, Y., Li, X., Smith, K. S., Kukurba, K. R., Zhang, R., Li, J. B., Van Der Kooy, D., Montgomery, S. B., and Fraser, H. B. 2015. Genetic conflict reflected in tissue-specific maps of genomic imprinting in human and mouse. *Nature Genetics*, 47(5): 544–549.

Baird, D. J., Barber, I., Bradley, M., Soares, A. M. V. M., and Calow, P. 1991. A comparative study of genotype sensitivity to acute toxic stress using clones of *Daphnia magna straus*. *Ecotoxicology and Environmental Safety*, 21: 257–265.

Bannister, A. J. and Kouzarides, T. 2011. Regulation of chromatin by histone modifications. *Cell Research*, 21(3): 381–395.

Bao, Y. Y., Qin, X., Yu, B., Chen, L. B., Wang, Z. C., and Zhang, C. X. 2014. Genomic insights into the serine protease gene family and expression profile analysis in the planthopper, *Nilaparvata lugens*. *BMC Genomics*, 15(1).

Barlow, D. P. 2011. Genomic Imprinting: A Mammalian Epigenetic Discovery Model. *Annual Review of Genetics*, 45(1): 379–403.

Barlow, D. P. and Bartolomei, M. S. 2014. Genomic Imprinting in Mammals. *Cold Spring Harb Perspect Biol*, 6(a018282).

Bassett, A. R. and Liu, J. L. 2014. CRISPR/Cas9 and Genome Editing in *Drosophila*. *Journal of Genetics and Genomics*, 41(1): 7–19.

Bebane, P., Hunt, B. J., Pegoraro, M., Jones, A., Marshall, H., Rosato, E., and Mallon, E. 2019. The effects of the neonicotinoid imidacloprid on gene expression and DNA methylation in the buff-tailed bumblebee *Bombus terrestris*. *Proc. R. Soc. B*, 286: 20190718.

Benjamini, Y. and Hochberg, Y. 1995. Controlling the false discovery rate: a practical and powerful approach to multiple testing. *Journal of the Royal Statistical Society*, 57(1): 289–300.

Berg, S., Jeppesen, E., Sandergaard, M., and Mortensen, E. 1994. Environmental effects of introducing whitefish, *Coregonus lavaretus* (L.), in Lake Ring. *Hydrobiologia*, 275-276(1): 71–79.

Bewick, A. J. and Schmitz, R. J. 2017. Gene body DNA methylation in plants. *Current Opinion in Plant Biology*, 36: 103–110.

Bewick, A. J., Vogel, K. J., Moore, A. J., and Schmitz, R. J. 2016. Evolution of DNA methylation across insects. *Molecular Biology and Evolution*, 34(3): 654–665.

Bewick, A. J., Sanchez, Z., McKinney, E. C., Moore, A. J., Moore, P. J., and Schmitz, R. J. 2019. Dnmt1 is essential for egg production and embryo viability in the large milkweed bug, *Oncopeltus fasciatus*. *Epigenetics and Chromatin*, 12(1): 1–14.

Blecher-Gonen, R., Barnett-Itzhaki, Z., Jaitin, D., Amann-Zalcenstein, D., Lara-Astiaso, D., and Amit, I. 2013. High-throughput chromatin immunoprecipitation for

genome-wide mapping of in vivo protein-DNA interactions and epigenomic states. *Nature Protocols*, 8(3): 539–554.

Blinova, I., Kanarbik, L., Irha, N., and Kahru, A. 2017. Ecotoxicity of nanosized magnetite to crustacean *Daphnia magna* and duckweed *Lemna minor*. *Hydrobiologia*, 798(1): 141–149.

Bloch, G. 1999. Regulation of queen-worker conflict in bumble-bee (*Bombus terrestris*) colonies. *Proc. R. Soc. Lond. B*, (266): 2465–2469.

Bonasio, R., Li, Q., Lian, J., Mutti, N. S., Jin, L., Zhao, H., Zhang, P., Wen, P., Xiang, H., Ding, Y., Jin, Z., Shen, S. S., Wang, Z., Wang, W., Wang, J., Berger, S. L., Liebig, J. J., Zhang, G., and Reinberg, D. 2012. Genome-wide and caste-specific DNA methylomes of the ants *Camponotus floridanus* and *Harpegnathos saltator*. *Current Biology*, 22(19): 1755–1764.

Broad Institute 2018. Picard Tools - By Broad Institute. *http://broadinstitute.github.io/picard/*.

Brown, A. H. and Yan, N. D. 2015. Food quantity affects the sensitivity of Daphnia to road salt. *Environmental Science and Technology*, 49(7): 4673–4680.

Buenrostro, J. D., Wu, B., Chang, H. Y., and Greenleaf, W. J. 2015. ATAC-seq: A method for assaying chromatin accessibility genome-wide. *Current Protocols in Molecular Biology*, January: 1–21.

Burggren, W. 2016. Epigenetic Inheritance and Its Role in Evolutionary Biology: Re-Evaluation and New Perspectives. *Biology*, 5(2): 24.

Burggren, W. W. and Crews, D. 2014. Epigenetics in comparative biology: Why we should pay attention. *Integrative and Comparative Biology*, 54(1): 7–20.

Camacho, C., Coulouris, G., Avagyan, V., Ma, N., Papadopoulos, J., Bealer, K., and Madden, T. L. 2009. BLAST+: Architecture and applications. *BMC Bioinformatics*, 10: 1–9.

Cardoso-Júnior, C. A., Fujimura, P. T., Santos-Júnior, C. D., Borges, N. A., Ueira-Vieira, C., Hartfelder, K., Goulart, L. R., and Bonetti, A. M. 2017. Epigenetic

modifications and their relation to caste and sex determination and adult division of labor in the stingless bee *Melipona scutellaris*. *Genetics and Molecular Biology*, 40(1): 61–68.

Charalambous, M., Smith, F. M., Bennett, W. R., Crew, T. E., Mackenzie, F., and Ward, A. 2003. Disruption of the imprinted Grb10 gene leads to disproportionate overgrowth by an Igf2-independent mechanism. *Proceedings of the National Academy of Sciences*, 100(14): 8292–8297.

Cheng, L. and Zhu, Y. 2014. A classification approach for DNA methylation profiling with bisulfite next-generation sequencing data. *Bioinformatics*, 30(2): 172–179.

Chevin, L.-M., Lande, R., and Mace, G. M. 2010. Adaptation, Plasticity, and Extinction in a Changing Environment: Towards a Predictive Theory. *PLoS Biology*, 8(4): e1000357.

Christman, J. K. 2002. 5-Azacytidine and 5-aza-2′-deoxycytidine as inhibitors of DNA methylation: Mechanistic studies and their implications for cancer therapy. *Oncogene*, 21(35 REV. ISS. 3): 5483–5495.

Colgan, T. J., Carolan, J. C., Bridgett, S. J., Sumner, S., Blaxter, M. L., and Brown, M. J. 2011. Polyphenism in social insects: insights from a transcriptome-wide analysis of gene expression in the life stages of the key pollinator, *Bombus terrestris*. *BMC genomics*, 12(1): 623.

Collins, D. H., Mohorianu, I., Beckers, M., Moulton, V., Dalmay, T., and Bourke, A. F. 2017. MicroRNAs Associated with Caste Determination and Differentiation in a Primitively Eusocial Insect. *Scientific Reports*, 7(45674).

Cook, N., DJ, P., Tauber, E., BA, P., and Shuker, D. M. 2019. Validating the demethylating effects of 5-aza-2'-deoxycytidine in insects requires a whole-genome approach (A reply to Ellers et al.). *The American Naturalist*, 194(3).

Corona, M., Libbrecht, R., and Wheeler, D. E. 2016. Molecular mechanisms of phenotypic plasticity in social insects. *Current Opinion in Insect Science*, 13: 55–60.

Crouse, H. V., Brown, A., and Mumford, B. C. 1971. L-chromosome inheritance and the

problem of chromosome "imprinting" in Sciara (Sciaridae, Diptera). *Chromosoma*, 34(3): 324–339.

Cuenca Cambronero, M., Marshall, H., De Meester, L., Davidson, T. A., Beckerman, A. P., and Orsini, L. 2018. Predictability of the impact of multiple stressors on the keystone species Daphnia. *Scientific Reports*, 8(1): 17572.

Day, T. and Bonduriansky, R. 2004. Intralocus sexual conflict can drive the evolution of genomic imprinting. *Genetics*, 167(4): 1537–1546.

Delaval, K. and Feil, R. 2004. Epigenetic regulation of mammalian genomic imprinting. *Current Opinion in Genetics & Development*, 14: 188–195.

Dixon, G., Liao, Y., Bay, L. K., and Matz, M. V. 2018. Role of gene body methylation in acclimatization and adaptation in a basal metazoan. *Proceedings of the National Academy of Sciences*, 115(52): 13342–13346.

Dobin, A., Gingeras, T. R., and Spring, C. 2016. Mapping RNA-seq Reads with STAR Alexander. *Current Protocols in Bioinformatics*, (51): 1–11.

Dowen, R. H., Pelizzola, M., Schmitz, R. J., Lister, R., Dowen, J. M., Nery, J. R., Dixon, J. E., and Ecker, J. R. 2012. Widespread dynamic DNA methylation in response to biotic stress. *Proceedings of the National Academy of Sciences of the United States of America*, 109(32): 2183–91.

Drewell, R. a., Lo, N., Oxley, P. R., and Oldroyd, B. P. 2012. Kin conflict in insect societies: A new epigenetic perspective. *Trends in Ecology and Evolution*, 27(7): 367–373.

Drewell, R. A., Bush, E. C., Remnant, E. J., Wong, G. T., Beeler, S. M., Stringham, J. L., Lim, J., and Oldroyd, B. P. 2014. The dynamic DNA methylation cycle from egg to sperm in the honey bee *Apis mellifera*. *Development*, 141(13): 2702–2711.

Duchateau, M. J. and Velthuis, H. H. W. 1988. Development and reproductive strategies in *Bombus terrestris* colonies. *Behaviour*, 107(3): 186–207.

Edwards, J. R., Yarychkivska, O., Boulard, M., and Bestor, T. H. 2017. DNA methylation and DNA methyltransferases. *Epigenetics and Chromatin*, 10(1): 1–10.

Elango, N., Hunt, B. G., Goodisman, M. a. D., and Yi, S. V. 2009. DNA methylation is widespread and associated with differential gene expression in castes of the honeybee, *Apis mellifera*. *Proceedings of the National Academy of Sciences of the United States of America*, 106(27): 11206–11211.

Eyer, P. A., Leniaud, L., Darras, H., and Aron, S. 2013. Hybridogenesis through thelytokous parthenogenesis in two *Cataglyphis* desert ants. *Molecular Ecology*, 22(4): 947–955.

Falckenhayn, C., Boerjan, B., Raddatz, G., Frohme, M., Schoofs, L., and Lyko, F. 2013. Characterization of genome methylation patterns in the desert locust *Schistocerca gregaria*. *Journal of Experimental Biology*, 216(8): 1423–1429.

Fang, F., Hodges, E., Molaro, a., Dean, M., Hannon, G. J., and Smith, a. D. 2012. Genomic landscape of human allele-specific DNA methylation. *Proceedings of the National Academy of Sciences*, 109(19): 7332–7337.

Feil, R. and Fraga, M. F. 2012. Epigenetics and the environment: Emerging patterns and implications. *Nature Reviews Genetics*, 13(2): 97–109.

Feng, S., Cokus, S. J., Zhang, X., Chen, P.-Y., Bostick, M., Goll, M. G., Hetzel, J., Jain, J., Strauss, S. H., Halpern, M. E., Ukomadu, C., Sadler, K. C., Pradhan, S., Pellegrini, M., and Jacobsen, S. E. 2010. Conservation and divergence of methylation patterning in plants and animals. *Proceedings of the National Academy of Sciences*, 107(19): 8689–8694.

Flores, K. B., Wolschin, F., and Amdam, G. V. 2013. The role of methylation of DNA in environmental adaptation. *Integrative and Comparative Biology*, 53(2): 359–372.

Foret, S., Kucharski, R., Pittelkow, Y., Lockett, G. A., and Maleszka, R. 2009. Epigenetic regulation of the honey bee transcriptome: unravelling the nature of methylated genes. *BMC Genomics*, 10(1): 472.

Foster, R. L., Brunskill, A., Verdirame, D., and O'Donnell, S. 2004. Reproductive physiology, dominance interactions, and division of labour among bumble bee workers. *Physiological Entomology*, 29(4): 327–334.

Frisch, D., Morton, P. K., Chowdhury, P. R., Culver, B. W., Colbourne, J. K., Weider, L. J., and Jeyasingh, P. D. 2014. A millennial-scale chronicle of evolutionary responses to cultural eutrophication in Daphnia. *Ecology Letters*, 17(3): 360–368.

Galbraith, D. A., Yi, S. V., and Grozinger, C. M. 2016a. Evaluation of possible proximate mechanisms underlying the kinship theory of intragenomic conflict in social insects. *Integrative and Comparative Biology*, 56(6): 1206–1214.

Galbraith, D. A., Kocher, S. D., Glenn, T., Albert, I., Hunt, G. J., Strassmann, J. E., Queller, D. C., and Grozinger, C. M. 2016b. Testing the kinship theory of intragenomic conflict in honey bees (*Apis mellifera*). *Proceedings of the National Academy of Sciences*, 113(4): 1020–1025.

Garrison, E. and Marth, G. 2012. Haplotype-based variant detection from short-read sequencing. *arXiv*, 1207.3907.

Gatzmann, F., Falckenhayn, C., Gutekunst, J., Hanna, K., Raddatz, G., Carneiro, V. C., and Lyko, F. 2018. The methylome of the marbled crayfish links gene body methylation to stable expression of poorly accessible genes. *Epigenetics & Chromatin*, 11(1): 57.

Geoghegan, J. L. and Spencer, H. G. 2012. Population-epigenetic models of selection. *Theoretical Population Biology*, 81(3): 232–242.

Geva, S., Hartfelder, K., and Bloch, G. 2005. Reproductive division of labor, dominance, and ecdysteroid levels in hemolymph and ovary of the bumble bee *Bombus terrestris*. *Journal of Insect Physiology*, 51(7): 811–823.

Gibson, J. D., Arechavaleta-Velasco, M. E., Tsuruda, J. M., and Hunt, G. J. 2015. Biased allele expression and aggression in hybrid honeybees may be influenced by inappropriate nuclear-cytoplasmic signaling. *Frontiers in Genetics*, 6(343).

Gilles, A. F., Schinko, J. B., and Averof, M. 2015. Efficient CRISPR-mediated gene targeting and transgene replacement in the beetle *Tribolium castaneum*. *Development*, 142(16): 2832–2839.

Glastad, K. M., Hunt, B. G., Yi, S. V., and Goodisman, M. A. 2011. DNA methylation

in insects: On the brink of the epigenomic era. *Insect Molecular Biology*, 20(5): 553–565.

Glastad, K. M., Hunt, B. G., and Goodisman, M. A. 2013. Evidence of a conserved functional role for DNA methylation in termites. *Insect Molecular Biology*, 22(2): 143–154.

Glastad, K. M., Hunt, B. G., Yi, S. V., and Goodisman, M. a. D. 2014. Epigenetic inheritance and genome regulation: is DNA methylation linked to ploidy in haplodiploid insects? *Proceedings. Biological sciences / The Royal Society*, 281(1785): 20140411.

Glastad, K. M., Chau, L. M., and Goodisman, M. A. 2015. Epigenetics in Social Insects. In *Physiology, Behavior, Genomics of Social Insects*, volume 48, pages 227–269. Elsevier Ltd., 1 edition.

Glastad, K. M., Gokhale, K., Liebig, J., and Goodisman, M. A. D. 2016. The caste- and sex-specific DNA methylome of the termite *Zootermopsis nevadensis*. *Scientific Reports*, 6(37110).

Glastad, K. M., Arsenault, S. V., Vertacnik, K. L., Geib, S. M., Kay, S., Danforth, B. N., Rehan, S. M., Linnen, C. R., Kocher, S. D., and Hunt, B. G. 2017. Variation in DNA methylation is not consistently reflected by sociality in hymenoptera. *Genome Biology and Evolution*, 9(6): 1687–1698.

Glastad, K. M., Hunt, B. G., and Goodisman, M. A. 2018. Epigenetics in Insects: Genome Regulation and the Generation of Phenotypic Diversity. *Annual Review of Entomology*, 64(1): 185–203.

Gopal, B. 2005. Does inland aquatic biodiversity have a future in Asian developing countries? *Hydrobiologia*, 542(1): 69–75.

Gorman, M. J. and Paskewitz, S. M. 2001. Serine proteases as mediators of mosquito immune responses. *Insect Biochemistry and Molecular Biology*, 31(3): 257–262.

Grant, P. R. and Grant, B. R. 2002. Unpredictable evolution in a 30-year study of Darwin's finches. *Science*, 296(5568): 707–711.

Grothendieck, G. 2017. sqldf: Manipulate R Data Frames Using SQL. R package: *https://cran.r–project.org/package=sqldf*.

Guo, W., Wu, Z., Yang, L., Cai, Z., Zhao, L., and Zhou, S. 2019. Juvenile hormone-dependent Kazal-type serine protease inhibitor Greglin safeguards insect vitellogenesis and egg production. *FASEB Journal*, 33(1): 917–927.

Gutierrez-Arcelus, M., Lappalainen, T., Montgomery, S. B., Buil, A., Ongen, H., Yurovsky, A., Bryois, J., Giger, T., Romano, L., Planchon, A., Falconnet, E., Bielser, D., Gagnebin, M., Padioleau, I., Borel, C., Letourneau, A., Makrythanasis, P., Guipponi, M., Gehrig, C., Antonarakis, S. E., and Dermitzakis, E. T. 2013. Passive and active DNA methylation and the interplay with genetic variation in gene regulation. *eLife*, 2013(2): 1–18.

Guzman-Novoa, E., Hunt, G. J., Page, R. E., Uribe-Rubio, J. L., Prieto-Merlos, D., and Becerra-Guzman, F. 2005. Paternal effects on the defensive behavior of honeybees. *Journal of Heredity*, 96(4): 376–380.

Haig, D. 1996. Placental hormones, genomic imprinting, and maternal-fetal communication. *Journal of Evolutionary Biology*, 9(3): 357–380.

Haig, D. 2000. The Kinship Theory of Genomic Imprinting. *Annual Review of Ecology, Evolution, and Systematics*, (31): 9–32.

Harris, K. D. M., Bartlett, N. J., and Lloyd, V. K. 2012. Daphnia as an emerging epigenetic model organism. *Genetics research international*, 2012: 147892.

Hatorangan, M. R., Laenen, B., Steige, K. A., Slotte, T., and Köhler, C. 2016. Rapid Evolution of Genomic Imprinting in Two Species of the Brassicaceae. *The Plant Cell*, 28(8): 1815–1827.

Haydak, M. H. 1943. Larval Food and Development of Castes in the Honeybee. *Journal of Economic Entomology*, 36(5): 778–792.

Hearn, J., Pearson, M., Blaxter, M., Wilson, P. J., and Little, T. J. 2019. Genome-wide methylation is modified by caloric restriction in *Daphnia magna*. *BMC Genomics*, 20(1): 1–11.

Hebert, P. D. N. 1978. The Population Bilogy of Daphnia (Crustacea, Daphnidae). *Biological Reviews*, 53(3): 387–426.

Heckwolf, M. J., Meyer, B. S., Häsler, R., and Höppner, M. P. 2019. DNA methylation facilitates local adaptation and adaptive transgenerational plasticity. *biorXiv*, doi: http://dx.doi.org/10.1101/649574.

Herb, B. R., Wolschin, F., Hansen, K. D., Aryee, M. J., Langmead, B., Irizarry, R., Amdam, G. V., and Feinberg, A. P. 2012. Reversible switching between epigenetic states in honeybee behavioral subcastes. *Nature Neuroscience*, 15(10): 1371–1373.

Hodson, C. N., Hamilton, P. T., Dilworth, D., Nelson, C. J., Curtis, C. I., and Perlman, S. J. 2017. Paternal Genome Elimination in *Liposcelis* Booklice. *Genetics*, 206: 1091–1100.

Hunt, B. G., Brisson, J. A., Yi, S. V., and Goodisman, M. A. D. 2010. Functional conservation of DNA methylation in the pea aphid and the honeybee. *Genome Biology and Evolution*, 2(1): 719–728.

Hunt, B. G., Glastad, K. M., Yi, S. V., and Goodisman, M. A. D. 2013. The function of intragenic DNA methylation: Insights from insect epigenomes. *Integrative and Comparative Biology*, 53(2): 319–328.

Inoue, A., Jiang, L., Lu, F., Suzuki, T., and Zhang, Y. 2017. Maternal H3K27me3 controls DNA methylation-independent imprinting. *Nature*, 457: 419–424.

Jeremias, G., Barbosa, J., Marques, S. M., De Schamphelaere, K. A., Van Nieuwerburgh, F., Deforce, D., Gonçalves, F. J., Pereira, J. L., and Asselman, J. 2018. Transgenerational Inheritance of DNA Hypomethylation in *Daphnia magna* in Response to Salinity Stress. *Environmental Science and Technology*, 52(17): 10114–10123.

Joanis, V. and Lloyd, V. 2002. Genomic imprinting in Drosophila is maintained by the products of Suppressor of variegation and trithorax group, but not Polycomb group, genes. *Molecular Genetics and Genomics*, 268: 103–112.

Jones, P. A. 2012. Functions of DNA methylation: Islands, start sites, gene bodies and beyond. *Nature Reviews Genetics*, 13(7): 484–492.

Kay, S., Skowronski, D., and Hunt, B. G. 2018. Developmental DNA methyltransferase expression in the fire ant *Solenopsis invicta*. *Insect Science*, 25(1): 57–65.

Kerfoot, W. C., Robbins, J. A., Weider, L. J., and Robbins, A. 1999. A new approach to historical reconstruction : and Combining descriptive experimental paleolimnology. *Limnology*, 44(5): 1232–1247.

Knight, J. C. 2004. Allele-specific gene expression uncovered. *Trends in Genetics*, 20(3): 116–122.

Kocher, S. D., Tsuruda, J. M., Gibson, J. D., Emore, C. M., Arechavaleta-Velasco, M. E., Queller, D. C., Strassmann, J. E., Grozinger, C. M., Gribskov, M. R., San Miguel, P., Westerman, R., and Hunt, G. J. 2015. A Search for Parent-of-Origin Effects on Honey Bee Gene Expression. *G3*, 5(8): 1657–1662.

Kohno, H., Suenami, S., Takeuchi, H., Sasaki, T., and Kubo, T. 2016. Production of Knockout Mutants by CRISPR/Cas9 in the European Honeybee, *Apis mellifera L.* *Zoological Science*, 33(5): 505–512.

Kooke, R. and Keurentjes, J. J. 2015. Epigenetic variation contributes to environmental adaptation of *Arabidopsis thaliana*. *Plant Signaling and Behavior*, 10(9): e1057368.

Krueger, F. and Andrews, S. R. 2011. Bismark: A flexible aligner and methylation caller for Bisulfite-Seq applications. *Bioinformatics*, 27(11): 1571–1572.

Krueger, F., Andrews, S. R., and Osborne, C. S. 2011. Large scale loss of data in low-diversity illumina sequencing libraries can be recovered by deferred cluster calling. *PLoS ONE*, 6(1): 4–10.

Kucharski, R., Maleszka, J., Foret, S., and Maleszka, R. 2008. Nutritional control of reproductive status in honeybees via DNA methylation. *Science*, 319(5871): 1827–1830.

Kuhn, A., Darras, H., and Aron, S. 2018. Phenotypic plasticity in an ant with strong caste-genotype association. *Biology Letters*, 14(1): 20170705.

Kvist, J., Athanàsio, C. G., Solari, O. S., Brown, J. B., Colbourne, J. K., Pfrender,

M. E., and Mirbahai, L. 2018. Pattern of DNA methylation in Daphnia: Evolutionary perspective. *Genome Biology and Evolution*, 10(August 2018): 1988–2007.

Langmead, B. and Salzberg, S. L. 2012. Fast gapped-read alignment with Bowtie 2. *Nat Methods*, 9(4): 357–359.

Lea, A. J., Vilgalys, T. P., Durst, P. A. P., and Tung, J. 2017. Maximizing ecological and evolutionary insight in bisulfite sequencing data sets. *Nature Ecology & Evolution*, 1(8): 1074–1083.

LeBlanc, G. A. and Medlock, E. K. 2015. Males on demand: The environmental-neuroendocrine control of male sex determination in daphnids. *FEBS Journal*, 282(21): 4080–4093.

Leniaud, L., Darras, H., Boulay, R., and Aron, S. 2012. Social hybridogenesis in the clonal ant *Cataglyphis hispanica*. *Current Biology*, 22(13): 1188–1193.

Lex, A., Gehlenborg, N., and Strobelt, H. 2016. UpSet : Visualization of Intersecting Sets. *Europe PMC Funders Group*, 20(12): 1983–1992.

Li, B., Hou, L., Zhu, D., Xu, X., An, S., and Wang, X. 2018. Identification and caste-dependent expression patterns of DNA methylation associated genes in *Bombus terrestris*. *Scientific Reports*, 8(2332): DOI:10.1038/s41598–018–20831–1.

Li, E., Beard, C., and Jaenisch, R. 2003. Role for DNA methylation in genomic imprinting. *Trends in Genetics*, 10(3): 78.

Li, H. and Durbin, R. 2009. Fast and accurate short read alignment with Burrows-Wheeler transform. *Bioinformatics*, 25(14): 1754–1760.

Li, H., Handsaker, B., Wysoker, A., Fennell, T., Ruan, J., Homer, N., Marth, G., Abecasis, G., Durbin, R., and Subgroup, . G. P. D. P. 2009. The Sequence Alignment/Map format and SAMtools. *Bioinformatics*, 25(16): 2078–2079.

Li, M., Au, L. Y. C., Douglah, D., Chong, A., White, B. J., Ferree, P. M., and Akbari, O. S. 2017. Generation of heritable germline mutations in the jewel wasp Nasonia vitripennis using CRISPR/Cas9. *Scientific Reports*, 7(1): 1–7.

Li-Byarlay, H. 2016. The Function of DNA Methylation Marks in Social Insects. *Frontiers in Ecology and Evolution*, 4(57).

Li-Byarlay, H., Li, Y., Stroud, H., Feng, S., Newman, T. C., Kaneda, M., Hou, K. K., Worley, K. C., Elsik, C. G., Wickline, S. A., Jacobsen, S. E., Ma, J., and Robinson, G. E. 2013. RNA interference knockdown of DNA methyl-transferase 3 affects gene alternative splicing in the honey bee. *Proceedings of the National Academy of Sciences*, 110(31): 12750–12755.

Libbrecht, R. and Keller, L. 2012. Genetic compatibility affects division of labor in ants. *Evolution*, 67(2): 517–524.

Libbrecht, R., Schwander, T., and Keller, L. 2011. Genetic Components to Caste Allocation in a Multiple-Queen Ant Species. *Evolution*, 65(10): 2907–2915.

Libbrecht, R., Oxley, P. R., Keller, L., and Kronauer, D. J. C. 2016. Robust DNA Methylation in the Clonal Raider Ant Brain. *Current Biology*, 26: 1–5.

Lind, M. I. and Spagopoulou, F. 2018. Evolutionary consequences of epigenetic inheritance. *Heredity*, 121: 205–209.

Liu, L., Pei, C., Liu, S., Guo, X., Du, N., and Guo, W. 2018. Genetic and epigenetic changes during the invasion of a cosmopolitan species (*Phragmites australis*). *Ecology and Evolution*, (March): 1–10.

Liu, S., Sun, K., Jiang, T., and Feng, J. 2015. Natural epigenetic variation in bats and its role in evolution. *Journal of Experimental Biology*, 218: 100–106.

Liu, S., Aageaard, A., Bechsgaard, J., and Bilde, T. 2019. DNA Methylation Patterns in the Social Spider, *Stegodyphus dumicola*. *Genes*, 10(2): 137.

Liu, X. S., Wu, H., Ji, X., Stelzer, Y., Wu, X., Czauderna, S., Shu, J., Dadon, D., Young, R. A., and Jaenisch, R. 2016. Editing DNA Methylation in the Mammalian Genome. *Cell*, 167(1): 233–247.

Liu, Y., Siegmund, K. D., Laird, P. W., and Berman, B. P. 2012. Bis-SNP: combined DNA methylation and SNP calling for Bisulfite-seq data. *Genome biology*, 13(7): R61.

Liu, Y., Ma, S., Wang, X., Chang, J., Gao, J., Shi, R., Zhang, J., Lu, W., Liu, Y., Zhao, P., and Xia, Q. 2014. Highly efficient multiplex targeted mutagenesis and genomic structure variation in *Bombyx mori* cells using CRISPR/Cas9. *Insect Biochemistry and Molecular Biology*, 49(1): 35–42.

Lockett, G. A., Almond, E. J., Huggins, T. J., Parker, J. D., and Bourke, A. F. 2016. Gene expression differences in relation to age and social environment in queen and worker bumble bees. *Experimental Gerontology*, 77: 52–61.

Lonsdale, Z., Lee, K., Kiriakidu, M., Amarasinghe, H., Nathanael, D., O'Connor, C. J., and Mallon, E. B. 2017. Allele specific expression and methylation in the bumblebee, *Bombus terrestris*. *PeerJ*, 5(e3798).

Love, M. I., Huber, W., and Anders, S. 2014. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome biology*, 15(12): 550.

Lu, Y., Wang, B., Jiang, F., Mo, X., Wu, L., He, P., Lu, X., Deng, F., and Lei, S. 2019. Multi-omics integrative analysis identified SNP-methylation-mRNA: Interaction in peripheral blood mononuclear cells. *Journal of Cellular and Molecular Medicine*, (October 2018): 4601–4610.

Lyko, F., Foret, S., Kucharski, R., Wolf, S., Falckenhayn, C., and Maleszka, R. 2010. The honey bee epigenomes: Differential methylation of brain DNA in queens and workers. *PLoS Biology*, 8(11).

Martin, M. 2011. Cutadapt removes adapter sequences from high-throughput sequencing reads. *EMBnet.journal*, 17(1): 10.

Matsuura, K., Mizumoto, N., Kobayashi, K., Nozaki, T., Fujita, T., Yashiro, T., Fuchikawa, T., Mitaka, Y., and Vargo, E. L. 2018. A Genomic Imprinting Model of Termite Caste Determination: Not Genetic but Epigenetic Inheritance Influences Offspring Caste Fate. *The American Naturalist*, 191(6).

Mcafee, A., Pettis, J. S., Tarpy, D. R., and Foster, L. J. 2019. *Feminizer* and *doublesex* knock-outs cause honey bees to switch sexes. *PLoS Biology*, 17(5): e3000256.

McCann, J. A., Zheng, H., Islam, A., Goodyer, C. G., and Polychronakos, C. 2001.

Evidence against GRB10 as the gene responsible for Silver-Russell syndrome. *Biochemical and Biophysical Research Communications*, 286(5): 943–948.

McGrath, J. and Solter, D. 1984. Completion of mouse embryogenesis requires both the maternal and paternal genomes. *Cell*, 37(1): 179–183.

McKenna, A., Hanna, M., Banks, E., Sivachenko, A., Cibulskis, K., Kernytsky, A., Garimella, K., Altshuler, D., Gabriel, S., Daly, M., and DePristo, M. A. 2010. The Genome Analysis Toolkit: A MapReduce framework for analyzing next-generation DNA sequencing data. *Genome Research*, 20: 1297–1303.

Meaburn, E. L., Schalkwyk, L. C., and Mill, J. 2010. Allele-specific methylation in the human genome: Implications for genetic studies of complex disease. *Epigenetics*, 5(7): 578–582.

Messerschmidt, D. M., Knowles, B. B., and Solter, D. 2014. DNA methylation dynamics during epigenetic reprogramming in the germline and preimplantation embryos. *Genes and Development*, 28(8): 812–828.

Michels, H. 2007. Micro-evolutionary response of *Daphnia magna* to changes in biotic stress associated with habitat degradation and restoration of a shallow lake. *Thesis*, KU Leuven.

Mott, B. M., Gadau, J., and Anderson, K. E. 2015. Phylogeography of *Pogonomyrmex barbatus* and *P. rugosus* harvester ants with genetic and environmental caste determination. *Ecology and Evolution*, 5(14): 2798–2826.

Oldroyd, B. P., Allsopp, M. H., Roth, K. M., Remnant, E. J., Drewell, R. A., and Beekman, M. 2014. A parent-of-origin effect on honeybee worker ovary size. *Proceedings of the Royal Society B: Biological Sciences*, 281(1775): 20132388.

Orsini, L., Marshall, H., Cuenca Cambronero, M., Chaturvedi, A., Thomas, K. W., Pfrender, M. E., Spanier, K. I., and De Meester, L. 2016. Temporal genetic stability in natural populations of the waterflea *Daphnia magna* in response to strong selection pressure. *Molecular Ecology*, 25: 6024–6038.

Padilla, M., Amsalem, E., Altman, N., Hefetz, A., and Grozinger, C. M. 2016. Chemical

communication is not sufficient to explain reproductive inhibition in the bumblebee *Bombus impatiens*. *Royal Society Open Science*, 3(10): 160576.

Park, J., Peng, Z., Zeng, J., Elango, N., Park, T., Wheeler, D., Werren, J. H., and Yi, S. V. 2011. Comparative analyses of DNA methylation and sequence evolution using Nasonia genomes. *Molecular Biology and Evolution*, 28(12): 3345–3354.

Patalano, S., Vlasova, A., Wyatt, C., Ewels, P., Camara, F., Ferreira, P. G., Asher, C. L., Jurkowski, T. P., Segonds-Pichon, A., Bachman, M., González-Navarrete, I., Minoche, A. E., Krueger, F., Lowy, E., Marcet-Houben, M., Rodriguez-Ales, J. L., Nascimento, F. S., Balasubramanian, S., Gabaldon, T., Tarver, J. E., Andrews, S., Himmelbauer, H., Hughes, W. O. H., Guigó, R., Reik, W., and Sumner, S. 2015. Molecular signatures of plastic phenotypes in two eusocial insect species with simple societies. *Proceedings of the National Academy of Sciences*, 112(45): 13970–13975.

Patten, M. M., Ross, L., Curley, J. P., Queller, D. C., Bonduriansky, R., and Wolf, J. B. 2014. The evolution of genomic imprinting: theories, predictions and empirical tests. *Heredity*, 113(2): 119–28.

Pegoraro, M., Bafna, A., Davies, N. J., Shuker, D. M., and Tauber, E. 2016. DNA methylation changes induced by long and short photoperiods in *Nasonia*. *Genome research*, 26(2): 203–10.

Pegoraro, M., Marshall, H., Lonsdale, Z. N., and Mallon, E. B. 2017. Do social insects support Haig's kin theory for the evolution of genomic imprinting? *Epigenetics*, 12(9): 725–742.

Platt, A., Gugger, P. F., Pellegrini, M., and Sork, V. L. 2015. Genome-wide signature of local adaptation linked to variable CpG methylation in oak populations. *Molecular Ecology*, 24(15): 3823–3830.

Provataris, P., Meusemann, K., Niehuis, O., Grath, S., and Misof, B. 2018. Signatures of DNA Methylation across Insects Suggest Reduced DNA Methylation Levels in Holometabola. *Genome biology and evolution*, 10(4): 1185–1197.

Qian, C., Fang, Q., Wang, L., and Ye, G. Y. 2015. Molecular cloning and functional

studies of two Kazal-type serine protease inhibitors specifically expressed by *Nasonia vitripennis* venom apparatus. *Toxins*, 7(8): 2888–2905.

Queller, D. C. 2003. Theory of genomic imprinting conflict in social insects. *BMC Evolutionary Biology*, 3(15).

Quinlan, A. R. and Hall, I. M. 2010. BEDTools: A flexible suite of utilities for comparing genomic features. *Bioinformatics*, 26(6): 841–842.

Radford, E. J., Ferrón, S. R., and Ferguson-Smith, A. C. 2011. Genomic imprinting as an adaptative model of developmental plasticity. *FEBS Letters*, 585(13): 2059–2066.

Remnant, E. J., Ashe, A., Young, P. E., Buchmann, G., Beekman, M., Allsopp, M. H., Suter, C. M., Drewell, R. A., and Oldroyd, B. P. 2016. Parent-of-origin effects on genome-wide DNA methylation in the Cape honey bee (Apis mellifera capensis) may be confounded by allele-specific methylation. *BMC genomics*, 17(1): 226.

Richards, C. L., Bossdorf, O., and Pigliucci, M. 2010. What Role Does Heritable Epigenetic Variation Play in Phenotypic Evolution? *BioScience*, 60(3): 232–237.

Rivals, I., Personnaz, L., Taing, L., and Potier, M. C. 2007. Enrichment or depletion of a GO category within a class of genes: Which test? *Bioinformatics*, 23(4): 401–407.

Rodrigues, J. A. and Zilberman, D. 2015. Evolution and function of genomic imprinting in plants. *Genes and Development*, 29(24): 2517–2531.

Rosenzweig, C., Karoly, D., Vicarelli, M., Neofotis, P., Wu, Q., Casassa, G., Menzel, A., Root, T. L., Estrella, N., Seguin, B., Tryjanowski, P., Liu, C., Rawlins, S., and Imeson, A. 2008. Attributing physical and biological impacts to anthropogenic climate change. *Nature*, 453(7193): 353–7.

Sadd, B. M., Barribeau, S. M., Bloch, G., de Graaf, D. C., Dearden, P., Elsik, C. G., Gadau, J., Grimmelikhuijzen, C. J., Hasselmann, M., Lozier, J. D., Robertson, H. M., Smagghe, G., Stolle, E., Van Vaerenbergh, M., Waterhouse, R. M., Bornberg-Bauer, E., Klasberg, S., Bennett, A. K., Câmara, F., Guigó, R., Hoff, K., Mariotti, M., Munoz-Torres, M., Murphy, T., Santesmasses, D., Amdam, G. V., Beckers, M., Beye, M., Biewer, M., Bitondi, M. M., Blaxter, M. L., Bourke, A. F., Brown, M. J., Buechel,

S. D., Cameron, R., Cappelle, K., Carolan, J. C., Christiaens, O., Ciborowski, K. L., Clarke, D. F., Colgan, T. J., Collins, D. H., Cridge, A. G., Dalmay, T., Dreier, S., du Plessis, L., Duncan, E., Erler, S., Evans, J., Falcon, T., Flores, K., Freitas, F. C., Fuchikawa, T., Gempe, T., Hartfelder, K., Hauser, F., Helbing, S., Humann, F. C., Irvine, F., Jermiin, L. S., Johnson, C. E., Johnson, R. M., Jones, A. K., Kadowaki, T., Kidner, J. H., Koch, V., Köhler, A., Kraus, F. B., Lattorff, H. M. G., Leask, M., Lockett, G. A., Mallon, E. B., Antonio, D. S., Marxer, M., Meeus, I., Moritz, R. F., Nair, A., Näpflin, K., Nissen, I., Niu, J., Nunes, F. M., Oakeshott, J. G., Osborne, A., Otte, M., Pinheiro, D. G., Rossié, N., Rueppell, O., Santos, C. G., Schmid-Hempel, R., Schmitt, B. D., Schulte, C., Simões, Z. L., Soares, M. P., Swevers, L., Winnebeck, E. C., Wolschin, F., Yu, N., Zdobnov, E. M., Aqrawi, P. K., Blankenburg, K. P., Coyle, M., Francisco, L., Hernandez, A. G., Holder, M., Hudson, M. E., Jackson, L. R., Jayaseelan, J., Joshi, V., Kovar, C., Lee, S. L., Mata, R., Mathew, T., Newsham, I. F., Ngo, R., Okwuonu, G., Pham, C., Pu, L. L., Saada, N., Santibanez, J., Simmons, D. N., Thornton, R., Venkat, A., Walden, K. K., Wu, Y. Q., Debyser, G., Devreese, B., Asher, C., Blommaert, J., Chipman, A. D., Chittka, L., Fouks, B., Liu, J., O'Neill, M. P., Sumner, S., Puiu, D., Qu, J., Salzberg, S. L., Scherer, S. E., Muzny, D. M., Richards, S., Robinson, G. E., Gibbs, R. A., Schmid-Hempel, P., and Worley, K. C. 2015. The genomes of two key bumblebee species with primitive eusocial organization. *Genome Biology*, 16(1): 76.

Saebelfeld, M., Minguez, L., Griebel, J., Gessner, M. O., and Wolinska, J. 2017. Humic dissolved organic carbon drives oxidative stress and severe fitness impairments in Daphnia. *Aquatic Toxicology*, 182: 31–38.

Sarapultseva, E. I., Ustenko, K., and Dubrova, Y. E. 2019. The combined effects of acute irradiation and food supply on survival and fertility in *Daphnia magna*. *Journal of Environmental Radioactivity*, 199-200(August 2018): 75–83.

Sarda, S., Zeng, J., Hunt, B. G., and Yi, S. V. 2012. The evolution of invertebrate gene body methylation. *Molecular Biology and Evolution*, 29(8): 1907–1916.

Satyaki, P. R. and Gehring, M. 2017. DNA methylation and imprinting in plants: machinery and mechanisms. *Critical Reviews in Biochemistry and Molecular Biology*,

52(2): 163–175.

Schneider, C. A., Rasband, W. S., and Eliceiri, K. W. 2012. NIH Image to ImageJ: 25 years of image analysis. *Nature Methods*, 9(7): 671–675.

Schultz, M. D., Schmitz, R. J., and Ecker, J. R. 2012. 'Leveling' the playing field for analyses of single-base resolution DNA methylomes. *Trends in Genetics*, 28(12): 583–585.

Scott, R. J. and Spielman, M. 2006. Genomic imprinting in plants and mammals: How life history constrains convergence. *Cytogenetic and Genome Research*, 113(1-4): 53–67.

Shaham, R., Ben-Shlomo, R., Motro, U., and Keasar, T. 2016. Genome methylation patterns across castes and generations in a parasitoid wasp. *Ecology and Evolution*, 6(22): 7943–7953.

Simola, D. F., Graham, R. J., Brady, C. M., Enzmann, B. L., Desplan, C., Ray, A., Zwiebel, L. J., Bonasio, R., Reinberg, D., Liebig, J., and Berger, S. L. 2016. Epigenetic (re)programming of caste-specific behavior in the ant *Camponotus floridanus*. *Science*, 351(6268).

Singer, M., Kosti, I., Pachter, L., and Mandel-Gutfreund, Y. 2015. A diverse epigenetic landscape at human exons with implication for expression. *Nucleic Acids Research*, 43(7): 3498–3508.

Spencer, H. G. and Clark, A. G. 2014. Non-conflict theories for the evolution of genomic imprinting. *Heredity*, 113(2): 112–118.

Standage, D. S., Berens, A. J., Glastad, K. M., Severin, A. J., Brendel, V. P., and Toth, A. L. 2016. Genome, transcriptome, and methylome sequencing of a primitively eusocial wasp reveal a greatly reduced DNA methylation system in a social insect. *Molecular Ecology*, 25(8): 1769–1784.

Supek, F., Bošnjak, M., Škunca, N., and Šmuc, T. 2011. Revigo summarizes and visualizes long lists of gene ontology terms. *PLoS ONE*, 6(7).

Thomas, G. W. C., Dohmen, E., Hughes, D. S. T., Murali, S. C., Poelchau, M., Glastad,

K., Anstead, C. A., Ayoub, N. A., Batterham, P., Bellair, M., Binford, G. J., Chao, H., Chen, Y. H., Childers, C., Dinh, H., Doddapaneni, H., Duan, J. J., Dugan, S., Esposito, L. A., Friedrich, M., Garb, J., Gasser, R. B. B., Goodisman, M. A. D., Gundersen-Rindal, D. E., Han, Y., Handler, A. M., Hatakeyama, M., Hering, L., Hunter, W. B., Ioannidis, P., Jayaseelan, J. C., Kalra, D., Khila, A., Korhonen, P. K., Lee, C. E., Lee, S. L., Li, Y., Lindsey, A. R., Mayer, G., McGregor, A. P., McKenna, D. D., Misof, B., Munidasa, M., Munoz-Torres, M., Muzny, D. M., Niehuis, O., Osuji-Lacy, N., Palli, S. R., Panfilio, K. A., Pechmann, M., Perry, T., Peters, R. S., Poynton, H. C., Prpic, N.-M., Qu, J., Rotenberg, D., Schal, C., Schoville, S. D., Scully, E. D., Skinner, E., Sloan, D. B., Stouthamer, R., Strand, M. R., Szucsich, N. U., Wijeratne, A., Young, N. D., Zattara, E. E., Benoit, J. B., Zdobnov, E. M., Pfrender, M. E., Hackett, K. J., Werren, J. H., Worley, K. C., Gibbs, R. A., Chipman, A. D., Waterhouse, R. M., Bornberg-Bauer, E., Hahn, M. W., and Richards, S. 2018. The genomic basis of Arthropod diversity. *bioRxiv Genomics*, (August): 382945.

Tian, X. C. 2013. Genomic Imprinting in Farm Animals. *Annual Review of Animal Biosciences*, 2(1): 23–40.

Tycko, B. 2010. Allele-specific DNA methylation: Beyond imprinting. *Human Molecular Genetics*, 19(R2): 210–220.

Tycko, B. and Morison, I. M. 2002. Physiological functions of imprinted genes. *Journal of Cellular Physiology*, 192(3): 245–258.

van der Graaf, A., Wardenaar, R., Neumann, D. A., Taudt, A., Shaw, R. G., Jansen, R. C., Schmitz, R. J., Colomé-Tatché, M., and Johannes, F. 2015. Rate, spectrum, and evolutionary dynamics of spontaneous epimutations. *Proceedings of the National Academy of Sciences*, 112(21): 6676–6681.

Vandegehuchte, M. B., Lemière, F., and Janssen, C. R. 2009. Quantitative DNA-methylation in Daphnia magna and effects of multigeneration Zn exposure. *Comparative Biochemistry and Physiology - C Toxicology and Pharmacology*, 150(3): 343–348.

Vandegehuchte, M. B., De Coninck, D., Vandenbrouck, T., De Coen, W. M., and

Janssen, C. R. 2010. Gene transcription profiles, global DNA methylation and potential transgenerational epigenetic effects related to Zn exposure history in *Daphnia magna*. *Environmental Pollution*, 158(10): 3323–3329.

Verhoeven, K. J., vonHoldt, B. M., and Sork, V. L. 2016. Epigenetics in ecology and evolution: what we know and what we need to know. *Molecular Ecology*, 25: 1631–1638.

Vogt, G. 2017. *Evolution of Epigenetic Mechanisms in Animals and Their Role in Speciation*. Elsevier Inc., second edi edition.

Vojta, A., Dobrinic, P., Tadic, V., Bockor, L., Korac, P., Julg, B., Klasic, M., and Zoldos, V. 2016. Repurposing the CRISPR-Cas9 system for targeted DNA methylation. *Nucleic Acids Research*, 44(12): 5615–5628.

Voon, H. P., Hughes, J. R., Rode, C., DeLaRosa-Velázquez, I. A., Jenuwein, T., Feil, R., Higgs, D. R., and Gibbons, R. J. 2015. ATRX Plays a Key Role in Maintaining Silencing at Interstitial Heterochromatic Loci and Imprinted Genes. *Cell Reports*, 11(3): 405–418.

Wakefield, R. I., Smith, B. O., Nan, X., Free, A., Soteriou, A., Uhrin, D., Bird, A. P., and Barlow, P. N. 1999. The solution structure of the domain from MeCP2 that binds to methylated DNA. *Journal of Molecular Biology*, 291(5): 1055–1065.

Wang, X., Wheeler, D., Avery, A., Rago, A., Choi, J. H., Colbourne, J. K., Clark, A. G., and Werren, J. H. 2013. Function and Evolution of DNA Methylation in *Nasonia vitripennis*. *PLoS Genetics*, 9(10).

Wang, X., Werren, J. H., and Clark, A. G. 2016. Allele-Specific Transcriptome and Methylome Analysis Reveals Stable Inheritance and Cis-Regulation of DNA Methylation in Nasonia. *PLOS Biology*, 14(7): e1002500.

Wedd, L., Kucharski, R., and Maleszka, R. 2016. Differentially methylated obligatory epialleles modulate context-dependent LAM gene expression in the honeybee *Apis mellifera*. *Epigenetics*, 11(1): 1–10.

Weiner, S. A., Galbraith, D. A., Adams, D. C., Valenzuela, N., Noll, F. B., Grozinger,

C. M., and Toth, A. L. 2013. A survey of DNA methylation across social insect species, life stages, and castes reveals abundant and caste-associated methylation in a primitively social wasp. *Naturwissenschaften*, 100(8): 795–799.

Weyrich, A., Lenz, D., Jeschek, M., Chung, T. H., Rubensam, K., Gritz, F., Jewgenow, K., Fickel, J. J., Rubensam, K., Goritz, F., Jewgenow, K., and Fickel, J. J. 2015. Paternal intergenerational epigenetic response to heat exposure in male Wild guinea pigs. *Molecular Ecology*, 25(8): 1729–1740.

Wilkins, J. F. and Haig, D. 2003. What good is genomic imprinting: the function of parent-specific gene expression. *Nature Reviews Genetics*, 4(5): 359–368.

Winkler, A. M., Webster, M. A., Vidaurre, D., Nichols, T. E., and Smith, S. M. 2015. Multi-level block permutation. *NeuroImage*, 123: 253–268.

Wolf, J. B. and Hager, R. 2006. A maternal-offspring coadaptation theory for the evolution of genomic imprinting. *PLoS Biology*, 4(12): 2238–2243.

Woodard, S. H., Lozier, J. D., Goulson, D., Williams, P. H., Strange, J. P., and Jha, S. 2015. Molecular tools and bumble bees: Revealing hidden details of ecology and evolution in a model system. *Molecular Ecology*, 24(12): 2916–2936.

Yang, L., Lin, Z., Fang, Q., Wang, J., Yan, Z., Zou, Z., Song, Q., and Ye, G. 2017. The genomic and transcriptomic analyses of serine proteases and their homologs in an endoparasitoid, *Pteromalus puparum*. *Developmental and Comparative Immunology*, 77: 56–68.

Yoshimura, H. and Yamada, Y. Y. 2018. Caste-fate determination primarily occurs after adult emergence in a primitively eusocial paper wasp: significance of the photoperiod during the adult stage. *Science of Nature*, 105(1-2).

Yu, H. M., Zhu, B. J., Sun, Y., Wei, G. Q., Wang, L., Qian, C., Nadeem Abbas, M., and Liu, C. L. 2017. Characterization and functional analysis of serpin-1 like gene from oak silkworm *Antheraea pernyi*. *Bulletin of Entomological Research*, (2017): 1–7.

Zhang, H., Lang, Z., and Zhu, J. K. 2018. Dynamics and function of DNA methylation in plants. *Nature Reviews Molecular Cell Biology*, 19(8): 489–506.

Zhang, Y., Gou, W., Ma, J., Zhang, H., Zhang, Y., and Zhang, H. 2017. Genome methylation and regulatory functions for hypoxic adaptation in Tibetan chicken embryos. *PeerJ*, 5: e3891.

Zilberman, D. 2017. An evolutionary case for functional gene body methylation in plants and animals. *Genome Biology*, 18(1): 17–19.

Zou, Z., Picheng, Z., Weng, H., Mita, K., and Jiang, H. 2009. A comparative analysis of serpin genes in the silkworm genome. *Genomics*, 93(4): 367–375.

Chapter 2: supplementary

Supplementary 1.0.0: ovary weight and length of the largest oocyte for all samples used.

Colony	Date_Eclosed	Date_Sampled	Sample_Name	Ovary_Weight(g)	Mean Oocyte Length(mm	Reproductive score	Reproductive Status
1	19/01/2016	25/01/2016	J1_3	0.0245	1.8295	4	Reproductive
1	19/01/2016	25/01/2016	J1_5	0.0022	N/A	0	Sterile
1	20/01/2016	26/01/2016	J1_6	0.0341	2.3075	4	Reproductive
1	20/01/2016	26/01/2016	J1_7	0.0227	1.6975	4	Reproductive
1	20/01/2016	26/01/2016	J1_8	0.0025	N/A	0	Sterile
1	23/01/2016	29/01/2016	J1_17	0.001	N/A	0	Sterile
5	20/01/2016	26/01/2016	J5_6	0.0177	1.8745	4	Reproductive
5	20/01/2016	26/01/2016	J5_7	0.0024	N/A	0	Sterile
5	20/01/2016	26/01/2016	J5_13	0.018	1.7675	4	Reproductive
5	20/01/2016	26/01/2016	J5_15	0.0014	N/A	0	Sterile
5	03/02/2016	09/02/2016	J5_33	0.0183	2.495	4	Reproductive
5	03/02/2016	09/02/2016	J5_34	0.0004	N/A	0	Sterile
8	04/02/2016	10/02/2016	J8_12	0.0119	1.365	3	Reproductive
8	17/02/2016	23/02/2016	J8_18	0.0077	N/A	0	Sterile
8	18/02/2016	24/02/2016	J8_23	0.001	N/A	0	Sterile
8	18/02/2016	24/02/2016	J8_24	0.0282	2.185	4	Reproductive
8	19/02/2016	25/02/2016	J8_29	0.0011	N/A	0	Sterile
8	19/02/2016	25/02/2016	J8_30	0.0791	2.49	4	Reproductive

Supplementary 1.0.1: Quantity and quality values for all extracted samples. 260/280 and 260/230 values were determined using a Nanodrop 2000. Final volume was estimated, taking into account the maximum volume loss during the elution step of the DNA extraction procedure and QUBIT concentration levels. Sample names refer to unique colony and reproductive status (R= reproductive, NR= non-reproductive).

Sample	Nanodrop Concentration (ng/µl)	QUBIT Concentration (ng/µl)	Final Volume (µl)	Total DNA (µg)	260/280	260/230
J1_R	143.9	13.8	100	1.38	2.1	1.8
J1_NR	136.4	13.5	92.5	1.25	2.11	1.91
J5_R	146	17.3	83.5	1.44	2.05	1.76
J5_NR	139.2	15.1	100	1.51	2.09	1.95
J8_R	141.2	12.8	100	1.28	2.08	1.73
J8_NR	145.6	19	100	1.9	2.08	1.86

Supplementary 1.0.2: Quantity and quality values for all extracted RNA samples, generated using an Agilent 2100. RIN (RNA integrity score) indicates the level of degredation of the sample, 0 being full degraded and 10 being fully intact. Sample names refer to unique colony and reproductive status (R= reproductive, NR= non-reproductive).

Sample	Concentration (ng/µl)	Final Volume (µl)	Total RNA (µg)	RIN
J1_3	128	30	3.84	6.9
J1_5	151	34	5.13	8.4
J1_6	156	33	5.15	8.2
J1_7	199	33	6.57	8.3
J1_8	127	33	4.19	8.8
J1_17	124	44	5.46	8.6
J5_6	158	35	5.53	7.6
J5_7	102	35	3.57	8.3
J5_13	149	33	4.92	6.9
J5_15	116	37	4.29	8.3
J5_33	117	35	4.1	8.7
J5_34	72	33	2.38	8.9
J8_18	50	45	2.25	8.9
J8_23	77	67	5.16	8.9
J8_24	113	46	5.2	9.1
J8_29	33	50	1.65	8.9
J8_12	115	54	6.21	9.6
J8_30	94	59	5.55	6

Supplementary information 1.0.3: GO terms enriched in methylated genes compared to all genes.

term_ID	description	frequency	log10 p-value
GO:0009987	cellular process	63.78%	-7.0104
GO:0044238	primary metabolic process	53.74%	-27.5577
GO:0044260	cellular macromolecule metabolic process	34.28%	-9.7671
GO:0034641	cellular nitrogen compound metabolic process	34.14%	-23.33
GO:1901360	organic cyclic compound metabolic process	30.32%	-24.481
GO:0044249	cellular biosynthetic process	30.05%	-6.8917
GO:0046483	heterocycle metabolic process	29.66%	-28.9828
GO:0006725	cellular aromatic compound metabolic process	29.63%	-25.9827
GO:0065007	biological regulation	20.50%	-12.3755
GO:0010467	gene expression	19.67%	-18.4399
GO:0050794	regulation of cellular process	18.84%	-2.6693
GO:1901564	organonitrogen compound metabolic process	17.89%	-10.0459
GO:0016070	RNA metabolic process	15.95%	-16.1026
GO:0034654	nucleobase-containing compound biosynthetic process	14.53%	-3.2603
GO:0044267	cellular protein metabolic process	14.29%	-15.1215
GO:0006796	phosphate-containing compound metabolic process	13.11%	-4.1174
GO:0060255	regulation of macromolecule metabolic process	11.72%	-11.0342
GO:0009889	regulation of biosynthetic process	10.83%	-12.5445
GO:0097659	nucleic acid-templated transcription	10.72%	-15.3706
GO:2000112	regulation of cellular macromolecule biosynthetic process	10.68%	-5.2786
GO:0019219	regulation of nucleobase-containing compound metabolic process	10.26%	-11.0378
GO:2001141	regulation of RNA biosynthetic process	9.97%	-7.5852
GO:0006355	regulation of transcription, DNA-templated	9.92%	-5.2584
GO:0051716	cellular response to stimulus	9.56%	-5.8745
GO:0036211	protein modification process	7.73%	-19.9971
GO:0071702	organic substance transport	4.98%	-5.5921
GO:1901575	organic substance catabolic process	4.61%	-5.4965

GO:0006950	response to stress	4.58%	-8.3841
GO:0044085	cellular component biogenesis	4.36%	-5.4194
GO:0006468	protein phosphorylation	4.14%	-4.5072
GO:0035556	intracellular signal transduction	4.00%	-2.6685
GO:0032259	methylation	3.10%	-4.5914
GO:0008104	protein localization	2.63%	-3.7532
GO:0043933	macromolecular complex subunit organization	2.37%	-13.8678
GO:0006974	cellular response to DNA damage stimulus	2.36%	-4.26
GO:0009161	ribonucleoside monophosphate metabolic process	2.27%	-2.4276
GO:0015031	protein transport	2.25%	-2.6824
GO:0006281	DNA repair	2.23%	-2.6643
GO:0051641	cellular localization	2.04%	-4.5478
GO:0009126	purine nucleoside monophosphate metabolic process	1.92%	-2.3221
GO:0007049	cell cycle	1.89%	-6.3181
GO:0048523	negative regulation of cellular process	1.83%	-6.9323
GO:0065009	regulation of molecular function	1.73%	-8.2552
GO:0051649	establishment of localization in cell	1.68%	-15.0911
GO:0042592	homeostatic process	1.66%	-2.2598
GO:0051128	regulation of cellular component organization	1.59%	-3.1986
GO:0048522	positive regulation of cellular process	1.59%	-5.0824
GO:0009124	nucleoside monophosphate biosynthetic process	1.49%	-2.2442
GO:0051276	chromosome organization	1.48%	-12.7487
GO:0032268	regulation of cellular protein metabolic process	1.47%	-4.0696
GO:0006366	transcription from RNA polymerase II promoter	1.43%	-2.5802
GO:0042254	ribosome biogenesis	1.42%	-2.7083
GO:0006357	regulation of transcription from RNA polymerase II promoter	1.27%	-3.4132
GO:0044265	cellular macromolecule catabolic process	1.27%	-3.9287
GO:0051301	cell division	1.23%	-5.5119
GO:0006886	intracellular protein transport	1.20%	-11.7884
GO:0010605	negative regulation of macromolecule metabolic process	1.17%	-2.7164

GO:0043039	tRNA aminoacylation	1.12%	-2.5907
GO:0016192	vesicle-mediated transport	1.09%	-3.1122
GO:0071103	DNA conformation change	1.08%	-2.7727
GO:0030163	protein catabolic process	1.00%	-7.9865
GO:0010604	positive regulation of macromolecule metabolic process	0.99%	-6.9478
GO:0009966	regulation of signal transduction	0.86%	-7.7216
GO:0070647	protein modification by small protein conjugation or removal	0.82%	-8.7922
GO:0043085	positive regulation of catalytic activity	0.82%	-6.0689
GO:0007010	cytoskeleton organization	0.79%	-6.4333
GO:0000003	reproduction	0.77%	-4.0138
GO:0031327	negative regulation of cellular biosynthetic process	0.77%	-3.9442
GO:0034655	nucleobase-containing compound catabolic process	0.76%	-3.9985
GO:0051603	proteolysis involved in cellular protein catabolic process	0.76%	-9.2285
GO:0051704	multi-organism process	0.75%	-2.3799
GO:0010558	negative regulation of macromolecule biosynthetic process	0.74%	-5.6079
GO:0010608	posttranscriptional regulation of gene expression	0.72%	-4.6206
GO:0022604	regulation of cell morphogenesis	0.71%	-3.1851
GO:0045934	negative regulation of nucleobase-containing compound metabolic proce	0.70%	-4.4972
GO:0034248	regulation of cellular amide metabolic process	0.70%	-4.2628
GO:0051173	positive regulation of nitrogen compound metabolic process	0.69%	-5.4376
GO:0009891	positive regulation of biosynthetic process	0.67%	-6.1728
GO:0010628	positive regulation of gene expression	0.65%	-3.3508
GO:0043632	modification-dependent macromolecule catabolic process	0.63%	-12.6318
GO:1902679	negative regulation of RNA biosynthetic process	0.61%	-2.933
GO:0045935	positive regulation of nucleobase-containing compound metabolic proces	0.60%	-8.0208
GO:0032508	DNA duplex unwinding	0.59%	-2.2434
GO:0006470	protein dephosphorylation	0.59%	-2.4491
GO:0006511	ubiquitin-dependent protein catabolic process	0.58%	-4.5812
GO:0019220	regulation of phosphate metabolic process	0.58%	-7.7481
GO:0048468	cell development	0.57%	-4.6661

GO:0000278	mitotic cell cycle	0.56%	-2.8346
GO:0006397	mRNA processing	0.56%	-4.2733
GO:0016567	protein ubiquitination	0.52%	-3.2879
GO:1902680	positive regulation of RNA biosynthetic process	0.52%	-6.2899
GO:0045893	positive regulation of transcription, DNA-templated	0.52%	-2.3426
GO:1903047	mitotic cell cycle process	0.51%	-4.5291
GO:0072594	establishment of protein localization to organelle	0.49%	-2.4073
GO:0043547	positive regulation of GTPase activity	0.47%	-2.3883
GO:0048285	organelle fission	0.46%	-6.6885
GO:0048584	positive regulation of response to stimulus	0.46%	-6.3296
GO:0031668	cellular response to extracellular stimulus	0.44%	-2.6309
GO:0051248	negative regulation of protein metabolic process	0.44%	-5.8185
GO:0001932	regulation of protein phosphorylation	0.43%	-2.3222
GO:0016569	covalent chromatin modification	0.42%	-7.0876
GO:0022411	cellular component disassembly	0.42%	-2.1588
GO:0042180	cellular ketone metabolic process	0.42%	-3.3326
GO:0022008	neurogenesis	0.42%	-2.6631
GO:2000026	regulation of multicellular organismal development	0.42%	-3.0819
GO:0043086	negative regulation of catalytic activity	0.40%	-3.8912
GO:0030029	actin filament-based process	0.40%	-2.5029
GO:0051130	positive regulation of cellular component organization	0.37%	-3.9653
GO:0016570	histone modification	0.37%	-6.5078
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	0.37%	-3.3751
GO:0051338	regulation of transferase activity	0.37%	-7.1663
GO:0022618	ribonucleoprotein complex assembly	0.36%	-2.9842
GO:0010647	positive regulation of cell communication	0.36%	-7.2087
GO:0023056	positive regulation of signaling	0.36%	-7.008
GO:0018205	peptidyl-lysine modification	0.36%	-5.4204
GO:0010941	regulation of cell death	0.34%	-2.395
GO:0006479	protein methylation	0.34%	-4.4447

GO:0042886	amide transport	0.34%	-15.4923
GO:0009725	response to hormone	0.34%	-3.5851
GO:0044703	multi-organism reproductive process	0.34%	-3.6674
GO:0030182	neuron differentiation	0.33%	-2.9594
GO:0044764	multi-organism cellular process	0.33%	-2.6691
GO:0000375	RNA splicing, via transesterification reactions	0.32%	-12.5525
GO:0040007	growth	0.32%	-2.3018
GO:0000398	mRNA splicing, via spliceosome	0.32%	-8.5986
GO:0010564	regulation of cell cycle process	0.31%	-5.5921
GO:0030162	regulation of proteolysis	0.30%	-2.7036
GO:0031401	positive regulation of protein modification process	0.30%	-6.2096
GO:0003006	developmental process involved in reproduction	0.30%	-3.7569
GO:0045859	regulation of protein kinase activity	0.30%	-3.1252
GO:0010562	positive regulation of phosphorus metabolic process	0.28%	-6.0201
GO:0007167	enzyme linked receptor protein signaling pathway	0.28%	-3.0768
GO:0007346	regulation of mitotic cell cycle	0.27%	-2.2949
GO:0044419	interspecies interaction between organisms	0.26%	-2.3188
GO:0051052	regulation of DNA metabolic process	0.25%	-2.2025
GO:0042327	positive regulation of phosphorylation	0.25%	-2.9912
GO:0000819	sister chromatid segregation	0.24%	-2.1637
GO:0071824	protein-DNA complex subunit organization	0.24%	-2.1701
GO:0006913	nucleocytoplasmic transport	0.24%	-2.8745
GO:0006402	mRNA catabolic process	0.23%	-4.2543
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	0.23%	-2.9929
GO:0007265	Ras protein signal transduction	0.23%	-4.4543
GO:0051056	regulation of small GTPase mediated signal transduction	0.22%	-5.5183
GO:0006887	exocytosis	0.21%	-2.7116
GO:0044770	cell cycle phase transition	0.21%	-3.516
GO:1905114	cell surface receptor signaling pathway involved in cell-cell signaling	0.21%	-3.0789
GO:0065004	protein-DNA complex assembly	0.20%	-2.9193

GO:0043254	regulation of protein complex assembly	0.20%	-4.1947
GO:0016579	protein deubiquitination	0.20%	-3.2302
GO:0044089	positive regulation of cellular component biogenesis	0.19%	-4.3891
GO:0002520	immune system development	0.19%	-3.6139
GO:0051050	positive regulation of transport	0.19%	-3.1649
GO:0010563	negative regulation of phosphorus metabolic process	0.18%	-3.4384
GO:0006473	protein acetylation	0.18%	-4.4545
GO:0048858	cell projection morphogenesis	0.17%	-2.4875
GO:0007276	gamete generation	0.16%	-5.7373
GO:1901990	regulation of mitotic cell cycle phase transition	0.16%	-7.6209
GO:0009792	embryo development ending in birth or egg hatching	0.16%	-2.5484
GO:0051223	regulation of protein transport	0.15%	-3.2535
GO:0031400	negative regulation of protein modification process	0.15%	-4.5315
GO:0032784	regulation of DNA-templated transcription, elongation	0.15%	-3.2379
GO:0033674	positive regulation of kinase activity	0.15%	-3.7731
GO:0050767	regulation of neurogenesis	0.15%	-3.2992
GO:0009894	regulation of catabolic process	0.15%	-8.3775
GO:0018393	internal peptidyl-lysine acetylation	0.14%	-3.5528
GO:0007420	brain development	0.14%	-2.4775
GO:0198738	cell-cell signaling by wnt	0.14%	-2.1802
GO:0006338	chromatin remodeling	0.14%	-2.964
GO:0032271	regulation of protein polymerization	0.14%	-2.3946
GO:0007034	vacuolar transport	0.13%	-2.7185
GO:0045930	negative regulation of mitotic cell cycle	0.13%	-2.5394
GO:1903827	regulation of cellular protein localization	0.13%	-4.8723
GO:0016032	viral process	0.13%	-2.535
GO:0040029	regulation of gene expression, epigenetic	0.13%	-4.1656
GO:0007088	regulation of mitotic nuclear division	0.13%	-3.1625
GO:0006888	ER to Golgi vesicle-mediated transport	0.13%	-2.4545
GO:0035023	regulation of Rho protein signal transduction	0.13%	-4.0445

GO:0010942	positive regulation of cell death	0.11%	-3.4782
GO:0043410	positive regulation of MAPK cascade	0.11%	-3.5893
GO:0071383	cellular response to steroid hormone stimulus	0.11%	-2.5069
GO:0032386	regulation of intracellular transport	0.11%	-2.6304
GO:0006606	protein import into nucleus	0.10%	-2.6594
GO:0051236	establishment of RNA localization	0.10%	-8.8922
GO:0050657	nucleic acid transport	0.10%	-8.8922
GO:0034976	response to endoplasmic reticulum stress	0.10%	-4.6932
GO:0034968	histone lysine methylation	0.10%	-3.0742
GO:1904951	positive regulation of establishment of protein localization	0.10%	-2.9111
GO:0071426	ribonucleoprotein complex export from nucleus	0.10%	-4.4397
GO:0044091	membrane biogenesis	0.10%	-2.3993
GO:0009267	cellular response to starvation	0.09%	-3.0295
GO:0018209	peptidyl-serine modification	0.09%	-3.0975
GO:0007283	spermatogenesis	0.09%	-2.8779
GO:0071417	cellular response to organonitrogen compound	0.09%	-2.334
GO:1901988	negative regulation of cell cycle phase transition	0.09%	-8.094
GO:0017148	negative regulation of translation	0.09%	-2.5307
GO:0031047	gene silencing by RNA	0.09%	-3.1357
GO:0051962	positive regulation of nervous system development	0.09%	-3.1326
GO:0010720	positive regulation of cell development	0.09%	-2.3889
GO:0002694	regulation of leukocyte activation	0.09%	-2.4942
GO:0048638	regulation of developmental growth	0.09%	-2.478
GO:0016236	macroautophagy	0.08%	-2.4002
GO:0007051	spindle organization	0.08%	-4.5351
GO:0035601	protein deacylation	0.08%	-2.5333
GO:0032147	activation of protein kinase activity	0.08%	-2.6002
GO:0061640	cytoskeleton-dependent cytokinesis	0.08%	-2.1512
GO:0016482	cytosolic transport	0.08%	-7.3532
GO:0051028	mRNA transport	0.08%	-4.7418

GO:0090068	positive regulation of cell cycle process	0.07%	-4.8591
GO:0000077	DNA damage checkpoint	0.07%	-3.2313
GO:0006469	negative regulation of protein kinase activity	0.07%	-2.4545
GO:0022407	regulation of cell-cell adhesion	0.07%	-3.5854
GO:0006405	RNA export from nucleus	0.07%	-2.6854
GO:0051494	negative regulation of cytoskeleton organization	0.07%	-2.7034
GO:1902275	regulation of chromatin organization	0.07%	-3.6081
GO:0000209	protein polyubiquitination	0.07%	-2.7822
GO:0031124	mRNA 3'-end processing	0.07%	-2.4281
GO:0090174	organelle membrane fusion	0.07%	-2.435
GO:1901652	response to peptide	0.06%	-3.3921
GO:0006891	intra-Golgi vesicle-mediated transport	0.06%	-2.397
GO:1903362	regulation of cellular protein catabolic process	0.06%	-4.9651
GO:0051784	negative regulation of nuclear division	0.06%	-2.397
GO:2001251	negative regulation of chromosome organization	0.06%	-2.2325
GO:0006904	vesicle docking involved in exocytosis	0.06%	-2.9532
GO:0031098	stress-activated protein kinase signaling cascade	0.06%	-2.2586
GO:0009952	anterior/posterior pattern specification	0.06%	-2.7045
GO:0031331	positive regulation of cellular catabolic process	0.06%	-2.2797
GO:0051403	stress-activated MAPK cascade	0.06%	-4.6084
GO:0001701	in utero embryonic development	0.06%	-3.5494
GO:0006406	mRNA export from nucleus	0.06%	-4.0631
GO:0042147	retrograde transport, endosome to Golgi	0.06%	-3.2625
GO:0045732	positive regulation of protein catabolic process	0.05%	-2.556
GO:0048477	oogenesis	0.05%	-3.731
GO:0050867	positive regulation of cell activation	0.05%	-3.1047
GO:0090316	positive regulation of intracellular protein transport	0.05%	-2.6027
GO:0051961	negative regulation of nervous system development	0.05%	-2.2391
GO:0036293	response to decreased oxygen levels	0.05%	-2.8113
GO:0006997	nucleus organization	0.05%	-2.444

GO:0030010	establishment of cell polarity	0.05%	-2.2825
GO:0006909	phagocytosis	0.05%	-3.5643
GO:0045931	positive regulation of mitotic cell cycle	0.05%	-2.9657
GO:1902115	regulation of organelle assembly	0.05%	-2.1612
GO:0030433	ER-associated ubiquitin-dependent protein catabolic process	0.05%	-4.3201
GO:0033048	negative regulation of mitotic sister chromatid segregation	0.05%	-2.4157
GO:1902850	microtubule cytoskeleton organization involved in mitosis	0.05%	-4.2283
GO:0016575	histone deacetylation	0.05%	-3.8017
GO:0061136	regulation of proteasomal protein catabolic process	0.05%	-3.0366
GO:0051251	positive regulation of lymphocyte activation	0.05%	-3.7783
GO:0071375	cellular response to peptide hormone stimulus	0.05%	-2.8906
GO:0043044	ATP-dependent chromatin remodeling	0.05%	-2.4201
GO:0050821	protein stabilization	0.05%	-3.8807
GO:0000245	spliceosomal complex assembly	0.04%	-2.1894
GO:0060491	regulation of cell projection assembly	0.04%	-2.5643
GO:0032868	response to insulin	0.04%	-3.2496
GO:1902749	regulation of cell cycle G2/M phase transition	0.04%	-3.3875
GO:0043484	regulation of RNA splicing	0.04%	-7.0914
GO:0010976	positive regulation of neuron projection development	0.04%	-2.4754
GO:0007098	centrosome cycle	0.04%	-2.9999
GO:0035282	segmentation	0.04%	-2.3316
GO:1905037	autophagosome organization	0.04%	-2.4352
GO:0050684	regulation of mRNA processing	0.04%	-10.7308
GO:1903052	positive regulation of proteolysis involved in cellular protein catabolic pro	0.03%	-2.3361
GO:0050803	regulation of synapse structure or activity	0.03%	-2.517
GO:1903039	positive regulation of leukocyte cell-cell adhesion	0.03%	-2.4378
GO:1902806	regulation of cell cycle G1/S phase transition	0.03%	-3.8711
GO:0070304	positive regulation of stress-activated protein kinase signaling cascade	0.03%	-2.2728
GO:0009798	axis specification	0.03%	-2.3805
GO:0002262	myeloid cell homeostasis	0.03%	-2.9526

GO:0002066	columnar/cuboidal epithelial cell development	0.03%	-2.8588
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	0.03%	-5.8036
GO:0016441	posttranscriptional gene silencing	0.03%	-2.2242
GO:0072331	signal transduction by p53 class mediator	0.03%	-2.2962
GO:0032968	positive regulation of transcription elongation from RNA polymerase II pr	0.03%	-3.1102
GO:0031532	actin cytoskeleton reorganization	0.03%	-2.1656
GO:0046330	positive regulation of JNK cascade	0.03%	-2.4584
GO:0010972	negative regulation of G2/M transition of mitotic cell cycle	0.03%	-3.5085
GO:0031122	cytoplasmic microtubule organization	0.03%	-3.9027
GO:2001252	positive regulation of chromosome organization	0.03%	-6.021
GO:0071453	cellular response to oxygen levels	0.03%	-3.3394
GO:0044033	multi-organism metabolic process	0.03%	-2.6691
GO:0010501	RNA secondary structure unwinding	0.03%	-2.2434
GO:0030518	intracellular steroid hormone receptor signaling pathway	0.02%	-2.1757
GO:0008286	insulin receptor signaling pathway	0.02%	-3.2394
GO:0007272	ensheathment of neurons	0.02%	-3.0335
GO:0090307	mitotic spindle assembly	0.02%	-2.7089
GO:0042552	myelination	0.02%	-2.4584
GO:0040014	regulation of multicellular organism growth	0.02%	-2.1881
GO:0051781	positive regulation of cell division	0.02%	-2.3353
GO:0031110	regulation of microtubule polymerization or depolymerization	0.02%	-2.4062
GO:0071456	cellular response to hypoxia	0.02%	-2.5907
GO:0010977	negative regulation of neuron projection development	0.02%	-2.3679
GO:0009994	oocyte differentiation	0.02%	-2.6286
GO:0035195	gene silencing by miRNA	0.02%	-3.5176
GO:0090630	activation of GTPase activity	0.02%	-6.0161
GO:0031338	regulation of vesicle fusion	0.02%	-3.2534
GO:0043488	regulation of mRNA stability	0.02%	-2.1894
GO:2000144	positive regulation of DNA-templated transcription, initiation	0.02%	-2.1672
GO:0048268	clathrin coat assembly	0.02%	-2.224

GO:2000177	regulation of neural precursor cell proliferation	0.02%	-3.5878
GO:2000134	negative regulation of G1/S transition of mitotic cell cycle	0.02%	-3.9629
GO:0046579	positive regulation of Ras protein signal transduction	0.02%	-3.4516
GO:0000381	regulation of alternative mRNA splicing, via spliceosome	0.02%	-7.8622
GO:0031050	dsRNA fragmentation	0.02%	-2.3993
GO:0008298	intracellular mRNA localization	0.02%	-2.2779
GO:1900076	regulation of cellular response to insulin stimulus	0.01%	-2.6827
GO:0007350	blastoderm segmentation	0.01%	-2.2204
GO:0050982	detection of mechanical stimulus	0.01%	-2.7721
GO:0044804	nucleophagy	0.01%	-2.1672
GO:0007095	mitotic G2 DNA damage checkpoint	0.01%	-2.4201
GO:0043954	cellular component maintenance	0.01%	-2.4378
GO:0038083	peptidyl-tyrosine autophosphorylation	0.01%	-2.5054
GO:0070936	protein K48-linked ubiquitination	0.01%	-2.6814
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	0.01%	-2.6021
GO:2000058	regulation of protein ubiquitination involved in ubiquitin-dependent prote	0.01%	-4.3868
GO:0008595	anterior/posterior axis specification, embryo	0.01%	-2.7586
GO:0034501	protein localization to kinetochore	0.01%	-2.224
GO:0007298	border follicle cell migration	0.01%	-2.1919
GO:0030422	production of siRNA involved in RNA interference	0.01%	-2.2386
GO:0045736	negative regulation of cyclin-dependent protein serine/threonine kinase a	0.01%	-2.3748
GO:0051642	centrosome localization	0.01%	-2.451
GO:1904396	regulation of neuromuscular junction development	0.01%	-2.6211
GO:0061014	positive regulation of mRNA catabolic process	0.01%	-2.4484
GO:0045475	locomotor rhythm	0.01%	-2.1894
GO:2000725	regulation of cardiac muscle cell differentiation	0.01%	-2.3748
GO:0043984	histone H4-K16 acetylation	0.01%	-3.5804
GO:0033522	histone H2A ubiquitination	0.01%	-2.2386
GO:0007289	spermatid nucleus differentiation	0.01%	-2.6044
GO:0098722	asymmetric stem cell division	0.01%	-2.1656

GO:1900117	regulation of execution phase of apoptosis	0.01%	-2.6691
GO:1902803	regulation of synaptic vesicle transport	0.01%	-2.3748
GO:0031937	positive regulation of chromatin silencing	0.00%	-2.3748
GO:0060292	long term synaptic depression	0.00%	-2.224
GO:1902043	positive regulation of extrinsic apoptotic signaling pathway via death don	0.00%	-2.224
GO:0010606	positive regulation of cytoplasmic mRNA processing body assembly	0.00%	-2.6691
GO:0001675	acrosome assembly	0.00%	-2.224
GO:0007406	negative regulation of neuroblast proliferation	0.00%	-2.7721
GO:0048853	forebrain morphogenesis	0.00%	-2.224
GO:1905208	negative regulation of cardiocyte differentiation	0.00%	-2.3748
GO:0031053	primary miRNA processing	0.00%	-3.1143
GO:0007549	dosage compensation	0.00%	-2.7721
GO:1903649	regulation of cytoplasmic transport	0.00%	-2.6388
GO:2000831	regulation of steroid hormone secretion	0.00%	-2.6691
GO:0045764	positive regulation of cellular amino acid metabolic process	0.00%	-4.3214
GO:0090160	Golgi to lysosome transport	0.00%	-2.6691
GO:0016334	establishment or maintenance of polarity of follicular epithelium	0.00%	-2.4484
GO:0007294	germarium-derived oocyte fate determination	0.00%	-2.2386
GO:0007362	terminal region determination	0.00%	-2.1672
GO:0072499	photoreceptor cell axon guidance	0.00%	-2.5054
GO:0016080	synaptic vesicle targeting	0.00%	-2.3748
GO:1903421	regulation of synaptic vesicle recycling	0.00%	-2.3748
GO:0031442	positive regulation of mRNA 3'-end processing	0.00%	-2.3748

Supplementary information 1.0.4: list of differentially methylated CpGs between reproductive and sterile workers, a positive methylation difference indicates hypermethylation in sterile workers.

gene_id	chromosome	CpG_position	p-value	q-value	methylation_difference
LOC100649679	NC_015762.1	376997	0.00061086	0.02712047	-19.551282
LOC100649317	NC_015762.1	422492	0.00184886	0.04435045	21.031746
LOC100643028	NC_015762.1	545521	0.00166287	0.0424353	-32.358491
LOC100650265	NC_015762.1	959134	0.00053552	0.02534089	21.2765957
LOC100650139	NC_015762.1	964221	8.53E-05	0.01104368	34.5706619
LOC100650139	NC_015762.1	964231	0.00233014	0.0484507	13.0434783
LOC100644709	NC_015762.1	1197187	0.00230063	0.04837402	27.7777778
LOC100642191	NC_015762.1	2030026	0.00212284	0.0466812	30.2336235
LOC100642674	NC_015762.1	2064279	0.00053564	0.02534089	24.1401687
LOC100647602	NC_015762.1	2738546	0.0004096	0.02291082	30.7878788
LOC100643434	NC_015762.1	4114367	0.00095589	0.03456307	12.7659574
LOC100644747	NC_015762.1	4149170	0.00057583	0.02604982	26.7904509
LOC100647009	NC_015762.1	4433898	0.00148474	0.0411148	15.1960784
LOC100647009	NC_015762.1	4440579	0.00083019	0.03223778	15.3846154
LOC100647685	NC_015762.1	4468971	0.00141597	0.04073846	19.0829528
LOC100649435	NC_015762.1	4552747	0.00124452	0.03843553	16.2162162
LOC100650267	NC_015762.1	4636836	0.00246413	0.04993636	21.0160428
LOC100644473	NC_015762.1	4862491	0.00043603	0.02323745	-29.837329
LOC100650992	NC_015762.1	5577577	0.00033153	0.02121127	-27.083333
LOC100646331	NC_015762.1	7097883	0.00223058	0.04792228	19.6744186
LOC100645181	NC_015762.1	9501657	0.00021111	0.01783907	-31.18541
LOC100645309	NC_015762.1	9501657	0.00021111	0.01783907	-31.18541
LOC100645181	NC_015762.1	9502971	5.26E-05	0.00942173	-44.688875
LOC100645309	NC_015762.1	9502971	5.26E-05	0.00942173	-44.688875
LOC100645740	NC_015762.1	10122973	0.00233313	0.0484507	-29.008152
LOC105665612	NC_015762.1	10130097	0.00205827	0.04626133	17.9411765

LOC100648778	NC_015762.1	10301740	5.01E-06	0.00269224	22.4137931
LOC100645113	NC_015762.1	14533119	0.00244803	0.04992576	10.6666667
LOC100644837	NC_015763.1	2414718	0.00029505	0.02016154	24.6212121
LOC100645311	NC_015763.1	2447308	8.69E-05	0.01112041	17.6470588
LOC100645434	NC_015763.1	2447308	8.69E-05	0.01112041	17.6470588
LOC100646975	NC_015763.1	2692973	0.00184496	0.04434456	23.8175676
LOC100651983	NC_015763.1	3559220	0.00127015	0.03879755	-12.5
LOC100651275	NC_015763.1	5242081	0.00217175	0.04737333	17.2115385
LOC100652309	NC_015763.1	5824201	0.00150039	0.0411148	-31.791383
LOC100647451	NC_015763.1	8037643	0.00168265	0.0424353	-24.540338
LOC100648426	NC_015763.1	8385770	0.00243628	0.04992576	-19.317382
LOC100644712	NC_015763.1	8385770	0.00243628	0.04992576	-19.317382
LOC105667022	NC_015763.1	8385770	0.00243628	0.04992576	-19.317382
LOC100651477	NC_015763.1	8891390	0.00180411	0.0439126	19.5581015
LOC100647370	NC_015763.1	10268093	0.00011891	0.01331362	26.7857143
LOC100649615	NC_015763.1	10436471	0.00211867	0.0466812	-23.435948
LOC105665621	NC_015763.1	10518301	0.00190511	0.04490677	-24.071807
LOC100650355	NC_015763.1	10605433	0.00167241	0.0424353	19.1158537
LOC100650355	NC_015763.1	10605602	0.00010966	0.0126086	-31.296841
LOC100645236	NC_015763.1	13312160	1.01E-05	0.00355553	29.5454545
LOC100645437	NC_015764.1	1081801	0.00072299	0.02979752	-30.166667
LOC100642440	NC_015764.1	1192228	0.00218957	0.04737333	30.1020408
LOC100646404	NC_015764.1	1192228	0.00218957	0.04737333	30.1020408
LOC100652224	NC_015764.1	1208992	0.00182064	0.04415497	10.7692308
LOC100652224	NC_015764.1	1211692	0.00041575	0.02294401	24.4318182
LOC100642600	NC_015764.1	3884911	0.00012883	0.01349954	-29.727047
LOC100642600	NC_015764.1	3885630	0.00169376	0.04261648	19.89093
LOC100648621	NC_015764.1	5109757	0.00188021	0.04471202	30.8913309
LOC100643521	NC_015764.1	5994954	0.00208772	0.04646083	-19.285714
LOC100642513	NC_015764.1	6108207	0.00217965	0.04737333	21.032571

LOC100645706	NC_015764.1	6525137	9.78E-05	0.01205311	15.1898734
LOC100651317	NC_015764.1	6549445	0.00189719	0.04490677	17.0512821
LOC100651317	NC_015764.1	6552420	0.00173552	0.04294337	-33.245243
LOC100646895	NC_015764.1	6574361	0.00010395	0.01246974	-36.111111
LOC100642558	NC_015764.1	6610854	6.86E-06	0.00291254	31.6110305
LOC100642720	NC_015764.1	9050155	0.00241695	0.04992576	20
LOC100645747	NC_015764.1	10420316	0.00129881	0.03912695	-24.848485
LOC100645045	NC_015764.1	10828316	0.00038817	0.02257766	-19.807692
LOC100644799	NC_015764.1	10851881	0.00105756	0.03561222	14.7058824
LOC100651673	NC_015764.1	11040965	0.00104921	0.03554808	24.0348692
LOC100651673	NC_015764.1	11041325	0.00202925	0.04619753	30.6715064
LOC100651673	NC_015764.1	11042591	0.00125683	0.03855396	-23.943877
LOC100650433	NC_015764.1	13036970	6.43E-08	0.00012344	41.9076611
LOC100646137	NC_015764.1	14245742	0.00147626	0.0411148	17.071638
LOC100649804	NC_015765.1	522907	0.00122276	0.0382068	-23.732252
LOC100643318	NC_015765.1	1949136	9.88E-06	0.00355553	16.6666667
LOC100643035	NC_015765.1	1958122	7.80E-05	0.01080157	34.3137255
LOC100643924	NC_015765.1	1965037	0.0011625	0.03754602	28.9583333
LOC100644247	NC_015765.1	1971932	0.00228894	0.04835523	-23.291667
LOC100643605	NC_015765.1	2412424	0.00172237	0.04293826	27.8787879
LOC100647255	NC_015765.1	2636068	0.00108992	0.03598034	-24.424552
LOC100646058	NC_015765.1	5271524	0.00077765	0.0310823	-40.714286
LOC100645870	NC_015765.1	7352866	0.00211992	0.0466812	27.8409091
LOC100648856	NC_015765.1	11511032	0.00244317	0.04992576	29.9641577
LOC100648856	NC_015765.1	11512985	3.38E-05	0.00743885	-38.333333
LOC100647893	NC_015765.1	11591893	0.00025811	0.01922711	-28.742369
LOC100651439	NC_015765.1	13314211	0.00026303	0.01941807	27.1712159
LOC100650957	NC_015765.1	13333033	0.00061161	0.02712047	-25.439408
LOC100649877	NC_015765.1	13435437	0.00041249	0.02291082	28.2296651
LOC100645672	NC_015765.1	13445583	0.00094949	0.03456307	31.8603382

LOC100649921	NC_015765.1	13713316	8.44E-06	0.00323724	-38.235294
LOC100643402	NC_015766.1	269713	0.00048465	0.02457229	-18.939164
LOC100645906	NC_015766.1	349423	3.33E-05	0.00743885	-35.25554
LOC100643571	NC_015766.1	942671	0.00055335	0.02547583	-25.040128
LOC100650882	NC_015766.1	1046736	0.00016323	0.01608316	-22.727273
LOC100648246	NC_015766.1	1150262	0.00151332	0.0411148	20.3636364
LOC100644128	NC_015766.1	5765098	0.00161558	0.04223102	-29.122807
LOC100644128	NC_015766.1	5765286	0.0016083	0.04218494	20.90301
LOC100651835	NC_015766.1	6144945	0.00095957	0.03456307	-22.530395
LOC100652191	NC_015766.1	6144945	0.00095957	0.03456307	-22.530395
LOC100647771	NC_015766.1	6667656	0.00186215	0.04451879	24.9154834
LOC100649448	NC_015766.1	7432526	0.00133357	0.03985811	16.0177976
LOC100648130	NC_015766.1	7833701	0.00028498	0.01985697	-40.12987
LOC100647296	NC_015766.1	9314237	0.00118769	0.03799449	26.9690577
LOC100650881	NC_015766.1	9370618	0.00036944	0.02202871	29.2307692
LOC100650881	NC_015766.1	9371786	0.00050901	0.02505116	-29.524887
LOC100647181	NC_015766.1	9390841	3.41E-06	0.0019932	-34.011544
LOC100642689	NC_015767.1	1275891	0.00214014	0.04698485	-26.868687
LOC100642366	NC_015767.1	2374714	0.00029177	0.02010375	18.5290266
LOC100651077	NC_015767.1	2731010	2.90E-05	0.00696239	30.3296703
LOC100644964	NC_015767.1	9555097	0.00120379	0.03813389	-25.972851
LOC100645080	NC_015767.1	9563475	0.00014385	0.01464163	34.6590909
LOC100648674	NC_015767.1	11847984	5.89E-05	0.00962609	33.9421613
LOC100649926	NC_015767.1	12180711	0.00223129	0.04792228	31.0897436
LOC100649926	NC_015767.1	12181522	0.00173025	0.04293826	-26.394921
LOC100650322	NC_015768.1	765065	0.00087602	0.0332487	10.4477612
LOC100651404	NC_015768.1	892901	0.00063122	0.0274464	20.4545455
LOC100648278	NC_015768.1	1546328	0.00160387	0.04217105	-23.676324
LOC100648278	NC_015768.1	1546732	0.00146023	0.0411148	28.8372093
LOC100649770	NC_015768.1	1598781	0.00026943	0.01951202	15.2173913

LOC100644254	NC_015768.1	4196510	0.00052	0.02511765	31.6202946
LOC100644254	NC_015768.1	4196804	0.00037782	0.02218122	11.7647059
LOC100646948	NC_015768.1	5104057	0.00135203	0.03992475	19.5195195
LOC100646949	NC_015768.1	5208587	2.49E-05	0.00655373	22.6797386
LOC100648362	NC_015768.1	5378538	4.77E-05	0.00916367	22.8571429
LOC100645875	NC_015768.1	7715313	0.00048826	0.02466234	25.7058288
LOC100643044	NC_015768.1	8271746	7.55E-05	0.01068653	-35.673981
LOC100643044	NC_015768.1	8271759	0.00231566	0.0484507	-26.979167
LOC100644134	NC_015768.1	8295523	5.03E-05	0.00936481	23.6842105
LOC100644329	NC_015768.1	11153303	4.54E-05	0.00883099	-35.649087
LOC100644329	NC_015768.1	11153311	0.00032914	0.02121127	-28.888889
LOC100648136	NC_015768.1	12747660	8.64E-06	0.00323724	22.0338983
LOC100648899	NC_015768.1	12919785	0.00232351	0.0484507	23.3117484
LOC100650528	NC_015768.1	16012015	0.0015103	0.0411148	-20.196078
LOC100644967	NC_015768.1	17499101	0.00075934	0.03058643	29.2277615
LOC100645448	NC_015768.1	17521199	8.51E-05	0.01104368	32.2619048
LOC100645562	NC_015768.1	17686921	0.00013062	0.01349954	37.3745819
LOC100649334	NC_015769.1	2819659	0.00180354	0.0439126	-33.846154
LOC100650204	NC_015769.1	2938428	3.02E-05	0.00698925	33.3734758
LOC100643205	NC_015769.1	3480833	0.00033103	0.02121127	18.4210526
LOC100645949	NC_015769.1	5257648	0.00154584	0.04115267	-26.280323
LOC100646150	NC_015769.1	5290732	0.00149788	0.0411148	23.5014469
LOC100646866	NC_015769.1	8216699	0.00107826	0.03598034	29.0598291
LOC100647342	NC_015769.1	8392163	0.00188955	0.04485463	10.5263158
LOC100645451	NC_015770.1	1033899	0.00102092	0.03526209	-23.043185
LOC100644764	NC_015770.1	1065111	4.43E-05	0.00875103	37.037037
LOC100642213	NC_015770.1	1148005	0.00198038	0.04541963	22.5262576
LOC100649963	NC_015770.1	1456528	0.00224785	0.04800988	22.1417069
LOC100648442	NC_015770.1	1554684	0.0001766	0.01642384	16.6666667
LOC100647029	NC_015770.1	1643501	0.00151403	0.0411148	24.4840041

LOC100646112	NC_015770.1	2118039	0.00051216	0.02507962	15.3846154
LOC100643368	NC_015770.1	2186602	0.00193848	0.04514313	12.195122
LOC100643368	NC_015770.1	2186792	2.75E-05	0.0069411	19.2982456
LOC100643207	NC_015770.1	7668378	0.00223747	0.04792228	19.4871795
LOC100649337	NC_015770.1	11445974	0.00152245	0.0411148	-32.564272
LOC100647859	NC_015770.1	11529433	0.00118063	0.03794928	29.9275362
LOC100645253	NC_015770.1	13479511	0.00041908	0.02294401	11.1111111
LOC100645253	NC_015770.1	13479600	0.00095337	0.03456307	23.9795193
LOC100648868	NC_015770.1	14498902	0.00171392	0.04293826	10.6060606
LOC100651013	NC_015771.1	2452636	0.00118714	0.03799449	-31.591837
LOC100651571	NC_015771.1	3602996	0.00138406	0.04007767	-26.638951
LOC100647268	NC_015771.1	4395371	0.00149194	0.0411148	12.1212121
LOC100646067	NC_015771.1	4493679	0.00211411	0.0466812	27.1842911
LOC100651532	NC_015771.1	5842740	0.00047387	0.02420881	30.0677966
LOC100648217	NC_015771.1	6510648	0.00205899	0.04626133	17.1294747
LOC100644567	NC_015771.1	6792425	1.05E-07	0.0001758	53.8095238
LOC100645382	NC_015771.1	6820441	0.0008539	0.03277969	-29.52381
LOC100645255	NC_015771.1	6820441	0.0008539	0.03277969	-29.52381
LOC100644263	NC_015771.1	6896443	0.00051881	0.02511765	22.9880775
LOC100649584	NC_015771.1	8281942	0.00063467	0.02750764	24.7985348
LOC100645723	NC_015771.1	9283019	0.00202252	0.04613631	21.7830109
LOC100652128	NC_015771.1	9994075	8.40E-05	0.01104368	34.08368
LOC100650816	NC_015771.1	10001523	5.23E-05	0.00942173	25.5789474
LOC100651290	NC_015771.1	10837173	0.00128648	0.03895375	22.6911103
LOC100651290	NC_015771.1	10837220	0.0004713	0.02420881	33.6871069
LOC100651651	NC_015771.1	12129265	0.00197866	0.04541963	11.8644068
LOC100646628	NC_015771.1	13458703	0.00022422	0.01800386	31.9640565
LOC100646628	NC_015771.1	13458772	0.00195419	0.04519154	12.8205128
LOC105666203	NC_015772.1	796430	0.00053198	0.02534089	-31.983679
LOC100651455	NC_015772.1	2281052	0.00165714	0.0424353	-31.777778

LOC100651455	NC_015772.1	2283781	0.00116223	0.03754602	18.1733458
LOC100650367	NC_015772.1	2360167	0.00017459	0.01642384	32.1153846
LOC100642815	NC_015772.1	2479485	0.00166799	0.0424353	27.9753266
LOC100647987	NC_015772.1	3923672	0.00034493	0.02147532	-28.787879
LOC100650609	NC_015772.1	5332776	1.54E-06	0.00107365	44.9430199
LOC100651534	NC_015772.1	5379162	0.00206761	0.04633041	26.7761194
LOC100651092	NC_015772.1	6576984	0.00147463	0.0411148	-19.979716
LOC100646957	NC_015772.1	6868157	6.30E-05	0.00973903	33.75
LOC100646957	NC_015772.1	6868204	0.00049508	0.02485664	-32.909699
LOC100646513	NC_015772.1	6892324	0.00113096	0.03688221	13.5294118
LOC105666262	NC_015772.1	7443880	0.00153004	0.0411148	18.6046512
LOC100650735	NC_015772.1	7498078	0.00216302	0.04733244	19.7222222
LOC100650735	NC_015772.1	7498103	0.00047263	0.02420881	14.2857143
LOC100650735	NC_015772.1	7498114	6.10E-05	0.00963462	22.7430269
LOC100648990	NC_015772.1	7594758	0.00120703	0.03813389	-24.292453
LOC100646308	NC_015772.1	7953581	0.00135029	0.03992475	-24.008529
LOC100646190	NC_015772.1	7968705	0.00070943	0.02958876	30.4395604
LOC100645726	NC_015772.1	7982092	0.00138342	0.04007767	-32.979664
LOC100644215	NC_015772.1	8077342	0.00181903	0.04415497	10.6666667
LOC100644215	NC_015772.1	8077516	0.00079589	0.03127612	22.605364
LOC100651892	NC_015772.1	8168722	0.00109982	0.03621811	26.6898955
LOC100649664	NC_015772.1	8236242	0.002262	0.04808856	20.8061002
LOC100644688	NC_015772.1	8738116	4.10E-05	0.0082459	15.8536585
LOC100643619	NC_015772.1	9383369	5.47E-05	0.00947187	-34.009009
LOC100651377	NC_015772.1	9545548	0.00157575	0.04167626	27.9378531
LOC100651377	NC_015772.1	9545561	3.50E-05	0.00747449	37.5038521
LOC100647867	NC_015772.1	10722659	2.58E-05	0.00666436	43.4782609
LOC100645094	NC_015772.1	14959999	0.0016553	0.0424353	-25.641026
LOC100643089	NC_015772.1	15212675	0.00020394	0.0177431	-25.396825
LOC100652204	NC_015772.1	15230384	0.00071132	0.02958876	30.4621849

LOC100643777	NC_015772.1	15939621	1.61E-08	4.32E-05	-12.221606
LOC100643777	NC_015772.1	15939902	4.66E-08	0.00010431	-12.359809
LOC100651216	NC_015772.1	16386110	0.00230046	0.04837402	33.6415363
LOC100650493	NC_015772.1	16399837	0.00099992	0.03489548	32.6388889
LOC100642580	NC_015772.1	16531620	0.0003744	0.02216048	30.1829268
LOC100650050	NC_015773.1	245608	6.68E-06	0.00291254	-41.960784
LOC100648410	NC_015773.1	459127	0.00242457	0.04992576	30.6547619
LOC100642413	NC_015773.1	4243504	0.00093615	0.03455507	-20.05772
LOC100644532	NC_015773.1	4361543	0.00052667	0.02527231	-31.25
LOC100644222	NC_015773.1	5753989	2.01E-05	0.00562279	-26.236423
LOC100644222	NC_015773.1	5754212	0.00039615	0.02264944	-22.922923
LOC100644222	NC_015773.1	5757638	0.00135869	0.03994558	28.0107527
LOC100644653	NC_015773.1	5833060	5.65E-05	0.00948452	25.8012821
LOC100652208	NC_015773.1	6707294	0.00121978	0.03820221	-32.166593
LOC100647514	NC_015773.1	8137938	0.0001877	0.01670161	24.7058824
LOC100645462	NC_015773.1	8538053	0.0001076	0.0126086	33.56974
LOC100643255	NC_015773.1	8693427	0.00134962	0.03992475	21.6403162
LOC100643132	NC_015773.1	8711022	2.32E-05	0.00635459	-40.851064
LOC100650496	NC_015773.1	8969074	0.00020488	0.0177431	36.3601824
LOC100648763	NC_015773.1	8993234	0.00075608	0.03058643	-26.190476
LOC100648650	NC_015773.1	9006078	0.00197333	0.04541963	-24.603175
LOC100646432	NC_015773.1	9318039	0.00191729	0.04503575	16.995614
LOC100646004	NC_015773.1	9334506	0.00079611	0.03127612	18.3064516
LOC100649591	NC_015773.1	9388052	5.09E-05	0.00936481	20.4081633
LOC100643499	NC_015773.1	9815173	0.0003419	0.02147532	38.7533875
LOC100644817	NC_015773.1	12030891	0.00025902	0.01922711	27.0168856
LOC100645419	NC_015773.1	12039311	0.00011176	0.01272564	-38.465447
LOC100648066	NC_015773.1	12272759	0.00204991	0.04621203	14.2857143
LOC100647077	NC_015773.1	12676859	0.00203856	0.04619753	-25.904203
LOC100645060	NC_015774.1	1310371	2.45E-05	0.00655373	26.9855072

LOC100642774	NC_015774.1	5691417	0.00089356	0.0336296	19.8160535
LOC100646316	NC_015775.1	107793	0.00028671	0.01985697	-30.005672
LOC105666437	NC_015775.1	729753	0.0017278	0.04293826	22.3015873
LOC100647592	NC_015775.1	1689877	0.00098837	0.03469842	13.4328358
LOC100649596	NC_015775.1	1816614	0.00041266	0.02291082	-35.470085
LOC100650617	NC_015775.1	1853559	0.00041997	0.02294401	26.9824561
LOC100650375	NC_015775.1	1870848	0.00194356	0.04514313	-23.726274
LOC100647078	NC_015775.1	2994553	0.00229271	0.04835881	16.6666667
LOC100644498	NC_015775.1	6118499	0.00095749	0.03456307	16.3050847
LOC100646125	NC_015775.1	6304890	0.00010913	0.0126086	19.2281421
LOC100642819	NC_015775.1	8070714	0.00027848	0.0197966	-25.918004
LOC100648458	NC_015775.1	8247478	0.00040035	0.02269652	15.9126984
LOC100642419	NC_015775.1	8847655	0.00030997	0.02051555	22.9166667
LOC100643343	NC_015776.1	1247761	7.56E-05	0.01068653	36.6183575
LOC100647790	NC_015776.1	2305956	0.00098091	0.0345914	14.4444444
LOC100651855	NC_015776.1	2925261	0.00020601	0.0177431	-33.196961
LOC100651618	NC_015776.1	2935313	0.00147694	0.0411148	28.9240973
LOC100651777	NC_015776.1	4508053	2.14E-06	0.00137156	38.8176933
LOC100652059	NC_015776.1	4895559	2.29E-10	3.07E-06	42.0099256
LOC100652059	NC_015776.1	4897707	0.00037054	0.02202871	11.2676056
LOC100647479	NC_015776.1	5138454	0.00031737	0.0206996	-28.256812
LOC100646364	NC_015776.1	7180846	1.68E-05	0.0049208	21.4035088
LOC100647913	NC_015776.1	8637804	0.00033877	0.02147532	13.9534884
LOC100647000	NC_015776.1	8662688	0.00133371	0.03985811	16.3636364
LOC100643745	NC_015776.1	9266346	0.00168112	0.0424353	28.0371353
LOC100643987	NC_015776.1	9266346	0.00168112	0.0424353	28.0371353
LOC100648462	NC_015776.1	9893543	0.00035403	0.02171986	28.5761371
LOC100643219	NC_015776.1	10571715	0.00012206	0.01342364	-30.795455
LOC100648917	NC_015777.1	2555811	0.00043731	0.02323745	-30.890805
LOC100647678	NC_015777.1	2576943	0.00026706	0.01951202	35.0195724

LOC100649192	NC_015777.1	2646358	0.0003927	0.02264479	20.0938086
LOC100649192	NC_015777.1	2646669	8.78E-07	0.00079478	26.4285714
LOC100649192	NC_015777.1	2653266	0.00034524	0.02147532	39.2857143
LOC100642980	NC_015777.1	2666116	0.00045348	0.02398781	15.7894737
LOC100647123	NC_015777.1	2710303	0.00020918	0.01778768	29.9843014
LOC100649277	NC_015777.1	3146401	0.00144367	0.0411148	10.2040816
LOC100650098	NC_015777.1	3153025	1.40E-05	0.00437392	22.5806452
LOC100650098	NC_015777.1	3153048	0.00162754	0.04237864	20.67283
LOC100651858	NC_015777.1	3226690	0.00076034	0.03058643	33.4525939
LOC100651974	NC_015777.1	3228259	0.00232084	0.0484507	-22.699758
LOC100642228	NC_015777.1	3242576	0.00165631	0.0424353	27.1428571
LOC100642822	NC_015777.1	3254918	0.00212135	0.0466812	32.8191489
LOC100643786	NC_015777.1	3686978	0.00063993	0.02755756	13.7244766
LOC100644503	NC_015777.1	3686978	0.00063993	0.02755756	13.7244766
LOC100647755	NC_015777.1	4704892	0.00029939	0.02016154	37.6466529
LOC100647755	NC_015777.1	4706455	0.00022978	0.01800386	28.0965392
LOC100648841	NC_015777.1	4763424	1.19E-05	0.00401335	24.3589744
LOC100650422	NC_015777.1	5041073	0.00022775	0.01800386	-35.757576
LOC100651778	NC_015778.1	572614	1.57E-05	0.00468538	-32.788462
LOC100645779	NC_015778.1	1985910	0.0018676	0.04456568	16.998557
LOC100631084	NC_015778.1	2734791	0.00038149	0.02228525	-27.482993
LOC100650018	NC_015778.1	3244001	0.00155289	0.04115267	-18.543372
LOC100649830	NC_015779.1	2821981	0.00037805	0.02218122	28.5714286
LOC100649830	NC_015779.1	2822065	0.00148137	0.0411148	14.9122807
LOC100649830	NC_015779.1	2822115	6.85E-05	0.01022965	31.1904762
LOC100649830	NC_015779.1	2822147	0.00017997	0.01642384	34.5221445
LOC100647710	NW_003565404.	174935	0.00042772	0.02313049	22.5258045
LOC100648347	NW_003565426.	771633	0.00040782	0.02291082	18.5185185
LOC100647711	NW_003565557.	1460735	9.99E-05	0.01220648	-40.563725
LOC100649789	NW_003565760.	1739	5.95E-05	0.00962609	-30.632411

LOC100650748	NW_003565787.	4187	0.00120418	0.03813389	16.7857143
LOC100650829	NW_003565947.	258209	0.00012719	0.01349954	18.5185185
LOC100650829	NW_003565947.	260930	0.00095121	0.03456307	20.6596036
LOC100650829	NW_003565947.	262080	5.36E-06	0.00276925	28.5714286
LOC100649280	NW_003565947.	814375	0.00201194	0.04597318	25.3928867
LOC100642946	NW_003566036.	1519664	0.00036258	0.02202871	23.0769231
LOC100650136	NW_003566042.	54133	0.00164465	0.0424353	10.5263158
LOC100649607	NW_003566126.	478265	0.00246177	0.04993636	32.9302987
LOC100650987	NW_003566126.	759206	0.0010296	0.0352896	-25.519126
LOC100645305	NW_003566135.	1286754	0.00086518	0.03293034	29.1612903
LOC105666915	NW_003566269.	3063	0.00154974	0.04115267	12.244898
LOC100645663	NW_003566384.	417159	0.00034991	0.02156593	18.75
LOC100643431	NW_003566384.	828989	0.00143579	0.0411148	36.5546218
LOC100643307	NW_003566384.	833502	0.00073603	0.03015022	-33.462819
LOC100644353	NW_003566384.	876138	0.00207585	0.04633041	30.2222222
LOC100646212	NW_003566384.	1180695	0.00012316	0.01342364	-30.925285
LOC100647885	NW_003566384.	1506956	0.00167039	0.0424353	20.1149425
LOC100647885	NW_003566384.	1507063	0.00068991	0.02906118	28.2229965
LOC100650627	NW_003566384.	1638092	0.00110717	0.03636988	26.2731481
LOC100643229	NW_003566384.	1918733	3.40E-07	0.00045678	43.2285115
LOC100642867	NW_003566384.	1934762	0.00223991	0.04792228	16.3414634
LOC100643472	NW_003566384.	1970056	0.00168278	0.0424353	12.9032258
LOC100645476	NW_003566384.	2118650	0.00121181	0.03813389	21.8039003
LOC100645971	NW_003566384.	2155391	0.00024403	0.01873566	20.4848485
LOC100647919	NW_003566384.	2279539	0.00152929	0.0411148	-29.291717
LOC100648846	NW_003566384.	2320454	0.00223838	0.04792228	23.0635551
LOC100648846	NW_003566384.	2320463	0.00036789	0.02202871	19.6521739
LOC100649677	NW_003566384.	2416892	0.00193235	0.04514313	10.6382979
LOC100649244	NW_003566440.	3798	0.00083688	0.03231103	-19.047619
LOC100651907	NW_003566591.	394287	0.00015242	0.01528247	17.3913043

LOC100651907	NW_003566591.	395387	0.00209011	0.04646083	13.3333333
LOC100644471	NW_003566591.	777561	0.00025589	0.01922711	24.1967871
LOC100650871	NW_003568921.	616	0.00097389	0.03456307	16.4869029
LOC100644590	NC_015762.1	1207762	0.00034515	0.02147532	-17.489228
LOC100642191	NC_015762.1	2026758	0.0003986	0.02269278	-17.021277
LOC100647009	NC_015762.1	4440218	0.00017734	0.01642384	-14.364207
LOC100648080	NC_015762.1	4495874	0.00183203	0.04427138	-19.80464
LOC100649013	NC_015762.1	4526996	0.00116767	0.03762275	-29.091653
LOC100649435	NC_015762.1	4552004	0.0024494	0.04992576	-19.907407
LOC100643752	NC_015762.1	4833460	0.00056748	0.02575891	-22.673532
LOC100643752	NC_015762.1	4833497	0.00030011	0.02016154	-32.692308
LOC100649681	NC_015762.1	6095755	1.09E-05	0.00374178	-37.142857
LOC105665938	NC_015762.1	7003250	1.06E-08	3.56E-05	-31.599455
LOC105665938	NC_015762.1	7003268	0.00050173	0.0249289	-17.173616
LOC100652151	NC_015762.1	10271327	0.00222547	0.04792228	-11.111111
LOC100648270	NC_015762.1	10284728	0.00031487	0.0206996	-18.918919
LOC100644794	NC_015763.1	1140608	0.00145611	0.0411148	-33.044365
LOC100649798	NC_015763.1	3275343	8.67E-06	0.00323724	-37.915022
LOC100651983	NC_015763.1	3556693	0.00110984	0.03636988	-12.857143
LOC100650915	NC_015763.1	5221226	0.00123165	0.0383063	-12.797838
LOC100652224	NC_015764.1	1213482	0.00021798	0.01796785	-17.321429
LOC100646498	NC_015764.1	5681807	0.00138759	0.04009363	-16.520147
LOC100643521	NC_015764.1	5995155	0.00056588	0.02575891	-29.57529
LOC100642513	NC_015764.1	6107987	0.00061758	0.02729535	-14.660895
LOC100651317	NC_015764.1	6554254	8.31E-05	0.01104368	-16.018128
LOC100645866	NC_015764.1	10413935	0.0002224	0.01800386	-16.33263
LOC100644361	NC_015764.1	10871523	0.00074897	0.03043578	-16.614944
LOC100651635	NC_015765.1	2144566	0.00054375	0.02543848	-23.748339
LOC100644957	NC_015765.1	2477243	0.00017626	0.01642384	-19.230769
LOC100650316	NC_015765.1	2613871	0.00024977	0.0189594	-13.043478

LOC100643888	NC_015766.1	2570556	0.00108428	0.03598034	-32.82795
LOC100651678	NC_015766.1	3402397	0.00149131	0.0411148	-13.432836
LOC100651562	NC_015766.1	3425666	0.00174444	0.04308481	-13.685889
LOC100649806	NC_015766.1	3650055	7.79E-05	0.01080157	-21.296296
LOC100646622	NC_015766.1	4170158	3.18E-05	0.00723564	-31.108597
LOC100650320	NC_015766.1	5005663	0.00124112	0.03843553	-15.235732
LOC100647771	NC_015766.1	6667690	0.0009202	0.03415392	-23.548387
LOC100652158	NC_015766.1	7403353	0.00178536	0.04369369	-28.325762
LOC100648974	NC_015766.1	7696208	0.00144553	0.0411148	-25.503686
LOC100648782	NC_015766.1	7696208	0.00144553	0.0411148	-25.503686
LOC100650881	NC_015766.1	9368475	2.44E-07	0.00036465	-46.274218
LOC100650881	NC_015766.1	9370761	0.00199276	0.0456123	-12.545038
LOC105665830	NC_015767.1	124877	0.00105368	0.03557064	-12.94772
LOC100648319	NC_015767.1	133909	0.00054717	0.02543848	-19.866071
LOC100648319	NC_015767.1	133933	2.79E-05	0.0069411	-21.473684
LOC100648319	NC_015767.1	140310	0.00128667	0.03895375	-12.820513
LOC100643649	NC_015767.1	4844299	0.0020719	0.04633041	-21.581395
LOC100649926	NC_015767.1	12180011	0.0001092	0.0126086	-29.444998
LOC100646110	NC_015768.1	5064305	0.00194972	0.04516598	-12
LOC100650442	NC_015768.1	5542929	0.00020034	0.017593	-23.404255
LOC100646298	NC_015768.1	9053237	4.01E-07	0.00048173	-42.346014
LOC100648635	NC_015768.1	9644114	0.00024875	0.0189594	-16.071429
LOC100652194	NC_015768.1	10971383	0.00054371	0.02543848	-21.900161
LOC100650204	NC_015769.1	2937871	0.00102489	0.0352896	-15.039973
LOC100650204	NC_015769.1	2938762	0.00152827	0.0411148	-20.675766
LOC100642640	NC_015769.1	3267580	0.00091955	0.03415392	-27.964427
LOC100649260	NC_015769.1	3494038	7.33E-05	0.01058752	-35.768501
LOC100650648	NC_015769.1	3521779	0.00102878	0.0352896	-20.303605
LOC100649811	NC_015769.1	3556735	0.00134119	0.03992475	-15.789474
LOC100650244	NC_015769.1	3572122	2.84E-05	0.00694862	-15.174129

LOC100651406	NC_015769.1	4972748	2.95E-05	0.00696239	-34.210526
LOC100645250	NC_015769.1	7946176	6.28E-06	0.00290984	-28.928571
LOC100645720	NC_015769.1	8206633	0.00066245	0.0283328	-17.307692
LOC100648096	NC_015769.1	8427230	0.00013992	0.0143511	-15.591398
LOC100649659	NC_015770.1	91560	0.00124725	0.03843553	-15.602035
LOC100646867	NC_015770.1	401229	0.00012332	0.01342364	-32.585416
LOC100645201	NC_015770.1	1031102	0.00015631	0.01555699	-18.032787
LOC100642571	NC_015770.1	2258005	5.89E-05	0.00962609	-18.604651
LOC100648984	NC_015770.1	14505162	0.00245236	0.04992576	-30.431979
LOC100643944	NC_015771.1	1081673	0.00046302	0.02420641	-18.287671
LOC100648946	NC_015771.1	2351675	1.29E-06	0.0010198	-38.745471
LOC100648946	NC_015771.1	2351677	7.91E-05	0.01080788	-30.555556
LOC100650967	NC_015771.1	3617043	0.00028356	0.01985697	-19.518944
LOC100649459	NC_015771.1	11530518	0.00027012	0.01951202	-28.888889
LOC100649968	NC_015772.1	1159366	0.001526	0.0411148	-22.286184
LOC100645645	NC_015772.1	2066455	0.00204583	0.04619753	-21.481481
LOC100651534	NC_015772.1	5378937	0.0009	0.03377724	-28.070175
LOC100650491	NC_015772.1	7519867	0.00021606	0.01791969	-12.195122
LOC100649343	NC_015772.1	7541405	0.00082679	0.03219908	-24.90566
LOC105666257	NC_015772.1	7909278	6.94E-06	0.00291254	-26.064421
LOC100646190	NC_015772.1	7963524	0.00173212	0.04293826	-24.205508
LOC100650819	NC_015772.1	8214789	0.00023361	0.01814337	-32.710623
LOC100649664	NC_015772.1	8237014	0.00056267	0.02571714	-13.611111
LOC100643819	NC_015772.1	9386870	0.00162221	0.04232197	-20.786963
LOC100650452	NC_015772.1	10062659	1.38E-05	0.00437392	-20
LOC100647546	NC_015772.1	15745254	0.00046724	0.02420881	-36.842105
LOC100643294	NC_015772.1	15931078	9.01E-05	0.01120883	-27.707897
LOC100652208	NC_015773.1	6716460	0.00096301	0.03456307	-20.512821
LOC100643380	NC_015773.1	7515210	1.91E-09	1.28E-05	-56.895223
LOC100642532	NC_015773.1	8746795	5.41E-05	0.00947187	-24.583333

LOC100631073	NC_015773.1	8806951	0.0018518	0.04435045	-15.151515
LOC100648529	NC_015773.1	8815726	0.00172374	0.04293826	-24.94073
LOC100645771	NC_015773.1	9351280	0.00105037	0.03554808	-13.888889
LOC100647938	NC_015773.1	11565044	0.00021446	0.01789686	-14.634146
LOC100643091	NC_015773.1	12019053	0.00218412	0.04737333	-18.150685
LOC100647474	NC_015773.1	12067331	0.00125458	0.03855396	-12.121212
LOC100647077	NC_015773.1	12676872	0.00072107	0.02979752	-24.095238
LOC100650252	NC_015774.1	7695745	3.69E-05	0.00775375	-22.9811
LOC100646438	NC_015775.1	6650239	4.30E-07	0.00048173	-39.554731
LOC100642658	NC_015775.1	6963096	0.00147572	0.0411148	-10.606061
LOC100644906	NC_015775.1	7895469	0.00086382	0.03293034	-23.467784
LOC100650786	NC_015775.1	7908723	0.00070027	0.02931077	-19.763023
LOC100643058	NC_015775.1	8936201	0.00137681	0.04007767	-10.11236
LOC100646998	NC_015775.1	11078682	0.0003922	0.02264479	-15.789474
LOC100647553	NC_015776.1	2705860	0.00011615	0.01311401	-26.653061
LOC100645389	NC_015776.1	5263064	0.0001098	0.0126086	-20.833333
LOC100644347	NC_015776.1	9251933	0.0006298	0.0274464	-34.047619
LOC100647794	NC_015777.1	2535852	0.00052158	0.02511765	-23.051948
LOC100649192	NC_015777.1	2642369	0.00218223	0.04737333	31.1749571
LOC100649192	NC_015777.1	2645324	0.00029921	0.02016154	-11.667102
LOC100647123	NC_015777.1	2720352	7.32E-05	0.01058752	-17.777778
LOC100649976	NC_015777.1	3161644	1.39E-06	0.00103961	-21.411483
LOC100651974	NC_015777.1	3228178	0.00066774	0.02839149	-31.111111
LOC100643786	NC_015777.1	3686912	0.00194538	0.04514313	-19.1
LOC100644503	NC_015777.1	3686912	0.00194538	0.04514313	-19.1
LOC100645696	NC_015777.1	4259206	0.00043757	0.02323745	-24.603175
LOC100647755	NC_015777.1	4705209	0.00057936	0.02612161	-29.665072
LOC100648841	NC_015777.1	4762026	0.00022412	0.01800386	-17.884525
LOC100645779	NC_015778.1	1985608	0.00203405	0.04619753	-23.59988
LOC100648492	NC_015778.1	3384957	0.00244015	0.04992576	-12.395833

LOC100644156	NW_003565911.	2844	0.00158488	0.04175353	-18.421053
LOC100647485	NW_003566126.	349992	0.00022244	0.01800386	-12
LOC100649195	NW_003566135.	83799	0.00083354	0.03227458	-30.35807
LOC100643146	NW_003566135.	273577	0.00218905	0.04737333	-17.89993
LOC105666928	NW_003566384.	128572	0.001551	0.04115267	-30.355731
LOC100651063	NW_003566384.	433230	0.00016399	0.01608316	-20.634921
LOC100644587	NW_003566384.	1266239	0.0020452	0.04619753	-20.030395
LOC100644587	NW_003566384.	1266272	1.40E-05	0.00437392	-30.753968
LOC100645783	NW_003566384.	1402790	1.28E-06	0.0010198	-19.417476
LOC100646812	NW_003566384.	1473277	0.00027788	0.0197966	-14.318285
LOC100648421	NW_003566384.	1524988	0.00100889	0.03511734	-25.498188
LOC100649011	NW_003566384.	1562183	0.00091246	0.03405465	-12.857143
LOC100651907	NW_003566591.	393779	0.00043533	0.02323745	-15.120594
LOC100642986	NW_003566591.	464563	6.38E-05	0.00973903	-27.224824
LOC100651357	NC_015762.1	6274051	7.21E-05	0.01058752	22.7150538
LOC100647408	NC_015763.1	4768505	0.00207274	0.04633041	17.1875
LOC100652224	NC_015764.1	1208259	0.00111857	0.0365668	10.6796117
LOC100652224	NC_015764.1	1211673	6.34E-05	0.00973903	14.1269841
LOC100651791	NC_015764.1	4372228	4.11E-05	0.0082459	16.6666667
LOC100645706	NC_015764.1	6525147	0.00104362	0.03549868	11.25
LOC100642241	NC_015765.1	10954741	0.00042779	0.02313049	11.9402985
LOC100650805	NC_015765.1	11122729	0.00187074	0.04456568	11.1111111
LOC100643402	NC_015766.1	271766	0.00039502	0.02264944	14.8648649
LOC100648474	NC_015766.1	1153468	0.00183809	0.0443382	21.3095238
LOC100650640	NC_015766.1	3472066	0.00121192	0.03813389	15.9090909
LOC100650881	NC_015766.1	9370604	0.0008087	0.03158606	11.3207547
LOC100646180	NC_015767.1	4660438	0.00190413	0.04490677	17.6847662
LOC100651639	NC_015767.1	8818124	0.00145864	0.0411148	16.1347518
LOC100649926	NC_015767.1	12182718	0.00193758	0.04514313	17.0424403
LOC100643848	NC_015768.1	3030077	0.00245022	0.04992576	21.0786739

LOC100648165	NC_015768.1	4596907	0.00056273	0.02571714	13.2352941
LOC100645248	NC_015768.1	11201782	0.00165624	0.0424353	12.7906977
LOC100651603	NC_015769.1	3036554	0.0002854	0.01985697	19.5665446
LOC100651603	NC_015769.1	3039331	5.89E-06	0.00290984	26.6911453
LOC100651603	NC_015769.1	3039342	0.00012617	0.01349954	23.5785081
LOC100648098	NC_015770.1	256437	0.00121714	0.03820221	14.6537162
LOC100644567	NC_015771.1	6788507	0.00182686	0.04422608	13.5135135
LOC100644897	NC_015771.1	6863468	0.00095568	0.03456307	17.0212766
LOC100649664	NC_015772.1	8233007	0.00065275	0.0280201	13.3333333
LOC100649664	NC_015772.1	8238004	0.00119776	0.03813389	10.3896104
LOC100644688	NC_015772.1	8738518	1.60E-06	0.00107365	27.4948484
LOC100651377	NC_015772.1	9543638	0.00049651	0.02485664	12.0535714
LOC100649781	NC_015772.1	14825684	0.00099864	0.03489548	10.3896104
LOC100644652	NC_015773.1	4373179	0.00050467	0.0249289	16.6666667
LOC100645060	NC_015774.1	1310359	0.00113904	0.03705584	19.4361526
LOC105666468	NC_015775.1	6302038	0.00108784	0.03598034	12.244898
LOC100642940	NC_015775.1	7869420	0.00089114	0.0336296	13.128655
LOC100650786	NC_015775.1	7907587	0.00127055	0.03879755	22.8021978
LOC100643909	NC_015776.1	3217662	5.62E-05	0.00948452	18.4848485
LOC100652059	NC_015776.1	4887270	0.00054569	0.02543848	17.710944
LOC100652059	NC_015776.1	4894655	8.87E-07	0.00079478	24.2929293
LOC100646364	NC_015776.1	7169239	0.0007498	0.03043578	14.0350877
LOC100646391	NC_015776.1	9112473	0.00032599	0.0211591	20.3703704
LOC100649192	NC_015777.1	2652130	0.0016321	0.04241536	28.6231884
LOC100649192	NC_015777.1	2654325	0.00062372	0.0274337	-30.835459
LOC100650421	NC_015777.1	3171763	0.00036135	0.02202871	16.2790698
LOC100648695	NC_015778.1	3471635	9.93E-09	3.56E-05	40.4365079
LOC100648695	NC_015778.1	3471747	0.00031675	0.0206996	22.5931446
LOC100651665	NW_003566384.	791632	0.00204147	0.04619753	11.3207547
LOC100651511	NW_003566384.	1772578	0.00120302	0.03813389	22.1680217

LOC100651511	NW_003566384.	1772588	0.00137895	0.04007767	17.5
LOC100643472	NW_003566384.	1965662	6.09E-05	0.00963462	18.6666667
LOC100643718	NW_003566384.	2085160	0.00034146	0.02147532	13.1147541
LOC100648266	NW_003566384.	2300905	0.00042867	0.02313049	25.7386537
LOC100649677	NW_003566384.	2412863	0.00018088	0.01642384	20.3929539
LOC100644952	NC_015762.1	9997675	0.0006248	0.0274337	-25.489362
LOC100646734	NC_015763.1	2496195	0.00047949	0.02440312	-22.569444
LOC100648009	NC_015763.1	10599998	0.00104308	0.03549868	-12.336142
LOC100645706	NC_015764.1	6528545	0.00036514	0.02202871	-15.789474
LOC100649130	NC_015764.1	6774464	0.00024333	0.01873566	-21.153846
LOC100648856	NC_015765.1	11512673	0.00124707	0.03843553	-24.697268
LOC100645906	NC_015766.1	349552	0.00096626	0.03456307	-14.068826
LOC100649806	NC_015766.1	3650091	0.00060875	0.02712047	-18.937806
LOC100647417	NC_015766.1	4091145	0.00025637	0.01922711	-14.285714
LOC100651717	NC_015766.1	6774651	0.00163826	0.0424353	-15.517241
LOC105665838	NC_015767.1	4644150	0.00030177	0.02017155	-16.666667
LOC100646258	NC_015768.1	2264303	0.00050309	0.0249289	-14.893617
LOC100648362	NC_015768.1	5380549	0.00095393	0.03456307	-16.216216
LOC100651805	NC_015768.1	16159476	0.0005347	0.02534089	-12.727273
LOC100651603	NC_015769.1	3034552	2.60E-06	0.00158687	-25
LOC100651603	NC_015769.1	3041656	0.00016778	0.01633506	-22.561108
LOC100648096	NC_015769.1	8426463	0.0019045	0.04490677	-14
LOC100642571	NC_015770.1	2257628	0.00104131	0.03549868	-12.5
LOC100648097	NC_015770.1	2309522	0.00139352	0.04017851	-13.207547
LOC100644892	NC_015770.1	2309522	0.00139352	0.04017851	-13.207547
LOC100651885	NC_015770.1	3327651	0.00198096	0.04541963	-19.362821
LOC100648905	NC_015770.1	11463574	0.00134658	0.03992475	-21.033592
LOC100642457	NC_015770.1	11718426	8.55E-05	0.01104368	-13.924051
LOC100646957	NC_015772.1	6867861	0.00018091	0.01642384	-17.021277
LOC100648873	NC_015772.1	7600753	0.00071874	0.02979752	-17.948718

LOC105666316	NC_015773.1	1411984	3.95E-05	0.00817199	-20
LOC100644653	NC_015773.1	5832860	0.00034962	0.02156593	-15.384615
LOC100643011	NC_015773.1	8702205	0.00020774	0.01777803	-15.254237
LOC100642532	NC_015773.1	8744895	6.57E-05	0.00991686	-24.444444
LOC100650375	NC_015775.1	1871457	0.00097753	0.03456307	-35.61828
LOC100650375	NC_015775.1	1871459	0.00017955	0.01642384	-37.222222
LOC100631090	NC_015775.1	7891443	0.00244914	0.04992576	-15.384615
LOC100646559	NC_015775.1	8223823	0.00116217	0.03754602	-35.366795
LOC100648914	NC_015775.1	11184167	0.00231381	0.0484507	-23.269231
LOC100643137	NC_015776.1	2273841	0.00078473	0.03110195	-10.526316
LOC100652059	NC_015776.1	4890830	0.00240197	0.04972665	-12.74794
LOC100649429	NC_015776.1	6165090	0.00122562	0.03820704	-16
LOC100648917	NC_015777.1	2554494	0.00013054	0.01349954	-25.180375
LOC100647123	NC_015777.1	2716797	0.00161068	0.04218494	-22.009292
LOC100650667	NC_015777.1	3188993	0.00192514	0.04514134	-12.068966
LOC100644504	NC_015777.1	3231073	0.00018632	0.01670161	-19.58168
LOC100646686	NC_015777.1	3826337	0.00167069	0.0424353	-15.09434
LOC100646806	NC_015777.1	3851777	0.00084089	0.03237269	-16.289934
LOC100645391	NC_015777.1	4443238	0.00088431	0.0334691	-25.246305
LOC100644154	NC_015779.1	2199288	0.00045716	0.02399337	-20
LOC100648347	NW_003565426.	771711	0.00069215	0.02906118	-11.363636
LOC100644421	NW_003565443.	189004	0.00245868	0.04993636	-11.904762
LOC100649399	NW_003565557.	10497	0.00019467	0.01720806	-25.34153
LOC100649676	NW_003566135.	321890	0.00171802	0.04293826	-22.435897
LOC100650022	NW_003566384.	1609337	0.00077961	0.0310823	-17.948718
LOC100646211	NW_003566384.	2184430	0.00074009	0.03022415	-23.275261
LOC100649558	NW_003566384.	2401494	0.001967	0.04540952	-14.0625
LOC100642314	NC_015762.1	2042315	0.00023016	0.01800386	14
LOC100644954	NC_015763.1	2426585	0.00030008	0.02016154	13.8888889
LOC100652224	NC_015764.1	1213599	0.00023048	0.01800386	11.5044248

LOC100647721	NC_015764.1	5504714	0.0022703	0.04812563	12
LOC100647721	NC_015764.1	5504844	0.00059455	0.02671517	11.1111111
LOC100645517	NC_015764.1	8892515	0.00045654	0.02399337	16
LOC105665731	NC_015766.1	7412643	0.00233159	0.0484507	12
LOC100645193	NC_015766.1	11001047	0.00028503	0.01985697	10.9589041
LOC100651995	NC_015767.1	4701299	0.00138013	0.04007767	11.9047619
LOC100647499	NC_015767.1	4752460	0.00129016	0.03895375	18.875
LOC100651158	NC_015767.1	8785489	0.00017427	0.01642384	11.6883117
LOC100649499	NC_015767.1	12310611	0.00037048	0.02202871	16.6666667
LOC100648825	NC_015768.1	5398913	0.00047138	0.02420881	10.1010101
LOC100645448	NC_015768.1	17521059	0.00097418	0.03456307	12.5
LOC100651603	NC_015769.1	3041482	0.00177228	0.04345278	13.4050881
LOC100649141	NC_015769.1	5230270	0.00021279	0.0178687	13.2963477
LOC100648096	NC_015769.1	8427047	0.00012959	0.01349954	15.8231707
LOC100651571	NC_015771.1	3603556	0.00022695	0.01800386	23.0392157
LOC100650607	NC_015771.1	5943407	0.00096759	0.03456307	11.6883117
LOC100644529	NC_015771.1	9462240	0.00212233	0.0466812	15.7894737
LOC100651651	NC_015771.1	12129229	0.0023242	0.0484507	12.4675325
LOC100646871	NC_015772.1	8697482	0.00095984	0.03456307	19.5121951
LOC100643089	NC_015772.1	15212592	0.00092829	0.03435905	12
LOC100646678	NC_015775.1	129530	0.0001515	0.01528247	19.047619
LOC100643058	NC_015775.1	8936643	0.00234372	0.04859552	13.1147541
LOC100643137	NC_015776.1	2280361	0.00073051	0.03001557	11.4754098
LOC100649192	NC_015777.1	2653524	0.00051332	0.02507962	17.5
LOC100649976	NC_015777.1	3161554	4.68E-06	0.00262214	16
LOC100651900	NC_015777.1	4129918	0.00016903	0.01633905	13.6363636
LOC100648492	NC_015778.1	3385457	0.00026794	0.01951202	12.1212121
LOC100643961	NW_003566384.	1255296	0.00040802	0.02291082	12.3076923
LOC100645971	NW_003566384.	2159747	0.00146867	0.0411148	10.6666667
LOC100642868	NW_003566591.	461381	0.00137199	0.04007767	12.3076923

LOC100650139	NC_015762.1	966360	3.50E-05	0.00747449	-19.444444
LOC100646974	NC_015763.1	1082594	0.00030841	0.0205136	-16.216216
LOC100650430	NC_015763.1	5197991	0.00067422	0.0285764	-16.542474
LOC100648856	NC_015765.1	11514635	0.00245246	0.04992576	-14.893617
LOC100648856	NC_015765.1	11516752	0.00042009	0.02294401	-19.565217
LOC100649877	NC_015765.1	13437883	5.50E-05	0.00947187	-11.650485
LOC100651678	NC_015766.1	3402413	0.0006384	0.02755756	-10.344828
LOC100649770	NC_015768.1	1599169	0.0015291	0.0411148	-15
LOC100650041	NC_015769.1	3587817	0.00176829	0.04343423	-13.793103
LOC100643368	NC_015770.1	2187684	0.00135663	0.03994558	-12.048193
LOC100651885	NC_015770.1	3327231	0.00215872	0.04731527	-10.769231
LOC100647509	NC_015771.1	2690140	0.00049766	0.02485664	-14.634146
LOC100647155	NC_015772.1	1898960	0.00101835	0.03526209	-17.073171
LOC100651534	NC_015772.1	5378933	0.00221989	0.04792228	-16
LOC100647113	NC_015773.1	4870286	0.00055366	0.02547583	-20.37037
LOC100644222	NC_015773.1	5750425	0.00086287	0.03293034	-15.384615
LOC100642532	NC_015773.1	8744760	8.97E-05	0.01120883	-25.977011
LOC100650376	NC_015775.1	7290296	0.00171772	0.04293826	-14.611212
LOC100652138	NC_015775.1	7534029	0.00128838	0.03895375	-17.647059
LOC100649150	NC_015775.1	7921759	0.00106669	0.03582985	-11.111111
LOC100648113	NC_015775.1	8194391	0.00228625	0.04835523	-14.285714
LOC100643137	NC_015776.1	2273687	1.79E-05	0.00510851	-25.925926
LOC100645812	NC_015776.1	9187656	0.0009891	0.03469842	-13.461538
LOC100647318	NC_015776.1	9925744	0.00010273	0.01243453	-15.384615
LOC100643219	NC_015776.1	10570435	0.00055084	0.02547583	-17.307692
LOC100643911	NC_015777.1	207062	0.00209207	0.04646083	-11.169208
LOC100646247	NC_015778.1	974769	0.0005965	0.02671517	-22.684458
LOC100651179	NW_003565407.	389479	6.27E-06	0.00290984	-25.862069
LOC100651181	NW_003565557.	708516	4.95E-05	0.00936481	-11.764706
LOC100649982	NW_003565947.	848331	0.0005174	0.02511765	-16.153846

LOC100650136	NW_003566042.	55647	0.00102003	0.03526209	-10.169492
LOC100642867	NW_003566384.	1934790	0.00133494	0.03985811	-14.084507

Supplementary 1.0.5: Location of differentially methylated CpGs found outside of genes along with the expression levels of genes found within 5000bp.

Gene	Chromosome	CpG Position	pvalue	qvalue	Percentage Methylation Difference	Location	FPKM Repro	FPKM Sterile
LOC100644051	NC_015765.1	12720757	0.00107953	0.03598034	15.6862745	promotor	22.0771489	22.0185103
LOC100644165	NC_015765.1	12720757	0.00107953	0.03598034	15.6862745	promotor	19.7185199	17.4114759
LOC100644269	NC_015775.1	10519648	0.00054701	0.02543848	-17.741935	downstream	4.96172188	5.28835964
LOC100647669	NC_015773.1	7088437	0.0016834	0.0424353	16.873706	promotor	5.0230992	5.93958681
LOC100647784	NC_015773.1	7088437	0.0016834	0.0424353	16.873706	promotor	3.07423198	3.36082349
LOC100648764	NC_015773.1	7088437	0.0016834	0.0424353	16.873706	downstream	34.438568	35.3322893
LOC100648818	NC_015765.1	13414299	5.81E-07	0.00060048	30.6122449	promotor	10.1584966	10.6711456
LOC100648934	NC_015765.1	13414299	5.81E-07	0.00060048	30.6122449	promotor	102.062509	95.5049872
LOC100649133	NC_015765.1	13414299	5.81E-07	0.00060048	30.6122449	downstream	40.1316789	35.4865418
LOC100649254	NC_015765.1	13414299	5.81E-07	0.00060048	30.6122449	downstream	9.19447606	9.7747434
LOC100651999	NC_015769.1	1238707	0.00174807	0.04309524	-22.002551	downstream	7.25259771	6.79301995
LOC100652121	NC_015769.1	1238707	0.00174807	0.04309524	-22.002551	promotor	10.4540248	9.04276021
LOC100652238	NC_015769.1	1238707	0.00174807	0.04309524	-22.002551	promotor	78.8213943	65.8684876

Supplementary 1.0.6: Results of the post-hoc Dunn's test, p-values have been corrected for multiple testing using the Benjamini-Hochberg method.* indicates a significant difference ($p < 0.05$) in the weighted methylation of the features compared, using weighted methylation calculated from all samples.

Genomic feature comparisons

Comparison	Z	P.unadj	P.adj	
CDS - exon	9.2068272	3.36E-20	1.18E-19	*
CDS - gene	7.1073223	1.18E-12	3.31E-12	*
exon - gene	-1.4070275	1.59E-01	1.72E-01	
CDS - intron	23.3015946	4.27E-120	5.98E-119	*
exon - intron	19.0442184	7.34E-81	4.11E-80	*
gene - intron	19.0876352	3.20E-81	2.24E-80	*
CDS - mRNA	6.7661733	1.32E-11	3.37E-11	*
exon - mRNA	-1.7583463	7.87E-02	9.18E-02	
gene - mRNA	-0.3223292	7.47E-01	7.47E-01	
intron - mRNA	-19.253152	1.33E-82	1.24E-81	*
CDS - ncRNA	4.7261802	2.29E-06	4.00E-06	*
exon - ncRNA	3.3820797	7.19E-04	1.06E-03	*
gene - ncRNA	3.5715618	3.55E-04	5.52E-04	*
intron - ncRNA	-1.2477562	2.12E-01	2.20E-01	
mRNA - ncRNA	3.621967	2.92E-04	4.82E-04	*
CDS - promotor	-2.0617532	3.92E-02	4.78E-02	*
exon - promotor	-11.746421	7.37E-32	3.44E-31	*
gene - promotor	-9.3496151	8.80E-21	3.52E-20	*
intron - promotor	-24.77811	1.54E-135	4.32E-134	*
mRNA - promotor	-8.993068	2.40E-19	7.48E-19	*
ncRNA - promotor	-5.0716511	3.94E-07	8.49E-07	*
CDS - transcript	4.9336895	8.07E-07	1.61E-06	*
exon - transcript	2.7036072	6.86E-03	8.73E-03	*
gene - transcript	3.0148295	2.57E-03	3.43E-03	*
intron - transcript	-4.8010013	1.58E-06	2.95E-06	*

Linkage group comparisons

Comparison	Z	P.unadj	P.adj	
NC_015762.1 - NC_015763.1	3.60079083	3.17E-04	1.31E-03	*
NC_015762.1 - NC_015764.1	2.86760552	4.14E-03	1.22E-02	*
NC_015763.1 - NC_015764.1	-0.7747158	4.39E-01	5.04E-01	
NC_015762.1 - NC_015765.1	3.63768602	2.75E-04	1.17E-03	*
NC_015763.1 - NC_015765.1	0.10605196	9.16E-01	9.34E-01	
NC_015764.1 - NC_015765.1	0.86724665	3.86E-01	4.58E-01	
NC_015762.1 - NC_015766.1	-0.3935225	6.94E-01	7.48E-01	
NC_015763.1 - NC_015766.1	-3.8848302	1.02E-04	5.05E-04	*
NC_015764.1 - NC_015766.1	-3.175573	1.50E-03	5.20E-03	*
NC_015765.1 - NC_015766.1	-3.9172875	8.96E-05	4.72E-04	*
NC_015762.1 - NC_015767.1	3.30591454	9.47E-04	3.45E-03	*
NC_015763.1 - NC_015767.1	0.20368677	8.39E-01	8.73E-01	
NC_015764.1 - NC_015767.1	0.8742291	3.82E-01	4.60E-01	
NC_015765.1 - NC_015767.1	0.10850393	9.14E-01	9.38E-01	
NC_015766.1 - NC_015767.1	3.57004686	3.57E-04	1.40E-03	*
NC_015762.1 - NC_015768.1	1.15063168	2.50E-01	3.48E-01	
NC_015763.1 - NC_015768.1	-2.61042	9.04E-03	2.27E-02	*
NC_015764.1 - NC_015768.1	-1.8342141	6.66E-02	1.21E-01	
NC_015765.1 - NC_015768.1	-2.6670884	7.65E-03	2.02E-02	*
NC_015766.1 - NC_015768.1	1.52207519	1.28E-01	2.00E-01	
NC_015767.1 - NC_015768.1	-2.4381715	1.48E-02	3.37E-02	*
NC_015762.1 - NC_015769.1	-1.4037905	1.60E-01	2.38E-01	
NC_015763.1 - NC_015769.1	-4.4363317	9.15E-06	8.75E-05	*
NC_015764.1 - NC_015769.1	-3.8188785	1.34E-04	6.22E-04	*
NC_015765.1 - NC_015769.1	-4.4648232	8.01E-06	8.17E-05	*

mRNA - transcript	3.098549	1.94E-03	2.72E-03	*	NC_015766.1 - NC_015769.1	-1.0397112	2.98E-01	3.81E-01	
ncRNA - transcript	-1.5255875	1.27E-01	1.42E-01		NC_015767.1 - NC_015769.1	-4.1464141	3.38E-05	2.46E-04	*
promotor - transcript	5.5111164	3.57E-08	8.32E-08	*	NC_015768.1 - NC_015769.1	-2.4003926	1.64E-02	3.58E-02	*
					NC_015762.1 - NC_015770.1	2.67681266	7.43E-03	2.00E-02	*
					NC_015763.1 - NC_015770.1	-0.9758035	3.29E-01	4.06E-01	
					NC_015764.1 - NC_015770.1	-0.2012839	8.40E-01	8.69E-01	
					NC_015765.1 - NC_015770.1	-1.0646654	2.87E-01	3.75E-01	
					NC_015766.1 - NC_015770.1	2.9911992	2.78E-03	9.05E-03	*
					NC_015767.1 - NC_015770.1	-1.0473841	2.95E-01	3.79E-01	
					NC_015768.1 - NC_015770.1	1.63200012	1.03E-01	1.67E-01	
					NC_015769.1 - NC_015770.1	3.65909933	2.53E-04	1.11E-03	*
					NC_015762.1 - NC_015771.1	1.47604843	1.40E-01	2.16E-01	
					NC_015763.1 - NC_015771.1	-2.0981372	3.59E-02	6.86E-02	
					NC_015764.1 - NC_015771.1	-1.3523924	1.76E-01	2.59E-01	
					NC_015765.1 - NC_015771.1	-2.1645267	3.04E-02	5.97E-02	
					NC_015766.1 - NC_015771.1	1.82118178	6.86E-02	1.23E-01	
					NC_015767.1 - NC_015771.1	-2.0183319	4.36E-02	8.23E-02	
					NC_015768.1 - NC_015771.1	0.40172342	6.88E-01	7.46E-01	
					NC_015769.1 - NC_015771.1	2.63643992	8.38E-03	2.17E-02	*
					NC_015770.1 - NC_015771.1	-1.1586036	2.47E-01	3.46E-01	
					NC_015762.1 - NC_015772.1	-1.1870007	2.35E-01	3.33E-01	
					NC_015763.1 - NC_015772.1	-4.9314863	8.16E-07	1.39E-05	*
					NC_015764.1 - NC_015772.1	-4.1891937	2.80E-05	2.14E-04	*
					NC_015765.1 - NC_015772.1	-4.9374412	7.92E-07	1.51E-05	*
					NC_015766.1 - NC_015772.1	-0.7361495	4.62E-01	5.23E-01	
					NC_015767.1 - NC_015772.1	-4.4040161	1.06E-05	9.56E-05	*
					NC_015768.1 - NC_015772.1	-2.4523177	1.42E-02	3.29E-02	*
					NC_015769.1 - NC_015772.1	0.46871754	6.39E-01	7.04E-01	
					NC_015770.1 - NC_015772.1	-3.9954928	6.46E-05	3.80E-04	*
					NC_015771.1 - NC_015772.1	-2.7126998	6.67E-03	1.86E-02	*

NC_015762.1 - NC_015773.1	1.12848386	2.59E-01	3.54E-01	
NC_015763.1 - NC_015773.1	-2.3302349	1.98E-02	4.15E-02	*
NC_015764.1 - NC_015773.1	-1.6099663	1.07E-01	1.73E-01	
NC_015765.1 - NC_015773.1	-2.3916555	1.68E-02	3.61E-02	*
NC_015766.1 - NC_015773.1	1.47385746	1.41E-01	2.15E-01	
NC_015767.1 - NC_015773.1	-2.2294511	2.58E-02	5.19E-02	
NC_015768.1 - NC_015773.1	0.07655504	9.39E-01	9.45E-01	
NC_015769.1 - NC_015773.1	2.31876196	2.04E-02	4.22E-02	*
NC_015770.1 - NC_015773.1	-1.4230057	1.55E-01	2.32E-01	
NC_015771.1 - NC_015773.1	-0.296489	7.67E-01	8.15E-01	
NC_015772.1 - NC_015773.1	2.30426953	2.12E-02	4.33E-02	*
NC_015762.1 - NC_015774.1	6.22221504	4.90E-10	1.50E-08	*
NC_015763.1 - NC_015774.1	3.06177781	2.20E-03	7.48E-03	*
NC_015764.1 - NC_015774.1	3.76813129	1.64E-04	7.40E-04	*
NC_015765.1 - NC_015774.1	2.92532525	3.44E-03	1.07E-02	*
NC_015766.1 - NC_015774.1	6.42581307	1.31E-10	5.02E-09	*
NC_015767.1 - NC_015774.1	2.55490285	1.06E-02	2.58E-02	*
NC_015768.1 - NC_015774.1	5.42953088	5.65E-08	1.44E-06	*
NC_015769.1 - NC_015774.1	6.7174894	1.85E-11	9.43E-10	*
NC_015770.1 - NC_015774.1	3.95035382	7.80E-05	4.42E-04	*
NC_015771.1 - NC_015774.1	4.89432241	9.86E-07	1.51E-05	*
NC_015772.1 - NC_015774.1	7.42706923	1.11E-13	1.70E-11	*
NC_015773.1 - NC_015774.1	5.04080648	4.64E-07	1.01E-05	*
NC_015762.1 - NC_015775.1	1.79011708	7.34E-02	1.29E-01	
NC_015763.1 - NC_015775.1	-1.783105	7.46E-02	1.30E-01	
NC_015764.1 - NC_015775.1	-1.0339627	3.01E-01	3.81E-01	
NC_015765.1 - NC_015775.1	-1.855469	6.35E-02	1.17E-01	
NC_015766.1 - NC_015775.1	2.12572845	3.35E-02	6.49E-02	
NC_015767.1 - NC_015775.1	-1.746587	8.07E-02	1.36E-01	
NC_015768.1 - NC_015775.1	0.72990054	4.65E-01	5.24E-01	

NC_015769.1 - NC_015775.1	2.90121251	3.72E-03	1.12E-02	*
NC_015770.1 - NC_015775.1	-0.8393362	4.01E-01	4.72E-01	
NC_015771.1 - NC_015775.1	0.31218066	7.55E-01	8.08E-01	
NC_015772.1 - NC_015775.1	3.03874452	2.38E-03	7.90E-03	*
NC_015773.1 - NC_015775.1	0.59862116	5.49E-01	6.09E-01	
NC_015774.1 - NC_015775.1	-4.6169553	3.89E-06	4.58E-05	*
NC_015762.1 - NC_015776.1	2.60055151	9.31E-03	2.30E-02	*
NC_015763.1 - NC_015776.1	-1.0595511	2.89E-01	3.75E-01	
NC_015764.1 - NC_015776.1	-0.2844695	7.76E-01	8.19E-01	
NC_015765.1 - NC_015776.1	-1.1469196	2.51E-01	3.47E-01	
NC_015766.1 - NC_015776.1	2.91774432	3.53E-03	1.08E-02	*
NC_015767.1 - NC_015776.1	-1.1193215	2.63E-01	3.56E-01	
NC_015768.1 - NC_015776.1	1.55015101	1.21E-01	1.91E-01	
NC_015769.1 - NC_015776.1	3.59569023	3.24E-04	1.30E-03	*
NC_015770.1 - NC_015776.1	-0.083011	9.34E-01	9.46E-01	
NC_015771.1 - NC_015776.1	1.07971133	2.80E-01	3.76E-01	
NC_015772.1 - NC_015776.1	3.91955695	8.87E-05	4.85E-04	*
NC_015773.1 - NC_015776.1	1.34711471	1.78E-01	2.59E-01	
NC_015774.1 - NC_015776.1	-4.027885	5.63E-05	3.59E-04	*
NC_015775.1 - NC_015776.1	0.75981846	4.47E-01	5.11E-01	
NC_015762.1 - NC_015777.1	-1.7798443	7.51E-02	1.29E-01	
NC_015763.1 - NC_015777.1	-4.6372243	3.53E-06	4.50E-05	*
NC_015764.1 - NC_015777.1	-4.0545342	5.02E-05	3.34E-04	*
NC_015765.1 - NC_015777.1	-4.6649269	3.09E-06	4.29E-05	*
NC_015766.1 - NC_015777.1	-1.4306743	1.53E-01	2.31E-01	
NC_015767.1 - NC_015777.1	-4.3639893	1.28E-05	1.09E-04	*
NC_015768.1 - NC_015777.1	-2.7223925	6.48E-03	1.84E-02	*
NC_015769.1 - NC_015777.1	-0.4082797	6.83E-01	7.46E-01	
NC_015770.1 - NC_015777.1	-3.9039941	9.46E-05	4.83E-04	*
NC_015771.1 - NC_015777.1	-2.9391619	3.29E-03	1.05E-02	*

NC_015772.1 - NC_015777.1	-0.9118668	3.62E-01	4.39E-01
NC_015773.1 - NC_015777.1	-2.6357693	8.39E-03	2.14E-02 *
NC_015774.1 - NC_015777.1	-6.8174801	9.27E-12	7.09E-10 *
NC_015775.1 - NC_015777.1	-3.1887289	1.43E-03	5.08E-03 *
NC_015776.1 - NC_015777.1	-3.8442958	1.21E-04	5.78E-04 *
NC_015762.1 - NC_015778.1	-0.039703	9.68E-01	9.68E-01
NC_015763.1 - NC_015778.1	-2.43601	1.49E-02	3.34E-02 *
NC_015764.1 - NC_015778.1	-1.9302747	5.36E-02	1.00E-01
NC_015765.1 - NC_015778.1	-2.487239	1.29E-02	3.03E-02 *
NC_015766.1 - NC_015778.1	0.22331775	8.23E-01	8.63E-01
NC_015767.1 - NC_015778.1	-2.4156617	1.57E-02	3.48E-02 *
NC_015768.1 - NC_015778.1	-0.7791728	4.36E-01	5.05E-01
NC_015769.1 - NC_015778.1	0.97104876	3.32E-01	4.06E-01
NC_015770.1 - NC_015778.1	-1.8002942	7.18E-02	1.28E-01
NC_015771.1 - NC_015778.1	-1.0179225	3.09E-01	3.87E-01
NC_015772.1 - NC_015778.1	0.71558517	4.74E-01	5.30E-01
NC_015773.1 - NC_015778.1	-0.8001777	4.24E-01	4.95E-01
NC_015774.1 - NC_015778.1	-4.5106084	6.46E-06	7.06E-05 *
NC_015775.1 - NC_015778.1	-1.2277572	2.20E-01	3.14E-01
NC_015776.1 - NC_015778.1	-1.7475981	8.05E-02	1.37E-01
NC_015777.1 - NC_015778.1	1.27859086	2.01E-01	2.90E-01
NC_015762.1 - NC_015779.1	3.3103147	9.32E-04	3.48E-03 *
NC_015763.1 - NC_015779.1	1.07290646	2.83E-01	3.74E-01
NC_015764.1 - NC_015779.1	1.56131194	1.18E-01	1.89E-01
NC_015765.1 - NC_015779.1	0.99738256	3.19E-01	3.96E-01
NC_015766.1 - NC_015779.1	3.51589762	4.38E-04	1.68E-03 *
NC_015767.1 - NC_015779.1	0.86976404	3.84E-01	4.60E-01
NC_015768.1 - NC_015779.1	2.67695189	7.43E-03	2.03E-02 *
NC_015769.1 - NC_015779.1	4.02667502	5.66E-05	3.46E-04 *
NC_015770.1 - NC_015779.1	1.68651087	9.17E-02	1.51E-01

NC_015771.1 - NC_015779.1	2.38761162	1.70E-02	3.60E-02	*
NC_015772.1 - NC_015779.1	4.06226288	4.86E-05	3.38E-04	*
NC_015773.1 - NC_015779.1	2.54660107	1.09E-02	2.60E-02	*
NC_015774.1 - NC_015779.1	-1.0756875	2.82E-01	3.75E-01	
NC_015775.1 - NC_015779.1	2.19126079	2.84E-02	5.65E-02	
NC_015776.1 - NC_015779.1	1.73847629	8.21E-02	1.37E-01	
NC_015777.1 - NC_015779.1	4.23266714	2.31E-05	1.86E-04	*
NC_015778.1 - NC_015779.1	2.75018457	5.96E-03	1.72E-02	*

Supplementary 1.0.7: Final list of differentially methylated genes between castes after filtering for each gene to contain at least one differentially methylated CpG and a minimum weighted methylation difference of 10%.

geneID	Repro_weighted_methylation	Sterile_weighted_methylation	Hypermethylated_caste
LOC100642413	0.486673699	0.36948701	repro
LOC100642419	0.096431293	0.253553928	sterile
LOC100642580	0.695427928	0.802442529	sterile
LOC100642640	0.530504606	0.395066783	repro
LOC100642822	0.107855028	0.219075847	sterile
LOC100642946	0.025641026	0.25042735	sterile
LOC100642986	0.693094478	0.54264703	repro
LOC100643219	0.608551213	0.472661807	repro
LOC100643229	0.099390567	0.27865665	sterile
LOC100643343	0.211091897	0.409292929	sterile
LOC100643380	0.371490457	0.090793651	repro
LOC100643521	0.481074639	0.332544512	repro
LOC100643649	0.257834758	0.055944056	repro
LOC100643752	0.300757576	0.130777187	repro
LOC100643888	0.383036046	0.211195286	repro
LOC100643909	0.275388019	0.381664062	sterile
LOC100643944	0.191837433	0.057431717	repro
LOC100643961	0.01816092	0.139607522	sterile
LOC100644156	0.181623932	0	repro
LOC100644329	0.513931198	0.366078329	repro
LOC100644353	0.103940887	0.28065784	sterile
LOC100644498	0.038461538	0.215964412	sterile
LOC100644529	0.009803922	0.137820513	sterile
LOC100644532	0.422596939	0.317948217	repro
LOC100644587	0.324653731	0.183271357	repro

LOC100644712	0.925524476	0.801087801	repro
LOC100644747	0.075757576	0.333939394	sterile
LOC100644897	0.168181818	0.322590012	sterile
LOC100645060	0.031714841	0.277375867	sterile
LOC100645094	0.85024517	0.730543478	repro
LOC100645181	0.557876582	0.446039562	repro
LOC100645236	0	0.305882353	sterile
LOC100645305	0.140350877	0.442649573	sterile
LOC100645309	0.53495352	0.42253032	repro
LOC100645419	0.809090909	0.412121212	repro
LOC100645562	0.380698006	0.529587472	sterile
LOC100645672	0.44283647	0.561050061	sterile
LOC100645870	0.066666667	0.35	sterile
LOC100646004	0.696709719	0.913352884	sterile
LOC100646110	0.13115942	0	repro
LOC100646180	0.021354688	0.161877395	sterile
LOC100646212	0.897176644	0.687794198	repro
LOC100646298	0.692063492	0.473669468	repro
LOC100646498	0.188888889	0.013333333	repro
LOC100646559	0.328251184	0.197751323	repro
LOC100646622	0.509268235	0.3677802	repro
LOC100646866	0.136825397	0.3414603	sterile
LOC100646867	0.311096777	0.076190476	repro
LOC100646895	0.911111111	0.551587302	repro
LOC100646998	0.214076246	0.043209877	repro
LOC100647181	0.629024532	0.491788738	repro
LOC100647268	0	0.121212121	sterile
LOC100647451	0.685442759	0.452991453	repro
LOC100647499	0.058355011	0.163145582	sterile
LOC100647514	0.023809524	0.280934343	sterile

LOC100647553	0.32833239	0.225071225	repro
LOC100647602	0.211650668	0.520757021	sterile
LOC100647893	0.90058345	0.796089829	repro
LOC100648130	0.76340007	0.640090657	repro
LOC100648165	0	0.103448276	sterile
LOC100648246	0.501851852	0.604821944	sterile
LOC100648529	0.321225662	0.160882872	repro
LOC100648621	0.142863417	0.358918129	sterile
LOC100648763	0.213015572	0.092390204	repro
LOC100648778	0.00952381	0.24366791	sterile
LOC100648782	0.173223042	0.071056338	repro
LOC100648846	0.292393269	0.394629274	sterile
LOC100648899	0.42635315	0.581058429	sterile
LOC100648905	0.265478313	0.014492754	repro
LOC100648914	0.245858429	0.141504329	repro
LOC100648917	0.193147432	0.085995799	repro
LOC100648974	0.318161838	0.198858367	repro
LOC100648984	0.40942029	0.127777778	repro
LOC100649195	0.207498029	0.098184746	repro
LOC100649317	0.427770905	0.531879122	sterile
LOC100649337	0.537734323	0.360978203	repro
LOC100649429	0.122764228	0.01010101	repro
LOC100649459	0.383806417	0.274809118	repro
LOC100649584	0.676262626	0.944444444	sterile
LOC100649607	0.315003779	0.471957672	sterile
LOC100649615	0.298124098	0.111428571	repro
LOC100649676	0.292352092	0.188221344	repro
LOC100649679	0.373866279	0.207552615	repro
LOC100649830	0.254272313	0.41916532	sterile
LOC100649921	0.415194081	0.201454817	repro

LOC100649982	0.238188943	0.093911249	repro
LOC100650022	0.437548321	0.322129283	repro
LOC100650375	0.530987587	0.360302547	repro
LOC100650452	0.18369453	0	repro
LOC100650493	0.353680309	0.485484432	sterile
LOC100650607	0.048051495	0.17216089	sterile
LOC100650819	0.353818692	0.148484848	repro
LOC100651181	0.145720477	0.040464552	repro
LOC100651216	0.426757162	0.607674624	sterile
LOC100651275	0.575163399	0.73017736	sterile
LOC100651477	0.708294429	0.88780573	sterile
LOC100651635	0.286195286	0.064563463	repro
LOC100651855	0.598997494	0.376355406	repro
LOC100651858	0.134287356	0.244060226	sterile
LOC100651995	0	0.151282051	sterile
LOC100652128	0.216341829	0.422199688	sterile
LOC100652158	0.418134172	0.261742738	repro
LOC100652204	0.090909091	0.356521739	sterile
LOC100652208	0.241320787	0.133955045	repro
LOC105665612	0.013333333	0.169348659	sterile
LOC105665621	0.361111111	0.146825397	repro
LOC105665830	0.247620796	0.137391167	repro
LOC105666203	0.567640693	0.453663341	repro
LOC105666262	0	0.161064426	sterile
LOC105666915	0	0.108130081	sterile
LOC105667022	0.925524476	0.801087801	repro

Supplementary 1.0.8: List of the GO terms associaited with differentially methylated genes between castes.

term_ID	description	frequency	log10 p-value
GO:0016043	cellular component organization	7.24%	-1.69
GO:0009605	response to external stimulus	1.37%	-1.4644
GO:0035335	peptidyl-tyrosine dephosphorylation	0.26%	-2.2548
GO:0051321	meiotic cell cycle	0.18%	-1.595
GO:0045936	negative regulation of phosphate metabolic process	0.18%	-1.3538
GO:0050776	regulation of immune response	0.15%	-1.6772
GO:0031400	negative regulation of protein modification process	0.15%	-1.3984
GO:0016050	vesicle organization	0.13%	-1.5177
GO:0006661	phosphatidylinositol biosynthetic process	0.12%	-1.8891
GO:0007062	sister chromatid cohesion	0.10%	-1.4104
GO:0000027	ribosomal large subunit assembly	0.08%	-1.3404
GO:0002757	immune response-activating signal transduction	0.07%	-2.077
GO:0001731	formation of translation preinitiation complex	0.07%	-1.4186
GO:0010631	epithelial cell migration	0.06%	-1.9574
GO:0007229	integrin-mediated signaling pathway	0.06%	-2.1509
GO:0090130	tissue migration	0.06%	-1.8903
GO:0007020	microtubule nucleation	0.04%	-1.6068
GO:0002218	activation of innate immune response	0.04%	-1.7455
GO:0045995	regulation of embryonic development	0.04%	-1.3213
GO:0001649	osteoblast differentiation	0.04%	-1.6201
GO:0043409	negative regulation of MAPK cascade	0.04%	-1.3647
GO:1903725	regulation of phospholipid metabolic process	0.03%	-2.0269
GO:0002221	pattern recognition receptor signaling pathway	0.03%	-2.2548
GO:0043550	regulation of lipid kinase activity	0.02%	-1.8598
GO:0010594	regulation of endothelial cell migration	0.02%	-1.6068
GO:0042149	cellular response to glucose starvation	0.02%	-1.8598
GO:0034446	substrate adhesion-dependent cell spreading	0.02%	-2.1509

GO:0001570	vasculogenesis	0.02%	-1.6068
GO:0000076	DNA replication checkpoint	0.02%	-1.5066
GO:0051897	positive regulation of protein kinase B signaling	0.02%	-1.6068
GO:0043279	response to alkaloid	0.02%	-1.3404
GO:0043552	positive regulation of phosphatidylinositol 3-kinase activity	0.01%	-2.9996
GO:0050435	beta-amyloid metabolic process	0.01%	-1.4975
GO:0006509	membrane protein ectodomain proteolysis	0.01%	-1.7227
GO:0045022	early endosome to late endosome transport	0.01%	-1.7227
GO:0031638	zymogen activation	0.01%	-1.4186
GO:0042572	retinol metabolic process	0.01%	-1.4975
GO:0031938	regulation of chromatin silencing at telomere	0.01%	-1.4975
GO:1900087	positive regulation of G1/S transition of mitotic cell cycle	0.01%	-1.5066
GO:0048208	COPII vesicle coating	0.01%	-1.7227
GO:0048199	vesicle targeting, to, from or within Golgi	0.01%	-1.6068
GO:0006267	pre-replicative complex assembly involved in nuclear cell cycle DNA replication	0.01%	-1.4975
GO:0033627	cell adhesion mediated by integrin	0.01%	-1.6068
GO:0002504	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	0.01%	-1.4186
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	0.01%	-1.5066
GO:0036388	pre-replicative complex assembly	0.01%	-1.4975
GO:0051647	nucleus localization	0.01%	-1.3404
GO:0051415	interphase microtubule nucleation by interphase microtubule organizing center	0.00%	-2.9996
GO:0003365	establishment of cell polarity involved in ameboidal cell migration	0.00%	-1.4975
GO:0038128	ERBB2 signaling pathway	0.00%	-2.9996
GO:2000209	regulation of anoikis	0.00%	-2.5316
GO:1902954	regulation of early endosome to recycling endosome transport	0.00%	-1.4975
GO:0032495	response to muramyl dipeptide	0.00%	-1.4975
GO:0032487	regulation of Rap protein signal transduction	0.00%	-1.4975
GO:0044026	DNA hypermethylation	0.00%	-1.4975
GO:0018406	protein C-linked glycosylation via 2'-alpha-mannosyl-L-tryptophan	0.00%	-1.4975
GO:0044313	protein K6-linked deubiquitination	0.00%	-1.4975

GO:0034421	post-translational protein acetylation	0.00%	-1.4975
GO:0043686	co-translational protein modification	0.00%	-1.4975
GO:0016321	female meiosis chromosome segregation	0.00%	-2.0269
GO:0018211	peptidyl-tryptophan modification	0.00%	-1.4975
GO:0042574	retinal metabolic process	0.00%	-1.4975
GO:0090309	positive regulation of methylation-dependent chromatin silencing	0.00%	-1.4975
GO:0021693	cerebellar Purkinje cell layer structural organization	0.00%	-1.4975
GO:0021685	cerebellar granular layer structural organization	0.00%	-1.4975
GO:0021681	cerebellar granular layer development	0.00%	-1.4975
GO:0033624	negative regulation of integrin activation	0.00%	-1.4975
GO:1901562	response to paraquat	0.00%	-1.4975
GO:0060613	fat pad development	0.00%	-1.4975
GO:0060465	pharynx development	0.00%	-1.4975
GO:0048567	ectodermal digestive tract morphogenesis	0.00%	-1.4975
GO:0007319	negative regulation of oskar mRNA translation	0.00%	-1.4975
GO:0050872	white fat cell differentiation	0.00%	-1.4975
GO:0008359	regulation of bicoid mRNA localization	0.00%	-1.4975
GO:0042070	maintenance of oocyte nucleus location involved in oocyte dorsal/ventral axis specification	0.00%	-1.4975
GO:0034162	toll-like receptor 9 signaling pathway	0.00%	-1.4975
GO:0070433	negative regulation of nucleotide-binding oligomerization domain containing 2 signaling pat	0.00%	-1.4975
GO:0070424	regulation of nucleotide-binding oligomerization domain containing signaling pathway	0.00%	-1.4975
GO:0090522	vesicle tethering involved in exocytosis	0.00%	-1.4975
GO:0048194	Golgi vesicle budding	0.00%	-1.4186
GO:0018103	protein C-linked glycosylation	0.00%	-1.4975
GO:1902977	mitotic DNA replication preinitiation complex assembly	0.00%	-1.4975
GO:0038007	netrin-activated signaling pathway	0.00%	-1.4975
GO:0061781	mitotic cohesin unloading	0.00%	-1.4975
GO:2000588	positive regulation of platelet-derived growth factor receptor-beta signaling pathway	0.00%	-1.4975
GO:0008335	female germline ring canal stabilization	0.00%	-1.4975
GO:0043569	negative regulation of insulin-like growth factor receptor signaling pathway	0.00%	-1.4975

GO:0051038	negative regulation of transcription involved in meiotic cell cycle	0.00%	-1.4975
GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II	0.00%	-1.5066
GO:0002021	response to dietary excess	0.00%	-1.4975

Supplementary information 1.0.9: differentially expressed genes between reproductive and sterile workers, a negative log2FoldChange indicates up-regulation in sterile workers.

baseMean	log2FoldChange	lfcSE	stat	p-value	q-value	gene_id
11.3567093	-4.488518312	0.81537489	-5.5048523	3.69E-08	1.13E-05	LOC100651038
11.8690588	-3.862324737	0.72382098	-5.3360221	9.50E-08	2.44E-05	LOC100647644
61.7361475	-3.85103381	0.57459749	-6.7021417	2.05E-11	1.77E-08	LOC100643020
30.1435913	-3.459065041	0.78731241	-4.3935101	1.12E-05	0.00123026	LOC100648933
9.02736348	-3.458374295	0.56228481	-6.1505739	7.72E-10	4.07E-07	LOC110120021
10.0760116	-3.092897571	0.62005057	-4.9881376	6.10E-07	0.00011339	LOC100649153
158.048327	-3.071666469	0.25764699	-11.921996	9.09E-33	8.62E-29	LOC100646246
163.438035	-3.064131209	0.60249198	-5.0857626	3.66E-07	7.55E-05	LOC100648955
1036.76763	-3.039496446	0.47488965	-6.4004268	1.55E-10	1.05E-07	LOC100651509
19.4282135	-2.97336517	0.90898583	-3.2710798	0.00107138	0.03691617	LOC100647208
54.2780104	-2.902568554	0.68002526	-4.2683246	1.97E-05	0.00186572	LOC100646729
12.4230108	-2.892027356	0.69595692	-4.1554689	3.25E-05	0.00274942	LOC100650753
9.59449013	-2.804643458	0.63327992	-4.4287579	9.48E-06	0.0010832	LOC100649475
39.4422058	-2.738961222	0.71581499	-3.8263536	0.00013006	0.00806344	LOC100649275
9.58075754	-2.512199845	0.5833839	-4.306255	1.66E-05	0.00165797	LOC100646491
2247.2073	-2.181516247	0.65105511	-3.3507398	0.00080596	0.03106939	LOC100645985
1407.05753	-2.181340156	0.67632804	-3.2252694	0.00125854	0.04088537	LOC100644839
2823.13619	-2.019447755	0.43887707	-4.6013973	4.20E-06	0.00057695	LOC100650495
2040.89772	-2.002943835	0.24541407	-8.1614874	3.31E-16	1.05E-12	LOC100649840
166.876296	-1.995131114	0.2707237	-7.3696212	1.71E-13	2.71E-10	LOC100651467
73.6048298	-1.990125352	0.21438855	-9.2827967	1.65E-20	7.83E-17	LOC100644783
13.5235108	-1.741493211	0.39995278	-4.3542471	1.34E-05	0.00140735	LOC100648001
961.60374	-1.691072814	0.35824479	-4.7204394	2.35E-06	0.00036006	LOC100647578
9151.772	-1.585014276	0.21712577	-7.2999821	2.88E-13	3.90E-10	LOC100648427
144.940922	-1.461079053	0.45239535	-3.2296509	0.00123941	0.04054167	LOC100652047
18.170127	-1.457118761	0.37828868	-3.8518699	0.00011722	0.00741295	LOC100644454
260.409289	-1.441093383	0.45859604	-3.1424026	0.00167567	0.04846174	LOC100644249

23484.5535	-1.347473829	0.1952983	-6.8995675	5.22E-12	4.95E-09	LOC100648624
137.845524	-1.314599636	0.22057507	-5.959874	2.52E-09	1.14E-06	LOC100645024
91.4582385	-1.301299702	0.20779877	-6.2623071	3.79E-10	2.25E-07	LOC105666762
16.542805	-1.275200077	0.30485852	-4.1829241	2.88E-05	0.00257539	LOC100651957
43.6545746	-1.266267008	0.32953206	-3.8426216	0.00012173	0.00764704	LOC105666682
28.5236575	-1.254841707	0.36619837	-3.426672	0.00061103	0.02498361	LOC100643275
33.9253392	-1.238016449	0.35099877	-3.5271248	0.0004201	0.01901393	LOC105665690
3244.37604	-1.227332866	0.17135689	-7.1624365	7.93E-13	9.40E-10	LOC100651787
346.637328	-1.226639931	0.35493688	-3.4559382	0.00054838	0.02343217	LOC100648239
457.928401	-1.198309484	0.3356323	-3.5703044	0.00035657	0.01722302	LOC100645349
29.8712032	-1.192235358	0.33226543	-3.5882017	0.00033297	0.0163654	LOC105666033
44.1798588	-1.17201358	0.32084582	-3.6528872	0.00025931	0.01359004	LOC100648311
648.757471	-1.142171807	0.21336303	-5.3531851	8.64E-08	2.28E-05	LOC100645221
1762.07051	-1.105945143	0.20407308	-5.4193582	5.98E-08	1.67E-05	LOC100645016
172.489444	-1.094106141	0.24169765	-4.5267553	5.99E-06	0.0007678	LOC100631088
109.681543	-1.070265523	0.25746268	-4.1569735	3.22E-05	0.00274942	LOC100648252
26.5513113	-1.064922783	0.27131629	-3.9250235	8.67E-05	0.00613909	LOC100649092
9104.46729	-1.063348147	0.13531607	-7.8582544	3.90E-15	7.39E-12	npve
11.0360278	-1.062474952	0.32755306	-3.2436728	0.00117999	0.0394134	LOC110119514
70.0680392	-1.047908692	0.33256206	-3.151017	0.00162703	0.04808103	LOC100643152
54.0932549	-1.026363575	0.29185805	-3.5166533	0.00043702	0.01955477	LOC110120082
11.4080873	-1.003780369	0.3105404	-3.2323664	0.0012277	0.04054167	LOC100651599
1600.09569	-0.998814169	0.14344741	-6.9629292	3.33E-12	3.51E-09	LOC100648426
80.76665	-0.977071461	0.27589511	-3.5414599	0.00039792	0.01841299	LOC100642296
25214.604	-0.94182169	0.17034275	-5.5289803	3.22E-08	1.05E-05	LOC100645577
42.4401804	-0.936715417	0.25915337	-3.6145214	0.0003009	0.01528689	LOC100648402
57.3208682	-0.926386532	0.28676582	-3.2304635	0.0012359	0.04054167	LOC105665691
25.0331609	-0.889781495	0.26489022	-3.3590575	0.00078209	0.03053039	LOC105666966
75.611397	-0.876330071	0.23184403	-3.779826	0.00015694	0.00942675	LOC105665901
1548.95647	-0.87597224	0.19614584	-4.4659231	7.97E-06	0.00093366	LOC100649364

280.915451	-0.871241462	0.16129322	-5.4015999	6.60E-08	1.79E-05	LOC100644889
65.0328186	-0.86895995	0.25708074	-3.3801052	0.00072458	0.02852023	LOC100648121
155.141466	-0.855214368	0.14837159	-5.7640035	8.21E-09	3.26E-06	LOC100649705
83.0647948	-0.843857362	0.25850076	-3.264429	0.00109685	0.03720137	LOC100644557
200.965955	-0.843163838	0.24713264	-3.4117866	0.00064539	0.02602303	LOC100644036
239880.167	-0.84311337	0.20972081	-4.0201703	5.82E-05	0.00444894	LOC100650111
1125.3684	-0.833206835	0.20189019	-4.1270298	3.67E-05	0.00300509	LOC100651196
583.134147	-0.825125093	0.24066409	-3.4285344	0.00060685	0.02492024	LOC100652160
82.6314925	-0.81213565	0.16370324	-4.9610238	7.01E-07	0.00012318	LOC100644956
1788.1095	-0.785350968	0.21037489	-3.7331023	0.00018914	0.01121339	LOC100646723
783.554204	-0.774379156	0.19917838	-3.8878675	0.00010113	0.00668524	LOC100650007
143.765103	-0.767692367	0.1966481	-3.903889	9.47E-05	0.00636835	LOC105665671
797.725388	-0.765085437	0.17450257	-4.3843793	1.16E-05	0.00126826	LOC100643830
27.6977638	-0.762154483	0.20440228	-3.7286985	0.00019247	0.0112627	LOC105666352
440.161834	-0.760974136	0.15313722	-4.9692305	6.72E-07	0.00012031	LOC100644850
8398.2454	-0.745420265	0.15857381	-4.7007779	2.59E-06	0.00037823	LOC100645892
48.8525532	-0.736836215	0.22406942	-3.2884283	0.00100748	0.03633839	LOC105666950
880.753043	-0.734372943	0.16007527	-4.5876727	4.48E-06	0.00060739	LOC100649912
969.843741	-0.712202085	0.20822448	-3.4203571	0.00062539	0.02535234	LOC100652206
110.140109	-0.708540817	0.17574269	-4.0316945	5.54E-05	0.00430572	LOC100645287
82.5882606	-0.699305545	0.2200034	-3.1786124	0.00147982	0.04572493	LOC100645257
314.415888	-0.69707051	0.1392921	-5.0043794	5.60E-07	0.00010632	LOC100643765
380.284603	-0.688175005	0.209668	-3.2822129	0.00102996	0.03659244	LOC100648720
12276.2145	-0.677431979	0.16574117	-4.0872884	4.36E-05	0.00345009	LOC100642903
1447.73391	-0.66964473	0.20604191	-3.2500414	0.00115388	0.03881463	LOC100650005
536.369744	-0.659587801	0.20820373	-3.1679923	0.00153496	0.04637131	LOC100647225
449.079198	-0.649313083	0.1829781	-3.5485835	0.00038731	0.01815357	LOC100642374
60.6067988	-0.649150387	0.17249986	-3.7631937	0.00016776	0.01000845	LOC100652321
758.018756	-0.645611728	0.14185932	-4.5510701	5.34E-06	0.00069357	LOC100645828
46.4927938	-0.640203245	0.19102935	-3.3513345	0.00080423	0.03106939	LOC105666733

81.6237878	-0.634143122	0.18417148	-3.4432211	0.00057483	0.0242348	LOC105666563
142.802568	-0.616364449	0.14235923	-4.3296417	1.49E-05	0.00153995	LOC100645258
4506.48155	-0.613052817	0.09917933	-6.1812558	6.36E-10	3.55E-07	LOC100647918
66.2815921	-0.612390518	0.16531299	-3.7044306	0.00021187	0.0120345	LOC100644526
145.657175	-0.606374383	0.177774	-3.4109284	0.00064742	0.02602303	LOC100650646
2267.5204	-0.595493739	0.16607647	-3.58566	0.00033623	0.01644045	LOC100649988
73.7320151	-0.590195433	0.16546675	-3.5668522	0.0003613	0.01730932	LOC100645051
144.199859	-0.565544731	0.17982991	-3.144887	0.00166151	0.04833772	LOC100647103
6572.27263	-0.555315491	0.12917325	-4.2989975	1.72E-05	0.00167978	LOC100646012
272.830339	-0.549593951	0.1737241	-3.1636022	0.0015583	0.04663092	LOC100650183
93.2582281	-0.549538212	0.16740202	-3.2827454	0.00102801	0.03659244	LOC100642988
133.661793	-0.547927383	0.16400751	-3.3408677	0.00083517	0.03143819	LOC100646619
755.60027	-0.543182387	0.17317188	-3.1366663	0.00170881	0.04867786	LOC100650345
86.9185727	-0.540482042	0.13370292	-4.0424101	5.29E-05	0.00414754	LOC100651727
84287.3889	-0.540076544	0.15284672	-3.533452	0.00041017	0.01879651	LOC100647343
443.737955	-0.538939477	0.16009037	-3.3664702	0.00076137	0.02984437	LOC100650865
121.488246	-0.535607331	0.16762527	-3.1952661	0.00139702	0.04413264	LOC100648691
193.931367	-0.524599888	0.15947087	-3.2896284	0.0010032	0.03632188	LOC110119151
134.855164	-0.523582939	0.16291661	-3.2138095	0.00130987	0.04197765	LOC100651214
115.913149	-0.523274662	0.14727274	-3.5530994	0.00038072	0.01805758	LOC100649387
106.107431	-0.514634872	0.15477521	-3.3250471	0.00088404	0.03237824	LOC100649987
168.460224	-0.505530016	0.12018072	-4.2064152	2.59E-05	0.00234398	LOC100650416
297.241738	-0.501717033	0.11226841	-4.4689064	7.86E-06	0.00093224	LOC100643960
2103.69794	-0.490836041	0.14665428	-3.3468921	0.00081723	0.03113351	LOC100651171
11995.0488	-0.488462394	0.13252109	-3.6859219	0.00022788	0.01242319	LOC100650354
175.583135	-0.47953525	0.11518483	-4.1631807	3.14E-05	0.00273131	LOC100652040
448.697293	-0.475999367	0.12884161	-3.6944538	0.00022036	0.01229609	LOC100646422
167.252334	-0.475802504	0.1149216	-4.1402358	3.47E-05	0.00288698	LOC100645132
895.393786	-0.475243107	0.13448062	-3.5339151	0.00040945	0.01879651	LOC105666388
1224.85137	-0.470249615	0.11954777	-3.9335708	8.37E-05	0.00596927	LOC100647588

3936.70682	-0.470050477	0.11049531	-4.254031	2.10E-05	0.00193364	LOC100650219
290.102878	-0.468759232	0.12060168	-3.8868384	0.00010156	0.00668524	LOC100645563
427.630113	-0.456898408	0.13478206	-3.3899053	0.00069917	0.02775023	LOC100645609
929.785668	-0.444187486	0.12338356	-3.600054	0.00031815	0.01580095	LOC100646835
192.375124	-0.434224798	0.12472583	-3.4814345	0.00049874	0.02180188	LOC100649737
1479.24182	-0.433928611	0.13351107	-3.250132	0.00115351	0.03881463	LOC100647483
747.44187	-0.433591351	0.13520404	-3.2069407	0.00134155	0.04256157	LOC100649765
789.929754	-0.430121192	0.10302303	-4.1750002	2.98E-05	0.00263782	LOC100648538
1856.84725	-0.425034852	0.08346546	-5.0923443	3.54E-07	7.46E-05	LOC100648828
2279.27969	-0.41235454	0.12612776	-3.2693401	0.00107799	0.03691617	LOC100645683
534.305901	-0.405972896	0.12181295	-3.3327565	0.0008599	0.03204571	LOC100642565
783.847816	-0.404708656	0.09181599	-4.4078231	1.04E-05	0.00116527	LOC100649251
72.6110262	-0.397729666	0.12111071	-3.2840172	0.00102339	0.03659244	LOC100644081
201.931285	-0.393614335	0.1137372	-3.4607351	0.0005387	0.02312277	LOC100644312
415.936531	-0.386437666	0.12039525	-3.2097419	0.00132854	0.04231768	LOC100648522
446.820608	-0.38302317	0.11434557	-3.3496983	0.000809	0.03106939	LOC100650995
397.938134	-0.382070555	0.11401637	-3.3510149	0.00080516	0.03106939	LOC100647110
2165.68207	-0.378016415	0.11863977	-3.1862537	0.00144128	0.04497367	LOC105666719
7287.1757	-0.37746705	0.11760722	-3.2095568	0.0013294	0.04231768	LOC100647566
342.676165	-0.374557473	0.08671135	-4.3195897	1.56E-05	0.00159446	LOC100646658
176.394342	-0.373714596	0.09875494	-3.7842624	0.00015417	0.00937442	LOC105665619
7870.06023	-0.367281941	0.09457094	-3.883666	0.00010289	0.00668524	LOC105666492
807.312836	-0.366998903	0.06188091	-5.9307291	3.02E-09	1.30E-06	LOC100642303
147.358916	-0.354922793	0.10277068	-3.4535413	0.00055328	0.02353539	LOC100648374
1262.51632	-0.354735129	0.09307855	-3.8111372	0.00013833	0.00852071	LOC105667061
1098.20056	-0.352793998	0.10551483	-3.3435489	0.00082714	0.03126	LOC100651051
2192.94864	-0.34763779	0.08669831	-4.0097413	6.08E-05	0.00459617	LOC100651968
2917.32942	-0.346078581	0.10561965	-3.2766495	0.00105047	0.03691617	LOC100644162
762.961	-0.318938608	0.09918883	-3.2154689	0.00130232	0.04187719	LOC100651733
342.507794	-0.317400523	0.09512379	-3.3367101	0.00084776	0.03178609	LOC100648393

386.266999	-0.315528408	0.08060344	-3.9145776	9.06E-05	0.00627064	LOC100650465
3756.20457	-0.311360622	0.0776709	-4.0087164	6.10E-05	0.00459617	LOC100652262
2774.42429	-0.308943429	0.06938827	-4.4523872	8.49E-06	0.00098239	LOC100648375
1183.07732	-0.308847501	0.09762371	-3.1636524	0.00155803	0.04663092	LOC100648521
931.001677	-0.302552905	0.08119561	-3.7262223	0.00019437	0.0112627	LOC100649011
535.670904	-0.302319236	0.08249316	-3.6647796	0.00024755	0.01319255	LOC100648640
1573.49268	-0.297801014	0.09338734	-3.1888799	0.00142825	0.04471419	LOC100645214
1448.30258	-0.293635014	0.09115314	-3.2213374	0.00127594	0.04130906	LOC100650186
6622.79946	-0.290509302	0.09166178	-3.1693613	0.00152774	0.04637131	LOC100650576
235.775898	-0.284921103	0.07786971	-3.6589467	0.00025325	0.01334648	LOC110120279
1300.10294	-0.272645049	0.07308941	-3.730295	0.00019126	0.0112627	LOC100645813
1855.90073	-0.270479504	0.08613443	-3.140202	0.00168831	0.04853134	LOC100647817
1343.46502	-0.256780536	0.07451634	-3.4459629	0.00056903	0.02409734	LOC100648214
1586.39425	-0.239513187	0.07564452	-3.1662993	0.00154392	0.046494	LOC100643887
461.183475	-0.221324177	0.05745127	-3.8523813	0.00011697	0.00741295	LOC100647553
853.936168	0.207225522	0.06522757	3.17696196	0.00148827	0.04575335	LOC100645041
1144.34813	0.215621385	0.06797877	3.17189296	0.00151449	0.04633792	LOC100645533
604.755726	0.223025815	0.05641455	3.95333889	7.71E-05	0.0056236	LOC100646267
1009.3758	0.22426419	0.06170571	3.63441578	0.00027861	0.01452146	LOC100651961
974.860303	0.238532033	0.07578589	3.14744632	0.00164703	0.04822148	LOC100646695
1083.82211	0.242390766	0.07275567	3.33157213	0.00086357	0.03204571	LOC100652162
679.273649	0.243151416	0.06612581	3.67710296	0.0002359	0.01276885	LOC100651795
309.053218	0.250169313	0.07168624	3.48978152	0.00048342	0.02132875	LOC100647182
446.903499	0.257155594	0.07864508	3.26982437	0.00107614	0.03691617	LOC100651065
216.243036	0.262120398	0.07617777	3.44090417	0.00057977	0.02433511	LOC100646195
650.207523	0.263190846	0.07746494	3.39754777	0.00067993	0.02709995	LOC100649399
314.108101	0.269433112	0.07329496	3.67601153	0.00023691	0.01276885	LOC100651339
374.046294	0.27361647	0.07581436	3.60903219	0.00030734	0.01550767	LOC100647630
1203.73704	0.291378042	0.09307963	3.1304169	0.00174558	0.04957667	LOC100647058
322.380293	0.291391735	0.08907787	3.27120221	0.00107091	0.03691617	LOC100651724

588.854608	0.295819352	0.07826516	3.7797069	0.00015701	0.00942675	LOC100646627
359.480809	0.298350289	0.09008533	3.31186326	0.00092677	0.03381279	LOC100646241
250.571125	0.300112825	0.08616154	3.48314134	0.00049557	0.02176364	LOC100647451
9315.55766	0.30175986	0.08519819	3.5418577	0.00039732	0.01841299	LOC100647111
376.162822	0.303925108	0.08514527	3.56948903	0.00035768	0.01722302	LOC100645954
529.395499	0.308809746	0.09543789	3.23571429	0.00121339	0.04024544	LOC100649534
571.274401	0.309978076	0.07452372	4.15945536	3.19E-05	0.00274942	LOC100649054
1928.09148	0.313966767	0.09883894	3.17654937	0.00149038	0.04575335	LOC100646880
286.402236	0.319501907	0.09597529	3.32900176	0.00087158	0.03204571	LOC100649593
878.633827	0.320537755	0.09626168	3.32985814	0.0008689	0.03204571	LOC100650985
250.778824	0.328225983	0.09976042	3.29014239	0.00100137	0.03632188	LOC105666531
398.367754	0.328659724	0.07335732	4.48025813	7.46E-06	0.00090668	LOC100649142
611.82522	0.329827804	0.10477222	3.14804647	0.00164366	0.04822148	LOC100646329
668.938541	0.330408119	0.07992846	4.13379816	3.57E-05	0.00294327	LOC110119183
4583.47718	0.331344854	0.08542389	3.87883121	0.00010496	0.00675329	LOC100643802
521.229803	0.339419533	0.09433776	3.59791819	0.00032077	0.01584826	LOC100648645
367.122997	0.342403509	0.09854464	3.474603	0.00051161	0.02216042	LOC100650741
754.066587	0.345239062	0.10818989	3.19104746	0.00141758	0.04452703	LOC100647508
504.694439	0.347022258	0.09854086	3.52160775	0.00042894	0.01928393	LOC100644723
1209.9968	0.349762304	0.10828822	3.22992014	0.00123825	0.04054167	LOC100645274
264.252104	0.3498907	0.10173659	3.43918264	0.00058347	0.02438251	LOC100648754
592.776869	0.350213324	0.09399747	3.72577409	0.00019472	0.0112627	LOC100649858
1333.82904	0.359609592	0.10980196	3.27507432	0.00105634	0.03691617	LOC100652097
656.723011	0.360895893	0.11056482	3.26411147	0.00109808	0.03720137	LOC100645881
1422.45315	0.369433408	0.11288906	3.27253507	0.00106588	0.03691617	LOC100643972
357.133586	0.369584375	0.11402585	3.24123328	0.00119014	0.03961279	LOC100645904
1340.18947	0.371126754	0.09570316	3.87789448	0.00010536	0.00675329	LOC105666621
477.32713	0.380528942	0.09277044	4.10183404	4.10E-05	0.00332325	LOC100652286
138.048865	0.383207905	0.12136479	3.15748817	0.00159135	0.04725809	LOC100645497
283.564825	0.39242941	0.10638629	3.68872167	0.00022538	0.01238022	LOC100646990

120.238188	0.393608679	0.1250221	3.14831281	0.00164216	0.04822148	LOC100645791
994.159136	0.398189117	0.11291012	3.52660247	0.00042093	0.01901393	LOC110119287
178.110447	0.403642969	0.12543665	3.21790285	0.00129132	0.04166469	LOC100643808
188.55834	0.4108135	0.10493546	3.91491606	9.04E-05	0.00627064	LOC100651510
1899.104	0.411588728	0.09130293	4.50794635	6.55E-06	0.00081702	LOC100648227
438.035612	0.421489381	0.08068215	5.22407197	1.75E-07	4.15E-05	LOC100644625
154.41667	0.424128583	0.13415362	3.16151424	0.00156951	0.04681882	LOC100647604
1226.12962	0.428226788	0.11848673	3.61413289	0.00030135	0.01528689	LOC100642544
1021.65538	0.428489395	0.13284431	3.22550052	0.00125753	0.04088537	LOC100647412
758.121935	0.433133414	0.10230233	4.23385688	2.30E-05	0.00209529	LOC100651362
167.73335	0.433575182	0.13253488	3.27140438	0.00107015	0.03691617	LOC100652278
151.348928	0.440388635	0.11940246	3.68827107	0.00022578	0.01238022	LOC100645495
313.159947	0.442340218	0.10794573	4.0978019	4.17E-05	0.003353	LOC100644831
158.302701	0.443040213	0.12235044	3.62107563	0.00029338	0.01516903	LOC100647340
404.163008	0.446041607	0.12572398	3.54778474	0.00038849	0.01815357	LOC100644863
107.671242	0.44749608	0.14065928	3.18141871	0.00146556	0.04543225	LOC100650980
160.530334	0.448715621	0.13666748	3.28326539	0.00102612	0.03659244	LOC100649522
239.291781	0.453149102	0.10858494	4.1732224	3.00E-05	0.00263782	LOC100649491
651.72824	0.455369141	0.12751088	3.5712179	0.00035533	0.01722302	LOC100650936
846.317702	0.456790188	0.10645552	4.29090182	1.78E-05	0.00172247	LOC105665781
157.109364	0.457181592	0.1373191	3.32933716	0.00087053	0.03204571	LOC100647958
712.913536	0.46404468	0.12479605	3.71842447	0.00020047	0.0114651	LOC100648998
619.100863	0.465820762	0.14815964	3.14404626	0.00166629	0.04833772	LOC100644842
239.435567	0.4718041	0.12064406	3.91071127	9.20E-05	0.0063257	LOC105666410
347.71323	0.475880562	0.11911733	3.9950573	6.47E-05	0.00483103	LOC100646646
198.172835	0.478194697	0.10631959	4.49771004	6.87E-06	0.00084622	LOC100643216
90.8257974	0.485858403	0.15449602	3.14479564	0.00166203	0.04833772	LOC100645907
145.513673	0.491560023	0.15501777	3.17099148	0.0015192	0.04633792	LOC100648047
1411.03583	0.494419724	0.10825946	4.56698845	4.95E-06	0.00065187	LOC100650051
1285.56719	0.495555858	0.13960261	3.54976059	0.00038558	0.01815357	LOC100650785

44662.4585	0.498447319	0.10647212	4.68148204	2.85E-06	0.00040935	LOC100646145
116.191264	0.500081381	0.14934559	3.34848451	0.00081255	0.03107997	LOC100644917
78.9923149	0.505928858	0.12684357	3.98860455	6.65E-05	0.00492554	LOC100647507
207.571877	0.506809339	0.15922692	3.18293755	0.00145789	0.04534279	LOC100650526
1229.50093	0.529638892	0.13636195	3.88406653	0.00010272	0.00668524	LOC100646039
786.197247	0.545186011	0.09556127	5.70509392	1.16E-08	4.07E-06	LOC100642250
236.014578	0.549784114	0.11448358	4.80229648	1.57E-06	0.00024799	LOC100649392
13949.4785	0.56267152	0.12575224	4.47444518	7.66E-06	0.0009199	LOC105666319
82.7001146	0.574935111	0.16978341	3.38628566	0.00070846	0.02800172	LOC100651535
178.625184	0.582785023	0.17806286	3.27291739	0.00106444	0.03691617	LOC100645461
59.9533074	0.587406802	0.15893383	3.69592052	0.00021909	0.01229609	LOC105665959
163.325704	0.589050002	0.10768142	5.47030288	4.49E-08	1.29E-05	LOC100649793
339.668897	0.596680087	0.13985546	4.26640528	1.99E-05	0.00186572	LOC100646310
864.021993	0.607536222	0.17714195	3.42965755	0.00060434	0.02492024	LOC100648566
358.209461	0.616503418	0.17947707	3.43499826	0.00059256	0.02465352	LOC105666289
5306.17478	0.616600522	0.17319279	3.56019736	0.00037058	0.01766475	LOC100642650
1254539.91	0.617512128	0.1581683	3.90414591	9.46E-05	0.00636835	LOC100644055
545.433351	0.625397526	0.09747076	6.41625756	1.40E-10	1.02E-07	LOC100652085
146.392325	0.629196508	0.19856393	3.16873515	0.00153104	0.04637131	LOC100647788
376.423018	0.643891868	0.13024483	4.94370393	7.67E-07	0.0001322	LOC100650185
13173.6707	0.644294169	0.14960818	4.30654378	1.66E-05	0.00165797	LOC100650230
3146.11374	0.651136332	0.14432224	4.51168394	6.43E-06	0.00081346	LOC100646546
207.869189	0.653267958	0.12901983	5.06331452	4.12E-07	8.32E-05	LOC100643207
878.868941	0.657413569	0.15332954	4.28758576	1.81E-05	0.00173072	LOC100651134
760.233313	0.659793639	0.17236781	3.8278239	0.00012928	0.00806344	LOC100647696
534.554053	0.671097026	0.15389857	4.36064496	1.30E-05	0.00138218	LOC100649872
365.997906	0.673849932	0.18367279	3.66875201	0.00024374	0.01306267	LOC100650674
909.351868	0.676585273	0.1830147	3.69689028	0.00021826	0.01229609	LOC100649299
552.603857	0.681935632	0.16669405	4.09094164	4.30E-05	0.00342473	LOC100645481
5002.8927	0.686374895	0.20148414	3.40659512	0.00065779	0.0263281	LOC100646667

792.108767	0.692510277	0.14721709	4.70400732	2.55E-06	0.00037823	LOC100649621
33.0855727	0.694647377	0.20256635	3.42923378	0.00060529	0.02492024	LOC100648015
796.038754	0.712032812	0.19437395	3.66321112	0.00024907	0.01319948	LOC100646078
1540.76719	0.717110727	0.22715189	3.15696575	0.0015942	0.04725809	LOC100644671
547.986085	0.717460097	0.16833533	4.26208875	2.03E-05	0.00188348	LOC100649601
33.3290284	0.731461591	0.23307214	3.13834843	0.00169903	0.04862361	LOC100648154
256.883315	0.732121505	0.21389196	3.42285662	0.00061967	0.02522818	LOC105667110
348.493536	0.733153294	0.15441595	4.74791157	2.06E-06	0.00031961	LOC100648706
6674.66685	0.754152894	0.15430238	4.88749995	1.02E-06	0.00017299	LOC100651198
44.6377133	0.790538775	0.16806487	4.70377181	2.55E-06	0.00037823	LOC100644424
212.296764	0.802916921	0.22286916	3.60263808	0.000315	0.01572699	LOC100650700
164.05595	0.827672421	0.21196308	3.90479516	9.43E-05	0.00636835	LOC100646186
680.914628	0.834620139	0.24112111	3.4614147	0.00053734	0.02312277	LOC100651268
251.05457	0.837419797	0.23167622	3.61461268	0.0003008	0.01528689	LOC100647616
3270.04817	0.872112335	0.16948724	5.14559293	2.67E-07	5.75E-05	LOC100649785
165.574202	0.872816076	0.27321826	3.19457444	0.00140037	0.04413264	LOC100650573
439.735514	0.891448952	0.22374878	3.98415115	6.77E-05	0.00497991	LOC100650521
37.5129045	0.897253451	0.24131277	3.71821786	0.00020063	0.0114651	LOC105666145
51.0669246	0.898232987	0.20573358	4.36600084	1.27E-05	0.00136407	LOC100645993
137.698661	0.901917529	0.2287899	3.9421213	8.08E-05	0.005804	LOC110119544
76.7625747	0.906378521	0.1590313	5.6993718	1.20E-08	4.07E-06	LOC100648563
133476.951	0.921264694	0.24315223	3.7888391	0.00015135	0.0092628	LOC100651683
23.6087747	0.92265577	0.28238376	3.26738253	0.00108547	0.0370387	LOC100642459
21617.1688	0.952441554	0.17350732	5.48934511	4.03E-08	1.20E-05	LOC100644867
317.470257	0.954537789	0.23691752	4.02898772	5.60E-05	0.00432018	LOC100647765
69.1976574	0.980007179	0.27165252	3.60757626	0.00030907	0.01551241	LOC100643594
80.5804911	0.982078936	0.23678762	4.14750961	3.36E-05	0.00282155	LOC100649112
31981.6517	0.999099619	0.18795275	5.31569574	1.06E-07	2.65E-05	LOC100650343
125.35645	1.010330064	0.21847885	4.62438387	3.76E-06	0.00053194	LOC100645974
560.356188	1.045075269	0.3328008	3.14024262	0.00168808	0.04853134	LOC100645678

1547.09493	1.057505654	0.30178404	3.50418022	0.00045802	0.02039781	LOC100651812
634.811643	1.085617798	0.21834972	4.97192219	6.63E-07	0.00012031	LOC100650592
785.78304	1.098040081	0.19941998	5.5061689	3.67E-08	1.13E-05	LOC100648012
22.4571623	1.116113536	0.31904198	3.49832819	0.00046818	0.02075327	LOC100650899
335.237318	1.12419749	0.26151756	4.29874574	1.72E-05	0.00167978	LOC100648980
1969.75123	1.151338229	0.22163033	5.19485861	2.05E-07	4.58E-05	LOC100651923
13.0524932	1.167534516	0.3720781	3.13787485	0.00170178	0.04862361	LOC110119604
4614.61218	1.20392794	0.22801303	5.28008402	1.29E-07	3.14E-05	LOC100648126
2071.46049	1.205272586	0.30779906	3.91577734	9.01E-05	0.00627064	LOC100648602
82.5420514	1.210607772	0.34321127	3.5272961	0.00041983	0.01901393	LOC100643810
30.3845309	1.304969623	0.30110382	4.33395235	1.46E-05	0.00152668	LOC100648274
126758.602	1.342415813	0.41369749	3.24492134	0.00117483	0.03937966	LOC100645916
73.4708784	1.373635309	0.27400246	5.01322247	5.35E-07	0.00010362	LOC105666640
170.071491	1.3943714	0.17491961	7.9714983	1.57E-15	3.72E-12	LOC100643625
136.317555	1.476192733	0.40775149	3.62032457	0.00029423	0.01516903	LOC100645800
5250.70454	1.4828515	0.30494574	4.86267334	1.16E-06	0.00019273	LOC100631053
51176.6573	1.564125091	0.24660832	6.34254783	2.26E-10	1.43E-07	LOC100645956
11.0332947	1.635661899	0.34031314	4.80634362	1.54E-06	0.00024747	LOC100646752
699.177349	1.6361135	0.5000875	3.27165444	0.0010692	0.03691617	LOC100645453
20.738888	1.653200819	0.47520537	3.4789186	0.00050344	0.02190663	LOC110119410
11.3506749	1.662938826	0.45060064	3.6904937	0.00022382	0.01238022	LOC100645738
683.974913	1.711482766	0.43344042	3.94859983	7.86E-05	0.0056923	LOC100647051
2592.17146	1.724192633	0.29917706	5.76311787	8.26E-09	3.26E-06	LOC100646873
842.11782	1.725354414	0.33227497	5.19255009	2.07E-07	4.58E-05	LOC100643669
184822.395	1.789797457	0.40490667	4.42027157	9.86E-06	0.00111322	LOC100646942
75.7571962	1.814739208	0.37759272	4.80607572	1.54E-06	0.00024747	LOC100650927
10328.2912	1.99087284	0.51020901	3.90207311	9.54E-05	0.00637114	LOC100643149
69.4238745	2.014700722	0.32977762	6.10927055	1.00E-09	5.00E-07	LOC100642491
1681.1668	2.060619704	0.36085451	5.71038916	1.13E-08	4.07E-06	LOC100644966
385.790275	2.172940158	0.37796703	5.74902045	8.98E-09	3.41E-06	LOC100645125

316.203054	2.194106412	0.43634889	5.02833043	4.95E-07	9.78E-05	LOC100647178
401.074213	2.2154169	0.36342841	6.0958825	1.09E-09	5.16E-07	LOC100650035
2838.67701	2.274993351	0.43762605	5.19848706	2.01E-07	4.58E-05	LOC100648482
181.960578	2.296179665	0.6864358	3.34507561	0.0008226	0.03121279	LOC100631078
1879.56713	2.562526717	0.55651427	4.60460201	4.13E-06	0.00057649	LOC100652301
665.065754	2.819904711	0.43131417	6.53793658	6.24E-11	4.93E-08	LOC100651307
62688.4188	2.929620134	0.64087036	4.57131473	4.85E-06	0.00064755	LOC100650436

Supplementary information 1.1.0: GO terms enriched for differentially expressed genes between reproductive and sterile workers.

term_ID	description	frequency	log10 p-value
GO:0055114	oxidation-reduction process	15.06%	-3.873
GO:0043436	oxoacid metabolic process	9.01%	-3.3251
GO:0044283	small molecule biosynthetic process	5.68%	-3.5978
GO:0005975	carbohydrate metabolic process	5.26%	-1.6688
GO:0046394	carboxylic acid biosynthetic process	4.16%	-2.3177
GO:1901605	alpha-amino acid metabolic process	3.63%	-1.5497
GO:0006732	coenzyme metabolic process	3.11%	-2.8645
GO:0044255	cellular lipid metabolic process	2.70%	-7.7045
GO:0032787	monocarboxylic acid metabolic process	2.49%	-4.2161
GO:0006820	anion transport	1.96%	-2.0193
GO:0072524	pyridine-containing compound metabolic process	1.35%	-1.3656
GO:0044282	small molecule catabolic process	1.27%	-2.1464
GO:0044272	sulfur compound biosynthetic process	1.24%	-2.1085
GO:0006766	vitamin metabolic process	1.23%	-1.8857
GO:0042364	water-soluble vitamin biosynthetic process	1.16%	-1.4386
GO:0046942	carboxylic acid transport	1.02%	-1.7946
GO:0046395	carboxylic acid catabolic process	0.95%	-1.4518
GO:0006081	cellular aldehyde metabolic process	0.75%	-1.4225
GO:0006633	fatty acid biosynthetic process	0.62%	-1.6107
GO:0008299	isoprenoid biosynthetic process	0.44%	-6.6192
GO:1901136	carbohydrate derivative catabolic process	0.42%	-2.5364
GO:0016042	lipid catabolic process	0.40%	-1.9973
GO:0006098	pentose-phosphate shunt	0.29%	-1.4386
GO:0006869	lipid transport	0.27%	-1.6622
GO:0035383	thioester metabolic process	0.25%	-3.6454
GO:0016114	terpenoid biosynthetic process	0.25%	-1.7966
GO:0033865	nucleoside bisphosphate metabolic process	0.24%	-1.3515

GO:0046184	aldehyde biosynthetic process	0.19%	-1.5379
GO:0042822	pyridoxal phosphate metabolic process	0.17%	-2.4583
GO:0015936	coenzyme A metabolic process	0.17%	-1.3515
GO:0006084	acetyl-CoA metabolic process	0.17%	-1.7193
GO:0071616	acyl-CoA biosynthetic process	0.15%	-3.1113
GO:0015696	ammonium transport	0.15%	-1.9525
GO:0006826	iron ion transport	0.13%	-1.4386
GO:0006694	steroid biosynthetic process	0.12%	-1.3944
GO:0006595	polyamine metabolic process	0.12%	-1.653
GO:0046165	alcohol biosynthetic process	0.11%	-1.8783
GO:0009062	fatty acid catabolic process	0.11%	-1.5877
GO:0006071	glycerol metabolic process	0.11%	-1.4386
GO:0016125	sterol metabolic process	0.11%	-2.0806
GO:1902652	secondary alcohol metabolic process	0.10%	-1.6322
GO:0042402	cellular biogenic amine catabolic process	0.09%	-1.4386
GO:0008615	pyridoxine biosynthetic process	0.09%	-2.4583
GO:0019395	fatty acid oxidation	0.09%	-1.5877
GO:0006030	chitin metabolic process	0.08%	-1.5448
GO:0046900	tetrahydrofolylpolyglutamate metabolic process	0.07%	-1.4617
GO:0008295	spermidine biosynthetic process	0.06%	-2.1672
GO:0016999	antibiotic metabolic process	0.06%	-1.3103
GO:0015695	organic cation transport	0.05%	-1.4386
GO:0050992	dimethylallyl diphosphate biosynthetic process	0.04%	-1.4617
GO:0019303	D-ribose catabolic process	0.03%	-1.4617
GO:0030148	sphingolipid biosynthetic process	0.03%	-1.5037
GO:0019427	acetyl-CoA biosynthetic process from acetate	0.03%	-1.4617
GO:0019521	D-gluconate metabolic process	0.03%	-1.4617
GO:0006646	phosphatidylethanolamine biosynthetic process	0.03%	-1.9553
GO:0033559	unsaturated fatty acid metabolic process	0.03%	-2.0046
GO:0009698	phenylpropanoid metabolic process	0.02%	-1.653

GO:0015772	oligosaccharide transport	0.02%	-2.741
GO:0006656	phosphatidylcholine biosynthetic process	0.02%	-1.9553
GO:0046466	membrane lipid catabolic process	0.02%	-1.9525
GO:0009443	pyridoxal 5'-phosphate salvage	0.02%	-1.4617
GO:0006690	icosanoid metabolic process	0.02%	-2.1361
GO:0006574	valine catabolic process	0.02%	-1.4617
GO:0006695	cholesterol biosynthetic process	0.01%	-2.2629
GO:0009437	carnitine metabolic process	0.01%	-1.4617
GO:0046274	lignin catabolic process	0.01%	-1.9553
GO:1901570	fatty acid derivative biosynthetic process	0.01%	-1.5822
GO:0042761	very long-chain fatty acid biosynthetic process	0.01%	-3.1113
GO:0033539	fatty acid beta-oxidation using acyl-CoA dehydrogenase	0.01%	-3.6078
GO:0043103	hypoxanthine salvage	0.01%	-1.4617
GO:0042074	cell migration involved in gastrulation	0.01%	-1.4386
GO:0006693	prostaglandin metabolic process	0.01%	-2.0462
GO:0046477	glycosylceramide catabolic process	0.01%	-1.4617
GO:0045337	farnesyl diphosphate biosynthetic process	0.01%	-2.9254
GO:0010054	trichoblast differentiation	0.01%	-1.4617
GO:0035337	fatty-acyl-CoA metabolic process	0.01%	-1.9525
GO:0042538	hyperosmotic salinity response	0.00%	-2.1672
GO:0002121	inter-male aggressive behavior	0.00%	-1.7141
GO:0002092	positive regulation of receptor internalization	0.00%	-1.3515
GO:0019367	fatty acid elongation, saturated fatty acid	0.00%	-2.3901
GO:0016119	carotene metabolic process	0.00%	-1.4617
GO:0042360	vitamin E metabolic process	0.00%	-1.4617
GO:0033690	positive regulation of osteoblast proliferation	0.00%	-1.4617
GO:0045138	nematode male tail tip morphogenesis	0.00%	-1.4617
GO:0042759	long-chain fatty acid biosynthetic process	0.00%	-2.6988
GO:0015771	trehalose transport	0.00%	-2.8541
GO:0002138	retinoic acid biosynthetic process	0.00%	-1.4617

GO:0035338	long-chain fatty-acyl-CoA biosynthetic process	0.00%	-2.9254
GO:0014866	skeletal myofibril assembly	0.00%	-1.9553
GO:1901374	acetate ester transport	0.00%	-1.4617
GO:0051918	negative regulation of fibrinolysis	0.00%	-1.4617
GO:0016139	glycoside catabolic process	0.00%	-1.4617
GO:0034625	fatty acid elongation, monounsaturated fatty acid	0.00%	-2.3901
GO:0034626	fatty acid elongation, polyunsaturated fatty acid	0.00%	-2.3901
GO:0019376	galactolipid catabolic process	0.00%	-2.1672
GO:0070672	response to interleukin-15	0.00%	-1.4617
GO:0035426	extracellular matrix-cell signaling	0.00%	-1.4617
GO:0090383	phagosome acidification	0.00%	-1.4617
GO:0060136	embryonic process involved in female pregnancy	0.00%	-2.4583
GO:1904430	negative regulation of t-circle formation	0.00%	-1.4617
GO:0035309	wing and notum subfield formation	0.00%	-1.7892
GO:0070837	dehydroascorbic acid transport	0.00%	-1.4617
GO:0061526	acetylcholine secretion	0.00%	-1.4617
GO:0014057	positive regulation of acetylcholine secretion, neurotransmission	0.00%	-1.4617
GO:1902262	apoptotic process involved in blood vessel morphogenesis	0.00%	-1.4617
GO:0033540	fatty acid beta-oxidation using acyl-CoA oxidase	0.00%	-4.3502
GO:0033386	geranylgeranyl diphosphate biosynthetic process	0.00%	-1.4617
GO:0061064	negative regulation of nematode larval development	0.00%	-1.4617
GO:0045297	post-mating behavior	0.00%	-1.653
GO:0090326	positive regulation of locomotion involved in locomotory behavior	0.00%	-1.4617
GO:1901046	positive regulation of oviposition	0.00%	-1.4617
GO:0030070	insulin processing	0.00%	-1.4617
GO:0001579	medium-chain fatty acid transport	0.00%	-1.4617
GO:0015917	aminophospholipid transport	0.00%	-1.4617
GO:2000192	negative regulation of fatty acid transport	0.00%	-1.4617
GO:0090474	arg-arg specific dibasic protein processing	0.00%	-1.4617
GO:0031637	regulation of neuronal synaptic plasticity in response to neurotrophin	0.00%	-1.4617

GO:0071689	muscle thin filament assembly	0.00%	-2.4583
GO:1904810	negative regulation of dense core granule transport	0.00%	-1.4617
GO:0009609	response to symbiotic bacterium	0.00%	-1.4617
GO:0090212	negative regulation of establishment of blood-brain barrier	0.00%	-1.4617
GO:0060764	cell-cell signaling involved in mammary gland development	0.00%	-1.4617
GO:0021556	central nervous system formation	0.00%	-1.4617
GO:0061330	Malpighian tubule stellate cell differentiation	0.00%	-1.4617
GO:0007502	digestive tract mesoderm development	0.00%	-1.4617
GO:0033384	geranyl diphosphate biosynthetic process	0.00%	-2.9254
GO:0019442	tryptophan catabolic process to acetyl-CoA	0.00%	-1.4617
GO:0009951	polarity specification of dorsal/ventral axis	0.00%	-1.4617
GO:0070904	transepithelial L-ascorbic acid transport	0.00%	-1.4617
GO:1902435	regulation of male mating behavior	0.00%	-1.4617
GO:0061096	negative regulation of turning behavior involved in mating	0.00%	-1.4617
GO:0035238	vitamin A biosynthetic process	0.00%	-1.4617
GO:0050929	induction of negative chemotaxis	0.00%	-1.4617
GO:0032307	negative regulation of prostaglandin secretion	0.00%	-1.4617
GO:0007477	notum development	0.00%	-1.4617

Supplementary information 1.1.1: differentially expressed genes between reproductive and sterile workers, a negative log2FoldChange indicates up-regulation in sterile workers.

gene_id	exon	exonBaseMean	dispersion	stat	pvalue	qvalue	sterile	repro
LOC100642316	E005	139.9675642	0.00137057	22.9080341	1.70E-06	0.00624232	18.8525488	20.3225585
LOC100642450+LOC100651402	E002	74.94552772	0.00463883	26.9168677	2.12E-07	0.00117028	16.4971895	13.8747364
LOC100642450+LOC100651402	E027	82.67105184	0.00100698	15.7940046	7.06E-05	0.08319492	15.0637351	16.360283
LOC100642976	E006	53.42037811	0.0067113	15.5173488	8.18E-05	0.09122847	13.9855609	12.2853499
LOC100643147	E001	49.19202389	0.00609829	17.0947647	3.56E-05	0.05805399	11.7676458	13.6197126
LOC100643199	E003	35.77290784	0.00192871	15.2642098	9.35E-05	0.09927959	10.355157	11.921335
LOC100643335	E001	95.05430836	0.0021851	18.176577	2.01E-05	0.04127842	15.9290775	17.5740231
LOC100643457	E003	77.82234812	0.00108149	15.4404305	8.51E-05	0.09382986	15.8562666	14.8916007
LOC100644050	E001	153.7997828	0.00737175	26.6817286	2.40E-07	0.00124396	19.0859328	21.5875157
LOC100644055	E001	402.3067144	0.15080504	36.0500748	1.92E-09	8.48E-05	34.9436451	19.5349896
LOC100644055	E002	327.9087074	0.15125079	31.7686656	1.74E-08	0.00032958	32.7546983	18.5380145
LOC100644055	E003	419.4090973	0.15060215	30.1857227	3.93E-08	0.00038455	35.0404538	20.7958445
LOC100644055	E004	664.1530672	0.15508751	29.4276113	5.80E-08	0.00045183	39.607722	24.7522298
LOC100644055	E005	325.9855434	0.15370397	28.9793738	7.32E-08	0.00045183	32.473328	19.0902286
LOC100644055	E006	645.3450396	0.14461986	30.3935261	3.53E-08	0.00038455	39.1920815	24.8567682
LOC100644055	E007	670.1917992	0.17168689	24.4671358	7.56E-07	0.00302896	39.4242984	25.5990807
LOC100644055	E008	381.3230206	0.15576493	25.1979412	5.17E-07	0.00228053	33.6582041	21.1646831
LOC100644429	E004	275.5297076	0.00085933	29.9490652	4.44E-08	0.00039102	24.7845411	26.3725122
LOC100644484	E007	5.880848964	0.00885193	18.590372	1.62E-05	0.0375917	3.47334056	5.42186527
LOC100644708	E006	58.56184513	0.00255145	16.6003798	4.61E-05	0.06431823	14.3638412	12.9534085
LOC100645228	E010	13.77270542	0.00901779	21.6003814	3.36E-06	0.01020763	7.90749104	5.76770248
LOC100645229	E004	199.0859802	0.00071061	16.6420469	4.51E-05	0.06431823	22.9257613	21.7455385
LOC100645331	E008	203.4829943	0.0032946	15.3801688	8.79E-05	0.09567434	23.5674078	21.9559283
LOC100645869	E002	1184.340379	0.00103117	15.2953685	9.19E-05	0.09884625	33.4314825	32.9664914
LOC100646273	E002	3118.18913	0.00279866	15.777839	7.12E-05	0.08319492	48.6073097	49.9841719
LOC100646273	E003	2911.192372	0.00178527	15.6952999	7.44E-05	0.08519136	47.9835143	49.1712935
LOC100646273	E010	7074.862766	0.00140878	16.0578862	6.14E-05	0.07737152	58.1128753	57.3174591

LOC100646787	E004	1.784517173	0.06802399	16.5688675	4.69E-05	0.06431823	1.59223219	3.56325849
LOC100646942	E001	16.33964753	0.10545725	22.5632192	2.03E-06	0.00717044	9.72493043	5.91122024
LOC100646951	E003	45.9634061	0.00329678	17.2356472	3.30E-05	0.05597736	11.3733135	13.1132631
LOC100647378	E001	154.2841167	0.00879225	16.5985952	4.62E-05	0.06431823	19.4605095	21.4737025
LOC100647409	E003	2.697020834	0.01234544	16.8831847	3.98E-05	0.06148199	3.83211099	1.8534867
LOC100647530	E015	2.879995443	0.01267068	15.7648854	7.17E-05	0.08319492	3.92288033	2.02082041
LOC100647760	E008	69.42263645	0.01028612	16.4590381	4.97E-05	0.06541141	15.7144645	13.5862805
LOC100647810	E001	95.36774523	0.01070132	21.7132025	3.17E-06	0.0099683	15.8241329	17.5686171
LOC100648012	E001	740.6162019	0.09460751	17.8009176	2.45E-05	0.04504597	28.9977733	38.2997201
LOC100648012	E005	24.58948843	0.02660734	20.2232335	6.89E-06	0.01794438	9.33406124	9.01090731
LOC100648012	E008	21.04551999	0.0491087	16.7420991	4.28E-05	0.0639821	8.90470622	8.21704226
LOC100648012	E009	17.58951075	0.04117651	26.3474706	2.85E-07	0.00139678	8.54138806	7.23025614
LOC100648012	E012	15.49560936	0.0227414	22.2447692	2.40E-06	0.00783665	7.59572874	7.00196221
LOC100648012	E013	14.69491209	0.04959429	17.0452438	3.65E-05	0.05850434	7.63578313	6.77743704
LOC100648012	E014	11.50729789	0.04653717	16.1011943	6.00E-05	0.0767181	6.78152749	6.06471978
LOC100648195	E025	103.2523995	0.01370992	18.4808886	1.72E-05	0.03802106	16.6415943	18.0058089
LOC100648281	E010	5.429071926	0.01108338	17.8413191	2.40E-05	0.04503789	3.55943157	5.44666882
LOC100648473	E008	25.64800923	0.02265821	25.461569	4.51E-07	0.00209391	7.2979796	10.5724774
LOC100648602	E002	125.65315	0.03486063	18.0049289	2.20E-05	0.04316485	21.2018415	16.8994941
LOC100648602	E003	187.4441672	0.02545695	20.2150502	6.92E-06	0.01794438	24.192736	20.1714503
LOC100648602	E008	125.7499153	0.04522214	15.8797201	6.75E-05	0.0815137	21.216945	16.8501255
LOC100648602	E015	151.4057004	0.01042726	18.327122	1.86E-05	0.03904972	17.7521941	20.9274504
LOC100648842	E005	48.98601112	0.00315247	18.0241275	2.18E-05	0.04316485	13.4167945	11.949298
LOC100648955	E007	22.11472877	0.21197472	23.7957766	1.07E-06	0.00410576	5.72065084	11.6611089
LOC100648980	E001	190.2332976	0.01395068	22.440857	2.17E-06	0.00734813	20.3022894	22.4451509
LOC100648980	E013	31.63877809	0.01374217	21.1328631	4.29E-06	0.01218617	11.6073294	9.26347187
LOC100648980	E015	6.257553971	0.04784269	29.1012297	6.87E-08	0.00045183	6.47625316	3.42044181
LOC100649013	E007	181.7744416	0.00359289	17.6279286	2.69E-05	0.04736103	22.5281362	20.8653851
LOC100649302	E001	284.2461733	0.00078818	15.9108743	6.64E-05	0.08129654	24.9211952	25.9793305
LOC100649392	E008	116.702716	0.0111521	36.9615975	1.20E-09	8.48E-05	16.37867	19.5238999

LOC100649583	E004	2.00031448	0.02462309	15.9392569	6.54E-05	0.08121456	2.99913011	1.04593783
LOC100649610	E003	1.849306007	0.03582653	17.8842833	2.35E-05	0.04498967	1.72716743	3.41442053
LOC100649679	E010	29.79242743	0.00220066	16.5828725	4.66E-05	0.06431823	10.6426808	9.64086048
LOC100650035	E001	6.161154856	0.02593671	28.8831444	7.69E-08	0.00045183	5.71758629	3.77959528
LOC100650035	E002	51.61732122	0.08130367	34.3749615	4.55E-09	0.00013357	14.8541994	10.9365778
LOC100650035	E003	370.2491643	0.07578386	31.535852	1.96E-08	0.00032958	22.9803848	27.6178347
LOC100650351	E004	43.15442547	0.01319771	15.6655698	7.56E-05	0.08543156	10.4812542	12.6990316
LOC100650528	E002	104.9421893	0.01024313	17.161892	3.43E-05	0.0570954	16.7436885	18.4918278
LOC100650572	E006	50.61816078	0.0104916	16.4809257	4.91E-05	0.06541141	13.8149619	11.5401185
LOC100650646	E011	60.83561233	0.00494086	31.271815	2.24E-08	0.00032958	12.8810058	15.0173565
LOC100650648	E001	103.2530125	0.00648007	21.321362	3.88E-06	0.01141292	18.2839138	16.4742204
LOC100650743	E018	7.889683511	0.01433295	19.2089511	1.17E-05	0.02951095	5.99740765	4.18062909
LOC100650865	E007	11.79213959	0.01980247	18.3515876	1.84E-05	0.03904972	6.90987785	5.12154286
LOC100650865	E009	71.27400787	0.01421299	16.5484538	4.74E-05	0.06431823	14.8370663	13.7717437
LOC100650865	E017	199.420465	0.0324938	29.1616371	6.66E-08	0.00045183	19.8494662	25.543416
LOC100651376	E002	584.5966118	0.01255503	18.4709571	1.73E-05	0.03802106	33.8118777	30.5981035
LOC100651787	E001	33.20040351	0.03599287	30.2582023	3.78E-08	0.00038455	8.5636104	13.1411525
LOC100651787	E006	73.3121002	0.01082588	20.2765081	6.70E-06	0.01794438	15.0242199	12.6707992
LOC100651987	E009	6.223688548	0.01858453	16.1015712	6.00E-05	0.0767181	5.56720411	3.58885132
LOC100652183	E009	90.44965541	0.00117463	25.0541278	5.57E-07	0.0023401	17.3478688	15.7395082
LOC100652301	E005	517.3686345	0.0063955	19.0609686	1.27E-05	0.03100418	27.2920949	29.6659698
LOC105666289	E001	1.717497588	0.02119037	18.6444565	1.58E-05	0.0375278	3.36348168	1.33736831
LOC105666631+LOC105666630	E007	56.16569155	0.00321255	16.8474334	4.05E-05	0.06157087	12.6464259	14.3600682
LOC105667093	E006	29.35497497	0.0061918	17.6564559	2.65E-05	0.04736103	10.4177741	9.47463715
LOC110119151	E003	9.688044271	0.01189851	16.9767319	3.78E-05	0.05957078	6.65972126	4.57964632
LOC110119633	E010	104.4271306	0.00111882	17.5556977	2.79E-05	0.04822994	16.8788851	18.4145613

log2foldChange	chromosome	start	end	width	strand
0.274543713	NC_015763.1	3581899	3583139	1241	+
-0.581265708	NC_015767.1	3188823	3189058	236	-
0.279965096	NC_015767.1	3207262	3207407	146	-
-0.420218709	NC_015776.1	10591855	10592051	197	-
0.470473559	NC_015762.1	492943	493282	340	-
0.442744436	NC_015767.1	12054895	12055209	315	+
0.33974569	NC_015772.1	7178881	7179120	240	-
-0.211532614	NC_015772.1	7176155	7176392	238	+
0.457255724	NC_015765.1	1976415	1976684	270	-
-2.479549241	NC_015766.1	4460168	4460376	209	+
-2.346514993	NC_015766.1	4467037	4467165	129	+
-2.262246527	NC_015766.1	4467254	4467450	197	+
-2.239371816	NC_015766.1	4467683	4468042	360	+
-2.198975031	NC_015766.1	4469152	4469299	148	+
-2.162969348	NC_015766.1	4469383	4469700	318	+
-2.074690729	NC_015766.1	4469792	4470162	371	+
-1.993251629	NC_015766.1	4470247	4470395	149	+
0.258068909	NC_015762.1	5859556	5859675	120	-
1.303262681	NC_015767.1	9377924	9381792	3869	-
-0.338012512	NW_0035663	1271168	1271737	570	-
-0.941273546	NW_0035661	538720	538936	217	+
-0.204713892	NW_0035705	1108	1164	57	-
-0.276835138	NC_015770.1	9350576	9351049	474	+
-0.068848037	NC_015765.1	11920906	11921161	256	-
0.190271823	NC_015777.1	2046978	2047298	321	-
0.164365102	NC_015777.1	2047724	2048020	297	-
-0.108754011	NC_015777.1	2057192	2057354	163	-

2.335061	NC_015770.1	11743610	11743823	214	-
-1.499132068	NC_015764.1	8837873	8838083	211	+
0.454976769	NC_015770.1	2080700	2080889	190	-
0.366506377	NC_015767.1	3229471	3231443	1973	-
-2.107713824	NC_015763.1	6363989	6364175	187	+
-1.925920816	NC_015763.1	6486202	6486335	134	+
-0.484030911	NW_0035661	21695	21917	223	+
0.361148275	NC_015768.1	9099338	9100682	1345	-
1.376322192	NC_015764.1	8784687	8785123	437	-
-0.107877768	NC_015764.1	8785882	8786100	219	-
-0.244255649	NC_015764.1	8786788	8787014	227	-
-0.502585783	NC_015764.1	8787525	8787740	216	-
-0.243982146	NC_015764.1	8788309	8788471	163	-
-0.357097826	NC_015764.1	8788543	8788722	180	-
-0.332048489	NC_015764.1	8788795	8788880	86	-
0.275396412	NC_015762.1	1465100	1465239	140	+
1.245430066	NC_015769.1	307578	307960	383	-
1.130828049	NC_015765.1	6646462	6646648	187	+
-0.819604156	NC_015772.1	6768841	6768962	122	+
-0.701280424	NC_015772.1	6769071	6769253	183	+
-0.832436661	NC_015772.1	6771342	6771481	140	+
0.59840867	NC_015772.1	6774994	6775179	186	+
-0.372812599	NW_0035654	209279	209702	424	-
2.163116745	NC_015776.1	5321551	5321720	170	+
0.380729321	NC_015769.1	973690	976253	2564	-
-0.701896267	NC_015769.1	1003489	1006820	3332	-
-1.873911165	NC_015769.1	1008732	1010131	1400	-
-0.292947748	NC_015762.1	4533886	4534082	197	-
0.172324225	NC_015771.1	2544189	2545367	1179	-
0.621288798	NC_015776.1	2789389	2789747	359	+

-3.047869591	NC_015771.1	479160	479400	241	+
1.975659022	NC_015762.1	4838949	4839231	283	-
-0.306493133	NC_015762.1	377399	377782	384	-
-1.213807797	NC_015766.1	6367480	6367734	255	-
-0.988021515	NC_015766.1	6367833	6369220	1388	-
0.758526135	NC_015766.1	6371319	6372602	1284	-
0.607295718	NW_0035663	2613840	2614383	544	-
0.349080562	NC_015768.1	16004061	16004285	225	+
-0.578927723	NC_015773.1	3221414	3221500	87	+
0.504252562	NC_015768.1	15999132	15999819	688	+
-0.364666005	NC_015769.1	3517284	3518043	760	+
-1.060778278	NC_015775.1	8506957	8506972	16	-
-0.886866339	NW_0035655	463213	463305	93	+
-0.246388137	NW_0035655	463419	464524	1106	+
0.982915922	NW_0035655	477117	478786	1670	+
-0.48017905	NC_015772.1	1094460	1094807	348	+
1.339148059	NC_015762.1	3670520	3670688	169	+
-0.55882412	NC_015762.1	3673367	3673471	105	+
-1.286016599	NC_015764.1	6287222	6287422	201	-
-0.335038419	NW_0035664	123873	123985	113	+
0.369440441	NW_0035658	1260	1381	122	-
-2.671211707	NC_015762.1	372508	372821	314	+
0.414489865	NC_015777.1	4174845	4175193	349	+
-0.293428052	NC_015763.1	10322488	10327946	5459	+
-1.105134912	NC_015764.1	6725635	6725847	213	-
0.306277534	NC_015771.1	12278734	12278745	12	+

Supplementary 1.1.2: List of enriched GO terms associaited with genes containing differentially used exons between castes.

term_ID	description	frequency	log10 p-value
GO:0044406	adhesion of symbiont to host	0.01%	-1.7326
GO:0048678	response to axon injury	0.01%	-2.3701
GO:1903034	regulation of response to wounding	0.03%	-2.149
GO:1903725	regulation of phospholipid metabolic process	0.03%	-2.7004
GO:0045834	positive regulation of lipid metabolic process	0.03%	-1.707
GO:0043552	positive regulation of phosphatidylinositol 3-kinase activity	0.01%	-1.7326
GO:0030242	pexophagy	0.01%	-1.609
GO:0035609	C-terminal protein deglutamylation	0.00%	-2.2071
GO:0035610	protein side chain deglutamylation	0.00%	-2.2071
GO:0042160	lipoprotein modification	0.00%	-1.7326
GO:0008283	cell proliferation	0.39%	-1.3046
GO:1903475	mitotic actomyosin contractile ring assembly	0.01%	-2.2071
GO:1902410	mitotic cytokinetic process	0.05%	-1.609
GO:0006545	glycine biosynthetic process	0.08%	-1.609
GO:1904059	regulation of locomotor rhythm	0.00%	-1.7326
GO:0042632	cholesterol homeostasis	0.02%	-2.3174
GO:1904589	regulation of protein import	0.04%	-2.3701
GO:1900180	regulation of protein localization to nucleus	0.05%	-1.8921
GO:0042308	negative regulation of protein import into nucleus	0.01%	-1.4355
GO:0046822	regulation of nucleocytoplasmic transport	0.05%	-1.707
GO:0006828	manganese ion transport	0.02%	-1.4355
GO:0045324	late endosome to vacuole transport	0.03%	-1.3132
GO:0098581	detection of external biotic stimulus	0.00%	-2.2071
GO:0032497	detection of lipopolysaccharide	0.00%	-2.2071
GO:0034334	adherens junction maintenance	0.00%	-1.5134
GO:0006006	glucose metabolic process	0.43%	-1.5504

GO:0034368	protein-lipid complex remodeling	0.01%	-1.609
GO:0034375	high-density lipoprotein particle remodeling	0.00%	-1.609
GO:0071827	plasma lipoprotein particle organization	0.01%	-1.4355
GO:0031104	dendrite regeneration	0.00%	-2.2071
GO:0048680	positive regulation of axon regeneration	0.00%	-1.9074
GO:0070570	regulation of neuron projection regeneration	0.01%	-1.4355
GO:0031102	neuron projection regeneration	0.01%	-1.4462
GO:0014012	peripheral nervous system axon regeneration	0.00%	-1.609
GO:0009605	response to external stimulus	1.37%	-1.3465
GO:0043654	recognition of apoptotic cell	0.00%	-2.2071
GO:0034162	toll-like receptor 9 signaling pathway	0.00%	-1.9074
GO:0006702	androgen biosynthetic process	0.00%	-1.7326
GO:0019102	male somatic sex determination	0.00%	-1.9074
GO:0034384	high-density lipoprotein particle clearance	0.00%	-2.2071
GO:0034383	low-density lipoprotein particle clearance	0.00%	-1.4355
GO:0006796	phosphate-containing compound metabolic process	13.11%	-1.4436
GO:0035298	regulation of Malpighian tubule size	0.00%	-2.2071
GO:0006707	cholesterol catabolic process	0.00%	-2.2071
GO:1902775	mitochondrial large ribosomal subunit assembly	0.00%	-1.9074
GO:0060292	long term synaptic depression	0.00%	-1.9074
GO:0008362	chitin-based embryonic cuticle biosynthetic process	0.00%	-1.4355
GO:0035461	vitamin transmembrane transport	0.07%	-2.2071
GO:0071896	protein localization to adherens junction	0.00%	-1.609
GO:0051000	positive regulation of nitric-oxide synthase activity	0.00%	-1.7326
GO:0032768	regulation of monooxygenase activity	0.01%	-1.3699
GO:0051353	positive regulation of oxidoreductase activity	0.01%	-1.3699
GO:0000768	syncytium formation by plasma membrane fusion	0.01%	-1.8345
GO:1901739	regulation of myoblast fusion	0.00%	-1.3699
GO:0007601	visual perception	0.05%	-1.9756
GO:0050906	detection of stimulus involved in sensory perception	0.29%	-1.5207

GO:0007600	sensory perception	0.43%	-1.4383
GO:0046460	neutral lipid biosynthetic process	0.02%	-2.5521
GO:0006639	acylglycerol metabolic process	0.04%	-1.6838
GO:0006651	diacylglycerol biosynthetic process	0.00%	-1.609
GO:0010867	positive regulation of triglyceride biosynthetic process	0.00%	-1.4355
GO:0019432	triglyceride biosynthetic process	0.02%	-1.5241
GO:2000035	regulation of stem cell division	0.00%	-1.7326
GO:0031848	protection from non-homologous end joining at telomere	0.00%	-1.609
GO:0015920	lipopolysaccharide transport	0.03%	-2.2071
GO:0070508	cholesterol import	0.00%	-1.9074
GO:0043691	reverse cholesterol transport	0.00%	-1.609
GO:0019915	lipid storage	0.03%	-1.8073
GO:0035382	sterol transmembrane transport	0.16%	-2.2071
GO:0014902	myotube differentiation	0.03%	-1.707
GO:0042335	cuticle development	0.01%	-1.4346
GO:1902221	erythrose 4-phosphate/phosphoenolpyruvate family amino acid metabolic process	0.08%	-1.4355
GO:0007164	establishment of tissue polarity	0.02%	-1.3725
GO:0016476	regulation of embryonic cell shape	0.00%	-1.4355
GO:0046663	dorsal closure, leading edge cell differentiation	0.00%	-1.7326
GO:0007395	dorsal closure, spreading of leading edge cells	0.00%	-1.609
GO:0030589	pseudocleavage involved in syncytial blastoderm formation	0.00%	-1.5134
GO:0033540	fatty acid beta-oxidation using acyl-CoA oxidase	0.00%	-1.3699
GO:0007374	posterior midgut invagination	0.00%	-2.2071
GO:0007370	ventral furrow formation	0.00%	-1.609
GO:0007377	germ-band extension	0.00%	-1.5134
GO:2000405	negative regulation of T cell migration	0.00%	-1.7326
GO:0002686	negative regulation of leukocyte migration	0.01%	-1.3699
GO:2000401	regulation of lymphocyte migration	0.01%	-1.4355
GO:0090251	protein localization involved in establishment of planar polarity	0.00%	-2.2071
GO:0042249	establishment of planar polarity of embryonic epithelium	0.00%	-1.609

GO:0001737	establishment of imaginal disc-derived wing hair orientation	0.00%	-1.3132
GO:0034442	regulation of lipoprotein oxidation	0.00%	-1.7326
GO:0050748	negative regulation of lipoprotein metabolic process	0.00%	-1.7326
GO:0060588	negative regulation of lipoprotein lipid oxidation	0.00%	-1.7326
GO:0007089	traversing start control point of mitotic cell cycle	0.00%	-1.9074
GO:0090254	cell elongation involved in imaginal disc-derived wing morphogenesis	0.00%	-1.9074
GO:0044255	cellular lipid metabolic process	2.70%	-2.3169
GO:0035149	lumen formation, open tracheal system	0.00%	-1.609
GO:0010642	negative regulation of platelet-derived growth factor receptor signaling pathway	0.00%	-1.5134
GO:0016054	organic acid catabolic process	0.95%	-1.7469
GO:0009063	cellular amino acid catabolic process	0.65%	-1.3578
GO:0021702	cerebellar Purkinje cell differentiation	0.00%	-1.7326
GO:0021692	cerebellar Purkinje cell layer morphogenesis	0.00%	-1.4355
GO:0021697	cerebellar cortex formation	0.01%	-1.4355
GO:0046622	positive regulation of organ growth	0.01%	-1.4355
GO:0003008	system process	0.66%	-1.6751
GO:0010631	epithelial cell migration	0.06%	-1.5931
GO:0090130	tissue migration	0.06%	-1.5609
GO:0050884	neuromuscular process controlling posture	0.00%	-1.7326
GO:0010810	regulation of cell-substrate adhesion	0.04%	-1.5978
GO:2000098	negative regulation of smooth muscle cell-matrix adhesion	0.00%	-1.7326
GO:0051895	negative regulation of focal adhesion assembly	0.00%	-1.4355
GO:0006572	tyrosine catabolic process	0.01%	-1.5134
GO:0006559	L-phenylalanine catabolic process	0.03%	-1.4355
GO:0090596	sensory organ morphogenesis	0.08%	-1.6023
GO:0030950	establishment or maintenance of actin cytoskeleton polarity	0.01%	-1.7326
GO:0045199	maintenance of epithelial cell apical/basal polarity	0.00%	-1.5134
GO:0034440	lipid oxidation	0.09%	-1.6614
GO:0050910	detection of mechanical stimulus involved in sensory perception of sound	0.00%	-1.9074
GO:0050982	detection of mechanical stimulus	0.01%	-1.3699

GO:0010886	positive regulation of cholesterol storage	0.00%	-1.9074
GO:1900016	negative regulation of cytokine production involved in inflammatory response	0.00%	-1.609
GO:0071638	negative regulation of monocyte chemotactic protein-1 production	0.00%	-1.5134
GO:0006706	steroid catabolic process	0.00%	-1.7326
GO:0055088	lipid homeostasis	0.04%	-1.7308
GO:0070593	dendrite self-avoidance	0.00%	-1.609
GO:0021772	olfactory bulb development	0.01%	-1.4355
GO:0030098	lymphocyte differentiation	0.06%	-1.4678
GO:0045321	leukocyte activation	0.15%	-1.3041
GO:0033151	V(D)J recombination	0.00%	-1.4355
GO:0051480	regulation of cytosolic calcium ion concentration	0.06%	-1.5778
GO:0010899	regulation of phosphatidylcholine catabolic process	0.00%	-2.2071
GO:0046475	glycerophospholipid catabolic process	0.01%	-1.3699
GO:0045017	glycerolipid biosynthetic process	0.30%	-2.0416
GO:0006567	threonine catabolic process	0.04%	-1.609
GO:0048699	generation of neurons	0.37%	-1.5505
GO:0048666	neuron development	0.27%	-1.5976

Supplementary 1.1.3: Lists of overlapping genes from all analyses.

Genes both differentially methylated and differentially expressed between reproductive and sterile workers.
LOC100647553 SWI/SNF complex subunit SMARCC2
LOC100647451 retinoblastoma-binding protein 5 homolog

Genes both differentially methylated and containing a differentially expressed exon between reproductive and sterile workers.
LOC100649679 phosphoinositide 3-kinase regulatory subunit 4

Genes both differentially expressed and containing a differentially expressed exon between reproductive and sterile workers.
LOC100644055 uncharacterized
LOC100646942 venom acid phosphatase Acph-1
LOC100648012 replication factor C subunit 1
LOC100648602 uncharacterized
LOC100648955 probable peroxisomal acyl-coenzyme A oxidase 1
LOC100648980 insulin-like growth factor I, juvenile form
LOC100649392 flavin-containing monooxygenase FMO GS-OX-like 2
LOC100650035 protein artichoke
LOC100650646 SPARC-related modular calcium-binding protein 2
LOC100650865 allatotropin receptor
LOC100651787 3-hydroxy-3-methylglutaryl-coenzyme A reductase
LOC100652301 serine protease inhibitor 3/4
LOC105666289 uncharacterized
LOC110119151 probable low-specificity L-threonine aldolase 1

Chapter 3: supplementary

Supplementary 3.0.0: mapping statistics for all samples aligned to the Bter_1.0 reference genome using STAR.

Sample	Mapping Percentage	Unique Mapped Reads
j1_17	89.7	9693065
j1_3	88.26	11104601
j1_5	89.88	11515820
j1_6	89.01	10229854
j1_7	89.18	9516528
j1_8	89.18	10519352
j5_13	90.97	10731961
j5_15	89.55	9686764
j5_33	88.27	9489124
j5_34	90.19	9712769
j5_6	87.96	10366533
j5_7	89.21	11452674
j8_12	89.32	10570796
j8_18	90.34	3354181
j8_23	88.63	11390055
j8_24	90.14	11574958
j8_29	89.12	11426249
j8_30	90.49	9741303

Supplementary 3.0.1: Genes showing significant allelic expression bias for both reproductive and sterile workers.

geneID	status	proportion expression	SE	z	p	average proportion expression	padj
LOC100642305	repro	0.736679144	0.00965787	20.6635346	7.38E-95	0.70050866	1.42E-93
LOC100642399	repro	0.737093529	0.00754579	26.475406	1.86E-154	0.750128558	5.86E-153
LOC100642453	repro	0.888013257	0.0353335	5.82769608	5.62E-09	0.867197672	1.47E-08
LOC100642458	repro	0.890416206	0.01504345	13.5886343	4.68E-42	0.805380701	4.34E-41
LOC100642687	repro	0.759144573	0.04556545	4.60665221	4.09E-06	0.785674209	8.22E-06
LOC100642816	repro	0.706620495	0.02336699	7.79857589	6.26E-15	0.722268629	2.45E-14
LOC100642850	repro	0.784684303	0.02129458	10.2602793	1.06E-24	0.750857404	6.36E-24
LOC100643315	repro	0.605401066	0.0234113	4.36755949	1.26E-05	0.703457616	2.39E-05
LOC100643320	repro	0.714637322	0.00736281	25.4266304	1.28E-142	0.711308485	3.71E-141
LOC100643517	repro	0.828148614	0.03333378	6.71405189	1.89E-11	0.809073758	6.00E-11
LOC100643745	repro	0.761495132	0.00153851	137.043239	0	0.760363245	0
LOC100643777	repro	0.89069253	0.00762676	26.7798754	5.54E-158	0.850872527	1.78E-156
LOC100643807	repro	0.743295752	0.01236857	16.4012806	1.87E-60	0.727148598	2.37E-59
LOC100643863	repro	0.809620245	0.00520128	42.8967017	0	0.793818733	0
LOC100643871	repro	0.743580589	0.0025503	79.5976146	0	0.752958411	0
LOC100644365	repro	0.714637322	0.00736281	25.4266304	1.28E-142	0.711308485	3.71E-141
LOC100644487	repro	0.812149609	0.07420836	3.00987099	0.00261359	0.795916158	0.00364336
LOC100644669	repro	0.750326175	0.00279268	73.8132344	0	0.740078622	0
LOC100644791	repro	0.692776894	0.02105973	8.2178194	2.07E-16	0.700892792	8.82E-16
LOC100644807	repro	0.808980545	0.07551302	2.95379561	0.00313892	0.789415457	0.0043292
LOC100644832	repro	0.740984192	0.0253552	7.95624618	1.77E-15	0.711523593	7.20E-15
LOC100644957	repro	0.742297564	0.03463938	5.84237499	5.15E-09	0.71484163	1.35E-08
LOC100645175	repro	0.792275738	0.05039937	4.37140555	1.23E-05	0.71184577	2.35E-05
LOC100645358	repro	0.824326567	0.00502872	44.5184657	0	0.823949287	0
LOC100645564	repro	0.713118	0.02376849	7.83753048	4.59E-15	0.726270502	1.81E-14

LOC100645627	repro	0.789845057	0.01251928	17.554452	5.50E-69	0.771949237	7.91E-68
LOC100645719	repro	0.851192409	0.05816364	3.7979019	0.00014593	0.768129603	0.00024254
LOC100645947	repro	0.73012084	0.02002247	9.79427743	1.19E-22	0.741014695	6.61E-22
LOC100646175	repro	0.823662521	0.01824855	12.2678963	1.35E-34	0.794744205	1.06E-33
LOC100646202	repro	0.812057621	0.00591984	37.7289906	0	0.807756207	0
LOC100646400	repro	0.897700263	0.00915882	21.7777033	3.78E-105	0.908434733	8.07E-104
LOC100646568	repro	0.873918537	0.01948273	10.9494167	6.69E-28	0.877379839	4.45E-27
LOC100646958	repro	0.69434788	0.0159118	10.9440296	7.10E-28	0.707925028	4.72E-27
LOC100646980	repro	0.839383621	0.01946667	11.4525435	2.28E-30	0.726879114	1.64E-29
LOC100647016	repro	0.676841621	0.01333323	12.1278721	7.52E-34	0.721429521	5.85E-33
LOC100647088	repro	0.736486008	0.01250206	15.9546931	2.64E-57	0.764640408	3.19E-56
LOC100647105	repro	0.786512845	0.0428826	5.10604751	3.29E-07	0.826919845	7.37E-07
LOC100647488	repro	0.743593867	0.01714777	11.8385081	2.47E-32	0.754341135	1.85E-31
LOC100647574	repro	0.887488887	0.035918	5.74167485	9.37E-09	0.8707976	2.40E-08
LOC100647684	repro	0.695702885	0.00965708	18.1275254	1.93E-73	0.703453069	2.94E-72
LOC100647760	repro	0.73126965	0.03303648	5.9547915	2.60E-09	0.774200964	7.03E-09
LOC100647826	repro	0.776670009	0.03343115	6.46662326	1.00E-10	0.802896379	3.00E-10
LOC100647842	repro	0.692748329	0.0156006	11.0922269	1.37E-28	0.707779846	9.29E-28
LOC100648000	repro	0.782981277	0.01236676	17.6303791	1.44E-69	0.726343031	2.09E-68
LOC100648009	repro	0.660242434	0.02233158	6.67369443	2.49E-11	0.716448851	7.85E-11
LOC100648502	repro	0.753561454	0.01353586	15.3343663	4.51E-53	0.729500237	5.08E-52
LOC100648602	repro	0.72282103	0.00372823	51.5086486	0	0.783275328	0
LOC100648717	repro	0.728063425	0.01258296	15.4956791	3.71E-54	0.727328197	4.25E-53
LOC100648857	repro	0.720808007	0.01695994	11.2544242	2.20E-29	0.71615805	1.53E-28
LOC100649041	repro	0.690988004	0.04471499	3.84281629	0.00012163	0.717840087	0.00020423
LOC100649123	repro	0.66768563	0.00754747	20.5121517	1.68E-93	0.798816918	3.17E-92
LOC100649244	repro	0.796687211	0.01602265	13.8063445	2.33E-43	0.758281513	2.23E-42
LOC100649421	repro	0.710457944	0.01158697	15.9355675	3.59E-57	0.711625046	4.31E-56
LOC100649524	repro	0.75993245	0.03538939	5.94024589	2.85E-09	0.779473866	7.66E-09
LOC100649753	repro	0.747557038	0.01932841	10.5996495	2.99E-26	0.753426324	1.88E-25

LOC100649760	repro	0.677231712	0.02532618	6.39621298	1.59E-10	0.72259014	4.70E-10
LOC100650186	repro	0.72313699	0.00837081	22.9627351	1.10E-116	0.729431366	2.57E-115
LOC100650242	repro	0.900394367	0.03823077	5.16469628	2.41E-07	0.826855452	5.46E-07
LOC100650244	repro	0.747749062	0.03524238	5.81581116	6.03E-09	0.761632715	1.57E-08
LOC100650256	repro	0.796353096	0.06007822	3.68104382	0.00023228	0.793171194	0.00037554
LOC100650626	repro	0.928339309	0.00382307	44.5720378	0	0.946858952	0
LOC100650837	repro	0.925942123	0.00924193	18.7421704	2.24E-78	0.848654015	3.60E-77
LOC100651045	repro	0.838366691	0.03655543	6.10205131	1.05E-09	0.714452342	2.91E-09
LOC100651252	repro	0.70762866	0.03342743	5.470635	4.48E-08	0.711935879	1.09E-07
LOC100651324	repro	0.692799742	0.02111085	8.19865995	2.43E-16	0.707943715	1.03E-15
LOC100651336	repro	0.740924998	0.01820652	11.0786139	1.59E-28	0.702270061	1.08E-27
LOC100651419	repro	0.758373234	0.01754886	11.9432424	7.04E-33	0.742867483	5.35E-32
LOC100651556	repro	0.769017309	0.01717799	12.4372961	1.64E-35	0.762170295	1.32E-34
LOC100651785	repro	0.825928637	0.03048464	7.34326962	2.08E-13	0.837367106	7.47E-13
LOC100651786	repro	0.799712858	0.00779149	28.4616488	3.50E-178	0.791206373	1.23E-176
LOC100651908	repro	0.924483695	0.02291679	7.63087458	2.33E-14	0.838698043	8.77E-14
LOC100651943	repro	0.734644362	0.02443456	8.12425091	4.50E-16	0.732907569	1.88E-15
LOC100652111	repro	0.731099155	0.05263985	3.73545417	0.00018738	0.72636093	0.00030717
LOC100652132	repro	0.837204778	0.02014903	11.0769608	1.62E-28	0.821734602	1.10E-27
LOC100652299	repro	0.691904455	0.03137764	5.49642311	3.88E-08	0.713895968	9.43E-08
LOC105665810	repro	0.828947042	0.02572122	8.70008036	3.32E-18	0.838885862	1.54E-17
LOC105666051	repro	0.714739348	0.01929489	9.70584501	2.85E-22	0.745760983	1.56E-21
LOC105666165	repro	0.741849076	0.01406019	14.3779898	7.11E-47	0.703711439	7.28E-46
LOC105666343	repro	0.80880423	0.04539807	4.91278341	8.98E-07	0.789798513	1.93E-06
LOC105666469	repro	0.77763504	0.0096187	22.5065297	3.58E-112	0.801523288	8.07E-111
LOC105666638	repro	0.769767441	0.02840993	7.52944416	5.10E-14	0.796736156	1.89E-13
LOC105666711	repro	0.707984002	0.01804868	10.14445	3.51E-24	0.73518166	2.06E-23
LOC105666829	repro	0.655570737	0.02449551	5.93281807	2.98E-09	0.705564418	8.00E-09
LOC105666882	repro	0.934155603	0.0121438	13.4342721	3.81E-41	0.93372898	3.45E-40
LOC105667011	repro	0.706798239	0.02659321	6.85672623	7.05E-12	0.704354951	2.29E-11

LOC105667013	repro	0.868046076	0.01067813	20.2070483	8.49E-91	0.744566428	1.55E-89
LOC105667035	repro	0.732133094	0.00559839	35.2221925	9.15E-272	0.722023507	4.88E-270
LOC105667037	repro	0.866102295	0.0033522	64.5861685	0	0.841393142	0
LOC105667038	repro	0.687139592	0.06441049	2.62598651	0.00863982	0.770207772	0.01116635
LOC105667042	repro	0.726658554	0.04926514	3.94200587	8.08E-05	0.720732093	0.00013845
LOC105667061	repro	0.762193608	0.00878603	24.0284856	1.40E-127	0.785044704	3.58E-126
LOC105667073	repro	0.760479888	0.01742048	12.0800596	1.35E-33	0.717648944	1.04E-32
LOC105667086	repro	0.795477971	0.01324357	16.6858533	1.66E-62	0.78098703	2.16E-61
LOC100642305	non_repro	0.765860285	0.00825242	25.7508699	3.15E-146	0.70050866	9.30E-145
LOC100642399	non_repro	0.747825664	0.00710899	28.8365062	7.48E-183	0.750128558	2.71E-181
LOC100642453	non_repro	0.852226801	0.04745088	4.6503302	3.31E-06	0.867197672	6.72E-06
LOC100642458	non_repro	0.832083711	0.0193535	11.5543959	7.01E-31	0.805380701	5.10E-30
LOC100642687	non_repro	0.760143147	0.0471313	4.46213061	8.11E-06	0.785674209	1.57E-05
LOC100642816	non_repro	0.672355616	0.02386855	6.63466853	3.25E-11	0.722268629	1.02E-10
LOC100642850	non_repro	0.803826432	0.01913105	11.6252188	3.07E-31	0.750857404	2.25E-30
LOC100643315	non_repro	0.642762768	0.01571643	8.58162483	9.35E-18	0.703457616	4.27E-17
LOC100643320	non_repro	0.712114278	0.00809577	22.9342296	2.12E-116	0.711308485	4.93E-115
LOC100643437	non_repro	0.726091327	0.06444852	3.00840102	0.00262626	0.712035368	0.00366001
LOC100643517	non_repro	0.85309998	0.03114708	7.07784376	1.46E-12	0.809073758	4.97E-12
LOC100643745	non_repro	0.736471532	0.00160224	124.487882	0	0.760363245	0
LOC100643777	non_repro	0.880342638	0.00798542	26.3259415	9.68E-153	0.850872527	3.01E-151
LOC100643807	non_repro	0.756123001	0.0106158	19.6553448	5.20E-86	0.727148598	9.07E-85
LOC100643863	non_repro	0.77117846	0.0053285	40.2360623	0	0.793818733	0
LOC100643871	non_repro	0.750433487	0.00259427	79.477122	0	0.752958411	0
LOC100644365	non_repro	0.712114278	0.00809577	22.9342296	2.12E-116	0.711308485	4.93E-115
LOC100644487	non_repro	0.824774642	0.07280654	3.07484868	0.00210609	0.795916158	0.0029776
LOC100644669	non_repro	0.744525814	0.00264744	76.8481204	0	0.740078622	0
LOC100644791	non_repro	0.708646574	0.01950109	9.41032676	4.95E-21	0.700892792	2.61E-20
LOC100644807	non_repro	0.828409411	0.07213867	3.10230405	0.00192021	0.789415457	0.00273186
LOC100644832	non_repro	0.733432182	0.02584476	7.65634414	1.91E-14	0.711523593	7.24E-14

LOC100644839	non_repro	0.720032005	0.06539638	2.91181487	0.00359336	0.726812412	0.00491634
LOC100644957	non_repro	0.700994496	0.03905937	4.572225	4.83E-06	0.71484163	9.61E-06
LOC100645301	non_repro	0.752717223	0.09869342	2.09939413	0.03578217	0.718646803	0.04209634
LOC100645358	non_repro	0.828089157	0.00478547	46.7680009	0	0.823949287	0
LOC100645564	non_repro	0.735985537	0.01736748	11.4702188	1.86E-30	0.726270502	1.34E-29
LOC100645627	non_repro	0.785455588	0.01278359	17.1070934	1.31E-65	0.771949237	1.78E-64
LOC100645719	non_repro	0.872281726	0.04583132	4.6702423	3.01E-06	0.768129603	6.13E-06
LOC100645947	non_repro	0.759460994	0.01945257	10.7971397	3.55E-27	0.741014695	2.31E-26
LOC100646175	non_repro	0.830447632	0.01543087	14.4975872	1.25E-47	0.794744205	1.30E-46
LOC100646202	non_repro	0.807682572	0.00583785	38.1825554	0	0.807756207	0
LOC100646400	non_repro	0.914133655	0.00739566	25.1027192	4.64E-139	0.908434733	1.30E-137
LOC100646568	non_repro	0.856298829	0.03068168	7.15840785	8.16E-13	0.877379839	2.81E-12
LOC100646958	non_repro	0.704659614	0.01471127	12.3016876	8.87E-35	0.707925028	7.05E-34
LOC100646980	non_repro	0.87970977	0.01569406	13.4158631	4.88E-41	0.726879114	4.41E-40
LOC100647016	non_repro	0.647441462	0.01330044	10.4312124	1.79E-25	0.721429521	1.09E-24
LOC100647088	non_repro	0.703949836	0.01358205	13.2907315	2.62E-40	0.764640408	2.34E-39
LOC100647105	non_repro	0.824598266	0.03775398	5.92970698	3.03E-09	0.826919845	8.14E-09
LOC100647488	non_repro	0.732091758	0.01703489	11.5742072	5.57E-31	0.754341135	4.06E-30
LOC100647574	non_repro	0.858199402	0.03018185	7.25927094	3.89E-13	0.8707976	1.37E-12
LOC100647684	non_repro	0.677535174	0.00982556	16.5095076	3.13E-61	0.703453069	3.99E-60
LOC100647760	non_repro	0.70377967	0.03289564	5.48417119	4.15E-08	0.774200964	1.01E-07
LOC100647826	non_repro	0.827386035	0.03048031	7.34332746	2.08E-13	0.802896379	7.47E-13
LOC100647842	non_repro	0.688699288	0.01504061	11.3185217	1.06E-29	0.707779846	7.50E-29
LOC100648000	non_repro	0.777495847	0.01162282	18.6220742	2.13E-77	0.726343031	3.37E-76
LOC100648009	non_repro	0.694173901	0.0197922	8.79238802	1.46E-18	0.716448851	6.92E-18
LOC100648482	non_repro	0.772039657	0.05923103	3.62460851	0.0002894	0.733244334	0.00046174
LOC100648502	non_repro	0.709459634	0.01961981	9.37939118	6.64E-21	0.729500237	3.48E-20
LOC100648602	non_repro	0.786264461	0.00635058	34.4688962	2.35E-260	0.783275328	1.21E-258
LOC100648717	non_repro	0.707820968	0.02067881	8.8491988	8.81E-19	0.727328197	4.20E-18
LOC100648857	non_repro	0.679970522	0.01509307	10.8658621	1.68E-27	0.71615805	1.11E-26

LOC100649041	non_repro	0.667810396	0.04378533	3.53794965	0.00040325	0.717840087	0.00063078
LOC100649123	non_repro	0.652352933	0.00544857	26.1977579	2.82E-151	0.798816918	8.57E-150
LOC100649244	non_repro	0.813101115	0.01698067	13.1582719	1.53E-39	0.758281513	1.33E-38
LOC100649421	non_repro	0.757397529	0.0090716	23.0597499	1.17E-117	0.711625046	2.77E-116
LOC100649524	non_repro	0.809904595	0.03031395	7.36119551	1.82E-13	0.779473866	6.55E-13
LOC100649753	non_repro	0.780600756	0.01869754	11.6251794	3.07E-31	0.753426324	2.25E-30
LOC100649760	non_repro	0.676084424	0.02407582	6.69317535	2.18E-11	0.72259014	6.90E-11
LOC100650186	non_repro	0.717564538	0.00792464	23.8456427	1.12E-125	0.729431366	2.84E-124
LOC100650242	non_repro	0.847076944	0.04298442	5.15884107	2.48E-07	0.826855452	5.63E-07
LOC100650244	non_repro	0.739468022	0.03474835	5.78383781	7.30E-09	0.761632715	1.89E-08
LOC100650256	non_repro	0.697028179	0.08540747	2.06014945	0.03938426	0.793171194	0.04602226
LOC100650626	non_repro	0.92187085	0.00430072	41.3327355	0	0.946858952	0
LOC100650837	non_repro	0.913232505	0.01224046	15.2371134	2.01E-52	0.848654015	2.25E-51
LOC100651045	non_repro	0.725879427	0.0305055	6.35191748	2.13E-10	0.714452342	6.22E-10
LOC100651252	non_repro	0.737214933	0.03091329	6.46452969	1.02E-10	0.711935879	3.04E-10
LOC100651324	non_repro	0.672312046	0.02449319	6.46412763	1.02E-10	0.707943715	3.05E-10
LOC100651336	non_repro	0.718866933	0.01484373	12.7824085	2.06E-37	0.702270061	1.73E-36
LOC100651419	non_repro	0.754152112	0.01844904	11.2644845	1.96E-29	0.742867483	1.37E-28
LOC100651556	non_repro	0.732433403	0.02223541	8.87536171	6.97E-19	0.762170295	3.34E-18
LOC100651785	non_repro	0.825656588	0.02707488	8.26820468	1.36E-16	0.837367106	5.85E-16
LOC100651786	non_repro	0.789655207	0.00744032	29.5316486	1.13E-191	0.791206373	4.26E-190
LOC100651908	non_repro	0.816871011	0.03138642	7.12679592	1.03E-12	0.838698043	3.52E-12
LOC100651943	non_repro	0.767249932	0.02464071	8.64486941	5.39E-18	0.732907569	2.48E-17
LOC100652111	non_repro	0.674555237	0.05340107	2.99632891	0.00273252	0.72636093	0.00380064
LOC100652132	non_repro	0.796531383	0.02000374	11.0571625	2.02E-28	0.821734602	1.36E-27
LOC100652299	non_repro	0.703830436	0.03060836	5.89506238	3.75E-09	0.713895968	9.96E-09
LOC105665810	non_repro	0.794464925	0.02799349	7.88673104	3.10E-15	0.838885862	1.24E-14
LOC105665975	non_repro	0.804610011	0.03165109	7.03017431	2.06E-12	0.708710452	6.95E-12
LOC105666051	non_repro	0.74500764	0.0134511	15.142237	8.53E-52	0.745760983	9.46E-51
LOC105666165	non_repro	0.718690217	0.01140267	16.6307069	4.18E-62	0.703711439	5.36E-61

LOC105666343	non_repro	0.819577248	0.04263945	5.24865416	1.53E-07	0.789798513	3.54E-07
LOC105666469	non_repro	0.792285508	0.00945868	23.2927109	5.26E-120	0.801523288	1.26E-118
LOC105666638	non_repro	0.76590541	0.02900934	7.32603981	2.37E-13	0.796736156	8.47E-13
LOC105666711	non_repro	0.697802315	0.0189001	9.33704405	9.91E-21	0.73518166	5.16E-20
LOC105666829	non_repro	0.702084328	0.02053061	8.73343044	2.47E-18	0.705564418	1.16E-17
LOC105666882	non_repro	0.929767912	0.01314651	12.8305717	1.11E-37	0.93372898	9.37E-37
LOC105667011	non_repro	0.662506285	0.02657622	5.67457808	1.39E-08	0.704354951	3.52E-08
LOC105667013	non_repro	0.811661256	0.01148141	19.4501134	2.91E-84	0.744566428	4.95E-83
LOC105667035	non_repro	0.753473511	0.00509232	40.7527335	0	0.722023507	0
LOC105667037	non_repro	0.832582809	0.00289424	77.2518655	0	0.841393142	0
LOC105667038	non_repro	0.697131034	0.07128492	2.46926277	0.01353918	0.770207772	0.01699538
LOC105667042	non_repro	0.746333812	0.0455571	4.48459233	7.31E-06	0.720732093	1.43E-05
LOC105667061	non_repro	0.783235111	0.00774872	28.1466011	2.64E-174	0.785044704	9.14E-173
LOC105667073	non_repro	0.742834825	0.01201266	16.8686516	7.65E-64	0.717648944	1.01E-62
LOC105667086	non_repro	0.784357198	0.01311613	16.6513959	2.96E-62	0.78098703	3.81E-61

Supplementary 3.0.2: Enriched GO terms for genes showing allele-specific expression in either both castes, just reproductive workers or just sterile workers.

Allelically expressed genes in both castes.

term_ID	description	frequency	log10 p-value
GO:0000469	cleavage involved in rRNA processing	0.05%	-2.3396
GO:0046960	sensitization	0.00%	-1.9186
GO:0072488	ammonium transmembrane transport	0.09%	-1.9186
GO:2000117	negative regulation of cysteine-type endopeptidase activity	0.02%	-2.3396
GO:0010466	negative regulation of peptidase activity	0.17%	-1.8288
GO:2001268	negative regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	0.00%	-2.2184
GO:1900117	regulation of execution phase of apoptosis	0.01%	-1.5245
GO:2001271	negative regulation of cysteine-type endopeptidase activity involved in execution phase of apoptosis	0.00%	-1.7438
GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	0.04%	-1.5236
GO:0006921	cellular component disassembly involved in execution phase of apoptosis	0.01%	-1.3242
GO:0044247	cellular polysaccharide catabolic process	0.10%	-1.381
GO:0009251	glucan catabolic process	0.10%	-1.381
GO:0061484	hematopoietic stem cell homeostasis	0.00%	-1.7438
GO:0044205	'de novo' UMP biosynthetic process	0.22%	-1.7438
GO:0046049	UMP metabolic process	0.27%	-1.5245
GO:0009174	pyrimidine ribonucleoside monophosphate biosynthetic process	0.28%	-1.4466
GO:0006207	'de novo' pyrimidine nucleobase biosynthetic process	0.19%	-1.4466
GO:0090263	positive regulation of canonical Wnt signaling pathway	0.02%	-2.2435
GO:0030111	regulation of Wnt signaling pathway	0.07%	-1.9596
GO:0198738	cell-cell signaling by wnt	0.14%	-1.4615
GO:0010378	temperature compensation of the circadian clock	0.00%	-1.7438
GO:0002931	response to ischemia	0.00%	-1.3242
GO:0043063	intercellular bridge organization	0.00%	-1.3242
GO:0061709	reticulophagy	0.00%	-2.2184
GO:0001826	inner cell mass cell differentiation	0.00%	-1.9186
GO:0043570	maintenance of DNA repeat elements	0.06%	-1.9186

GO:1904901	positive regulation of myosin II filament organization	0.00%	-2.2184
GO:0007166	cell surface receptor signaling pathway	0.92%	-1.3606
GO:0060279	positive regulation of ovulation	0.00%	-2.2184
GO:1903356	positive regulation of distal tip cell migration	0.00%	-2.2184
GO:1902903	regulation of supramolecular fiber organization	0.17%	-1.7772
GO:0010891	negative regulation of sequestering of triglyceride	0.00%	-1.9186
GO:0001889	liver development	0.02%	-1.9138
GO:0048538	thymus development	0.01%	-1.6202
GO:0010898	positive regulation of triglyceride catabolic process	0.00%	-1.6202
GO:1900244	positive regulation of synaptic vesicle endocytosis	0.00%	-1.6202
GO:1903421	regulation of synaptic vesicle recycling	0.00%	-1.381
GO:1903382	negative regulation of endoplasmic reticulum stress-induced neuron intrinsic apoptotic signaling path	0.00%	-2.2184
GO:1903298	negative regulation of hypoxia-induced intrinsic apoptotic signaling pathway	0.00%	-2.2184
GO:1900037	regulation of cellular response to hypoxia	0.00%	-1.3242
GO:2000331	regulation of terminal button organization	0.00%	-1.3242
GO:0045035	sensory organ precursor cell division	0.00%	-1.5245
GO:0048025	negative regulation of mRNA splicing, via spliceosome	0.00%	-1.4466
GO:0006610	ribosomal protein import into nucleus	0.00%	-1.4466
GO:0010635	regulation of mitochondrial fusion	0.00%	-1.4466
GO:0035114	imaginal disc-derived appendage morphogenesis	0.02%	-1.4252
GO:0048800	antennal morphogenesis	0.00%	-1.381
GO:0030263	apoptotic chromosome condensation	0.00%	-1.9186
GO:0051574	positive regulation of histone H3-K9 methylation	0.00%	-1.5245
GO:0031061	negative regulation of histone methylation	0.01%	-1.5245
GO:0006996	organelle organization	3.60%	-1.3485
GO:0045657	positive regulation of monocyte differentiation	0.00%	-2.2184
GO:0090257	regulation of muscle system process	0.04%	-1.4718
GO:0045987	positive regulation of smooth muscle contraction	0.00%	-1.6202
GO:0010614	negative regulation of cardiac muscle hypertrophy	0.00%	-1.4466
GO:0061179	negative regulation of insulin secretion involved in cellular response to glucose stimulus	0.00%	-2.2184

GO:0048806	genitalia development	0.01%	-1.8288
GO:0000710	meiotic mismatch repair	0.01%	-1.7438
GO:1903318	negative regulation of protein maturation	0.01%	-1.4393
GO:0070613	regulation of protein processing	0.02%	-1.3497
GO:1990001	inhibition of cysteine-type endopeptidase activity involved in apoptotic process	0.00%	-1.5245
GO:0097341	zymogen inhibition	0.00%	-1.5245
GO:0000472	endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rF	0.02%	-1.7438
GO:0000480	endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	0.02%	-1.6202
GO:0034471	ncRNA 5'-end processing	0.05%	-1.381
GO:0000447	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistroni	0.02%	-1.5245
GO:0048536	spleen development	0.01%	-1.4466
GO:0009129	pyrimidine nucleoside monophosphate metabolic process	0.34%	-1.381
GO:0042274	ribosomal small subunit biogenesis	0.26%	-1.5603
GO:0007615	anesthesia-resistant memory	0.00%	-1.4466
GO:0007313	maternal specification of dorsal/ventral axis, oocyte, soma encoded	0.00%	-1.7438
GO:0007301	female germline ring canal formation	0.00%	-1.4466
GO:0030723	ovarian fusome organization	0.00%	-1.4466
GO:0030242	pexophagy	0.01%	-1.6202
GO:0032271	regulation of protein polymerization	0.14%	-1.4081
GO:0031116	positive regulation of microtubule polymerization	0.01%	-1.5245
GO:0060298	positive regulation of sarcomere organization	0.00%	-1.4466
GO:0051493	regulation of cytoskeleton organization	0.23%	-1.3086
GO:0043069	negative regulation of programmed cell death	0.18%	-1.7123
GO:2001234	negative regulation of apoptotic signaling pathway	0.04%	-1.4931
GO:0010941	regulation of cell death	0.34%	-1.6571
GO:0006915	apoptotic process	0.41%	-1.7056
GO:0061723	glycophagy	0.00%	-1.6202
GO:0046673	negative regulation of compound eye retinal cell programmed cell death	0.00%	-1.4466
GO:0007292	female gamete generation	0.06%	-1.611
GO:0044705	multi-organism reproductive behavior	0.02%	-1.3088

GO:0007619	courtship behavior	0.01%	-1.5059
GO:0007298	border follicle cell migration	0.01%	-1.4554
GO:1903131	mononuclear cell differentiation	0.01%	-1.4466
GO:0016080	synaptic vesicle targeting	0.00%	-1.3242
GO:0072375	medium-term memory	0.00%	-1.4466
GO:0048815	hermaphrodite genitalia morphogenesis	0.00%	-1.9186
GO:0030717	karyosome formation	0.00%	-1.3242

Allelically expressed genes in reproductive workers.

term_ID	description	frequency	log10 p
GO:0045464	R8 cell fate specification	0.00%	-3.7982
GO:0001752	compound eye photoreceptor fate commitment	0.00%	-2.321
GO:0001754	eye photoreceptor cell differentiation	0.02%	-1.8391
GO:0016330	second mitotic wave involved in compound eye morphogenesis	0.00%	-3.0992
GO:0045465	R8 cell differentiation	0.00%	-2.8951
GO:0048665	neuron fate specification	0.01%	-2.7982
GO:0046552	photoreceptor cell fate commitment	0.00%	-2.293
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	0.37%	-1.3541
GO:0007541	sex determination, primary response to X:A ratio	0.00%	-3.321
GO:0035019	somatic stem cell population maintenance	0.01%	-2.5429
GO:0061382	Malpighian tubule tip cell differentiation	0.00%	-3.321
GO:0030707	ovarian follicle cell development	0.02%	-1.7451
GO:0002064	epithelial cell development	0.07%	-1.5781
GO:0002065	columnar/cuboidal epithelial cell differentiation	0.04%	-1.6398
GO:0061326	renal tubule development	0.02%	-2.3068
GO:0098727	maintenance of cell number	0.04%	-2.0347
GO:0007292	female gamete generation	0.06%	-1.3557
GO:0007281	germ cell development	0.09%	-1.3082
GO:0045596	negative regulation of cell differentiation	0.13%	-1.5677
GO:0007422	peripheral nervous system development	0.02%	-2.145
GO:0061101	neuroendocrine cell differentiation	0.00%	-3.0992
GO:0001655	urogenital system development	0.07%	-1.8897
GO:0008407	chaeta morphogenesis	0.00%	-2.4971
GO:0045165	cell fate commitment	0.09%	-1.5381
GO:0051962	positive regulation of nervous system development	0.09%	-1.7263
GO:0010720	positive regulation of cell development	0.09%	-1.691

GO:0050767	regulation of neurogenesis	0.15%	-1.4907
GO:0045666	positive regulation of neuron differentiation	0.06%	-1.9005
GO:0048749	compound eye development	0.02%	-1.652
GO:0090596	sensory organ morphogenesis	0.08%	-1.5405
GO:0007538	primary sex determination	0.00%	-2.8439
GO:0018993	somatic sex determination	0.00%	-2.8439

Allelically expressed genes in sterile workers.

term_ID	description	frequency	log10 p
GO:0006238	CMP salvage	0.00%	-3.1961
GO:0046132	pyrimidine ribonucleoside biosynthetic process	0.40%	-2.197
GO:0009220	pyrimidine ribonucleotide biosynthetic process	0.42%	-2.1181
GO:0032262	pyrimidine nucleotide salvage	0.04%	-2.8952
GO:0009209	pyrimidine ribonucleoside triphosphate biosynthetic process	0.14%	-2.3516
GO:0044206	UMP salvage	0.04%	-2.8952
GO:0044211	CTP salvage	0.02%	-2.8952
GO:0046049	UMP metabolic process	0.27%	-2.4976
GO:0009174	pyrimidine ribonucleoside monophosphate biosynthetic process	0.28%	-2.4185
GO:0046036	CTP metabolic process	0.14%	-2.3516
GO:0043174	nucleoside salvage	0.15%	-2.2937
GO:0040011	locomotion	1.00%	-1.3915
GO:0014722	regulation of skeletal muscle contraction by calcium ion signaling	0.00%	-2.8952
GO:0045989	positive regulation of striated muscle contraction	0.00%	-2.5944
GO:0003009	skeletal muscle contraction	0.01%	-2.3516
GO:0006937	regulation of muscle contraction	0.03%	-1.6809
GO:0009698	phenylpropanoid metabolic process	0.02%	-2.3516
GO:0046274	lignin catabolic process	0.01%	-2.4976
GO:1905552	positive regulation of protein localization to endoplasmic reticulum	0.00%	-2.8952
GO:0043062	extracellular structure organization	0.06%	-1.3521
GO:0006909	phagocytosis	0.05%	-1.312
GO:0008302	female germline ring canal formation, actin assembly	0.00%	-2.7192
GO:0007303	cytoplasmic transport, nurse cell to oocyte	0.00%	-2.1558
GO:0030725	germline ring canal formation	0.00%	-2.3516
GO:0035023	regulation of Rho protein signal transduction	0.13%	-1.6316
GO:0050879	multicellular organismal movement	0.01%	-2.1558
GO:0048149	behavioral response to ethanol	0.01%	-1.8367

GO:0007635	chemosensory behavior	0.02%	-1.5197
GO:0045611	negative regulation of hemocyte differentiation	0.00%	-2.4976
GO:0035204	negative regulation of lamellocyte differentiation	0.00%	-2.5944
GO:0035168	larval lymph gland hemocyte differentiation	0.00%	-2.197
GO:0045613	regulation of plasmatocyte differentiation	0.00%	-2.4976
GO:0030431	sleep	0.01%	-1.6316
GO:0051130	positive regulation of cellular component organization	0.37%	-1.7567
GO:0019932	second-messenger-mediated signaling	0.08%	-1.3521
GO:0008340	determination of adult lifespan	0.02%	-1.4854
GO:0048542	lymph gland development	0.00%	-1.722
GO:0015937	coenzyme A biosynthetic process	0.15%	-2.3516
GO:0033866	nucleoside bisphosphate biosynthetic process	0.16%	-2.3516
GO:0033875	ribonucleoside bisphosphate metabolic process	0.24%	-2.197
GO:0046129	purine ribonucleoside biosynthetic process	0.92%	-1.5875
GO:0034032	purine nucleoside bisphosphate metabolic process	0.24%	-2.197
GO:0048138	germ-line cyst encapsulation	0.00%	-2.4185
GO:0030708	germarium-derived female germ-line cyst encapsulation	0.00%	-2.5944
GO:0060298	positive regulation of sarcomere organization	0.00%	-2.4185
GO:0030239	myofibril assembly	0.02%	-1.5288
GO:0051149	positive regulation of muscle cell differentiation	0.02%	-1.9426
GO:0051153	regulation of striated muscle cell differentiation	0.02%	-1.7837
GO:0009129	pyrimidine nucleoside monophosphate metabolic process	0.34%	-2.3516
GO:0048580	regulation of post-embryonic development	0.03%	-2.1558
GO:0046035	CMP metabolic process	0.00%	-3.1961
GO:0031034	myosin filament assembly	0.00%	-2.3516
GO:0030241	skeletal muscle myosin thick filament assembly	0.00%	-2.5944
GO:0003012	muscle system process	0.08%	-1.3175
GO:0009147	pyrimidine nucleoside triphosphate metabolic process	0.25%	-2.1558
GO:0009124	nucleoside monophosphate biosynthetic process	1.49%	-1.3521
GO:0009142	nucleoside triphosphate biosynthetic process	0.65%	-1.41

GO:0048646	anatomical structure formation involved in morphogenesis	0.41%	-1.6952
GO:0006206	pyrimidine nucleobase metabolic process	0.27%	-2.0834
GO:0072528	pyrimidine-containing compound biosynthetic process	0.90%	-1.8367
GO:0006220	pyrimidine nucleotide metabolic process	0.67%	-1.876
GO:0006213	pyrimidine nucleoside metabolic process	0.46%	-2.0215
GO:0008045	motor neuron axon guidance	0.01%	-1.609
GO:1902115	regulation of organelle assembly	0.05%	-1.4386
GO:0045595	regulation of cell differentiation	0.35%	-1.5848
GO:1901659	glycosyl compound biosynthetic process	1.47%	-1.4772
GO:0042278	purine nucleoside metabolic process	2.01%	-1.3287
GO:0035166	post-embryonic hemopoiesis	0.00%	-1.7366
GO:1903706	regulation of hemopoiesis	0.07%	-1.4241
GO:0008355	olfactory learning	0.01%	-1.7366
GO:0007612	learning	0.03%	-1.3898
GO:0007616	long-term memory	0.01%	-1.6434
GO:0030036	actin cytoskeleton organization	0.38%	-2.1178
GO:0051495	positive regulation of cytoskeleton organization	0.12%	-1.6338

Supplementary 3.0.3: mapping statistics for the qhole genome bilsulfite sequencing libraries to the reference genome, Bter_1.0, using bismark.

Sample	Number of unique mapped	Num C's analysed	Mapping efficency (%)
J1_NR	28698284	1087748846	65.5
J1_R	27571744	1060315142	63
J5_NR	26855289	1059186214	61.5
J5_R	28222365	1020744881	64.3
J8_NR	26855289	1059186214	63.1
J8_R	28052314	1069428548	64.1

Supplementary 3.0.4: allelically methylated regions identified in reproductive workers.

scaffold	amr_start	amr_end	pval	gene	feature
NC_015762.1	367039	367558	4.07E-07	LOC100646694	gene
NC_015762.1	473192	474345	2.31E-10	LOC100643270	gene
NC_015762.1	493944	494642	4.52E-07	LOC100643147	gene
NC_015762.1	531804	533457	2.71E-11	NA	NA
NC_015762.1	535809	536556	6.68E-08	LOC100652148	gene
NC_015762.1	535809	536556	6.68E-08	LOC100652148	exon
NC_015762.1	543007	543989	3.00E-10	LOC100642673	gene
NC_015762.1	564528	565277	9.45E-07	LOC100642190	gene
NC_015762.1	946306	947331	7.74E-13	LOC100650629	gene
NC_015762.1	946306	947331	7.74E-13	LOC100650629	exon
NC_015762.1	946306	947331	7.74E-13	LOC105666912	gene
NC_015762.1	950290	950844	7.47E-11	LOC100650511	gene
NC_015762.1	950290	950844	7.47E-11	LOC100650511	exon
NC_015762.1	2025582	2026757	1.81E-09	LOC100642191	gene
NC_015762.1	4119909	4120613	2.30E-08	LOC100643434	gene
NC_015762.1	4119909	4120613	2.30E-08	LOC100643874	gene
NC_015762.1	4149169	4150225	1.63E-08	NA	NA
NC_015762.1	4407836	4408511	4.33E-08	LOC100646250	gene
NC_015762.1	4862235	4863303	6.25E-14	LOC100644473	gene
NC_015762.1	4862235	4863303	6.25E-14	LOC100644473	exon
NC_015762.1	4862235	4863303	6.25E-14	LOC100644473	exon
NC_015762.1	6273602	6274307	2.16E-08	LOC100651357	gene
NC_015762.1	6273602	6274307	2.16E-08	LOC100651357	exon
NC_015762.1	6307796	6308331	1.20E-09	LOC100648082	gene
NC_015762.1	6563227	6564090	9.92E-08	LOC100643839	gene
NC_015762.1	6968788	6969418	3.68E-09	LOC100644670	gene
NC_015762.1	7326268	7330570	8.67E-08	NA	NA

NC_015762.1	7413801	7416257	1.09E-08	LOC100644474	gene
NC_015762.1	10122170	10123337	4.12E-08	LOC100645740	exon
NC_015762.1	10122170	10123337	4.12E-08	LOC100645740	gene
NC_015762.1	11909337	11910798	3.96E-08	LOC105666120	gene
NC_015762.1	11917861	11918788	2.33E-12	LOC100647802	gene
NC_015762.1	11924257	11925181	1.59E-09	LOC100648045	gene
NC_015762.1	16821730	16822751	3.04E-07	LOC100644430	gene
NC_015763.1	1120925	1121735	6.54E-07	LOC100646134	gene
NC_015763.1	2420152	2420783	1.47E-08	LOC100644837	gene
NC_015763.1	2420152	2420783	1.47E-08	LOC100644837	intron
NC_015763.1	2444911	2445951	1.36E-07	LOC100645311	gene
NC_015763.1	2444911	2445951	1.36E-07	LOC100645434	gene
NC_015763.1	2461471	2461985	1.11E-07	NA	NA
NC_015763.1	2465555	2467208	5.59E-09	NA	NA
NC_015763.1	2747568	2750400	5.50E-07	LOC100647328	gene
NC_015763.1	3161460	3162465	7.62E-09	LOC100648084	gene
NC_015763.1	3316670	3317920	1.42E-07	LOC100650027	gene
NC_015763.1	3555245	3557504	7.18E-10	LOC100651983	gene
NC_015763.1	4553072	4553609	5.05E-08	LOC100644390	gene
NC_015763.1	5208981	5210056	4.90E-09	LOC100650675	gene
NC_015763.1	5459937	5460694	7.27E-09	LOC100648389	gene
NC_015763.1	7973648	7974339	3.57E-08	LOC100646170	gene
NC_015763.1	8386823	8387814	9.15E-07	LOC100648426	gene
NC_015763.1	11992319	11993224	4.29E-07	LOC100643559	gene
NC_015763.1	13318102	13318983	5.20E-08	LOC100645586	gene
NC_015763.1	13318102	13318983	5.20E-08	LOC100645586	intron
NC_015763.1	13477395	13478526	2.44E-10	LOC100646334	gene
NC_015764.1	330860	331767	2.54E-07	LOC100650595	gene
NC_015764.1	336572	337774	1.00E-06	LOC100650358	gene
NC_015764.1	430355	431303	6.91E-10	LOC100649724	gene

NC_015764.1	430355	431303	6.91E-10	LOC100649724	exon
NC_015764.1	970034	970786	1.30E-07	LOC100646018	gene
NC_015764.1	1082222	1082975	4.12E-07	LOC100645437	gene
NC_015764.1	1082222	1082975	4.12E-07	LOC100645437	exon
NC_015764.1	2268218	2268946	4.45E-08	LOC100648931	exon
NC_015764.1	2268218	2268946	4.45E-08	LOC100648931	gene
NC_015764.1	2942178	2942945	6.72E-08	LOC100647213	gene
NC_015764.1	3883484	3885409	2.22E-16	LOC100642600	gene
NC_015764.1	3883484	3885409	2.22E-16	LOC100642600	exon
NC_015764.1	6420128	6421355	7.74E-07	LOC100642991	gene
NC_015764.1	9061728	9063796	2.00E-08	LOC100642482	exon
NC_015764.1	9061728	9063796	2.00E-08	LOC100642482	gene
NC_015764.1	9072521	9073762	1.53E-10	LOC100647767	gene
NC_015764.1	9340660	9342768	8.62E-07	LOC100644245	gene
NC_015764.1	10425349	10426157	1.19E-11	NA	NA
NC_015764.1	11551726	11552961	1.87E-09	LOC100649016	gene
NC_015764.1	11551726	11552961	1.87E-09	LOC100649016	exon
NC_015764.1	13313220	13313796	9.58E-07	LOC100646405	gene
NC_015764.1	13313220	13313796	9.58E-07	LOC100649205	gene
NC_015764.1	14303402	14303940	3.72E-08	LOC100647292	gene
NC_015764.1	14526747	14527924	6.22E-07	LOC100643685	gene
NC_015765.1	39414	40362	8.27E-07	LOC100649371	gene
NC_015765.1	521112	521725	5.13E-12	LOC100649804	gene
NC_015765.1	521112	521725	5.13E-12	LOC100649804	intron
NC_015765.1	1449048	1450208	7.18E-07	LOC105667203	exon
NC_015765.1	1449048	1450208	7.18E-07	LOC105667203	gene
NC_015765.1	2354613	2355187	7.90E-08	LOC100642320	gene
NC_015765.1	3771597	3772502	6.04E-10	LOC100647495	gene
NC_015765.1	4130868	4131886	1.50E-11	LOC100647807	gene
NC_015765.1	6101422	6102089	7.39E-07	LOC100651035	gene

NC_015765.1	7367492	7368692	7.86E-11	LOC100645239	gene
NC_015765.1	7371259	7373325	1.94E-07	LOC100644881	exon
NC_015765.1	7371259	7373325	1.94E-07	LOC100644881	gene
NC_015765.1	7724195	7724996	9.52E-13	NA	NA
NC_015765.1	7733806	7734454	5.55E-16	NA	NA
NC_015765.1	9766284	9767303	1.83E-08	LOC100645708	gene
NC_015765.1	11094831	11095708	7.43E-07	LOC100651123	gene
NC_015765.1	11517823	11518406	1.09E-12	LOC100648856	gene
NC_015765.1	13671353	13671946	9.82E-07	LOC100651598	gene
NC_015766.1	95590	96499	2.30E-08	LOC100642364	gene
NC_015766.1	421114	422241	2.24E-08	LOC100647419	gene
NC_015766.1	668693	669210	0	LOC105665778	gene
NC_015766.1	4822642	4824203	4.39E-13	LOC105665753	gene
NC_015766.1	4822642	4824203	4.39E-13	LOC105665753	exon
NC_015766.1	4822642	4824203	4.39E-13	LOC105665753	exon
NC_015766.1	4822642	4824203	4.39E-13	LOC105665753	exon
NC_015766.1	4822642	4824203	4.39E-13	LOC105665753	exon
NC_015766.1	5189379	5190091	1.35E-07	LOC105665745	gene
NC_015766.1	6087420	6088485	2.42E-07	NA	NA
NC_015766.1	6793009	6794544	9.56E-07	LOC100651001	gene
NC_015766.1	6834950	6835948	3.87E-08	LOC100649572	gene
NC_015766.1	7308304	7309375	1.30E-07	LOC100644289	exon
NC_015766.1	7308304	7309375	1.30E-07	LOC100644289	gene
NC_015766.1	7308304	7309375	1.30E-07	LOC100645710	gene
NC_015766.1	7411219	7413823	2.22E-07	LOC105665731	gene
NC_015766.1	8068872	8069385	2.39E-12	LOC100647333	gene
NC_015766.1	8068872	8069385	2.39E-12	LOC105665725	exon
NC_015766.1	8068872	8069385	2.39E-12	LOC105665725	gene
NC_015766.1	8505717	8506617	9.75E-13	LOC100644844	gene
NC_015766.1	8505717	8506617	9.75E-13	LOC100644844	intron

NC_015766.1	8538257	8539107	4.05E-07	LOC100649290	gene
NC_015766.1	9373530	9375012	5.52E-10	LOC100650881	gene
NC_015766.1	9404556	9405118	1.03E-08	LOC100643321	gene
NC_015767.1	1436198	1436720	2.25E-07	LOC100651157	gene
NC_015767.1	4539876	4590253	0	NA	NA
NC_015767.1	4663148	4663679	8.64E-08	NA	NA
NC_015767.1	4916698	4918429	5.43E-07	LOC100645004	gene
NC_015767.1	8694658	8695232	3.98E-07	LOC100650201	gene
NC_015767.1	9656252	9656871	1.70E-14	NA	NA
NC_015767.1	12071832	12072431	2.63E-12	LOC100642691	gene
NC_015767.1	12071832	12072431	2.63E-12	LOC100642691	intron
NC_015767.1	12074507	12075461	1.24E-07	LOC100642569	gene
NC_015767.1	12150388	12151380	6.09E-11	LOC100651079	gene
NC_015767.1	12495567	12496267	1.32E-07	LOC100650845	gene
NC_015767.1	12500165	12500905	5.34E-09	LOC100651759	gene
NC_015768.1	569455	569990	0	LOC100648438	gene
NC_015768.1	569455	569990	0	LOC105665864	gene
NC_015768.1	573263	573776	9.66E-15	LOC100648438	gene
NC_015768.1	573263	573776	9.66E-15	LOC105665864	gene
NC_015768.1	2045933	2047307	1.85E-08	LOC100642997	exon
NC_015768.1	2045933	2047307	1.85E-08	LOC100642997	gene
NC_015768.1	2055946	2056770	2.67E-09	LOC100643118	gene
NC_015768.1	2058285	2058816	5.68E-09	LOC100643118	gene
NC_015768.1	2083745	2085697	7.94E-11	LOC100643806	gene
NC_015768.1	2105990	2106730	2.33E-08	NA	NA
NC_015768.1	2292896	2293615	2.32E-10	LOC100646623	gene
NC_015768.1	2407903	2408537	3.32E-09	LOC100648475	gene
NC_015768.1	2644222	2645130	1.05E-07	LOC100651248	gene
NC_015768.1	2651977	2654335	1.33E-07	LOC100651760	gene
NC_015768.1	4199216	4200943	7.38E-07	LOC100644254	gene

NC_015768.1	4730249	4731117	2.85E-08	LOC100652280	gene
NC_015768.1	4730249	4731117	2.85E-08	LOC100652280	exon
NC_015768.1	4968193	4969296	1.10E-10	LOC100649626	gene
NC_015768.1	5177240	5178464	5.84E-08	NA	NA
NC_015768.1	5388165	5388786	3.36E-07	LOC100648597	gene
NC_015768.1	6599163	6600035	6.30E-08	LOC100642693	gene
NC_015768.1	6615739	6617661	6.55E-08	LOC100643807	gene
NC_015768.1	6615739	6617661	6.55E-08	LOC100643807	exon
NC_015768.1	11162664	11163249	2.05E-07	LOC100644135	gene
NC_015768.1	11162664	11163249	2.05E-07	LOC100644135	exon
NC_015768.1	11578621	11579198	1.83E-11	NA	NA
NC_015768.1	13305979	13306877	2.07E-07	LOC100651130	gene
NC_015768.1	13568190	13569156	3.17E-09	LOC100652163	gene
NC_015768.1	14737762	14738639	9.84E-08	LOC100644258	gene
NC_015768.1	14756691	14758029	3.31E-08	LOC100644806	gene
NC_015768.1	14817428	14818605	8.40E-07	LOC100645524	exon
NC_015768.1	14817428	14818605	8.40E-07	LOC100645524	gene
NC_015768.1	16000586	16001878	6.26E-08	LOC100650770	gene
NC_015768.1	17491274	17492413	1.11E-16	LOC100644607	gene
NC_015768.1	17491274	17492413	1.11E-16	LOC100644607	exon
NC_015768.1	17664535	17668774	1.86E-10	LOC100647903	gene
NC_015769.1	208825	210356	3.98E-07	LOC100644296	gene
NC_015769.1	216711	218268	7.73E-07	LOC100646661	gene
NC_015769.1	1467993	1469230	6.24E-08	LOC100643936	gene
NC_015769.1	1467993	1469230	6.24E-08	LOC100643936	exon
NC_015769.1	2770282	2771880	9.68E-11	LOC100648865	gene
NC_015769.1	2933350	2934584	1.37E-08	LOC100650204	gene
NC_015769.1	3268386	3269732	3.07E-07	LOC100642640	gene
NC_015769.1	4969478	4971368	4.28E-09	LOC100651406	gene
NC_015769.1	5027347	5029044	2.63E-07	LOC100651956	gene

NC_015769.1	5160796	5162003	1.02E-09	LOC100644563	gene
NC_015769.1	7548538	7549196	2.74E-09	LOC100644446	gene
NC_015769.1	7958780	7959772	8.88E-16	LOC100645450	gene
NC_015769.1	8426483	8427376	1.29E-08	LOC100648096	gene
NC_015769.1	8426483	8427376	1.29E-08	LOC100648096	exon
NC_015769.1	8490950	8492986	0	LOC100644808	gene
NC_015770.1	82353	83483	6.18E-07	LOC100649537	gene
NC_015770.1	101342	101987	6.74E-12	LOC100649297	gene
NC_015770.1	243301	244285	5.07E-11	LOC100645494	gene
NC_015770.1	613038	613751	0	LOC100644765	gene
NC_015770.1	1034167	1035026	7.18E-10	LOC100645451	exon
NC_015770.1	1034167	1035026	7.18E-10	LOC100645451	gene
NC_015770.1	1095088	1096029	1.26E-10	LOC100643245	gene
NC_015770.1	1188954	1190217	8.44E-11	LOC100651720	gene
NC_015770.1	1507401	1507946	1.38E-09	LOC100642888	gene
NC_015770.1	1551604	1552378	7.54E-08	LOC100648560	gene
NC_015770.1	2256493	2258026	2.48E-11	LOC100642571	gene
NC_015770.1	2319102	2319614	2.00E-07	LOC100643850	gene
NC_015770.1	2319102	2319614	2.00E-07	LOC100648097	gene
NC_015770.1	3225646	3226314	2.89E-08	LOC100643287	gene
NC_015770.1	3329423	3329956	6.47E-09	LOC100651885	gene
NC_015770.1	5668953	5669601	2.19E-07	LOC100645564	gene
NC_015770.1	5668953	5669601	2.19E-07	LOC105666051	gene
NC_015770.1	5668953	5669601	2.19E-07	LOC105666051	exon
NC_015770.1	8113304	8113845	5.07E-14	LOC100642214	gene
NC_015770.1	9147034	9148534	4.70E-09	LOC100651252	gene
NC_015770.1	11436610	11438052	7.92E-09	LOC100649538	gene
NC_015770.1	11444163	11445888	8.81E-12	LOC100649337	gene
NC_015770.1	11449662	11450183	1.91E-08	LOC100649217	gene
NC_015770.1	11449662	11450183	1.91E-08	LOC100649217	intron

NC_015770.1	12634121	12634623	3.98E-08	LOC100644895	gene
NC_015770.1	12634121	12634623	3.98E-08	LOC100644895	exon
NC_015770.1	12634121	12634623	3.98E-08	LOC100644895	exon
NC_015770.1	13317220	13320734	5.66E-14	LOC100643941	gene
NC_015770.1	13317220	13320734	5.66E-14	LOC100643941	intron
NC_015770.1	13638751	13639409	4.70E-10	LOC100644811	gene
NC_015770.1	13638751	13639409	4.70E-10	LOC100644932	gene
NC_015770.1	13638751	13639409	4.70E-10	LOC100644932	exon
NC_015770.1	14381123	14382305	9.77E-10	LOC100646788	gene
NC_015771.1	10	535	6.55E-15	LOC100651450	exon
NC_015771.1	10	535	6.55E-15	LOC100651450	exon
NC_015771.1	10	535	6.55E-15	LOC100651450	gene
NC_015771.1	1546713	1547464	6.60E-07	LOC100650691	gene
NC_015771.1	1584160	1585747	2.87E-08	LOC100651572	gene
NC_015771.1	2354017	2354613	3.14E-09	LOC100648946	gene
NC_015771.1	2470471	2471024	2.92E-10	LOC100650292	gene
NC_015771.1	3606343	3607303	3.39E-07	LOC105666151	exon
NC_015771.1	3606343	3607303	3.39E-07	LOC105666151	gene
NC_015771.1	3609281	3610141	6.67E-08	LOC100651335	gene
NC_015771.1	3616391	3618164	7.92E-09	LOC100650967	gene
NC_015771.1	7090703	7091239	2.71E-10	LOC100643659	gene
NC_015771.1	7090703	7091239	2.71E-10	LOC100643659	exon
NC_015771.1	8323429	8324445	1.20E-09	LOC100648642	gene
NC_015771.1	9281100	9283329	3.86E-07	LOC100645723	gene
NC_015771.1	9314502	9315379	3.99E-08	LOC100645254	gene
NC_015771.1	9314502	9315379	3.99E-08	LOC100645254	exon
NC_015771.1	10498564	10499699	2.66E-15	LOC100644372	gene
NC_015771.1	10832972	10833965	2.14E-09	LOC100648830	gene
NC_015771.1	11529378	11530565	1.48E-07	LOC100649459	gene
NC_015771.1	11923517	11924746	2.87E-09	NA	NA

NC_015772.1	1833470	1834113	2.65E-07	LOC100648449	gene
NC_015772.1	2150409	2151166	1.27E-08	LOC100646748	gene
NC_015772.1	2478801	2479329	9.75E-10	LOC100642815	gene
NC_015772.1	3759231	3760016	1.26E-09	LOC100644335	gene
NC_015772.1	3759231	3760016	1.26E-09	LOC100652167	gene
NC_015772.1	6575117	6575645	2.58E-07	LOC100651092	gene
NC_015772.1	6577590	6578647	4.09E-09	LOC100651092	gene
NC_015772.1	6755707	6757090	2.39E-12	LOC100648833	gene
NC_015772.1	6877593	6878095	1.23E-07	LOC100646718	gene
NC_015772.1	7513683	7515425	9.40E-09	LOC100650368	gene
NC_015772.1	7596455	7597347	7.65E-07	LOC100648990	gene
NC_015772.1	7653609	7654429	1.13E-09	LOC100647781	gene
NC_015772.1	7653609	7654429	1.13E-09	LOC105665622	gene
NC_015772.1	7653609	7654429	1.13E-09	LOC105665622	exon
NC_015772.1	7906749	7907607	1.04E-08	LOC105666257	gene
NC_015772.1	7979798	7980975	1.34E-14	LOC100645726	gene
NC_015772.1	8026122	8027148	5.30E-07	LOC100644972	gene
NC_015772.1	8153021	8154211	3.24E-07	LOC100642223	gene
NC_015772.1	8168863	8169377	4.80E-10	LOC100651892	gene
NC_015772.1	8168863	8169377	4.80E-10	LOC100651892	exon
NC_015772.1	8234686	8235385	1.41E-10	LOC100649664	gene
NC_015772.1	8234686	8235385	1.41E-10	LOC100649664	exon
NC_015772.1	8242302	8242802	4.93E-08	LOC100649777	gene
NC_015772.1	8257927	8258897	8.77E-15	NA	NA
NC_015772.1	8653940	8654753	8.31E-07	LOC100647746	gene
NC_015772.1	8697784	8698424	1.82E-10	LOC100646871	gene
NC_015772.1	8697784	8698424	1.82E-10	LOC100646871	exon
NC_015772.1	8730893	8731646	4.88E-07	LOC100646189	gene
NC_015772.1	9385840	9387665	0	LOC100643819	gene
NC_015772.1	9560063	9561157	1.70E-11	LOC100651609	gene

NC_015772.1	9560063	9561157	1.70E-11	LOC100651609	exon
NC_015772.1	9560063	9561157	1.70E-11	LOC100651609	exon
NC_015772.1	12134155	12137215	0	LOC100652318	gene
NC_015772.1	12134155	12137215	0	LOC100652318	exon
NC_015772.1	14623796	14624552	3.70E-10	LOC100652132	gene
NC_015772.1	14626504	14628040	0	LOC100652132	gene
NC_015772.1	14629926	14630550	0	NA	NA
NC_015772.1	14954193	14956549	8.76E-10	LOC100644858	gene
NC_015772.1	15439138	15440573	1.33E-11	LOC100650494	gene
NC_015772.1	15685079	15686349	1.82E-12	LOC100648221	gene
NC_015772.1	15856017	15858644	6.16E-07	LOC100645958	gene
NC_015772.1	15939450	15940698	0	LOC100643777	gene
NC_015772.1	15990253	15991479	1.36E-10	LOC100642736	gene
NC_015772.1	16567705	16568880	9.73E-09	LOC100651846	gene
NC_015772.1	16669538	16670182	2.20E-07	LOC100650856	gene
NC_015772.1	16729466	16732267	4.02E-08	LOC100647430	gene
NC_015773.1	8028191	8028834	4.73E-08	LOC100650337	gene
NC_015773.1	8183200	8183708	1.16E-07	LOC100646632	gene
NC_015773.1	8702835	8705195	6.88E-11	LOC100643011	gene
NC_015773.1	8707867	8708527	1.76E-07	LOC100643706	gene
NC_015773.1	8707867	8708527	1.76E-07	LOC100643706	exon
NC_015773.1	8746228	8747382	1.50E-09	LOC100642532	gene
NC_015773.1	9390040	9390608	1.98E-11	LOC100649591	gene
NC_015773.1	9390040	9390608	1.98E-11	LOC100649591	exon
NC_015773.1	11585640	11586331	7.69E-09	LOC100647702	gene
NC_015773.1	12212599	12213268	1.17E-07	LOC100643256	gene
NC_015773.1	12676473	12678133	2.36E-09	LOC100647077	gene
NC_015773.1	12692639	12693684	1.60E-14	LOC100644735	gene
NC_015773.1	12735323	12735836	8.39E-07	LOC100646154	gene
NC_015773.1	12809057	12809672	2.62E-07	NA	NA

NC_015774.1	3346059	3346941	1.58E-08	LOC100645651	gene
NC_015774.1	3346059	3346941	1.58E-08	LOC105666384	exon
NC_015774.1	3346059	3346941	1.58E-08	LOC105666384	gene
NC_015774.1	4019188	4020073	1.11E-11	NA	NA
NC_015774.1	5693008	5694357	1.66E-07	LOC100642774	gene
NC_015774.1	6381860	6383332	5.80E-10	LOC100647750	gene
NC_015774.1	7695525	7696940	6.71E-08	LOC100650252	gene
NC_015774.1	8466303	8466919	7.09E-08	LOC100648721	gene
NC_015774.1	8591008	8591639	4.66E-13	LOC100648143	gene
NC_015775.1	126357	126886	2.89E-12	LOC100646678	gene
NC_015775.1	643814	644480	1.54E-07	LOC100648998	gene
NC_015775.1	737066	738025	6.03E-09	LOC100649825	gene
NC_015775.1	742583	744276	2.03E-08	LOC100649944	gene
NC_015775.1	887063	887586	4.57E-07	LOC100643710	gene
NC_015775.1	1636242	1637024	6.79E-12	LOC100646996	gene
NC_015775.1	2314122	2315226	2.57E-07	LOC100652053	gene
NC_015775.1	2995008	2995976	2.15E-09	LOC100647078	gene
NC_015775.1	2995008	2995976	2.15E-09	LOC100647078	exon
NC_015775.1	4461343	4462437	5.39E-07	LOC100652136	exon
NC_015775.1	4461343	4462437	5.39E-07	LOC100652136	gene
NC_015775.1	5117836	5118483	1.45E-07	LOC100644499	gene
NC_015775.1	6318742	6319862	1.67E-15	LOC100648298	gene
NC_015775.1	7494961	7496723	2.87E-07	LOC100651541	gene
NC_015775.1	7494961	7496723	2.87E-07	LOC105666474	gene
NC_015775.1	7768840	7769349	2.92E-08	LOC100642467	gene
NC_015775.1	7909501	7910780	7.74E-11	LOC100650786	gene
NC_015775.1	8088408	8088908	1.09E-07	LOC100651775	gene
NC_015775.1	8103135	8103636	8.18E-13	LOC100642705	gene
NC_015775.1	8103135	8103636	8.18E-13	LOC100642705	exon
NC_015775.1	8153400	8154594	1.06E-08	LOC100652055	gene

NC_015775.1	8170032	8170909	4.28E-07	LOC100651298	gene
NC_015775.1	8192291	8193066	1.58E-07	LOC100648113	gene
NC_015775.1	8247758	8249986	3.03E-11	LOC100648458	gene
NC_015775.1	8847166	8848376	8.94E-07	LOC100642419	gene
NC_015775.1	11133641	11134693	3.95E-07	LOC105665609	gene
NC_015775.1	11484245	11485271	3.64E-07	LOC100649898	gene
NC_015776.1	2305991	2306506	1.68E-07	LOC100647790	gene
NC_015776.1	2355493	2356040	2.04E-07	LOC100649310	gene
NC_015776.1	2702418	2706355	4.67E-07	NA	NA
NC_015776.1	2761043	2763491	8.72E-09	LOC100649002	gene
NC_015776.1	2929432	2930548	2.46E-13	LOC100651618	gene
NC_015776.1	4531256	4532704	1.18E-07	LOC100642421	gene
NC_015776.1	4890577	4893162	1.51E-08	LOC100652059	gene
NC_015776.1	4961666	4963404	2.05E-08	LOC100649713	gene
NC_015776.1	5138054	5138775	2.16E-07	LOC100647479	gene
NC_015776.1	5269308	5270653	5.85E-08	LOC100645142	gene
NC_015776.1	6041275	6042088	1.48E-10	LOC100650461	gene
NC_015776.1	6437017	6438638	3.71E-08	NA	NA
NC_015776.1	9225468	9226471	1.21E-14	LOC100644943	gene
NC_015776.1	9241197	9241879	5.94E-10	LOC100644823	gene
NC_015776.1	9271719	9273024	2.05E-07	LOC100643628	gene
NC_015776.1	9902655	9903431	1.23E-09	LOC100648229	gene
NC_015776.1	10570984	10571687	3.05E-07	LOC100643219	gene
NC_015776.1	10904576	10906408	3.49E-07	LOC100643910	gene
NC_015777.1	188846	189468	3.24E-12	LOC100652019	exon
NC_015777.1	188846	189468	3.24E-12	LOC100652019	gene
NC_015777.1	756421	757111	5.42E-07	LOC100649861	gene
NC_015777.1	818017	819135	6.39E-08	LOC100642663	gene
NC_015777.1	2544787	2546162	1.26E-09	LOC100650133	gene
NC_015777.1	2634987	2636277	1.19E-09	LOC100645851	gene

NC_015777.1	2716271	2717110	1.57E-09	LOC100647123	gene
NC_015777.1	2716271	2717110	1.57E-09	LOC100647123	exon
NC_015777.1	3125840	3126533	3.83E-12	LOC100644383	gene
NC_015777.1	3231048	3232300	5.27E-09	LOC100644504	gene
NC_015777.1	3242575	3243865	1.57E-10	LOC100642228	gene
NC_015777.1	3658735	3659499	4.88E-07	LOC100643546	gene
NC_015777.1	3696223	3697290	1.85E-08	LOC100644740	gene
NC_015777.1	3699357	3700529	3.99E-07	LOC100644622	gene
NC_015777.1	3787931	3788526	3.06E-10	LOC100645658	gene
NC_015777.1	4127822	4131550	5.43E-09	NA	NA
NC_015777.1	4304244	4304838	8.47E-08	LOC100644741	exon
NC_015777.1	4304244	4304838	8.47E-08	LOC100644741	gene
NC_015778.1	574257	576097	6.33E-07	LOC100651778	gene
NC_015778.1	1128489	1130162	6.47E-12	LOC100650462	gene
NC_015778.1	2734320	2735042	2.95E-07	LOC100631084	gene
NC_015778.1	3009353	3010839	1.24E-07	LOC100643670	gene
NC_015778.1	3081318	3082085	7.42E-07	LOC100652095	gene
NC_015778.1	3226455	3228629	1.69E-09	LOC100650381	gene
NC_015778.1	3226455	3228629	1.69E-09	LOC100650381	exon
NC_015778.1	3230448	3231175	4.09E-08	NA	NA
NC_015778.1	3351339	3353219	4.91E-12	LOC100648918	gene
NC_015778.1	3385575	3386571	1.42E-10	LOC100648492	gene
NC_015779.1	2271770	2272460	1.43E-10	NA	NA
NC_015779.1	2821601	2822283	0	NA	NA

Supplementary 3.0.5: allelically methylated regions identified in sterile workers.

scaffold	amr_start	amr_end	pval	gene	feature
NC_015762.1	536261	537380	1.45E-09	LOC100652148	gene
NC_015762.1	946221	947331	1.26E-12	LOC100650629	gene
NC_015762.1	946221	947331	1.26E-12	LOC100650629	exon
NC_015762.1	946221	947331	1.26E-12	LOC105666912	gene
NC_015762.1	2024933	2026751	3.00E-07	LOC100642191	gene
NC_015762.1	4494791	4495841	7.81E-08	LOC100648080	gene
NC_015762.1	4861900	4862519	8.53E-11	LOC100644473	gene
NC_015762.1	4861900	4862519	8.53E-11	LOC100644473	exon
NC_015762.1	4861900	4862519	8.53E-11	LOC100644473	exon
NC_015762.1	5125204	5125725	3.17E-08	LOC100646051	gene
NC_015762.1	6967340	6969418	8.85E-09	LOC100644670	gene
NC_015762.1	7326268	7326838	1.32E-07	LOC100643721	gene
NC_015762.1	7413625	7414670	1.34E-09	LOC100644474	gene
NC_015762.1	7413625	7414670	1.34E-09	LOC100644474	exon
NC_015762.1	7741997	7742817	6.40E-07	LOC100643273	gene
NC_015762.1	7741997	7742817	6.40E-07	LOC105665993	gene
NC_015762.1	9501415	9503211	7.86E-08	LOC100645181	gene
NC_015762.1	9501415	9503211	7.86E-08	LOC100645309	gene
NC_015762.1	10122170	10123337	1.33E-15	LOC100645740	exon
NC_015762.1	10122170	10123337	1.33E-15	LOC100645740	gene
NC_015762.1	10285547	10286538	1.08E-14	LOC100648270	gene
NC_015762.1	11917861	11918788	3.85E-09	LOC100647802	gene
NC_015763.1	2420152	2420807	1.63E-09	LOC100644837	gene
NC_015763.1	2420152	2420807	1.63E-09	LOC100644837	intron
NC_015763.1	2433487	2435412	1.13E-07	LOC100645183	gene
NC_015763.1	2655355	2658573	4.79E-14	LOC100646252	gene
NC_015763.1	3161460	3162465	6.71E-10	LOC100648084	gene

NC_015763.1	3554945	3557377	2.51E-08	LOC100651983	gene
NC_015763.1	4691558	4692476	4.91E-07	NA	NA
NC_015763.1	7259986	7260487	9.99E-08	NA	NA
NC_015763.1	7973686	7974339	1.50E-08	LOC100646170	gene
NC_015763.1	8986025	8986898	6.66E-07	LOC100642397	gene
NC_015763.1	11887502	11888454	3.02E-08	LOC100642989	gene
NC_015764.1	429904	431720	1.88E-10	LOC100649724	gene
NC_015764.1	472934	473995	4.28E-08	LOC100648622	gene
NC_015764.1	3140925	3141646	7.20E-08	LOC100645116	exon
NC_015764.1	3140925	3141646	7.20E-08	LOC100645116	gene
NC_015764.1	3883872	3885782	3.22E-15	LOC100642600	gene
NC_015764.1	3883872	3885782	3.22E-15	LOC100642600	exon
NC_015764.1	4370527	4372233	3.50E-10	LOC100651791	gene
NC_015764.1	6449586	6450256	1.45E-07	LOC100648930	gene
NC_015764.1	6782058	6782638	2.78E-07	NA	NA
NC_015764.1	8858272	8859730	1.14E-11	LOC100645746	gene
NC_015764.1	8865268	8866642	2.17E-08	LOC100645865	gene
NC_015764.1	8880279	8881111	3.90E-09	LOC100645623	gene
NC_015764.1	9038757	9039258	7.66E-14	LOC100642601	gene
NC_015764.1	9049296	9050641	1.23E-08	LOC100642720	gene
NC_015764.1	10925642	10926308	3.57E-10	LOC100649326	gene
NC_015764.1	11042099	11042755	2.45E-07	LOC100651673	gene
NC_015764.1	11551329	11552961	4.39E-11	LOC100649016	gene
NC_015764.1	11551329	11552961	4.39E-11	LOC100649016	exon
NC_015764.1	13313220	13313796	6.13E-09	LOC100646405	gene
NC_015764.1	13313220	13313796	6.13E-09	LOC100649205	gene
NC_015764.1	13585114	13585918	1.35E-10	LOC100642798	gene
NC_015764.1	14232979	14233902	1.63E-07	LOC100646774	gene
NC_015765.1	520712	522008	3.34E-12	LOC100649804	gene
NC_015765.1	520712	522008	3.34E-12	LOC100649804	intron

NC_015765.1	1922473	1923635	7.51E-08	LOC100642561	gene
NC_015765.1	1946943	1947810	2.14E-08	LOC100643318	gene
NC_015765.1	2445195	2445806	4.97E-09	LOC100644515	gene
NC_015765.1	2490730	2491256	1.68E-08	NA	NA
NC_015765.1	2582621	2583294	4.81E-08	LOC100646288	gene
NC_015765.1	6728813	6729418	6.51E-07	LOC100647769	gene
NC_015765.1	7724195	7725130	1.61E-13	NA	NA
NC_015766.1	95590	96819	2.41E-10	LOC100642364	gene
NC_015766.1	348813	349485	1.46E-08	LOC100645906	gene
NC_015766.1	668693	669210	0	LOC105665778	gene
NC_015766.1	3650734	3652270	1.08E-09	LOC100649806	gene
NC_015766.1	3854921	3856133	1.67E-08	NA	NA
NC_015766.1	6144209	6145336	5.36E-07	LOC100651835	gene
NC_015766.1	6144209	6145336	5.36E-07	LOC100652191	gene
NC_015766.1	6144209	6145336	5.36E-07	LOC100652191	exon
NC_015766.1	6144209	6145336	5.36E-07	LOC100652191	exon
NC_015766.1	6640448	6641448	3.34E-08	LOC100648203	gene
NC_015766.1	6855651	6856381	1.66E-08	LOC100645002	exon
NC_015766.1	6855651	6856381	1.66E-08	LOC100645002	gene
NC_015766.1	8068872	8069380	8.75E-09	LOC100647333	gene
NC_015766.1	8068872	8069380	8.75E-09	LOC105665725	exon
NC_015766.1	8068872	8069380	8.75E-09	LOC105665725	gene
NC_015766.1	9404556	9405118	4.42E-07	LOC100643321	gene
NC_015766.1	10636625	10638533	1.64E-07	NA	NA
NC_015767.1	1436198	1436720	1.59E-10	LOC100651157	gene
NC_015767.1	2373045	2373741	1.42E-07	LOC100642366	gene
NC_015767.1	2373045	2373741	1.42E-07	LOC100642366	exon
NC_015767.1	4649846	4651221	3.74E-07	LOC100645793	gene
NC_015767.1	4700870	4702425	4.82E-08	LOC100651995	gene
NC_015767.1	9656362	9656871	3.78E-13	NA	NA

NC_015767.1	12500165	12500905	1.90E-08	LOC100651759	gene
NC_015768.1	573263	573776	2.32E-14	LOC100648438	gene
NC_015768.1	573263	573776	2.32E-14	LOC105665864	gene
NC_015768.1	2292921	2293692	1.94E-11	LOC100646623	gene
NC_015768.1	2407764	2408537	7.55E-07	LOC100648475	gene
NC_015768.1	3092878	3094623	5.37E-10	LOC100645286	gene
NC_015768.1	5540396	5541166	9.32E-08	LOC100650442	gene
NC_015768.1	6616566	6617727	4.20E-12	LOC100643807	gene
NC_015768.1	6616566	6617727	4.20E-12	LOC100643807	exon
NC_015768.1	7693965	7695129	2.32E-08	LOC100646108	gene
NC_015768.1	7716618	7717501	6.78E-12	NA	NA
NC_015768.1	14806687	14807515	1.10E-07	LOC100645288	exon
NC_015768.1	14806687	14807515	1.10E-07	LOC100645288	gene
NC_015768.1	17491274	17492176	2.96E-11	LOC100644607	gene
NC_015768.1	17491274	17492176	2.96E-11	LOC100644607	exon
NC_015769.1	1467993	1469230	5.52E-12	LOC100643936	gene
NC_015769.1	1467993	1469230	5.52E-12	LOC100643936	exon
NC_015769.1	2188684	2189578	1.18E-07	LOC100646625	gene
NC_015769.1	2933350	2934640	4.96E-08	LOC100650204	gene
NC_015769.1	3268386	3269418	1.29E-09	LOC100642640	gene
NC_015769.1	3554001	3557188	1.94E-09	LOC100649811	gene
NC_015769.1	4970450	4971391	3.42E-08	LOC100651406	gene
NC_015769.1	4970450	4971391	3.42E-08	LOC100651406	exon
NC_015769.1	5027293	5029150	6.22E-09	LOC100651956	gene
NC_015769.1	7957933	7959772	7.94E-12	LOC100645450	gene
NC_015769.1	8491426	8492986	1.11E-16	LOC100644808	gene
NC_015770.1	101920	102940	3.15E-09	LOC100649297	gene
NC_015770.1	387554	388601	1.54E-07	LOC100645378	gene
NC_015770.1	613038	613751	0	LOC100644765	gene
NC_015770.1	1034167	1035292	5.68E-13	LOC100645451	exon

NC_015770.1	1034167	1035292	5.68E-13	LOC100645451	gene
NC_015770.1	1188721	1189484	1.88E-07	LOC100651720	gene
NC_015770.1	1589422	1590487	2.12E-10	LOC100647736	gene
NC_015770.1	2256493	2257018	4.61E-07	LOC100642571	gene
NC_015770.1	2256493	2257018	4.61E-07	LOC100642571	exon
NC_015770.1	2318724	2319646	5.64E-09	LOC100643850	gene
NC_015770.1	2318724	2319646	5.64E-09	LOC100648097	gene
NC_015770.1	4688190	4689554	2.36E-08	LOC100647811	gene
NC_015770.1	5668623	5669601	6.55E-07	LOC100645564	gene
NC_015770.1	5668623	5669601	6.55E-07	LOC105666051	gene
NC_015770.1	5668623	5669601	6.55E-07	LOC105666051	exon
NC_015770.1	7668414	7668930	1.07E-11	LOC100643207	gene
NC_015770.1	8974722	8975877	1.37E-07	LOC100648828	gene
NC_015770.1	9146164	9148534	5.37E-08	LOC100651252	gene
NC_015770.1	11449662	11450195	1.89E-07	LOC100649217	gene
NC_015770.1	11449662	11450195	1.89E-07	LOC100649217	intron
NC_015770.1	12634121	12634623	2.81E-08	LOC100644895	gene
NC_015770.1	12634121	12634623	2.81E-08	LOC100644895	exon
NC_015770.1	12634121	12634623	2.81E-08	LOC100644895	exon
NC_015770.1	13317225	13320916	1.12E-12	LOC100643941	gene
NC_015770.1	13317225	13320916	1.12E-12	LOC100643941	intron
NC_015770.1	13638751	13639409	5.51E-13	LOC100644811	gene
NC_015770.1	13638751	13639409	5.51E-13	LOC100644932	gene
NC_015770.1	13638751	13639409	5.51E-13	LOC100644932	exon
NC_015770.1	14380641	14382050	8.12E-08	LOC100646788	gene
NC_015770.1	14391223	14392149	2.63E-07	LOC100647303	gene
NC_015771.1	8640	9233	4.27E-07	LOC100651210	gene
NC_015771.1	2316661	2317859	1.17E-09	LOC100645206	gene
NC_015771.1	3597120	3598215	7.29E-09	LOC100651689	gene
NC_015771.1	3616430	3618284	9.31E-10	LOC100650967	gene

NC_015771.1	3819568	3820111	1.04E-07	LOC100649541	gene
NC_015771.1	3832983	3834428	2.18E-07	LOC100649182	gene
NC_015771.1	4915573	4917897	4.11E-09	LOC100643415	gene
NC_015771.1	8323429	8324445	3.65E-09	LOC100648642	gene
NC_015771.1	9281864	9283018	1.98E-08	LOC100645723	gene
NC_015771.1	9314173	9315379	4.37E-07	LOC100645254	gene
NC_015771.1	9473291	9473796	1.21E-08	LOC100643700	gene
NC_015771.1	9993202	9994434	7.75E-08	LOC100652128	gene
NC_015771.1	9999505	10001803	2.73E-12	LOC100650816	gene
NC_015771.1	10498564	10499699	2.65E-14	LOC100644372	gene
NC_015771.1	10832972	10833965	2.48E-09	LOC100648830	gene
NC_015771.1	13461846	13462863	1.13E-07	LOC100646988	exon
NC_015771.1	13461846	13462863	1.13E-07	LOC100646988	gene
NC_015772.1	2476486	2479811	0	NA	NA
NC_015772.1	5351312	5352527	4.68E-08	LOC100646551	gene
NC_015772.1	5383364	5384522	3.76E-09	LOC100650734	gene
NC_015772.1	6576949	6577679	2.79E-07	LOC100651092	gene
NC_015772.1	7442913	7444842	1.90E-08	LOC105666262	gene
NC_015772.1	7513683	7515173	2.27E-08	LOC100650368	gene
NC_015772.1	7927565	7928404	1.15E-07	LOC100646750	gene
NC_015772.1	7946301	7947197	1.98E-08	LOC100646956	gene
NC_015772.1	7967137	7969114	7.08E-09	LOC100646190	gene
NC_015772.1	7972680	7973381	4.95E-08	LOC100645844	gene
NC_015772.1	8153458	8154127	2.33E-08	LOC100642223	gene
NC_015772.1	8168863	8169583	9.84E-14	LOC100651892	gene
NC_015772.1	8168863	8169583	9.84E-14	LOC100651892	exon
NC_015772.1	8234732	8235385	8.69E-08	LOC100649664	gene
NC_015772.1	8234732	8235385	8.69E-08	LOC100649664	exon
NC_015772.1	8258045	8258897	0	NA	NA
NC_015772.1	8697912	8698424	4.72E-12	LOC100646871	gene

NC_015772.1	8697912	8698424	4.72E-12	LOC100646871	exon
NC_015772.1	8730893	8731727	5.43E-09	LOC100646189	gene
NC_015772.1	8737638	8738324	8.94E-09	LOC100644688	gene
NC_015772.1	8737638	8738324	8.94E-09	LOC100644688	exon
NC_015772.1	9387029	9387637	1.09E-07	LOC100643819	gene
NC_015772.1	12134146	12134729	2.25E-08	LOC100652318	gene
NC_015772.1	12134146	12134729	2.25E-08	LOC100652318	exon
NC_015772.1	12136107	12137215	2.36E-13	LOC100652318	gene
NC_015772.1	12136107	12137215	2.36E-13	LOC100652318	exon
NC_015772.1	14626504	14628040	0	LOC100652132	gene
NC_015772.1	14629926	14630550	0	NA	NA
NC_015772.1	14954193	14955597	4.02E-09	LOC100644858	gene
NC_015772.1	15203708	15204564	7.49E-07	LOC100643540	gene
NC_015772.1	15203708	15204564	7.49E-07	LOC100643540	exon
NC_015772.1	15203708	15204564	7.49E-07	LOC100643540	exon
NC_015772.1	15439138	15439936	2.14E-11	LOC100650494	gene
NC_015772.1	15442094	15443137	3.51E-07	LOC100649970	gene
NC_015772.1	15939450	15940613	0	LOC100643777	gene
NC_015772.1	15990202	15991661	2.56E-07	LOC100642736	gene
NC_015773.1	221988	222845	1.05E-10	LOC100646479	gene
NC_015773.1	5753988	5758907	1.03E-07	LOC100644222	gene
NC_015773.1	8193011	8194064	9.02E-08	LOC100646268	gene
NC_015773.1	8564088	8564801	7.27E-07	LOC100645212	gene
NC_015773.1	8702835	8704548	6.50E-12	LOC100643011	gene
NC_015773.1	8707867	8708840	3.09E-09	LOC100643706	gene
NC_015773.1	8707867	8708840	3.09E-09	LOC100643706	exon
NC_015773.1	9390040	9390625	4.04E-08	LOC100649591	gene
NC_015773.1	9390040	9390625	4.04E-08	LOC100649591	exon
NC_015773.1	12692639	12693684	1.31E-12	LOC100644735	gene
NC_015774.1	8591008	8591639	1.57E-13	LOC100648143	gene

NC_015775.1	1636242	1637002	2.19E-10	LOC100646996	gene
NC_015775.1	4461343	4462387	2.47E-12	LOC100652136	exon
NC_015775.1	4461343	4462387	2.47E-12	LOC100652136	gene
NC_015775.1	5117714	5119114	6.04E-09	LOC100644499	gene
NC_015775.1	6305133	6306514	3.97E-07	LOC100646125	gene
NC_015775.1	7589539	7590046	2.83E-09	LOC100651659	gene
NC_015775.1	7910080	7910780	1.28E-10	LOC100650786	gene
NC_015775.1	8192291	8193066	8.88E-16	LOC100648113	gene
NC_015775.1	8387775	8388882	3.14E-07	LOC100650377	gene
NC_015775.1	11071298	11071928	3.00E-08	LOC100646635	gene
NC_015776.1	1247160	1247840	8.09E-13	LOC100643343	gene
NC_015776.1	2761331	2762094	1.44E-07	LOC100649002	gene
NC_015776.1	2934772	2935340	2.57E-07	LOC100651618	gene
NC_015776.1	2934772	2935340	2.57E-07	LOC100651618	exon
NC_015776.1	6041092	6041899	1.45E-11	LOC100650461	gene
NC_015776.1	6059369	6062232	8.33E-11	LOC100650344	gene
NC_015776.1	6376242	6377573	5.77E-10	LOC100647914	gene
NC_015776.1	7160788	7163636	1.50E-07	LOC100646364	gene
NC_015776.1	9241197	9242054	3.07E-08	LOC100644823	gene
NC_015776.1	9912558	9913802	2.09E-09	LOC100647997	gene
NC_015776.1	10904576	10906408	5.40E-07	LOC100643910	gene
NC_015776.1	11276047	11276969	4.95E-07	LOC105666542	gene
NC_015777.1	2634868	2636277	1.98E-07	LOC100645851	gene
NC_015777.1	3144512	3146461	2.57E-07	LOC100649277	gene
NC_015777.1	3241991	3244186	1.10E-08	LOC100642228	gene
NC_015777.1	3669679	3670952	3.98E-10	LOC100643912	gene
NC_015777.1	4119267	4120076	5.85E-07	LOC100650983	gene
NC_015777.1	4127371	4131631	2.24E-11	NA	NA
NC_015777.1	4181588	4182252	2.37E-10	LOC100642781	gene
NC_015777.1	4304155	4304838	5.41E-11	LOC100644741	exon

NC_015777.1	4304155	4304838	5.41E-11	LOC100644741	gene
NC_015777.1	4317850	4319935	3.10E-07	LOC100645144	gene
NC_015777.1	4735373	4736685	8.04E-08	LOC100648611	gene
NC_015777.1	4735373	4736685	8.04E-08	LOC100648611	intron
NC_015777.1	4756815	4757703	1.07E-08	LOC100648841	gene
NC_015778.1	575134	576097	6.74E-08	LOC100651778	gene
NC_015778.1	1128489	1130147	4.02E-09	LOC100650462	gene
NC_015778.1	2898542	2899468	4.53E-07	LOC105666648	gene
NC_015778.1	2898542	2899468	4.53E-07	LOC105666648	exon
NC_015778.1	3226348	3228629	9.37E-10	LOC100650381	gene
NC_015778.1	3230497	3231095	2.14E-08	NA	NA
NC_015778.1	3255183	3256254	6.32E-07	LOC100651507	gene
NC_015778.1	3255183	3256254	6.32E-07	LOC100651507	intron
NC_015778.1	3342637	3344856	2.57E-07	LOC100648727	gene
NC_015778.1	3375112	3376997	3.48E-08	LOC100649038	gene
NC_015778.1	3385575	3386597	2.43E-14	LOC100648492	gene
NC_015779.1	2144125	2145039	3.11E-15	LOC100642623	gene
NC_015779.1	2477628	2478310	2.22E-16	LOC105666711	gene
NC_015779.1	2821642	2822283	5.55E-08	NA	NA

Supplementary 3.0.6: Enriched GO terms for genes showing allele-specific methylation in either both castes, just reproductive workers or just sterile workers.

Allelically methylated genes in both castes.

term_ID	description	frequency	log10 p
GO:0033120	positive regulation of RNA splicing	0.01%	-2.9883
GO:0031328	positive regulation of cellular biosynthetic process	0.67%	-1.9173
GO:0019217	regulation of fatty acid metabolic process	0.02%	-1.6216
GO:0051254	positive regulation of RNA metabolic process	0.54%	-2.1895
GO:0006376	mRNA splice site selection	0.02%	-1.453
GO:0010628	positive regulation of gene expression	0.65%	-1.5251
GO:1903508	positive regulation of nucleic acid-templated transcription	0.52%	-2.2508
GO:2000144	positive regulation of DNA-templated transcription, initiation	0.02%	-1.6216
GO:0000381	regulation of alternative mRNA splicing, via spliceosome	0.02%	-1.9681
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	0.37%	-1.7727
GO:0000375	RNA splicing, via transesterification reactions	0.32%	-1.341
GO:0000398	mRNA splicing, via spliceosome	0.32%	-1.3576
GO:0010557	positive regulation of macromolecule biosynthetic process	0.63%	-2.0302
GO:0032968	positive regulation of transcription elongation from RNA polymerase II promoter	0.03%	-1.3167
GO:0046889	positive regulation of lipid biosynthetic process	0.02%	-1.6216
GO:0051130	positive regulation of cellular component organization	0.37%	-1.4576
GO:0051173	positive regulation of nitrogen compound metabolic process	0.69%	-1.7037
GO:0050684	regulation of mRNA processing	0.04%	-1.5292
GO:0050685	positive regulation of mRNA processing	0.01%	-1.3816
GO:0040007	growth	0.32%	-1.4681
GO:0098655	cation transmembrane transport	2.29%	-1.8723
GO:0098660	inorganic ion transmembrane transport	2.32%	-1.397
GO:0071229	cellular response to acid chemical	0.07%	-2.8174
GO:0071233	cellular response to leucine	0.00%	-2.3607
GO:0043200	response to amino acid	0.02%	-1.3167
GO:0032526	response to retinoic acid	0.01%	-1.8401

GO:0071417	cellular response to organonitrogen compound	0.09%	-1.5195
GO:0060359	response to ammonium ion	0.02%	-1.3816
GO:0043933	macromolecular complex subunit organization	2.37%	-2.6964
GO:1901360	organic cyclic compound metabolic process	30.32%	-1.7448
GO:0006725	cellular aromatic compound metabolic process	29.63%	-1.9141
GO:0043610	regulation of carbohydrate utilization	0.00%	-1.5589
GO:0045838	positive regulation of membrane potential	0.00%	-1.3816
GO:0042749	regulation of circadian sleep/wake cycle	0.01%	-2.1467
GO:0007623	circadian rhythm	0.06%	-1.3506
GO:0048520	positive regulation of behavior	0.01%	-1.3914
GO:0010841	positive regulation of circadian sleep/wake cycle, wakefulness	0.00%	-1.5589
GO:0022410	circadian sleep/wake cycle process	0.01%	-1.8401
GO:1904000	positive regulation of eating behavior	0.00%	-1.5589
GO:0042789	mRNA transcription from RNA polymerase II promoter	0.00%	-2.6539
GO:0016071	mRNA metabolic process	0.80%	-1.863
GO:0023041	neuronal signal transduction	0.00%	-1.5589
GO:0099003	vesicle-mediated transport in synapse	0.04%	-1.4992
GO:0046483	heterocycle metabolic process	29.66%	-1.7276
GO:0051028	mRNA transport	0.08%	-1.7456
GO:0050657	nucleic acid transport	0.10%	-1.7642
GO:0051236	establishment of RNA localization	0.10%	-1.7642
GO:0034654	nucleobase-containing compound biosynthetic process	14.53%	-1.6971
GO:0051253	negative regulation of RNA metabolic process	0.63%	-1.8416
GO:0045814	negative regulation of gene expression, epigenetic	0.09%	-1.7099
GO:0021553	olfactory nerve development	0.00%	-1.5589
GO:1904056	positive regulation of cholangiocyte proliferation	0.00%	-1.5589
GO:0031668	cellular response to extracellular stimulus	0.44%	-2.6112
GO:0009267	cellular response to starvation	0.09%	-2.203
GO:0032094	response to food	0.01%	-2.3607
GO:0007584	response to nutrient	0.03%	-1.6216

GO:0046928	regulation of neurotransmitter secretion	0.01%	-2.5451
GO:0030072	peptide hormone secretion	0.04%	-1.6178
GO:0061670	evoked neurotransmitter secretion	0.00%	-1.5589
GO:0099643	signal release from synapse	0.04%	-1.7099
GO:0016080	synaptic vesicle targeting	0.00%	-1.8401
GO:0050806	positive regulation of synaptic transmission	0.02%	-1.6178
GO:0050796	regulation of insulin secretion	0.03%	-1.3167
GO:0051590	positive regulation of neurotransmitter transport	0.00%	-1.9784
GO:1903307	positive regulation of regulated secretory pathway	0.01%	-1.6216
GO:0046883	regulation of hormone secretion	0.04%	-1.4766
GO:0017158	regulation of calcium ion-dependent exocytosis	0.02%	-1.453
GO:0060025	regulation of synaptic activity	0.00%	-1.5589
GO:0072553	terminal button organization	0.00%	-1.6216
GO:0002128	tRNA nucleoside ribose methylation	0.01%	-1.5589
GO:0035158	regulation of tube diameter, open tracheal system	0.00%	-1.5589
GO:0000022	mitotic spindle elongation	0.01%	-2.1467
GO:1904594	regulation of termination of RNA polymerase II transcription	0.00%	-1.5589
GO:0034641	cellular nitrogen compound metabolic process	34.14%	-1.3402
GO:1904193	negative regulation of cholangiocyte apoptotic process	0.00%	-1.5589
GO:0009914	hormone transport	0.07%	-1.3543
GO:0030034	microvillar actin bundle assembly	0.00%	-1.5589
GO:0042542	response to hydrogen peroxide	0.03%	-2.1392
GO:1901701	cellular response to oxygen-containing compound	0.35%	-1.3576
GO:0007389	pattern specification process	0.15%	-1.6653
GO:0097309	cap1 mRNA methylation	0.00%	-1.5589
GO:0090702	non-reproductive fruiting body development	0.01%	-1.5589
GO:0031152	aggregation involved in sorocarp development	0.00%	-1.5589
GO:1902474	positive regulation of protein localization to synapse	0.00%	-1.5589
GO:0048752	semicircular canal morphogenesis	0.00%	-1.5589
GO:0035167	larval lymph gland hemopoiesis	0.00%	-1.453

GO:0010890	positive regulation of sequestering of triglyceride	0.00%	-1.5589
GO:0035886	vascular smooth muscle cell differentiation	0.00%	-1.5589
GO:0060999	positive regulation of dendritic spine development	0.00%	-1.8401
GO:0006606	protein import into nucleus	0.10%	-2.4091
GO:0006913	nucleocytoplasmic transport	0.24%	-1.8812
GO:0010611	regulation of cardiac muscle hypertrophy	0.01%	-1.723
GO:0014736	negative regulation of muscle atrophy	0.00%	-1.5589
GO:0014733	regulation of skeletal muscle adaptation	0.00%	-1.5589
GO:1904206	positive regulation of skeletal muscle hypertrophy	0.00%	-1.5589
GO:0061051	positive regulation of cell growth involved in cardiac muscle cell development	0.00%	-1.5589
GO:0014888	striated muscle adaptation	0.01%	-1.5589
GO:0014897	striated muscle hypertrophy	0.01%	-1.5324
GO:0042493	response to drug	0.27%	-1.318
GO:0098942	retrograde trans-synaptic signaling by trans-synaptic protein complex	0.00%	-1.5589
GO:0021762	substantia nigra development	0.01%	-1.5589
GO:0031529	ruffle organization	0.01%	-1.8401
GO:0016569	covalent chromatin modification	0.42%	-2.2089
GO:0031887	lipid particle transport along microtubule	0.00%	-1.5589
GO:0051703	intraspecies interaction between organisms	0.02%	-1.3816
GO:0019219	regulation of nucleobase-containing compound metabolic process	10.26%	-2.0642
GO:2001141	regulation of RNA biosynthetic process	9.97%	-1.3953
GO:0006355	regulation of transcription, DNA-templated	9.92%	-1.4104
GO:1904197	positive regulation of granulosa cell proliferation	0.00%	-1.5589
GO:0051549	positive regulation of keratinocyte migration	0.00%	-1.5589
GO:0051262	protein tetramerization	0.04%	-1.453
GO:0090304	nucleic acid metabolic process	21.45%	-1.4744
GO:0060566	positive regulation of DNA-templated transcription, termination	0.00%	-1.5589
GO:0009953	dorsal/ventral pattern formation	0.03%	-1.5996
GO:0021796	cerebral cortex regionalization	0.00%	-1.5589
GO:0048190	wing disc dorsal/ventral pattern formation	0.00%	-1.5324

GO:0007637	proboscis extension reflex	0.00%	-1.5589
GO:1900244	positive regulation of synaptic vesicle endocytosis	0.00%	-2.3607
GO:2000302	positive regulation of synaptic vesicle exocytosis	0.00%	-2.3607
GO:1903421	regulation of synaptic vesicle recycling	0.00%	-1.8401
GO:0003215	cardiac right ventricle morphogenesis	0.00%	-1.5589
GO:0003226	right ventricular compact myocardium morphogenesis	0.00%	-1.5589
GO:1901950	dense core granule transport	0.00%	-1.5589
GO:1990049	retrograde neuronal dense core vesicle transport	0.00%	-1.5589
GO:0044057	regulation of system process	0.09%	-1.3506
GO:0051276	chromosome organization	1.48%	-1.3028
GO:1902373	negative regulation of mRNA catabolic process	0.00%	-1.8401
GO:0050995	negative regulation of lipid catabolic process	0.00%	-1.5589
GO:0045840	positive regulation of mitotic nuclear division	0.02%	-1.5324
GO:0019090	mitochondrial rRNA export from mitochondrion	0.00%	-1.5589
GO:1905606	regulation of presynapse assembly	0.00%	-1.5589
GO:0097115	neurexin clustering involved in presynaptic membrane assembly	0.00%	-1.5589
GO:1905520	positive regulation of presynaptic active zone assembly	0.00%	-1.5589
GO:0003062	regulation of heart rate by chemical signal	0.00%	-1.5589
GO:1990253	cellular response to leucine starvation	0.00%	-2.6539
GO:0043984	histone H4-K16 acetylation	0.01%	-1.5324
GO:0007628	adult walking behavior	0.01%	-1.9784
GO:0007616	long-term memory	0.01%	-1.3167
GO:0030534	adult behavior	0.04%	-1.4677
GO:0051656	establishment of organelle localization	0.18%	-2.0604
GO:1902803	regulation of synaptic vesicle transport	0.01%	-1.8401
GO:0097480	establishment of synaptic vesicle localization	0.04%	-1.9681
GO:0051648	vesicle localization	0.08%	-1.3399
GO:0060421	positive regulation of heart growth	0.01%	-1.5589
GO:0048869	cellular developmental process	1.90%	-1.4755
GO:0034765	regulation of ion transmembrane transport	0.20%	-1.921

GO:0090087	regulation of peptide transport	0.03%	-1.6357
GO:1904213	negative regulation of iodide transmembrane transport	0.00%	-1.5589
GO:2000310	regulation of N-methyl-D-aspartate selective glutamate receptor activity	0.00%	-1.5589
GO:1903960	negative regulation of anion transmembrane transport	0.00%	-1.5589
GO:0051046	regulation of secretion	0.14%	-1.9006
GO:1904201	regulation of iodide transport	0.00%	-1.5589
GO:0032388	positive regulation of intracellular transport	0.06%	-1.8757
GO:1903795	regulation of inorganic anion transmembrane transport	0.00%	-1.5589
GO:0033157	regulation of intracellular protein transport	0.08%	-1.4205
GO:0016480	negative regulation of transcription from RNA polymerase III promoter	0.01%	-1.5589
GO:0023061	signal release	0.09%	-1.4769
GO:0032252	secretory granule localization	0.00%	-1.5589
GO:0002087	regulation of respiratory gaseous exchange by neurological system process	0.00%	-1.5589
GO:0030719	P granule organization	0.00%	-1.5589
GO:2000806	positive regulation of termination of RNA polymerase II transcription, poly(A)-coupl	0.00%	-1.5589
GO:0051931	regulation of sensory perception	0.00%	-1.5589
GO:1904058	positive regulation of sensory perception of pain	0.00%	-1.5589
GO:0021510	spinal cord development	0.02%	-1.3167
GO:1900029	positive regulation of ruffle assembly	0.00%	-1.5589

Allelically methylated genes in reproductive workers.

term_ID	description	frequency	log10 p
GO:0006043	glucosamine catabolic process	0.00%	-1.3166
GO:0006998	nuclear envelope organization	0.02%	-2.2224
GO:0090204	protein localization to nuclear pore	0.00%	-1.3166
GO:0007608	sensory perception of smell	0.27%	-3.2671
GO:0003015	heart process	0.05%	-1.7158
GO:0045823	positive regulation of heart contraction	0.01%	-1.3166
GO:0086004	regulation of cardiac muscle cell contraction	0.01%	-1.8861
GO:1905024	regulation of membrane repolarization during ventricular cardiac muscle cell action potential	0.00%	-1.3166
GO:1903947	positive regulation of ventricular cardiac muscle cell action potential	0.00%	-1.3166
GO:0007600	sensory perception	0.43%	-1.4682
GO:1903762	positive regulation of voltage-gated potassium channel activity involved in ventricular cardiac muscle	0.00%	-1.3166
GO:1903522	regulation of blood circulation	0.05%	-1.5682
GO:0006942	regulation of striated muscle contraction	0.02%	-1.3835
GO:0033058	directional locomotion	0.00%	-1.3166
GO:0043268	positive regulation of potassium ion transport	0.01%	-2.1732
GO:1901018	positive regulation of potassium ion transmembrane transporter activity	0.00%	-2.1732
GO:1904064	positive regulation of cation transmembrane transport	0.02%	-1.8658
GO:0036150	phosphatidylserine acyl-chain remodeling	0.00%	-1.3166
GO:1900044	regulation of protein K63-linked ubiquitination	0.00%	-1.3166
GO:1902915	negative regulation of protein polyubiquitination	0.00%	-1.3166
GO:1901315	negative regulation of histone H2A K63-linked ubiquitination	0.00%	-1.3166
GO:1902402	signal transduction involved in mitotic DNA damage checkpoint	0.01%	-2.1281
GO:1902400	intracellular signal transduction involved in G1 DNA damage checkpoint	0.00%	-1.3835
GO:0072401	signal transduction involved in DNA integrity checkpoint	0.01%	-1.9887
GO:0072425	signal transduction involved in G2 DNA damage checkpoint	0.00%	-1.3166
GO:0072413	signal transduction involved in mitotic cell cycle checkpoint	0.01%	-2.1281

GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	0.00%	-1.5158
GO:1902504	regulation of signal transduction involved in mitotic G2 DNA damage checkpoint	0.00%	-1.3166
GO:0051642	centrosome localization	0.01%	-1.5682
GO:1903326	regulation of tRNA metabolic process	0.00%	-1.3166
GO:0015931	nucleobase-containing compound transport	0.20%	-1.4338
GO:0018002	N-terminal peptidyl-glutamic acid acetylation	0.00%	-1.3166
GO:0017198	N-terminal peptidyl-serine acetylation	0.00%	-1.3166
GO:0007216	G-protein coupled glutamate receptor signaling pathway	0.01%	-1.3166
GO:0060260	regulation of transcription initiation from RNA polymerase II promoter	0.02%	-1.6576
GO:0086009	membrane repolarization	0.01%	-1.8861
GO:0043401	steroid hormone mediated signaling pathway	0.10%	-1.7131
GO:0048545	response to steroid hormone	0.12%	-1.3966
GO:1900169	regulation of glucocorticoid mediated signaling pathway	0.00%	-1.3166
GO:0033147	negative regulation of intracellular estrogen receptor signaling pathway	0.00%	-1.8861
GO:0071385	cellular response to glucocorticoid stimulus	0.01%	-1.6781
GO:0033143	regulation of intracellular steroid hormone receptor signaling pathway	0.01%	-1.5682
GO:0006366	transcription from RNA polymerase II promoter	1.43%	-1.3016
GO:0048583	regulation of response to stimulus	1.12%	-1.3149
GO:0071500	cellular response to nitrosative stress	0.00%	-1.3166
GO:1905259	negative regulation of nitrosative stress-induced intrinsic apoptotic signaling pathway	0.00%	-1.3166
GO:2000237	positive regulation of tRNA processing	0.00%	-1.3166
GO:0030035	microspike assembly	0.00%	-1.3166
GO:2000152	regulation of ubiquitin-specific protease activity	0.00%	-1.3166
GO:1902946	protein localization to early endosome	0.00%	-1.3166
GO:0009408	response to heat	0.17%	-1.3653
GO:0009631	cold acclimation	0.00%	-1.3166
GO:1905090	negative regulation of parkin-mediated mitophagy in response to mitochondrial depolarization	0.00%	-1.3166
GO:1902373	negative regulation of mRNA catabolic process	0.00%	-1.3835
GO:0007318	pole plasm protein localization	0.00%	-2.1732
GO:0048599	oocyte development	0.02%	-1.8505

GO:0051235	maintenance of location	0.13%	-1.4882
GO:0043489	RNA stabilization	0.01%	-1.3835
GO:0070935	3'-UTR-mediated mRNA stabilization	0.00%	-1.3166
GO:0042770	signal transduction in response to DNA damage	0.02%	-1.3425
GO:1903019	negative regulation of glycoprotein metabolic process	0.00%	-1.3166
GO:0042985	negative regulation of amyloid precursor protein biosynthetic process	0.00%	-1.3166
GO:1990168	protein K33-linked deubiquitination	0.00%	-1.3166
GO:0001967	suckling behavior	0.00%	-1.3166
GO:0006408	snRNA export from nucleus	0.00%	-1.3166
GO:1901741	positive regulation of myoblast fusion	0.00%	-1.3166
GO:0048875	chemical homeostasis within a tissue	0.00%	-1.3166
GO:0046552	photoreceptor cell fate commitment	0.00%	-2.7223
GO:0001752	compound eye photoreceptor fate commitment	0.00%	-1.3938
GO:0007464	R3/R4 cell fate commitment	0.00%	-1.6781
GO:0072160	nephron tubule epithelial cell differentiation	0.00%	-1.3166
GO:2001013	epithelial cell proliferation involved in renal tubule morphogenesis	0.00%	-1.3166
GO:0042795	snRNA transcription from RNA polymerase II promoter	0.00%	-1.3835
GO:0042796	snRNA transcription from RNA polymerase III promoter	0.00%	-1.3166
GO:0032057	negative regulation of translational initiation in response to stress	0.00%	-1.3166
GO:0034383	low-density lipoprotein particle clearance	0.00%	-1.3166
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	0.04%	-1.7562
GO:2000036	regulation of stem cell population maintenance	0.01%	-1.8861
GO:0042066	perineurial glial growth	0.00%	-1.3166
GO:0072344	rescue of stalled ribosome	0.00%	-1.3166
GO:0046000	positive regulation of ecdysteroid secretion	0.00%	-1.3166
GO:0032941	secretion by tissue	0.01%	-1.3835
GO:0015862	uridine transport	0.00%	-1.3166
GO:0051482	positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G-protei	0.00%	-1.3166
GO:0007129	synapsis	0.02%	-1.8861
GO:0045141	meiotic telomere clustering	0.00%	-1.3166

GO:0070197	meiotic attachment of telomere to nuclear envelope	0.00%	-1.3166
GO:1903781	positive regulation of cardiac conduction	0.00%	-1.3166
GO:0002164	larval development	0.02%	-2.5296
GO:0002165	instar larval or pupal development	0.04%	-1.3059
GO:0007560	imaginal disc morphogenesis	0.02%	-1.6131
GO:0040025	vulval development	0.01%	-1.8861
GO:0009886	post-embryonic animal morphogenesis	0.04%	-1.6462
GO:0007476	imaginal disc-derived wing morphogenesis	0.02%	-1.3291
GO:0043053	dauer entry	0.00%	-1.3166
GO:0010883	regulation of lipid storage	0.01%	-2.1281
GO:0010891	negative regulation of sequestering of triglyceride	0.00%	-1.3166
GO:0010886	positive regulation of cholesterol storage	0.00%	-1.3166
GO:0035882	defecation rhythm	0.00%	-1.3166
GO:0015801	aromatic amino acid transport	0.01%	-1.3166
GO:0021885	forebrain cell migration	0.01%	-1.8861
GO:0021817	nucleokinesis involved in cell motility in cerebral cortex radial glia guided migration	0.00%	-1.3166
GO:0021814	cell motility involved in cerebral cortex radial glia guided migration	0.00%	-1.3166
GO:0021795	cerebral cortex cell migration	0.01%	-1.8861
GO:0035666	TRIF-dependent toll-like receptor signaling pathway	0.00%	-1.3166
GO:0035523	protein K29-linked deubiquitination	0.00%	-1.3166
GO:0035107	appendage morphogenesis	0.06%	-1.5816
GO:0070327	thyroid hormone transport	0.00%	-1.3166
GO:2000400	positive regulation of thymocyte aggregation	0.00%	-1.3166
GO:0033081	regulation of T cell differentiation in thymus	0.01%	-1.3166
GO:0061393	positive regulation of transcription from RNA polymerase II promoter in response to osmotic stress	0.00%	-1.3166
GO:0042538	hyperosmotic salinity response	0.00%	-1.3166
GO:0061404	positive regulation of transcription from RNA polymerase II promoter in response to increased salt	0.00%	-1.3166
GO:0061416	regulation of transcription from RNA polymerase II promoter in response to salt stress	0.00%	-1.3166
GO:0071474	cellular hyperosmotic response	0.00%	-1.3166
GO:0043403	skeletal muscle tissue regeneration	0.01%	-1.3166

GO:0003231	cardiac ventricle development	0.03%	-1.6576
GO:0003290	atrial septum secundum morphogenesis	0.00%	-1.3166
GO:0003149	membranous septum morphogenesis	0.00%	-1.3166
GO:0036245	cellular response to menadione	0.00%	-1.3166
GO:2000011	regulation of adaxial/abaxial pattern formation	0.00%	-1.3166
GO:0090188	negative regulation of pancreatic juice secretion	0.00%	-1.3166
GO:0042327	positive regulation of phosphorylation	0.25%	-1.6525
GO:0010562	positive regulation of phosphorus metabolic process	0.28%	-1.3971
GO:0010606	positive regulation of cytoplasmic mRNA processing body assembly	0.00%	-1.5158
GO:2001137	positive regulation of endocytic recycling	0.00%	-1.3166
GO:0086023	adrenergic receptor signaling pathway involved in heart process	0.00%	-1.3166
GO:0071883	activation of MAPK activity by adrenergic receptor signaling pathway	0.00%	-1.3166
GO:0060348	bone development	0.04%	-1.5682
GO:0032332	positive regulation of chondrocyte differentiation	0.00%	-1.3166
GO:0034340	response to type I interferon	0.01%	-1.3166
GO:0002244	hematopoietic progenitor cell differentiation	0.03%	-1.3425
GO:0007089	traversing start control point of mitotic cell cycle	0.00%	-1.3166
GO:2001234	negative regulation of apoptotic signaling pathway	0.04%	-1.6489
GO:2001236	regulation of extrinsic apoptotic signaling pathway	0.03%	-1.4116
GO:0043069	negative regulation of programmed cell death	0.18%	-1.3789
GO:0044770	cell cycle phase transition	0.21%	-1.6779
GO:0001975	response to amphetamine	0.00%	-1.3166
GO:0048569	post-embryonic animal organ development	0.04%	-1.3037
GO:0022605	oogenesis stage	0.00%	-1.3166
GO:0048387	negative regulation of retinoic acid receptor signaling pathway	0.00%	-1.3166
GO:0008406	gonad development	0.04%	-1.4711
GO:0060707	trophoblast giant cell differentiation	0.00%	-1.3166
GO:0060708	spongiotrophoblast differentiation	0.00%	-1.3166
GO:0007548	sex differentiation	0.06%	-1.3291
GO:0001550	ovarian cumulus expansion	0.00%	-1.3166

GO:0001541	ovarian follicle development	0.01%	-1.5158
GO:1901207	regulation of heart looping	0.00%	-1.3166
GO:0048729	tissue morphogenesis	0.18%	-1.3039
GO:0048523	negative regulation of cellular process	1.83%	-1.3289
GO:1903077	negative regulation of protein localization to plasma membrane	0.00%	-1.3166
GO:1903748	negative regulation of establishment of protein localization to mitochondrion	0.00%	-1.3166
GO:0035456	response to interferon-beta	0.00%	-1.3166
GO:0099625	ventricular cardiac muscle cell membrane repolarization	0.00%	-1.8861
GO:0099623	regulation of cardiac muscle cell membrane repolarization	0.00%	-1.8861
GO:1903954	positive regulation of voltage-gated potassium channel activity involved in atrial cardiac muscle cell acti	0.00%	-1.3166
GO:0086013	membrane repolarization during cardiac muscle cell action potential	0.00%	-1.3166
GO:0046628	positive regulation of insulin receptor signaling pathway	0.00%	-1.3166
GO:0098901	regulation of cardiac muscle cell action potential	0.01%	-1.6781
GO:0098903	regulation of membrane repolarization during action potential	0.00%	-1.3166
GO:0033182	regulation of histone ubiquitination	0.01%	-1.3166
GO:0033083	regulation of immature T cell proliferation	0.00%	-1.3166
GO:0033092	positive regulation of immature T cell proliferation in thymus	0.00%	-1.3166
GO:0034764	positive regulation of transmembrane transport	0.02%	-2.1222
GO:0032411	positive regulation of transporter activity	0.01%	-1.9887
GO:0008626	granzyme-mediated apoptotic signaling pathway	0.00%	-1.3166

Allelically methylated genes in sterile workers.

term_ID	description	frequency	log10 p
GO:0043484	regulation of RNA splicing	0.04%	-2.6834
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine	0.32%	-2.4681
GO:0000380	alternative mRNA splicing, via spliceosome	0.02%	-1.3048
GO:0045087	innate immune response	0.15%	-2.7629
GO:0002683	negative regulation of immune system process	0.08%	-1.3373
GO:0050852	T cell receptor signaling pathway	0.02%	-1.4948
GO:0002757	immune response-activating signal transduction	0.07%	-1.5348
GO:0065007	biological regulation	20.50%	-1.3755
GO:0097150	neuronal stem cell population maintenance	0.01%	-2.6989
GO:0001578	microtubule bundle formation	0.03%	-1.3577
GO:0018095	protein polyglutamylation	0.01%	-1.5815
GO:0019284	L-methionine biosynthetic process from S-adenosylmethionine	0.04%	-1.5815
GO:0035332	positive regulation of hippo signaling	0.00%	-2.6989
GO:2000286	receptor internalization involved in canonical Wnt signaling pathway	0.00%	-1.5815
GO:0034474	U2 snRNA 3'-end processing	0.00%	-1.5815
GO:0007166	cell surface receptor signaling pathway	0.92%	-1.4213
GO:0030717	karyosome formation	0.00%	-2.4053
GO:0007281	germ cell development	0.09%	-1.757
GO:0006723	cuticle hydrocarbon biosynthetic process	0.00%	-1.5815
GO:0046960	sensitization	0.00%	-1.5815
GO:0006468	protein phosphorylation	4.14%	-1.5351
GO:0034198	cellular response to amino acid starvation	0.02%	-1.6642
GO:0046824	positive regulation of nucleocytoplasmic transport	0.03%	-1.6642
GO:0090277	positive regulation of peptide hormone secretion	0.01%	-1.5746
GO:0050794	regulation of cellular process	18.84%	-1.4283
GO:0051567	histone H3-K9 methylation	0.01%	-1.5746

GO:1900114	positive regulation of histone H3-K9 trimethylation	0.00%	-1.5815
GO:0051647	nucleus localization	0.01%	-1.4948
GO:0038083	peptidyl-tyrosine autophosphorylation	0.01%	-1.5746
GO:0097374	sensory neuron axon guidance	0.00%	-1.5815
GO:0009653	anatomical structure morphogenesis	1.54%	-2.0587
GO:0000902	cell morphogenesis	0.95%	-1.5128
GO:0009790	embryo development	0.31%	-1.6775
GO:0007391	dorsal closure	0.01%	-1.7854
GO:0000165	MAPK cascade	0.25%	-1.3275
GO:0023057	negative regulation of signaling	0.29%	-2.0798
GO:0051716	cellular response to stimulus	9.56%	-1.483
GO:0007516	hemocyte development	0.00%	-1.5815
GO:0018212	peptidyl-tyrosine modification	0.22%	-1.4112
GO:0007446	imaginal disc growth	0.00%	-1.766
GO:0098868	bone growth	0.01%	-1.5815
GO:0003417	growth plate cartilage development	0.00%	-1.5815
GO:0034125	negative regulation of MyD88-dependent toll-like receptor signaling pathway	0.00%	-1.5815
GO:2000255	negative regulation of male germ cell proliferation	0.00%	-1.5815
GO:0098727	maintenance of cell number	0.04%	-1.3026
GO:0072205	metanephric collecting duct development	0.00%	-1.5815
GO:0001764	neuron migration	0.03%	-1.423
GO:0060465	pharynx development	0.00%	-1.5815
GO:0000349	generation of catalytic spliceosome for first transesterification step	0.00%	-1.5815
GO:0045879	negative regulation of smoothened signaling pathway	0.01%	-1.423
GO:0000096	sulfur amino acid metabolic process	0.54%	-1.423
GO:0042473	outer ear morphogenesis	0.00%	-1.5815
GO:0042474	middle ear morphogenesis	0.00%	-1.5815
GO:0008359	regulation of bicoid mRNA localization	0.00%	-1.5815
GO:0042070	maintenance of oocyte nucleus location involved in oocyte dorsal/ventral axis spe	0.00%	-1.5815
GO:0003402	planar cell polarity pathway involved in axis elongation	0.00%	-1.5815

GO:0002314	germinal center B cell differentiation	0.00%	-1.5815
GO:0071678	olfactory bulb axon guidance	0.00%	-1.5815
GO:0035745	T-helper 2 cell cytokine production	0.00%	-1.5815
GO:0010648	negative regulation of cell communication	0.29%	-2.025
GO:1902532	negative regulation of intracellular signal transduction	0.13%	-1.6873
GO:0009966	regulation of signal transduction	0.86%	-1.7596
GO:0048749	compound eye development	0.02%	-1.3056
GO:0060441	epithelial tube branching involved in lung morphogenesis	0.01%	-1.5815
GO:0001738	morphogenesis of a polarized epithelium	0.02%	-1.4112
GO:0000381	regulation of alternative mRNA splicing, via spliceosome	0.02%	-2.0466
GO:0050684	regulation of mRNA processing	0.04%	-1.8358
GO:0060711	labyrinthine layer development	0.01%	-1.5815
GO:0048585	negative regulation of response to stimulus	0.34%	-1.7261
GO:0007300	ovarian nurse cell to oocyte transport	0.00%	-1.5746

Chapter 4: supplementary

Supplementary 4.0.0: Behavioural data for each sample selected for RNA-Seq along with ovary score, age, weight and final caste classification.

	Parental genomes									
Nest	Mother	Father	Worker	**A:** sit idle	**B:** standing close to brood	**C:** standing far from brood	**D:** walking in nest	**E:** incubating	**F:** feeding larvae	**G:** inspecting brood cells
14-Feb	B. t. dalmatin	B. t. audax, far	44	0	2	0	1	2	0	1
14-Feb	B. t. dalmatin	B. t. audax, far	35	0	0	0	2	0	0	0
14-Feb	B. t. dalmatin	B. t. audax, far	37	0	2	1	1	4	1	1
14-Feb	B. t. dalmatin	B. t. audax, far	54	0	0	3	2	1	0	1
14-Feb	B. t. dalmatin	B. t. audax, far	10	1	4	1	4	0	0	3
14-Feb	B. t. dalmatin	B. t. audax, far	18	0	7	0	2	0	0	4
14-Feb	B. t. dalmatin	B. t. audax, far	22	0	6	0	1	4	1	6
14-Feb	B. t. dalmatin	B. t. audax, far	12	1	4	0	0	2	0	2
14-Dec	B. t. audax, far	B. t. dalmatin	74	0	3	0	0	0	1	1
14-Dec	B. t. audax, far	B. t. dalmatin	78	0	0	0	0	0	0	0
14-Dec	B. t. audax, far	B. t. dalmatin	75	0	1	3	2	1	1	2
14-Dec	B. t. audax, far	B. t. dalmatin	76	0	4	0	0	0	1	1
14-Dec	B. t. audax, far	B. t. dalmatin	85	2	6	0	2	0	0	4
14-Dec	B. t. audax, far	B. t. dalmatin	89	1	8	1	2	1	0	3

14-Dec	B. t. audax, far	B. t. dalmatini	84	0	3	0	0	3	0	1
14-Dec	B. t. audax, far	B. t. dalmatini	82	0	4	0	0	1	0	2
14-22	B. t. dalmatini	B. t. audax, far	49	0	1	0	0	2	0	0
14-22	B. t. dalmatini	B. t. audax, far	30	0	3	0	1	4	0	0
14-22	B. t. dalmatini	B. t. audax, far	26	0	3	1	1	5	1	1
14-22	B. t. dalmatini	B. t. audax, far	35	0	2	0	0	4	0	0
14-22	B. t. dalmatini	B. t. audax, far	21	2	5	0	5	5	0	8
14-22	B. t. dalmatini	B. t. audax, far	9	0	8	1	2	6	2	5
14-22	B. t. dalmatini	B. t. audax, far	23	0	8	0	1	8	1	5
14-22	B. t. dalmatini	B. t. audax, far	18	0	2	1	0	0	1	0
14-31	B. t. audax, far	B. t. dalmatini	64	0	1	0	2	2	0	0
14-31	B. t. audax, far	B. t. dalmatini	44	0	3	1	0	0	0	2
14-31	B. t. audax, far	B. t. dalmatini	45	0	3	1	0	3	0	1
14-31	B. t. audax, far	B. t. dalmatini	65	0	1	0	0	0	1	0
14-31	B. t. audax, far	B. t. dalmatini	79	5	8	0	0	0	0	4
14-31	B. t. audax, far	B. t. dalmatini	89	0	11	0	0	2	0	7
14-31	B. t. audax, far	B. t. dalmatini	86	0	16	0	0	4	2	6
14-31	B. t. audax, far	B. t. dalmatini	84	0	9	0	0	8	0	2

		Behaviour								
H: building egg cup	**I:** building periphery	**J:** ventilation < 4 sec	**K:** biting/grasping	**L:** push / bump	**M:** egg-laying	**N:** eating eggs	**O:** ventilation > 4 sec	**P:** leaving nest	**Q:** foraging	**R:** feeding self
0	0	0	0	0	0	0	0	0	9	0
0	0	1	0	0	0	0	0	0	8	0
0	0	0	0	0	0	0	0	0	0	2
0	4	1	0	0	0	0	0	0	0	2
15	1	8	7	15	0	2	0	0	0	1
10	0	6	4	2	1	3	0	0	0	0
5	0	1	0	0	1	0	0	0	0	0
1	1	0	0	0	1	0	0	0	0	1
0	1	0	0	0	0	0	0	0	3	0
0	0	0	0	0	0	0	0	0	2	0
0	1	2	0	0	0	0	0	0	0	1
0	2	0	0	0	0	0	0	0	0	1
7	0	20	6	9	0	3	0	0	0	0
1	0	7	3	2	0	2	0	0	0	1

1	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	1

0	0	0	0	0	0	0	0	0	8	1
1	0	0	0	0	0	0	0	0	6	0
0	1	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0

10	0	6	5	8	0	0	0	0	0	0
2	1	1	0	0	0	0	0	0	0	1
2	0	1	0	0	0	0	0	0	0	0
1	1	2	0	0	0	0	0	0	0	2

0	0	0	0	0	0	0	0	0	7	0
0	1	0	0	0	0	0	0	0	6	1
0	0	0	0	0	0	0	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0

10	0	0	0	13	0	0	0	0	0	0
3	0	0	0	2	0	0	0	0	0	0
4	1	3	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0

S: grooming	Ovary development	Age at sampling (days)	Weight (mg)	Role/ Caste
0	0	10	262	FOR
0	1	12	229	FOR
0	1	11	162	NUR
0	1	6	144	NUR
		9.756	**199.25118**	
1	4	19	329	DOM
0	4	16	234	DOM
0	4	15	258	SUB
0	4	17	283	SUB
		16.754	**27695**	
0	1	6	196	FOR
0	0.5	14	202	FOR
0	1	6	183	NUR
0	1.5	8	203	NUR
		8.58	**19620**	
0	4	18	370	DOM
0	4	19	286	DOM

0	4	18	262	SUB
0	4	16	306	SUB
		17.75	**306**	
		3	**108**	
0	0	6	233	FOR
0	1	13	237	FOR
1	0	14	245	NUR
0	1	11	204	NUR
		11	**229.75**	
		8	**41**	
1	4	17	412	DOM
0	4	20	252	SUB
0	4	16	285	SUB
0	4	18	253	SUB
		17.75	**300.5**	
		4	**160**	
0	0	12	233	FOR
0	0	7	184	FOR
0	0	7	166	NUR
0	1.5	12	157	NUR
		9.5	**185**	
		5	**76**	
0	4	17	330	DOM
0	4	19	293	DOM
0	4	18	245	SUB
0	4	18	238	SUB
		18	**276.5**	
		2	**92**	

Supplementary 4.0.1: mapping statistics for the parental whole genome sequencing data and for the RNA-seq samples mapped to the parental reference genomes.

Parental WGS mapped to Bter_1.0

Sample	Percentage of Mapped Reads	Total Mapped Reads	Coverage
m02	97.86	41863548	15.13
m12	97.97	41461013	14.99
m22	97.67	39533179	14.29
m31	98.18	39032037	14.11
q02	98.32	43531647	15.73
q12	97.87	39689801	14.35
q22	98.69	35668767	12.89
q31	97.82	34957377	12.64

Worker abdomen RNA-Seq mapped to parental genomes

	Paternal Genome		**Maternal Genome**	
Sample	Percentage of Mapped Reads	Total Mapped Reads	Percentage of Mapped Reads	Total Mapped Reads
02_10	93.13	14754786	93.07	14745504
02_12	92.58	15272716	92.52	15262602
02_18	92.86	12317557	92.74	12300982
02_22	93.18	10947368	93.05	10932839
02_35	92.34	15191942	92.18	15165617
02_37	90.86	13246569	91.11	13282822
02_44	91.15	14127795	91.34	14157733
02_54	90.56	13752077	90.73	13779212
12_74	90.9	13035223	90.48	12974937
12_75	90.96	15198375	90.72	15157671
12_76	89.2	16483230	88.97	16439047
12_78	90.75	14009175	90.48	13966953
12_82	93.06	13600770	92.71	13550077
12_84	92.99	13272187	92.75	13238064
12_85	93.48	15048159	93.17	14997214
12_89	93.05	14483283	92.8	14443890
22_09	93	14309997	92.61	14249718
22_18	93.2	15986761	92.85	15927663
22_21	93.48	14190777	93.08	14130041
22_23	93.24	12288914	92.88	12241348
22_26	91.47	16999307	91.08	16925609
22_30	85.74	11634205	85.37	11584193

22_35	90.85	13723569	90.85	13723563
22_49	90.09	13727569	89.58	13650555
31_44	90.29	14379784	90.11	14351648
31_45	87.57	14561577	87.39	14531173
31_64	91.07	14352054	90.86	14318659
31_65	90.68	14991514	90.48	14957640
31_79	93.55	15374149	93.63	15387184
31_84	93.14	15261471	93.14	15261557
31_86	93.36	14610038	93.4	14616367
31_89	92.63	13531829	92.69	13540027

Worker head RNA-Seq mapped to parental genomes

	Paternal Genome		Maternal Genome	
Sample	Percentage of Mapped Reads	Total Mapped Reads	Percentage of Mapped Reads	Total Mapped Reads
02_10	92.5	12234262	92.4	12220522
02_12	92.01	18445396	91.88	18418390
02_18	91.98	13652644	91.77	13621317
02_22	92.03	15539787	91.82	15504809
02_35	90.96	15133462	91.32	15193469
02_37	91.89	16301027	91.73	16273302
02_44	92.58	5581688	92.42	5572097
02_54	92.29	18289385	92.08	18246721
12_74	91.94	13283125	91.44	13210084
12_75	91.89	15072775	91.45	15001400
12_76	91.32	14182576	90.92	14119295
12_78	92.35	19337930	91.91	19245971
12_82	91.81	12157812	91.35	12096521
12_84	91.88	10101121	91.44	10052733
12_85	92.23	11686549	91.73	11623167
12_89	91.52	10946168	91.17	10905373
22_09	91.1	16755324	90.67	16675479
22_18	91.03	11955094	90.69	11910993
22_21	91.26	13018423	90.87	12963229
22_23	90.73	13635334	90.22	13558347
22_26	91.54	10468646	91.19	10429470
22_30	91.65	12624668	91.26	12570410

22_35	91.2	14145292	90.76	14077968
22_49	92.21	15308840	91.78	15236109
31_44	91.12	11816031	91.09	11812325
31_45	90.8	11978793	90.84	11983950
31_64	91.61	11318189	91.61	11317945
31_65	91.23	12445807	91.36	12463755
31_79	90.59	14084171	90.91	14132944
31_84	90.56	17139602	90.98	17219844
31_86	89.77	12960080	90.17	13017412
31_89	90.35	14579551	90.59	14618272

Supplementary 4.0.2: genes showing parent-of-origin expression in reproductive workers, 'avgpropmatexpr' refers to the average proportion of maternal expression.

geneID	direction cross	reprstatus1	proportion maternal expression	SE	z	p	Av. Prop. Mat. Exp. Bias	padj
LOC100642393	initial	NONREPR	0.38841319	0.08104611	-5.6015915	2.12E-08	0.38632327	2.88E-07
LOC100642393	reciprocal	NONREPR	0.37758186	0.06948371	-7.1934087	6.32E-13	0.38632327	1.45E-11
LOC100642393	initial	REPR	0.39509933	0.07442987	-5.7225285	1.05E-08	0.38632327	1.49E-07
LOC100642393	reciprocal	REPR	0.38419868	0.0625769	-7.5389567	4.74E-14	0.38632327	1.19E-12
LOC100642707	initial	NONREPR	0.66025154	0.0435908	15.2421011	1.86E-52	0.69362557	2.34E-50
LOC100642707	reciprocal	NONREPR	0.68694378	0.04615734	17.0258866	5.28E-65	0.69362557	8.90E-63
LOC100642707	initial	REPR	0.70124965	0.04874456	17.5046352	1.32E-68	0.69362557	2.43E-66
LOC100642707	reciprocal	REPR	0.72605731	0.05119901	19.0376735	8.31E-81	0.69362557	1.85E-78
LOC100642787	initial	NONREPR	0.97517253	0.72813306	5.04119912	4.63E-07	0.94353096	5.13E-06
LOC100642787	reciprocal	NONREPR	0.98792925	0.79233964	5.55926467	2.71E-08	0.94353096	3.62E-07
LOC100642787	initial	REPR	0.87511725	0.30280682	6.42978434	1.28E-10	0.94353096	2.32E-09
LOC100642787	reciprocal	REPR	0.93590482	0.50274483	5.3330128	9.66E-08	0.94353096	1.20E-06
LOC100642895	initial	NONREPR	0.38251109	0.03702498	-12.934605	2.87E-38	0.38308973	2.43E-36
LOC100642895	reciprocal	NONREPR	0.37345058	0.03902235	-13.260143	3.94E-40	0.38308973	3.49E-38
LOC100642895	initial	REPR	0.39277492	0.04437368	-9.818045	9.42E-23	0.38308973	4.17E-21
LOC100642895	reciprocal	REPR	0.38362233	0.04964397	-9.5520429	1.27E-21	0.38308973	5.26E-20
LOC100642916	initial	NONREPR	0.3811223	0.13256804	-3.6568947	0.00025529	0.39249297	0.00163404
LOC100642916	reciprocal	NONREPR	0.4128962	0.12805467	-2.7488683	0.00598014	0.39249297	0.02457193
LOC100642916	initial	REPR	0.37221877	0.1272058	-4.1091677	3.97E-05	0.39249297	0.00030597
LOC100642916	reciprocal	REPR	0.40373462	0.11987351	-3.2528292	0.00114262	0.39249297	0.00602893
LOC100643010	initial	NONREPR	0.35318301	0.03460968	-17.482886	1.93E-68	0.36629107	3.54E-66
LOC100643010	reciprocal	NONREPR	0.35325019	0.03630359	-16.659041	2.60E-62	0.36629107	4.18E-60
LOC100643010	initial	REPR	0.37933091	0.04088513	-12.043232	2.11E-33	0.36629107	1.50E-31
LOC100643010	reciprocal	REPR	0.37940016	0.04542902	-10.832174	2.42E-27	0.36629107	1.39E-25

LOC100643108	initial	NONREPR	0.38106302	0.02998213	-16.177592	7.26E-59	0.39344496	1.07E-56
LOC100643108	reciprocal	NONREPR	0.43796222	0.02988552	-8.3463983	7.04E-17	0.39344496	2.21E-15
LOC100643108	initial	REPR	0.34973604	0.04910873	-12.629112	1.46E-36	0.39344496	1.17E-34
LOC100643108	reciprocal	REPR	0.40501854	0.05247131	-7.3296697	2.31E-13	0.39344496	5.46E-12
LOC100643295	initial	NONREPR	0.62013218	0.07152076	6.852686	7.25E-12	0.60531803	1.52E-10
LOC100643295	reciprocal	NONREPR	0.58726699	0.07922566	4.4515709	8.52E-06	0.60531803	7.48E-05
LOC100643295	initial	REPR	0.62332219	0.0711559	7.07844808	1.46E-12	0.60531803	3.26E-11
LOC100643295	reciprocal	REPR	0.59055077	0.08371276	4.37499286	1.21E-05	0.60531803	0.00010353
LOC100643431	initial	NONREPR	0.66479578	0.16582459	4.1293026	3.64E-05	0.63362524	0.00028262
LOC100643431	reciprocal	NONREPR	0.59663498	0.14058085	2.78461545	0.00535912	0.63362524	0.02238472
LOC100643431	initial	REPR	0.67038679	0.17483736	4.06054505	4.90E-05	0.63362524	0.00037003
LOC100643431	reciprocal	REPR	0.60268342	0.14586214	2.85652377	0.00428308	0.63362524	0.01863406
LOC100643442	initial	NONREPR	0.59416183	0.08272003	4.60828221	4.06E-06	0.62324831	3.80E-05
LOC100643442	reciprocal	NONREPR	0.64736739	0.06830137	8.89421675	5.88E-19	0.62324831	2.10E-17
LOC100643442	initial	REPR	0.59926801	0.08153521	4.93548828	8.00E-07	0.62324831	8.56E-06
LOC100643442	reciprocal	REPR	0.65219601	0.06727981	9.34464663	9.22E-21	0.62324831	3.62E-19
LOC100643517	initial	NONREPR	0.18492856	0.1303616	-11.378398	5.36E-30	0.1633029	3.44E-28
LOC100643517	reciprocal	NONREPR	0.14424183	0.14356722	-12.401832	2.55E-35	0.1633029	1.94E-33
LOC100643517	initial	REPR	0.18210769	0.12824022	-11.713426	1.09E-31	0.1633029	7.37E-30
LOC100643517	reciprocal	REPR	0.14193351	0.14190648	-12.679638	7.67E-37	0.1633029	6.17E-35
LOC100643622	initial	NONREPR	0.34634929	0.03310388	-19.18583	4.86E-82	0.333425	1.12E-79
LOC100643622	reciprocal	NONREPR	0.32404036	0.02949708	-24.926716	3.82E-137	0.333425	1.62E-134
LOC100643622	initial	REPR	0.34275058	0.04132608	-15.754228	6.42E-56	0.333425	8.97E-54
LOC100643622	reciprocal	REPR	0.32055977	0.04104867	-18.300239	8.24E-75	0.333425	1.69E-72
LOC100644111	initial	NONREPR	0.24476908	0.10069922	-11.188848	4.62E-29	0.29481958	2.85E-27
LOC100644111	reciprocal	NONREPR	0.38694109	0.10199617	-4.5118224	6.43E-06	0.29481958	5.81E-05
LOC100644111	initial	REPR	0.20850204	0.10821352	-12.327281	6.46E-35	0.29481958	4.81E-33
LOC100644111	reciprocal	REPR	0.33906611	0.10396266	-6.4201771	1.36E-10	0.29481958	2.47E-09
LOC100644232	initial	NONREPR	0.12419132	0.32464898	-6.0167275	1.78E-09	0.16538919	2.80E-08

LOC100644232	reciprocal	NONREPR	0.22432229	0.26613276	-4.6617835	3.13E-06	0.16538919	3.00E-05
LOC100644232	initial	REPR	0.11065269	0.33959381	-6.1370124	8.41E-10	0.16538919	1.38E-08
LOC100644232	reciprocal	REPR	0.20239047	0.26829047	-5.1116998	3.19E-07	0.16538919	3.65E-06
LOC100644288	initial	NONREPR	0.22726439	0.11068836	-11.056474	2.04E-28	0.29141764	1.24E-26
LOC100644288	reciprocal	NONREPR	0.32310966	0.10981537	-6.7341891	1.65E-11	0.29141764	3.32E-10
LOC100644288	initial	REPR	0.25643152	0.11010118	-9.6692809	4.07E-22	0.29141764	1.74E-20
LOC100644288	reciprocal	REPR	0.358865	0.1185888	-4.8933268	9.91E-07	0.29141764	1.04E-05
LOC100644543	initial	NONREPR	0.63457549	0.05433257	10.1577481	3.06E-24	0.62197847	1.50E-22
LOC100644543	reciprocal	NONREPR	0.60070877	0.06100986	6.6943149	2.17E-11	0.62197847	4.31E-10
LOC100644543	initial	REPR	0.64309627	0.04929601	11.9447482	6.92E-33	0.62197847	4.85E-31
LOC100644543	reciprocal	REPR	0.60953334	0.06024558	7.39226072	1.44E-13	0.62197847	3.47E-12
LOC100644548	initial	NONREPR	0.78836373	0.07402106	17.7664368	1.29E-70	0.73001389	2.49E-68
LOC100644548	reciprocal	NONREPR	0.73703949	0.06999709	14.7240063	4.52E-49	0.73001389	5.18E-47
LOC100644548	initial	REPR	0.72727071	0.07841502	12.5080519	6.75E-36	0.73001389	5.22E-34
LOC100644548	reciprocal	REPR	0.66738162	0.08017434	8.68564982	3.77E-18	0.73001389	1.27E-16
LOC100644669	initial	NONREPR	0.60864235	0.0255374	17.2926342	5.35E-67	0.61252856	9.55E-65
LOC100644669	reciprocal	NONREPR	0.60913305	0.02615901	16.9604867	1.61E-64	0.61252856	2.69E-62
LOC100644669	initial	REPR	0.61592576	0.02694602	17.527285	8.87E-69	0.61252856	1.64E-66
LOC100644669	reciprocal	REPR	0.61641308	0.02839299	16.7066249	1.17E-62	0.61252856	1.90E-60
LOC100644671	initial	NONREPR	0.92092358	0.19278105	12.7344588	3.80E-37	0.86123122	3.12E-35
LOC100644671	reciprocal	NONREPR	0.86988619	0.16690036	11.383755	5.04E-30	0.86123122	3.25E-28
LOC100644671	initial	REPR	0.86617561	0.20397982	9.15560799	5.41E-20	0.86123122	2.04E-18
LOC100644671	reciprocal	REPR	0.78793952	0.1897977	6.91552018	4.66E-12	0.86123122	9.99E-11
LOC100644680	initial	NONREPR	0.65077586	0.13128166	4.74134263	2.12E-06	0.75802555	2.10E-05
LOC100644680	reciprocal	NONREPR	0.87066275	0.25426339	7.49943347	6.41E-14	0.75802555	1.60E-12
LOC100644680	initial	REPR	0.64358754	0.13820551	4.27601916	1.90E-05	0.75802555	0.00015661
LOC100644680	reciprocal	REPR	0.86707604	0.25803483	7.26781513	3.65E-13	0.75802555	8.50E-12
LOC100644719	initial	NONREPR	0.38718131	0.11585172	-3.9634804	7.39E-05	0.36508996	0.00053822
LOC100644719	reciprocal	NONREPR	0.32015868	0.15035873	-5.0083069	5.49E-07	0.36508996	6.01E-06

LOC100644719	initial	REPR	0.41092927	0.10862908	-3.3151818	0.00091584	0.36508996	0.0049784
LOC100644719	reciprocal	REPR	0.34209056	0.1363746	-4.7955542	1.62E-06	0.36508996	1.64E-05
LOC100644771	initial	NONREPR	0.57423027	0.08304154	3.602195	0.00031554	0.6255245	0.00196987
LOC100644771	reciprocal	NONREPR	0.66000051	0.12468488	5.31978325	1.04E-07	0.6255245	1.29E-06
LOC100644771	initial	REPR	0.59182071	0.05104638	7.27764009	3.40E-13	0.6255245	7.92E-12
LOC100644771	reciprocal	REPR	0.6760465	0.10814626	6.80247195	1.03E-11	0.6255245	2.12E-10
LOC100645035	initial	NONREPR	0.72219428	0.03820408	25.0070736	5.12E-138	0.65184368	2.26E-135
LOC100645035	reciprocal	NONREPR	0.58250622	0.03127168	10.6508573	1.73E-26	0.65184368	9.54E-25
LOC100645035	initial	REPR	0.72127798	0.03811827	24.9436758	2.50E-137	0.65184368	1.07E-134
LOC100645035	reciprocal	REPR	0.58139624	0.03249833	10.1084484	5.07E-24	0.65184368	2.45E-22
LOC100645056	initial	NONREPR	0.35000603	0.15624264	-3.9618681	7.44E-05	0.36618684	0.00054095
LOC100645056	reciprocal	NONREPR	0.40495257	0.12266458	-3.1375899	0.00170343	0.36618684	0.00848691
LOC100645056	initial	REPR	0.32812998	0.15733101	-4.5550784	5.24E-06	0.36618684	4.81E-05
LOC100645056	reciprocal	REPR	0.38165877	0.13567356	-3.55643	0.00037593	0.36618684	0.00230187
LOC100645087	initial	NONREPR	0.56215964	0.12234102	2.0429084	0.04106151	0.60904292	0.11708031
LOC100645087	reciprocal	NONREPR	0.62521055	0.13246933	3.86296267	0.00011202	0.60904292	0.00077989
LOC100645087	initial	REPR	0.59375426	0.08339833	4.55053837	5.35E-06	0.60904292	4.91E-05
LOC100645087	reciprocal	REPR	0.65504723	0.09835694	6.52012835	7.02E-11	0.60904292	1.32E-09
LOC100645154	initial	NONREPR	0.22418168	0.05339763	-23.249377	1.44E-119	0.23303833	5.10E-117
LOC100645154	reciprocal	NONREPR	0.23169951	0.05017234	-23.892441	3.67E-126	0.23303833	1.40E-123
LOC100645154	initial	REPR	0.23426088	0.06011061	-19.70378	2.00E-86	0.23303833	4.97E-84
LOC100645154	reciprocal	REPR	0.24201126	0.05753986	-19.841624	1.30E-87	0.23303833	3.31E-85
LOC100645509	initial	NONREPR	0.54688978	0.04153793	4.52867734	5.94E-06	0.62244867	5.40E-05
LOC100645509	reciprocal	NONREPR	0.57898406	0.06585195	4.83819032	1.31E-06	0.62244867	1.35E-05
LOC100645509	initial	REPR	0.66781616	0.05039848	13.8560592	1.17E-43	0.62244867	1.17E-41
LOC100645509	reciprocal	REPR	0.69610467	0.07504539	11.0442049	2.34E-28	0.62244867	1.42E-26
LOC100645681	initial	NONREPR	0.56664242	0.11403162	2.35167437	0.01868913	0.60586506	0.06268258
LOC100645681	reciprocal	NONREPR	0.61420586	0.12348164	3.76595437	0.00016591	0.60586506	0.00111083
LOC100645681	initial	REPR	0.59816875	0.0757979	5.2487038	1.53E-07	0.60586506	1.84E-06

LOC100645681	reciprocal	REPR	0.64444321	0.09447177	6.29501994	3.07E-10	0.60586506	5.32E-09
LOC100645789	initial	NONREPR	0.6307522	0.12666377	4.22729498	2.37E-05	0.6454837	0.00019092
LOC100645789	reciprocal	NONREPR	0.67764929	0.16805442	4.42112589	9.82E-06	0.6454837	8.53E-05
LOC100645789	initial	REPR	0.612791	0.13981906	3.28323852	0.00102622	0.6454837	0.00549292
LOC100645789	reciprocal	REPR	0.66074231	0.17718028	3.7622921	0.00016836	0.6454837	0.00112522
LOC100645833	initial	NONREPR	0.68592847	0.11736549	6.65572655	2.82E-11	0.6385525	5.53E-10
LOC100645833	reciprocal	NONREPR	0.61216217	0.10719271	4.25784528	2.06E-05	0.6385525	0.00016848
LOC100645833	initial	REPR	0.66589023	0.12193932	5.65572491	1.55E-08	0.6385525	2.16E-07
LOC100645833	reciprocal	REPR	0.59022912	0.1112282	3.28075622	0.00103529	0.6385525	0.00553261
LOC100646012	initial	NONREPR	0.63906623	0.08106551	7.04755428	1.82E-12	0.63095595	4.04E-11
LOC100646012	reciprocal	NONREPR	0.62922383	0.06398202	8.26620516	1.38E-16	0.63095595	4.21E-15
LOC100646012	initial	REPR	0.6327235	0.08537844	6.37067842	1.88E-10	0.63095595	3.34E-09
LOC100646012	reciprocal	REPR	0.62281023	0.07347189	6.82564985	8.75E-12	0.63095595	1.82E-10
LOC100646202	initial	NONREPR	0.70540002	0.04117647	21.2049893	8.59E-100	0.71959813	2.55E-97
LOC100646202	reciprocal	NONREPR	0.72419078	0.0558569	17.2824757	6.38E-67	0.71959813	1.13E-64
LOC100646202	initial	REPR	0.71519999	0.04666575	19.7312806	1.16E-86	0.71959813	2.93E-84
LOC100646202	reciprocal	REPR	0.73360173	0.05144051	19.6921425	2.52E-86	0.71959813	6.20E-84
LOC100646322	initial	NONREPR	0.50278181	0.23439276	0.0474731	0.96213617	0.65510339	0.98265115
LOC100646322	reciprocal	NONREPR	0.60462004	0.10240603	4.14773434	3.36E-05	0.65510339	0.00026251
LOC100646322	initial	REPR	0.71865176	0.24853016	3.77331957	0.00016109	0.65510339	0.00108142
LOC100646322	reciprocal	REPR	0.79435994	0.12607535	10.7190607	8.28E-27	0.65510339	4.66E-25
LOC100646468	initial	NONREPR	0.69555501	0.13797431	5.98821393	2.12E-09	0.69414015	3.29E-08
LOC100646468	reciprocal	NONREPR	0.66393423	0.14570604	4.67294431	2.97E-06	0.69414015	2.86E-05
LOC100646468	initial	REPR	0.72353327	0.07878004	12.211926	2.68E-34	0.69414015	1.95E-32
LOC100646468	reciprocal	REPR	0.69353806	0.08807508	9.27291315	1.81E-20	0.69414015	7.02E-19
LOC100646523	initial	NONREPR	0.64911559	0.10071926	6.10760994	1.01E-09	0.61827262	1.64E-08
LOC100646523	reciprocal	NONREPR	0.58768985	0.10067092	3.52061424	0.00043055	0.61827262	0.00259609
LOC100646523	initial	REPR	0.64886344	0.09809339	6.25982133	3.85E-10	0.61827262	6.58E-09
LOC100646523	reciprocal	REPR	0.58742162	0.10239894	3.45039322	0.00055977	0.61827262	0.0032487

LOC100646607	initial	NONREPR	0.43193193	0.07385997	-3.7093606	0.00020778	0.37867007	0.00135726
LOC100646607	reciprocal	NONREPR	0.32185556	0.07517227	-9.9139932	3.62E-23	0.37867007	1.64E-21
LOC100646607	initial	REPR	0.43568927	0.06741991	-3.8367851	0.00012466	0.37867007	0.00086069
LOC100646607	reciprocal	REPR	0.32520353	0.06546116	-11.151039	7.08E-29	0.37867007	4.35E-27
LOC100646622	initial	NONREPR	0.35626171	0.1687756	-3.5054041	0.00045591	0.34130715	0.00272171
LOC100646622	reciprocal	NONREPR	0.29524378	0.13818294	-6.2963674	3.05E-10	0.34130715	5.29E-09
LOC100646622	initial	REPR	0.38874811	0.16352647	-2.7676101	0.0056469	0.34130715	0.02340119
LOC100646622	reciprocal	REPR	0.32497502	0.12270094	-5.957586	2.56E-09	0.34130715	3.92E-08
LOC100646719	initial	NONREPR	0.64629811	0.08769648	6.87378108	6.25E-12	0.6587505	1.32E-10
LOC100646719	reciprocal	NONREPR	0.70537471	0.11772787	7.41561753	1.21E-13	0.6587505	2.94E-12
LOC100646719	initial	REPR	0.61065732	0.10515514	4.28011496	1.87E-05	0.6587505	0.00015401
LOC100646719	reciprocal	REPR	0.67267186	0.12918009	5.57589371	2.46E-08	0.6587505	3.31E-07
LOC100646727	initial	NONREPR	0.42877067	0.10809605	-2.6538301	0.00795839	0.38298487	0.03124394
LOC100646727	reciprocal	NONREPR	0.34690417	0.0748361	-8.4541459	2.81E-17	0.38298487	9.09E-16
LOC100646727	initial	REPR	0.41867123	0.10148125	-3.2343956	0.001219	0.38298487	0.00636506
LOC100646727	reciprocal	REPR	0.33759342	0.06154899	-10.951231	6.56E-28	0.38298487	3.89E-26
LOC100646825	initial	NONREPR	0.32718712	0.22381307	-3.2211479	0.00127678	0.32838658	0.00662506
LOC100646825	reciprocal	NONREPR	0.30351338	0.15805069	-5.2554209	1.48E-07	0.32838658	1.78E-06
LOC100646825	initial	REPR	0.35375074	0.21688706	-2.7783712	0.00546322	0.32838658	0.02274989
LOC100646825	reciprocal	REPR	0.32909509	0.14182492	-5.0222533	5.11E-07	0.32838658	5.62E-06
LOC100646847	initial	NONREPR	0.42045727	0.0857672	-3.7414832	0.00018294	0.37301809	0.00121237
LOC100646847	reciprocal	NONREPR	0.33259564	0.08443993	-8.2480958	1.61E-16	0.37301809	4.89E-15
LOC100646847	initial	REPR	0.41310432	0.07502678	-4.6802881	2.86E-06	0.37301809	2.77E-05
LOC100646847	reciprocal	REPR	0.32591512	0.0704034	-10.322215	5.59E-25	0.37301809	2.86E-23
LOC100646910	initial	NONREPR	0.79770396	0.13147295	10.4356478	1.70E-25	0.71165353	9.00E-24
LOC100646910	reciprocal	NONREPR	0.62944785	0.10405507	5.09200416	3.54E-07	0.71165353	4.02E-06
LOC100646910	initial	REPR	0.79455335	0.13388798	10.1024282	5.39E-24	0.71165353	2.60E-22
LOC100646910	reciprocal	REPR	0.62490895	0.1030273	4.95438732	7.26E-07	0.71165353	7.83E-06
LOC100646945	initial	NONREPR	0.40083636	0.08938708	-4.4970872	6.89E-06	0.39364736	6.20E-05

LOC100646945	reciprocal	NONREPR	0.3946168	0.07242996	-5.908418	3.45E-09	0.39364736	5.21E-08
LOC100646945	initial	REPR	0.3926554	0.0913454	-4.7748869	1.80E-06	0.39364736	1.80E-05
LOC100646945	reciprocal	REPR	0.3864809	0.0712757	-6.483682	8.95E-11	0.39364736	1.66E-09
LOC100646967	initial	NONREPR	0.42399199	0.08180665	-3.7455024	0.00018003	0.37598142	0.00119576
LOC100646967	reciprocal	NONREPR	0.34237639	0.07810859	-8.3565974	6.46E-17	0.37598142	2.03E-15
LOC100646967	initial	REPR	0.40896523	0.07165511	-5.139127	2.76E-07	0.37598142	3.18E-06
LOC100646967	reciprocal	REPR	0.32859209	0.06685009	-10.688986	1.15E-26	0.37598142	6.40E-25
LOC100647061	initial	NONREPR	0.3653001	0.01645381	-33.574783	3.92E-247	0.35944645	4.20E-244
LOC100647061	reciprocal	NONREPR	0.3551934	0.01619966	-36.808668	1.34E-296	0.35944645	2.01E-293
LOC100647061	initial	REPR	0.36368963	0.0162976	-34.323187	3.54E-258	0.35944645	3.94E-255
LOC100647061	reciprocal	REPR	0.35360267	0.0154394	-39.071492	0	0.35944645	0
LOC100647088	initial	NONREPR	0.30951953	0.03336829	-24.04578	9.24E-128	0.29721636	3.56E-125
LOC100647088	reciprocal	NONREPR	0.35100658	0.03493178	-17.594798	2.70E-69	0.29721636	5.10E-67
LOC100647088	initial	REPR	0.24594429	0.03368844	-33.256544	1.64E-242	0.29721636	1.70E-239
LOC100647088	reciprocal	REPR	0.28239503	0.03540659	-26.340078	6.67E-153	0.29721636	3.45E-150
LOC100647189	initial	NONREPR	0.56998181	0.11020496	2.55684459	0.01056264	0.62274018	0.03936638
LOC100647189	reciprocal	NONREPR	0.6467052	0.13193161	4.58258422	4.59E-06	0.62274018	4.26E-05
LOC100647189	initial	REPR	0.59992005	0.07100139	5.70597275	1.16E-08	0.62274018	1.64E-07
LOC100647189	reciprocal	REPR	0.67435366	0.09762159	7.45678015	8.87E-14	0.62274018	2.18E-12
LOC100647211	initial	NONREPR	0.66577652	0.11704254	5.88798033	3.91E-09	0.64173132	5.86E-08
LOC100647211	reciprocal	NONREPR	0.59655891	0.13091889	2.98770873	0.00281077	0.64173132	0.01302498
LOC100647211	initial	REPR	0.68600892	0.11401299	6.85471104	7.15E-12	0.64173132	1.50E-10
LOC100647211	reciprocal	REPR	0.61858094	0.13227298	3.65554164	0.00025664	0.64173132	0.0016407
LOC100647228	initial	NONREPR	0.65887215	0.10325587	6.3751545	1.83E-10	0.67592392	3.26E-09
LOC100647228	reciprocal	NONREPR	0.68036966	0.09987485	7.56417789	3.90E-14	0.67592392	9.87E-13
LOC100647228	initial	REPR	0.67169378	0.10027604	7.13885177	9.41E-13	0.67592392	2.14E-11
LOC100647228	reciprocal	REPR	0.69276008	0.1004383	8.09506738	5.72E-16	0.67592392	1.66E-14
LOC100647251	initial	NONREPR	0.7389909	0.07460078	13.9506631	3.12E-44	0.71803742	3.15E-42
LOC100647251	reciprocal	NONREPR	0.72666657	0.08795924	11.1162318	1.05E-28	0.71803742	6.41E-27

LOC100647251	initial	REPR	0.70981437	0.09461184	9.45423647	3.25E-21	0.71803742	1.31E-19
LOC100647251	reciprocal	REPR	0.69667785	0.10702586	7.76940916	7.89E-15	0.71803742	2.11E-13
LOC100647278	initial	NONREPR	0.64897985	0.03009559	20.4202045	1.11E-92	0.63286709	3.08E-90
LOC100647278	reciprocal	NONREPR	0.58873027	0.03255318	11.0194724	3.08E-28	0.63286709	1.85E-26
LOC100647278	initial	REPR	0.67604925	0.02920518	25.1898636	5.17E-140	0.63286709	2.35E-137
LOC100647278	reciprocal	REPR	0.61770897	0.0309345	15.5113278	2.91E-54	0.63286709	3.92E-52
LOC100647282	initial	NONREPR	0.32310162	0.11889996	-6.219971	4.97E-10	0.30740515	8.37E-09
LOC100647282	reciprocal	NONREPR	0.28312953	0.11684404	-7.9506897	1.85E-15	0.30740515	5.21E-14
LOC100647282	initial	REPR	0.33199404	0.11239565	-6.2207041	4.95E-10	0.30740515	8.34E-09
LOC100647282	reciprocal	REPR	0.29139542	0.1114035	-7.976558	1.50E-15	0.30740515	4.24E-14
LOC100647304	initial	NONREPR	0.57148086	0.11251577	2.55871316	0.01050604	0.62118313	0.03920307
LOC100647304	reciprocal	NONREPR	0.64385961	0.13477156	4.39377332	1.11E-05	0.62118313	9.57E-05
LOC100647304	initial	REPR	0.59950629	0.07196894	5.60531261	2.08E-08	0.62118313	2.83E-07
LOC100647304	reciprocal	REPR	0.66988578	0.10065335	7.03074985	2.05E-12	0.62118313	4.53E-11
LOC100647326	initial	NONREPR	0.70397969	0.01764551	49.0958631	0	0.61235604	0
LOC100647326	reciprocal	NONREPR	0.52177356	0.01657769	5.25702501	1.46E-07	0.61235604	1.77E-06
LOC100647326	initial	REPR	0.70303161	0.01735749	49.6486669	0	0.61235604	0
LOC100647326	reciprocal	REPR	0.52063928	0.01594249	5.18137722	2.20E-07	0.61235604	2.58E-06
LOC100647368	initial	NONREPR	0.64098855	0.0990587	5.8516546	4.87E-09	0.63618446	7.22E-08
LOC100647368	reciprocal	NONREPR	0.63792591	0.11869844	4.77153114	1.83E-06	0.63618446	1.83E-05
LOC100647368	initial	REPR	0.63445486	0.12601451	4.37549892	1.21E-05	0.63618446	0.00010338
LOC100647368	reciprocal	REPR	0.63136854	0.14382183	3.74138176	0.00018301	0.63618446	0.00121259
LOC100647417	initial	NONREPR	0.40488512	0.01421267	-27.09914	1.01E-161	0.38873015	5.93E-159
LOC100647417	reciprocal	NONREPR	0.36843172	0.01119104	-48.159144	0	0.38873015	0
LOC100647417	initial	REPR	0.40909956	0.01390424	-26.444387	4.23E-154	0.38873015	2.23E-151
LOC100647417	reciprocal	REPR	0.37250422	0.01072393	-48.628503	0	0.38873015	0
LOC100647426	initial	NONREPR	0.56960134	0.1133941	2.47124666	0.01346429	0.61754449	0.04802354
LOC100647426	reciprocal	NONREPR	0.63795706	0.13475495	4.20398782	2.62E-05	0.61754449	0.00020955
LOC100647426	initial	REPR	0.59806098	0.07305356	5.43973947	5.34E-08	0.61754449	6.87E-07

LOC100647426	reciprocal	REPR	0.66455859	0.10189365	6.70969925	1.95E-11	0.61754449	3.90E-10
LOC100647466	initial	NONREPR	0.75345807	0.15181043	7.35879147	1.86E-13	0.70558491	4.41E-12
LOC100647466	reciprocal	NONREPR	0.61581284	0.20939598	2.25321079	0.02424586	0.70558491	0.07697766
LOC100647466	initial	REPR	0.78975264	0.17565179	7.53442409	4.90E-14	0.70558491	1.23E-12
LOC100647466	reciprocal	REPR	0.66331608	0.22761066	2.97924114	0.00288963	0.70558491	0.01333895
LOC100647560	initial	NONREPR	0.65489949	0.06618801	9.67918662	3.70E-22	0.75764199	1.58E-20
LOC100647560	reciprocal	NONREPR	0.8394216	0.08273577	19.9905164	6.66E-89	0.75764199	1.74E-86
LOC100647560	initial	REPR	0.6813712	0.07231434	10.5107844	7.71E-26	0.75764199	4.15E-24
LOC100647560	reciprocal	REPR	0.85487566	0.08639341	20.5266245	1.25E-93	0.75764199	3.49E-91
LOC100647603	initial	NONREPR	0.72332658	0.2399128	4.00571776	6.18E-05	0.8401237	0.00045718
LOC100647603	reciprocal	NONREPR	0.68881656	0.23113548	3.43777765	0.00058651	0.8401237	0.00338088
LOC100647603	initial	REPR	0.97626485	0.210465	17.659834	8.55E-70	0.8401237	1.62E-67
LOC100647603	reciprocal	REPR	0.97208683	0.19241411	18.4515907	5.06E-76	0.8401237	1.06E-73
LOC100647654	initial	NONREPR	0.35610465	0.04542962	-13.038005	7.44E-39	0.34637328	6.38E-37
LOC100647654	reciprocal	NONREPR	0.34112257	0.04399361	-14.963437	1.27E-50	0.34637328	1.53E-48
LOC100647654	initial	REPR	0.35157856	0.04503272	-13.592509	4.44E-42	0.34637328	4.18E-40
LOC100647654	reciprocal	REPR	0.33668734	0.04271673	-15.874149	9.57E-57	0.34637328	1.36E-54
LOC100647684	initial	NONREPR	0.63039182	0.03816033	13.9909182	1.77E-44	0.65005203	1.80E-42
LOC100647684	reciprocal	NONREPR	0.6351267	0.04474	12.3887859	3.01E-35	0.65005203	2.27E-33
LOC100647684	initial	REPR	0.66508312	0.03582798	19.1478757	1.01E-81	0.65005203	2.31E-79
LOC100647684	reciprocal	REPR	0.6696065	0.04361676	16.1957421	5.40E-59	0.65005203	8.03E-57
LOC100647716	initial	NONREPR	0.56280097	0.13080647	1.93061928	0.05353015	0.63431177	0.14381349
LOC100647716	reciprocal	NONREPR	0.60641612	0.11531788	3.74852732	0.00017788	0.63431177	0.001183
LOC100647716	initial	REPR	0.66460958	0.11379816	6.00980264	1.86E-09	0.63431177	2.91E-08
LOC100647716	reciprocal	REPR	0.70342042	0.10760594	8.02594364	1.01E-15	0.63431177	2.87E-14
LOC100647760	initial	NONREPR	0.09682084	0.2033847	-10.979482	4.80E-28	0.12504473	2.86E-26
LOC100647760	reciprocal	NONREPR	0.13922103	0.21200588	-8.5930397	8.47E-18	0.12504473	2.81E-16
LOC100647760	initial	REPR	0.10871266	0.18518763	-11.361226	6.52E-30	0.12504473	4.18E-28
LOC100647760	reciprocal	REPR	0.15542439	0.20289374	-8.3426668	7.26E-17	0.12504473	2.27E-15

LOC100647772	initial	NONREPR	0.37089262	0.03961799	-13.337108	1.41E-40	0.36204654	1.27E-38
LOC100647772	reciprocal	NONREPR	0.35719013	0.04259604	-13.794257	2.76E-43	0.36204654	2.72E-41
LOC100647772	initial	REPR	0.36687037	0.03846503	-14.186044	1.12E-45	0.36204654	1.20E-43
LOC100647772	reciprocal	REPR	0.35323305	0.04074388	-14.845371	7.45E-50	0.36204654	8.74E-48
LOC100647792	initial	NONREPR	0.32893255	0.07610119	-9.3693264	7.30E-21	0.31144274	2.88E-19
LOC100647792	reciprocal	NONREPR	0.2732194	0.07806196	-12.532987	4.93E-36	0.31144274	3.85E-34
LOC100647792	initial	REPR	0.35070513	0.08383748	-7.3468472	2.03E-13	0.31144274	4.81E-12
LOC100647792	reciprocal	REPR	0.29291389	0.08570491	-10.282652	8.44E-25	0.31144274	4.26E-23
LOC100647880	initial	NONREPR	0.20779289	0.29009391	-4.6132682	3.96E-06	0.24741563	3.72E-05
LOC100647880	reciprocal	NONREPR	0.29867185	0.29874733	-2.8573658	0.00427173	0.24741563	0.01859817
LOC100647880	initial	REPR	0.19758664	0.29627076	-4.7302903	2.24E-06	0.24741563	2.21E-05
LOC100647880	reciprocal	REPR	0.28561116	0.28421925	-3.225665	0.0012568	0.24741563	0.00653381
LOC100647914	initial	NONREPR	0.4137638	0.06651188	-5.2385754	1.62E-07	0.39048604	1.93E-06
LOC100647914	reciprocal	NONREPR	0.36842854	0.07382131	-7.3009315	2.86E-13	0.39048604	6.71E-12
LOC100647914	initial	REPR	0.41251804	0.07385151	-4.7875203	1.69E-06	0.39048604	1.70E-05
LOC100647914	reciprocal	REPR	0.36723378	0.08241925	-6.6016425	4.07E-11	0.39048604	7.81E-10
LOC100647965	initial	NONREPR	0.35572436	0.04944858	-12.011881	3.08E-33	0.34359309	2.19E-31
LOC100647965	reciprocal	NONREPR	0.33907647	0.04756266	-14.032278	9.89E-45	0.34359309	1.02E-42
LOC100647965	initial	REPR	0.34802223	0.04936576	-12.716186	4.81E-37	0.34359309	3.92E-35
LOC100647965	reciprocal	REPR	0.33154931	0.04659084	-15.049871	3.46E-51	0.34359309	4.27E-49
LOC100648000	initial	NONREPR	0.37554094	0.09992457	-5.0890214	3.60E-07	0.36772516	4.07E-06
LOC100648000	reciprocal	NONREPR	0.36074685	0.09965771	-5.7408915	9.42E-09	0.36772516	1.35E-07
LOC100648000	initial	REPR	0.37469643	0.10453096	-4.8992287	9.62E-07	0.36772516	1.02E-05
LOC100648000	reciprocal	REPR	0.35991643	0.10103007	-5.6985694	1.21E-08	0.36772516	1.70E-07
LOC100648001	initial	NONREPR	0.77969968	0.06269766	20.1589202	2.25E-90	0.77655331	6.03E-88
LOC100648001	reciprocal	NONREPR	0.74284806	0.06032514	17.5851141	3.20E-69	0.77655331	6.01E-67
LOC100648001	initial	REPR	0.80854196	0.03236629	44.5081553	0	0.77655331	0
LOC100648001	reciprocal	REPR	0.77512354	0.03599237	34.3814893	4.77E-259	0.77655331	5.51E-256
LOC100648033	initial	NONREPR	0.29186843	0.13623699	-6.505772	7.73E-11	0.34909862	1.45E-09

LOC100648033	reciprocal	NONREPR	0.27700519	0.16874307	-5.6853644	1.31E-08	0.34909862	1.83E-07
LOC100648033	initial	REPR	0.42261763	0.11195213	-2.7872353	0.00531599	0.34909862	0.02223857
LOC100648033	reciprocal	REPR	0.40490323	0.13842947	-2.7817482	0.0054067	0.34909862	0.02253954
LOC100648034	initial	NONREPR	0.32135471	0.02742035	-27.262708	1.17E-163	0.31284487	7.06E-161
LOC100648034	reciprocal	NONREPR	0.3145378	0.05180051	-15.038252	4.12E-51	0.31284487	5.03E-49
LOC100648034	initial	REPR	0.3110919	0.03219174	-24.696381	1.17E-134	0.31284487	4.75E-132
LOC100648034	reciprocal	REPR	0.30439505	0.05539271	-14.919933	2.45E-50	0.31284487	2.94E-48
LOC100648162	initial	NONREPR	0.36708347	0.0581371	-9.3700807	7.25E-21	0.34896643	2.86E-19
LOC100648162	reciprocal	NONREPR	0.34092925	0.05461108	-12.070003	1.52E-33	0.34896643	1.09E-31
LOC100648162	initial	REPR	0.35682937	0.05867245	-10.041379	1.00E-23	0.34896643	4.69E-22
LOC100648162	reciprocal	REPR	0.33102363	0.05421583	-12.977003	1.65E-38	0.34896643	1.40E-36
LOC100648188	initial	NONREPR	0.65096455	0.06334283	9.83981528	7.58E-23	0.65549332	3.38E-21
LOC100648188	reciprocal	NONREPR	0.65879863	0.05976757	11.0083966	3.48E-28	0.65549332	2.08E-26
LOC100648188	initial	REPR	0.65219461	0.06460893	9.73085197	2.23E-22	0.65549332	9.69E-21
LOC100648188	reciprocal	REPR	0.6600155	0.06218169	10.6681446	1.43E-26	0.65549332	7.95E-25
LOC100648261	initial	NONREPR	0.3230608	0.09037857	-8.184915	2.72E-16	0.29268604	8.09E-15
LOC100648261	reciprocal	NONREPR	0.25737579	0.10303778	-10.284121	8.31E-25	0.29268604	4.20E-23
LOC100648261	initial	REPR	0.3283243	0.10223375	-7.0013457	2.54E-12	0.29268604	5.54E-11
LOC100648261	reciprocal	REPR	0.26198328	0.11547955	-8.9685645	3.00E-19	0.29268604	1.09E-17
LOC100648300	initial	NONREPR	0.44400549	0.1873757	-1.2003771	0.22999293	0.67223483	0.41416658
LOC100648300	reciprocal	NONREPR	0.49005939	0.18177858	-0.2187698	0.82682936	0.67223483	0.9089251
LOC100648300	initial	REPR	0.86750063	0.09341074	20.1158697	5.36E-90	0.67223483	1.41E-87
LOC100648300	reciprocal	REPR	0.88737382	0.09922137	20.8039074	3.99E-96	0.67223483	1.14E-93
LOC100648410	initial	NONREPR	0.32747414	0.03237918	-22.22513	1.96E-109	0.33809677	6.48E-107
LOC100648410	reciprocal	NONREPR	0.32837042	0.02728861	-26.222096	1.49E-151	0.33809677	7.57E-149
LOC100648410	initial	REPR	0.34780972	0.03806103	-16.517706	2.74E-61	0.33809677	4.30E-59
LOC100648410	reciprocal	REPR	0.34873279	0.0366246	-17.054492	3.24E-65	0.33809677	5.49E-63
LOC100648417	initial	NONREPR	0.5539509	0.27697283	0.78219592	0.43409944	0.68877683	0.62518647
LOC100648417	reciprocal	NONREPR	0.52661465	0.28233758	0.37741816	0.70586287	0.68877683	0.83325502

LOC100648417	initial	REPR	0.84476603	0.22881199	7.40401014	1.32E-13	0.68877683	3.19E-12
LOC100648417	reciprocal	REPR	0.82977572	0.1920662	8.24735721	1.62E-16	0.68877683	4.91E-15
LOC100648509	initial	NONREPR	0.35309261	0.04297043	-14.090452	4.35E-45	0.34238999	4.56E-43
LOC100648509	reciprocal	NONREPR	0.3386714	0.04342141	-15.412225	1.35E-53	0.34238999	1.78E-51
LOC100648509	initial	REPR	0.3460384	0.04338313	-14.671575	9.80E-49	0.34238999	1.12E-46
LOC100648509	reciprocal	REPR	0.33175754	0.04374948	-16.005829	1.16E-57	0.34238999	1.67E-55
LOC100648528	initial	NONREPR	0.3168915	0.03262298	-23.544578	1.43E-122	0.32265617	5.16E-120
LOC100648528	reciprocal	NONREPR	0.31632292	0.03080959	-25.015656	4.13E-138	0.32265617	1.85E-135
LOC100648528	initial	REPR	0.32899505	0.03959906	-17.998755	1.99E-72	0.32265617	3.96E-70
LOC100648528	reciprocal	REPR	0.3284152	0.04105413	-17.424838	5.35E-68	0.32265617	9.73E-66
LOC100648624	initial	NONREPR	0.60429718	0.06087021	6.9558264	3.51E-12	0.62634774	7.60E-11
LOC100648624	reciprocal	NONREPR	0.68113257	0.07695867	9.86219722	6.07E-23	0.62634774	2.72E-21
LOC100648624	initial	REPR	0.57016975	0.06889034	4.10135534	4.11E-05	0.62634774	0.00031552
LOC100648624	reciprocal	REPR	0.64979146	0.08289588	7.45661478	8.88E-14	0.62634774	2.18E-12
LOC100648630	initial	NONREPR	0.39088882	0.15818552	-2.8041608	0.00504477	0.36972321	0.02131183
LOC100648630	reciprocal	NONREPR	0.41463534	0.15334379	-2.2487741	0.02452687	0.36972321	0.07771371
LOC100648630	initial	REPR	0.32566135	0.1636585	-4.4475198	8.69E-06	0.36972321	7.62E-05
LOC100648630	reciprocal	REPR	0.34770731	0.15589691	-4.0355662	5.45E-05	0.36972321	0.00040789
LOC100648770	initial	NONREPR	0.31191322	0.01726598	-45.823623	0	0.31462682	0
LOC100648770	reciprocal	NONREPR	0.32383474	0.02122682	-34.682736	1.43E-263	0.31462682	1.79E-260
LOC100648770	initial	REPR	0.30548509	0.01980227	-41.475678	0	0.31462682	0
LOC100648770	reciprocal	REPR	0.31727421	0.02388992	-32.077411	9.11E-226	0.31462682	7.81E-223
LOC100648955	initial	NONREPR	0.35144868	0.04060977	-15.086948	1.97E-51	0.39238614	2.45E-49
LOC100648955	reciprocal	NONREPR	0.46451484	0.04434391	-3.2062951	0.00134456	0.39238614	0.00692292
LOC100648955	initial	REPR	0.3218492	0.05273024	-14.13395	2.35E-45	0.39238614	2.49E-43
LOC100648955	reciprocal	REPR	0.43173183	0.05733725	-4.7925003	1.65E-06	0.39238614	1.66E-05
LOC100648995	initial	NONREPR	0.62353483	0.08160737	6.18300888	6.29E-10	0.62688237	1.04E-08
LOC100648995	reciprocal	NONREPR	0.62162696	0.08091588	6.13550291	8.49E-10	0.62688237	1.39E-08
LOC100648995	initial	REPR	0.63212892	0.09710739	5.57486752	2.48E-08	0.62688237	3.33E-07

LOC100648995	reciprocal	REPR	0.63023878	0.09902446	5.38494515	7.25E-08	0.62688237	9.18E-07
LOC100649275	initial	NONREPR	0.23435532	0.0803775	-14.728995	4.20E-49	0.27934317	4.83E-47
LOC100649275	reciprocal	NONREPR	0.300767	0.07743561	-10.894834	1.22E-27	0.27934317	7.13E-26
LOC100649275	initial	REPR	0.25614679	0.09243268	-11.533725	8.92E-31	0.27934317	5.97E-29
LOC100649275	reciprocal	REPR	0.32610358	0.09451847	-7.679572	1.60E-14	0.27934317	4.16E-13
LOC100649394	initial	NONREPR	0.25080957	0.08927655	-12.25741	1.53E-34	0.26932012	1.12E-32
LOC100649394	reciprocal	NONREPR	0.26809984	0.10254829	-9.7932849	1.20E-22	0.26932012	5.30E-21
LOC100649394	initial	REPR	0.27013063	0.10264	-9.6839426	3.53E-22	0.26932012	1.51E-20
LOC100649394	reciprocal	REPR	0.28824042	0.11808579	-7.6549881	1.93E-14	0.26932012	5.01E-13
LOC100649421	initial	NONREPR	0.77129737	0.04866387	24.9805751	9.94E-138	0.74049882	4.33E-135
LOC100649421	reciprocal	NONREPR	0.74109289	0.04284409	24.5461282	4.76E-133	0.74049882	1.90E-130
LOC100649421	initial	REPR	0.74114331	0.04879715	21.5569851	4.55E-103	0.74049882	1.42E-100
LOC100649421	reciprocal	REPR	0.70846171	0.0470427	18.8748657	1.84E-79	0.74049882	3.91E-77
LOC100649428	initial	NONREPR	0.44095816	0.06185491	-3.8359822	0.00012506	0.39279605	0.00086272
LOC100649428	reciprocal	NONREPR	0.36022461	0.06031384	-9.5233433	1.68E-21	0.39279605	6.90E-20
LOC100649428	initial	REPR	0.42480175	0.05403523	-5.6091587	2.03E-08	0.39279605	2.77E-07
LOC100649428	reciprocal	REPR	0.34519969	0.05203534	-12.303317	8.69E-35	0.39279605	6.45E-33
LOC100649524	initial	NONREPR	0.65962822	0.21930787	3.01693637	0.00255343	0.76784185	0.01199726
LOC100649524	reciprocal	NONREPR	0.87443961	0.23450487	8.2761454	1.27E-16	0.76784185	3.90E-15
LOC100649524	initial	REPR	0.66180008	0.23107481	2.90523381	0.00366979	0.76784185	0.01636418
LOC100649524	reciprocal	REPR	0.8754995	0.25359818	7.69124151	1.46E-14	0.76784185	3.81E-13
LOC100649553	initial	NONREPR	0.43049982	0.05515825	-5.0728986	3.92E-07	0.38443047	4.40E-06
LOC100649553	reciprocal	NONREPR	0.34475104	0.05041583	-12.737919	3.64E-37	0.38443047	2.99E-35
LOC100649553	initial	REPR	0.42384107	0.04884688	-6.2854578	3.27E-10	0.38443047	5.63E-09
LOC100649553	reciprocal	REPR	0.33862997	0.04250168	-15.750095	6.86E-56	0.38443047	9.49E-54
LOC100649672	initial	NONREPR	0.4340949	0.08636001	-3.0704401	0.00213744	0.39233764	0.01030223
LOC100649672	reciprocal	NONREPR	0.34890793	0.0865439	-7.2083995	5.66E-13	0.39233764	1.31E-11
LOC100649672	initial	REPR	0.43583222	0.07457583	-3.4608307	0.00053851	0.39233764	0.00313928
LOC100649672	reciprocal	REPR	0.35051549	0.07402528	-8.3319386	7.95E-17	0.39233764	2.48E-15

LOC100649728	initial	NONREPR	0.35835934	0.17321894	-3.3627512	0.0007717	0.33779416	0.00430157
LOC100649728	reciprocal	NONREPR	0.2883758	0.15024366	-6.0121371	1.83E-09	0.33779416	2.87E-08
LOC100649728	initial	REPR	0.38871824	0.16889492	-2.6803839	0.00735378	0.33779416	0.02925532
LOC100649728	reciprocal	REPR	0.31572324	0.1349652	-5.7310805	9.98E-09	0.33779416	1.42E-07
LOC100649839	initial	NONREPR	0.35283326	0.16581504	-3.6583434	0.00025385	0.32853706	0.00162633
LOC100649839	reciprocal	NONREPR	0.28559906	0.17222914	-5.3234624	1.02E-07	0.32853706	1.26E-06
LOC100649839	initial	REPR	0.37246928	0.16129112	-3.2341401	0.0012201	0.32853706	0.00636944
LOC100649839	reciprocal	REPR	0.30324662	0.15862087	-5.2444872	1.57E-07	0.32853706	1.88E-06
LOC100649867	initial	NONREPR	0.99430888	0.3347273	15.4249153	1.11E-53	0.98394533	1.47E-51
LOC100649867	reciprocal	NONREPR	0.97325187	0.19899544	18.0616107	6.39E-73	0.98394533	1.28E-70
LOC100649867	initial	REPR	0.99442665	0.31021009	16.7118037	1.08E-62	0.98394533	1.75E-60
LOC100649867	reciprocal	REPR	0.97379392	0.24657086	14.6619438	1.13E-48	0.98394533	1.29E-46
LOC100649900	initial	NONREPR	0.43572776	0.09999707	-2.5852678	0.00973034	0.38384652	0.03685916
LOC100649900	reciprocal	NONREPR	0.33565261	0.08765099	-7.7891698	6.75E-15	0.38384652	1.82E-13
LOC100649900	initial	REPR	0.43185761	0.09138534	-3.0013144	0.00268817	0.38384652	0.01253811
LOC100649900	reciprocal	REPR	0.33214812	0.07359465	-9.4909811	2.29E-21	0.38384652	9.31E-20
LOC100649904	initial	NONREPR	0.75065856	0.17513085	6.29316708	3.11E-10	0.77287405	5.38E-09
LOC100649904	reciprocal	NONREPR	0.80058456	0.19290285	7.20545014	5.79E-13	0.77287405	1.33E-11
LOC100649904	initial	REPR	0.74473181	0.18750176	5.71039671	1.13E-08	0.77287405	1.60E-07
LOC100649904	reciprocal	REPR	0.79552126	0.2123442	6.3977899	1.58E-10	0.77287405	2.83E-09
LOC100649986	initial	NONREPR	0.32913982	0.09768907	-7.2892299	3.12E-13	0.35605636	7.28E-12
LOC100649986	reciprocal	NONREPR	0.41341957	0.10232534	-3.4189652	0.0006286	0.35605636	0.00359124
LOC100649986	initial	REPR	0.30028714	0.09948401	-8.5031849	1.84E-17	0.35605636	6.03E-16
LOC100649986	reciprocal	REPR	0.3813789	0.10463481	-4.6227407	3.79E-06	0.35605636	3.56E-05
LOC100649992	initial	NONREPR	0.34601092	0.0821201	-7.7523084	9.02E-15	0.39329737	2.40E-13
LOC100649992	reciprocal	NONREPR	0.40971717	0.06967317	-5.2406781	1.60E-07	0.39329737	1.91E-06
LOC100649992	initial	REPR	0.37598105	0.07644477	-6.6275565	3.41E-11	0.39329737	6.62E-10
LOC100649992	reciprocal	REPR	0.44148033	0.05963922	-3.9429818	8.05E-05	0.39329737	0.00058019
LOC100650015	initial	NONREPR	0.42842154	0.09907079	-2.9099812	0.0036145	0.37928329	0.01614511

LOC100650015	reciprocal	NONREPR	0.33166911	0.09845991	-7.1160491	1.11E-12	0.37928329	2.51E-11
LOC100650015	initial	REPR	0.42682116	0.08879035	-3.3205484	0.00089841	0.37928329	0.00489785
LOC100650015	reciprocal	REPR	0.33022135	0.08381453	-8.4374883	3.24E-17	0.37928329	1.04E-15
LOC100650024	initial	NONREPR	0.51199386	0.12474526	0.38466095	0.70048863	0.61486688	0.82965837
LOC100650024	reciprocal	NONREPR	0.64148819	0.11535099	5.04398972	4.56E-07	0.61486688	5.06E-06
LOC100650024	initial	REPR	0.59296706	0.12116149	3.10531596	0.00190076	0.61486688	0.00932462
LOC100650024	reciprocal	REPR	0.71301843	0.11153936	8.15935563	3.37E-16	0.61486688	9.93E-15
LOC100650131	initial	NONREPR	0.41106035	0.08055525	-4.4638138	8.05E-06	0.3790036	7.11E-05
LOC100650131	reciprocal	NONREPR	0.34468042	0.07832219	-8.2033627	2.34E-16	0.3790036	7.00E-15
LOC100650131	initial	REPR	0.41340457	0.06970229	-5.020045	5.17E-07	0.3790036	5.67E-06
LOC100650131	reciprocal	REPR	0.34686904	0.06287848	-10.06434	7.94E-24	0.3790036	3.77E-22
LOC100650219	initial	NONREPR	0.6310083	0.05128075	10.4628907	1.28E-25	0.63254196	6.80E-24
LOC100650219	reciprocal	NONREPR	0.66656218	0.0385601	17.9635693	3.76E-72	0.63254196	7.38E-70
LOC100650219	initial	REPR	0.59784892	0.05068284	7.82336318	5.14E-15	0.63254196	1.40E-13
LOC100650219	reciprocal	REPR	0.63474843	0.04315281	12.8066392	1.51E-37	0.63254196	1.25E-35
LOC100650253	initial	NONREPR	0.63741169	0.10804415	5.22145515	1.78E-07	0.61409953	2.11E-06
LOC100650253	reciprocal	NONREPR	0.57405505	0.12732684	2.34369432	0.01909381	0.61409953	0.06378119
LOC100650253	initial	REPR	0.65363542	0.11604055	5.47272337	4.43E-08	0.61409953	5.76E-07
LOC100650253	reciprocal	REPR	0.59129595	0.12918952	2.85878708	0.00425264	0.61409953	0.01852848
LOC100650257	initial	NONREPR	0.41700441	0.06857605	-4.8862953	1.03E-06	0.37314664	1.08E-05
LOC100650257	reciprocal	NONREPR	0.35415022	0.0538033	-11.167452	5.88E-29	0.37314664	3.62E-27
LOC100650257	initial	REPR	0.39130293	0.06226014	-7.0966547	1.28E-12	0.37314664	2.87E-11
LOC100650257	reciprocal	REPR	0.330129	0.04628892	-15.286633	9.39E-53	0.37314664	1.20E-50
LOC100650263	initial	NONREPR	0.25495879	0.18179513	-5.8986047	3.67E-09	0.30355463	5.52E-08
LOC100650263	reciprocal	NONREPR	0.37263052	0.16244354	-3.20695	0.0013415	0.30355463	0.00690955
LOC100650263	initial	REPR	0.23671188	0.16869762	-6.94018	3.92E-12	0.30355463	8.47E-11
LOC100650263	reciprocal	REPR	0.34991735	0.14095773	-4.3942432	1.11E-05	0.30355463	9.55E-05
LOC100650386	initial	NONREPR	0.23578677	0.17370136	-6.7697741	1.29E-11	0.28314862	2.63E-10
LOC100650386	reciprocal	NONREPR	0.34677908	0.15642459	-4.0481324	5.16E-05	0.28314862	0.00038806

LOC100650386	initial	REPR	0.22144266	0.16271986	-7.7266475	1.10E-14	0.28314862	2.92E-13
LOC100650386	reciprocal	REPR	0.32858596	0.13610647	-5.2502096	1.52E-07	0.28314862	1.83E-06
LOC100650448	initial	NONREPR	0.66281405	0.09173858	7.36723756	1.74E-13	0.64033114	4.15E-12
LOC100650448	reciprocal	NONREPR	0.65105252	0.07201913	8.65976657	4.73E-18	0.64033114	1.58E-16
LOC100650448	initial	REPR	0.62985297	0.09304039	5.7134982	1.11E-08	0.64033114	1.57E-07
LOC100650448	reciprocal	REPR	0.61760502	0.07787833	6.15569244	7.48E-10	0.64033114	1.23E-08
LOC100650586	initial	NONREPR	0.62626626	0.07458442	6.9214451	4.47E-12	0.611337	9.61E-11
LOC100650586	reciprocal	NONREPR	0.61324506	0.07798397	5.91112968	3.40E-09	0.611337	5.14E-08
LOC100650586	initial	REPR	0.60953254	0.08078956	5.51244126	3.54E-08	0.611337	4.65E-07
LOC100650586	reciprocal	REPR	0.59630414	0.08860701	4.40246285	1.07E-05	0.611337	9.23E-05
LOC100650744	initial	NONREPR	0.43297006	0.09436266	-2.8585832	0.00425538	0.36921308	0.01853771
LOC100650744	reciprocal	NONREPR	0.33752225	0.09913484	-6.8024071	1.03E-11	0.36921308	2.12E-10
LOC100650744	initial	REPR	0.3991979	0.08319463	-4.9138787	8.93E-07	0.36921308	9.47E-06
LOC100650744	reciprocal	REPR	0.30716212	0.08878356	-9.1618354	5.10E-20	0.36921308	1.93E-18
LOC100651112	initial	NONREPR	0.99832505	0.13218003	48.3453889	0	0.99612166	0
LOC100651112	reciprocal	NONREPR	0.99442318	0.13132851	39.4700616	0	0.99612166	0
LOC100651112	initial	REPR	0.99809101	0.12764835	49.0352731	0	0.99612166	0
LOC100651112	reciprocal	REPR	0.99364742	0.12586679	40.1418119	0	0.99612166	0
LOC100651152	initial	NONREPR	0.63813745	0.04573191	12.4046692	2.47E-35	0.65594858	1.88E-33
LOC100651152	reciprocal	NONREPR	0.7066549	0.04613696	19.0561484	5.84E-81	0.65594858	1.31E-78
LOC100651152	initial	REPR	0.60363764	0.05043447	8.34043102	7.40E-17	0.65594858	2.31E-15
LOC100651152	reciprocal	REPR	0.67536431	0.05033572	14.5532562	5.57E-48	0.65594858	6.26E-46
LOC100651153	initial	NONREPR	0.73796667	0.07169583	14.4419416	2.82E-47	0.77233021	3.11E-45
LOC100651153	reciprocal	NONREPR	0.81361461	0.08091834	18.2118217	4.16E-74	0.77233021	8.44E-72
LOC100651153	initial	REPR	0.73021915	0.07220027	13.7912881	2.88E-43	0.77233021	2.82E-41
LOC100651153	reciprocal	REPR	0.8075204	0.08230666	17.4223833	5.58E-68	0.77233021	1.01E-65
LOC100651339	initial	NONREPR	0.79201446	0.31475856	4.24805314	2.16E-05	0.73079153	0.00017534
LOC100651339	reciprocal	NONREPR	0.66127256	0.26595412	2.5153598	0.0118911	0.73079153	0.04337534
LOC100651339	initial	REPR	0.79902311	0.31671008	4.35792863	1.31E-05	0.73079153	0.00011141

LOC100651339	reciprocal	REPR	0.670856	0.27752147	2.56578048	0.0102944	0.73079153	0.03857074
LOC100651450	initial	NONREPR	0.97831013	0.29705786	12.8223558	1.23E-37	0.94866566	1.02E-35
LOC100651450	reciprocal	NONREPR	0.93477699	0.24624326	10.812461	3.00E-27	0.94866566	1.71E-25
LOC100651450	initial	REPR	0.97007291	0.26899912	12.9316678	2.98E-38	0.94866566	2.52E-36
LOC100651450	reciprocal	REPR	0.9115026	0.22847163	10.2074871	1.84E-24	0.94866566	9.11E-23
LOC100651509	initial	NONREPR	0.92050677	0.05936133	41.2600653	0	0.91548644	0
LOC100651509	reciprocal	NONREPR	0.91060321	0.05753872	40.3384425	0	0.91548644	0
LOC100651509	initial	REPR	0.92037697	0.12870289	19.0165105	1.24E-80	0.91548644	2.75E-78
LOC100651509	reciprocal	REPR	0.91045881	0.14097229	16.4518136	8.14E-61	0.91548644	1.25E-58
LOC100651763	initial	NONREPR	0.69355962	0.09708629	8.41327821	3.99E-17	0.68147758	1.28E-15
LOC100651763	reciprocal	NONREPR	0.66360977	0.07621001	8.9151332	4.87E-19	0.68147758	1.74E-17
LOC100651763	initial	REPR	0.69920107	0.0997637	8.45494218	2.79E-17	0.68147758	9.04E-16
LOC100651763	reciprocal	REPR	0.66953988	0.07951187	8.88049507	6.66E-19	0.68147758	2.37E-17
LOC100651775	initial	NONREPR	0.65928784	0.04263813	15.4819695	4.59E-54	0.67188853	6.13E-52
LOC100651775	reciprocal	NONREPR	0.65704345	0.04385416	14.8251945	1.01E-49	0.67188853	1.18E-47
LOC100651775	initial	REPR	0.68668654	0.03947142	19.8795446	6.12E-88	0.67188853	1.58E-85
LOC100651775	reciprocal	REPR	0.68453628	0.04050499	19.1259872	1.53E-81	0.67188853	3.49E-79
LOC100651786	initial	NONREPR	0.26759864	0.09258488	-10.874782	1.52E-27	0.24079492	8.85E-26
LOC100651786	reciprocal	NONREPR	0.21464925	0.08900751	-14.57321	4.16E-48	0.24079492	4.69E-46
LOC100651786	initial	REPR	0.26689105	0.09823108	-10.286498	8.11E-25	0.24079492	4.11E-23
LOC100651786	reciprocal	REPR	0.21404075	0.09534029	-13.643115	2.22E-42	0.24079492	2.12E-40
LOC100651849	initial	NONREPR	0.56539761	0.09272896	2.83727614	0.00455002	0.64425369	0.0195995
LOC100651849	reciprocal	NONREPR	0.72729303	0.12979022	7.55782398	4.10E-14	0.64425369	1.04E-12
LOC100651849	initial	REPR	0.56077426	0.09136742	2.67387369	0.00749807	0.64425369	0.02976233
LOC100651849	reciprocal	REPR	0.72354984	0.13320142	7.22318815	5.08E-13	0.64425369	1.17E-11
LOC100651955	initial	NONREPR	0.47781621	0.06237396	-1.4235663	0.15457206	0.38627571	0.31361418
LOC100651955	reciprocal	NONREPR	0.34783125	0.05452666	-11.528047	9.53E-31	0.38627571	6.36E-29
LOC100651955	initial	REPR	0.42142771	0.05825986	-5.4396841	5.34E-08	0.38627571	6.87E-07
LOC100651955	reciprocal	REPR	0.29802766	0.05195193	-16.490392	4.30E-61	0.38627571	6.66E-59

LOC100652123	initial	NONREPR	0.28768831	0.33751044	-2.6862516	0.00722587	0.29287194	0.02884582
LOC100652123	reciprocal	NONREPR	0.30364013	0.33931357	-2.4461839	0.01443773	0.29287194	0.05089051
LOC100652123	initial	REPR	0.28219238	0.33797532	-2.762369	0.00573836	0.29287194	0.02373436
LOC100652123	reciprocal	REPR	0.29796694	0.34038912	-2.5177009	0.01181236	0.29287194	0.04314579
LOC100652255	initial	NONREPR	0.73344172	0.06182649	16.3708989	3.09E-60	0.6428411	4.68E-58
LOC100652255	reciprocal	NONREPR	0.53865278	0.05240483	2.95622002	0.00311435	0.6428411	0.01423404
LOC100652255	initial	REPR	0.74532775	0.05734461	18.7261987	3.03E-78	0.6428411	6.40E-76
LOC100652255	reciprocal	REPR	0.55394215	0.04543175	4.76784651	1.86E-06	0.6428411	1.86E-05
LOC100652265	initial	NONREPR	0.9998089	3.09242421	2.76886877	0.00562513	0.98728652	0.02334965
LOC100652265	reciprocal	NONREPR	0.97415718	1.40125546	2.5902058	0.00959186	0.98728652	0.03642649
LOC100652265	initial	REPR	0.99981803	3.09710293	2.78049998	0.00542753	0.98728652	0.0226044
LOC100652265	reciprocal	REPR	0.97536198	1.40805663	2.61247861	0.00898883	0.98728652	0.03452061
LOC100652299	initial	NONREPR	0.42348993	0.04862802	-6.3433194	2.25E-10	0.32105855	3.96E-09
LOC100652299	reciprocal	NONREPR	0.38098277	0.04709315	-10.306786	6.57E-25	0.32105855	3.34E-23
LOC100652299	initial	REPR	0.25599095	0.04209175	-25.347272	9.63E-142	0.32105855	4.45E-139
LOC100652299	reciprocal	REPR	0.22377054	0.03996255	-31.12482	1.11E-212	0.32105855	9.02E-210
LOC100652301	initial	NONREPR	0.93176014	0.25978579	10.0623155	8.11E-24	0.89043339	3.83E-22
LOC100652301	reciprocal	NONREPR	0.90879557	0.27080288	8.48963154	2.07E-17	0.89043339	6.77E-16
LOC100652301	initial	REPR	0.87938732	0.18703458	10.6217847	2.36E-26	0.89043339	1.30E-24
LOC100652301	reciprocal	REPR	0.84179052	0.18692548	8.9426609	3.80E-19	0.89043339	1.37E-17
LOC105665800	initial	NONREPR	0.35411704	0.0439569	-13.672275	1.49E-42	0.3536681	1.43E-40
LOC105665800	reciprocal	NONREPR	0.35314679	0.03774364	-16.03543	7.23E-58	0.3536681	1.04E-55
LOC105665800	initial	REPR	0.35418946	0.0432493	-13.888645	7.42E-44	0.3536681	7.45E-42
LOC105665800	reciprocal	REPR	0.35321912	0.03570061	-16.944218	2.12E-64	0.3536681	3.52E-62
LOC105665983	initial	NONREPR	0.6439928	0.11819746	5.01479976	5.31E-07	0.64686015	5.82E-06
LOC105665983	reciprocal	NONREPR	0.61378031	0.13612356	3.40301633	0.00066646	0.64686015	0.00377595
LOC105665983	initial	REPR	0.67925595	0.11713429	6.40593443	1.49E-10	0.64686015	2.70E-09
LOC105665983	reciprocal	REPR	0.65041154	0.13242493	4.68830654	2.75E-06	0.64686015	2.68E-05
LOC105666148	initial	NONREPR	0.61630082	0.11163349	4.24492979	2.19E-05	0.63934609	0.00017755

LOC105666148	reciprocal	NONREPR	0.69107589	0.1160983	6.93510611	4.06E-12	0.63934609	8.76E-11
LOC105666148	initial	REPR	0.58628753	0.11258564	3.09665725	0.00195716	0.63934609	0.00955293
LOC105666148	reciprocal	REPR	0.66372013	0.11906998	5.7102287	1.13E-08	0.63934609	1.60E-07
LOC105666149	initial	NONREPR	0.13971215	0.11105352	-16.367629	3.26E-60	0.17743907	4.91E-58
LOC105666149	reciprocal	NONREPR	0.16949132	0.10009934	-15.876595	9.20E-57	0.17743907	1.31E-54
LOC105666149	initial	REPR	0.18202303	0.11305514	-13.291752	2.58E-40	0.17743907	2.31E-38
LOC105666149	reciprocal	REPR	0.21852976	0.10614912	-12.004385	3.37E-33	0.17743907	2.39E-31
LOC105666191	initial	NONREPR	0.67171354	0.19966578	3.58571908	0.00033615	0.70742178	0.00208423
LOC105666191	reciprocal	NONREPR	0.72360894	0.18648429	5.16094057	2.46E-07	0.70742178	2.86E-06
LOC105666191	initial	REPR	0.6922339	0.13912191	5.82642806	5.66E-09	0.70742178	8.37E-08
LOC105666191	reciprocal	REPR	0.74213076	0.11950241	8.84561928	9.10E-19	0.70742178	3.20E-17
LOC105666212	initial	NONREPR	0.57697095	0.11617395	2.67143409	0.00755279	0.60038393	0.02994787
LOC105666212	reciprocal	NONREPR	0.58506818	0.11268448	3.04934769	0.00229339	0.60038393	0.01095385
LOC105666212	initial	REPR	0.61582901	0.11868927	3.97577299	7.02E-05	0.60038393	0.0005139
LOC105666212	reciprocal	REPR	0.62366759	0.10996371	4.59374017	4.35E-06	0.60038393	4.05E-05
LOC105666325	initial	NONREPR	0.49329642	0.2748643	-0.0975606	0.9222812	0.30215742	0.96240826
LOC105666325	reciprocal	NONREPR	0.31210255	0.35436298	-2.2302216	0.02573274	0.30215742	0.08071687
LOC105666325	initial	REPR	0.26155147	0.34254675	-3.0300107	0.00244545	0.30215742	0.01156531
LOC105666325	reciprocal	REPR	0.14167923	0.42225901	-4.2661312	1.99E-05	0.30215742	0.00016296
LOC105666541	initial	NONREPR	0.37356663	0.10359726	-4.9899582	6.04E-07	0.35915921	6.58E-06
LOC105666541	reciprocal	NONREPR	0.32157578	0.0947937	-7.875413	3.40E-15	0.35915921	9.36E-14
LOC105666541	initial	REPR	0.39749331	0.11048021	-3.7646622	0.00016677	0.35915921	0.00111559
LOC105666541	reciprocal	REPR	0.34400112	0.10061776	-6.4155094	1.40E-10	0.35915921	2.54E-09
LOC105666566	initial	NONREPR	0.4308379	0.0452796	-6.1492003	7.79E-10	0.38865068	1.28E-08
LOC105666566	reciprocal	NONREPR	0.35200063	0.04298298	-14.197638	9.48E-46	0.38865068	1.02E-43
LOC105666566	initial	REPR	0.42509535	0.0397379	-7.5970473	3.03E-14	0.38865068	7.71E-13
LOC105666566	reciprocal	REPR	0.34666885	0.0361371	-17.536383	7.56E-69	0.38865068	1.41E-66
LOC105666573	initial	NONREPR	0.37582125	0.13161107	-3.8547149	0.00011586	0.36796284	0.00080447
LOC105666573	reciprocal	NONREPR	0.3581673	0.11719807	-4.9772789	6.45E-07	0.36796284	7.01E-06

LOC105666573	initial	REPR	0.37777782	0.14315888	-3.4855749	0.00049108	0.36796284	0.00290108
LOC105666573	reciprocal	REPR	0.36008498	0.13309265	-4.3202634	1.56E-05	0.36796284	0.00013024
LOC105666595	initial	NONREPR	0.44783602	0.06526985	-3.2084943	0.00133432	0.39462895	0.0068749
LOC105666595	reciprocal	NONREPR	0.35583821	0.06196844	-9.577032	9.99E-22	0.39462895	4.18E-20
LOC105666595	initial	REPR	0.43283318	0.05766738	-4.6872443	2.77E-06	0.39462895	2.69E-05
LOC105666595	reciprocal	REPR	0.34200839	0.05363902	-12.19927	3.14E-34	0.39462895	2.27E-32
LOC105666606	initial	NONREPR	0.45764021	0.27897996	-0.6088118	0.54264918	0.69044105	0.71580872
LOC105666606	reciprocal	NONREPR	0.47011485	0.26073761	-0.459018	0.64622121	0.69044105	0.79322775
LOC105666606	initial	REPR	0.91509599	0.16952685	14.0243721	1.11E-44	0.69044105	1.13E-42
LOC105666606	reciprocal	REPR	0.91891314	0.16219194	14.9678869	1.19E-50	0.69044105	1.44E-48
LOC105666672	initial	NONREPR	0.71550819	0.15293846	6.03045534	1.63E-09	0.64964521	2.58E-08
LOC105666672	reciprocal	NONREPR	0.62848575	0.14032643	3.74645116	0.00017935	0.64964521	0.00119178
LOC105666672	initial	REPR	0.67347009	0.07559293	9.57658416	1.00E-21	0.64964521	4.19E-20
LOC105666672	reciprocal	REPR	0.58111679	0.07065754	4.63304561	3.60E-06	0.64964521	3.41E-05
LOC105666723	initial	NONREPR	0.8638186	0.15411202	11.9872217	4.15E-33	0.86209304	2.93E-31
LOC105666723	reciprocal	NONREPR	0.8590434	0.38749514	4.6642324	3.10E-06	0.86209304	2.97E-05
LOC105666723	initial	REPR	0.8651235	0.19020978	9.77085811	1.50E-22	0.86209304	6.58E-21
LOC105666723	reciprocal	REPR	0.86038666	0.42484073	4.28043978	1.87E-05	0.86209304	0.00015387
LOC105666923	initial	NONREPR	0.98984023	0.9345716	4.89968587	9.60E-07	0.9646269	1.01E-05
LOC105666923	reciprocal	NONREPR	0.94657568	0.55463382	5.18285187	2.19E-07	0.9646269	2.56E-06
LOC105666923	initial	REPR	0.98744377	0.84087668	5.19089521	2.09E-07	0.9646269	2.46E-06
LOC105666923	reciprocal	REPR	0.93464791	0.52893994	5.02964555	4.91E-07	0.9646269	5.42E-06
LOC105666928	initial	NONREPR	0.29719354	0.07692488	-11.188811	4.63E-29	0.36330298	2.85E-27
LOC105666928	reciprocal	NONREPR	0.31568243	0.08598539	-8.9978702	2.30E-19	0.36330298	8.41E-18
LOC105666928	initial	REPR	0.40957046	0.06186294	-5.912124	3.38E-09	0.36330298	5.11E-08
LOC105666928	reciprocal	REPR	0.43076547	0.07264934	-3.8366313	0.00012473	0.36330298	0.00086103
LOC105666931	initial	NONREPR	0.26048393	0.10400953	-10.032301	1.10E-23	0.32062044	5.11E-22
LOC105666931	reciprocal	NONREPR	0.31440418	0.12194663	-6.3930336	1.63E-10	0.32062044	2.91E-09
LOC105666931	initial	REPR	0.32369086	0.08657659	-8.5110921	1.72E-17	0.32062044	5.65E-16

LOC105666931	reciprocal	REPR	0.38390278	0.10644714	-4.4436648	8.84E-06	0.32062044	7.74E-05
LOC105666969	initial	NONREPR	0.92731574	0.80169804	3.17597046	0.00149336	0.91544596	0.00758631
LOC105666969	reciprocal	NONREPR	0.9504721	0.82267558	3.59123659	0.00032911	0.91544596	0.00204484
LOC105666969	initial	REPR	0.87252523	0.46307254	4.15371887	3.27E-05	0.91544596	0.00025653
LOC105666969	reciprocal	REPR	0.91147075	0.51231332	4.55136807	5.33E-06	0.91544596	4.89E-05
LOC105666984	initial	NONREPR	0.87756234	0.41450623	4.75154733	2.02E-06	0.85388038	2.01E-05
LOC105666984	reciprocal	NONREPR	0.94481123	0.44165177	6.43091662	1.27E-10	0.85388038	2.31E-09
LOC105666984	initial	REPR	0.72826026	0.1318601	7.47620929	7.65E-14	0.85388038	1.90E-12
LOC105666984	reciprocal	REPR	0.86488771	0.20936538	8.86724189	7.50E-19	0.85388038	2.66E-17
LOC105666994	initial	NONREPR	0.9123007	0.26621203	8.79770822	1.40E-18	0.92074766	4.87E-17
LOC105666994	reciprocal	NONREPR	0.94638883	0.34722297	8.26816273	1.36E-16	0.92074766	4.15E-15
LOC105666994	initial	REPR	0.89133042	0.27185513	7.74089975	9.87E-15	0.92074766	2.62E-13
LOC105666994	reciprocal	REPR	0.93297068	0.36256745	7.26276901	3.79E-13	0.92074766	8.80E-12
LOC105666995	initial	NONREPR	0.9933537	1.08688491	4.60676793	4.09E-06	0.9766882	3.83E-05
LOC105666995	reciprocal	NONREPR	0.99063412	0.93021113	5.01098236	5.42E-07	0.9766882	5.93E-06
LOC105666995	initial	REPR	0.96774451	0.51787613	6.56774804	5.11E-11	0.9766882	9.71E-10
LOC105666995	reciprocal	REPR	0.95502046	0.62039041	4.9251647	8.43E-07	0.9766882	8.99E-06
LOC105667011	initial	NONREPR	0.84379845	0.12185389	13.8425326	1.41E-43	0.87743158	1.40E-41
LOC105667011	reciprocal	NONREPR	0.89951113	0.14787096	14.8224131	1.05E-49	0.87743158	1.22E-47
LOC105667011	initial	REPR	0.85753763	0.13542149	13.2548181	4.23E-40	0.87743158	3.74E-38
LOC105667011	reciprocal	REPR	0.90887912	0.16482001	13.9547692	2.94E-44	0.87743158	2.99E-42
LOC105667016	initial	NONREPR	0.96817668	0.41059319	8.31775922	8.96E-17	0.95794002	2.78E-15
LOC105667016	reciprocal	NONREPR	0.9535156	0.34121863	8.85367564	8.47E-19	0.95794002	2.99E-17
LOC105667016	initial	REPR	0.9634034	0.38367566	8.52417059	1.54E-17	0.95794002	5.06E-16
LOC105667016	reciprocal	REPR	0.94666439	0.31099566	9.2488124	2.27E-20	0.95794002	8.75E-19
LOC105667035	initial	NONREPR	0.82188852	0.32055555	4.77045282	1.84E-06	0.84108064	1.84E-05
LOC105667035	reciprocal	NONREPR	0.85219032	0.29197163	6.00018686	1.97E-09	0.84108064	3.07E-08
LOC105667035	initial	REPR	0.83058436	0.33938285	4.68430974	2.81E-06	0.84108064	2.72E-05
LOC105667035	reciprocal	REPR	0.85965936	0.3260278	5.55923021	2.71E-08	0.84108064	3.62E-07

LOC105667042	initial	NONREPR	0.98737554	0.25382613	17.1748054	4.10E-66	0.98972093	7.16E-64
LOC105667042	reciprocal	NONREPR	0.98898958	0.35365783	12.7180595	4.69E-37	0.98972093	3.84E-35
LOC105667042	initial	REPR	0.99066054	0.30780509	15.152849	7.26E-52	0.98972093	9.12E-50
LOC105667042	reciprocal	REPR	0.99185806	0.36849635	13.0328317	7.96E-39	0.98972093	6.81E-37
LOC105667061	initial	NONREPR	0.73436058	0.1622412	6.2675839	3.67E-10	0.80134271	6.27E-09
LOC105667061	reciprocal	NONREPR	0.86423488	0.1866703	9.91544055	3.57E-23	0.80134271	1.62E-21
LOC105667061	initial	REPR	0.73947483	0.16808152	6.20675462	5.41E-10	0.80134271	9.07E-09
LOC105667061	reciprocal	REPR	0.86730054	0.21000155	8.93945166	3.91E-19	0.80134271	1.40E-17
LOC105667069	initial	NONREPR	0.99670027	0.20893058	27.3325663	1.74E-164	0.99292344	1.09E-161
LOC105667069	reciprocal	NONREPR	0.9941846	0.18848036	27.2782465	7.69E-164	0.99292344	4.71E-161
LOC105667069	initial	REPR	0.99304031	0.18707883	26.516289	6.29E-155	0.99292344	3.43E-152
LOC105667069	reciprocal	REPR	0.98776859	0.16495724	26.6216931	3.81E-156	0.99292344	2.12E-153
LOC105667070	initial	NONREPR	0.97824488	0.19291659	19.7282723	1.23E-86	0.98013163	3.09E-84
LOC105667070	reciprocal	NONREPR	0.98231229	0.18526836	21.6822728	3.02E-104	0.98013163	9.63E-102
LOC105667070	initial	REPR	0.97792129	0.20068769	18.8891271	1.40E-79	0.98013163	3.01E-77
LOC105667070	reciprocal	REPR	0.98204808	0.2038364	19.633114	8.06E-86	0.98013163	1.97E-83
LOC105667072	initial	NONREPR	0.99895252	0.67490837	10.1648102	2.85E-24	0.99728589	1.40E-22
LOC105667072	reciprocal	NONREPR	0.99791693	0.54012184	11.4267312	3.07E-30	0.99728589	2.02E-28
LOC105667072	initial	REPR	0.99741229	0.66605869	8.93974029	3.90E-19	0.99728589	1.40E-17
LOC105667072	reciprocal	REPR	0.99486181	0.51847828	10.1564586	3.10E-24	0.99728589	1.51E-22
LOC105667073	initial	NONREPR	0.99908798	0.21806311	32.0959438	5.02E-226	0.9992886	4.44E-223
LOC105667073	reciprocal	NONREPR	0.99941513	0.22850109	32.5755213	9.11E-233	0.9992886	8.55E-230
LOC105667073	initial	REPR	0.99917824	0.23034084	30.8379486	8.13E-209	0.9992886	6.42E-206
LOC105667073	reciprocal	REPR	0.99947303	0.21507899	35.0933375	8.52E-270	0.9992886	1.11E-266
LOC105667075	initial	NONREPR	0.90856147	0.43489311	5.27990793	1.29E-07	0.86667382	1.57E-06
LOC105667075	reciprocal	NONREPR	0.7938872	0.35358037	3.81389316	0.00013679	0.86667382	0.00093441
LOC105667075	initial	REPR	0.92897888	0.46813751	5.49220817	3.97E-08	0.86667382	5.19E-07
LOC105667075	reciprocal	REPR	0.83526775	0.39996786	4.0589033	4.93E-05	0.86667382	0.00037245
LOC105667080	initial	NONREPR	0.78309655	0.19112323	6.71715139	1.85E-11	0.78578731	3.72E-10

LOC105667080	reciprocal	NONREPR	0.75349236	0.19005624	5.87892235	4.13E-09	0.78578731	6.18E-08
LOC105667080	initial	REPR	0.81641772	0.14736779	10.1261146	4.23E-24	0.78578731	2.05E-22
LOC105667080	reciprocal	REPR	0.79014263	0.16708306	7.93488778	2.11E-15	0.78578731	5.90E-14
LOC105667082	initial	NONREPR	0.96605158	0.14961399	22.3800924	6.15E-111	0.97963085	2.08E-108
LOC105667082	reciprocal	NONREPR	0.99039377	0.16076603	28.8350124	7.81E-183	0.97963085	5.33E-180
LOC105667082	initial	REPR	0.97042088	0.16183981	21.5686185	3.54E-103	0.97963085	1.12E-100
LOC105667082	reciprocal	REPR	0.99165718	0.14811901	32.2576857	2.74E-228	0.97963085	2.50E-225
LOC105667161	initial	NONREPR	0.17658143	0.23726377	-6.4893286	8.62E-11	0.25102504	1.60E-09
LOC105667161	reciprocal	NONREPR	0.30039772	0.24489838	-3.4520631	0.00055632	0.25102504	0.00323054
LOC105667161	initial	REPR	0.19729843	0.21251859	-6.603025	4.03E-11	0.25102504	7.74E-10
LOC105667161	reciprocal	REPR	0.32982257	0.22467036	-3.1556796	0.00160125	0.25102504	0.00804454
LOC105667164	initial	NONREPR	0.19560007	0.24568842	-5.7553566	8.65E-09	0.24848172	1.24E-07
LOC105667164	reciprocal	NONREPR	0.2984445	0.2772553	-3.0827762	0.00205079	0.24848172	0.00993726
LOC105667164	initial	REPR	0.19810712	0.2249867	-6.2144434	5.15E-10	0.24848172	8.66E-09
LOC105667164	reciprocal	REPR	0.30177521	0.25989232	-3.2277163	0.00124783	0.24848172	0.00649614
LOC105667165	initial	NONREPR	0.17516422	0.24404533	-6.349068	2.17E-10	0.26351197	3.83E-09
LOC105667165	reciprocal	NONREPR	0.31584841	0.24861102	-3.1089415	0.00187759	0.26351197	0.00922905
LOC105667165	initial	REPR	0.20451262	0.21371237	-6.3558573	2.07E-10	0.26351197	3.67E-09
LOC105667165	reciprocal	REPR	0.35852265	0.21876003	-2.6594531	0.00782676	0.26351197	0.03081044

Supplementary 4.0.3: genes showing parent-of-origin expression in sterile workers, 'avgpropmatexpr' refers to the average proportion o
maternal expression.

geneID	direction cross	reprstatus1	proportion maternal expression	SE	z	p	Av. Prop. Mat. Exp. Bias	padj
LOC100642213	initial	NONREPR	0.31823385	0.30430521	-2.5037369	0.01228894	0.32590959	0.04452904
LOC100642213	reciprocal	NONREPR	0.31702089	0.30167998	-2.5440754	0.01095674	0.32590959	0.04056332
LOC100642213	initial	REPR	0.33481443	0.29579954	-2.3207933	0.020298	0.32590959	0.06693481
LOC100642213	reciprocal	REPR	0.33356919	0.29101531	-2.3781774	0.01739845	0.32590959	0.059113
LOC100642367	initial	NONREPR	0.29642134	0.21575187	-4.0064441	6.16E-05	0.34514829	0.000456
LOC100642367	reciprocal	NONREPR	0.34952164	0.23406032	-2.6537713	0.00795978	0.34514829	0.03124394
LOC100642367	initial	REPR	0.3391013	0.21754355	-3.0674395	0.00215901	0.34514829	0.01038955
LOC100642367	reciprocal	REPR	0.39554887	0.26340573	-1.6098605	0.10742832	0.34514829	0.24127581
LOC100642393	initial	NONREPR	0.38841319	0.08104611	-5.6015915	2.12E-08	0.38632327	2.88E-07
LOC100642393	reciprocal	NONREPR	0.37758186	0.06948371	-7.1934087	6.32E-13	0.38632327	1.45E-11
LOC100642393	initial	REPR	0.39509933	0.07442987	-5.7225285	1.05E-08	0.38632327	1.49E-07
LOC100642393	reciprocal	REPR	0.38419868	0.0625769	-7.5389567	4.74E-14	0.38632327	1.19E-12
LOC100642707	initial	NONREPR	0.66025154	0.0435908	15.2421011	1.86E-52	0.69362557	2.34E-50
LOC100642707	reciprocal	NONREPR	0.68694378	0.04615734	17.0258866	5.28E-65	0.69362557	8.90E-63
LOC100642707	initial	REPR	0.70124965	0.04874456	17.5046352	1.32E-68	0.69362557	2.43E-66
LOC100642707	reciprocal	REPR	0.72605731	0.05119901	19.0376735	8.31E-81	0.69362557	1.85E-78
LOC100642787	initial	NONREPR	0.97517253	0.72813306	5.04119912	4.63E-07	0.94353096	5.13E-06
LOC100642787	reciprocal	NONREPR	0.98792925	0.79233964	5.55926467	2.71E-08	0.94353096	3.62E-07
LOC100642787	initial	REPR	0.87511725	0.30280682	6.42978434	1.28E-10	0.94353096	2.32E-09
LOC100642787	reciprocal	REPR	0.93590482	0.50274483	5.3330128	9.66E-08	0.94353096	1.20E-06
LOC100642895	initial	NONREPR	0.38251109	0.03702498	-12.934605	2.87E-38	0.38308973	2.43E-36
LOC100642895	reciprocal	NONREPR	0.37345058	0.03902235	-13.260143	3.94E-40	0.38308973	3.49E-38
LOC100642895	initial	REPR	0.39277492	0.04437368	-9.818045	9.42E-23	0.38308973	4.17E-21
LOC100642895	reciprocal	REPR	0.38362233	0.04964397	-9.5520429	1.27E-21	0.38308973	5.26E-20

LOC100642916	initial	NONREPR	0.3811223	0.13256804	-3.6568947	0.00025529	0.39249297	0.00163404
LOC100642916	reciprocal	NONREPR	0.4128962	0.12805467	-2.7488683	0.00598014	0.39249297	0.02457193
LOC100642916	initial	REPR	0.37221877	0.1272058	-4.1091677	3.97E-05	0.39249297	0.00030597
LOC100642916	reciprocal	REPR	0.40373462	0.11987351	-3.2528292	0.00114262	0.39249297	0.00602893
LOC100643010	initial	NONREPR	0.35318301	0.03460968	-17.482886	1.93E-68	0.36629107	3.54E-66
LOC100643010	reciprocal	NONREPR	0.35325019	0.03630359	-16.659041	2.60E-62	0.36629107	4.18E-60
LOC100643010	initial	REPR	0.37933091	0.04088513	-12.043232	2.11E-33	0.36629107	1.50E-31
LOC100643010	reciprocal	REPR	0.37940016	0.04542902	-10.832174	2.42E-27	0.36629107	1.39E-25
LOC100643108	initial	NONREPR	0.38106302	0.02998213	-16.177592	7.26E-59	0.39344496	1.07E-56
LOC100643108	reciprocal	NONREPR	0.43796222	0.02988552	-8.3463983	7.04E-17	0.39344496	2.21E-15
LOC100643108	initial	REPR	0.34973604	0.04910873	-12.629112	1.46E-36	0.39344496	1.17E-34
LOC100643108	reciprocal	REPR	0.40501854	0.05247131	-7.3296697	2.31E-13	0.39344496	5.46E-12
LOC100643295	initial	NONREPR	0.62013218	0.07152076	6.852686	7.25E-12	0.60531803	1.52E-10
LOC100643295	reciprocal	NONREPR	0.58726699	0.07922566	4.4515709	8.52E-06	0.60531803	7.48E-05
LOC100643295	initial	REPR	0.62332219	0.0711559	7.07844808	1.46E-12	0.60531803	3.26E-11
LOC100643295	reciprocal	REPR	0.59055077	0.08371276	4.37499286	1.21E-05	0.60531803	0.00010353
LOC100643431	initial	NONREPR	0.66479578	0.16582459	4.1293026	3.64E-05	0.63362524	0.00028262
LOC100643431	reciprocal	NONREPR	0.59663498	0.14058085	2.78461545	0.00535912	0.63362524	0.02238472
LOC100643431	initial	REPR	0.67038679	0.17483736	4.06054505	4.90E-05	0.63362524	0.00037003
LOC100643431	reciprocal	REPR	0.60268342	0.14586214	2.85652377	0.00428308	0.63362524	0.01863406
LOC100643442	initial	NONREPR	0.59416183	0.08272003	4.60828221	4.06E-06	0.62324831	3.80E-05
LOC100643442	reciprocal	NONREPR	0.64736739	0.06830137	8.89421675	5.88E-19	0.62324831	2.10E-17
LOC100643442	initial	REPR	0.59926801	0.08153521	4.93548828	8.00E-07	0.62324831	8.56E-06
LOC100643442	reciprocal	REPR	0.65219601	0.06727981	9.34464663	9.22E-21	0.62324831	3.62E-19
LOC100643517	initial	NONREPR	0.18492856	0.1303616	-11.378398	5.36E-30	0.1633029	3.44E-28
LOC100643517	reciprocal	NONREPR	0.14424183	0.14356722	-12.401832	2.55E-35	0.1633029	1.94E-33
LOC100643517	initial	REPR	0.18210769	0.12824022	-11.713426	1.09E-31	0.1633029	7.37E-30
LOC100643517	reciprocal	REPR	0.14193351	0.14190648	-12.679638	7.67E-37	0.1633029	6.17E-35
LOC100643622	initial	NONREPR	0.34634929	0.03310388	-19.18583	4.86E-82	0.333425	1.12E-79

LOC100643622	reciprocal	NONREPR	0.32404036	0.02949708	-24.926716	3.82E-137	0.333425	1.62E-134
LOC100643622	initial	REPR	0.34275058	0.04132608	-15.754228	6.42E-56	0.333425	8.97E-54
LOC100643622	reciprocal	REPR	0.32055977	0.04104867	-18.300239	8.24E-75	0.333425	1.69E-72
LOC100643818	initial	NONREPR	0.6977559	0.20057696	4.17113889	3.03E-05	0.64351854	0.00023981
LOC100643818	reciprocal	NONREPR	0.63115827	0.20107133	2.67163399	0.00754829	0.64351854	0.02993399
LOC100643818	initial	REPR	0.65768354	0.20515342	3.18292651	0.00145795	0.64351854	0.0074328
LOC100643818	reciprocal	REPR	0.58747646	0.19808444	1.78480913	0.07429228	0.64351854	0.18426106
LOC100643869	initial	NONREPR	0.65562729	0.16099163	3.9993876	6.35E-05	0.63084454	0.00046901
LOC100643869	reciprocal	NONREPR	0.60279813	0.14767754	2.82465252	0.00473319	0.63084454	0.02024619
LOC100643869	initial	REPR	0.65879397	0.25589824	2.57103893	0.01013939	0.63084454	0.03808201
LOC100643869	reciprocal	REPR	0.60615878	0.23737584	1.8165039	0.06929311	0.63084454	0.1746537
LOC100643931	initial	NONREPR	0.38618429	0.14376392	-3.2232014	0.00126766	0.38559244	0.00658116
LOC100643931	reciprocal	NONREPR	0.37050544	0.13433369	-3.9457643	7.95E-05	0.38559244	0.00057405
LOC100643931	initial	REPR	0.40079001	0.18826601	-2.1362033	0.03266285	0.38559244	0.09768924
LOC100643931	reciprocal	REPR	0.38489001	0.18292457	-2.5630427	0.01037593	0.38559244	0.03881505
LOC100644111	initial	NONREPR	0.24476908	0.10069922	-11.188848	4.62E-29	0.29481958	2.85E-27
LOC100644111	reciprocal	NONREPR	0.38694109	0.10199617	-4.5118224	6.43E-06	0.29481958	5.81E-05
LOC100644111	initial	REPR	0.20850204	0.10821352	-12.327281	6.46E-35	0.29481958	4.81E-33
LOC100644111	reciprocal	REPR	0.33906611	0.10396266	-6.4201771	1.36E-10	0.29481958	2.47E-09
LOC100644232	initial	NONREPR	0.12419132	0.32464898	-6.0167275	1.78E-09	0.16538919	2.80E-08
LOC100644232	reciprocal	NONREPR	0.22432229	0.26613276	-4.6617835	3.13E-06	0.16538919	3.00E-05
LOC100644232	initial	REPR	0.11065269	0.33959381	-6.1370124	8.41E-10	0.16538919	1.38E-08
LOC100644232	reciprocal	REPR	0.20239047	0.26829047	-5.1116998	3.19E-07	0.16538919	3.65E-06
LOC100644288	initial	NONREPR	0.22726439	0.11068836	-11.056474	2.04E-28	0.29141764	1.24E-26
LOC100644288	reciprocal	NONREPR	0.32310966	0.10981537	-6.7341891	1.65E-11	0.29141764	3.32E-10
LOC100644288	initial	REPR	0.25643152	0.11010118	-9.6692809	4.07E-22	0.29141764	1.74E-20
LOC100644288	reciprocal	REPR	0.358865	0.1185888	-4.8933268	9.91E-07	0.29141764	1.04E-05
LOC100644543	initial	NONREPR	0.63457549	0.05433257	10.1577481	3.06E-24	0.62197847	1.50E-22
LOC100644543	reciprocal	NONREPR	0.60070877	0.06100986	6.6943149	2.17E-11	0.62197847	4.31E-10

LOC100644543	initial	REPR	0.64309627	0.04929601	11.9447482	6.92E-33	0.62197847	4.85E-31
LOC100644543	reciprocal	REPR	0.60953334	0.06024558	7.39226072	1.44E-13	0.62197847	3.47E-12
LOC100644548	initial	NONREPR	0.78836373	0.07402106	17.7664368	1.29E-70	0.73001389	2.49E-68
LOC100644548	reciprocal	NONREPR	0.73703949	0.06999709	14.7240063	4.52E-49	0.73001389	5.18E-47
LOC100644548	initial	REPR	0.72727071	0.07841502	12.5080519	6.75E-36	0.73001389	5.22E-34
LOC100644548	reciprocal	REPR	0.66738162	0.08017434	8.68564982	3.77E-18	0.73001389	1.27E-16
LOC100644669	initial	NONREPR	0.60864235	0.0255374	17.2926342	5.35E-67	0.61252856	9.55E-65
LOC100644669	reciprocal	NONREPR	0.60913305	0.02615901	16.9604867	1.61E-64	0.61252856	2.69E-62
LOC100644669	initial	REPR	0.61592576	0.02694602	17.527285	8.87E-69	0.61252856	1.64E-66
LOC100644669	reciprocal	REPR	0.61641308	0.02839299	16.7066249	1.17E-62	0.61252856	1.90E-60
LOC100644671	initial	NONREPR	0.92092358	0.19278105	12.7344588	3.80E-37	0.86123122	3.12E-35
LOC100644671	reciprocal	NONREPR	0.86988619	0.16690036	11.383755	5.04E-30	0.86123122	3.25E-28
LOC100644671	initial	REPR	0.86617561	0.20397982	9.15560799	5.41E-20	0.86123122	2.04E-18
LOC100644671	reciprocal	REPR	0.78793952	0.1897977	6.91552018	4.66E-12	0.86123122	9.99E-11
LOC100644680	initial	NONREPR	0.65077586	0.13128166	4.74134263	2.12E-06	0.75802555	2.10E-05
LOC100644680	reciprocal	NONREPR	0.87066275	0.25426339	7.49943347	6.41E-14	0.75802555	1.60E-12
LOC100644680	initial	REPR	0.64358754	0.13820551	4.27601916	1.90E-05	0.75802555	0.00015661
LOC100644680	reciprocal	REPR	0.86707604	0.25803483	7.26781513	3.65E-13	0.75802555	8.50E-12
LOC100644719	initial	NONREPR	0.38718131	0.11585172	-3.9634804	7.39E-05	0.36508996	0.00053822
LOC100644719	reciprocal	NONREPR	0.32015868	0.15035873	-5.0083069	5.49E-07	0.36508996	6.01E-06
LOC100644719	initial	REPR	0.41092927	0.10862908	-3.3151818	0.00091584	0.36508996	0.0049784
LOC100644719	reciprocal	REPR	0.34209056	0.1363746	-4.7955542	1.62E-06	0.36508996	1.64E-05
LOC100644771	initial	NONREPR	0.57423027	0.08304154	3.602195	0.00031554	0.6255245	0.00196987
LOC100644771	reciprocal	NONREPR	0.66000051	0.12468488	5.31978325	1.04E-07	0.6255245	1.29E-06
LOC100644771	initial	REPR	0.59182071	0.05104638	7.27764009	3.40E-13	0.6255245	7.92E-12
LOC100644771	reciprocal	REPR	0.6760465	0.10814626	6.80247195	1.03E-11	0.6255245	2.12E-10
LOC100645035	initial	NONREPR	0.72219428	0.03820408	25.0070736	5.12E-138	0.65184368	2.26E-135
LOC100645035	reciprocal	NONREPR	0.58250622	0.03127168	10.6508573	1.73E-26	0.65184368	9.54E-25
LOC100645035	initial	REPR	0.72127798	0.03811827	24.9436758	2.50E-137	0.65184368	1.07E-134

LOC100645035	reciprocal	REPR	0.58139624	0.03249833	10.1084484	5.07E-24	0.65184368	2.45E-22
LOC100645056	initial	NONREPR	0.35000603	0.15624264	-3.9618681	7.44E-05	0.36618684	0.00054095
LOC100645056	reciprocal	NONREPR	0.40495257	0.12266458	-3.1375899	0.00170343	0.36618684	0.00848691
LOC100645056	initial	REPR	0.32812998	0.15733101	-4.5550784	5.24E-06	0.36618684	4.81E-05
LOC100645056	reciprocal	REPR	0.38165877	0.13567356	-3.55643	0.00037593	0.36618684	0.00230187
LOC100645154	initial	NONREPR	0.22418168	0.05339763	-23.249377	1.44E-119	0.23303833	5.10E-117
LOC100645154	reciprocal	NONREPR	0.23169951	0.05017234	-23.892441	3.67E-126	0.23303833	1.40E-123
LOC100645154	initial	REPR	0.23426088	0.06011061	-19.70378	2.00E-86	0.23303833	4.97E-84
LOC100645154	reciprocal	REPR	0.24201126	0.05753986	-19.841624	1.30E-87	0.23303833	3.31E-85
LOC100645486	initial	NONREPR	0.68816148	0.15492251	5.10925132	3.23E-07	0.62887758	3.69E-06
LOC100645486	reciprocal	NONREPR	0.6260068	0.14902706	3.45657767	0.00054708	0.62887758	0.0031848
LOC100645486	initial	REPR	0.63376306	0.13805231	3.97236846	7.12E-05	0.62887758	0.00052055
LOC100645486	reciprocal	REPR	0.56757899	0.12860977	2.11477135	0.03444944	0.62887758	0.1018458
LOC100645509	initial	NONREPR	0.54688978	0.04153793	4.52867734	5.94E-06	0.62244867	5.40E-05
LOC100645509	reciprocal	NONREPR	0.57898406	0.06585195	4.83819032	1.31E-06	0.62244867	1.35E-05
LOC100645509	initial	REPR	0.66781616	0.05039848	13.8560592	1.17E-43	0.62244867	1.17E-41
LOC100645509	reciprocal	REPR	0.69610467	0.07504539	11.0442049	2.34E-28	0.62244867	1.42E-26
LOC100645789	initial	NONREPR	0.6307522	0.12666377	4.22729498	2.37E-05	0.6454837	0.00019092
LOC100645789	reciprocal	NONREPR	0.67764929	0.16805442	4.42112589	9.82E-06	0.6454837	8.53E-05
LOC100645789	initial	REPR	0.612791	0.13981906	3.28323852	0.00102622	0.6454837	0.00549292
LOC100645789	reciprocal	REPR	0.66074231	0.17718028	3.7622921	0.00016836	0.6454837	0.00112522
LOC100645833	initial	NONREPR	0.68592847	0.11736549	6.65572655	2.82E-11	0.6385525	5.53E-10
LOC100645833	reciprocal	NONREPR	0.61216217	0.10719271	4.25784528	2.06E-05	0.6385525	0.00016848
LOC100645833	initial	REPR	0.66589023	0.12193932	5.65572491	1.55E-08	0.6385525	2.16E-07
LOC100645833	reciprocal	REPR	0.59022912	0.1112282	3.28075622	0.00103529	0.6385525	0.00553261
LOC100646012	initial	NONREPR	0.63906623	0.08106551	7.04755428	1.82E-12	0.63095595	4.04E-11
LOC100646012	reciprocal	NONREPR	0.62922383	0.06398202	8.26620516	1.38E-16	0.63095595	4.21E-15
LOC100646012	initial	REPR	0.6327235	0.08537844	6.37067842	1.88E-10	0.63095595	3.34E-09
LOC100646012	reciprocal	REPR	0.62281023	0.07347189	6.82564985	8.75E-12	0.63095595	1.82E-10

LOC100646186	initial	NONREPR	0.64237701	0.10922765	5.36215934	8.22E-08	0.62606412	1.03E-06
LOC100646186	reciprocal	NONREPR	0.65429379	0.19537278	3.26538407	0.00109316	0.62606412	0.00580466
LOC100646186	initial	REPR	0.59754091	0.12680847	3.11674225	0.00182861	0.62606412	0.00901932
LOC100646186	reciprocal	REPR	0.61004477	0.20601688	2.17215414	0.02984404	0.62606412	0.09088811
LOC100646194	initial	NONREPR	0.65514577	0.21353457	3.00530235	0.00265317	0.60138409	0.01239809
LOC100646194	reciprocal	NONREPR	0.59513041	0.1341458	2.87161831	0.00408376	0.60138409	0.0179477
LOC100646194	initial	REPR	0.60887626	0.21344331	2.07357671	0.03811864	0.60138409	0.11043189
LOC100646194	reciprocal	REPR	0.54638391	0.13227488	1.40669686	0.1595173	0.60138409	0.32086533
LOC100646202	initial	NONREPR	0.70540002	0.04117647	21.2049893	8.59E-100	0.71959813	2.55E-97
LOC100646202	reciprocal	NONREPR	0.72419078	0.0558569	17.2824757	6.38E-67	0.71959813	1.13E-64
LOC100646202	initial	REPR	0.71519999	0.04666575	19.7312806	1.16E-86	0.71959813	2.93E-84
LOC100646202	reciprocal	REPR	0.73360173	0.05144051	19.6921425	2.52E-86	0.71959813	6.20E-84
LOC100646431	initial	NONREPR	0.69488864	0.02215323	37.1537092	3.82E-302	0.60397498	6.04E-299
LOC100646431	reciprocal	NONREPR	0.52262476	0.02291618	3.95183223	7.76E-05	0.60397498	0.00056143
LOC100646431	initial	REPR	0.68606773	0.02202645	35.4936541	6.16E-276	0.60397498	8.81E-273
LOC100646431	reciprocal	REPR	0.5123188	0.02432936	2.02574957	0.04279045	0.60397498	0.12079644
LOC100646468	initial	NONREPR	0.69555501	0.13797431	5.98821393	2.12E-09	0.69414015	3.29E-08
LOC100646468	reciprocal	NONREPR	0.66393423	0.14570604	4.67294431	2.97E-06	0.69414015	2.86E-05
LOC100646468	initial	REPR	0.72353327	0.07878004	12.211926	2.68E-34	0.69414015	1.95E-32
LOC100646468	reciprocal	REPR	0.69353806	0.08807508	9.27291315	1.81E-20	0.69414015	7.02E-19
LOC100646523	initial	NONREPR	0.64911559	0.10071926	6.10760994	1.01E-09	0.61827262	1.64E-08
LOC100646523	reciprocal	NONREPR	0.58768985	0.10067092	3.52061424	0.00043055	0.61827262	0.00259609
LOC100646523	initial	REPR	0.64886344	0.09809339	6.25982133	3.85E-10	0.61827262	6.58E-09
LOC100646523	reciprocal	REPR	0.58742162	0.10239894	3.45039322	0.00055977	0.61827262	0.0032487
LOC100646582	initial	NONREPR	0.61415141	0.16240938	2.86188189	0.00421134	0.61394535	0.0183939
LOC100646582	reciprocal	NONREPR	0.60548178	0.17436068	2.45674161	0.01402035	0.61394535	0.04968174
LOC100646582	initial	REPR	0.62237464	0.17660185	2.82918682	0.00466664	0.61394535	0.02000143
LOC100646582	reciprocal	REPR	0.61377357	0.21891763	2.11587474	0.03435546	0.61394535	0.10163801
LOC100646607	initial	NONREPR	0.43193193	0.07385997	-3.7093606	0.00020778	0.37867007	0.00135726

LOC100646607	reciprocal	NONREPR	0.32185556	0.07517227	-9.9139932	3.62E-23	0.37867007	1.64E-21
LOC100646607	initial	REPR	0.43568927	0.06741991	-3.8367851	0.00012466	0.37867007	0.00086069
LOC100646607	reciprocal	REPR	0.32520353	0.06546116	-11.151039	7.08E-29	0.37867007	4.35E-27
LOC100646622	initial	NONREPR	0.35626171	0.1687756	-3.5054041	0.00045591	0.34130715	0.00272171
LOC100646622	reciprocal	NONREPR	0.29524378	0.13818294	-6.2963674	3.05E-10	0.34130715	5.29E-09
LOC100646622	initial	REPR	0.38874811	0.16352647	-2.7676101	0.0056469	0.34130715	0.02340119
LOC100646622	reciprocal	REPR	0.32497502	0.12270094	-5.957586	2.56E-09	0.34130715	3.92E-08
LOC100646719	initial	NONREPR	0.64629811	0.08769648	6.87378108	6.25E-12	0.6587505	1.32E-10
LOC100646719	reciprocal	NONREPR	0.70537471	0.11772787	7.41561753	1.21E-13	0.6587505	2.94E-12
LOC100646719	initial	REPR	0.61065732	0.10515514	4.28011496	1.87E-05	0.6587505	0.00015401
LOC100646719	reciprocal	REPR	0.67267186	0.12918009	5.57589371	2.46E-08	0.6587505	3.31E-07
LOC100646727	initial	NONREPR	0.42877067	0.10809605	-2.6538301	0.00795839	0.38298487	0.03124394
LOC100646727	reciprocal	NONREPR	0.34690417	0.0748361	-8.4541459	2.81E-17	0.38298487	9.09E-16
LOC100646727	initial	REPR	0.41867123	0.10148125	-3.2343956	0.001219	0.38298487	0.00636506
LOC100646727	reciprocal	REPR	0.33759342	0.06154899	-10.951231	6.56E-28	0.38298487	3.89E-26
LOC100646825	initial	NONREPR	0.32718712	0.22381307	-3.2211479	0.00127678	0.32838658	0.00662506
LOC100646825	reciprocal	NONREPR	0.30351338	0.15805069	-5.2554209	1.48E-07	0.32838658	1.78E-06
LOC100646825	initial	REPR	0.35375074	0.21688706	-2.7783712	0.00546322	0.32838658	0.02274989
LOC100646825	reciprocal	REPR	0.32909509	0.14182492	-5.0222533	5.11E-07	0.32838658	5.62E-06
LOC100646847	initial	NONREPR	0.42045727	0.0857672	-3.7414832	0.00018294	0.37301809	0.00121237
LOC100646847	reciprocal	NONREPR	0.33259564	0.08443993	-8.2480958	1.61E-16	0.37301809	4.89E-15
LOC100646847	initial	REPR	0.41310432	0.07502678	-4.6802881	2.86E-06	0.37301809	2.77E-05
LOC100646847	reciprocal	REPR	0.32591512	0.0704034	-10.322215	5.59E-25	0.37301809	2.86E-23
LOC100646910	initial	NONREPR	0.79770396	0.13147295	10.4356478	1.70E-25	0.71165353	9.00E-24
LOC100646910	reciprocal	NONREPR	0.62944785	0.10405507	5.09200416	3.54E-07	0.71165353	4.02E-06
LOC100646910	initial	REPR	0.79455335	0.13388798	10.1024282	5.39E-24	0.71165353	2.60E-22
LOC100646910	reciprocal	REPR	0.62490895	0.1030273	4.95438732	7.26E-07	0.71165353	7.83E-06
LOC100646945	initial	NONREPR	0.40083636	0.08938708	-4.4970872	6.89E-06	0.39364736	6.20E-05
LOC100646945	reciprocal	NONREPR	0.3946168	0.07242996	-5.908418	3.45E-09	0.39364736	5.21E-08

LOC100646945	initial	REPR	0.3926554	0.0913454	-4.7748869	1.80E-06	0.39364736	1.80E-05
LOC100646945	reciprocal	REPR	0.3864809	0.0712757	-6.483682	8.95E-11	0.39364736	1.66E-09
LOC100646967	initial	NONREPR	0.42399199	0.08180665	-3.7455024	0.00018003	0.37598142	0.00119576
LOC100646967	reciprocal	NONREPR	0.34237639	0.07810859	-8.3565974	6.46E-17	0.37598142	2.03E-15
LOC100646967	initial	REPR	0.40896523	0.07165511	-5.139127	2.76E-07	0.37598142	3.18E-06
LOC100646967	reciprocal	REPR	0.32859209	0.06685009	-10.688986	1.15E-26	0.37598142	6.40E-25
LOC100647061	initial	NONREPR	0.3653001	0.01645381	-33.574783	3.92E-247	0.35944645	4.20E-244
LOC100647061	reciprocal	NONREPR	0.3551934	0.01619966	-36.808668	1.34E-296	0.35944645	2.01E-293
LOC100647061	initial	REPR	0.36368963	0.0162976	-34.323187	3.54E-258	0.35944645	3.94E-255
LOC100647061	reciprocal	REPR	0.35360267	0.0154394	-39.071492	0	0.35944645	0
LOC100647088	initial	NONREPR	0.30951953	0.03336829	-24.04578	9.24E-128	0.29721636	3.56E-125
LOC100647088	reciprocal	NONREPR	0.35100658	0.03493178	-17.594798	2.70E-69	0.29721636	5.10E-67
LOC100647088	initial	REPR	0.24594429	0.03368844	-33.256544	1.64E-242	0.29721636	1.70E-239
LOC100647088	reciprocal	REPR	0.28239503	0.03540659	-26.340078	6.67E-153	0.29721636	3.45E-150
LOC100647097	initial	NONREPR	0.63924156	0.14559209	3.92929195	8.52E-05	0.6084933	0.00061042
LOC100647097	reciprocal	NONREPR	0.60256567	0.13484274	3.08631328	0.00202655	0.6084933	0.00984681
LOC100647097	initial	REPR	0.61484112	0.14679057	3.18622633	0.00144142	0.6084933	0.00735853
LOC100647097	reciprocal	REPR	0.57732483	0.13104236	2.37939181	0.01734123	0.6084933	0.0589653
LOC100647189	initial	NONREPR	0.56998181	0.11020496	2.55684459	0.01056264	0.62274018	0.03936638
LOC100647189	reciprocal	NONREPR	0.6467052	0.13193161	4.58258422	4.59E-06	0.62274018	4.26E-05
LOC100647189	initial	REPR	0.59992005	0.07100139	5.70597275	1.16E-08	0.62274018	1.64E-07
LOC100647189	reciprocal	REPR	0.67435366	0.09762159	7.45678015	8.87E-14	0.62274018	2.18E-12
LOC100647211	initial	NONREPR	0.66577652	0.11704254	5.88798033	3.91E-09	0.64173132	5.86E-08
LOC100647211	reciprocal	NONREPR	0.59655891	0.13091889	2.98770873	0.00281077	0.64173132	0.01302498
LOC100647211	initial	REPR	0.68600892	0.11401299	6.85471104	7.15E-12	0.64173132	1.50E-10
LOC100647211	reciprocal	REPR	0.61858094	0.13227298	3.65554164	0.00025664	0.64173132	0.0016407
LOC100647228	initial	NONREPR	0.65887215	0.10325587	6.3751545	1.83E-10	0.67592392	3.26E-09
LOC100647228	reciprocal	NONREPR	0.68036966	0.09987485	7.56417789	3.90E-14	0.67592392	9.87E-13
LOC100647228	initial	REPR	0.67169378	0.10027604	7.13885177	9.41E-13	0.67592392	2.14E-11

LOC100647228	reciprocal	REPR	0.69276008	0.1004383	8.09506738	5.72E-16	0.67592392	1.66E-14
LOC100647251	initial	NONREPR	0.7389909	0.07460078	13.9506631	3.12E-44	0.71803742	3.15E-42
LOC100647251	reciprocal	NONREPR	0.72666657	0.08795924	11.1162318	1.05E-28	0.71803742	6.41E-27
LOC100647251	initial	REPR	0.70981437	0.09461184	9.45423647	3.25E-21	0.71803742	1.31E-19
LOC100647251	reciprocal	REPR	0.69667785	0.10702586	7.76940916	7.89E-15	0.71803742	2.11E-13
LOC100647278	initial	NONREPR	0.64897985	0.03009559	20.4202045	1.11E-92	0.63286709	3.08E-90
LOC100647278	reciprocal	NONREPR	0.58873027	0.03255318	11.0194724	3.08E-28	0.63286709	1.85E-26
LOC100647278	initial	REPR	0.67604925	0.02920518	25.1898636	5.17E-140	0.63286709	2.35E-137
LOC100647278	reciprocal	REPR	0.61770897	0.0309345	15.5113278	2.91E-54	0.63286709	3.92E-52
LOC100647282	initial	NONREPR	0.32310162	0.11889996	-6.219971	4.97E-10	0.30740515	8.37E-09
LOC100647282	reciprocal	NONREPR	0.28312953	0.11684404	-7.9506897	1.85E-15	0.30740515	5.21E-14
LOC100647282	initial	REPR	0.33199404	0.11239565	-6.2207041	4.95E-10	0.30740515	8.34E-09
LOC100647282	reciprocal	REPR	0.29139542	0.1114035	-7.976558	1.50E-15	0.30740515	4.24E-14
LOC100647304	initial	NONREPR	0.57148086	0.11251577	2.55871316	0.01050604	0.62118313	0.03920307
LOC100647304	reciprocal	NONREPR	0.64385961	0.13477156	4.39377332	1.11E-05	0.62118313	9.57E-05
LOC100647304	initial	REPR	0.59950629	0.07196894	5.60531261	2.08E-08	0.62118313	2.83E-07
LOC100647304	reciprocal	REPR	0.66988578	0.10065335	7.03074985	2.05E-12	0.62118313	4.53E-11
LOC100647326	initial	NONREPR	0.70397969	0.01764551	49.0958631	0	0.61235604	0
LOC100647326	reciprocal	NONREPR	0.52177356	0.01657769	5.25702501	1.46E-07	0.61235604	1.77E-06
LOC100647326	initial	REPR	0.70303161	0.01735749	49.6486669	0	0.61235604	0
LOC100647326	reciprocal	REPR	0.52063928	0.01594249	5.18137722	2.20E-07	0.61235604	2.58E-06
LOC100647368	initial	NONREPR	0.64098855	0.0990587	5.8516546	4.87E-09	0.63618446	7.22E-08
LOC100647368	reciprocal	NONREPR	0.63792591	0.11869844	4.77153114	1.83E-06	0.63618446	1.83E-05
LOC100647368	initial	REPR	0.63445486	0.12601451	4.37549892	1.21E-05	0.63618446	0.00010338
LOC100647368	reciprocal	REPR	0.63136854	0.14382183	3.74138176	0.00018301	0.63618446	0.00121259
LOC100647417	initial	NONREPR	0.40488512	0.01421267	-27.09914	1.01E-161	0.38873015	5.93E-159
LOC100647417	reciprocal	NONREPR	0.36843172	0.01119104	-48.159144	0	0.38873015	0
LOC100647417	initial	REPR	0.40909956	0.01390424	-26.444387	4.23E-154	0.38873015	2.23E-151
LOC100647417	reciprocal	REPR	0.37250422	0.01072393	-48.628503	0	0.38873015	0

LOC100647426	initial	NONREPR	0.56960134	0.1133941	2.47124666	0.01346429	0.61754449	0.04802354
LOC100647426	reciprocal	NONREPR	0.63795706	0.13475495	4.20398782	2.62E-05	0.61754449	0.00020955
LOC100647426	initial	REPR	0.59806098	0.07305356	5.43973947	5.34E-08	0.61754449	6.87E-07
LOC100647426	reciprocal	REPR	0.66455859	0.10189365	6.70969925	1.95E-11	0.61754449	3.90E-10
LOC100647560	initial	NONREPR	0.65489949	0.06618801	9.67918662	3.70E-22	0.75764199	1.58E-20
LOC100647560	reciprocal	NONREPR	0.8394216	0.08273577	19.9905164	6.66E-89	0.75764199	1.74E-86
LOC100647560	initial	REPR	0.6813712	0.07231434	10.5107844	7.71E-26	0.75764199	4.15E-24
LOC100647560	reciprocal	REPR	0.85487566	0.08639341	20.5266245	1.25E-93	0.75764199	3.49E-91
LOC100647603	initial	NONREPR	0.72332658	0.2399128	4.00571776	6.18E-05	0.8401237	0.00045718
LOC100647603	reciprocal	NONREPR	0.68881656	0.23113548	3.43777765	0.00058651	0.8401237	0.00338088
LOC100647603	initial	REPR	0.97626485	0.210465	17.659834	8.55E-70	0.8401237	1.62E-67
LOC100647603	reciprocal	REPR	0.97208683	0.19241411	18.4515907	5.06E-76	0.8401237	1.06E-73
LOC100647654	initial	NONREPR	0.35610465	0.04542962	-13.038005	7.44E-39	0.34637328	6.38E-37
LOC100647654	reciprocal	NONREPR	0.34112257	0.04399361	-14.963437	1.27E-50	0.34637328	1.53E-48
LOC100647654	initial	REPR	0.35157856	0.04503272	-13.592509	4.44E-42	0.34637328	4.18E-40
LOC100647654	reciprocal	REPR	0.33668734	0.04271673	-15.874149	9.57E-57	0.34637328	1.36E-54
LOC100647684	initial	NONREPR	0.63039182	0.03816033	13.9909182	1.77E-44	0.65005203	1.80E-42
LOC100647684	reciprocal	NONREPR	0.6351267	0.04474	12.3887859	3.01E-35	0.65005203	2.27E-33
LOC100647684	initial	REPR	0.66508312	0.03582798	19.1478757	1.01E-81	0.65005203	2.31E-79
LOC100647684	reciprocal	REPR	0.6696065	0.04361676	16.1957421	5.40E-59	0.65005203	8.03E-57
LOC100647760	initial	NONREPR	0.09682084	0.2033847	-10.979482	4.80E-28	0.12504473	2.86E-26
LOC100647760	reciprocal	NONREPR	0.13922103	0.21200588	-8.5930397	8.47E-18	0.12504473	2.81E-16
LOC100647760	initial	REPR	0.10871266	0.18518763	-11.361226	6.52E-30	0.12504473	4.18E-28
LOC100647760	reciprocal	REPR	0.15542439	0.20289374	-8.3426668	7.26E-17	0.12504473	2.27E-15
LOC100647772	initial	NONREPR	0.37089262	0.03961799	-13.337108	1.41E-40	0.36204654	1.27E-38
LOC100647772	reciprocal	NONREPR	0.35719013	0.04259604	-13.794257	2.76E-43	0.36204654	2.72E-41
LOC100647772	initial	REPR	0.36687037	0.03846503	-14.186044	1.12E-45	0.36204654	1.20E-43
LOC100647772	reciprocal	REPR	0.35323305	0.04074388	-14.845371	7.45E-50	0.36204654	8.74E-48
LOC100647792	initial	NONREPR	0.32893255	0.07610119	-9.3693264	7.30E-21	0.31144274	2.88E-19

LOC100647792	reciprocal	NONREPR	0.2732194	0.07806196	-12.532987	4.93E-36	0.31144274	3.85E-34
LOC100647792	initial	REPR	0.35070513	0.08383748	-7.3468472	2.03E-13	0.31144274	4.81E-12
LOC100647792	reciprocal	REPR	0.29291389	0.08570491	-10.282652	8.44E-25	0.31144274	4.26E-23
LOC100647880	initial	NONREPR	0.20779289	0.29009391	-4.6132682	3.96E-06	0.24741563	3.72E-05
LOC100647880	reciprocal	NONREPR	0.29867185	0.29874733	-2.8573658	0.00427173	0.24741563	0.01859817
LOC100647880	initial	REPR	0.19758664	0.29627076	-4.7302903	2.24E-06	0.24741563	2.21E-05
LOC100647880	reciprocal	REPR	0.28561116	0.28421925	-3.225665	0.0012568	0.24741563	0.00653381
LOC100647914	initial	NONREPR	0.4137638	0.06651188	-5.2385754	1.62E-07	0.39048604	1.93E-06
LOC100647914	reciprocal	NONREPR	0.36842854	0.07382131	-7.3009315	2.86E-13	0.39048604	6.71E-12
LOC100647914	initial	REPR	0.41251804	0.07385151	-4.7875203	1.69E-06	0.39048604	1.70E-05
LOC100647914	reciprocal	REPR	0.36723378	0.08241925	-6.6016425	4.07E-11	0.39048604	7.81E-10
LOC100647965	initial	NONREPR	0.35572436	0.04944858	-12.011881	3.08E-33	0.34359309	2.19E-31
LOC100647965	reciprocal	NONREPR	0.33907647	0.04756266	-14.032278	9.89E-45	0.34359309	1.02E-42
LOC100647965	initial	REPR	0.34802223	0.04936576	-12.716186	4.81E-37	0.34359309	3.92E-35
LOC100647965	reciprocal	REPR	0.33154931	0.04659084	-15.049871	3.46E-51	0.34359309	4.27E-49
LOC100648000	initial	NONREPR	0.37554094	0.09992457	-5.0890214	3.60E-07	0.36772516	4.07E-06
LOC100648000	reciprocal	NONREPR	0.36074685	0.09965771	-5.7408915	9.42E-09	0.36772516	1.35E-07
LOC100648000	initial	REPR	0.37469643	0.10453096	-4.8992287	9.62E-07	0.36772516	1.02E-05
LOC100648000	reciprocal	REPR	0.35991643	0.10103007	-5.6985694	1.21E-08	0.36772516	1.70E-07
LOC100648001	initial	NONREPR	0.77969968	0.06269766	20.1589202	2.25E-90	0.77655331	6.03E-88
LOC100648001	reciprocal	NONREPR	0.74284806	0.06032514	17.5851141	3.20E-69	0.77655331	6.01E-67
LOC100648001	initial	REPR	0.80854196	0.03236629	44.5081553	0	0.77655331	0
LOC100648001	reciprocal	REPR	0.77512354	0.03599237	34.3814893	4.77E-259	0.77655331	5.51E-256
LOC100648033	initial	NONREPR	0.29186843	0.13623699	-6.505772	7.73E-11	0.34909862	1.45E-09
LOC100648033	reciprocal	NONREPR	0.27700519	0.16874307	-5.6853644	1.31E-08	0.34909862	1.83E-07
LOC100648033	initial	REPR	0.42261763	0.11195213	-2.7872353	0.00531599	0.34909862	0.02223857
LOC100648033	reciprocal	REPR	0.40490323	0.13842947	-2.7817482	0.0054067	0.34909862	0.02253954
LOC100648034	initial	NONREPR	0.32135471	0.02742035	-27.262708	1.17E-163	0.31284487	7.06E-161
LOC100648034	reciprocal	NONREPR	0.3145378	0.05180051	-15.038252	4.12E-51	0.31284487	5.03E-49

LOC100648034	initial	REPR	0.3110919	0.03219174	-24.696381	1.17E-134	0.31284487	4.75E-132
LOC100648034	reciprocal	REPR	0.30439505	0.05539271	-14.919933	2.45E-50	0.31284487	2.94E-48
LOC100648162	initial	NONREPR	0.36708347	0.0581371	-9.3700807	7.25E-21	0.34896643	2.86E-19
LOC100648162	reciprocal	NONREPR	0.34092925	0.05461108	-12.070003	1.52E-33	0.34896643	1.09E-31
LOC100648162	initial	REPR	0.35682937	0.05867245	-10.041379	1.00E-23	0.34896643	4.69E-22
LOC100648162	reciprocal	REPR	0.33102363	0.05421583	-12.977003	1.65E-38	0.34896643	1.40E-36
LOC100648188	initial	NONREPR	0.65096455	0.06334283	9.83981528	7.58E-23	0.65549332	3.38E-21
LOC100648188	reciprocal	NONREPR	0.65879863	0.05976757	11.0083966	3.48E-28	0.65549332	2.08E-26
LOC100648188	initial	REPR	0.65219461	0.06460893	9.73085197	2.23E-22	0.65549332	9.69E-21
LOC100648188	reciprocal	REPR	0.6600155	0.06218169	10.6681446	1.43E-26	0.65549332	7.95E-25
LOC100648261	initial	NONREPR	0.3230608	0.09037857	-8.184915	2.72E-16	0.29268604	8.09E-15
LOC100648261	reciprocal	NONREPR	0.25737579	0.10303778	-10.284121	8.31E-25	0.29268604	4.20E-23
LOC100648261	initial	REPR	0.3283243	0.10223375	-7.0013457	2.54E-12	0.29268604	5.54E-11
LOC100648261	reciprocal	REPR	0.26198328	0.11547955	-8.9685645	3.00E-19	0.29268604	1.09E-17
LOC100648410	initial	NONREPR	0.32747414	0.03237918	-22.22513	1.96E-109	0.33809677	6.48E-107
LOC100648410	reciprocal	NONREPR	0.32837042	0.02728861	-26.222096	1.49E-151	0.33809677	7.57E-149
LOC100648410	initial	REPR	0.34780972	0.03806103	-16.517706	2.74E-61	0.33809677	4.30E-59
LOC100648410	reciprocal	REPR	0.34873279	0.0366246	-17.054492	3.24E-65	0.33809677	5.49E-63
LOC100648509	initial	NONREPR	0.35309261	0.04297043	-14.090452	4.35E-45	0.34238999	4.56E-43
LOC100648509	reciprocal	NONREPR	0.3386714	0.04342141	-15.412225	1.35E-53	0.34238999	1.78E-51
LOC100648509	initial	REPR	0.3460384	0.04338313	-14.671575	9.80E-49	0.34238999	1.12E-46
LOC100648509	reciprocal	REPR	0.33175754	0.04374948	-16.005829	1.16E-57	0.34238999	1.67E-55
LOC100648528	initial	NONREPR	0.3168915	0.03262298	-23.544578	1.43E-122	0.32265617	5.16E-120
LOC100648528	reciprocal	NONREPR	0.31632292	0.03080959	-25.015656	4.13E-138	0.32265617	1.85E-135
LOC100648528	initial	REPR	0.32899505	0.03959906	-17.998755	1.99E-72	0.32265617	3.96E-70
LOC100648528	reciprocal	REPR	0.3284152	0.04105413	-17.424838	5.35E-68	0.32265617	9.73E-66
LOC100648624	initial	NONREPR	0.60429718	0.06087021	6.9558264	3.51E-12	0.62634774	7.60E-11
LOC100648624	reciprocal	NONREPR	0.68113257	0.07695867	9.86219722	6.07E-23	0.62634774	2.72E-21
LOC100648624	initial	REPR	0.57016975	0.06889034	4.10135534	4.11E-05	0.62634774	0.00031552

LOC100648624	reciprocal	REPR	0.64979146	0.08289588	7.45661478	8.88E-14	0.62634774	2.18E-12
LOC100648770	initial	NONREPR	0.31191322	0.01726598	-45.823623	0	0.31462682	0
LOC100648770	reciprocal	NONREPR	0.32383474	0.02122682	-34.682736	1.43E-263	0.31462682	1.79E-260
LOC100648770	initial	REPR	0.30548509	0.01980227	-41.475678	0	0.31462682	0
LOC100648770	reciprocal	REPR	0.31727421	0.02388992	-32.077411	9.11E-226	0.31462682	7.81E-223
LOC100648955	initial	NONREPR	0.35144868	0.04060977	-15.086948	1.97E-51	0.39238614	2.45E-49
LOC100648955	reciprocal	NONREPR	0.46451484	0.04434391	-3.2062951	0.00134456	0.39238614	0.00692292
LOC100648955	initial	REPR	0.3218492	0.05273024	-14.13395	2.35E-45	0.39238614	2.49E-43
LOC100648955	reciprocal	REPR	0.43173183	0.05733725	-4.7925003	1.65E-06	0.39238614	1.66E-05
LOC100648995	initial	NONREPR	0.62353483	0.08160737	6.18300888	6.29E-10	0.62688237	1.04E-08
LOC100648995	reciprocal	NONREPR	0.62162696	0.08091588	6.13550291	8.49E-10	0.62688237	1.39E-08
LOC100648995	initial	REPR	0.63212892	0.09710739	5.57486752	2.48E-08	0.62688237	3.33E-07
LOC100648995	reciprocal	REPR	0.63023878	0.09902446	5.38494515	7.25E-08	0.62688237	9.18E-07
LOC100649153	initial	NONREPR	0.28461649	0.05554429	-16.593535	7.76E-62	0.37847454	1.23E-59
LOC100649153	reciprocal	NONREPR	0.46222853	0.04650647	-3.2549076	0.00113429	0.37847454	0.00599552
LOC100649153	initial	REPR	0.29375557	0.0646935	-13.559529	6.96E-42	0.37847454	6.47E-40
LOC100649153	reciprocal	REPR	0.47329756	0.06053334	-1.7661587	0.07736923	0.37847454	0.19011811
LOC100649230	initial	NONREPR	0.39016617	0.1590672	-2.8077052	0.00498959	0.39334346	0.02111707
LOC100649230	reciprocal	NONREPR	0.38564409	0.1383714	-3.3652874	0.00076464	0.39334346	0.00426698
LOC100649230	initial	REPR	0.40106493	0.18394016	-2.1802191	0.02924122	0.39334346	0.08938771
LOC100649230	reciprocal	REPR	0.39649866	0.17421654	-2.4112268	0.01589896	0.39334346	0.05502063
LOC100649275	initial	NONREPR	0.23435532	0.0803775	-14.728995	4.20E-49	0.27934317	4.83E-47
LOC100649275	reciprocal	NONREPR	0.300767	0.07743561	-10.894834	1.22E-27	0.27934317	7.13E-26
LOC100649275	initial	REPR	0.25614679	0.09243268	-11.533725	8.92E-31	0.27934317	5.97E-29
LOC100649275	reciprocal	REPR	0.32610358	0.09451847	-7.679572	1.60E-14	0.27934317	4.16E-13
LOC100649394	initial	NONREPR	0.25080957	0.08927655	-12.25741	1.53E-34	0.26932012	1.12E-32
LOC100649394	reciprocal	NONREPR	0.26809984	0.10254829	-9.7932849	1.20E-22	0.26932012	5.30E-21
LOC100649394	initial	REPR	0.27013063	0.10264	-9.6839426	3.53E-22	0.26932012	1.51E-20
LOC100649394	reciprocal	REPR	0.28824042	0.11808579	-7.6549881	1.93E-14	0.26932012	5.01E-13

LOC100649421	initial	NONREPR	0.77129737	0.04866387	24.9805751	9.94E-138	0.74049882	4.33E-135
LOC100649421	reciprocal	NONREPR	0.74109289	0.04284409	24.5461282	4.76E-133	0.74049882	1.90E-130
LOC100649421	initial	REPR	0.74114331	0.04879715	21.5569851	4.55E-103	0.74049882	1.42E-100
LOC100649421	reciprocal	REPR	0.70846171	0.0470427	18.8748657	1.84E-79	0.74049882	3.91E-77
LOC100649428	initial	NONREPR	0.44095816	0.06185491	-3.8359822	0.00012506	0.39279605	0.00086272
LOC100649428	reciprocal	NONREPR	0.36022461	0.06031384	-9.5233433	1.68E-21	0.39279605	6.90E-20
LOC100649428	initial	REPR	0.42480175	0.05403523	-5.6091587	2.03E-08	0.39279605	2.77E-07
LOC100649428	reciprocal	REPR	0.34519969	0.05203534	-12.303317	8.69E-35	0.39279605	6.45E-33
LOC100649524	initial	NONREPR	0.65962822	0.21930787	3.01693637	0.00255343	0.76784185	0.01199726
LOC100649524	reciprocal	NONREPR	0.87443961	0.23450487	8.2761454	1.27E-16	0.76784185	3.90E-15
LOC100649524	initial	REPR	0.66180008	0.23107481	2.90523381	0.00366979	0.76784185	0.01636418
LOC100649524	reciprocal	REPR	0.8754995	0.25359818	7.69124151	1.46E-14	0.76784185	3.81E-13
LOC100649553	initial	NONREPR	0.43049982	0.05515825	-5.0728986	3.92E-07	0.38443047	4.40E-06
LOC100649553	reciprocal	NONREPR	0.34475104	0.05041583	-12.737919	3.64E-37	0.38443047	2.99E-35
LOC100649553	initial	REPR	0.42384107	0.04884688	-6.2854578	3.27E-10	0.38443047	5.63E-09
LOC100649553	reciprocal	REPR	0.33862997	0.04250168	-15.750095	6.86E-56	0.38443047	9.49E-54
LOC100649672	initial	NONREPR	0.4340949	0.08636001	-3.0704401	0.00213744	0.39233764	0.01030223
LOC100649672	reciprocal	NONREPR	0.34890793	0.0865439	-7.2083995	5.66E-13	0.39233764	1.31E-11
LOC100649672	initial	REPR	0.43583222	0.07457583	-3.4608307	0.00053851	0.39233764	0.00313928
LOC100649672	reciprocal	REPR	0.35051549	0.07402528	-8.3319386	7.95E-17	0.39233764	2.48E-15
LOC100649728	initial	NONREPR	0.35835934	0.17321894	-3.3627512	0.0007717	0.33779416	0.00430157
LOC100649728	reciprocal	NONREPR	0.2883758	0.15024366	-6.0121371	1.83E-09	0.33779416	2.87E-08
LOC100649728	initial	REPR	0.38871824	0.16889492	-2.6803839	0.00735378	0.33779416	0.02925532
LOC100649728	reciprocal	REPR	0.31572324	0.1349652	-5.7310805	9.98E-09	0.33779416	1.42E-07
LOC100649739	initial	NONREPR	0.58928681	0.09344259	3.863526	0.00011176	0.61018678	0.00077841
LOC100649739	reciprocal	NONREPR	0.68795698	0.06006343	13.1625055	1.44E-39	0.61018678	1.26E-37
LOC100649739	initial	REPR	0.52970731	0.09579582	1.24190559	0.2142714	0.61018678	0.39604466
LOC100649739	reciprocal	REPR	0.63379603	0.06627098	8.27717871	1.26E-16	0.61018678	3.88E-15
LOC100649832	initial	NONREPR	0.64151307	0.09846691	5.90997874	3.42E-09	0.60149562	5.17E-08

LOC100649832	reciprocal	NONREPR	0.56747519	0.10496285	2.58717589	0.00967662	0.60149562	0.0366927
LOC100649832	initial	REPR	0.63570563	0.11915306	4.67275771	2.97E-06	0.60149562	2.86E-05
LOC100649832	reciprocal	REPR	0.56128859	0.12721598	1.93681143	0.0527684	0.60149562	0.14226337
LOC100649839	initial	NONREPR	0.35283326	0.16581504	-3.6583434	0.00025385	0.32853706	0.00162633
LOC100649839	reciprocal	NONREPR	0.28559906	0.17222914	-5.3234624	1.02E-07	0.32853706	1.26E-06
LOC100649839	initial	REPR	0.37246928	0.16129112	-3.2341401	0.0012201	0.32853706	0.00636944
LOC100649839	reciprocal	REPR	0.30324662	0.15862087	-5.2444872	1.57E-07	0.32853706	1.88E-06
LOC100649867	initial	NONREPR	0.99430888	0.3347273	15.4249153	1.11E-53	0.98394533	1.47E-51
LOC100649867	reciprocal	NONREPR	0.97325187	0.19899544	18.0616107	6.39E-73	0.98394533	1.28E-70
LOC100649867	initial	REPR	0.99442665	0.31021009	16.7118037	1.08E-62	0.98394533	1.75E-60
LOC100649867	reciprocal	REPR	0.97379392	0.24657086	14.6619438	1.13E-48	0.98394533	1.29E-46
LOC100649900	initial	NONREPR	0.43572776	0.09999707	-2.5852678	0.00973034	0.38384652	0.03685916
LOC100649900	reciprocal	NONREPR	0.33565261	0.08765099	-7.7891698	6.75E-15	0.38384652	1.82E-13
LOC100649900	initial	REPR	0.43185761	0.09138534	-3.0013144	0.00268817	0.38384652	0.01253811
LOC100649900	reciprocal	REPR	0.33214812	0.07359465	-9.4909811	2.29E-21	0.38384652	9.31E-20
LOC100649904	initial	NONREPR	0.75065856	0.17513085	6.29316708	3.11E-10	0.77287405	5.38E-09
LOC100649904	reciprocal	NONREPR	0.80058456	0.19290285	7.20545014	5.79E-13	0.77287405	1.33E-11
LOC100649904	initial	REPR	0.74473181	0.18750176	5.71039671	1.13E-08	0.77287405	1.60E-07
LOC100649904	reciprocal	REPR	0.79552126	0.2123442	6.3977899	1.58E-10	0.77287405	2.83E-09
LOC100649986	initial	NONREPR	0.32913982	0.09768907	-7.2892299	3.12E-13	0.35605636	7.28E-12
LOC100649986	reciprocal	NONREPR	0.41341957	0.10232534	-3.4189652	0.0006286	0.35605636	0.00359124
LOC100649986	initial	REPR	0.30028714	0.09948401	-8.5031849	1.84E-17	0.35605636	6.03E-16
LOC100649986	reciprocal	REPR	0.3813789	0.10463481	-4.6227407	3.79E-06	0.35605636	3.56E-05
LOC100649992	initial	NONREPR	0.34601092	0.0821201	-7.7523084	9.02E-15	0.39329737	2.40E-13
LOC100649992	reciprocal	NONREPR	0.40971717	0.06967317	-5.2406781	1.60E-07	0.39329737	1.91E-06
LOC100649992	initial	REPR	0.37598105	0.07644477	-6.6275565	3.41E-11	0.39329737	6.62E-10
LOC100649992	reciprocal	REPR	0.44148033	0.05963922	-3.9429818	8.05E-05	0.39329737	0.00058019
LOC100650015	initial	NONREPR	0.42842154	0.09907079	-2.9099812	0.0036145	0.37928329	0.01614511
LOC100650015	reciprocal	NONREPR	0.33166911	0.09845991	-7.1160491	1.11E-12	0.37928329	2.51E-11

LOC100650015	initial	REPR	0.42682116	0.08879035	-3.3205484	0.00089841	0.37928329	0.00489785
LOC100650015	reciprocal	REPR	0.33022135	0.08381453	-8.4374883	3.24E-17	0.37928329	1.04E-15
LOC100650131	initial	NONREPR	0.41106035	0.08055525	-4.4638138	8.05E-06	0.3790036	7.11E-05
LOC100650131	reciprocal	NONREPR	0.34468042	0.07832219	-8.2033627	2.34E-16	0.3790036	7.00E-15
LOC100650131	initial	REPR	0.41340457	0.06970229	-5.020045	5.17E-07	0.3790036	5.67E-06
LOC100650131	reciprocal	REPR	0.34686904	0.06287848	-10.06434	7.94E-24	0.3790036	3.77E-22
LOC100650219	initial	NONREPR	0.6310083	0.05128075	10.4628907	1.28E-25	0.63254196	6.80E-24
LOC100650219	reciprocal	NONREPR	0.66656218	0.0385601	17.9635693	3.76E-72	0.63254196	7.38E-70
LOC100650219	initial	REPR	0.59784892	0.05068284	7.82336318	5.14E-15	0.63254196	1.40E-13
LOC100650219	reciprocal	REPR	0.63474843	0.04315281	12.8066392	1.51E-37	0.63254196	1.25E-35
LOC100650257	initial	NONREPR	0.41700441	0.06857605	-4.8862953	1.03E-06	0.37314664	1.08E-05
LOC100650257	reciprocal	NONREPR	0.35415022	0.0538033	-11.167452	5.88E-29	0.37314664	3.62E-27
LOC100650257	initial	REPR	0.39130293	0.06226014	-7.0966547	1.28E-12	0.37314664	2.87E-11
LOC100650257	reciprocal	REPR	0.330129	0.04628892	-15.286633	9.39E-53	0.37314664	1.20E-50
LOC100650263	initial	NONREPR	0.25495879	0.18179513	-5.8986047	3.67E-09	0.30355463	5.52E-08
LOC100650263	reciprocal	NONREPR	0.37263052	0.16244354	-3.20695	0.0013415	0.30355463	0.00690955
LOC100650263	initial	REPR	0.23671188	0.16869762	-6.94018	3.92E-12	0.30355463	8.47E-11
LOC100650263	reciprocal	REPR	0.34991735	0.14095773	-4.3942432	1.11E-05	0.30355463	9.55E-05
LOC100650386	initial	NONREPR	0.23578677	0.17370136	-6.7697741	1.29E-11	0.28314862	2.63E-10
LOC100650386	reciprocal	NONREPR	0.34677908	0.15642459	-4.0481324	5.16E-05	0.28314862	0.00038806
LOC100650386	initial	REPR	0.22144266	0.16271986	-7.7266475	1.10E-14	0.28314862	2.92E-13
LOC100650386	reciprocal	REPR	0.32858596	0.13610647	-5.2502096	1.52E-07	0.28314862	1.83E-06
LOC100650448	initial	NONREPR	0.66281405	0.09173858	7.36723756	1.74E-13	0.64033114	4.15E-12
LOC100650448	reciprocal	NONREPR	0.65105252	0.07201913	8.65976657	4.73E-18	0.64033114	1.58E-16
LOC100650448	initial	REPR	0.62985297	0.09304039	5.7134982	1.11E-08	0.64033114	1.57E-07
LOC100650448	reciprocal	REPR	0.61760502	0.07787833	6.15569244	7.48E-10	0.64033114	1.23E-08
LOC100650586	initial	NONREPR	0.62626626	0.07458442	6.9214451	4.47E-12	0.611337	9.61E-11
LOC100650586	reciprocal	NONREPR	0.61324506	0.07798397	5.91112968	3.40E-09	0.611337	5.14E-08
LOC100650586	initial	REPR	0.60953254	0.08078956	5.51244126	3.54E-08	0.611337	4.65E-07

LOC100650586	reciprocal	REPR	0.59630414	0.08860701	4.40246285	1.07E-05	0.611337	9.23E-05
LOC100650600	initial	NONREPR	0.61531711	0.16424548	2.85985596	0.00423833	0.61195708	0.01848761
LOC100650600	reciprocal	NONREPR	0.62861233	0.16541041	3.18159106	0.00146468	0.61195708	0.00745956
LOC100650600	initial	REPR	0.5951751	0.18607282	2.07123746	0.03833661	0.61195708	0.11099911
LOC100650600	reciprocal	REPR	0.60872379	0.18814542	2.34898553	0.01882464	0.61195708	0.06306663
LOC100650744	initial	NONREPR	0.43297006	0.09436266	-2.8585832	0.00425538	0.36921308	0.01853771
LOC100650744	reciprocal	NONREPR	0.33752225	0.09913484	-6.8024071	1.03E-11	0.36921308	2.12E-10
LOC100650744	initial	REPR	0.3991979	0.08319463	-4.9138787	8.93E-07	0.36921308	9.47E-06
LOC100650744	reciprocal	REPR	0.30716212	0.08878356	-9.1618354	5.10E-20	0.36921308	1.93E-18
LOC100650910	initial	NONREPR	0.75230535	0.05240138	21.2006924	9.41E-100	0.64171555	2.77E-97
LOC100650910	reciprocal	NONREPR	0.56224498	0.05909449	4.23522072	2.28E-05	0.64171555	0.00018475
LOC100650910	initial	REPR	0.72506902	0.05109545	18.9791231	2.54E-80	0.64171555	5.56E-78
LOC100650910	reciprocal	REPR	0.52724286	0.05999368	1.81818263	0.06903622	0.64171555	0.17417407
LOC100651112	initial	NONREPR	0.99832505	0.13218003	48.3453889	0	0.99612166	0
LOC100651112	reciprocal	NONREPR	0.99442318	0.13132851	39.4700616	0	0.99612166	0
LOC100651112	initial	REPR	0.99809101	0.12764835	49.0352731	0	0.99612166	0
LOC100651112	reciprocal	REPR	0.99364742	0.12586679	40.1418119	0	0.99612166	0
LOC100651152	initial	NONREPR	0.63813745	0.04573191	12.4046692	2.47E-35	0.65594858	1.88E-33
LOC100651152	reciprocal	NONREPR	0.7066549	0.04613696	19.0561484	5.84E-81	0.65594858	1.31E-78
LOC100651152	initial	REPR	0.60363764	0.05043447	8.34043102	7.40E-17	0.65594858	2.31E-15
LOC100651152	reciprocal	REPR	0.67536431	0.05033572	14.5532562	5.57E-48	0.65594858	6.26E-46
LOC100651153	initial	NONREPR	0.73796667	0.07169583	14.4419416	2.82E-47	0.77233021	3.11E-45
LOC100651153	reciprocal	NONREPR	0.81361461	0.08091834	18.2118217	4.16E-74	0.77233021	8.44E-72
LOC100651153	initial	REPR	0.73021915	0.07220027	13.7912881	2.88E-43	0.77233021	2.82E-41
LOC100651153	reciprocal	REPR	0.8075204	0.08230666	17.4223833	5.58E-68	0.77233021	1.01E-65
LOC100651339	initial	NONREPR	0.79201446	0.31475856	4.24805314	2.16E-05	0.73079153	0.00017534
LOC100651339	reciprocal	NONREPR	0.66127256	0.26595412	2.5153598	0.0118911	0.73079153	0.04337534
LOC100651339	initial	REPR	0.79902311	0.31671008	4.35792863	1.31E-05	0.73079153	0.00011141
LOC100651339	reciprocal	REPR	0.670856	0.27752147	2.56578048	0.0102944	0.73079153	0.03857074

LOC100651450	initial	NONREPR	0.97831013	0.29705786	12.8223558	1.23E-37	0.94866566	1.02E-35
LOC100651450	reciprocal	NONREPR	0.93477699	0.24624326	10.812461	3.00E-27	0.94866566	1.71E-25
LOC100651450	initial	REPR	0.97007291	0.26899912	12.9316678	2.98E-38	0.94866566	2.52E-36
LOC100651450	reciprocal	REPR	0.9115026	0.22847163	10.2074871	1.84E-24	0.94866566	9.11E-23
LOC100651509	initial	NONREPR	0.92050677	0.05936133	41.2600653	0	0.91548644	0
LOC100651509	reciprocal	NONREPR	0.91060321	0.05753872	40.3384425	0	0.91548644	0
LOC100651509	initial	REPR	0.92037697	0.12870289	19.0165105	1.24E-80	0.91548644	2.75E-78
LOC100651509	reciprocal	REPR	0.91045881	0.14097229	16.4518136	8.14E-61	0.91548644	1.25E-58
LOC100651733	initial	NONREPR	0.56281128	0.08572236	2.94648208	0.00321411	0.60464661	0.01460331
LOC100651733	reciprocal	NONREPR	0.66916076	0.07259	9.70370238	2.91E-22	0.60464661	1.26E-20
LOC100651733	initial	REPR	0.53905229	0.08483552	1.84507584	0.06502651	0.60464661	0.16646342
LOC100651733	reciprocal	REPR	0.64756211	0.07929902	7.67147344	1.70E-14	0.60464661	4.42E-13
LOC100651763	initial	NONREPR	0.69355962	0.09708629	8.41327821	3.99E-17	0.68147758	1.28E-15
LOC100651763	reciprocal	NONREPR	0.66360977	0.07621001	8.9151332	4.87E-19	0.68147758	1.74E-17
LOC100651763	initial	REPR	0.69920107	0.0997637	8.45494218	2.79E-17	0.68147758	9.04E-16
LOC100651763	reciprocal	REPR	0.66953988	0.07951187	8.88049507	6.66E-19	0.68147758	2.37E-17
LOC100651775	initial	NONREPR	0.65928784	0.04263813	15.4819695	4.59E-54	0.67188853	6.13E-52
LOC100651775	reciprocal	NONREPR	0.65704345	0.04385416	14.8251945	1.01E-49	0.67188853	1.18E-47
LOC100651775	initial	REPR	0.68668654	0.03947142	19.8795446	6.12E-88	0.67188853	1.58E-85
LOC100651775	reciprocal	REPR	0.68453628	0.04050499	19.1259872	1.53E-81	0.67188853	3.49E-79
LOC100651786	initial	NONREPR	0.26759864	0.09258488	-10.874782	1.52E-27	0.24079492	8.85E-26
LOC100651786	reciprocal	NONREPR	0.21464925	0.08900751	-14.57321	4.16E-48	0.24079492	4.69E-46
LOC100651786	initial	REPR	0.26689105	0.09823108	-10.286498	8.11E-25	0.24079492	4.11E-23
LOC100651786	reciprocal	REPR	0.21404075	0.09534029	-13.643115	2.22E-42	0.24079492	2.12E-40
LOC100651849	initial	NONREPR	0.56539761	0.09272896	2.83727614	0.00455002	0.64425369	0.0195995
LOC100651849	reciprocal	NONREPR	0.72729303	0.12979022	7.55782398	4.10E-14	0.64425369	1.04E-12
LOC100651849	initial	REPR	0.56077426	0.09136742	2.67387369	0.00749807	0.64425369	0.02976233
LOC100651849	reciprocal	REPR	0.72354984	0.13320142	7.22318815	5.08E-13	0.64425369	1.17E-11
LOC100652255	initial	NONREPR	0.73344172	0.06182649	16.3708989	3.09E-60	0.6428411	4.68E-58

LOC100652255	reciprocal	NONREPR	0.53865278	0.05240483	2.95622002	0.00311435	0.6428411	0.01423404
LOC100652255	initial	REPR	0.74532775	0.05734461	18.7261987	3.03E-78	0.6428411	6.40E-76
LOC100652255	reciprocal	REPR	0.55394215	0.04543175	4.76784651	1.86E-06	0.6428411	1.86E-05
LOC100652265	initial	NONREPR	0.9998089	3.09242421	2.76886877	0.00562513	0.98728652	0.02334965
LOC100652265	reciprocal	NONREPR	0.97415718	1.40125546	2.5902058	0.00959186	0.98728652	0.03642649
LOC100652265	initial	REPR	0.99981803	3.09710293	2.78049998	0.00542753	0.98728652	0.0226044
LOC100652265	reciprocal	REPR	0.97536198	1.40805663	2.61247861	0.00898883	0.98728652	0.03452061
LOC100652299	initial	NONREPR	0.42348993	0.04862802	-6.3433194	2.25E-10	0.32105855	3.96E-09
LOC100652299	reciprocal	NONREPR	0.38098277	0.04709315	-10.306786	6.57E-25	0.32105855	3.34E-23
LOC100652299	initial	REPR	0.25599095	0.04209175	-25.347272	9.63E-142	0.32105855	4.45E-139
LOC100652299	reciprocal	REPR	0.22377054	0.03996255	-31.12482	1.11E-212	0.32105855	9.02E-210
LOC100652301	initial	NONREPR	0.93176014	0.25978579	10.0623155	8.11E-24	0.89043339	3.83E-22
LOC100652301	reciprocal	NONREPR	0.90879557	0.27080288	8.48963154	2.07E-17	0.89043339	6.77E-16
LOC100652301	initial	REPR	0.87938732	0.18703458	10.6217847	2.36E-26	0.89043339	1.30E-24
LOC100652301	reciprocal	REPR	0.84179052	0.18692548	8.9426609	3.80E-19	0.89043339	1.37E-17
LOC105665800	initial	NONREPR	0.35411704	0.0439569	-13.672275	1.49E-42	0.3536681	1.43E-40
LOC105665800	reciprocal	NONREPR	0.35314679	0.03774364	-16.03543	7.23E-58	0.3536681	1.04E-55
LOC105665800	initial	REPR	0.35418946	0.0432493	-13.888645	7.42E-44	0.3536681	7.45E-42
LOC105665800	reciprocal	REPR	0.35321912	0.03570061	-16.944218	2.12E-64	0.3536681	3.52E-62
LOC105665983	initial	NONREPR	0.6439928	0.11819746	5.01479976	5.31E-07	0.64686015	5.82E-06
LOC105665983	reciprocal	NONREPR	0.61378031	0.13612356	3.40301633	0.00066646	0.64686015	0.00377595
LOC105665983	initial	REPR	0.67925595	0.11713429	6.40593443	1.49E-10	0.64686015	2.70E-09
LOC105665983	reciprocal	REPR	0.65041154	0.13242493	4.68830654	2.75E-06	0.64686015	2.68E-05
LOC105666148	initial	NONREPR	0.61630082	0.11163349	4.24492979	2.19E-05	0.63934609	0.00017755
LOC105666148	reciprocal	NONREPR	0.69107589	0.1160983	6.93510611	4.06E-12	0.63934609	8.76E-11
LOC105666148	initial	REPR	0.58628753	0.11258564	3.09665725	0.00195716	0.63934609	0.00955293
LOC105666148	reciprocal	REPR	0.66372013	0.11906998	5.7102287	1.13E-08	0.63934609	1.60E-07
LOC105666149	initial	NONREPR	0.13971215	0.11105352	-16.367629	3.26E-60	0.17743907	4.91E-58
LOC105666149	reciprocal	NONREPR	0.16949132	0.10009934	-15.876595	9.20E-57	0.17743907	1.31E-54

LOC105666149	initial	REPR	0.18202303	0.11305514	-13.291752	2.58E-40	0.17743907	2.31E-38
LOC105666149	reciprocal	REPR	0.21852976	0.10614912	-12.004385	3.37E-33	0.17743907	2.39E-31
LOC105666191	initial	NONREPR	0.67171354	0.19966578	3.58571908	0.00033615	0.70742178	0.00208423
LOC105666191	reciprocal	NONREPR	0.72360894	0.18648429	5.16094057	2.46E-07	0.70742178	2.86E-06
LOC105666191	initial	REPR	0.6922339	0.13912191	5.82642806	5.66E-09	0.70742178	8.37E-08
LOC105666191	reciprocal	REPR	0.74213076	0.11950241	8.84561928	9.10E-19	0.70742178	3.20E-17
LOC105666195	initial	NONREPR	0.40001047	0.15271723	-2.6547199	0.00793743	0.39018436	0.0311766
LOC105666195	reciprocal	NONREPR	0.35672513	0.14314483	-4.1189512	3.81E-05	0.39018436	0.00029448
LOC105666195	initial	REPR	0.42412219	0.1530655	-1.9983205	0.04568193	0.39018436	0.12723652
LOC105666195	reciprocal	REPR	0.37987967	0.13994454	-3.5018087	0.00046211	0.39018436	0.00275323
LOC105666212	initial	NONREPR	0.57697095	0.11617395	2.67143409	0.00755279	0.60038393	0.02994787
LOC105666212	reciprocal	NONREPR	0.58506818	0.11268448	3.04934769	0.00229339	0.60038393	0.01095385
LOC105666212	initial	REPR	0.61582901	0.11868927	3.97577299	7.02E-05	0.60038393	0.0005139
LOC105666212	reciprocal	REPR	0.62366759	0.10996371	4.59374017	4.35E-06	0.60038393	4.05E-05
LOC105666397	initial	NONREPR	0.37652717	0.17090853	-2.9507888	0.00316964	0.38776681	0.01444058
LOC105666397	reciprocal	NONREPR	0.38373322	0.12913094	-3.6686203	0.00024386	0.38776681	0.00156971
LOC105666397	initial	REPR	0.39174798	0.19093385	-2.304309	0.02120531	0.38776681	0.06929113
LOC105666397	reciprocal	REPR	0.39905887	0.16253462	-2.5187742	0.01177641	0.38776681	0.0430564
LOC105666541	initial	NONREPR	0.37356663	0.10359726	-4.9899582	6.04E-07	0.35915921	6.58E-06
LOC105666541	reciprocal	NONREPR	0.32157578	0.0947937	-7.875413	3.40E-15	0.35915921	9.36E-14
LOC105666541	initial	REPR	0.39749331	0.11048021	-3.7646622	0.00016677	0.35915921	0.00111559
LOC105666541	reciprocal	REPR	0.34400112	0.10061776	-6.4155094	1.40E-10	0.35915921	2.54E-09
LOC105666566	initial	NONREPR	0.4308379	0.0452796	-6.1492003	7.79E-10	0.38865068	1.28E-08
LOC105666566	reciprocal	NONREPR	0.35200063	0.04298298	-14.197638	9.48E-46	0.38865068	1.02E-43
LOC105666566	initial	REPR	0.42509535	0.0397379	-7.5970473	3.03E-14	0.38865068	7.71E-13
LOC105666566	reciprocal	REPR	0.34666885	0.0361371	-17.536383	7.56E-69	0.38865068	1.41E-66
LOC105666573	initial	NONREPR	0.37582125	0.13161107	-3.8547149	0.00011586	0.36796284	0.00080447
LOC105666573	reciprocal	NONREPR	0.3581673	0.11719807	-4.9772789	6.45E-07	0.36796284	7.01E-06
LOC105666573	initial	REPR	0.37777782	0.14315888	-3.4855749	0.00049108	0.36796284	0.00290108

LOC105666573	reciprocal	REPR	0.36008498	0.13309265	-4.3202634	1.56E-05	0.36796284	0.00013024
LOC105666595	initial	NONREPR	0.44783602	0.06526985	-3.2084943	0.00133432	0.39462895	0.0068749
LOC105666595	reciprocal	NONREPR	0.35583821	0.06196844	-9.577032	9.99E-22	0.39462895	4.18E-20
LOC105666595	initial	REPR	0.43283318	0.05766738	-4.6872443	2.77E-06	0.39462895	2.69E-05
LOC105666595	reciprocal	REPR	0.34200839	0.05363902	-12.19927	3.14E-34	0.39462895	2.27E-32
LOC105666672	initial	NONREPR	0.71550819	0.15293846	6.03045534	1.63E-09	0.64964521	2.58E-08
LOC105666672	reciprocal	NONREPR	0.62848575	0.14032643	3.74645116	0.00017935	0.64964521	0.00119178
LOC105666672	initial	REPR	0.67347009	0.07559293	9.57658416	1.00E-21	0.64964521	4.19E-20
LOC105666672	reciprocal	REPR	0.58111679	0.07065754	4.63304561	3.60E-06	0.64964521	3.41E-05
LOC105666723	initial	NONREPR	0.8638186	0.15411202	11.9872217	4.15E-33	0.86209304	2.93E-31
LOC105666723	reciprocal	NONREPR	0.8590434	0.38749514	4.6642324	3.10E-06	0.86209304	2.97E-05
LOC105666723	initial	REPR	0.8651235	0.19020978	9.77085811	1.50E-22	0.86209304	6.58E-21
LOC105666723	reciprocal	REPR	0.86038666	0.42484073	4.28043978	1.87E-05	0.86209304	0.00015387
LOC105666923	initial	NONREPR	0.98984023	0.9345716	4.89968587	9.60E-07	0.9646269	1.01E-05
LOC105666923	reciprocal	NONREPR	0.94657568	0.55463382	5.18285187	2.19E-07	0.9646269	2.56E-06
LOC105666923	initial	REPR	0.98744377	0.84087668	5.19089521	2.09E-07	0.9646269	2.46E-06
LOC105666923	reciprocal	REPR	0.93464791	0.52893994	5.02964555	4.91E-07	0.9646269	5.42E-06
LOC105666928	initial	NONREPR	0.29719354	0.07692488	-11.188811	4.63E-29	0.36330298	2.85E-27
LOC105666928	reciprocal	NONREPR	0.31568243	0.08598539	-8.9978702	2.30E-19	0.36330298	8.41E-18
LOC105666928	initial	REPR	0.40957046	0.06186294	-5.912124	3.38E-09	0.36330298	5.11E-08
LOC105666928	reciprocal	REPR	0.43076547	0.07264934	-3.8366313	0.00012473	0.36330298	0.00086103
LOC105666931	initial	NONREPR	0.26048393	0.10400953	-10.032301	1.10E-23	0.32062044	5.11E-22
LOC105666931	reciprocal	NONREPR	0.31440418	0.12194663	-6.3930336	1.63E-10	0.32062044	2.91E-09
LOC105666931	initial	REPR	0.32369086	0.08657659	-8.5110921	1.72E-17	0.32062044	5.65E-16
LOC105666931	reciprocal	REPR	0.38390278	0.10644714	-4.4436648	8.84E-06	0.32062044	7.74E-05
LOC105666969	initial	NONREPR	0.92731574	0.80169804	3.17597046	0.00149336	0.91544596	0.00758631
LOC105666969	reciprocal	NONREPR	0.9504721	0.82267558	3.59123659	0.00032911	0.91544596	0.00204484
LOC105666969	initial	REPR	0.87252523	0.46307254	4.15371887	3.27E-05	0.91544596	0.00025653
LOC105666969	reciprocal	REPR	0.91147075	0.51231332	4.55136807	5.33E-06	0.91544596	4.89E-05

LOC105666984	initial	NONREPR	0.87756234	0.41450623	4.75154733	2.02E-06	0.85388038	2.01E-05
LOC105666984	reciprocal	NONREPR	0.94481123	0.44165177	6.43091662	1.27E-10	0.85388038	2.31E-09
LOC105666984	initial	REPR	0.72826026	0.1318601	7.47620929	7.65E-14	0.85388038	1.90E-12
LOC105666984	reciprocal	REPR	0.86488771	0.20936538	8.86724189	7.50E-19	0.85388038	2.66E-17
LOC105666994	initial	NONREPR	0.9123007	0.26621203	8.79770822	1.40E-18	0.92074766	4.87E-17
LOC105666994	reciprocal	NONREPR	0.94638883	0.34722297	8.26816273	1.36E-16	0.92074766	4.15E-15
LOC105666994	initial	REPR	0.89133042	0.27185513	7.74089975	9.87E-15	0.92074766	2.62E-13
LOC105666994	reciprocal	REPR	0.93297068	0.36256745	7.26276901	3.79E-13	0.92074766	8.80E-12
LOC105666995	initial	NONREPR	0.9933537	1.08688491	4.60676793	4.09E-06	0.9766882	3.83E-05
LOC105666995	reciprocal	NONREPR	0.99063412	0.93021113	5.01098236	5.42E-07	0.9766882	5.93E-06
LOC105666995	initial	REPR	0.96774451	0.51787613	6.56774804	5.11E-11	0.9766882	9.71E-10
LOC105666995	reciprocal	REPR	0.95502046	0.62039041	4.9251647	8.43E-07	0.9766882	8.99E-06
LOC105667011	initial	NONREPR	0.84379845	0.12185389	13.8425326	1.41E-43	0.87743158	1.40E-41
LOC105667011	reciprocal	NONREPR	0.89951113	0.14787096	14.8224131	1.05E-49	0.87743158	1.22E-47
LOC105667011	initial	REPR	0.85753763	0.13542149	13.2548181	4.23E-40	0.87743158	3.74E-38
LOC105667011	reciprocal	REPR	0.90887912	0.16482001	13.9547692	2.94E-44	0.87743158	2.99E-42
LOC105667016	initial	NONREPR	0.96817668	0.41059319	8.31775922	8.96E-17	0.95794002	2.78E-15
LOC105667016	reciprocal	NONREPR	0.9535156	0.34121863	8.85367564	8.47E-19	0.95794002	2.99E-17
LOC105667016	initial	REPR	0.9634034	0.38367566	8.52417059	1.54E-17	0.95794002	5.06E-16
LOC105667016	reciprocal	REPR	0.94666439	0.31099566	9.2488124	2.27E-20	0.95794002	8.75E-19
LOC105667035	initial	NONREPR	0.82188852	0.32055555	4.77045282	1.84E-06	0.84108064	1.84E-05
LOC105667035	reciprocal	NONREPR	0.85219032	0.29197163	6.00018686	1.97E-09	0.84108064	3.07E-08
LOC105667035	initial	REPR	0.83058436	0.33938285	4.68430974	2.81E-06	0.84108064	2.72E-05
LOC105667035	reciprocal	REPR	0.85965936	0.3260278	5.55923021	2.71E-08	0.84108064	3.62E-07
LOC105667042	initial	NONREPR	0.98737554	0.25382613	17.1748054	4.10E-66	0.98972093	7.16E-64
LOC105667042	reciprocal	NONREPR	0.98898958	0.35365783	12.7180595	4.69E-37	0.98972093	3.84E-35
LOC105667042	initial	REPR	0.99066054	0.30780509	15.152849	7.26E-52	0.98972093	9.12E-50
LOC105667042	reciprocal	REPR	0.99185806	0.36849635	13.0328317	7.96E-39	0.98972093	6.81E-37
LOC105667061	initial	NONREPR	0.73436058	0.1622412	6.2675839	3.67E-10	0.80134271	6.27E-09

LOC105667061	reciprocal	NONREPR	0.86423488	0.1866703	9.91544055	3.57E-23	0.80134271	1.62E-21
LOC105667061	initial	REPR	0.73947483	0.16808152	6.20675462	5.41E-10	0.80134271	9.07E-09
LOC105667061	reciprocal	REPR	0.86730054	0.21000155	8.93945166	3.91E-19	0.80134271	1.40E-17
LOC105667069	initial	NONREPR	0.99670027	0.20893058	27.3325663	1.74E-164	0.99292344	1.09E-161
LOC105667069	reciprocal	NONREPR	0.9941846	0.18848036	27.2782465	7.69E-164	0.99292344	4.71E-161
LOC105667069	initial	REPR	0.99304031	0.18707883	26.516289	6.29E-155	0.99292344	3.43E-152
LOC105667069	reciprocal	REPR	0.98776859	0.16495724	26.6216931	3.81E-156	0.99292344	2.12E-153
LOC105667070	initial	NONREPR	0.97824488	0.19291659	19.7282723	1.23E-86	0.98013163	3.09E-84
LOC105667070	reciprocal	NONREPR	0.98231229	0.18526836	21.6822728	3.02E-104	0.98013163	9.63E-102
LOC105667070	initial	REPR	0.97792129	0.20068769	18.8891271	1.40E-79	0.98013163	3.01E-77
LOC105667070	reciprocal	REPR	0.98204808	0.2038364	19.633114	8.06E-86	0.98013163	1.97E-83
LOC105667072	initial	NONREPR	0.99895252	0.67490837	10.1648102	2.85E-24	0.99728589	1.40E-22
LOC105667072	reciprocal	NONREPR	0.99791693	0.54012184	11.4267312	3.07E-30	0.99728589	2.02E-28
LOC105667072	initial	REPR	0.99741229	0.66605869	8.93974029	3.90E-19	0.99728589	1.40E-17
LOC105667072	reciprocal	REPR	0.99486181	0.51847828	10.1564586	3.10E-24	0.99728589	1.51E-22
LOC105667073	initial	NONREPR	0.99908798	0.21806311	32.0959438	5.02E-226	0.9992886	4.44E-223
LOC105667073	reciprocal	NONREPR	0.99941513	0.22850109	32.5755213	9.11E-233	0.9992886	8.55E-230
LOC105667073	initial	REPR	0.99917824	0.23034084	30.8379486	8.13E-209	0.9992886	6.42E-206
LOC105667073	reciprocal	REPR	0.99947303	0.21507899	35.0933375	8.52E-270	0.9992886	1.11E-266
LOC105667075	initial	NONREPR	0.90856147	0.43489311	5.27990793	1.29E-07	0.86667382	1.57E-06
LOC105667075	reciprocal	NONREPR	0.7938872	0.35358037	3.81389316	0.00013679	0.86667382	0.00093441
LOC105667075	initial	REPR	0.92897888	0.46813751	5.49220817	3.97E-08	0.86667382	5.19E-07
LOC105667075	reciprocal	REPR	0.83526775	0.39996786	4.0589033	4.93E-05	0.86667382	0.00037245
LOC105667080	initial	NONREPR	0.78309655	0.19112323	6.71715139	1.85E-11	0.78578731	3.72E-10
LOC105667080	reciprocal	NONREPR	0.75349236	0.19005624	5.87892235	4.13E-09	0.78578731	6.18E-08
LOC105667080	initial	REPR	0.81641772	0.14736779	10.1261146	4.23E-24	0.78578731	2.05E-22
LOC105667080	reciprocal	REPR	0.79014263	0.16708306	7.93488778	2.11E-15	0.78578731	5.90E-14
LOC105667082	initial	NONREPR	0.96605158	0.14961399	22.3800924	6.15E-111	0.97963085	2.08E-108
LOC105667082	reciprocal	NONREPR	0.99039377	0.16076603	28.8350124	7.81E-183	0.97963085	5.33E-180

LOC105667082	initial	REPR	0.97042088	0.16183981	21.5686185	3.54E-103	0.97963085	1.12E-100
LOC105667082	reciprocal	REPR	0.99165718	0.14811901	32.2576857	2.74E-228	0.97963085	2.50E-225
LOC105667086	initial	NONREPR	0.88248996	0.4277908	4.71310653	2.44E-06	0.78344121	2.39E-05
LOC105667086	reciprocal	NONREPR	0.69453858	0.28869516	2.84529968	0.00443697	0.78344121	0.01917852
LOC105667086	initial	REPR	0.87577338	0.43788256	4.46009975	8.19E-06	0.78344121	7.22E-05
LOC105667086	reciprocal	REPR	0.68096292	0.31788009	2.38517775	0.01707087	0.78344121	0.05818769
LOC105667161	initial	NONREPR	0.17658143	0.23726377	-6.4893286	8.62E-11	0.25102504	1.60E-09
LOC105667161	reciprocal	NONREPR	0.30039772	0.24489838	-3.4520631	0.00055632	0.25102504	0.00323054
LOC105667161	initial	REPR	0.19729843	0.21251859	-6.603025	4.03E-11	0.25102504	7.74E-10
LOC105667161	reciprocal	REPR	0.32982257	0.22467036	-3.1556796	0.00160125	0.25102504	0.00804454
LOC105667164	initial	NONREPR	0.19560007	0.24568842	-5.7553566	8.65E-09	0.24848172	1.24E-07
LOC105667164	reciprocal	NONREPR	0.2984445	0.2772553	-3.0827762	0.00205079	0.24848172	0.00993726
LOC105667164	initial	REPR	0.19810712	0.2249867	-6.2144434	5.15E-10	0.24848172	8.66E-09
LOC105667164	reciprocal	REPR	0.30177521	0.25989232	-3.2277163	0.00124783	0.24848172	0.00649614
LOC105667165	initial	NONREPR	0.17516422	0.24404533	-6.349068	2.17E-10	0.26351197	3.83E-09
LOC105667165	reciprocal	NONREPR	0.31584841	0.24861102	-3.1089415	0.00187759	0.26351197	0.00922905
LOC105667165	initial	REPR	0.20451262	0.21371237	-6.3558573	2.07E-10	0.26351197	3.67E-09
LOC105667165	reciprocal	REPR	0.35852265	0.21876003	-2.6594531	0.00782676	0.26351197	0.03081044

f

Supplementary 4.0.4: enriched GO terms for the genes showing paternal expression bias in sterile and reproductive workers.

term_ID	description	frequency	log10 p-value
GO:0007049	cell cycle	1.89%	-1.5791
GO:0007610	behavior	0.17%	-1.5224
GO:0043900	regulation of multi-organism process	0.08%	-1.569
GO:0051179	localization	18.50%	-1.46
GO:0035282	segmentation	0.04%	-1.569
GO:0008283	cell proliferation	0.39%	-1.5224
GO:0030198	extracellular matrix organization	0.06%	-1.569
GO:0065008	regulation of biological quality	3.40%	-1.3616
GO:0016043	cellular component organization	7.24%	-1.3185
GO:0051094	positive regulation of developmental process	0.26%	-1.5224
GO:0090596	sensory organ morphogenesis	0.08%	-1.569
GO:0048729	tissue morphogenesis	0.18%	-1.569
GO:0060562	epithelial tube morphogenesis	0.10%	-1.569
GO:0009790	embryo development	0.31%	-1.5658
GO:0007389	pattern specification process	0.15%	-1.5224

Supplementary 4.0.5: enriched GO terms for the genes showing maternal expression bias in sterile and reproductive workers.

term_ID	description	frequency	log10 p-value
GO:0002252	immune effector process	0.19%	-1.3107
GO:0008152	metabolic process	75.39%	-1.6044
GO:0032535	regulation of cellular component size	0.18%	-1.3107
GO:0043170	macromolecule metabolic process	39.49%	-1.4268

Supplementary 4.0.6: enriched GO terms for the genes showing maternal or paternal expression bias in just reproductive or sterile workers.

Maternal bias in queen-right

term_ID	description	frequency	log10 p-value
GO:1901605	alpha-amino acid metabolic process	3.63%	-2.2294
GO:0032269	negative regulation of cellular protein metabolic process	0.42%	-1.4893
GO:0009890	negative regulation of biosynthetic process	0.77%	-1.4893
GO:2000113	negative regulation of cellular macromolecule biosynthetic process	0.72%	-1.4893
GO:0043412	macromolecule modification	9.79%	-1.3481
GO:0070997	neuron death	0.05%	-1.7713
GO:1901565	organonitrogen compound catabolic process	1.20%	-1.9521
GO:1901566	organonitrogen compound biosynthetic process	14.06%	-1.7297
GO:0043523	regulation of neuron apoptotic process	0.03%	-1.7713

Maternal bias in queen-less

term_ID	description	frequency	log10 p-value
GO:0045893	positive regulation of transcription, DNA-templated	0.52%	-1.504
GO:1902680	positive regulation of RNA biosynthetic process	0.52%	-1.504
GO:0009891	positive regulation of biosynthetic process	0.67%	-1.504
GO:0045935	positive regulation of nucleobase-containing compound metabolic process	0.60%	-1.3416
GO:0006796	phosphate-containing compound metabolic process	13.11%	-1.3792

Paternal bias in queen-right

term_ID	description	frequency	log10 p-value
GO:1901989	positive regulation of cell cycle phase transition	0.03%	-1.4433
GO:1902806	regulation of cell cycle G1/S phase transition	0.03%	-1.4433
GO:0045931	positive regulation of mitotic cell cycle	0.05%	-1.4433
GO:1900087	positive regulation of G1/S transition of mitotic cell cycle	0.01%	-1.4433

GO:0006513	protein monoubiquitination	0.02%	-1.4433
GO:0071482	cellular response to light stimulus	0.05%	-1.4433
GO:0070914	UV-damage excision repair	0.01%	-1.4433
GO:0051260	protein homooligomerization	0.11%	-1.4433
GO:0030431	sleep	0.01%	-1.4433
GO:0044248	cellular catabolic process	3.27%	-1.3163
GO:0001776	leukocyte homeostasis	0.02%	-1.4433
GO:0043029	T cell homeostasis	0.01%	-1.4433
GO:0034765	regulation of ion transmembrane transport	0.20%	-1.4433
GO:0055085	transmembrane transport	8.92%	-2.2401
GO:0006829	zinc II ion transport	0.03%	-1.4433
GO:0048706	embryonic skeletal system development	0.04%	-1.4433
GO:0048701	embryonic cranial skeleton morphogenesis	0.02%	-1.4433
GO:0006811	ion transport	5.34%	-1.7123
GO:0035518	histone H2A monoubiquitination	0.00%	-1.4433
GO:0016574	histone ubiquitination	0.02%	-1.4433
GO:0098655	cation transmembrane transport	2.29%	-1.4433
GO:0006813	potassium ion transport	0.48%	-1.4433
GO:0072511	divalent inorganic cation transport	0.39%	-1.4433
GO:0098660	inorganic ion transmembrane transport	2.32%	-1.4433
GO:0071805	potassium ion transmembrane transport	0.33%	-1.4433

Paternal bias in queen-less

term_ID	description	frequency	log10 p-value
GO:0046578	regulation of Ras protein signal transduction	0.19%	-2.5358
GO:0051057	positive regulation of small GTPase mediated signal transduction	0.02%	-1.4433
GO:0035025	positive regulation of Rho protein signal transduction	0.01%	-1.4433
GO:1902531	regulation of intracellular signal transduction	0.55%	-1.7123
GO:0061077	chaperone-mediated protein folding	0.04%	-1.4433

GO:0045214	sarcomere organization	0.01%	-1.4433
GO:0043065	positive regulation of apoptotic process	0.11%	-1.4433
GO:0010942	positive regulation of cell death	0.11%	-1.4433
GO:0043555	regulation of translation in response to stress	0.01%	-1.4433
GO:0017004	cytochrome complex assembly	0.21%	-1.4433
GO:0010998	regulation of translational initiation by eIF2 alpha phosphorylation	0.01%	-1.4433
GO:0042026	protein refolding	0.07%	-1.4433
GO:0033617	mitochondrial respiratory chain complex IV assembly	0.02%	-1.4433

Supplementary 4.0.7: mapping statistics for the RNA-seq data to the reference genome Bter_1.0.

Worker abdomen RNA-Seq mapped to Bter_1.0

Sample	Percentage of Mapped Reads	Total Mapped Reads
02_10	96.25	15248990
02_12	95.94	15825892
02_18	95.98	12731044
02_22	96.37	11322644
02_35	95.7	15745785
02_37	94.17	13728804
02_44	94.53	14652871
02_54	93.77	14240052
12_74	94.12	13497884
12_75	94.25	15747905
12_76	92.73	17133926
12_78	94.3	14557279
12_82	95.78	13998756
12_84	96.39	13757954
12_85	96.3	15501058
12_89	96.12	14961143
22_09	95.84	14746929
22_18	96	16466939
22_21	96.19	14602482
22_23	96.1	12667013
22_26	94.9	17636443
22_30	88.59	12021407
22_35	94.36	14253435

Worker head RNA-Seq mapped to Bter_1.0

Sample	Percentage of Mapped Reads	Total Mapped Reads
02_10	96.14	12715254
02_12	95.6	19164538
02_18	95.91	14235736
02_22	95.57	16136851
02_35	94.87	15784209
02_37	95.43	16929883
02_44	95.77	5774261
02_54	95.83	18990700
12_74	95.23	13758465
12_75	95.32	15636003
12_76	94.6	14691549
12_78	95.58	20013033
12_82	95.51	12648266
12_84	95.33	10481147
12_85	95.55	12107468
12_89	95.21	11387855
22_09	94.83	17440164
22_18	95.12	12492241
22_21	95.22	13584077
22_23	94.9	14261881
22_26	95.07	10873106
22_30	95.15	13106285
22_35	94.92	14722114

22_49	93.48	14244995	22_49	95.59	15869453
31_44	93.57	14902553	31_44	95.28	12354811
31_45	90.67	15077609	31_45	94.76	12500629
31_64	94.37	14871075	31_64	95.34	11779705
31_65	94.2	15573403	31_65	95.43	13018511
31_79	96.49	15857881	31_79	95.27	14810663
31_84	96.32	15781789	31_84	95.14	18006352
31_86	96.4	15085045	31_86	94.89	13698009
31_89	95.99	14022381	31_89	94.95	15321409

Supplementary 4.0.8: list of differentially expressed genes identified in whole abdomen tissue between reprodutive and sterile Bombus terrestris workers.

GeneID	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
LOC100650745	2731.60069	-8.597000836	0.68047937	-12.633742	1.38E-36	1.44E-35
LOC100650031	43.8741597	-7.358545751	1.4871037	-4.9482398	7.49E-07	1.29E-06
LOC100644839	4852.02834	-6.520201994	0.97302872	-6.7009348	2.07E-11	4.72E-11
LOC100643608	13741.1111	-5.704441211	0.84902457	-6.7188176	1.83E-11	4.19E-11
LOC105666966	21.1241478	-4.85999129	0.59378366	-8.1847845	2.73E-16	8.33E-16
LOC100649508	19.0820291	-4.808201064	0.83644269	-5.7483927	9.01E-09	1.75E-08
LOC100651509	1033.89623	-4.473130595	0.52475665	-8.5241999	1.54E-17	5.07E-17
LOC100648148	59.7046512	-4.338943289	0.53194706	-8.1567201	3.44E-16	1.05E-15
LOC100647803	44.9796833	-4.236088053	0.75771306	-5.590623	2.26E-08	4.29E-08
LOC100650111	317918.907	-4.210891918	0.42926848	-9.8094597	1.03E-22	4.49E-22
LOC100646729	157.670595	-4.210790062	1.11476728	-3.7772817	0.00015855	0.00023312
LOC100643115	186.310441	-4.105683943	0.83153446	-4.937479	7.91E-07	1.36E-06
LOC100652150	16916.5329	-4.089124111	0.26075899	-15.681623	2.02E-55	8.21E-54
LOC100643108	4517.40583	-4.034660832	0.32631533	-12.364301	4.08E-35	3.87E-34
LOC100645349	3171.71407	-3.958502232	0.27805738	-14.236278	5.46E-46	1.09E-44
LOC100646290	12.9496065	-3.951594136	0.62184154	-6.3546642	2.09E-10	4.46E-10
LOC100647875	10.4379083	-3.78741048	0.56823345	-6.6652368	2.64E-11	5.98E-11
LOC100650263	28.4343925	-3.761158001	0.42119108	-8.929814	4.27E-19	1.55E-18
LOC100649988	5405.36953	-3.732510573	0.28165094	-13.252257	4.38E-40	5.81E-39
LOC105667172	30.9086272	-3.645881467	0.57496741	-6.3410228	2.28E-10	4.87E-10
LOC100651567	159.064174	-3.64248597	0.42591381	-8.5521668	1.21E-17	4.01E-17
LOC100643435	58.422207	-3.608172422	0.7552559	-4.7774171	1.78E-06	2.98E-06
LOC100651730	44.018308	-3.566588942	1.07679006	-3.3122417	0.00092552	0.00128153
LOC100647779	36.076497	-3.534950256	0.45548236	-7.7608939	8.43E-15	2.36E-14
LOC105667190	21.4063222	-3.527136247	1.06528044	-3.3109932	0.00092965	0.0012869
LOC100646362	13.7045343	-3.475607688	0.54898312	-6.3309919	2.44E-10	5.19E-10

LOC100646754	23.0789964	-3.444241394	0.65348586	-5.2705676	1.36E-07	2.45E-07
LOC100649281	56.9167242	-3.410287543	0.93974703	-3.6289421	0.00028459	0.00041027
LOC100647588	2244.09699	-3.355422759	0.2530043	-13.262315	3.83E-40	5.11E-39
LOC100652157	358.516321	-3.34433995	1.18616487	-2.8194563	0.00481051	0.00627661
LOC105666341	15.1448051	-3.334327777	0.56827343	-5.8674709	4.42E-09	8.79E-09
LOC100646820	15.6810905	-3.291459137	0.55713254	-5.9078565	3.47E-09	6.93E-09
LOC100648242	194.9795	-3.287916832	0.59722227	-5.5053487	3.68E-08	6.88E-08
LOC100647448	1059.71947	-3.281495699	1.16954306	-2.805793	0.00501929	0.00654467
LOC100643622	620.820524	-3.276564944	0.31973729	-10.247678	1.21E-24	5.97E-24
LOC100649153	80.3635828	-3.250179276	0.57777665	-5.6253212	1.85E-08	3.53E-08
LOC100643580	1174.63554	-3.223687785	0.3778149	-8.5324529	1.43E-17	4.73E-17
LOC100651053	33.14691	-3.195028349	0.5739324	-5.5669071	2.59E-08	4.89E-08
LOC105665974	84.1496649	-3.177814326	0.42177751	-7.5343381	4.91E-14	1.32E-13
LOC100631088	196.776548	-3.166497726	0.45883014	-6.9012417	5.15E-12	1.23E-11
LOC100645792	17.4392875	-3.141851475	0.50309805	-6.2450083	4.24E-10	8.90E-10
LOC100648933	76.2886598	-3.120997905	0.86898237	-3.5915549	0.00032871	0.00047225
LOC100648029	3379.69751	-3.091551406	0.22908722	-13.495085	1.67E-41	2.48E-40
LOC100647566	16744.0248	-3.086801934	0.18998583	-16.247538	2.33E-59	1.29E-57
LOC100648823	65.4741933	-3.050768391	0.69789501	-4.3713859	1.23E-05	1.96E-05
LOC100642816	742.899405	-3.046294299	0.33335715	-9.13823	6.35E-20	2.41E-19
LOC100646558	12.9828964	-3.038121559	0.53271277	-5.7031138	1.18E-08	2.27E-08
LOC105666609	161.383485	-3.035919399	0.55284987	-5.4913993	3.99E-08	7.43E-08
LOC100643210	52.1930225	-3.001818171	0.27034155	-11.103799	1.20E-28	7.61E-28
LOC105666488	12.9179547	-2.968029788	0.49734058	-5.9678013	2.40E-09	4.85E-09
LOC100650508	11.553721	-2.967517228	0.55596107	-5.337635	9.42E-08	1.71E-07
LOC100648955	351.194314	-2.962091661	0.63721345	-4.6485078	3.34E-06	5.51E-06
LOC100646781	125.052179	-2.960107447	0.66540109	-4.4486063	8.64E-06	1.39E-05
LOC105666793	305.135994	-2.934054721	0.62367634	-4.7044509	2.55E-06	4.22E-06
LOC105666404	129.626928	-2.914418043	0.31337202	-9.300186	1.40E-20	5.53E-20

LOC105665682	18.5391494	-2.91052561	0.42844213	-6.7932759	1.10E-11	2.55E-11
LOC105665733	63.0148057	-2.887844999	0.38469104	-7.5069204	6.05E-14	1.62E-13
LOC100649305	14.9878262	-2.887821755	0.36276686	-7.9605446	1.71E-15	5.00E-15
LOC105665721	93.4924581	-2.886010477	0.46497231	-6.2068437	5.41E-10	1.13E-09
LOC105666827	11.4033114	-2.884541241	0.48677942	-5.9257667	3.11E-09	6.23E-09
LOC100642936	17587.3151	-2.881602073	0.19440908	-14.822364	1.05E-49	2.84E-48
LOC100645985	723.377218	-2.871108771	0.57044301	-5.0331211	4.83E-07	8.43E-07
LOC100643289	17.4655932	-2.870906861	0.73810652	-3.8895563	0.00010043	0.00014985
LOC100649230	14.8671368	-2.868021721	0.57676058	-4.9726383	6.60E-07	1.14E-06
LOC100647759	9742.48384	-2.865623462	0.34795479	-8.2356202	1.79E-16	5.54E-16
LOC100643109	26.8653368	-2.861300857	0.43554002	-6.5695475	5.05E-11	1.12E-10
LOC100649319	31.8996329	-2.842857301	0.33568812	-8.4687457	2.48E-17	8.06E-17
LOC105665932	12.8554749	-2.83493905	0.53134761	-5.3353755	9.53E-08	1.73E-07
LOC105666762	149.722652	-2.831637055	0.36309961	-7.798513	6.26E-15	1.77E-14
LOC100650690	1042.71903	-2.825616083	0.20300502	-13.918947	4.86E-44	8.48E-43
LOC100650209	26.8298121	-2.817013144	0.32704217	-8.6136084	7.08E-18	2.38E-17
LOC100643254	310.804888	-2.808402141	0.24613922	-11.409812	3.74E-30	2.61E-29
LOC100646193	241.599959	-2.806954703	0.31443828	-8.926886	4.38E-19	1.59E-18
LOC100649178	266.013196	-2.806566443	0.28151348	-9.9695632	2.07E-23	9.44E-23
LOC100647964	168.862216	-2.801585281	0.38288868	-7.3169707	2.54E-13	6.51E-13
LOC100651531	240.129514	-2.798658993	0.35701812	-7.838983	4.54E-15	1.29E-14
LOC100646587	36.7846017	-2.786000201	0.38059958	-7.3200296	2.48E-13	6.37E-13
LOC100650317	72.454683	-2.780385617	0.47457584	-5.8586751	4.67E-09	9.26E-09
LOC100643968	808.133086	-2.779467095	0.48841675	-5.6907694	1.26E-08	2.43E-08
LOC100648580	4369.15054	-2.761574185	0.37397891	-7.3843047	1.53E-13	3.99E-13
LOC100645101	1621.23224	-2.761353401	0.17624806	-15.667426	2.53E-55	1.01E-53
LOC100646078	8390.85371	-2.752151946	0.25944626	-10.607792	2.74E-26	1.50E-25
LOC100645026	20.9612099	-2.751836396	0.44371167	-6.2018571	5.58E-10	1.16E-09
LOC100651973	3406.97289	-2.749454642	0.20333345	-13.5219	1.16E-41	1.74E-40

LOC100646373	18666.8061	-2.746468612	0.23032617	-11.924258	8.85E-33	7.12E-32
LOC100642746	3162.06896	-2.713002978	0.35334904	-7.677969	1.62E-14	4.46E-14
LOC100649414	42.9973473	-2.710924956	0.4768202	-5.6854238	1.30E-08	2.51E-08
LOC100651987	672.631987	-2.710556732	0.35027364	-7.7383977	1.01E-14	2.81E-14
LOC100651262	59.5329658	-2.702897553	0.36164952	-7.4738039	7.79E-14	2.07E-13
LOC105666859	12.9450719	-2.70278209	0.44308558	-6.0999098	1.06E-09	2.18E-09
LOC100651059	644.027621	-2.702322417	0.24606871	-10.981983	4.67E-28	2.86E-27
LOC105665943	121.681157	-2.700976918	0.39990249	-6.7540888	1.44E-11	3.32E-11
LOC100645124	13.6277535	-2.699275723	0.68275348	-3.9535144	7.70E-05	0.00011609
LOC100649580	162.092088	-2.696162646	0.42957687	-6.2763217	3.47E-10	7.32E-10
LOC100649304	875.875576	-2.690833395	0.19866223	-13.544766	8.51E-42	1.29E-40
LOC100644242	30.7519297	-2.681148467	0.40855	-6.5625957	5.29E-11	1.17E-10
LOC100651029	787.945255	-2.674348464	0.2684891	-9.960734	2.26E-23	1.03E-22
LOC100647922	40.0547058	-2.66977967	0.34128218	-7.8227924	5.17E-15	1.46E-14
LOC105666505	15.1917428	-2.667798033	0.45637144	-5.8456727	5.05E-09	9.99E-09
LOC100645755	275.286455	-2.643470399	0.22698601	-11.645962	2.41E-31	1.79E-30
LOC100644732	1493.66557	-2.641379554	0.15063334	-17.535159	7.72E-69	9.45E-67
LOC100648867	29.6085608	-2.639439551	0.38534725	-6.8495092	7.41E-12	1.74E-11
LOC100647549	3605.69403	-2.638405526	0.19591873	-13.466836	2.45E-41	3.57E-40
LOC100648154	160.092284	-2.635467563	0.38935916	-6.7687314	1.30E-11	3.01E-11
LOC100642478	175.265479	-2.632501616	0.21979088	-11.977301	4.67E-33	3.84E-32
LOC100646941	35.2434742	-2.632215541	0.41019455	-6.416993	1.39E-10	2.99E-10
LOC100646043	46.3596367	-2.632214806	0.69481733	-3.7883551	0.00015165	0.00022324
LOC100649338	12675.3211	-2.630736281	0.2275597	-11.560642	6.52E-31	4.75E-30
LOC100646687	56810.511	-2.62674543	0.39170061	-6.706003	2.00E-11	4.57E-11
LOC100647220	448.977897	-2.620531267	0.25448519	-10.297382	7.24E-25	3.62E-24
LOC100651187	162.080753	-2.61810126	0.35432452	-7.3889927	1.48E-13	3.85E-13
LOC100649025	11.0958496	-2.603911942	0.47273471	-5.5081886	3.63E-08	6.77E-08
LOC105666352	34.3115976	-2.601467978	0.47192882	-5.5124159	3.54E-08	6.62E-08

LOC100650530	3129.19809	-2.599051728	0.74785058	-3.4753623	0.00051016	0.00072182
LOC100643869	2084.23002	-2.59702899	0.24960249	-10.40466	2.36E-25	1.22E-24
LOC105666066	99.1300956	-2.595129774	0.33841884	-7.6683962	1.74E-14	4.79E-14
LOC100651601	30.5451262	-2.593298189	0.44765092	-5.793126	6.91E-09	1.36E-08
LOC105666376	39.3161139	-2.592809497	0.41929726	-6.1837024	6.26E-10	1.30E-09
LOC105666246	73.3649764	-2.590252917	0.40899636	-6.3331931	2.40E-10	5.12E-10
LOC105665933	17.7947084	-2.589352535	0.46403705	-5.5800556	2.40E-08	4.55E-08
LOC100650566	3632.38269	-2.589226143	0.19348667	-13.381935	7.71E-41	1.09E-39
LOC100643485	174.104029	-2.586723035	0.27593962	-9.3742357	6.97E-21	2.79E-20
LOC105666035	54.0169871	-2.585982019	0.2662537	-9.7124734	2.67E-22	1.14E-21
LOC105666375	19.0083174	-2.578543387	0.4176277	-6.1742633	6.65E-10	1.38E-09
LOC100647945	2240.31916	-2.571074761	0.27217416	-9.4464323	3.51E-21	1.43E-20
LOC105666095	20.844861	-2.567541979	0.38988199	-6.5854337	4.54E-11	1.01E-10
LOC100644713	20757.1288	-2.566549061	0.36944404	-6.9470577	3.73E-12	8.94E-12
LOC100646799	104.837425	-2.553059787	0.61368489	-4.1602129	3.18E-05	4.92E-05
LOC100643714	679.926318	-2.547897528	0.3409892	-7.472077	7.89E-14	2.09E-13
LOC100644832	3488.74995	-2.545734751	0.1806704	-14.090491	4.35E-45	8.18E-44
LOC100644221	72.1087792	-2.543659227	0.42498359	-5.9853117	2.16E-09	4.37E-09
LOC100647285	3695.44909	-2.542618728	0.32892661	-7.7300488	1.08E-14	2.99E-14
LOC100649001	269.955976	-2.540257996	0.23069072	-11.011531	3.36E-28	2.08E-27
LOC100647031	2277.35746	-2.537585261	0.25481783	-9.958429	2.32E-23	1.05E-22
LOC105666378	18.2462101	-2.531448624	0.49452113	-5.1189899	3.07E-07	5.43E-07
LOC100642965	34.2987514	-2.528766635	0.38462895	-6.5745613	4.88E-11	1.09E-10
LOC100645841	1595.55965	-2.523655608	0.46347718	-5.4450482	5.18E-08	9.59E-08
LOC100649394	11.9925897	-2.522906169	0.41621914	-6.0614852	1.35E-09	2.76E-09
LOC100642704	724.585737	-2.513064929	0.23204946	-10.829868	2.49E-27	1.46E-26
LOC100651733	561.434764	-2.508703948	0.3214794	-7.8036228	6.02E-15	1.70E-14
LOC100649937	1877.17037	-2.508575554	0.46085424	-5.4433166	5.23E-08	9.68E-08
LOC105666655	228.645058	-2.506706855	0.90350301	-2.7744311	0.00552983	0.00719216

LOC100648133	1397.92806	-2.503116516	0.4804479	-5.2099645	1.89E-07	3.38E-07
LOC100651289	484.699035	-2.501274336	0.23515227	-10.636828	2.01E-26	1.11E-25
LOC100648294	1127.96094	-2.501230156	0.24241347	-10.318033	5.84E-25	2.94E-24
LOC100643050	11.122024	-2.495773522	0.49282173	-5.0642522	4.10E-07	7.19E-07
LOC100647625	289.645323	-2.486289059	0.35044571	-7.0946482	1.30E-12	3.19E-12
LOC100646106	6733.73703	-2.486238805	0.37571147	-6.6174152	3.66E-11	8.20E-11
LOC100650611	20.7004212	-2.485322091	0.46642611	-5.3284369	9.91E-08	1.80E-07
LOC100649566	14.8893992	-2.483241314	0.47021288	-5.2811002	1.28E-07	2.32E-07
LOC100644459	198.724648	-2.481850116	0.46825223	-5.300242	1.16E-07	2.09E-07
LOC105666518	16.4026747	-2.469947825	0.79621673	-3.1021049	0.0019215	0.00259925
LOC105666459	22.6889461	-2.469465467	0.39395276	-6.2684304	3.65E-10	7.69E-10
LOC100643480	105.81931	-2.464240584	0.34539407	-7.1345769	9.71E-13	2.41E-12
LOC100649919	179.999406	-2.464024177	0.62886101	-3.9182333	8.92E-05	0.00013368
LOC100646780	36.2816391	-2.462351841	0.8116776	-3.0336575	0.00241609	0.00324498
LOC105665851	989.40096	-2.461341534	0.50303836	-4.8929499	9.93E-07	1.70E-06
LOC100651231	18.8349764	-2.459800535	0.7025937	-3.5010284	0.00046347	0.00065842
LOC100652047	78.2937116	-2.458391603	0.34397523	-7.1470019	8.87E-13	2.21E-12
LOC100652258	3755.33167	-2.457154445	0.20671989	-11.886396	1.39E-32	1.11E-31
LOC100646798	161.621193	-2.451857282	0.27543393	-8.9017982	5.49E-19	1.98E-18
LOC100647539	4015.95525	-2.451565319	0.21386778	-11.462995	2.02E-30	1.43E-29
LOC100642930	957.144046	-2.451373126	0.23688668	-10.348295	4.26E-25	2.16E-24
LOC100647883	8468.64171	-2.446577128	0.23971611	-10.206144	1.86E-24	9.04E-24
LOC100646248	956.6494	-2.443535907	0.36306761	-6.7302503	1.69E-11	3.89E-11
LOC100647051	1915.95685	-2.440070315	0.31638763	-7.7122811	1.24E-14	3.43E-14
LOC100648557	527.352096	-2.433581319	0.3670033	-6.6309521	3.34E-11	7.49E-11
LOC100648767	145.660076	-2.432928391	0.33769583	-7.2044964	5.83E-13	1.47E-12
LOC100644658	59.2835564	-2.43283234	0.28524099	-8.5290419	1.48E-17	4.87E-17
LOC100646964	201.783363	-2.431077733	0.20870765	-11.648245	2.34E-31	1.75E-30
LOC100649157	705.975797	-2.428985254	0.23684712	-10.255498	1.12E-24	5.52E-24

LOC105667032	21.3533705	-2.428303994	0.79120622	-3.0691164	0.00214693	0.00289301
LOC100650702	78.3648212	-2.407950448	0.65019649	-3.7034196	0.00021271	0.00030997
LOC100646127	78.3343712	-2.407033458	0.28928518	-8.320625	8.75E-17	2.76E-16
LOC100645163	6688.96767	-2.404466071	0.22036972	-10.911055	1.02E-27	6.10E-27
LOC105666138	732.65349	-2.402925637	0.28649734	-8.3872529	4.98E-17	1.59E-16
LOC100646624	1142.01957	-2.401336158	0.44008592	-5.4565166	4.86E-08	8.99E-08
LOC105665681	69.7743384	-2.393908847	0.32447518	-7.3777873	1.61E-13	4.18E-13
LOC105666299	20.9661032	-2.392007935	0.47858211	-4.998114	5.79E-07	1.01E-06
LOC100647696	768.117723	-2.390761098	0.19960558	-11.977426	4.67E-33	3.83E-32
LOC105666263	32.5735927	-2.385726751	0.36182054	-6.5936741	4.29E-11	9.58E-11
LOC100645024	2381.25978	-2.383213477	0.21993279	-10.836099	2.32E-27	1.36E-26
LOC100649258	465.422179	-2.383030888	0.24298028	-9.8075074	1.05E-22	4.57E-22
LOC105666627	246.57965	-2.381845123	0.29251164	-8.1427362	3.86E-16	1.17E-15
LOC100645312	10.2503886	-2.376645333	0.61453646	-3.8673789	0.00011001	0.00016375
LOC100646002	405.632932	-2.376088187	0.18318893	-12.970698	1.79E-38	2.12E-37
LOC105665975	24.9489487	-2.375684356	0.40536716	-5.8605743	4.61E-09	9.16E-09
LOC100651870	1932.39993	-2.373322509	0.17397511	-13.641736	2.26E-42	3.53E-41
LOC100642295	436.543249	-2.371744329	0.5097415	-4.6528374	3.27E-06	5.40E-06
LOC100647854	503.100151	-2.369695398	0.28106067	-8.4312592	3.42E-17	1.10E-16
LOC100646439	69.7593721	-2.365426811	0.19450377	-12.161342	4.99E-34	4.40E-33
LOC100644904	851.75068	-2.357808775	0.24225153	-9.7328953	2.18E-22	9.39E-22
LOC100647148	14434.1809	-2.356149267	0.26211874	-8.9888623	2.50E-19	9.20E-19
LOC100651538	66.5384169	-2.356028581	0.29319822	-8.0356169	9.31E-16	2.76E-15
LOC100644867	15366.1123	-2.353532014	0.26912769	-8.7450386	2.23E-18	7.72E-18
LOC100643731	35279.6595	-2.3503804	0.22807469	-10.30531	6.67E-25	3.34E-24
LOC105665996	88.693987	-2.349976165	0.28184098	-8.3379506	7.56E-17	2.40E-16
LOC100649167	93.6869328	-2.345177331	0.32699922	-7.1718133	7.40E-13	1.85E-12
LOC100649660	1249.71618	-2.340758686	0.23682795	-9.8837939	4.89E-23	2.17E-22
LOC100644270	129.563986	-2.339747329	0.32183716	-7.2699727	3.60E-13	9.18E-13

LOC105666830	2512.38626	-2.339036853	0.40057684	-5.8391715	5.25E-09	1.04E-08
LOC100650618	435.265418	-2.338072851	0.25219796	-9.2707843	1.85E-20	7.22E-20
LOC100649785	3025.85737	-2.338039328	0.23887426	-9.7877406	1.27E-22	5.53E-22
LOC100649934	480.282568	-2.335466504	0.19528893	-11.959031	5.82E-33	4.74E-32
LOC100649255	615.073399	-2.331864272	0.29883353	-7.8032215	6.03E-15	1.70E-14
LOC100645777	71.4729366	-2.330357787	0.38464029	-6.058538	1.37E-09	2.81E-09
LOC105666492	9831.596	-2.32557583	0.19511753	-11.918846	9.44E-33	7.58E-32
LOC100646875	1211.20839	-2.322822175	0.48771436	-4.7626692	1.91E-06	3.20E-06
LOC105666574	11.0125869	-2.319483781	0.5785469	-4.0091543	6.09E-05	9.26E-05
LOC100648212	1392.37923	-2.318221586	0.24989653	-9.2767257	1.75E-20	6.84E-20
LOC100649149	617.068345	-2.315467767	0.18661768	-12.407547	2.38E-35	2.30E-34
LOC100645469	49.2933524	-2.3140895	0.40662784	-5.6909273	1.26E-08	2.43E-08
LOC100645619	287.513831	-2.312898035	0.29437165	-7.8570678	3.93E-15	1.12E-14
LOC100650488	37.0387206	-2.311016593	0.63658225	-3.6303504	0.00028304	0.00040819
LOC100643678	341.946398	-2.310711902	0.37785779	-6.1152951	9.64E-10	1.99E-09
LOC105665947	133.530841	-2.310626407	0.34945574	-6.6120718	3.79E-11	8.49E-11
LOC100652247	802.2598	-2.310449395	0.25949319	-8.9036994	5.40E-19	1.95E-18
LOC100649251	751.47078	-2.306937163	0.22928641	-10.061378	8.18E-24	3.82E-23
LOC100650330	396.108738	-2.306624927	0.25949229	-8.888992	6.17E-19	2.21E-18
LOC100647344	472.457334	-2.306069105	0.20757436	-11.109605	1.13E-28	7.18E-28
LOC100647447	2213.48198	-2.303607133	0.23226426	-9.918044	3.47E-23	1.56E-22
LOC100642554	19.1307549	-2.303519661	0.4669743	-4.9328617	8.10E-07	1.39E-06
LOC100649467	20.7762557	-2.302508544	0.3671981	-6.2704805	3.60E-10	7.60E-10
LOC100643830	600.053431	-2.300212876	0.2604019	-8.8333182	1.02E-18	3.59E-18
LOC105666838	511.060785	-2.29933127	0.83136901	-2.7657168	0.00567978	0.0073725
LOC100643278	117.830101	-2.298646489	0.32740015	-7.0209084	2.20E-12	5.35E-12
LOC100644137	140.546078	-2.297823367	0.3131921	-7.3367858	2.19E-13	5.64E-13
LOC100647872	1102.42343	-2.297819832	0.22935951	-10.01842	1.27E-23	5.84E-23
LOC100651683	142766.315	-2.297095322	0.27057729	-8.4896088	2.07E-17	6.77E-17

LOC100647290	281.100084	-2.296172868	0.18910307	-12.142441	6.29E-34	5.50E-33
LOC105666367	368.700642	-2.296118339	0.36358127	-6.3152822	2.70E-10	5.73E-10
LOC105666318	141.524226	-2.290714756	0.53972884	-4.2441956	2.19E-05	3.43E-05
LOC100648426	3538.95929	-2.287814887	0.19459854	-11.756588	6.53E-32	5.00E-31
LOC100644150	159.635735	-2.287519525	0.26074424	-8.7730396	1.74E-18	6.06E-18
LOC105667104	2491.66774	-2.285645421	0.22209963	-10.291082	7.73E-25	3.87E-24
LOC100648572	274.95153	-2.285023188	0.21371462	-10.691936	1.11E-26	6.22E-26
LOC100648391	20734.166	-2.284053974	0.20325909	-11.237156	2.68E-29	1.76E-28
LOC100650906	389.74043	-2.280146138	0.19599425	-11.63374	2.78E-31	2.07E-30
LOC100648126	6602.36879	-2.277901495	0.22178476	-10.270775	9.54E-25	4.74E-24
LOC100651728	870.589505	-2.277498075	0.19112177	-11.916476	9.71E-33	7.79E-32
LOC105665691	54.058275	-2.276949593	0.33470366	-6.8028822	1.03E-11	2.39E-11
LOC100644880	3550.968	-2.275971761	0.20747664	-10.969774	5.34E-28	3.26E-27
LOC100652129	40.8501278	-2.275453042	0.34345412	-6.6252024	3.47E-11	7.78E-11
LOC105666925	18.8004661	-2.275059865	0.42764033	-5.3200311	1.04E-07	1.88E-07
LOC105666572	116.626443	-2.264534081	0.2726027	-8.3070861	9.81E-17	3.09E-16
LOC100650437	5092.82127	-2.262972551	0.39121361	-5.7844934	7.27E-09	1.43E-08
LOC100643981	2850.73386	-2.259186834	0.15500932	-14.574522	4.08E-48	9.89E-47
LOC100644470	5910.3939	-2.25897478	0.45573341	-4.9567899	7.17E-07	1.24E-06
LOC100650874	4350.63546	-2.258060873	0.17208364	-13.12188	2.47E-39	3.09E-38
LOC100649665	562.357194	-2.257312976	0.20940059	-10.779879	4.28E-27	2.47E-26
LOC100644112	80.3623929	-2.257239035	0.22026075	-10.248031	1.21E-24	5.95E-24
LOC100645995	250.979214	-2.256110964	0.27453248	-8.218011	2.07E-16	6.39E-16
LOC105666445	191.612837	-2.255469899	0.36458404	-6.1864197	6.15E-10	1.28E-09
LOC100643481	2057.19546	-2.254735163	0.27186252	-8.2936596	1.10E-16	3.44E-16
LOC100642324	14.3276409	-2.25468136	0.69886582	-3.2262006	0.00125445	0.00171853
LOC100651196	3030.31968	-2.252353737	0.21428295	-10.51112	7.68E-26	4.08E-25
LOC100644232	13.3647573	-2.25206616	0.60139462	-3.7447394	0.00018058	0.00026472
LOC100650909	48.6270763	-2.252036948	0.29469739	-7.6418626	2.14E-14	5.86E-14

LOC100651840	10.9147567	-2.250998589	0.41206038	-5.4627882	4.69E-08	8.69E-08
LOC100651722	361.820048	-2.246309953	0.15769267	-14.24486	4.83E-46	9.78E-45
LOC100650561	1808.35762	-2.245730172	0.18235529	-12.315136	7.51E-35	7.01E-34
LOC100643092	511.902661	-2.24392513	0.22950868	-9.7770819	1.41E-22	6.13E-22
LOC100647785	11984.7479	-2.243748495	0.14817566	-15.142491	8.49E-52	2.68E-50
LOC100648838	245.933071	-2.243213936	0.348659	-6.4338335	1.24E-10	2.69E-10
LOC100652152	2682.78451	-2.242123855	0.34784828	-6.4456948	1.15E-10	2.49E-10
LOC100650509	339.894343	-2.238774886	0.48797846	-4.587856	4.48E-06	7.30E-06
LOC100649744	18757.5902	-2.236211676	0.29352117	-7.6185704	2.57E-14	6.99E-14
LOC100643066	277.804549	-2.23561875	0.21353293	-10.469667	1.19E-25	6.25E-25
LOC105666552	69.5139432	-2.233302156	0.35069103	-6.36829	1.91E-10	4.09E-10
LOC100650933	2041.67225	-2.231442998	0.28572224	-7.8098331	5.73E-15	1.62E-14
LOC100651905	615.963905	-2.230953953	0.29991044	-7.4387338	1.02E-13	2.68E-13
LOC100648711	24.4252409	-2.223538699	0.45106894	-4.9294875	8.24E-07	1.42E-06
LOC100646811	231.628223	-2.22338125	0.46476906	-4.7838409	1.72E-06	2.89E-06
LOC100647618	299.264656	-2.222391554	0.21779064	-10.204257	1.90E-24	9.22E-24
LOC100647198	771.07392	-2.221149345	0.27009501	-8.2235854	1.98E-16	6.11E-16
LOC100648450	885.573786	-2.219958591	0.27354913	-8.1153927	4.84E-16	1.46E-15
LOC105666501	40.8599926	-2.218400576	0.41457872	-5.3509755	8.75E-08	1.60E-07
LOC100642921	1669.72552	-2.217282288	0.22348295	-9.9214831	3.36E-23	1.51E-22
LOC105665864	53.6598015	-2.215619739	0.38282695	-5.787523	7.14E-09	1.40E-08
LOC100650704	1025.2929	-2.214650833	0.17774077	-12.460005	1.23E-35	1.21E-34
LOC100646175	402.667032	-2.213321563	0.20600872	-10.743825	6.34E-27	3.62E-26
LOC100644339	582.126637	-2.21304868	0.40113936	-5.5169073	3.45E-08	6.46E-08
LOC100652226	1629.72551	-2.208724377	0.17824363	-12.391603	2.90E-35	2.78E-34
LOC100650380	14.6411265	-2.208705005	0.63761928	-3.4639872	0.00053223	0.00075131
LOC100651071	178.576942	-2.207924351	0.38766228	-5.6954841	1.23E-08	2.37E-08
LOC100648239	296.15189	-2.207566428	0.29542176	-7.4725924	7.86E-14	2.09E-13
LOC100646302	27.4275466	-2.204535593	0.42859315	-5.1436557	2.69E-07	4.78E-07

LOC100649912	2235.0572	-2.204342952	0.26360581	-8.3622698	6.15E-17	1.96E-16
LOC100643181	2745.61385	-2.204252393	0.15549757	-14.175478	1.30E-45	2.56E-44
LOC100647833	80.479669	-2.202702458	0.24730593	-8.9067919	5.25E-19	1.90E-18
LOC100645396	10231.9031	-2.201882637	0.1810689	-12.160468	5.05E-34	4.44E-33
LOC100651518	230.654227	-2.200975631	0.18262236	-12.05206	1.89E-33	1.59E-32
LOC100648558	138.680669	-2.200912122	0.25008857	-8.8005308	1.36E-18	4.77E-18
LOC100650838	2756.58495	-2.200357133	0.2120427	-10.376953	3.16E-25	1.62E-24
LOC100646600	1510.91591	-2.199585549	0.4379392	-5.022582	5.10E-07	8.90E-07
LOC105665720	64.8590304	-2.198115385	0.29894261	-7.3529678	1.94E-13	5.01E-13
LOC100631058	28464.5163	-2.197951391	0.13937613	-15.769927	5.01E-56	2.12E-54
LOC100651631	147.82713	-2.194282294	0.56204271	-3.9041202	9.46E-05	0.00014145
LOC100648676	307.359117	-2.190653918	0.25104143	-8.7262644	2.63E-18	9.05E-18
LOC100652266	22.1938502	-2.190204661	0.36495931	-6.0012297	1.96E-09	3.97E-09
LOC100647965	253.444147	-2.187497989	0.22830875	-9.5813149	9.58E-22	3.99E-21
LOC100647601	6633.45574	-2.18697698	0.28335854	-7.7180556	1.18E-14	3.28E-14
LOC100645174	111.627644	-2.185487652	0.27264313	-8.0159279	1.09E-15	3.23E-15
LOC100643249	1279.98444	-2.185340844	0.2719773	-8.0350119	9.36E-16	2.77E-15
LOC100648599	2109.63663	-2.185003845	0.17433193	-12.533584	4.89E-36	4.88E-35
LOC100645061	26.5421402	-2.180806415	0.46039326	-4.7368339	2.17E-06	3.62E-06
LOC100651479	167.127207	-2.180109771	0.23748757	-9.1798898	4.32E-20	1.66E-19
LOC100649554	278.813922	-2.180002674	0.24056796	-9.0618996	1.28E-19	4.79E-19
LOC100643145	161.047227	-2.176561288	0.27543863	-7.9021643	2.74E-15	7.91E-15
LOC100648325	120.597108	-2.176031741	0.23390253	-9.303156	1.36E-20	5.38E-20
LOC105665671	132.734965	-2.175292475	0.32998367	-6.5921215	4.34E-11	9.67E-11
LOC105666254	16.8424277	-2.17478732	0.30060006	-7.2348199	4.66E-13	1.18E-12
LOC100649629	794.466843	-2.173969216	0.22652107	-9.5972052	8.21E-22	3.44E-21
LOC100645443	898.995348	-2.170853486	0.21391227	-10.148335	3.37E-24	1.61E-23
LOC100643013	125.6155	-2.170643512	0.24746453	-8.7715338	1.76E-18	6.14E-18
LOC100642368	80.8354188	-2.168357671	0.31995949	-6.7769756	1.23E-11	2.84E-11

LOC100644235	58.7353344	-2.164721692	0.30125547	-7.1856676	6.69E-13	1.68E-12
LOC100649515	116.346788	-2.164713502	0.24449907	-8.8536677	8.47E-19	3.01E-18
LOC105665901	39.3372836	-2.163865125	0.73124592	-2.9591483	0.00308491	0.00410608
LOC100642887	99.9862679	-2.16337504	0.24778457	-8.7308706	2.53E-18	8.70E-18
LOC100644575	424.671103	-2.163000918	0.41269966	-5.2411018	1.60E-07	2.87E-07
LOC100649306	237.537799	-2.161380458	0.25495737	-8.4774191	2.30E-17	7.50E-17
LOC100651735	6375.78476	-2.157791237	0.15113169	-14.277557	3.02E-46	6.21E-45
LOC100647822	1521.70623	-2.155124373	0.2060386	-10.459809	1.32E-25	6.91E-25
LOC100650174	272.416379	-2.154582648	0.29422177	-7.3229886	2.43E-13	6.24E-13
LOC100649911	49.4462765	-2.15374259	0.46065322	-4.6754098	2.93E-06	4.85E-06
LOC100646677	1930.50354	-2.153123545	0.19571744	-11.001184	3.77E-28	2.32E-27
LOC100644557	209.717335	-2.151498156	0.27037036	-7.9575964	1.75E-15	5.12E-15
LOC105666343	25110.9932	-2.151134318	0.21701965	-9.9121638	3.69E-23	1.65E-22
LOC100646273	17810.1105	-2.150270972	0.20466932	-10.506074	8.10E-26	4.30E-25
LOC100645676	354.264394	-2.148060081	0.51153872	-4.1992131	2.68E-05	4.17E-05
LOC100642915	18809.2838	-2.147669338	0.33030397	-6.5020997	7.92E-11	1.73E-10
LOC100648333	266.985247	-2.147181304	0.24355004	-8.8161813	1.18E-18	4.17E-18
LOC100649097	114.338648	-2.146946662	0.25722195	-8.3466696	7.02E-17	2.23E-16
LOC100647933	277.416948	-2.144376103	0.27687921	-7.7448072	9.57E-15	2.67E-14
LOC100643791	62.9804607	-2.142704727	0.32627102	-6.5672543	5.13E-11	1.14E-10
LOC100649325	572.285197	-2.142589504	0.2285357	-9.3752947	6.90E-21	2.76E-20
LOC100652024	1847.53695	-2.14147376	0.16316479	-13.124607	2.38E-39	2.98E-38
LOC105666034	180.803983	-2.139591963	0.15871565	-13.480661	2.03E-41	2.98E-40
LOC100643149	24680.4987	-2.137220057	0.36068672	-5.9254193	3.12E-09	6.24E-09
LOC100644661	29.9877193	-2.136944178	0.46249103	-4.6205094	3.83E-06	6.28E-06
LOC100643327	399.307808	-2.136353237	0.245809	-8.6911107	3.59E-18	1.22E-17
LOC100642676	25201.3202	-2.131641465	0.36116329	-5.9021543	3.59E-09	7.17E-09
LOC100643014	167.728956	-2.130922665	0.28885726	-7.3770785	1.62E-13	4.20E-13
LOC100642488	28.0672791	-2.130221613	0.41349528	-5.1517435	2.58E-07	4.58E-07

LOC100646167	728.678482	-2.127705594	0.37252574	-5.7115667	1.12E-08	2.17E-08
LOC100651487	16.8375225	-2.12726512	0.40094163	-5.3056728	1.12E-07	2.03E-07
LOC100649817	176.466795	-2.126316799	0.25962192	-8.190051	2.61E-16	8.00E-16
LOC100645386	5258.33486	-2.125119541	0.13725921	-15.482528	4.55E-54	1.65E-52
LOC105666564	115.32823	-2.117759298	0.17193099	-12.317496	7.29E-35	6.81E-34
LOC100645608	731.88344	-2.117715108	0.21266146	-9.9581517	2.32E-23	1.06E-22
LOC100648860	391.700729	-2.117674558	0.16240773	-13.039248	7.32E-39	8.87E-38
LOC100645408	209.401862	-2.116826085	0.31397309	-6.7420621	1.56E-11	3.59E-11
LOC100642198	72.6470251	-2.116732538	0.32708714	-6.4714637	9.71E-11	2.11E-10
LOC100652276	195.005732	-2.115896738	0.22340625	-9.4710725	2.77E-21	1.13E-20
LOC100646956	3249.92497	-2.108229956	0.24261904	-8.6894661	3.64E-18	1.24E-17
LOC100650938	12.3595773	-2.106952731	0.49656369	-4.2430665	2.20E-05	3.45E-05
LOC100645385	38.9110507	-2.106169411	0.42758831	-4.9256946	8.41E-07	1.44E-06
LOC100642288	999.677517	-2.106089132	0.27591718	-7.6330483	2.29E-14	6.26E-14
LOC100648995	9480.70564	-2.105599632	0.32143765	-6.5505694	5.73E-11	1.27E-10
LOC100650495	1855.09009	-2.105554418	0.31298164	-6.7274056	1.73E-11	3.96E-11
LOC100643151	2494.63592	-2.103623577	0.21409526	-9.8256429	8.73E-23	3.84E-22
LOC100644391	19.7770484	-2.103165798	0.68628419	-3.0645698	0.00217983	0.00293573
LOC105667112	27.229639	-2.102902791	0.33388325	-6.2983177	3.01E-10	6.38E-10
LOC100647261	865.959828	-2.101394726	0.2257566	-9.3082314	1.30E-20	5.13E-20
LOC100647646	573.4402	-2.097438683	0.27150169	-7.7253245	1.12E-14	3.10E-14
LOC105666070	32.8723826	-2.096913157	0.47414479	-4.4225165	9.76E-06	1.56E-05
LOC100643453	1169.98065	-2.096738509	0.1733891	-12.092677	1.15E-33	9.88E-33
LOC100647804	29.2770087	-2.095498882	0.36007016	-5.819696	5.90E-09	1.16E-08
LOC100643857	198.544014	-2.09515426	0.30909567	-6.7783358	1.22E-11	2.82E-11
LOC100647158	8024.14078	-2.094432942	0.16639358	-12.587222	2.48E-36	2.55E-35
LOC100645019	389.252132	-2.093789434	0.17598581	-11.89749	1.22E-32	9.72E-32
LOC100651128	170.253104	-2.093462844	0.18748474	-11.166044	5.98E-29	3.87E-28
LOC100647836	924.667145	-2.093394657	0.16346879	-12.806081	1.52E-37	1.68E-36

LOC100647796	25333.6688	-2.092582344	0.19107233	-10.951781	6.52E-28	3.95E-27
LOC100649504	1663.66247	-2.088736606	0.13751964	-15.188642	4.21E-52	1.36E-50
LOC100643173	524.209365	-2.08459929	0.1957629	-10.648592	1.77E-26	9.80E-26
LOC100649771	21.2712541	-2.084156572	0.3296562	-6.3222125	2.58E-10	5.48E-10
LOC100651245	288.295047	-2.083714697	0.14105711	-14.772135	2.22E-49	5.83E-48
LOC100649543	51.3104256	-2.083029328	0.21840076	-9.537647	1.46E-21	6.04E-21
LOC100642444	374.606097	-2.082721081	0.36704243	-5.6743333	1.39E-08	2.67E-08
LOC100648538	1562.02581	-2.082551426	0.18608288	-11.191526	4.49E-29	2.92E-28
LOC105665688	228.171923	-2.080745164	0.23612765	-8.8119506	1.23E-18	4.32E-18
LOC100642968	32.3810829	-2.080543295	0.34192108	-6.0848641	1.17E-09	2.39E-09
LOC100647936	3217.40564	-2.079561055	0.16270374	-12.781274	2.09E-37	2.30E-36
LOC100651052	1597.43199	-2.075437822	0.15825286	-13.114694	2.71E-39	3.38E-38
LOC100644828	1551.20796	-2.075334866	0.18277211	-11.354768	7.02E-30	4.80E-29
LOC100646862	526.583435	-2.074243373	0.20041368	-10.349809	4.19E-25	2.13E-24
LOC100650175	181.746115	-2.072461749	0.18633057	-11.1225	9.75E-29	6.23E-28
LOC105666111	97.4015979	-2.07079626	0.31031134	-6.6732858	2.50E-11	5.67E-11
LOC105666533	416.561866	-2.070577046	0.16508295	-12.542646	4.36E-36	4.37E-35
LOC100642772	812.799092	-2.068950192	0.25377065	-8.1528348	3.55E-16	1.08E-15
LOC100649409	722.702552	-2.067183	0.2174377	-9.5070127	1.96E-21	8.05E-21
LOC100651910	13.960787	-2.066522763	0.58329328	-3.5428537	0.00039582	0.00056502
LOC100645821	46.0709538	-2.066200042	0.29471302	-7.0108882	2.37E-12	5.73E-12
LOC100644963	906.968087	-2.065718546	0.3593365	-5.7487022	8.99E-09	1.75E-08
LOC100643664	30.6667154	-2.065134082	0.43450891	-4.7528003	2.01E-06	3.36E-06
LOC105666822	860.491205	-2.064793063	0.29321819	-7.0418315	1.90E-12	4.63E-12
LOC105666307	36.8010241	-2.06411275	0.28756406	-7.1779232	7.08E-13	1.77E-12
LOC100646129	444.809226	-2.063465477	0.21072718	-9.7921184	1.22E-22	5.30E-22
LOC105666458	27.1237202	-2.06168873	0.35374211	-5.8282254	5.60E-09	1.11E-08
LOC100647579	78.4474966	-2.060761932	0.3438141	-5.9938261	2.05E-09	4.15E-09
LOC100648214	3653.10393	-2.059705518	0.1355431	-15.195945	3.76E-52	1.23E-50

LOC100647808	4780.40377	-2.052765424	0.15667261	-13.102261	3.20E-39	3.98E-38
LOC100647453	2237.14295	-2.052067257	0.21297155	-9.6354055	5.67E-22	2.39E-21
LOC100646434	3016.43914	-2.051732619	0.14132238	-14.518101	9.31E-48	2.16E-46
LOC100646793	3295.6735	-2.050565892	0.18036535	-11.368957	5.97E-30	4.11E-29
LOC100643703	764.814781	-2.048488834	0.1679556	-12.196609	3.24E-34	2.90E-33
LOC105666310	57.5923105	-2.04835043	0.23105966	-8.8650284	7.65E-19	2.73E-18
LOC105666704	20.107569	-2.045895816	0.38583896	-5.3024604	1.14E-07	2.07E-07
LOC100646760	178.87679	-2.044935875	0.20166146	-10.14044	3.65E-24	1.74E-23
LOC100649754	425.858269	-2.044651069	0.18946612	-10.791645	3.77E-27	2.18E-26
LOC105665766	37.4453889	-2.044537321	0.30273609	-6.7535301	1.44E-11	3.33E-11
LOC100651697	47.1244285	-2.042223981	0.30954497	-6.5975034	4.18E-11	9.34E-11
LOC100649303	617.984048	-2.040549913	0.27432988	-7.4383072	1.02E-13	2.68E-13
LOC100650836	540.536263	-2.040403187	0.22868874	-8.9221848	4.57E-19	1.66E-18
LOC105666128	18.2676625	-2.040265325	0.5929278	-3.4410013	0.00057957	0.00081472
LOC100644555	37.9577102	-2.039801254	0.82333644	-2.4774821	0.01323131	0.01668784
LOC100646044	10537.9655	-2.038356826	0.2332164	-8.7401951	2.33E-18	8.05E-18
LOC100648531	80.4589021	-2.037506729	0.42641967	-4.7781725	1.77E-06	2.97E-06
LOC100643143	3148.13804	-2.03645649	0.15779213	-12.905944	4.17E-38	4.82E-37
LOC100643810	1719.88872	-2.035189262	0.32681717	-6.2273021	4.75E-10	9.94E-10
LOC100648138	273.65814	-2.034858472	0.39239711	-5.1857122	2.15E-07	3.84E-07
LOC100643389	39.3889391	-2.034275873	0.43156335	-4.7137364	2.43E-06	4.04E-06
LOC100631080	4668.90792	-2.032871601	0.17625851	-11.533466	8.95E-31	6.46E-30
LOC105667180	1310.06645	-2.032675206	0.34783301	-5.843825	5.10E-09	1.01E-08
LOC100645487	82.9790617	-2.023341766	0.28263736	-7.158791	8.14E-13	2.03E-12
LOC100651619	2245.67356	-2.022442818	0.30657156	-6.5969681	4.20E-11	9.37E-11
LOC100643152	77.711174	-2.021031914	0.24753165	-8.1647414	3.22E-16	9.81E-16
LOC105667206	47.2974092	-2.019640692	0.36331638	-5.5589034	2.71E-08	5.12E-08
LOC100649426	15117.3614	-2.01886667	0.28564453	-7.0677588	1.57E-12	3.85E-12
LOC100647800	45.99991	-2.017665482	0.3106967	-6.4940036	8.36E-11	1.83E-10

LOC100646060	1783.12946	-2.016472061	0.22643643	-8.9052458	5.33E-19	1.92E-18
LOC100644864	1751.05311	-2.016105519	0.15508494	-13.000008	1.22E-38	1.46E-37
LOC100643585	1507.99378	-2.015047494	0.16823346	-11.977686	4.65E-33	3.82E-32
LOC100650755	4705.64888	-2.014072486	0.18376341	-10.960139	5.94E-28	3.62E-27
LOC100647277	17.9917425	-2.01364393	0.61957106	-3.2500613	0.0011538	0.00158619
LOC100644225	1311.54463	-2.013388121	0.33642824	-5.984599	2.17E-09	4.39E-09
LOC105665778	97.1306537	-2.012055049	0.29676395	-6.7799846	1.20E-11	2.79E-11
LOC100644696	32.7360769	-2.010953419	0.28942442	-6.9481124	3.70E-12	8.87E-12
LOC100649066	31.9151424	-2.009260293	0.34471039	-5.8288359	5.58E-09	1.10E-08
LOC100647889	1631.58054	-2.00848315	0.15116904	-13.286339	2.78E-40	3.74E-39
LOC100642297	3983.80841	-2.008449519	0.20566385	-9.7656906	1.58E-22	6.85E-22
LOC100642449	10969.6271	-2.007736235	0.16515982	-12.156323	5.31E-34	4.65E-33
LOC105666139	571.494239	-2.007459767	0.23644159	-8.4902988	2.06E-17	6.73E-17
LOC100643572	88.207042	-2.006916277	0.23736355	-8.4550316	2.79E-17	9.02E-17
LOC100650643	575.768236	-2.006581601	0.24499111	-8.1904261	2.60E-16	7.97E-16
LOC100649907	5441.04975	-2.004936614	0.20899437	-9.5932565	8.53E-22	3.56E-21
LOC100647462	2374.763	-2.004409532	0.15887829	-12.616007	1.72E-36	1.79E-35
LOC100647778	344.772133	-2.00435546	0.14940157	-13.415893	4.88E-41	6.96E-40
LOC100647556	669.023419	-2.002510764	0.16130649	-12.414323	2.19E-35	2.11E-34
LOC100650075	1772.03073	-2.000997575	0.16166311	-12.377577	3.46E-35	3.30E-34
LOC100647612	1413.18983	-1.999978725	0.13170615	-15.185158	4.43E-52	1.43E-50
LOC100649327	126.740925	-1.999704238	0.22615159	-8.8423179	9.38E-19	3.32E-18
LOC100645322	60.5828257	-1.998387178	0.43446906	-4.5996076	4.23E-06	6.92E-06
LOC100642633	1171.50972	-1.99688963	0.13247452	-15.073763	2.41E-51	7.33E-50
LOC100650947	2873.48161	-1.995584763	0.18283708	-10.914552	9.82E-28	5.87E-27
LOC100648624	19653.9263	-1.995356554	0.2141583	-9.3172038	1.19E-20	4.72E-20
LOC100645184	4311.9028	-1.993929695	0.20847729	-9.5642537	1.13E-21	4.70E-21
LOC100644619	783.359217	-1.993085867	0.15632053	-12.749994	3.12E-37	3.40E-36
LOC105667095	11121.3953	-1.992698453	0.14027244	-14.205916	8.42E-46	1.67E-44

LOC100643465	143.57477	-1.990976343	0.25777645	-7.7236548	1.13E-14	3.14E-14
LOC100646779	24.795263	-1.989671137	0.43855792	-4.5368492	5.71E-06	9.26E-06
LOC100651417	2574.08276	-1.989294499	0.23078672	-8.619623	6.72E-18	2.26E-17
LOC100646650	140.077302	-1.98907569	0.16417221	-12.115788	8.71E-34	7.52E-33
LOC100651655	2056.62409	-1.988022268	0.32578541	-6.1022447	1.05E-09	2.15E-09
LOC100649469	3306.16875	-1.986851689	0.45962745	-4.3227438	1.54E-05	2.43E-05
LOC100650886	1184.01586	-1.985485463	0.14593582	-13.605196	3.73E-42	5.75E-41
LOC100644650	272.28332	-1.985108623	0.14641798	-13.55782	7.12E-42	1.08E-40
LOC105666112	22.4824127	-1.984839442	0.39684078	-5.0016015	5.69E-07	9.90E-07
LOC100642882	352.073797	-1.984791736	0.22793608	-8.7076679	3.10E-18	1.06E-17
LOC105666405	109.599756	-1.984146224	0.240868	-8.2374837	1.76E-16	5.45E-16
LOC105665991	9935.97499	-1.983450249	0.43424683	-4.5675641	4.93E-06	8.03E-06
LOC100644074	1043.304	-1.982791536	0.2513619	-7.8881946	3.07E-15	8.83E-15
LOC100642980	1749.97606	-1.982528511	0.19088151	-10.386174	2.87E-25	1.47E-24
LOC105666202	31.0831734	-1.98145053	0.34267924	-5.7822311	7.37E-09	1.44E-08
LOC100644847	32.6014787	-1.981311632	0.42941697	-4.6139575	3.95E-06	6.47E-06
LOC100651241	414.361763	-1.978607644	0.27632542	-7.1604258	8.04E-13	2.01E-12
LOC100648875	230.355401	-1.977718827	0.32635377	-6.0600459	1.36E-09	2.78E-09
LOC100649328	10006.0779	-1.975282295	0.17259754	-11.44444	2.51E-30	1.76E-29
LOC105666797	24.4456673	-1.974884976	0.40912771	-4.8270624	1.39E-06	2.35E-06
LOC100650964	951.214996	-1.974849236	0.25258228	-7.8186374	5.34E-15	1.51E-14
LOC100643150	32088.2504	-1.974541169	0.34564442	-5.7126372	1.11E-08	2.15E-08
LOC100650572	1860.59069	-1.974418753	0.24632324	-8.0155602	1.10E-15	3.24E-15
LOC100644889	259.354783	-1.972204332	0.24309224	-8.1129877	4.94E-16	1.49E-15
LOC100649441	53.7628098	-1.971475789	0.35787768	-5.5087979	3.61E-08	6.75E-08
LOC100652041	46.4370784	-1.970615095	0.47198268	-4.1751852	2.98E-05	4.62E-05
LOC100649382	502.827781	-1.970547302	0.15066588	-13.078922	4.35E-39	5.37E-38
LOC100642795	19635.0629	-1.970390847	0.30161369	-6.5328295	6.45E-11	1.42E-10
LOC100651204	90.2156242	-1.965389434	0.29123562	-6.7484515	1.49E-11	3.44E-11

LOC100644995	241.754182	-1.964474417	0.2376576	-8.2659862	1.39E-16	4.33E-16
LOC100644140	16.2463316	-1.964168022	0.55855871	-3.5164934	0.00043729	0.00062213
LOC100646280	72.3076148	-1.963371321	0.23368108	-8.4019268	4.39E-17	1.41E-16
LOC100647291	354.450779	-1.962582994	0.27203469	-7.2144586	5.41E-13	1.37E-12
LOC100644244	92.0812668	-1.962416203	0.32585691	-6.0223249	1.72E-09	3.50E-09
LOC100645346	2883.42612	-1.961836563	0.13112989	-14.961018	1.32E-50	3.77E-49
LOC100645597	117.213819	-1.961768157	0.50375967	-3.8942541	9.85E-05	0.00014708
LOC105666719	2213.00383	-1.961744526	0.15648345	-12.536434	4.72E-36	4.72E-35
LOC105667175	192.981815	-1.959711134	0.19583325	-10.00704	1.42E-23	6.52E-23
LOC100648476	165.776835	-1.958714979	0.2256701	-8.6795504	3.97E-18	1.35E-17
LOC100642782	311.301079	-1.957122466	0.1600591	-12.227499	2.22E-34	2.00E-33
LOC100642340	3660.07018	-1.956279076	0.15197807	-12.872114	6.46E-38	7.38E-37
LOC105665824	3331.45437	-1.956083496	0.1628507	-12.011514	3.09E-33	2.57E-32
LOC100647234	1655.66013	-1.955625522	0.44680283	-4.3769318	1.20E-05	1.91E-05
LOC105666003	2000.19174	-1.952643875	0.14641168	-13.336667	1.42E-40	1.96E-39
LOC100649423	16.0416596	-1.952575145	0.41480799	-4.7071783	2.51E-06	4.17E-06
LOC100650220	612.232693	-1.951826736	0.14652755	-13.320544	1.76E-40	2.40E-39
LOC100649479	659.569404	-1.950725331	0.33276773	-5.862123	4.57E-09	9.07E-09
LOC100643391	472.15977	-1.950142496	0.16032395	-12.163763	4.85E-34	4.28E-33
LOC100646466	297.250537	-1.949942212	0.25952144	-7.5136073	5.75E-14	1.54E-13
LOC100648992	45.0029028	-1.94788161	0.34305592	-5.6780294	1.36E-08	2.62E-08
LOC100647735	437.487462	-1.947658674	0.15939046	-12.219418	2.45E-34	2.20E-33
LOC100649899	6279.52009	-1.94627338	0.51847859	-3.7538163	0.00017416	0.00025558
LOC100644902	278.411889	-1.946022608	0.1697803	-11.462005	2.05E-30	1.45E-29
LOC100645567	4129.33282	-1.945335279	0.21488018	-9.0531165	1.39E-19	5.17E-19
LOC100646095	27057.5385	-1.943610441	0.17271478	-11.253295	2.23E-29	1.47E-28
LOC105666288	27.3790954	-1.943604771	0.46740406	-4.1582967	3.21E-05	4.96E-05
LOC100648564	40.223996	-1.941502811	0.25307419	-7.6716744	1.70E-14	4.68E-14
LOC105666140	1751.0425	-1.941424697	0.17816136	-10.897002	1.19E-27	7.09E-27

LOC105665690	83.5293748	-1.940676692	0.37841155	-5.1284816	2.92E-07	5.17E-07
LOC100643575	2367.17055	-1.939599994	0.24924534	-7.7818907	7.14E-15	2.01E-14
LOC100644939	398.097607	-1.939155218	0.27751993	-6.9874448	2.80E-12	6.74E-12
LOC100646642	266.785052	-1.938935134	0.20341667	-9.5318401	1.55E-21	6.38E-21
LOC105666456	16.9563298	-1.938826758	0.37455924	-5.1762887	2.26E-07	4.03E-07
LOC100644220	973.684853	-1.938173438	0.35711671	-5.4272829	5.72E-08	1.06E-07
LOC105666206	82.3668897	-1.937875323	0.402618	-4.813186	1.49E-06	2.51E-06
LOC105665942	70.5762736	-1.937828914	0.23753659	-8.1580228	3.41E-16	1.03E-15
LOC100648346	2581.76364	-1.936505102	0.12889244	-15.024195	5.10E-51	1.51E-49
LOC100643007	1460.17301	-1.936179715	0.19481127	-9.9387461	2.82E-23	1.27E-22
LOC105667090	6226.745	-1.935097439	0.15478112	-12.502155	7.27E-36	7.19E-35
LOC100650769	523.195886	-1.934394229	0.16442007	-11.764952	5.92E-32	4.54E-31
LOC100642292	78.6916024	-1.932333868	0.42083227	-4.5916961	4.40E-06	7.18E-06
LOC100651554	326.648319	-1.931279184	0.27034745	-7.143693	9.09E-13	2.26E-12
LOC100643411	14.374556	-1.929436571	0.42903097	-4.4971965	6.89E-06	1.11E-05
LOC100646447	48.2797669	-1.928699267	0.34789128	-5.5439713	2.96E-08	5.56E-08
LOC100649910	350.636935	-1.927830101	0.22027198	-8.752044	2.10E-18	7.26E-18
LOC100652008	2120.5219	-1.927544169	0.17214245	-11.197378	4.20E-29	2.74E-28
LOC100643522	675.473178	-1.92753838	0.16442713	-11.722752	9.75E-32	7.43E-31
LOC100647232	1731.4483	-1.927084735	0.17396188	-11.077627	1.61E-28	1.01E-27
LOC100644199	369.262007	-1.9270535	0.24393975	-7.8997109	2.80E-15	8.07E-15
LOC100651040	13.5417692	-1.92552891	0.55529608	-3.4675716	0.00052518	0.00074211
LOC100650863	36.8278189	-1.924941687	0.39853436	-4.830052	1.36E-06	2.31E-06
LOC100646641	12148.007	-1.924156912	0.49644696	-3.875856	0.00010625	0.00015827
LOC100651433	128.629119	-1.923568998	0.2483951	-7.7439894	9.63E-15	2.69E-14
LOC105665981	11.9826962	-1.923405887	0.49744448	-3.866574	0.00011037	0.00016426
LOC100646569	111.959483	-1.922439761	0.46373274	-4.145577	3.39E-05	5.24E-05
LOC100643008	1162.48862	-1.92164728	0.25204627	-7.6241845	2.46E-14	6.70E-14
LOC100647524	2385.49647	-1.920976816	0.23305211	-8.2426923	1.68E-16	5.23E-16

LOC100644749	2265.87686	-1.919394135	0.32097634	-5.9798618	2.23E-09	4.52E-09
LOC100648944	554.674482	-1.916473024	0.27315451	-7.0160768	2.28E-12	5.53E-12
LOC100644058	2348.53181	-1.915944545	0.14922308	-12.839466	9.86E-38	1.11E-36
LOC105666158	58.4509879	-1.915428309	0.27064173	-7.0773575	1.47E-12	3.60E-12
LOC100642871	275.344429	-1.913836357	0.31736895	-6.0303201	1.64E-09	3.33E-09
LOC105666141	4514.84244	-1.912637555	0.18151102	-10.537308	5.81E-26	3.11E-25
LOC100643360	1526.49292	-1.912594209	0.14813977	-12.910741	3.92E-38	4.54E-37
LOC100645656	634.331906	-1.910589255	0.35006569	-5.4578021	4.82E-08	8.93E-08
LOC100645782	682.289475	-1.909468022	0.16525017	-11.555014	6.96E-31	5.06E-30
LOC100649069	157.729458	-1.908105637	0.17416854	-10.955513	6.25E-28	3.80E-27
LOC100651766	26.5922694	-1.907205287	0.50312251	-3.7907374	0.0001502	0.00022124
LOC100644348	356.522362	-1.906869327	0.18007055	-10.589568	3.33E-26	1.81E-25
LOC100645815	600.094304	-1.906452984	0.13757387	-13.857668	1.14E-43	1.95E-42
LOC100651599	45.0933527	-1.904887391	0.2644875	-7.202183	5.93E-13	1.49E-12
LOC100650573	636.515544	-1.904602644	0.27804635	-6.8499465	7.39E-12	1.74E-11
LOC100643684	9276.97519	-1.903916212	0.13783783	-13.812726	2.14E-43	3.60E-42
LOC100642400	329.288609	-1.903443349	0.23577103	-8.0732707	6.84E-16	2.05E-15
LOC100648814	401.360643	-1.903047506	0.19004156	-10.013849	1.32E-23	6.10E-23
LOC100646914	6575.62246	-1.902965115	0.17347282	-10.969817	5.34E-28	3.26E-27
VSP	1716.15834	-1.901354154	0.23153968	-8.2117855	2.18E-16	6.72E-16
LOC100645836	4931.66149	-1.899141536	0.30872532	-6.1515575	7.67E-10	1.59E-09
LOC100649890	200.409702	-1.898760825	0.23792209	-7.9805991	1.46E-15	4.27E-15
LOC100643886	68.8917	-1.898520413	0.31862162	-5.9585424	2.54E-09	5.13E-09
LOC100646486	32.0591104	-1.89833173	0.54818051	-3.4629683	0.00053425	0.00075394
LOC100646701	6259.87323	-1.897894051	0.16091507	-11.794383	4.17E-32	3.24E-31
LOC100644877	265.072366	-1.896936202	0.35767535	-5.3035139	1.14E-07	2.06E-07
LOC100646240	57.1765972	-1.895781364	0.34569919	-5.4839045	4.16E-08	7.75E-08
LOC100648112	2683.39865	-1.895699917	0.11702352	-16.199307	5.10E-59	2.74E-57
LOC100644346	1921.78377	-1.894809235	0.3075561	-6.1608572	7.24E-10	1.50E-09

LOC100649490	955.504291	-1.894668871	0.18470722	-10.257687	1.09E-24	5.41E-24
LOC100647906	1397.6562	-1.89425148	0.20953815	-9.0401271	1.56E-19	5.81E-19
LOC100642661	65.0324139	-1.89363747	0.43118569	-4.3916983	1.12E-05	1.79E-05
LOC100646582	2359.16795	-1.892224033	0.41688105	-4.5390023	5.65E-06	9.17E-06
LOC100651551	391.971864	-1.891978782	0.16768275	-11.283085	1.59E-29	1.06E-28
LOC100649392	374.300747	-1.891253322	0.14490908	-13.05131	6.25E-39	7.63E-38
LOC100642628	1642.93586	-1.891054617	0.19696356	-9.6010378	7.91E-22	3.31E-21
LOC100643460	387.440761	-1.890610898	0.17556018	-10.769019	4.82E-27	2.77E-26
LOC105666578	23.5712395	-1.888995635	0.32710859	-5.7748273	7.70E-09	1.51E-08
LOC105665627	38105.7999	-1.888627621	0.3119683	-6.0539088	1.41E-09	2.89E-09
LOC100645507	22.9000757	-1.886771362	0.38410054	-4.912181	9.01E-07	1.54E-06
LOC100645387	5905.63338	-1.886498112	0.15673319	-12.036366	2.29E-33	1.91E-32
LOC105666702	177.055616	-1.886413234	0.20629087	-9.1444339	5.99E-20	2.28E-19
LOC100642883	453.506203	-1.886224077	0.24652996	-7.6510947	1.99E-14	5.48E-14
LOC105667207	852.130643	-1.884204578	0.21553362	-8.742045	2.29E-18	7.92E-18
LOC100645009	37.2174538	-1.883951931	0.23595314	-7.9844326	1.41E-15	4.14E-15
LOC100646918	284.333066	-1.883329254	0.22429294	-8.396739	4.59E-17	1.47E-16
LOC100647837	925.408441	-1.881157472	0.18205428	-10.332948	5.00E-25	2.53E-24
LOC100648637	3248.15393	-1.880638095	0.15172188	-12.395299	2.77E-35	2.66E-34
LOC100647265	207.579379	-1.88014483	0.2078841	-9.0441975	1.51E-19	5.60E-19
LOC100650649	132.68617	-1.879261253	0.45101485	-4.1667392	3.09E-05	4.79E-05
LOC100647224	494.832537	-1.878012165	0.26514494	-7.0829643	1.41E-12	3.46E-12
LOC100649475	6112.3051	-1.877711475	0.39728794	-4.7263238	2.29E-06	3.81E-06
LOC100647394	339.726878	-1.877609054	0.15263748	-12.301101	8.93E-35	8.32E-34
LOC100642919	94.8289917	-1.877285152	0.21816252	-8.6049845	7.63E-18	2.56E-17
LOC100648993	3143.05429	-1.876514015	0.14854636	-12.632514	1.40E-36	1.46E-35
LOC100646239	943.522669	-1.876308531	0.17466125	-10.742557	6.42E-27	3.67E-26
LOC100646719	6447.36704	-1.876206164	0.19089728	-9.8283545	8.50E-23	3.74E-22
LOC100649529	400.136914	-1.876199195	0.17287392	-10.852992	1.93E-27	1.14E-26

LOC100647412	1553.82333	-1.87604226	0.18737171	-10.012409	1.34E-23	6.19E-23
LOC100649342	341.973652	-1.875952624	0.18345758	-10.225539	1.52E-24	7.45E-24
LOC100651094	13424.6369	-1.875704973	0.18215197	-10.297473	7.23E-25	3.62E-24
LOC100647699	73.1930888	-1.875673109	0.21980262	-8.5334428	1.42E-17	4.69E-17
LOC100651034	1531.00807	-1.874227859	0.20740205	-9.0366892	1.61E-19	6.00E-19
LOC105666199	111.62364	-1.874102093	0.17582463	-10.658928	1.58E-26	8.78E-26
LOC100649518	126.052078	-1.873669781	0.17084723	-10.966931	5.51E-28	3.37E-27
LOC100643709	68.430926	-1.873629878	0.25926674	-7.2266497	4.95E-13	1.25E-12
LOC105666416	58.4639639	-1.87303687	0.22354368	-8.3788405	5.35E-17	1.71E-16
LOC100649871	2223.57701	-1.872391683	0.18438715	-10.154676	3.16E-24	1.51E-23
LOC100650001	116.149105	-1.869265518	0.30845091	-6.0601718	1.36E-09	2.78E-09
LOC100646485	21.0122066	-1.868258088	0.55237223	-3.3822448	0.00071896	0.00100261
LOC100644632	2218.65625	-1.867694163	0.17617793	-10.601181	2.94E-26	1.61E-25
LOC105666938	647.287199	-1.866930702	0.12859912	-14.517445	9.39E-48	2.17E-46
LOC100645892	9187.37896	-1.864225648	0.2117213	-8.8050928	1.31E-18	4.58E-18
LOC100644556	40.3895773	-1.862925707	0.32031748	-5.8158728	6.03E-09	1.19E-08
LOC100646730	526.708169	-1.862859245	0.13701582	-13.595943	4.23E-42	6.51E-41
LOC100648694	241.533169	-1.862553979	0.14848862	-12.543412	4.32E-36	4.33E-35
LOC100648542	97.9107163	-1.862466725	0.20785482	-8.9604212	3.23E-19	1.18E-18
LOC100646179	51.5997737	-1.862339503	0.42469973	-4.3850735	1.16E-05	1.85E-05
LOC100651586	1744.65508	-1.861909057	0.18467228	-10.082234	6.62E-24	3.11E-23
LOC100643765	542.853404	-1.861485706	0.27212115	-6.8406506	7.88E-12	1.85E-11
LOC100645347	414.961559	-1.859920788	0.25770788	-7.2171669	5.31E-13	1.34E-12
LOC100648508	5642.53427	-1.85952786	0.39483795	-4.7095976	2.48E-06	4.12E-06
LOC100642250	1109.89877	-1.858707382	0.22676396	-8.1966612	2.47E-16	7.59E-16
LOC100645137	123.149128	-1.85575224	0.18328472	-10.12497	4.28E-24	2.03E-23
LOC100643070	5197.95492	-1.855458893	0.14954886	-12.407041	2.39E-35	2.31E-34
LOC100646598	1714.10403	-1.853504253	0.13912925	-13.322175	1.72E-40	2.36E-39
LOC100646484	261.922773	-1.853112539	0.23859989	-7.7666109	8.06E-15	2.26E-14

LOC105666402	18.2420974	-1.852280698	0.42018937	-4.4082046	1.04E-05	1.66E-05
LOC100650869	1118.50678	-1.851162469	0.17175205	-10.77811	4.37E-27	2.51E-26
LOC100647368	3306.06302	-1.850555063	0.18154998	-10.193089	2.13E-24	1.03E-23
LOC100644253	1315.20332	-1.850411675	0.19499725	-9.4894246	2.32E-21	9.51E-21
LOC100644581	143.404281	-1.84996382	0.26458062	-6.992061	2.71E-12	6.53E-12
LOC100646009	4613.85528	-1.847263409	0.14936996	-12.367034	3.94E-35	3.75E-34
LOC100650077	3180.75618	-1.847037398	0.2006693	-9.2043844	3.44E-20	1.32E-19
LOC100650743	2440.4984	-1.846344425	0.19986116	-9.2381352	2.51E-20	9.73E-20
LOC100647409	172.220454	-1.8462495	0.26359655	-7.0040732	2.49E-12	6.01E-12
LOC100644450	3493.42594	-1.845542286	0.16734901	-11.028104	2.80E-28	1.74E-27
LOC100651682	607.316462	-1.845492949	0.15226032	-12.120643	8.21E-34	7.10E-33
LOC100643594	222.732711	-1.845423689	0.27421824	-6.7297627	1.70E-11	3.90E-11
LOC100645713	615.157499	-1.845188805	0.19231949	-9.594393	8.44E-22	3.53E-21
LOC100645006	38.0868703	-1.844907822	0.20024973	-9.2130351	3.17E-20	1.22E-19
LOC100651025	352.42074	-1.844251561	0.14936223	-12.34751	5.02E-35	4.73E-34
LOC105666319	11861.9233	-1.844093937	0.23086789	-7.987659	1.38E-15	4.04E-15
LOC100644382	113914.449	-1.842334868	0.25149963	-7.325398	2.38E-13	6.13E-13
LOC100652147	2872.57881	-1.842039031	0.18129199	-10.16062	2.97E-24	1.42E-23
LOC100648169	1947.04494	-1.841510292	0.14627445	-12.589419	2.41E-36	2.48E-35
LOC100646315	10175.2385	-1.841312942	0.16839659	-10.934384	7.89E-28	4.76E-27
LOC105665949	1100.21831	-1.837145882	0.15322819	-11.989608	4.03E-33	3.32E-32
LOC100647251	11663.5283	-1.835541396	0.17501276	-10.488043	9.80E-26	5.18E-25
LOC100651120	258.128645	-1.834980532	0.32667733	-5.617104	1.94E-08	3.69E-08
LOC105666151	315.13687	-1.833265666	0.16155698	-11.347486	7.63E-30	5.20E-29
LOC100648419	151.758745	-1.833250198	0.18510526	-9.9038255	4.01E-23	1.79E-22
LOC100649556	720.168455	-1.831323324	0.16688644	-10.97347	5.13E-28	3.14E-27
LOC100644524	95.18718	-1.830627952	0.26233541	-6.9781961	2.99E-12	7.19E-12
LOC100649787	1271.00383	-1.830301683	0.32093498	-5.7030296	1.18E-08	2.27E-08
LOC100646458	136.705906	-1.828151315	0.25312228	-7.2224038	5.11E-13	1.29E-12

LOC100647897	50.0501323	-1.825818918	0.2986065	-6.1144647	9.69E-10	2.00E-09
LOC100646229	506.91072	-1.823791146	0.15297811	-11.921909	9.10E-33	7.32E-32
LOC100644231	383.81504	-1.823787995	0.16191177	-11.264085	1.97E-29	1.31E-28
LOC100644720	44525.1487	-1.823663019	0.17069538	-10.683728	1.21E-26	6.79E-26
LOC100645035	918.804389	-1.822838173	0.15519333	-11.745596	7.44E-32	5.70E-31
LOC100646080	654.08586	-1.822446263	0.24643192	-7.3953335	1.41E-13	3.68E-13
LOC100648671	36.0945204	-1.822028774	0.30150204	-6.0431723	1.51E-09	3.08E-09
LOC100650085	3338.01758	-1.820807059	0.19160317	-9.503011	2.04E-21	8.36E-21
LOC100645595	1397.11652	-1.820710817	0.24270204	-7.5018356	6.29E-14	1.68E-13
LOC100643324	409.195182	-1.820347917	0.29748472	-6.1191307	9.41E-10	1.94E-09
LOC100648673	18585.4586	-1.81965645	0.2292622	-7.9370104	2.07E-15	6.03E-15
LOC100647225	394.74648	-1.819354178	0.1762952	-10.31993	5.73E-25	2.88E-24
LOC105666015	41.7417558	-1.819353862	0.368215	-4.9410096	7.77E-07	1.34E-06
LOC100649922	552.216404	-1.818668598	0.19154056	-9.4949527	2.20E-21	9.03E-21
LOC100648427	8087.0511	-1.818649796	0.24253978	-7.4983567	6.46E-14	1.72E-13
LOC100645555	6740.7006	-1.817889882	0.2332401	-7.794071	6.49E-15	1.83E-14
LOC105665994	48.9065097	-1.817043432	0.25294623	-7.1835165	6.79E-13	1.70E-12
LOC100650311	428.463749	-1.81682124	0.1848069	-9.8309167	8.29E-23	3.64E-22
LOC100648712	28.2996205	-1.815828673	0.32900477	-5.519156	3.41E-08	6.38E-08
LOC100642480	13669.4806	-1.81548888	0.17945388	-10.116744	4.66E-24	2.20E-23
LOC100645681	161.727508	-1.814557722	0.48821835	-3.716693	0.00020185	0.00029484
LOC100645461	579.584237	-1.81429694	0.15412028	-11.771955	5.44E-32	4.19E-31
LOC100643490	8157.13431	-1.813683667	0.14156784	-12.81141	1.42E-37	1.58E-36
LOC100642664	8354.23168	-1.81352554	0.12446827	-14.570184	4.35E-48	1.05E-46
LOC100643557	8045.19151	-1.813326707	0.15218376	-11.915376	9.84E-33	7.89E-32
LOC100643462	6445.72974	-1.812935414	0.17474795	-10.374573	3.24E-25	1.66E-24
LOC100643826	579.363559	-1.812757623	0.38049834	-4.7641669	1.90E-06	3.18E-06
LOC100652050	1622.52231	-1.812466271	0.27323075	-6.6334637	3.28E-11	7.37E-11
LOC100644526	75.3979944	-1.811425929	0.34252406	-5.2884634	1.23E-07	2.23E-07

LOC100645384	3406.89089	-1.8112904	0.16336452	-11.087416	1.44E-28	9.10E-28
LOC100643687	393.55697	-1.811030296	0.18242031	-9.9277886	3.15E-23	1.42E-22
LOC100643828	87.569702	-1.810688882	0.31802664	-5.6935132	1.24E-08	2.40E-08
LOC100646220	135.263766	-1.810256806	0.1968102	-9.1979826	3.65E-20	1.40E-19
LOC100644923	3501.35214	-1.810069011	0.19253128	-9.4014281	5.38E-21	2.17E-20
LOC100644182	4397.77138	-1.810005321	0.16412236	-11.02839	2.79E-28	1.73E-27
LOC100647860	6547.20994	-1.809453441	0.17377323	-10.412728	2.17E-25	1.12E-24
LOC100646804	29.3418982	-1.807046441	0.3347801	-5.3977117	6.75E-08	1.24E-07
LOC100644246	1599.68834	-1.804956489	0.12403725	-14.551729	5.69E-48	1.35E-46
LOC100648222	216.507838	-1.803672624	0.20939614	-8.6136862	7.07E-18	2.38E-17
LOC105665858	46.6849586	-1.803475601	0.23742979	-7.5958269	3.06E-14	8.30E-14
LOC100646763	37610.4204	-1.802780384	0.11866316	-15.192418	3.97E-52	1.30E-50
LOC100642321	2048.09836	-1.801808352	0.21584426	-8.3477243	6.96E-17	2.21E-16
LOC100646107	183.971111	-1.801569358	0.22566431	-7.9834042	1.42E-15	4.17E-15
LOC105665718	304.286268	-1.801380397	0.23296677	-7.7323491	1.06E-14	2.94E-14
LOC100645490	960.455754	-1.800658583	0.13713188	-13.130853	2.19E-39	2.76E-38
LOC100643148	5191.78655	-1.799771492	0.15064243	-11.947308	6.71E-33	5.45E-32
LOC100647939	369.759567	-1.798169586	0.24322503	-7.3930286	1.44E-13	3.74E-13
LOC100644013	251.333816	-1.797789005	0.292541	-6.1454259	7.97E-10	1.65E-09
LOC100652068	19106.8604	-1.797100965	0.11950414	-15.037981	4.14E-51	1.24E-49
LOC100642655	530.032536	-1.794461046	0.15547163	-11.542048	8.10E-31	5.87E-30
LOC100649104	171.255793	-1.793796268	0.20165123	-8.8955385	5.81E-19	2.09E-18
LOC100648073	12.4949711	-1.792841402	0.60777031	-2.9498667	0.00317911	0.00422572
LOC100651156	173.047454	-1.792028247	0.30852612	-5.8083519	6.31E-09	1.24E-08
LOC100646094	1876.59578	-1.791250521	0.19347035	-9.2585275	2.07E-20	8.06E-20
LOC100642219	317.555742	-1.790039424	0.24876406	-7.1957316	6.21E-13	1.56E-12
LOC100642987	838.034966	-1.789997775	0.15386537	-11.633533	2.78E-31	2.07E-30
LOC100644600	951.316081	-1.789670546	0.32971179	-5.4279848	5.70E-08	1.05E-07
LOC100644671	6863.53379	-1.788801304	0.18086322	-9.8903544	4.58E-23	2.04E-22

LOC100650653	1158.11173	-1.788712365	0.17498972	-10.221814	1.58E-24	7.72E-24
LOC100652253	388.039738	-1.788108839	0.14922132	-11.982931	4.37E-33	3.59E-32
LOC100644886	5638.34214	-1.786421999	0.1940042	-9.2081616	3.32E-20	1.28E-19
LOC100648275	3552.19754	-1.786062605	0.1440072	-12.402593	2.53E-35	2.44E-34
LOC100644753	58.0519262	-1.78477751	0.23874603	-7.4756321	7.68E-14	2.04E-13
LOC100650802	388.436002	-1.784429374	0.14159075	-12.602726	2.04E-36	2.10E-35
LOC100651843	307.998385	-1.78407427	0.19828335	-8.9976001	2.31E-19	8.51E-19
LOC100644438	91.6294581	-1.78405153	0.23694028	-7.5295411	5.09E-14	1.37E-13
LOC100650928	12.287494	-1.783567699	0.610282	-2.9225304	0.003472	0.00459135
LOC100646662	10301.7667	-1.783061488	0.12781349	-13.950495	3.12E-44	5.51E-43
LOC100649140	96.5964658	-1.781065726	0.27220483	-6.5431083	6.03E-11	1.33E-10
LOC100646983	360.706902	-1.780882804	0.26683957	-6.6739831	2.49E-11	5.65E-11
LOC100648661	1792.69096	-1.778931023	0.19502204	-9.1216924	7.40E-20	2.80E-19
LOC100644309	5966.51587	-1.778520222	0.14757224	-12.051862	1.90E-33	1.59E-32
LOC100650576	5218.79753	-1.77673139	0.1560588	-11.385013	4.97E-30	3.44E-29
LOC100645598	3251.83648	-1.776406556	0.21097783	-8.4198731	3.77E-17	1.21E-16
LOC100647339	6564.9398	-1.776199446	0.36883408	-4.815714	1.47E-06	2.48E-06
LOC100648227	1834.83663	-1.776147167	0.13135505	-13.521728	1.16E-41	1.74E-40
LOC105666544	85.9957758	-1.77550738	0.25916383	-6.8509074	7.34E-12	1.73E-11
LOC100648720	15272.6786	-1.774447264	0.21851426	-8.12051	4.64E-16	1.40E-15
LOC105666440	78.5716887	-1.77415587	0.20263776	-8.7553072	2.04E-18	7.07E-18
LOC100643004	339.906469	-1.774150919	0.20856576	-8.5064341	1.79E-17	5.87E-17
LOC100644814	2385.46737	-1.773156986	0.17413171	-10.182849	2.37E-24	1.14E-23
LOC100645730	534.835164	-1.77302008	0.14832302	-11.953775	6.20E-33	5.05E-32
LOC105665934	393.722711	-1.772942689	0.16631138	-10.660381	1.56E-26	8.66E-26
LOC100648545	316.900598	-1.772421446	0.19917607	-8.898767	5.65E-19	2.03E-18
LOC100644762	165.949595	-1.771222323	0.27441974	-6.4544275	1.09E-10	2.35E-10
LOC100644420	1276.64749	-1.770415385	0.10558284	-16.768022	4.18E-63	3.22E-61
LOC100642903	11351.0882	-1.769378199	0.2175224	-8.1342344	4.15E-16	1.25E-15

LOC100649207	2229.56811	-1.769295943	0.23958298	-7.3848982	1.53E-13	3.97E-13
LOC100645047	703.407137	-1.769226547	0.13113235	-13.491915	1.75E-41	2.57E-40
LOC100651344	3856.54363	-1.769179951	0.13841885	-12.781351	2.08E-37	2.30E-36
LOC105665740	44.2658856	-1.767977598	0.39765063	-4.4460576	8.75E-06	1.40E-05
LOC100645612	420.614006	-1.767463476	0.25104242	-7.0404973	1.92E-12	4.67E-12
LOC105667096	2471.86154	-1.767128432	0.18492738	-9.5557966	1.23E-21	5.09E-21
LOC100645073	60.6577821	-1.766061116	0.30661449	-5.7598749	8.42E-09	1.64E-08
LOC100646026	5533.54958	-1.764745126	0.16718463	-10.555666	4.78E-26	2.57E-25
LOC100646525	534.664531	-1.764470681	0.47099835	-3.7462353	0.00017951	0.00026323
LOC100648886	1502.0179	-1.763551474	0.14382848	-12.26149	1.46E-34	1.33E-33
LOC100642316	656.017147	-1.763016235	0.12427071	-14.186901	1.10E-45	2.18E-44
LOC100644903	1682.79529	-1.762168537	0.17792565	-9.9039603	4.00E-23	1.79E-22
LOC100649832	1757.91351	-1.761718977	0.11268215	-15.63441	4.24E-55	1.66E-53
LOC105665955	158.245082	-1.761115354	0.27488336	-6.4067732	1.49E-10	3.20E-10
LOC100650124	32.9772443	-1.759703049	0.31382428	-5.6072879	2.06E-08	3.90E-08
LOC100644145	91.2270228	-1.758649712	0.19961419	-8.810244	1.25E-18	4.38E-18
LOC100643680	216.730409	-1.758284321	0.18185736	-9.6684803	4.10E-22	1.74E-21
LOC100650772	668.211773	-1.758275841	0.24254036	-7.2494155	4.19E-13	1.07E-12
LOC100650856	379.577688	-1.757392164	0.15604746	-11.261908	2.02E-29	1.34E-28
LOC100652263	230.153872	-1.756502342	0.17986956	-9.7654227	1.58E-22	6.86E-22
LOC100644951	5478.57148	-1.755568083	0.21460036	-8.1806391	2.82E-16	8.62E-16
LOC100642573	112.981637	-1.7545114	0.25617967	-6.8487534	7.45E-12	1.75E-11
LOC100648579	1443.44333	-1.754304181	0.2230771	-7.8641159	3.72E-15	1.07E-14
LOC100646823	59.6140576	-1.753151234	0.19901425	-8.8091742	1.26E-18	4.42E-18
LOC100650457	302.146672	-1.751391635	0.17694592	-9.897892	4.25E-23	1.89E-22
LOC100645959	734.761413	-1.750459937	0.16272112	-10.757423	5.47E-27	3.13E-26
LOC100651038	196.289396	-1.750107672	0.37214338	-4.702778	2.57E-06	4.26E-06
LOC100643547	226.831316	-1.750070426	0.17431909	-10.039465	1.02E-23	4.75E-23
LOC100644445	43.376166	-1.750061414	0.26578314	-6.5845463	4.56E-11	1.02E-10

LOC100647809	735.76694	-1.748164164	0.16129542	-10.838275	2.27E-27	1.33E-26
LOC100643931	376.194982	-1.746021934	0.21878408	-7.9805712	1.46E-15	4.27E-15
LOC100650592	2196.53942	-1.745584867	0.21300423	-8.1950712	2.50E-16	7.68E-16
LOC100643512	50919.1459	-1.745474577	0.16995567	-10.270176	9.60E-25	4.77E-24
LOC100644384	435.881971	-1.744953932	0.17345958	-10.059715	8.32E-24	3.89E-23
LOC100642574	135.730056	-1.744586495	0.17922082	-9.7342845	2.15E-22	9.27E-22
LOC100651542	215.478613	-1.74312276	0.30920881	-5.6373645	1.73E-08	3.29E-08
LOC100650460	22230.6162	-1.74182828	0.24269494	-7.1770277	7.12E-13	1.78E-12
LOC100643695	132.317371	-1.739848533	0.45380663	-3.8338985	0.00012613	0.0001868
LOC100648281	161.682563	-1.739537755	0.19034934	-9.1386591	6.32E-20	2.41E-19
LOC105666242	775.831781	-1.739001418	0.12661181	-13.734907	6.27E-43	1.03E-41
LOC100643461	23.0160847	-1.736760118	0.3398726	-5.1100328	3.22E-07	5.69E-07
LOC100645271	542.642772	-1.735312319	0.18963756	-9.1506782	5.66E-20	2.16E-19
LOC100647993	687.371712	-1.735062507	0.16916158	-10.256836	1.10E-24	5.45E-24
LOC100643022	2082.68372	-1.733900122	0.1496714	-11.584712	4.93E-31	3.61E-30
LOC100649836	53.8137392	-1.733533546	0.27734041	-6.2505625	4.09E-10	8.60E-10
LOC100651768	2054.76078	-1.732846954	0.29570709	-5.8600115	4.63E-09	9.18E-09
LOC100651564	61.917005	-1.732513751	0.41512867	-4.173438	3.00E-05	4.65E-05
LOC100643760	1070.16109	-1.732286315	0.18376297	-9.426743	4.23E-21	1.71E-20
LOC100649657	1158.03832	-1.731290979	0.14437176	-11.991895	3.92E-33	3.23E-32
LOC100643213	2041.77875	-1.730943522	0.1224159	-14.139859	2.16E-45	4.18E-44
LOC100651465	790.002752	-1.730423356	0.22069179	-7.840905	4.47E-15	1.27E-14
LOC100645530	3286.82546	-1.729972194	0.14475674	-11.950892	6.42E-33	5.22E-32
LOC100647667	509.7008	-1.727841442	0.19897537	-8.6836951	3.83E-18	1.30E-17
LOC105665762	10.9777161	-1.727818304	0.59083637	-2.9243601	0.00345165	0.00456691
LOC100645831	18.2990416	-1.727252012	0.38373408	-4.5011692	6.76E-06	1.09E-05
LOC100644415	657.274749	-1.726712512	0.12254376	-14.090579	4.34E-45	8.18E-44
LOC100644333	13742.0608	-1.726437136	0.20374109	-8.4736818	2.38E-17	7.73E-17
LOC100648100	2917.76977	-1.7262143	0.22573033	-7.6472412	2.05E-14	5.63E-14

LOC100645335	1466.08635	-1.726105455	0.18517843	-9.3213096	1.15E-20	4.55E-20
LOC100642680	1374.48637	-1.725594062	0.32515803	-5.3069397	1.11E-07	2.02E-07
LOC100649548	2507.22108	-1.725509268	0.15655239	-11.021929	3.00E-28	1.86E-27
LOC100643203	198.001403	-1.723953608	0.31827471	-5.4165586	6.08E-08	1.12E-07
LOC105666529	1132.35412	-1.723865693	0.166517	-10.352491	4.08E-25	2.07E-24
LOC100651954	883.420588	-1.723380525	0.21974752	-7.8425483	4.41E-15	1.26E-14
LOC100645459	1077.75856	-1.723293126	0.14275042	-12.07207	1.48E-33	1.26E-32
LOC100645537	103.070783	-1.723227706	0.29699853	-5.8021423	6.55E-09	1.29E-08
LOC100642218	2462.08343	-1.722632833	0.13158163	-13.091742	3.67E-39	4.54E-38
LOC100648190	889.611867	-1.722387692	0.14190179	-12.137886	6.65E-34	5.80E-33
LOC100643073	1484.45544	-1.722006004	0.23875157	-7.2125431	5.49E-13	1.39E-12
LOC100646422	652.49433	-1.7216549	0.19943911	-8.6324839	6.00E-18	2.02E-17
LOC105666634	48.6465717	-1.721548687	0.34499559	-4.99006	6.04E-07	1.05E-06
LOC100647094	294.875857	-1.71943598	0.18554137	-9.2671301	1.91E-20	7.46E-20
LOC100644201	95.7432759	-1.717397868	0.62074581	-2.7666685	0.00566323	0.00735429
LOC105666538	1812.19602	-1.716016501	0.16153325	-10.623302	2.32E-26	1.27E-25
LOC105666821	625.485142	-1.715909258	0.29708706	-5.7757792	7.66E-09	1.50E-08
LOC100644169	3933.23406	-1.715843551	0.17235494	-9.9552908	2.39E-23	1.08E-22
LOC100649801	5107.35054	-1.715598595	0.21687102	-7.9106864	2.56E-15	7.40E-15
LOC100648414	723.498444	-1.715504759	0.16676208	-10.287139	8.05E-25	4.02E-24
LOC100649120	29.4772319	-1.715248267	0.37638973	-4.557107	5.19E-06	8.43E-06
LOC100652175	1968.04766	-1.715094411	0.12457414	-13.76766	3.99E-43	6.60E-42
LOC100643023	468.104214	-1.714670965	0.14578556	-11.761597	6.16E-32	4.72E-31
LOC100649282	1066.59093	-1.714365752	0.14092189	-12.165361	4.75E-34	4.21E-33
LOC100648022	891.989227	-1.713840479	0.11921309	-14.376278	7.29E-47	1.57E-45
LOC100649144	3633.49308	-1.713833705	0.21123425	-8.1134272	4.92E-16	1.48E-15
LOC100650646	216.739446	-1.713805886	0.15891765	-10.784239	4.09E-27	2.36E-26
LOC100631053	19607.0487	-1.712734341	0.28456465	-6.0187882	1.76E-09	3.57E-09
LOC100650722	20284.0031	-1.712126995	0.10482556	-16.333105	5.74E-60	3.36E-58

LOC100646115	37.5581253	-1.711575494	0.35261574	-4.8539396	1.21E-06	2.06E-06
LOC100642294	1953.19454	-1.711569619	0.09301414	-18.401177	1.29E-75	2.80E-73
LOC100651851	53.6286719	-1.71097751	0.50275476	-3.403205	0.000666	0.00093195
LOC100650084	1066.95338	-1.710754181	0.13445439	-12.723677	4.37E-37	4.70E-36
LOC100646291	2090.7188	-1.710540029	0.44024494	-3.8854281	0.00010215	0.0001523
LOC100649250	497.467504	-1.709344618	0.17290082	-9.8862722	4.77E-23	2.12E-22
LOC100647512	985.868763	-1.709101198	0.30329499	-5.6351118	1.75E-08	3.34E-08
LOC105666707	36.8202736	-1.708879927	0.49336237	-3.4637419	0.00053272	0.00075189
LOC100651812	6357.69409	-1.707861043	0.19895976	-8.5839519	9.17E-18	3.06E-17
LOC100646077	11.934385	-1.707621417	0.44431286	-3.843286	0.0001214	0.00018001
LOC105667184	20.7946816	-1.704714838	0.30948713	-5.5081929	3.63E-08	6.77E-08
LOC100650379	639.7163	-1.703212236	0.15022932	-11.337415	8.56E-30	5.81E-29
LOC100646819	343.911166	-1.702930403	0.16655803	-10.224247	1.54E-24	7.53E-24
LOC100651333	1007.44878	-1.702597806	0.09928304	-17.148928	6.40E-66	6.27E-64
LOC100649346	140.378548	-1.702591051	0.23994643	-7.0957133	1.29E-12	3.17E-12
LOC100647887	173.443506	-1.702370826	0.21273285	-8.0023882	1.22E-15	3.59E-15
LOC100646904	606.786666	-1.70225958	0.33041077	-5.1519495	2.58E-07	4.58E-07
LOC100642289	273.238862	-1.701884504	0.27818404	-6.1178367	9.49E-10	1.96E-09
LOC105666358	10.4790953	-1.700596496	0.41044047	-4.1433451	3.42E-05	5.28E-05
LOC100646603	8941.73228	-1.699341783	0.16661175	-10.199411	1.99E-24	9.66E-24
LOC100649792	1060.20756	-1.698143112	0.13996564	-12.132571	7.10E-34	6.18E-33
LOC100645013	1386.69022	-1.697076432	0.19807501	-8.5678473	1.05E-17	3.51E-17
LOC100642710	34.5210446	-1.69585179	0.34889463	-4.8606417	1.17E-06	1.99E-06
LOC105666460	577.526545	-1.69560907	0.13488401	-12.570867	3.05E-36	3.09E-35
LOC100643660	260.025521	-1.695505113	0.15067605	-11.252652	2.25E-29	1.48E-28
LOC100648311	450.705438	-1.694891279	0.27839092	-6.0881701	1.14E-09	2.35E-09
LOC100650234	23.3672721	-1.694181222	0.58417789	-2.9001119	0.0037303	0.00492095
LOC100649714	436.14584	-1.693808485	0.1581258	-10.711778	8.96E-27	5.06E-26
LOC100650434	27.4017394	-1.692107874	0.51268506	-3.3004821	0.00096519	0.0013342

LOC100643063	901.720133	-1.692027137	0.11650371	-14.523376	8.62E-48	2.01E-46
LOC100644115	1274.76639	-1.691363271	0.14992197	-11.281624	1.62E-29	1.08E-28
LOC100643593	371.857622	-1.690192611	0.21854072	-7.733994	1.04E-14	2.91E-14
LOC100645662	1543.00568	-1.689820015	0.24869191	-6.794833	1.08E-11	2.52E-11
LOC100643616	849.152256	-1.68981074	0.13464595	-12.55003	3.97E-36	4.01E-35
LOC100644042	1335.22883	-1.687576084	0.30741355	-5.4895957	4.03E-08	7.51E-08
LOC100651500	353.025374	-1.686421026	0.25506385	-6.6117604	3.80E-11	8.51E-11
LOC100649857	28.0898018	-1.686383986	0.44075028	-3.8261666	0.00013015	0.00019259
LOC100647100	1273.52356	-1.686248971	0.13333918	-12.646313	1.17E-36	1.23E-35
LOC100650351	3414.45116	-1.686118714	0.165568	-10.183844	2.34E-24	1.13E-23
LOC100643624	7929.0645	-1.684237424	0.24535443	-6.8645079	6.67E-12	1.58E-11
LOC105666563	63.8110618	-1.683790589	0.33122192	-5.0835723	3.70E-07	6.52E-07
LOC100651170	3493.84641	-1.683636371	0.12718717	-13.237471	5.33E-40	7.04E-39
LOC100650650	3472.42808	-1.683422481	0.14855667	-11.331854	9.13E-30	6.18E-29
LOC100643229	15.9504159	-1.683372995	0.37675144	-4.4681262	7.89E-06	1.27E-05
LOC100644223	14.4681743	-1.682266343	0.70007917	-2.4029658	0.01626271	0.02033825
LOC100648375	8979.13622	-1.682247767	0.16672896	-10.089715	6.13E-24	2.88E-23
LOC100651334	3555.16156	-1.681893189	0.20415504	-8.2383134	1.75E-16	5.42E-16
LOC100643574	2870.1216	-1.68139636	0.19179992	-8.7664078	1.84E-18	6.42E-18
LOC100649324	2728.0274	-1.680878953	0.10078691	-16.677553	1.91E-62	1.38E-60
LOC100644023	1951.15532	-1.68000383	0.14576897	-11.525113	9.86E-31	7.11E-30
LOC100650665	329.412644	-1.678873513	0.16742265	-10.027756	1.15E-23	5.33E-23
LOC105665776	325.900526	-1.677346368	0.15449443	-10.857003	1.85E-27	1.09E-26
LOC100644856	236.121108	-1.677255401	0.25255142	-6.6412433	3.11E-11	7.01E-11
LOC100644905	602.682928	-1.676813707	0.19496044	-8.6007896	7.92E-18	2.65E-17
LOC100647788	244.502513	-1.676135743	0.19079369	-8.7850689	1.56E-18	5.45E-18
LOC100644515	1000.40167	-1.675819724	0.12279982	-13.646761	2.11E-42	3.31E-41
LOC100651015	77.3439005	-1.675256991	0.25960153	-6.4531861	1.10E-10	2.37E-10
LOC100650291	24560.7072	-1.675226371	0.13140402	-12.748669	3.17E-37	3.45E-36

LOC100643858	5473.93347	-1.674012314	0.40207587	-4.163424	3.14E-05	4.85E-05
LOC100646995	106.318558	-1.673544505	0.28070095	-5.9620193	2.49E-09	5.03E-09
LOC100646186	751.353523	-1.673361254	0.17991744	-9.3007174	1.40E-20	5.50E-20
LOC100648821	78.4188641	-1.673339211	0.26993351	-6.1990791	5.68E-10	1.18E-09
LOC100644375	417.898524	-1.672096739	0.19931621	-8.3891656	4.90E-17	1.57E-16
LOC100645679	1305.80679	-1.671892673	0.15478164	-10.801621	3.38E-27	1.97E-26
LOC100647662	6840.7674	-1.670709198	0.19765776	-8.4525352	2.85E-17	9.21E-17
LOC100648589	698.058237	-1.670305974	0.18448267	-9.0539992	1.38E-19	5.14E-19
LOC105666781	312.30932	-1.66903305	0.13252621	-12.593985	2.28E-36	2.35E-35
LOC100646614	149.94271	-1.668844049	0.29439128	-5.6687958	1.44E-08	2.76E-08
LOC100643209	504.655961	-1.666718911	0.23630775	-7.0531707	1.75E-12	4.27E-12
LOC100647599	43.4921434	-1.666417982	0.2984278	-5.5839905	2.35E-08	4.45E-08
LOC100642912	3823.532	-1.666248836	0.13118913	-12.701119	5.83E-37	6.21E-36
LOC100644271	803.017707	-1.665803662	0.21616969	-7.7060001	1.30E-14	3.59E-14
LOC100650446	1389.36379	-1.665198207	0.12648298	-13.165393	1.39E-39	1.79E-38
LOC105667132	36.5237265	-1.664422457	0.4790703	-3.474276	0.00051223	0.00072454
LOC100647117	426.203914	-1.662943186	0.21756098	-7.6435727	2.11E-14	5.78E-14
LOC100644448	34.9590317	-1.662880065	0.37908144	-4.3866037	1.15E-05	1.83E-05
LOC100642377	117.494305	-1.662606218	0.31766345	-5.2338606	1.66E-07	2.98E-07
LOC100646790	1622.92523	-1.661843208	0.16802922	-9.8902037	4.59E-23	2.04E-22
LOC100647159	1661.36524	-1.659335043	0.15134319	-10.964055	5.69E-28	3.47E-27
LOC100644931	140.4502	-1.657471744	0.21165744	-7.8309166	4.84E-15	1.38E-14
LOC100651636	900.696895	-1.656478652	0.1896383	-8.7349372	2.44E-18	8.40E-18
LOC100645470	5110.06806	-1.65595766	0.18607512	-8.899404	5.61E-19	2.02E-18
LOC100646348	8871.46297	-1.655496075	0.25645223	-6.4553779	1.08E-10	2.34E-10
LOC100649427	162.24674	-1.655492826	0.27124808	-6.1032426	1.04E-09	2.14E-09
LOC100645650	2370.6386	-1.65514011	0.20742898	-7.9793099	1.47E-15	4.31E-15
LOC100642235	1581.86985	-1.654970712	0.14739162	-11.22839	2.96E-29	1.94E-28
LOC105667072	107.461436	-1.654054799	0.24061284	-6.8743415	6.23E-12	1.47E-11

LOC100650756	420.799863	-1.653596875	0.3145189	-5.2575437	1.46E-07	2.63E-07
LOC100650597	4071.83451	-1.652684127	0.10984914	-15.045034	3.72E-51	1.12E-49
LOC100650628	140.283106	-1.651838708	0.68728739	-2.4034177	0.01624262	0.02031573
LOC100647676	77.8760883	-1.651205624	0.21546815	-7.6633398	1.81E-14	4.98E-14
LOC100651348	193.554085	-1.649093498	0.24812315	-6.6462703	3.01E-11	6.78E-11
LOC100646769	711.829141	-1.648003769	0.18978872	-8.6833598	3.84E-18	1.31E-17
LOC100648878	125.612249	-1.647393588	0.27046124	-6.0910524	1.12E-09	2.30E-09
LOC100646476	80.2452996	-1.646806201	0.4148004	-3.9701172	7.18E-05	0.00010846
LOC100648162	628.788115	-1.645409892	0.20173346	-8.156356	3.45E-16	1.05E-15
LOC100645528	18.5681202	-1.645028292	0.3386732	-4.8572732	1.19E-06	2.03E-06
LOC100647596	544.416294	-1.644303035	0.25495256	-6.449447	1.12E-10	2.43E-10
LOC105667201	14.6859968	-1.643468616	0.7784377	-2.1112397	0.03475171	0.04227148
LOC100646943	1740.88462	-1.642082939	0.11628353	-14.121371	2.80E-45	5.40E-44
Trnaq-cug	13.6901603	-1.641817018	0.33168859	-4.9498749	7.43E-07	1.28E-06
LOC100642748	1664.75621	-1.641781846	0.1807386	-9.0837368	1.05E-19	3.93E-19
LOC100642954	1592.2135	-1.641647668	0.18125789	-9.0569724	1.34E-19	5.01E-19
LOC100644299	1589.24176	-1.641260471	0.14768593	-11.113181	1.08E-28	6.91E-28
LOC100645568	608.94705	-1.640586739	0.17606691	-9.317973	1.19E-20	4.69E-20
LOC100643423	6884.71073	-1.640230291	0.13129994	-12.492239	8.23E-36	8.12E-35
LOC100644306	1061.53839	-1.640217168	0.11942745	-13.734004	6.35E-43	1.04E-41
LOC105667113	886.360153	-1.640174425	0.25920546	-6.3277002	2.49E-10	5.30E-10
LOC100646398	334.395229	-1.639302568	0.18512004	-8.8553489	8.34E-19	2.97E-18
LOC100642438	45.6535184	-1.638954953	0.6536324	-2.5074567	0.01216035	0.01537474
LOC100643286	1532.86095	-1.638845517	0.10729355	-15.274409	1.13E-52	3.82E-51
LOC100647432	1674.92724	-1.63608703	0.12323915	-13.275708	3.20E-40	4.30E-39
LOC100647880	582.479294	-1.633597548	0.25043292	-6.5230943	6.89E-11	1.51E-10
LOC100646062	86.057882	-1.632501578	0.19734193	-8.2724517	1.31E-16	4.10E-16
LOC100649151	569.066848	-1.63156772	0.18493819	-8.8222324	1.12E-18	3.95E-18
LOC100649520	57.6979675	-1.631162631	0.29377805	-5.5523639	2.82E-08	5.31E-08

LOC100647958	382.930495	-1.631081832	0.15001432	-10.872841	1.55E-27	9.20E-27
LOC100650057	659.223005	-1.628878736	0.12891229	-12.635558	1.34E-36	1.41E-35
LOC105665982	302.236284	-1.626662867	0.18025195	-9.0243843	1.81E-19	6.69E-19
LOC100651268	2871.0664	-1.626639422	0.14321159	-11.358295	6.74E-30	4.62E-29
LOC100646399	2635.45144	-1.626333086	0.14549798	-11.177702	5.24E-29	3.40E-28
LOC100651948	125.64909	-1.626106917	0.43004296	-3.7812662	0.00015603	0.00022949
LOC105666735	68.2793959	-1.625880243	0.25266995	-6.4347987	1.24E-10	2.67E-10
LOC100643086	3327.03398	-1.624699746	0.13289119	-12.22579	2.26E-34	2.04E-33
LOC100651261	1166.24157	-1.623993608	0.19550679	-8.3065843	9.85E-17	3.10E-16
LOC100647489	1864.29721	-1.623640656	0.1738939	-9.3369615	9.91E-21	3.93E-20
LOC100643815	116.830324	-1.623632319	0.19104924	-8.498502	1.92E-17	6.28E-17
LOC100647713	126.87025	-1.623013034	0.18064729	-8.9844308	2.60E-19	9.57E-19
LOC100652245	59.9408011	-1.621629078	0.29698271	-5.4603485	4.75E-08	8.81E-08
LOC100642500	1565.44377	-1.621431962	0.18747362	-8.6488541	5.20E-18	1.76E-17
LOC100647797	141.734334	-1.621418447	0.21401295	-7.5762631	3.56E-14	9.61E-14
LOC100644243	14078.8076	-1.620540558	0.35276533	-4.5938203	4.35E-06	7.11E-06
LOC100643606	88.50812	-1.619155247	0.25133243	-6.4422854	1.18E-10	2.54E-10
LOC100643668	53.9798621	-1.618929032	0.22398347	-7.2278951	4.91E-13	1.24E-12
LOC100645182	1835.43567	-1.618687157	0.0852834	-18.980096	2.49E-80	7.62E-78
LOC100645135	628.941461	-1.618539493	0.20948427	-7.7263055	1.11E-14	3.08E-14
LOC100648384	52.8816468	-1.617252226	0.22739607	-7.11205	1.14E-12	2.83E-12
LOC105665677	89.6379111	-1.617163181	0.26915071	-6.0083928	1.87E-09	3.81E-09
LOC100642265	266.085376	-1.616209874	0.14546231	-11.11085	1.11E-28	7.09E-28
LOC100652073	11464.9023	-1.615815118	0.15295157	-10.564227	4.37E-26	2.36E-25
LOC100645442	471.399603	-1.61543467	0.23522971	-6.8674771	6.53E-12	1.54E-11
LOC105666858	10.3967039	-1.61490312	0.50891839	-3.1732064	0.00150765	0.00205305
LOC100650130	19121.7174	-1.614591943	0.28474177	-5.6703727	1.42E-08	2.73E-08
LOC105666583	384.750793	-1.614037379	0.34277463	-4.7087422	2.49E-06	4.14E-06
LOC100645788	647.299999	-1.612274896	0.19071317	-8.4539254	2.82E-17	9.10E-17

LOC100647222	28227.9253	-1.611831917	0.19424966	-8.2977333	1.06E-16	3.33E-16
LOC100647892	41721.87	-1.610892241	0.13864224	-11.619058	3.30E-31	2.44E-30
LOC100644523	1204.76691	-1.610717268	0.13311115	-12.100544	1.05E-33	9.01E-33
LOC100651915	2472.25265	-1.61068564	0.13249626	-12.156461	5.30E-34	4.65E-33
LOC100649431	578.878819	-1.610670632	0.12605389	-12.777635	2.19E-37	2.41E-36
LOC100644825	1210.76552	-1.609974003	0.13068899	-12.319125	7.15E-35	6.68E-34
LOC100644007	720.510141	-1.609168459	0.15464121	-10.405819	2.33E-25	1.21E-24
LOC105666090	173.917676	-1.607410279	0.17642146	-9.1111947	8.15E-20	3.08E-19
LOC100644554	643.580653	-1.607229454	0.17189312	-9.3501672	8.75E-21	3.48E-20
LOC100651734	1070.6439	-1.606003791	0.157871	-10.172887	2.62E-24	1.26E-23
LOC100650033	2336.61052	-1.605959231	0.20925303	-7.6747238	1.66E-14	4.57E-14
LOC100644668	2842.08529	-1.604661228	0.18961565	-8.4627047	2.61E-17	8.48E-17
LOC100651596	464.705014	-1.603368065	0.75803243	-2.1151708	0.03441539	0.04189495
LOC100649452	59.7658776	-1.602121076	0.2716188	-5.8984174	3.67E-09	7.32E-09
LOC100643451	698.911282	-1.601623467	0.4895016	-3.2719474	0.00106809	0.00147209
LOC100642731	227.707644	-1.601317612	0.15021782	-10.659971	1.57E-26	8.69E-26
LOC105666394	4153.47191	-1.601175994	0.17006017	-9.4153501	4.72E-21	1.90E-20
LOC100645460	1095.32561	-1.601080613	0.14295714	-11.199725	4.09E-29	2.67E-28
LOC100649235	56.233392	-1.600868444	0.2933601	-5.4570081	4.84E-08	8.97E-08
LOC100649351	66.6458134	-1.600284705	0.26235449	-6.0997039	1.06E-09	2.19E-09
LOC100644606	1319.70996	-1.598410168	0.13953273	-11.45545	2.21E-30	1.56E-29
LOC100643214	3437.00887	-1.597622403	0.14966849	-10.674407	1.34E-26	7.47E-26
LOC105665717	441.970296	-1.595830459	0.14842969	-10.751424	5.84E-27	3.34E-26
LOC100650309	86.1430608	-1.595783045	0.22762556	-7.0105618	2.37E-12	5.74E-12
LOC100646283	390.130277	-1.595039469	0.16080472	-9.9191087	3.44E-23	1.54E-22
LOC100648478	18.5787737	-1.594885664	0.4278426	-3.7277392	0.00019321	0.00028259
LOC100648666	66.2362275	-1.594575112	0.4805339	-3.3183406	0.00090554	0.00125547
LOC105666353	733.32157	-1.594145495	0.12987523	-12.274439	1.24E-34	1.14E-33
LOC100648266	4491.3283	-1.594127835	0.13838681	-11.519363	1.05E-30	7.60E-30

LOC100651335	355.650182	-1.593582613	0.17200698	-9.2646394	1.96E-20	7.63E-20
LOC100645741	127.556387	-1.591731303	0.29050438	-5.4791989	4.27E-08	7.95E-08
LOC100648859	1971.31194	-1.590065043	0.11219874	-14.171862	1.37E-45	2.68E-44
LOC100648433	20.1474531	-1.589621973	0.47243575	-3.3647368	0.00076617	0.00106662
LOC100649408	343.492588	-1.589110437	0.12849977	-12.36664	3.96E-35	3.77E-34
LOC100643447	125.089405	-1.588464285	0.23936095	-6.6362716	3.22E-11	7.24E-11
LOC100643247	698.356681	-1.588130025	0.10849048	-14.638428	1.60E-48	4.02E-47
LOC100646158	11268.385	-1.588128718	0.20569529	-7.7207832	1.16E-14	3.21E-14
LOC100650182	1173.84106	-1.587960348	0.13055376	-12.163268	4.88E-34	4.30E-33
LOC100631067	117.644504	-1.587842476	0.30369633	-5.2283887	1.71E-07	3.07E-07
LOC100646201	37.4508654	-1.587083686	0.34961766	-4.5394838	5.64E-06	9.15E-06
LOC100651713	1888.12042	-1.586454002	0.29120267	-5.4479377	5.10E-08	9.43E-08
LOC100646016	2360.02282	-1.586043098	0.18830791	-8.4226047	3.68E-17	1.18E-16
LOC100647826	841.490236	-1.585522189	0.14769331	-10.735233	6.95E-27	3.96E-26
LOC100643950	881.470576	-1.585487486	0.17197005	-9.2195559	2.98E-20	1.15E-19
LOC100644301	37.2020673	-1.585348243	0.3973459	-3.9898442	6.61E-05	0.00010008
LOC100646233	1337.36716	-1.584475307	0.18302785	-8.6570173	4.84E-18	1.64E-17
LOC100645409	193.337861	-1.584330983	0.23846393	-6.6439021	3.05E-11	6.89E-11
LOC105666039	213.561999	-1.584283159	0.38758699	-4.087555	4.36E-05	6.68E-05
LOC100642474	265.233517	-1.584020954	0.20118789	-7.8733414	3.45E-15	9.92E-15
LOC100643078	126.438536	-1.583991569	0.19524631	-8.112786	4.95E-16	1.49E-15
LOC100645224	1811.58062	-1.583942422	0.11228112	-14.106934	3.44E-45	6.57E-44
LOC100647287	1724.51094	-1.583373665	0.17921257	-8.8351706	9.99E-19	3.54E-18
LOC100648216	2215.82004	-1.583271636	0.20150778	-7.8571243	3.93E-15	1.12E-14
LOC100647598	160.264973	-1.583173544	0.19743568	-8.0186801	1.07E-15	3.16E-15
LOC100643720	508.845478	-1.579353118	0.16151265	-9.7785102	1.39E-22	6.05E-22
LOC100651054	127.736325	-1.579309688	0.35231487	-4.4826654	7.37E-06	1.19E-05
LOC100643972	3857.8822	-1.578389596	0.15786697	-9.9982256	1.55E-23	7.11E-23
LOC100642734	130.5881	-1.577364198	0.24031445	-6.5637509	5.25E-11	1.16E-10

LOC100644694	26525.258	-1.577259946	0.37222406	-4.2373939	2.26E-05	3.53E-05
LOC100643133	181.377987	-1.576639171	0.36399228	-4.3315182	1.48E-05	2.34E-05
LOC100643349	19686.8432	-1.57470689	0.31829079	-4.9473844	7.52E-07	1.30E-06
LOC100642595	528.345825	-1.574316166	0.24003966	-6.5585669	5.43E-11	1.20E-10
LOC100647003	435.413511	-1.572829632	0.14691021	-10.706061	9.53E-27	5.37E-26
LOC100645456	670.667985	-1.57253284	0.25714344	-6.1153915	9.63E-10	1.99E-09
LOC100648940	717.546055	-1.572477627	0.21550754	-7.2966246	2.95E-13	7.56E-13
LOC100651082	29.5290228	-1.570418901	0.56632495	-2.7729997	0.00555422	0.007221
LOC100647858	44.8854256	-1.570055577	0.29723547	-5.2821945	1.28E-07	2.30E-07
LOC100646384	11.210257	-1.569261758	0.52974685	-2.9622861	0.00305364	0.00406723
LOC100648776	3162.0857	-1.569049066	0.12932367	-12.132729	7.08E-34	6.17E-33
LOC100649904	4005.25838	-1.568268094	0.09008148	-17.40944	7.00E-68	8.06E-66
LOC100651198	11127.7795	-1.567935396	0.16014916	-9.7904694	1.24E-22	5.39E-22
LOC100644982	3265.84822	-1.567265808	0.26897194	-5.8268747	5.65E-09	1.11E-08
LOC100651254	830.096609	-1.565854104	0.22245316	-7.0390282	1.94E-12	4.72E-12
LOC100651423	898.181729	-1.565717168	0.11635195	-13.456734	2.81E-41	4.06E-40
LOC100649369	2508.81909	-1.565109202	0.19570572	-7.9972583	1.27E-15	3.74E-15
LOC100647510	354.99773	-1.564193137	0.13504049	-11.583142	5.02E-31	3.67E-30
LOC105665896	11.1174622	-1.564182756	0.57164543	-2.7362814	0.00621379	0.008039
LOC100644772	681.610285	-1.562755066	0.35118113	-4.4499972	8.59E-06	1.38E-05
LOC100649760	2247.42653	-1.562644962	0.21070901	-7.4161278	1.21E-13	3.16E-13
LOC100643641	155.045052	-1.562005967	0.21079926	-7.4099215	1.26E-13	3.30E-13
LOC100651447	506.040669	-1.561854828	0.15410423	-10.135055	3.86E-24	1.83E-23
LOC100643526	5497.28293	-1.561711098	0.10587966	-14.749869	3.08E-49	8.01E-48
LOC100644503	2189.59749	-1.561678914	0.21900142	-7.1309077	9.97E-13	2.47E-12
LOC100643644	20.1419058	-1.561575114	0.51068629	-3.0577972	0.0022297	0.00300124
LOC100645075	254.895646	-1.560831192	0.17525064	-8.9062798	5.28E-19	1.91E-18
LOC100648256	716.731318	-1.559860168	0.19425256	-8.0300623	9.74E-16	2.89E-15
LOC105666555	2937.65148	-1.558426429	0.23568573	-6.612307	3.78E-11	8.48E-11

LOC100651121	70.3631078	-1.558373767	0.26508306	-5.8788131	4.13E-09	8.22E-09
LOC100649022	307.828125	-1.556753327	0.43319024	-3.5936944	0.00032602	0.00046846
LOC100645154	723.225497	-1.556705111	0.1305118	-11.927697	8.49E-33	6.86E-32
LOC100648603	1431.09744	-1.55594212	0.13927894	-11.17141	5.63E-29	3.65E-28
LOC100646028	7910.53436	-1.554850262	0.156596	-9.929055	3.11E-23	1.40E-22
LOC105665951	556.947811	-1.554783478	0.11138259	-13.958945	2.78E-44	4.92E-43
LOC100643942	2117.56836	-1.553258311	0.12695146	-12.235056	2.02E-34	1.83E-33
LOC100644742	215.879783	-1.553170076	0.36846601	-4.215233	2.50E-05	3.89E-05
LOC105666387	52.4166764	-1.552160691	0.3897518	-3.9824337	6.82E-05	0.00010318
LOC100650827	307.798611	-1.551164748	0.14774926	-10.49863	8.76E-26	4.64E-25
LOC100650549	286.347299	-1.551163859	0.41876256	-3.7041608	0.00021209	0.00030915
LOC100647046	609.777919	-1.550105323	0.10623359	-14.59148	3.18E-48	7.77E-47
LOC100648818	196.437843	-1.549692626	0.2461014	-6.296968	3.04E-10	6.43E-10
LOC100651337	3270.45447	-1.549111546	0.16729992	-9.2594874	2.05E-20	8.00E-20
LOC100650682	34.2423833	-1.54908206	0.3333341	-4.6472354	3.36E-06	5.54E-06
LOC100652321	150.301567	-1.547800557	0.22529145	-6.8702143	6.41E-12	1.52E-11
LOC100651972	19.9017533	-1.546978742	0.39790009	-3.8878572	0.00010113	0.00015083
LOC100648997	780.710509	-1.545994701	0.17996399	-8.5905782	8.65E-18	2.89E-17
LOC100648400	1031.2718	-1.545404406	0.14307354	-10.801469	3.39E-27	1.97E-26
LOC105666996	900.805492	-1.544588121	0.13178953	-11.720113	1.01E-31	7.65E-31
LOC100644782	117.177169	-1.543962254	0.23674616	-6.5215937	6.96E-11	1.53E-10
LOC100647505	116.56171	-1.54344164	0.40655506	-3.7963902	0.00014682	0.00021636
LOC100645084	421.924162	-1.543273302	0.12265964	-12.581753	2.66E-36	2.72E-35
LOC100642775	13.2337014	-1.542719514	0.47710533	-3.2334988	0.00122284	0.0016771
LOC100644999	787.240383	-1.542477979	0.20931236	-7.3692636	1.72E-13	4.45E-13
LOC100645472	520.312153	-1.541955913	0.13601431	-11.336718	8.63E-30	5.85E-29
LOC100643824	825.340633	-1.541384956	0.1254222	-12.289571	1.03E-34	9.54E-34
LOC105665891	18.2055948	-1.540886013	0.31557875	-4.8827306	1.05E-06	1.79E-06
LOC100650366	1064.83768	-1.540522439	0.14818445	-10.395979	2.59E-25	1.33E-24

LOC100643100	95.7356152	-1.539740784	0.16229985	-9.4870127	2.38E-21	9.73E-21
LOC105666120	19454.7104	-1.539661326	0.09626981	-15.99319	1.43E-57	6.98E-56
LOC105667111	682.403701	-1.538611914	0.10793121	-14.255487	4.14E-46	8.42E-45
LOC100649636	379.590641	-1.538264738	0.12857099	-11.964322	5.46E-33	4.46E-32
LOC100644834	124.284184	-1.53704359	0.33351585	-4.6086073	4.05E-06	6.63E-06
LOC100647740	155.660302	-1.53548539	0.22088925	-6.9513811	3.62E-12	8.67E-12
LOC100647319	15.7791381	-1.535346663	0.49646581	-3.0925526	0.00198443	0.00268142
LOC100646355	216.982245	-1.534659006	0.17532804	-8.7530722	2.08E-18	7.20E-18
LOC100651354	52.3717225	-1.534455289	0.24425713	-6.282131	3.34E-10	7.06E-10
LOC100642657	13.7523187	-1.53366944	0.47601265	-3.221909	0.0012734	0.00174424
LOC100650918	875.888562	-1.533553812	0.12410332	-12.357074	4.46E-35	4.22E-34
LOC100647621	327.240014	-1.532986456	0.26629911	-5.7566337	8.58E-09	1.67E-08
LOC100645859	476.969119	-1.532224392	0.21569007	-7.1038243	1.21E-12	2.99E-12
LOC100650580	53.9579142	-1.53132497	0.30563109	-5.0103703	5.43E-07	9.47E-07
LOC100642344	797.679526	-1.529528883	0.17600958	-8.6900319	3.62E-18	1.24E-17
LOC100646629	225.934569	-1.528583307	0.13675155	-11.177813	5.24E-29	3.40E-28
LOC100651727	79.3360982	-1.528077264	0.23365428	-6.5399069	6.16E-11	1.36E-10
LOC100645105	770.986938	-1.527864084	0.40801571	-3.7446207	0.00018067	0.00026481
LOC100649390	191.298673	-1.526688846	0.15221014	-10.030139	1.12E-23	5.20E-23
LOC100647481	1230.25223	-1.526568699	0.24150109	-6.3211669	2.60E-10	5.52E-10
LOC100644032	6937.8175	-1.526381758	0.13633991	-11.195414	4.29E-29	2.80E-28
LOC100642958	1115.61386	-1.52601744	0.17270103	-8.8361806	9.90E-19	3.51E-18
LOC100647235	66.3505916	-1.525727836	0.38149132	-3.9993776	6.35E-05	9.63E-05
LOC100645056	134.49433	-1.525727046	0.3407752	-4.4772244	7.56E-06	1.22E-05
LOC100644917	355.95901	-1.525722145	0.16223816	-9.4042123	5.24E-21	2.11E-20
LOC100648563	200.660084	-1.524822899	0.22667374	-6.7269498	1.73E-11	3.97E-11
LOC100646387	55.7924936	-1.524713447	0.29030906	-5.2520353	1.50E-07	2.71E-07
LOC100650481	2495.45369	-1.522199698	0.15290894	-9.9549428	2.40E-23	1.09E-22
LOC100642764	381.531445	-1.521927362	0.18049532	-8.431949	3.40E-17	1.10E-16

LOC100647545	426.194033	-1.521175671	0.18618048	-8.1704358	3.07E-16	9.37E-16
LOC100644626	584.262987	-1.520924074	0.11550544	-13.167553	1.35E-39	1.74E-38
LOC105666181	23.6074649	-1.520911819	0.43420998	-3.5027104	0.00046055	0.00065446
LOC100643960	451.948961	-1.520906309	0.156829	-9.6978638	3.08E-22	1.31E-21
LOC100645954	890.734644	-1.520731054	0.12620347	-12.049835	1.94E-33	1.63E-32
LOC100648534	373.181531	-1.520425253	0.17989471	-8.4517507	2.87E-17	9.27E-17
LOC100650588	152.066234	-1.520423877	0.24506748	-6.2041029	5.50E-10	1.15E-09
LOC100648006	190.408525	-1.51995517	0.26695938	-5.6935822	1.24E-08	2.40E-08
LOC100644868	16.6271981	-1.519526477	0.51806969	-2.9330542	0.00335645	0.00444816
LOC100645890	364.678196	-1.51916165	0.14502821	-10.474939	1.13E-25	5.92E-25
LOC105667186	181.817303	-1.519129861	0.14834377	-10.240605	1.30E-24	6.41E-24
LOC100647870	2127.44839	-1.51902896	0.16961521	-8.9557356	3.37E-19	1.23E-18
LOC100643853	64.5603531	-1.518111581	0.32587214	-4.6586111	3.18E-06	5.25E-06
LOC105666359	126.682188	-1.517343743	0.23071065	-6.5768259	4.81E-11	1.07E-10
LOC105666703	75.5053005	-1.517252683	0.18256912	-8.3105659	9.52E-17	3.00E-16
LOC100651866	806.540972	-1.516856866	0.16663824	-9.1026938	8.81E-20	3.32E-19
LOC100651901	599.316249	-1.51613825	0.21716756	-6.9814214	2.92E-12	7.04E-12
LOC100643252	788.975928	-1.515176337	0.09783747	-15.486666	4.27E-54	1.56E-52
LOC100644812	279.457398	-1.514596416	0.25446872	-5.9519945	2.65E-09	5.33E-09
LOC100651828	5014.21774	-1.514398621	0.10156928	-14.910007	2.84E-50	7.80E-49
LOC100642826	3942.68343	-1.514393015	0.12063232	-12.553792	3.79E-36	3.82E-35
LOC105666503	67.6183911	-1.514079434	0.20612103	-7.3455843	2.05E-13	5.29E-13
LOC100650183	587.655382	-1.513895078	0.26113613	-5.7973406	6.74E-09	1.32E-08
LOC100651489	762.360056	-1.513415115	0.11386109	-13.291767	2.58E-40	3.48E-39
LOC105665950	7540.91692	-1.513108892	0.17216138	-8.7888987	1.51E-18	5.28E-18
LOC105665687	65.1240824	-1.511986907	0.20414699	-7.406364	1.30E-13	3.39E-13
LOC100647321	1384.88216	-1.511232272	0.17002545	-8.8882711	6.21E-19	2.22E-18
LOC100647116	633.397224	-1.511074806	0.168058	-8.9913889	2.44E-19	9.00E-19
LOC100649163	113.275438	-1.510787225	0.21762968	-6.9420092	3.87E-12	9.25E-12

LOC100651091	21.6360599	-1.509054345	0.59628586	-2.5307565	0.01138168	0.01443872
LOC100648107	35.9844231	-1.508899551	0.4220199	-3.5754227	0.00034966	0.00050125
LOC100647174	1121.07471	-1.508728838	0.10194259	-14.799789	1.47E-49	3.91E-48
LOC100651887	8802.89987	-1.50801197	0.12496846	-12.067141	1.58E-33	1.33E-32
LOC100645683	4858.17171	-1.507745005	0.17081113	-8.8269719	1.08E-18	3.79E-18
LOC105666543	384.820983	-1.507370861	0.13216228	-11.405454	3.93E-30	2.74E-29
LOC100643607	1592.59853	-1.506203064	0.15678513	-9.6067978	7.48E-22	3.14E-21
LOC105666936	39.3015038	-1.505399639	0.29783629	-5.0544534	4.32E-07	7.56E-07
LOC105665661	5213.19649	-1.505101433	0.16508473	-9.1171451	7.71E-20	2.92E-19
LOC105666654	16.3534443	-1.50505182	0.53441573	-2.8162566	0.00485868	0.00633694
LOC100646926	2650.5522	-1.504547741	0.14748009	-10.201701	1.95E-24	9.45E-24
LOC100645262	338.75521	-1.504493633	0.19965126	-7.5356081	4.86E-14	1.31E-13
LOC100646496	547.256847	-1.503807248	0.11905036	-12.63169	1.41E-36	1.47E-35
LOC100650710	40.276282	-1.499155736	0.28029201	-5.3485496	8.87E-08	1.62E-07
LOC100645856	704.097584	-1.498864508	0.08997536	-16.658611	2.62E-62	1.89E-60
LOC100651350	356.936954	-1.498250335	0.298375	-5.0213669	5.13E-07	8.95E-07
LOC100649502	720.196893	-1.49790814	0.12302668	-12.175474	4.20E-34	3.74E-33
LOC100648894	439.04631	-1.497640321	0.32307342	-4.6356037	3.56E-06	5.84E-06
LOC100644143	1238.20958	-1.495964751	0.15998909	-9.3504174	8.73E-21	3.47E-20
LOC100652162	1486.74837	-1.4953944	0.17033109	-8.7793392	1.64E-18	5.74E-18
LOC100646039	1249.06138	-1.494672565	0.21131551	-7.0731797	1.51E-12	3.71E-12
LOC100645780	11635.7512	-1.494622206	0.1095603	-13.642006	2.25E-42	3.52E-41
LOC100648724	389.441877	-1.493148341	0.1087361	-13.731854	6.54E-43	1.07E-41
LOC105667189	17.5591662	-1.492676471	0.52122963	-2.8637598	0.00418645	0.00550195
LOC100642719	2183.7253	-1.491966868	0.14921028	-9.999089	1.54E-23	7.05E-23
LOC100649421	837.975294	-1.491768098	0.1572689	-9.4854617	2.41E-21	9.87E-21
LOC100649407	2911.11826	-1.491113295	0.14226145	-10.481499	1.05E-25	5.54E-25
LOC105666238	49.5100082	-1.491032371	0.43359301	-3.4387832	0.00058433	0.00082095
LOC100643348	7375.92257	-1.489969544	0.13371185	-11.143137	7.73E-29	4.98E-28

LOC100648070	80.726057	-1.489605083	0.2652524	-5.6158024	1.96E-08	3.72E-08
LOC100643364	708.912875	-1.48864113	0.14850355	-10.024279	1.19E-23	5.51E-23
LOC100644800	4342.26897	-1.488623168	0.09097751	-16.36254	3.54E-60	2.13E-58
LOC100647320	87.8214732	-1.488309355	0.21842675	-6.8137686	9.51E-12	2.22E-11
LOC100647623	393.964023	-1.487869588	0.18420789	-8.077122	6.63E-16	1.99E-15
LOC100645131	594.759177	-1.487544571	0.13492593	-11.024898	2.90E-28	1.80E-27
LOC100645263	8225.25073	-1.487159399	0.1341992	-11.081731	1.54E-28	9.69E-28
LOC100644819	491.25779	-1.486849601	0.14577754	-10.199442	1.99E-24	9.66E-24
LOC100643623	298.504941	-1.486540129	0.19479386	-7.6313501	2.32E-14	6.34E-14
LOC100651917	211.253008	-1.486479176	0.33679109	-4.4136535	1.02E-05	1.62E-05
LOC100647223	850.712636	-1.486385098	0.14952209	-9.9409065	2.76E-23	1.25E-22
LOC100648282	1027.88444	-1.485894687	0.17910868	-8.2960509	1.08E-16	3.38E-16
LOC100643394	463.823542	-1.484634712	0.13902768	-10.678699	1.28E-26	7.14E-26
LOC100642767	1291.44907	-1.483971534	0.13622534	-10.893506	1.24E-27	7.36E-27
LOC100645883	1010.18162	-1.483540654	0.11642009	-12.742995	3.41E-37	3.69E-36
LOC105666240	201.4116	-1.482961588	0.20037463	-7.4009448	1.35E-13	3.53E-13
LOC105666534	31.4115211	-1.482915393	0.30588328	-4.847978	1.25E-06	2.12E-06
LOC100647153	248.026863	-1.482670778	0.10822928	-13.69935	1.02E-42	1.65E-41
LOC100647288	3527.19143	-1.482470939	0.14645305	-10.1225	4.39E-24	2.08E-23
LOC105666660	68.8434413	-1.481269552	0.22093561	-6.7045307	2.02E-11	4.61E-11
LOC105666345	387.751761	-1.48089584	0.25948845	-5.7069817	1.15E-08	2.22E-08
LOC105666575	34.1071914	-1.480084189	0.19972635	-7.4105603	1.26E-13	3.29E-13
LOC100651978	21.561637	-1.479968899	0.29220342	-5.0648582	4.09E-07	7.17E-07
LOC100650372	4146.15816	-1.479210778	0.28640278	-5.164792	2.41E-07	4.28E-07
LOC100645027	537.419251	-1.478210044	0.13308166	-11.107541	1.15E-28	7.31E-28
LOC100647012	1179.78032	-1.477346029	0.09753855	-15.146278	8.02E-52	2.54E-50
LOC100650310	153.483107	-1.477199156	0.14727563	-10.030167	1.12E-23	5.20E-23
LOC105666371	21.9695202	-1.476741272	0.39608415	-3.7283523	0.00019274	0.00028195
LOC100644147	30.8182156	-1.474107806	0.30273084	-4.8693679	1.12E-06	1.91E-06

LOC100649848	302.111357	-1.472850865	0.10954073	-13.445692	3.26E-41	4.68E-40
LOC100651102	1573.27138	-1.472305158	0.10090511	-14.590987	3.21E-48	7.81E-47
LOC100646420	507.609053	-1.471305571	0.18790693	-7.8299695	4.88E-15	1.39E-14
LOC100642669	2107.91627	-1.470749223	0.13835187	-10.630498	2.15E-26	1.18E-25
LOC100647555	1852.80711	-1.470334157	0.12657229	-11.616556	3.40E-31	2.51E-30
LOC100648472	169.259095	-1.470099351	0.25756448	-5.7076944	1.15E-08	2.21E-08
LOC100648204	4242.76944	-1.469518893	0.1232122	-11.926732	8.59E-33	6.93E-32
LOC100642947	11.3639611	-1.468291724	0.4523947	-3.2455988	0.00117204	0.00160991
LOC100651820	596.860703	-1.467538775	0.10677448	-13.744284	5.51E-43	9.08E-42
LOC100648002	5859.3299	-1.467530635	0.39033637	-3.7596564	0.00017015	0.00024984
LOC100648639	1159.19604	-1.466905423	0.1141422	-12.851561	8.43E-38	9.57E-37
LOC100648547	1208.27205	-1.46689407	0.19046554	-7.7016245	1.34E-14	3.72E-14
LOC100643891	278.918059	-1.466633767	0.18854651	-7.7786314	7.33E-15	2.06E-14
LOC100645034	104.798819	-1.466480187	0.353628	-4.1469572	3.37E-05	5.21E-05
LOC100649697	834.26565	-1.46574347	0.10704536	-13.692732	1.12E-42	1.80E-41
LOC100643649	1085.23241	-1.464090765	0.09385324	-15.59979	7.30E-55	2.78E-53
LOC100650927	3852.53909	-1.463808072	0.27201949	-5.3812616	7.40E-08	1.36E-07
LOC100643130	2370.54756	-1.463586184	0.09796745	-14.939514	1.82E-50	5.11E-49
LOC100648848	413.374534	-1.462273286	0.12418704	-11.774765	5.27E-32	4.06E-31
LOC100645043	29.9700325	-1.462212589	0.26740188	-5.468221	4.55E-08	8.44E-08
LOC105666167	46.2736208	-1.46073219	0.29562247	-4.9412083	7.76E-07	1.34E-06
LOC100643713	1266.87341	-1.460268054	0.14336137	-10.185925	2.29E-24	1.11E-23
LOC100642924	397.038006	-1.460183533	0.16106987	-9.0655289	1.24E-19	4.64E-19
LOC105665958	39.1791704	-1.46007585	0.36136829	-4.0404094	5.34E-05	8.14E-05
LOC100644403	772.566943	-1.460047127	0.19869461	-7.348197	2.01E-13	5.19E-13
LOC100642336	1612.42298	-1.460045744	0.2119654	-6.8881325	5.65E-12	1.34E-11
LOC100652268	24.3300784	-1.457643493	0.44284001	-3.2915804	0.00099626	0.0013756
LOC100646287	178.165876	-1.457569051	0.12173018	-11.973769	4.88E-33	3.99E-32
LOC100644990	102.02247	-1.456517051	0.17834957	-8.1666416	3.17E-16	9.66E-16

LOC105666757	16.7982427	-1.456304872	0.3982119	-3.6571104	0.00025507	0.00036933
LOC100644744	3662.98467	-1.455548822	0.14681098	-9.9144414	3.60E-23	1.61E-22
LOC100628631	2407.93504	-1.452362746	0.09316079	-15.58985	8.53E-55	3.23E-53
LOC100647940	343.599668	-1.452165687	0.41563859	-3.4938182	0.00047617	0.00067587
LOC100646327	1384.05012	-1.451636761	0.17464122	-8.3121084	9.40E-17	2.96E-16
LOC100650923	176.839631	-1.45129212	0.18774253	-7.7302256	1.07E-14	2.99E-14
LOC100649123	4006.80502	-1.451039959	0.16243738	-8.9329192	4.15E-19	1.51E-18
LOC100643745	6254.26401	-1.448317933	0.11352273	-12.757955	2.81E-37	3.08E-36
LOC105665900	33.0890146	-1.447824028	0.70129228	-2.0645087	0.03896951	0.04720991
LOC100647201	34.2846661	-1.445166033	0.35412536	-4.0809448	4.49E-05	6.87E-05
LOC100644998	60.0917743	-1.445103838	0.23624625	-6.1169386	9.54E-10	1.97E-09
LOC100651593	1242.63589	-1.445035987	0.08719657	-16.572165	1.11E-61	7.48E-60
LOC100643739	289.725907	-1.444615389	0.13467645	-10.726563	7.64E-27	4.33E-26
LOC100643293	453.164145	-1.444250662	0.14409229	-10.023094	1.21E-23	5.58E-23
LOC100649617	1655.19032	-1.443802002	0.19601469	-7.3657847	1.76E-13	4.57E-13
LOC100642221	759.567283	-1.443493834	0.11522052	-12.528097	5.24E-36	5.23E-35
LOC105666153	1604.83256	-1.442856023	0.1316939	-10.956134	6.21E-28	3.77E-27
LOC105666239	403.801315	-1.442016608	0.14096145	-10.229865	1.46E-24	7.14E-24
LOC100651229	1990.58184	-1.441158674	0.15656069	-9.2051122	3.41E-20	1.31E-19
LOC100649268	1286.60656	-1.440293666	0.13001211	-11.07815	1.60E-28	1.01E-27
LOC100649033	1071.99982	-1.439180439	0.18572042	-7.7491773	9.25E-15	2.59E-14
LOC105666640	254.950893	-1.438834955	0.18728689	-7.6825181	1.56E-14	4.31E-14
LOC100645389	849.979647	-1.438770898	0.15863257	-9.0698328	1.19E-19	4.46E-19
LOC100647053	252.156376	-1.438578951	0.15799367	-9.105295	8.60E-20	3.24E-19
LOC100650271	1163.38164	-1.438323574	0.11329955	-12.694874	6.31E-37	6.71E-36
Trnaa-cgc	12.7968056	-1.438036553	0.41620797	-3.4550913	0.00055011	0.00077576
LOC100642339	4691.45815	-1.437330953	0.1257006	-11.434559	2.81E-30	1.97E-29
LOC100651809	1141.77374	-1.43722543	0.16204948	-8.8690533	7.38E-19	2.63E-18
LOC100650370	132.162918	-1.436993235	0.29693848	-4.8393635	1.30E-06	2.21E-06

LOC105666208	39.47174	-1.436205481	0.2275735	-6.3109522	2.77E-10	5.89E-10
LOC100644608	57.4708821	-1.434529096	0.28200485	-5.0868951	3.64E-07	6.41E-07
LOC100647827	1294.94201	-1.43416547	0.13159741	-10.898128	1.18E-27	7.01E-27
LOC105666071	20.9889383	-1.431546486	0.54391976	-2.6319075	0.0084907	0.01088406
LOC100645159	923.94235	-1.431436444	0.12449555	-11.497893	1.35E-30	9.69E-30
LOC100642995	2348.33545	-1.430960705	0.12944043	-11.054975	2.07E-28	1.30E-27
LOC100647907	288.377327	-1.427420611	0.14135369	-10.09822	5.63E-24	2.65E-23
LOC100648628	291.873287	-1.427089206	0.18885516	-7.5565277	4.14E-14	1.12E-13
LOC100645016	2669.67391	-1.426123786	0.1909746	-7.4676098	8.17E-14	2.17E-13
LOC100648617	85.4694231	-1.424841537	0.21181938	-6.7266817	1.74E-11	3.98E-11
LOC100646087	646.490807	-1.424477785	0.11024867	-12.920589	3.44E-38	4.01E-37
LOC100643952	223.55576	-1.424373169	0.12578414	-11.323949	9.99E-30	6.75E-29
LOC100649691	1443.46469	-1.423436389	0.10960527	-12.986934	1.45E-38	1.73E-37
LOC105665637	62.5916985	-1.423195461	0.25275924	-5.6306366	1.80E-08	3.42E-08
LOC100648205	24.5847539	-1.422135827	0.32187436	-4.4182949	9.95E-06	1.59E-05
LOC100646612	657.777022	-1.421953222	0.13987045	-10.166216	2.81E-24	1.34E-23
LOC100643650	30281.9617	-1.421732493	0.1651419	-8.6091569	7.36E-18	2.47E-17
LOC100645687	1594.33608	-1.420677312	0.16238395	-8.7488778	2.15E-18	7.46E-18
LOC100652007	817.309984	-1.419996649	0.10489141	-13.537778	9.36E-42	1.41E-40
LOC100651167	518.637417	-1.419146149	0.26096246	-5.4381238	5.38E-08	9.95E-08
LOC105665952	472.369136	-1.419069133	0.16668179	-8.5136425	1.69E-17	5.54E-17
LOC105665907	19.9329991	-1.418914378	0.40172696	-3.5320367	0.00041237	0.00058788
LOC100649982	827.09978	-1.418899996	0.10638705	-13.337149	1.41E-40	1.95E-39
LOC105666424	155.268894	-1.418862159	0.22760989	-6.2337455	4.55E-10	9.55E-10
LOC100643113	62.2133946	-1.418071921	0.21186938	-6.6931423	2.18E-11	4.98E-11
LOC100650525	3819.30855	-1.417749524	0.09943417	-14.258173	3.99E-46	8.13E-45
LOC100647918	8549.18066	-1.41650513	0.1652767	-8.5705073	1.03E-17	3.43E-17
LOC105666524	101.251006	-1.416426398	0.51502843	-2.7501907	0.00595606	0.00771809
LOC100645775	139.960926	-1.41611259	0.24000309	-5.9003933	3.63E-09	7.24E-09

LOC100649321	108.939425	-1.415846596	0.24353563	-5.8137145	6.11E-09	1.20E-08
LOC100649687	178.423477	-1.415694034	0.15975529	-8.8616409	7.88E-19	2.81E-18
LOC100643126	2050.12373	-1.415323063	0.12371144	-11.440519	2.62E-30	1.84E-29
LOC100643300	379.637594	-1.414396753	0.17968353	-7.8715994	3.50E-15	1.01E-14
LOC100649678	8762.53549	-1.413917091	0.13800462	-10.245433	1.24E-24	6.10E-24
LOC100648195	1786.02729	-1.41272691	0.19280002	-7.327421	2.35E-13	6.04E-13
LOC105665853	14.5493518	-1.412530416	0.5480175	-2.5775279	0.00995098	0.0127044
LOC100642579	1612.08973	-1.412527729	0.21158794	-6.6758423	2.46E-11	5.58E-11
LOC100647817	3464.51317	-1.412513515	0.13290842	-10.62772	2.21E-26	1.22E-25
LOC105665679	141.311771	-1.410276031	0.15387008	-9.1653686	4.94E-20	1.89E-19
LOC100651320	563.957302	-1.410005724	0.14642834	-9.6293228	6.01E-22	2.53E-21
LOC100642653	906.07549	-1.409944004	0.22620965	-6.2329082	4.58E-10	9.60E-10
LOC100648124	1669.91617	-1.409614245	0.1479	-9.5308603	1.56E-21	6.44E-21
LOC100649621	2902.12682	-1.409550918	0.16821976	-8.379223	5.33E-17	1.70E-16
LOC100643392	39.1405228	-1.408709208	0.32214376	-4.372921	1.23E-05	1.95E-05
LOC100647780	582.621097	-1.407656207	0.36708805	-3.8346554	0.00012574	0.00018625
LOC100645299	118.075595	-1.406977324	0.23368337	-6.0208706	1.73E-09	3.53E-09
LOC100646463	1988.6922	-1.406174512	0.16032073	-8.7710088	1.77E-18	6.16E-18
LOC100644723	1080.42736	-1.406120617	0.14444234	-9.7348232	2.14E-22	9.22E-22
LOC100645021	355.418995	-1.405383871	0.16086083	-8.7366445	2.40E-18	8.28E-18
LOC100643910	365.273314	-1.404326888	0.22291147	-6.2999311	2.98E-10	6.31E-10
LOC100642318	716.351666	-1.403674501	0.18743871	-7.488712	6.96E-14	1.85E-13
LOC105666374	18.1301049	-1.403093637	0.31150692	-4.5042134	6.66E-06	1.08E-05
LOC100648833	6795.61261	-1.403021109	0.13174311	-10.649674	1.75E-26	9.70E-26
LOC100648892	5605.01055	-1.402620174	0.16279835	-8.6156905	6.95E-18	2.34E-17
LOC100642272	13762.5259	-1.402071031	0.20012854	-7.0058525	2.45E-12	5.93E-12
LOC100650808	1234.44836	-1.400770407	0.13171494	-10.634863	2.05E-26	1.13E-25
LOC100644228	2877.17299	-1.400463692	0.11855603	-11.812674	3.36E-32	2.62E-31
LOC105666447	12.9565673	-1.400251936	0.40413118	-3.4648451	0.00053054	0.00074935

LOC100651131	918.568132	-1.399678885	0.08324518	-16.813932	1.93E-63	1.54E-61
LOC100644396	971.456625	-1.399633036	0.15956078	-8.7717859	1.76E-18	6.13E-18
LOC100649384	1228.8835	-1.399574992	0.13447169	-10.407953	2.28E-25	1.18E-24
LOC100648071	36.2524467	-1.398976744	0.24088755	-5.8075925	6.34E-09	1.25E-08
LOC105665882	14.3064134	-1.398627409	0.4710453	-2.9691994	0.00298577	0.00398008
LOC100650349	116.833685	-1.397154215	0.22500882	-6.2093308	5.32E-10	1.11E-09
LOC100645107	6683.64524	-1.39713063	0.10744899	-13.002734	1.18E-38	1.41E-37
LOC100649983	115.386788	-1.396855993	0.28010188	-4.9869568	6.13E-07	1.07E-06
LOC100643561	127.562275	-1.396325889	0.20556745	-6.7925436	1.10E-11	2.56E-11
LOC100645376	2628.20907	-1.395203559	0.24741081	-5.6392184	1.71E-08	3.26E-08
LOC100647354	856.636065	-1.394781803	0.20679364	-6.7448002	1.53E-11	3.53E-11
LOC100643129	45.0247087	-1.394449387	0.4591511	-3.0370163	0.00238933	0.00320948
LOC100650230	26729.1031	-1.394409192	0.1236275	-11.279118	1.66E-29	1.11E-28
LOC100642559	81.0163597	-1.393396209	0.25748595	-5.4115428	6.25E-08	1.15E-07
LOC100648781	24.0724412	-1.393317398	0.55140672	-2.5268415	0.01150934	0.01459311
LOC100645497	392.662311	-1.392527103	0.13286596	-10.480691	1.06E-25	5.58E-25
LOC100649579	2066.05911	-1.392255862	0.23958737	-5.8110571	6.21E-09	1.22E-08
LOC100645697	1713.03024	-1.392173553	0.09030388	-15.416542	1.27E-53	4.45E-52
LOC100646646	890.259618	-1.391848954	0.13994823	-9.9454557	2.64E-23	1.19E-22
LOC100643729	3749.64145	-1.390956394	0.10139016	-13.71885	7.83E-43	1.28E-41
LOC105665868	12.5440462	-1.390569828	0.64902906	-2.1425386	0.03215016	0.03923498
LOC100643587	171.268971	-1.389387057	0.26695038	-5.2046641	1.94E-07	3.47E-07
LOC100649778	1763.13755	-1.38843449	0.07802241	-17.79533	7.68E-71	1.14E-68
LOC100645425	10.6543174	-1.387289392	0.52411042	-2.6469411	0.00812235	0.01042843
LOC100648010	340.614278	-1.386371995	0.16494482	-8.4050655	4.28E-17	1.37E-16
LOC100648183	133.311007	-1.385572251	0.24857585	-5.5740421	2.49E-08	4.71E-08
LOC100646417	489.130086	-1.384096057	0.19261493	-7.1858192	6.68E-13	1.68E-12
LOC100645545	39.9058509	-1.382889715	0.2498858	-5.5340869	3.13E-08	5.87E-08
LOC100647847	9559.33491	-1.382733678	0.11414599	-12.11373	8.93E-34	7.70E-33

LOC100643722	68.0137647	-1.381210117	0.28766033	-4.8015314	1.57E-06	2.65E-06
LOC100644920	2780.31687	-1.381169251	0.09408126	-14.680599	8.58E-49	2.18E-47
LOC100649960	260.655402	-1.379350825	0.22973291	-6.0041498	1.92E-09	3.90E-09
LOC100648752	5045.54516	-1.378900863	0.1384786	-9.9575018	2.34E-23	1.06E-22
LOC105666021	415.57193	-1.377806374	0.19112833	-7.2088026	5.64E-13	1.42E-12
LOC100646787	179.46905	-1.377660558	0.42647654	-3.2303314	0.00123647	0.00169508
LOC100650600	3203.4117	-1.37666143	0.24176031	-5.6943235	1.24E-08	2.39E-08
LOC100651459	360.601951	-1.376183887	0.16042481	-8.5783733	9.62E-18	3.21E-17
LOC105666052	102.97703	-1.374223002	0.15232777	-9.021487	1.86E-19	6.86E-19
LOC100651391	1155.09903	-1.372951615	0.09515035	-14.429287	3.39E-47	7.48E-46
LOC100647671	2325.30702	-1.372873249	0.12898153	-10.643952	1.86E-26	1.03E-25
LOC100642647	519.636305	-1.372839355	0.11668495	-11.76535	5.89E-32	4.53E-31
LOC100648128	1385.76333	-1.372818938	0.2532709	-5.4203579	5.95E-08	1.10E-07
LOC100642296	125.753444	-1.37222183	0.25372358	-5.4083339	6.36E-08	1.17E-07
LOC100646372	2162.72644	-1.371211386	0.13695402	-10.012203	1.35E-23	6.19E-23
LOC100647765	175.736918	-1.371004636	0.2649409	-5.1747565	2.28E-07	4.06E-07
LOC100642858	587.907191	-1.370566397	0.1318853	-10.392109	2.69E-25	1.39E-24
LOC100651338	2335.42757	-1.370357745	0.20562938	-6.6642118	2.66E-11	6.03E-11
LOC100646514	654.768812	-1.370114547	0.10668191	-12.842989	9.42E-38	1.06E-36
LOC100647762	133.125601	-1.370019078	0.18427056	-7.4348236	1.05E-13	2.76E-13
LOC100650878	63.1075617	-1.369637569	0.30848525	-4.4398803	9.00E-06	1.44E-05
LOC100644177	22.4262098	-1.369378655	0.4977232	-2.7512856	0.00593619	0.00769511
LOC100649111	17.1589787	-1.369091863	0.3652273	-3.7486022	0.00017782	0.00026087
LOC100651396	226.412695	-1.368609199	0.19009093	-7.1997608	6.03E-13	1.52E-12
LOC100647702	4382.0573	-1.368030719	0.11524328	-11.870807	1.68E-32	1.33E-31
LOC100643519	19.2847398	-1.366550693	0.31105447	-4.3932842	1.12E-05	1.78E-05
LOC100650849	854.86003	-1.36645391	0.1142587	-11.959298	5.81E-33	4.73E-32
LOC100647047	987.661036	-1.364133452	0.16467214	-8.283936	1.19E-16	3.73E-16
LOC105666556	41.9997552	-1.363942827	0.18616959	-7.3263459	2.37E-13	6.09E-13

LOC105665998	49.9129358	-1.363704184	0.3704059	-3.6816481	0.00023173	0.00033678
LOC100644679	367.12787	-1.362796939	0.14061458	-9.6917187	3.27E-22	1.39E-21
LOC100645318	706.788269	-1.360787173	0.18093301	-7.5209447	5.44E-14	1.46E-13
LOC100650936	815.897091	-1.360727178	0.13594261	-10.009571	1.38E-23	6.36E-23
LOC100645296	403.803497	-1.359706288	0.16519551	-8.2308914	1.86E-16	5.76E-16
LOC100647522	873.43918	-1.358263397	0.1124209	-12.081948	1.32E-33	1.12E-32
LOC100642685	101.554224	-1.357221884	0.36708562	-3.6972898	0.00021791	0.00031722
LOC100647723	193.689958	-1.356910252	0.25246854	-5.3745717	7.68E-08	1.40E-07
LOC100643314	383.968004	-1.356777855	0.14243384	-9.5256707	1.64E-21	6.76E-21
LOC100650233	245.795665	-1.356688866	0.29527632	-4.5946417	4.33E-06	7.08E-06
LOC100643838	14.349117	-1.356217578	0.61960737	-2.1888338	0.02860892	0.03507952
LOC100646055	593.539498	-1.355989629	0.12812592	-10.583258	3.56E-26	1.93E-25
LOC100647111	14053.0849	-1.355769894	0.10631651	-12.752205	3.03E-37	3.30E-36
LOC100648651	2548.13875	-1.354470687	0.17788043	-7.614501	2.65E-14	7.21E-14
LOC100646682	2190.8212	-1.353754899	0.12822649	-10.557529	4.69E-26	2.52E-25
LOC100649240	169.832532	-1.353555449	0.11655772	-11.612748	3.55E-31	2.62E-30
LOC100644949	406.504033	-1.353258332	0.14156412	-9.5593316	1.19E-21	4.92E-21
LOC100645536	105.98837	-1.353089198	0.26859834	-5.0375934	4.71E-07	8.25E-07
LOC100646337	5528.568	-1.353054799	0.14209676	-9.5220666	1.70E-21	6.99E-21
LOC100650343	24377.9851	-1.352593668	0.21591524	-6.2644659	3.74E-10	7.89E-10
LOC100642328	695.689287	-1.352424037	0.17342645	-7.7982569	6.28E-15	1.77E-14
LOC100646069	14.3461178	-1.352078599	0.43873846	-3.0817417	0.00205793	0.00277844
LOC100651650	662.261762	-1.350862005	0.10045138	-13.447918	3.17E-41	4.55E-40
LOC100647476	347.598588	-1.349937506	0.12880791	-10.480237	1.06E-25	5.61E-25
LOC100644871	2577.73108	-1.348736794	0.09883869	-13.645839	2.14E-42	3.34E-41
LOC100650502	433.374148	-1.348326864	0.19925969	-6.7666814	1.32E-11	3.05E-11
LOC100651232	7587.89342	-1.348267027	0.13551789	-9.9489969	2.55E-23	1.15E-22
LOC105666663	1760.7797	-1.347601221	0.10048412	-13.411087	5.21E-41	7.40E-40
LOC100650397	902.604311	-1.34697731	0.08495232	-15.855686	1.28E-56	5.64E-55

LOC100646402	333.560498	-1.346901858	0.27024887	-4.9839314	6.23E-07	1.08E-06
LOC100642851	142.797319	-1.346844436	0.25905325	-5.1991026	2.00E-07	3.58E-07
LOC100649476	1484.00732	-1.346512705	0.13183922	-10.213294	1.73E-24	8.42E-24
LOC100643511	323.947893	-1.345986734	0.13213479	-10.186467	2.28E-24	1.10E-23
LOC100647082	1638.97228	-1.345796012	0.17237876	-7.8072033	5.85E-15	1.65E-14
LOC100644486	23.138881	-1.345171731	0.37747082	-3.5636443	0.00036574	0.00052361
LOC100651559	989.390604	-1.345060108	0.09008183	-14.931536	2.05E-50	5.73E-49
LOC100652191	502.783088	-1.345053282	0.23219438	-5.79279	6.92E-09	1.36E-08
LOC100646978	316.786645	-1.344915427	0.1770368	-7.5968128	3.04E-14	8.24E-14
LOC105667093	53.8063749	-1.344860668	0.2471848	-5.4407095	5.31E-08	9.82E-08
LOC100649270	5957.37647	-1.343120865	0.13698601	-9.8048035	1.07E-22	4.69E-22
LOC100644763	36.3129703	-1.342813573	0.30910417	-4.3442105	1.40E-05	2.21E-05
LOC105666675	17.028099	-1.342542839	0.37110015	-3.6177373	0.00029719	0.00042778
LOC105667141	389.134514	-1.342093514	0.10060213	-13.340607	1.34E-40	1.87E-39
LOC100642814	764.663783	-1.341986286	0.15266326	-8.7904995	1.49E-18	5.20E-18
LOC100643813	1531.50152	-1.340889034	0.09167163	-14.627088	1.89E-48	4.69E-47
LOC100643404	1515.57636	-1.339866977	0.14539389	-9.2154285	3.10E-20	1.20E-19
LOC100647614	1401.93797	-1.339581185	0.12009162	-11.15466	6.80E-29	4.39E-28
LOC105666994	119.968259	-1.339347615	0.19137091	-6.9987	2.58E-12	6.24E-12
LOC105667110	599.360677	-1.338765596	0.13690508	-9.7787872	1.39E-22	6.03E-22
LOC100642415	445.268577	-1.33875338	0.1920154	-6.9721148	3.12E-12	7.51E-12
LOC100651939	22.2301432	-1.338657823	0.43227302	-3.0967879	0.0019563	0.00264523
LOC100652331	3368.10049	-1.338477176	0.10920872	-12.256138	1.56E-34	1.42E-33
LOC100648223	457.210764	-1.338033524	0.14249809	-9.3898347	6.01E-21	2.41E-20
LOC105666300	193.042101	-1.336449653	0.18144355	-7.3656497	1.76E-13	4.57E-13
LOC100647329	7539.98832	-1.3356997	0.15572796	-8.577135	9.73E-18	3.24E-17
LOC100645814	296.562901	-1.335573789	0.22471217	-5.9434866	2.79E-09	5.61E-09
LOC100643984	23.7996478	-1.33503445	0.33544314	-3.9799128	6.89E-05	0.0001042
LOC100649939	32.5363173	-1.333987825	0.31874234	-4.1851604	2.85E-05	4.43E-05

LOC105667075	39.1195516	-1.332264174	0.27113065	-4.913735	8.94E-07	1.53E-06
LOC100643367	329.761465	-1.332237318	0.11953451	-11.145211	7.56E-29	4.86E-28
LOC100645610	36.2979051	-1.332072256	0.3675139	-3.6245493	0.00028947	0.00041716
LOC100643502	291.551533	-1.331913109	0.2352451	-5.6618101	1.50E-08	2.87E-08
LOC100652170	292476.356	-1.331880224	0.26399991	-5.0450026	4.54E-07	7.94E-07
LOC100645415	15.0102232	-1.331822876	0.40074456	-3.323371	0.00088937	0.00123357
LOC100643897	72.895617	-1.331608616	0.44361684	-3.0017089	0.00268469	0.00359341
LOC100643873	1063.59651	-1.331039227	0.084861	-15.684935	1.92E-55	7.86E-54
LOC100642645	2199.62045	-1.330352694	0.07687093	-17.306318	4.22E-67	4.54E-65
LOC105665684	126.063816	-1.330328501	0.20502607	-6.4885823	8.66E-11	1.89E-10
LOC100649700	1592.3628	-1.330209971	0.16472287	-8.075442	6.72E-16	2.01E-15
LOC105665660	488.323909	-1.329533106	0.22329926	-5.9540417	2.62E-09	5.27E-09
LOC100644102	421.037105	-1.328130703	0.13754125	-9.6562357	4.63E-22	1.96E-21
LOC100645359	619.20212	-1.327593858	0.25945471	-5.1168616	3.11E-07	5.49E-07
LOC100648479	154.325333	-1.327218684	0.31406327	-4.2259595	2.38E-05	3.71E-05
LOC105667003	29.8392611	-1.326907144	0.37811539	-3.5092652	0.00044935	0.0006391
LOC100651633	540.011562	-1.326460868	0.11213145	-11.829517	2.75E-32	2.15E-31
LOC100645601	779.661351	-1.325322936	0.0881264	-15.038887	4.08E-51	1.22E-49
LOC100643565	526.977573	-1.324852829	0.10652416	-12.437111	1.64E-35	1.60E-34
LOC100645291	68.9753302	-1.324558564	0.26953257	-4.9142802	8.91E-07	1.53E-06
LOC100649831	20731.5666	-1.323676806	0.18603342	-7.1152636	1.12E-12	2.77E-12
LOC100649583	32.3556307	-1.323412143	0.39181754	-3.3776235	0.00073115	0.00101947
LOC100650673	725.538072	-1.323149134	0.09786174	-13.520597	1.18E-41	1.76E-40
LOC100652206	3032.54212	-1.323030228	0.21363747	-6.1928753	5.91E-10	1.23E-09
LOC100651446	3546.82266	-1.322514898	0.10774357	-12.274653	1.24E-34	1.14E-33
LOC100647299	966.484403	-1.322222037	0.15789592	-8.3740104	5.57E-17	1.78E-16
LOC100644239	496.093209	-1.321997311	0.11204174	-11.79915	3.94E-32	3.07E-31
LOC100645478	11.8871434	-1.321798484	0.3827665	-3.4532763	0.00055382	0.00078055
LOC100650864	159.320593	-1.321573952	0.3312486	-3.9896741	6.62E-05	0.00010014

LOC100642227	126.727642	-1.321234933	0.22273819	-5.9317845	3.00E-09	6.02E-09
LOC100650319	3525.66983	-1.320862027	0.14131617	-9.3468568	9.03E-21	3.59E-20
LOC100642498	77.1390413	-1.320096106	0.22284091	-5.9239396	3.14E-09	6.30E-09
LOC100645785	206.91571	-1.31944958	0.15615375	-8.4496825	2.92E-17	9.42E-17
LOC105666395	1963.00232	-1.319252873	0.15983005	-8.2540977	1.53E-16	4.76E-16
LOC100644319	140.728825	-1.317794737	0.28462655	-4.6299079	3.66E-06	6.01E-06
LOC100648840	40.3882501	-1.31737176	0.28825405	-4.5701761	4.87E-06	7.94E-06
LOC105665781	1119.3136	-1.317036409	0.12969081	-10.155202	3.14E-24	1.50E-23
LOC100649271	3013.64068	-1.316107657	0.08425998	-15.619605	5.35E-55	2.05E-53
LOC100652322	535.838496	-1.315774422	0.16043954	-8.2010606	2.38E-16	7.32E-16
LOC100650078	1101.74512	-1.315604093	0.25292381	-5.2015827	1.98E-07	3.53E-07
LOC100651024	7191.4058	-1.315437705	0.09989149	-13.168667	1.33E-39	1.72E-38
LOC100645429	261.206446	-1.314624464	0.29263148	-4.4924233	7.04E-06	1.14E-05
LOC100644108	2625.51103	-1.314528306	0.09461367	-13.89364	6.92E-44	1.20E-42
LOC100648903	643.675261	-1.314392752	0.14384513	-9.1375549	6.39E-20	2.43E-19
LOC100643863	2750.57404	-1.313565973	0.08405935	-15.62665	4.79E-55	1.85E-53
LOC100650599	178.530152	-1.313493661	0.23488313	-5.5921159	2.24E-08	4.25E-08
LOC100649442	2329.12175	-1.312315262	0.10835916	-12.110792	9.26E-34	7.96E-33
LOC100643186	30.4525279	-1.312240351	0.27000788	-4.8600075	1.17E-06	2.00E-06
LOC105665734	327.414893	-1.311815918	0.13324548	-9.8451066	7.20E-23	3.18E-22
LOC100645452	144.990288	-1.310862995	0.22251587	-5.8910989	3.84E-09	7.65E-09
LOC100644082	120.042743	-1.310217317	0.16820974	-7.7891882	6.74E-15	1.90E-14
LOC100646618	1210.75868	-1.309922573	0.11738497	-11.159202	6.46E-29	4.17E-28
LOC100643198	471.900518	-1.309786748	0.13504549	-9.6988558	3.05E-22	1.30E-21
LOC100649861	237.003642	-1.309271999	0.12423592	-10.538595	5.73E-26	3.07E-25
LOC100644974	2386.12317	-1.308875924	0.1672149	-7.8275077	4.98E-15	1.41E-14
LOC100648432	1988.39329	-1.306780134	0.11376893	-11.486266	1.55E-30	1.11E-29
LOC100648274	56.6793233	-1.306684565	0.54026407	-2.4186035	0.01558021	0.01951962
LOC100648625	21.9283967	-1.30609058	0.52549141	-2.4854651	0.01293823	0.01632661

LOC100648109	7009.47016	-1.305373627	0.08974814	-14.544855	6.30E-48	1.49E-46
LOC100649767	134.392927	-1.305110974	0.1843731	-7.078641	1.46E-12	3.57E-12
LOC105666233	230.584863	-1.304541513	0.12393547	-10.525974	6.56E-26	3.50E-25
LOC100646142	96.6195118	-1.303296671	0.19023213	-6.8510858	7.33E-12	1.72E-11
LOC100649527	347.106713	-1.30308969	0.14091864	-9.2471065	2.31E-20	8.96E-20
LOC100645139	494.942213	-1.30275449	0.15897761	-8.1945782	2.51E-16	7.71E-16
LOC100644105	57.7382573	-1.30237645	0.28244936	-4.6110087	4.01E-06	6.56E-06
LOC100644841	1805.79774	-1.299987906	0.28563309	-4.5512511	5.33E-06	8.67E-06
LOC100648791	529.669339	-1.299699389	0.10716003	-12.128584	7.45E-34	6.48E-33
LOC100642937	2568.38507	-1.299141194	0.20161876	-6.4435531	1.17E-10	2.52E-10
LOC105666115	83.4428499	-1.298525684	0.23188473	-5.5998758	2.15E-08	4.07E-08
LOC100642845	950.786352	-1.298303302	0.08306123	-15.630677	4.50E-55	1.74E-53
LOC100650715	421.015902	-1.297418039	0.12850226	-10.096461	5.73E-24	2.70E-23
LOC100642686	12947.4033	-1.296588608	0.15331039	-8.4572784	2.74E-17	8.86E-17
LOC105665666	267.536842	-1.29594131	0.09779392	-13.251757	4.41E-40	5.84E-39
LOC100648328	7269.28547	-1.295818152	0.12079155	-10.727721	7.54E-27	4.28E-26
LOC100647415	2572.52915	-1.295109252	0.13058422	-9.9178084	3.48E-23	1.56E-22
LOC100650867	1385.1371	-1.294968717	0.12389801	-10.451893	1.44E-25	7.50E-25
LOC100645111	452.217166	-1.294772919	0.12913304	-10.026659	1.16E-23	5.38E-23
LOC100643335	2217.37445	-1.294606157	0.09573579	-13.522698	1.15E-41	1.72E-40
LOC100644414	819.217736	-1.294405583	0.15761285	-8.2125637	2.17E-16	6.68E-16
LOC100650455	1024.95319	-1.293995231	0.16470084	-7.8566402	3.95E-15	1.13E-14
LOC100651118	3349.13535	-1.293399013	0.13438735	-9.6244103	6.31E-22	2.65E-21
LOC105666514	303.739314	-1.292933742	0.19467006	-6.6416672	3.10E-11	6.99E-11
LOC105666401	332.263629	-1.292656711	0.23912329	-5.4058168	6.45E-08	1.19E-07
LOC100645065	22.8873767	-1.292431447	0.32141527	-4.0210642	5.79E-05	8.82E-05
LOC100646052	334.406519	-1.292261177	0.20831395	-6.203431	5.52E-10	1.15E-09
LOC100645209	2914.29146	-1.291516115	0.15528735	-8.3169435	9.03E-17	2.85E-16
LOC105666074	23.9094414	-1.291145055	0.42833739	-3.0143179	0.00257558	0.00345209

LOC100650051	2271.59553	-1.290593422	0.15952022	-8.090469	5.94E-16	1.78E-15
LOC100651795	1232.35262	-1.289653537	0.1047296	-12.314126	7.60E-35	7.09E-34
LOC100649739	919.570784	-1.28955381	0.13206809	-9.7643103	1.60E-22	6.93E-22
LOC100647414	2601.24648	-1.289450843	0.10277097	-12.546839	4.14E-36	4.16E-35
LOC100644399	2376.78675	-1.289096849	0.12868616	-10.01737	1.28E-23	5.89E-23
LOC100642687	135.847336	-1.288835398	0.18035935	-7.1459304	8.94E-13	2.22E-12
LOC100649208	146.969491	-1.288680646	0.22042332	-5.8463899	5.02E-09	9.95E-09
LOC100644175	2171.76287	-1.287829746	0.08090463	-15.917874	4.76E-57	2.23E-55
LOC105666252	870.05942	-1.285563138	0.09965826	-12.899715	4.52E-38	5.21E-37
LOC100647259	162.102114	-1.285138017	0.23008435	-5.5855082	2.33E-08	4.41E-08
LOC100644351	15.5933815	-1.284994457	0.37093025	-3.4642482	0.00053172	0.00075073
LOC100649799	10681.2698	-1.284753161	0.15157729	-8.4758948	2.33E-17	7.60E-17
LOC100643543	1370.35274	-1.284727506	0.12935291	-9.9319564	3.02E-23	1.36E-22
LOC100649878	441.709669	-1.283520019	0.14115982	-9.0926726	9.66E-20	3.63E-19
LOC100648361	160.92108	-1.283316122	0.12115397	-10.59244	3.23E-26	1.76E-25
LOC100647132	1261.51266	-1.283290051	0.09638508	-13.314198	1.91E-40	2.61E-39
LOC100645806	620.040529	-1.283181779	0.14168159	-9.0567996	1.34E-19	5.01E-19
LOC100644654	238.028781	-1.28309837	0.19505482	-6.5781424	4.76E-11	1.06E-10
LOC100650749	1475.92547	-1.282908628	0.11729576	-10.937383	7.64E-28	4.61E-27
LOC100651520	834.753296	-1.282349937	0.11356066	-11.292202	1.43E-29	9.61E-29
LOC100644530	835.844977	-1.282043057	0.17877231	-7.1713739	7.42E-13	1.86E-12
LOC100646835	858.52667	-1.282026123	0.17823472	-7.1929089	6.34E-13	1.60E-12
LOC100651376	11261.3479	-1.28194305	0.18801811	-6.8181893	9.22E-12	2.15E-11
LOC100650004	1058.11438	-1.281555118	0.09165787	-13.981943	2.01E-44	3.62E-43
LOC100649008	1055.481	-1.281208187	0.09178901	-13.958187	2.80E-44	4.97E-43
LOC100646492	545.907189	-1.280970068	0.10867858	-11.786776	4.57E-32	3.54E-31
LOC100650700	568.357542	-1.280842236	0.18349588	-6.9802235	2.95E-12	7.09E-12
LOC105667139	713.944822	-1.280481266	0.1039355	-12.319961	7.07E-35	6.62E-34
LOC100650274	25482.1054	-1.279729767	0.18479246	-6.9252271	4.35E-12	1.04E-11

LOC100642539	55.8682803	-1.279206619	0.24249013	-5.2752936	1.33E-07	2.39E-07
LOC100644592	516.91677	-1.279161426	0.21470767	-5.9576886	2.56E-09	5.16E-09
LOC100647175	1909.07673	-1.27796629	0.09442161	-13.53468	9.76E-42	1.47E-40
LOC100644956	186.66647	-1.277441162	0.23164698	-5.5146032	3.50E-08	6.54E-08
LOC100642742	161.175448	-1.276800016	0.12387688	-10.307008	6.55E-25	3.29E-24
LOC100649290	427.535559	-1.276588812	0.12194606	-10.468471	1.21E-25	6.33E-25
LOC105666342	4846.05749	-1.275937755	0.06892554	-18.511828	1.66E-76	4.06E-74
LOC100648240	1058.7747	-1.275421404	0.07904798	-16.134775	1.45E-58	7.53E-57
LOC100645752	100.498199	-1.275054833	0.2992999	-4.2601245	2.04E-05	3.20E-05
LOC105665752	187.354797	-1.274715801	0.1793573	-7.107131	1.18E-12	2.93E-12
LOC100647272	115.44325	-1.274392355	0.20802893	-6.1260344	9.01E-10	1.86E-09
LOC100643802	6600.80599	-1.274139611	0.10460655	-12.180305	3.96E-34	3.53E-33
LOC100649759	2455.66513	-1.271448134	0.08628795	-14.734945	3.85E-49	9.88E-48
LOC100648122	30733.6274	-1.271128602	0.3111134	-4.0857404	4.39E-05	6.73E-05
LOC100648717	280.791129	-1.270858651	0.35442828	-3.5856581	0.00033623	0.0004827
LOC100644114	443.277106	-1.270354481	0.18259451	-6.9572435	3.47E-12	8.33E-12
LOC100647215	724.157963	-1.270255186	0.18558183	-6.8447175	7.66E-12	1.80E-11
LOC100646192	12213.6267	-1.270171023	0.07548744	-16.826256	1.57E-63	1.28E-61
LOC100645181	2901.61973	-1.268735176	0.12493041	-10.155535	3.13E-24	1.49E-23
LOC105667137	1554.88378	-1.268640318	0.10565465	-12.007426	3.25E-33	2.70E-32
LOC100645194	92.764585	-1.265481363	0.34357661	-3.6832582	0.00023027	0.00033476
LOC105665755	17.3518764	-1.264842414	0.43480617	-2.9089799	0.0036261	0.00478931
LOC100643477	57.2511902	-1.264537014	0.21084634	-5.997434	2.00E-09	4.06E-09
LOC100649872	2302.56795	-1.26370751	0.1448032	-8.7270687	2.61E-18	8.99E-18
LOC100651903	60.8054563	-1.262844479	0.22149625	-5.701426	1.19E-08	2.29E-08
LOC100651550	180.796037	-1.26237414	0.30142069	-4.1880805	2.81E-05	4.37E-05
LOC100650363	153.833628	-1.261824534	0.15658321	-8.0584922	7.72E-16	2.30E-15
LOC100648602	1741.06347	-1.260684201	0.28014042	-4.5001867	6.79E-06	1.10E-05
LOC100646968	699.988232	-1.260117809	0.16310785	-7.7256724	1.11E-14	3.09E-14

LOC100645881	2371.12633	-1.259904658	0.18178825	-6.9306164	4.19E-12	1.00E-11
LOC100642932	567.858461	-1.258215079	0.20840768	-6.0372779	1.57E-09	3.20E-09
LOC105666521	559.165107	-1.258153036	0.11454215	-10.984193	4.55E-28	2.80E-27
LOC100650782	250.728223	-1.257058604	0.15812958	-7.9495477	1.87E-15	5.46E-15
LOC100646562	2562.67307	-1.255967342	0.08715906	-14.410061	4.47E-47	9.80E-46
LOC100644775	100.309843	-1.254973069	0.22305299	-5.626345	1.84E-08	3.51E-08
LOC100642754	1086.00893	-1.254407603	0.14984391	-8.3714289	5.69E-17	1.82E-16
LOC100651693	701.410313	-1.253634111	0.16822097	-7.4523057	9.17E-14	2.42E-13
LOC100644046	1624.25717	-1.253215495	0.09793384	-12.796552	1.71E-37	1.90E-36
LOC100643441	2574.53068	-1.252717138	0.11695193	-10.711385	9.00E-27	5.07E-26
LOC100644809	2715.35975	-1.251764441	0.08794891	-14.232859	5.73E-46	1.15E-44
LOC100642711	594.298051	-1.250836893	0.13502746	-9.2635745	1.98E-20	7.71E-20
LOC100647178	579.899419	-1.25027468	0.35817611	-3.4906702	0.00048181	0.0006836
LOC100649595	27.6994575	-1.250229786	0.2819809	-4.4337392	9.26E-06	1.48E-05
LOC100642650	10634.1413	-1.250006309	0.1908629	-6.5492367	5.78E-11	1.28E-10
LOC100644148	223.225838	-1.249934805	0.1716374	-7.282415	3.28E-13	8.38E-13
LOC100651959	1589.49308	-1.249757591	0.08656936	-14.436488	3.05E-47	6.76E-46
LOC100647355	82.7496072	-1.249026385	0.16443768	-7.595743	3.06E-14	8.30E-14
LOC100643843	816.955052	-1.248788386	0.10109054	-12.353168	4.68E-35	4.42E-34
LOC100649362	1137.96326	-1.248742932	0.11002118	-11.350023	7.41E-30	5.06E-29
LOC100650141	920.934269	-1.24872474	0.11048874	-11.301828	1.29E-29	8.65E-29
LOC100649634	253.536252	-1.248085209	0.11067749	-11.276775	1.71E-29	1.14E-28
LOC100642418	230.503489	-1.247145637	0.228063	-5.468426	4.54E-08	8.43E-08
LOC100651811	128.806313	-1.247108549	0.35167233	-3.5462232	0.0003908	0.00055825
LOC100649446	166.031893	-1.24703202	0.21045202	-5.9254931	3.11E-09	6.24E-09
LOC105666814	50.8708767	-1.246720797	0.20898214	-5.965681	2.44E-09	4.92E-09
LOC105666871	85.2940227	-1.246174753	0.50324736	-2.4762668	0.01327643	0.0167426
LOC100647835	1986.73539	-1.245431307	0.16314084	-7.6340865	2.27E-14	6.21E-14
LOC100648764	962.527859	-1.245019226	0.09440191	-13.188496	1.02E-39	1.33E-38

LOC100644014	1925.02704	-1.243400594	0.21608717	-5.754162	8.71E-09	1.70E-08
LOC100650203	26.5184513	-1.243336619	0.48433726	-2.5670885	0.01025564	0.01307972
LOC100644040	48.677119	-1.243327484	0.24008228	-5.1787557	2.23E-07	3.98E-07
LOC100650171	50.7704415	-1.242304592	0.20541411	-6.0478056	1.47E-09	3.00E-09
LOC100649218	33.6433563	-1.242304157	0.32785819	-3.7891509	0.00015116	0.0002226
LOC100649608	7556.79175	-1.241923591	0.16745001	-7.4166827	1.20E-13	3.15E-13
LOC105665745	1350.9932	-1.241473231	0.11959808	-10.380377	3.05E-25	1.56E-24
LOC105667167	79.2647236	-1.241440632	0.21229109	-5.8478225	4.98E-09	9.87E-09
LOC100645904	914.55319	-1.241046218	0.09969462	-12.448477	1.43E-35	1.39E-34
LOC100646546	5625.3545	-1.240798776	0.13605872	-9.1195828	7.54E-20	2.86E-19
LOC105667125	21.2892233	-1.239955859	0.26948678	-4.601175	4.20E-06	6.87E-06
LOC100649274	939.995316	-1.239854112	0.13907938	-8.9147226	4.89E-19	1.77E-18
LOC100650242	136.980093	-1.238950484	0.35323316	-3.507458	0.00045241	0.00064317
LOC100649500	238.439535	-1.23815302	0.28556855	-4.3357471	1.45E-05	2.30E-05
LOC100648641	2695.40125	-1.237898877	0.09272039	-13.35088	1.17E-40	1.63E-39
LOC100647520	5570.36042	-1.237717233	0.10921277	-11.333082	9.00E-30	6.10E-29
LOC100646721	1310.21801	-1.237285068	0.10403286	-11.893214	1.28E-32	1.02E-31
LOC100647508	1991.49176	-1.236579113	0.07865569	-15.72142	1.08E-55	4.48E-54
LOC105666637	28.2291573	-1.236372201	0.4127387	-2.9955325	0.00273966	0.00366398
LOC100644099	249.259759	-1.236187565	0.22198847	-5.5687017	2.57E-08	4.85E-08
LOC100651189	12.8066959	-1.234735553	0.59493696	-2.0754057	0.03794895	0.04604191
LOC100645292	645.489708	-1.234297775	0.09803203	-12.59076	2.37E-36	2.44E-35
LOC100648810	1144.59552	-1.23331444	0.27409173	-4.4996411	6.81E-06	1.10E-05
LOC100651928	99.7705854	-1.232925461	0.31497945	-3.9143044	9.07E-05	0.00013578
LOC105665863	127.051462	-1.231862702	0.21097339	-5.8389482	5.25E-09	1.04E-08
LOC100645826	57.7981461	-1.231718966	0.21035924	-5.855312	4.76E-09	9.44E-09
LOC100648322	1128.29381	-1.231202602	0.09342052	-13.179145	1.16E-39	1.51E-38
LOC100651794	295.741286	-1.230491239	0.28450185	-4.3250729	1.52E-05	2.41E-05
LOC100649206	5024.57706	-1.230184853	0.10532339	-11.680073	1.61E-31	1.21E-30

LOC100642644	371.688812	-1.229739797	0.29812263	-4.1249461	3.71E-05	5.72E-05
LOC100649858	1038.23788	-1.229395445	0.08104625	-15.16906	5.67E-52	1.80E-50
LOC100643317	1520.79402	-1.2287089	0.0944384	-13.010691	1.06E-38	1.28E-37
LOC100650547	3102.38862	-1.228360705	0.08053095	-15.253275	1.57E-52	5.20E-51
LOC100650574	168.172506	-1.228137421	0.26433089	-4.6462123	3.38E-06	5.56E-06
LOC100650169	745.596518	-1.226669308	0.13275403	-9.2401663	2.46E-20	9.55E-20
LOC100644863	939.895915	-1.226149249	0.09681008	-12.665513	9.18E-37	9.72E-36
LOC105667097	2180.38934	-1.225903281	0.08480521	-14.455518	2.31E-47	5.15E-46
LOC100646705	55.3464411	-1.225046773	0.20391696	-6.0075767	1.88E-09	3.82E-09
LOC100647144	389.157482	-1.224150469	0.13760034	-8.8964203	5.77E-19	2.07E-18
LOC100646246	146.291503	-1.2235785	0.45932597	-2.6638566	0.00772505	0.0099325
LOC100645445	65.8263894	-1.223535645	0.28210785	-4.3371202	1.44E-05	2.29E-05
LOC100643839	315.46057	-1.222709683	0.11118999	-10.996581	3.97E-28	2.44E-27
LOC100649803	111.485339	-1.221038467	0.14795515	-8.2527611	1.55E-16	4.81E-16
LOC100649741	4599.43477	-1.220979703	0.14206884	-8.5942822	8.38E-18	2.80E-17
LOC100650335	546.397398	-1.220126035	0.0913534	-13.356109	1.09E-40	1.52E-39
LOC100648350	12161.5138	-1.21984808	0.08438535	-14.455685	2.31E-47	5.15E-46
LOC100651343	307.243952	-1.21978988	0.28804334	-4.2347443	2.29E-05	3.57E-05
LOC100648816	602.227933	-1.219026605	0.32577329	-3.7419477	0.0001826	0.00026756
LOC100649229	124.557839	-1.218562367	0.54915267	-2.2189865	0.02648764	0.03257228
LOC100645369	891.403296	-1.218389858	0.15463865	-7.878948	3.30E-15	9.50E-15
LOC100644881	820.380659	-1.217650017	0.14198269	-8.5760456	9.82E-18	3.27E-17
LOC100645259	352.885028	-1.217070315	0.19910527	-6.1126978	9.80E-10	2.02E-09
LOC100645947	505.916078	-1.216185728	0.12506051	-9.724778	2.36E-22	1.01E-21
LOC100644118	13466.4602	-1.215746004	0.17025924	-7.140558	9.30E-13	2.31E-12
LOC100642967	526.848445	-1.215621387	0.15293569	-7.948579	1.89E-15	5.50E-15
LOC100648950	141.34262	-1.213823405	0.33256126	-3.6499243	0.00026232	0.00037948
LOC100648555	21.5370161	-1.212862831	0.32938016	-3.6822583	0.00023118	0.00033602
LOC100644478	909.766925	-1.212794031	0.07727469	-15.694584	1.65E-55	6.80E-54

LOC100644623	913.758294	-1.212103745	0.08053333	-15.050957	3.40E-51	1.03E-49
LOC100643801	90.8149999	-1.211897634	0.3755168	-3.2272794	0.00124973	0.00171255
LOC105665867	2709.25991	-1.211197519	0.09264761	-13.073165	4.69E-39	5.77E-38
LOC100646665	368.385641	-1.209962392	0.26502542	-4.5654579	4.98E-06	8.11E-06
LOC105665957	802.53685	-1.209784167	0.08718805	-13.875574	8.91E-44	1.54E-42
LOC100651765	17.8610681	-1.208237337	0.42778464	-2.8244056	0.00473684	0.00618461
LOC100643095	362.956587	-1.207737294	0.18993142	-6.3588072	2.03E-10	4.35E-10
LOC100645214	4748.98343	-1.206589665	0.13092431	-9.2159329	3.09E-20	1.19E-19
LOC100646473	18.320708	-1.206356401	0.4174791	-2.8896211	0.00385706	0.00508134
LOC100650642	1104.35009	-1.206014829	0.17805731	-6.7731833	1.26E-11	2.92E-11
LOC105665707	176.423289	-1.205946278	0.12166338	-9.9121551	3.69E-23	1.65E-22
LOC100643535	450.369997	-1.205298009	0.17548906	-6.868223	6.50E-12	1.54E-11
LOC100649393	3547.92679	-1.205275697	0.15702045	-7.6759153	1.64E-14	4.53E-14
LOC100642223	2185.11358	-1.205054373	0.11834031	-10.182958	2.36E-24	1.14E-23
LOC105667178	697.076273	-1.204635911	0.11455356	-10.515918	7.30E-26	3.88E-25
LOC100648012	1318.04259	-1.203797223	0.13250925	-9.0846278	1.04E-19	3.90E-19
LOC100649340	491.655061	-1.203726602	0.14388637	-8.3658141	5.97E-17	1.90E-16
LOC100649302	594.769488	-1.203532394	0.32456921	-3.7080917	0.00020883	0.00030453
LOC100652262	12535.6134	-1.203259388	0.11393734	-10.560712	4.53E-26	2.44E-25
LOC100649822	148.179838	-1.202620538	0.1760817	-6.8299008	8.50E-12	1.99E-11
LOC100647851	584.680073	-1.202466096	0.15386388	-7.8151292	5.49E-15	1.55E-14
LOC100652012	2345.62631	-1.201769054	0.08005035	-15.012664	6.07E-51	1.78E-49
LOC100644508	910.374903	-1.201236458	0.11135185	-10.787755	3.93E-27	2.28E-26
LOC100647578	3467.33601	-1.20024717	0.27296916	-4.3970065	1.10E-05	1.75E-05
LOC100642804	1544.68155	-1.200237113	0.12334978	-9.730355	2.24E-22	9.62E-22
LOC100642279	27.2902405	-1.199968413	0.37672897	-3.18523	0.00144639	0.00197182
LOC100650575	1183.08128	-1.198981512	0.09750238	-12.296946	9.41E-35	8.74E-34
LOC105666000	18994.3244	-1.197606364	0.11149836	-10.741023	6.53E-27	3.72E-26
LOC100648636	68.1834052	-1.197575371	0.18041768	-6.637794	3.18E-11	7.17E-11

LOC100648506	7323.14728	-1.197172561	0.15282965	-7.8333788	4.75E-15	1.35E-14
LOC100651253	4094.48898	-1.196160471	0.07138009	-16.75762	4.98E-63	3.75E-61
LOC100647466	1627.12644	-1.195636232	0.09832544	-12.159989	5.08E-34	4.46E-33
LOC100646155	331.296403	-1.194634784	0.1187585	-10.059362	8.35E-24	3.90E-23
LOC100649418	1185.16075	-1.193063892	0.08827867	-13.514747	1.28E-41	1.90E-40
LOC100650742	982.933025	-1.19301759	0.13964126	-8.5434461	1.30E-17	4.32E-17
LOC100644492	81.3483197	-1.192860426	0.30088448	-3.964513	7.35E-05	0.00011099
LOC100647269	2148.53655	-1.192232037	0.08485892	-14.049577	7.75E-45	1.43E-43
LOC100644616	1039.27403	-1.191322629	0.16173737	-7.3657845	1.76E-13	4.57E-13
LOC105666198	47.0731965	-1.191005446	0.26266262	-4.5343545	5.78E-06	9.36E-06
LOC100651021	306.476916	-1.190575774	0.16024569	-7.4296898	1.09E-13	2.86E-13
LOC100651324	362.39748	-1.190407372	0.20933159	-5.6867067	1.30E-08	2.49E-08
LOC100644381	195.46068	-1.190227323	0.25264301	-4.7111033	2.46E-06	4.09E-06
LOC100646126	1283.19795	-1.190027602	0.09684302	-12.288212	1.05E-34	9.69E-34
LOC100645803	305.18205	-1.189878752	0.23745068	-5.0110563	5.41E-07	9.44E-07
LOC100647812	184.130751	-1.189699024	0.17066287	-6.9710476	3.15E-12	7.56E-12
LOC100645987	2034.73166	-1.18957822	0.13318809	-8.931566	4.20E-19	1.53E-18
LOC100645702	572.537775	-1.189293222	0.51613599	-2.3042246	0.02121004	0.02633703
LOC100652320	1102.01559	-1.188309116	0.08261433	-14.383814	6.54E-47	1.41E-45
LOC100643438	2018.11217	-1.187682783	0.12986718	-9.1453654	5.94E-20	2.27E-19
LOC100652210	3815.31232	-1.187291659	0.24460874	-4.8538399	1.21E-06	2.06E-06
LOC100647695	754.445924	-1.185764164	0.14556472	-8.1459583	3.76E-16	1.14E-15
LOC100651067	977.374854	-1.185683417	0.1214254	-9.7647071	1.60E-22	6.91E-22
LOC100646854	471.586147	-1.185304505	0.09806924	-12.086404	1.25E-33	1.06E-32
LOC100644893	740.66726	-1.18476807	0.17669428	-6.7051864	2.01E-11	4.59E-11
LOC100643794	371.364738	-1.184113205	0.18412843	-6.4309092	1.27E-10	2.74E-10
LOC100645496	1195.43913	-1.183415785	0.10994764	-10.763448	5.12E-27	2.94E-26
LOC100646691	20299.8859	-1.18318812	0.14671539	-8.0645129	7.35E-16	2.20E-15
LOC100643478	560.335554	-1.182375474	0.09185596	-12.872061	6.47E-38	7.38E-37

LOC100646807	584.219184	-1.182012285	0.15100301	-7.8277397	4.97E-15	1.41E-14
LOC100644965	276.46961	-1.181714219	0.21075302	-5.6071046	2.06E-08	3.91E-08
LOC100643642	47.1187729	-1.1816849	0.3590775	-3.290891	0.00099871	0.00137878
LOC100651143	3481.66496	-1.180889143	0.09808844	-12.039025	2.22E-33	1.86E-32
LOC100648736	1470.63636	-1.180785564	0.08519122	-13.860414	1.10E-43	1.89E-42
LOC100645549	37.8510657	-1.18077916	0.29154766	-4.0500382	5.12E-05	7.82E-05
LOC100642253	324.247206	-1.180664109	0.12923545	-9.1357601	6.49E-20	2.47E-19
LOC100646999	597.978139	-1.18066364	0.19775028	-5.9704778	2.37E-09	4.78E-09
LOC105666846	45.2407584	-1.180619111	0.29368574	-4.0200083	5.82E-05	8.86E-05
LOC100645727	454.818492	-1.180457206	0.32026718	-3.6858513	0.00022794	0.00033151
LOC105667140	37.4633101	-1.179318424	0.41592597	-2.8354046	0.00457677	0.00598759
LOC100645645	440.506107	-1.179030582	0.17555713	-6.7159367	1.87E-11	4.27E-11
LOC100643842	1542.17018	-1.178869486	0.16539788	-7.1274763	1.02E-12	2.54E-12
LOC100647369	5210.89638	-1.178777121	0.20176281	-5.8423904	5.15E-09	1.02E-08
LOC100651408	124.621868	-1.177753484	0.23099226	-5.0986708	3.42E-07	6.03E-07
LOC105665865	29.3359002	-1.177747466	0.28789134	-4.0909444	4.30E-05	6.59E-05
LOC105666911	100.862677	-1.177683893	0.13693218	-8.6004904	7.94E-18	2.66E-17
LOC100645690	5201.77535	-1.177501678	0.07424602	-15.859458	1.21E-56	5.38E-55
LOC100646353	18.7754394	-1.177357097	0.36301024	-3.2433165	0.00118147	0.00162195
LOC100651769	1050.02915	-1.177094762	0.15469732	-7.6090183	2.76E-14	7.52E-14
LOC100651535	148.270786	-1.176180934	0.18676128	-6.2977772	3.02E-10	6.40E-10
LOC100649219	110.197715	-1.175801107	0.23997361	-4.8997101	9.60E-07	1.64E-06
LOC100650132	1917.50513	-1.175098246	0.12474583	-9.4199404	4.51E-21	1.82E-20
LOC100642562	685.644521	-1.174975754	0.24330812	-4.8291679	1.37E-06	2.32E-06
LOC105667176	617.370884	-1.174955296	0.15724208	-7.4722699	7.88E-14	2.09E-13
LOC100647044	609.695838	-1.173648874	0.15145485	-7.7491665	9.25E-15	2.59E-14
LOC100646382	562.207609	-1.173439789	0.17948296	-6.5378898	6.24E-11	1.37E-10
LOC100649531	235.185791	-1.173330157	0.11945794	-9.8221198	9.04E-23	3.97E-22
LOC100644748	13.8323749	-1.172723446	0.37904543	-3.0938863	0.00197553	0.00267013

LOC100647629	529.026183	-1.172642676	0.16650768	-7.0425739	1.89E-12	4.60E-12
LOC100651076	703.615588	-1.172558598	0.15460131	-7.5844025	3.34E-14	9.04E-14
LOC100649630	153.437328	-1.17244133	0.12851814	-9.1227689	7.32E-20	2.78E-19
LOC100648416	1184.1555	-1.171580246	0.08078677	-14.50213	1.17E-47	2.70E-46
LOC100643338	2095.28722	-1.171524609	0.12144001	-9.6469412	5.06E-22	2.14E-21
LOC100644781	83.8805221	-1.17134635	0.35698734	-3.2811986	0.00103367	0.00142565
LOC100645613	253.552653	-1.171295131	0.14877405	-7.87298	3.46E-15	9.95E-15
LOC100644178	253.833654	-1.169507748	0.12106839	-9.6598937	4.46E-22	1.89E-21
LOC105665698	265.20681	-1.169112823	0.09472489	-12.342193	5.37E-35	5.05E-34
LOC100646359	1519.48023	-1.169097254	0.14035256	-8.3297178	8.10E-17	2.57E-16
LOC100650017	959.671362	-1.16849188	0.10682547	-10.938327	7.56E-28	4.56E-27
LOC100648114	74.1827855	-1.168375694	0.20405322	-5.725838	1.03E-08	2.00E-08
LOC100648669	1299.7219	-1.167157617	0.0980168	-11.90773	1.08E-32	8.61E-32
LOC100651648	551.754994	-1.166753779	0.17932434	-6.5063884	7.70E-11	1.69E-10
LOC105666607	16.5256479	-1.166550629	0.4821281	-2.4195865	0.01553817	0.01947941
LOC100650761	1584.33423	-1.166462094	0.07594201	-15.359906	3.04E-53	1.04E-51
LOC100645147	232.014609	-1.16555551	0.22562901	-5.1658051	2.39E-07	4.26E-07
LOC100646076	1051.5688	-1.165110986	0.15485202	-7.5240284	5.31E-14	1.42E-13
LOC100643142	185.910555	-1.16477775	0.24689859	-4.7176362	2.39E-06	3.97E-06
LOC100651688	14352.6208	-1.16442636	0.05983695	-19.459987	2.40E-84	1.02E-81
LOC105666943	16.0719062	-1.164053896	0.49515509	-2.3508875	0.0187287	0.02333283
LOC100648982	15.3813387	-1.163985907	0.52170365	-2.2311247	0.02567287	0.03162197
LOC100649652	216.850343	-1.163624423	0.12324578	-9.441495	3.67E-21	1.49E-20
LOC100642659	1000.11418	-1.163448658	0.07856417	-14.808896	1.28E-49	3.44E-48
LOC105665765	18.6360544	-1.163211818	0.31175431	-3.7311812	0.00019058	0.00027897
LOC100644605	3610.59384	-1.162295494	0.08316806	-13.975262	2.21E-44	3.95E-43
LOC100647035	5054.34653	-1.162063305	0.10225317	-11.36457	6.28E-30	4.31E-29
LOC100642901	1903.82005	-1.161817801	0.09544791	-12.17227	4.37E-34	3.88E-33
LOC100643761	775.355191	-1.161542877	0.0958242	-12.121603	8.12E-34	7.02E-33

LOC100644884	224.0631	-1.160797995	0.19501522	-5.9523455	2.64E-09	5.32E-09
LOC105666475	21.454248	-1.159502082	0.31301315	-3.7043238	0.00021196	0.00030905
LOC100650384	596.015511	-1.159493906	0.09511189	-12.190841	3.48E-34	3.11E-33
LOC100644823	5370.57617	-1.159173409	0.0952982	-12.163644	4.85E-34	4.29E-33
LOC100651062	1836.79265	-1.158570472	0.14095124	-8.2196543	2.04E-16	6.31E-16
LOC100646388	282.380953	-1.158256939	0.14482529	-7.997615	1.27E-15	3.73E-15
LOC100651183	1137.09983	-1.158246152	0.1467006	-7.8953061	2.90E-15	8.35E-15
LOC100646896	22.1051034	-1.158055985	0.40403588	-2.8662207	0.00415405	0.00546156
LOC100646385	1047.0163	-1.155976709	0.14664043	-7.8830696	3.19E-15	9.20E-15
LOC105666231	75.1603586	-1.155628801	0.3200269	-3.6110365	0.00030498	0.00043867
LOC100651443	394.432637	-1.155308206	0.0963213	-11.994316	3.81E-33	3.14E-32
LOC100646639	42.7360826	-1.154867249	0.27913368	-4.1373268	3.51E-05	5.42E-05
LOC100644797	943.119502	-1.154724834	0.10125104	-11.404573	3.97E-30	2.76E-29
LOC100651168	41648.946	-1.154688592	0.13527872	-8.5356262	1.39E-17	4.61E-17
LOC100645229	1972.05575	-1.154235969	0.07476651	-15.437874	9.11E-54	3.21E-52
LOC100643827	680.975831	-1.153790004	0.09124831	-12.644509	1.20E-36	1.26E-35
LOC100648250	3556.13903	-1.153521367	0.07919321	-14.565912	4.63E-48	1.11E-46
LOC100651173	461.295324	-1.152857918	0.08770912	-13.144105	1.84E-39	2.35E-38
LOC100647581	283.609296	-1.152817033	0.19256869	-5.9865238	2.14E-09	4.34E-09
LOC100651142	3512.46255	-1.151761666	0.10987995	-10.482	1.05E-25	5.51E-25
LOC100649028	499.64297	-1.151272199	0.09764156	-11.7908	4.35E-32	3.38E-31
LOC100646403	329.714676	-1.149464617	0.16352413	-7.0293274	2.08E-12	5.05E-12
LOC100650648	1312.51888	-1.148196235	0.12871735	-8.9202911	4.65E-19	1.68E-18
LOC100651221	162.415252	-1.148078773	0.27665526	-4.1498534	3.33E-05	5.14E-05
LOC100652097	4256.66255	-1.146944867	0.18445406	-6.2180517	5.03E-10	1.05E-09
LOC100644269	392.103872	-1.146411426	0.13283698	-8.6302127	6.12E-18	2.06E-17
LOC100650336	3988.65704	-1.146198221	0.0998957	-11.47395	1.78E-30	1.27E-29
LOC100652317	10162.174	-1.145282972	0.17428743	-6.571231	4.99E-11	1.11E-10
LOC100644569	9954.32721	-1.145010094	0.11134104	-10.28381	8.34E-25	4.15E-24

LOC100651171	12539.3768	-1.144864908	0.19459804	-5.8832293	4.02E-09	8.01E-09
LOC105666366	719.703958	-1.144223999	0.33075464	-3.4594344	0.00054131	0.00076369
LOC100642769	22.6646955	-1.143708713	0.49864811	-2.2936189	0.0218124	0.02704384
LOC100649204	761.749875	-1.143501895	0.0934702	-12.233866	2.05E-34	1.85E-33
LOC100643693	329.430155	-1.143429267	0.29137344	-3.9242742	8.70E-05	0.00013043
LOC100643446	24.646255	-1.143256614	0.41183905	-2.7759792	0.00550357	0.00715896
LOC105666016	138.892398	-1.143245835	0.21382768	-5.3465756	8.96E-08	1.63E-07
LOC100648065	3994.87591	-1.141351758	0.12797792	-8.9183492	4.73E-19	1.71E-18
LOC105665954	468.04486	-1.141054396	0.10837436	-10.528823	6.36E-26	3.40E-25
LOC100647005	108.116575	-1.140770955	0.14871231	-7.6709919	1.71E-14	4.70E-14
LOC100644476	222.231954	-1.140282549	0.27274436	-4.180774	2.91E-05	4.51E-05
LOC100642204	270.398671	-1.139528652	0.10317456	-11.044667	2.33E-28	1.45E-27
LOC100649606	5121.99312	-1.139016177	0.10398128	-10.95405	6.35E-28	3.85E-27
LOC100644966	4947.6965	-1.138668912	0.34231177	-3.3264089	0.00087973	0.00122055
LOC100651568	475.75487	-1.137795175	0.08378156	-13.580497	5.23E-42	8.00E-41
LOC100642913	3340.55803	-1.136755878	0.10419229	-10.910173	1.03E-27	6.15E-27
LOC100650654	16.0367532	-1.136688278	0.44823268	-2.5359335	0.0112148	0.01424178
LOC100652254	1503.97712	-1.136261844	0.08195199	-13.864969	1.03E-43	1.77E-42
LOC100645769	175.747689	-1.135038039	0.2753354	-4.1223833	3.75E-05	5.78E-05
LOC105666486	460.709731	-1.134802805	0.1030723	-11.009775	3.43E-28	2.12E-27
LOC100644355	196.399031	-1.134619827	0.14855964	-7.63747	2.22E-14	6.06E-14
LOC100645670	428.731557	-1.134060924	0.13034276	-8.7006053	3.30E-18	1.13E-17
LOC105666865	1502.90739	-1.133122696	0.1170886	-9.6774812	3.76E-22	1.60E-21
LOC100644444	2889.18575	-1.132828399	0.16488542	-6.8703976	6.40E-12	1.51E-11
LOC100649035	2680.90682	-1.132264385	0.13757777	-8.229995	1.87E-16	5.80E-16
LOC100650937	46.8729856	-1.131706322	0.24508493	-4.6176088	3.88E-06	6.36E-06
LOC100649755	595.1233	-1.131445044	0.12948071	-8.738329	2.37E-18	8.16E-18
LOC100644857	809.901362	-1.13063229	0.13435087	-8.4155191	3.91E-17	1.26E-16
LOC100643104	268.802756	-1.13033025	0.19546077	-5.7829007	7.34E-09	1.44E-08

LOC100649978	87.475364	-1.130285037	0.18715529	-6.0392898	1.55E-09	3.16E-09
LOC100648835	1044.54269	-1.13002988	0.08682003	-13.015774	9.95E-39	1.20E-37
LOC100647547	68.7489049	-1.129973839	0.21720967	-5.2022263	1.97E-07	3.52E-07
LOC100647664	3476.01603	-1.129585374	0.09126472	-12.377022	3.48E-35	3.32E-34
LOC105665652	726.63165	-1.129221537	0.13123647	-8.6044795	7.67E-18	2.57E-17
LOC100647488	3584.74075	-1.127605103	0.09983474	-11.294717	1.39E-29	9.36E-29
LOC100645374	1263.62664	-1.126954294	0.0996451	-11.309681	1.18E-29	7.92E-29
LOC100648756	197.058619	-1.126532535	0.22847072	-4.9307522	8.19E-07	1.41E-06
LOC100652238	1279.67027	-1.126515006	0.08373352	-13.453573	2.93E-41	4.24E-40
LOC100644919	575.02507	-1.125055262	0.14101818	-7.9780865	1.49E-15	4.35E-15
LOC100645579	155.70578	-1.124762362	0.15572611	-7.222696	5.10E-13	1.29E-12
LOC100644975	1164.44823	-1.124511806	0.07972245	-14.105335	3.52E-45	6.71E-44
LOC100651497	584.775894	-1.124077831	0.13609123	-8.2597372	1.46E-16	4.56E-16
LOC100647255	3290.40214	-1.12382738	0.08958476	-12.544851	4.24E-36	4.26E-35
LOC100644973	724.35691	-1.123603172	0.09341966	-12.027481	2.55E-33	2.13E-32
LOC100642652	19153.7204	-1.122957196	0.15291436	-7.3437	2.08E-13	5.36E-13
LOC100648568	2474.56891	-1.122580304	0.08682907	-12.928623	3.10E-38	3.63E-37
LOC100652213	1238.4782	-1.12168465	0.07282034	-15.403452	1.55E-53	5.43E-52
LOC100643845	1942.06144	-1.121557606	0.16186994	-6.9287579	4.25E-12	1.01E-11
LOC100644144	519.71412	-1.121461304	0.08976114	-12.49384	8.07E-36	7.97E-35
LOC100651925	162.878796	-1.120785653	0.16418399	-6.8264003	8.71E-12	2.04E-11
LOC100647240	2992.63166	-1.120412718	0.09131096	-12.270298	1.31E-34	1.20E-33
LOC100647731	169.786546	-1.120210831	0.21472577	-5.2169371	1.82E-07	3.26E-07
LOC100646075	2609.77274	-1.119972474	0.07692893	-14.558535	5.16E-48	1.23E-46
LOC100651710	645.954498	-1.11892757	0.12835903	-8.7171708	2.85E-18	9.80E-18
LOC100642567	3142.92822	-1.11811638	0.10219605	-10.940896	7.35E-28	4.44E-27
LOC100650298	196.50138	-1.118075656	0.26130852	-4.2787571	1.88E-05	2.95E-05
LOC105666511	60.2936726	-1.117974229	0.20764747	-5.3840013	7.28E-08	1.34E-07
LOC100647442	370.386628	-1.117834233	0.11088478	-10.081043	6.70E-24	3.14E-23

LOC100645070	2983.57472	-1.117381667	0.07634065	-14.636784	1.64E-48	4.11E-47
LOC100648497	582.03841	-1.117097399	0.09381217	-11.907809	1.08E-32	8.61E-32
LOC100646324	852.521941	-1.115533729	0.13078616	-8.5294477	1.47E-17	4.85E-17
LOC100642460	53.4649552	-1.11536378	0.49892013	-2.2355558	0.02538088	0.03127807
LOC100648003	3454.71682	-1.115343791	0.27058551	-4.1219642	3.76E-05	5.79E-05
LOC100650568	328.146621	-1.114885223	0.15384684	-7.2467215	4.27E-13	1.09E-12
LOC100645115	184.654641	-1.113347379	0.13037799	-8.5393813	1.35E-17	4.47E-17
LOC100646263	688.731725	-1.112734305	0.10334882	-10.766783	4.94E-27	2.84E-26
LOC100648770	542.871322	-1.112677067	0.14901612	-7.4668235	8.22E-14	2.18E-13
LOC105666325	1598.96942	-1.112626344	0.18658689	-5.9630467	2.48E-09	4.99E-09
LOC105666223	34.5816223	-1.112613273	0.29973219	-3.7120246	0.00020561	0.00030015
LOC100646676	461.473247	-1.1124585	0.08400527	-13.242723	4.97E-40	6.58E-39
LOC100643702	893.8646	-1.112211011	0.17740504	-6.2693314	3.63E-10	7.65E-10
LOC100646903	24.6132346	-1.111837687	0.29797721	-3.7312843	0.00019051	0.00027889
LOC100643717	137.267391	-1.111766376	0.16439031	-6.7629678	1.35E-11	3.13E-11
LOC100650327	1183.91029	-1.111168904	0.07938533	-13.997157	1.62E-44	2.93E-43
LOC100645830	1191.57021	-1.110129312	0.14959845	-7.4207274	1.16E-13	3.06E-13
LOC100648120	25.8169253	-1.109388181	0.4441939	-2.4975313	0.01250614	0.0157997
LOC100645936	215.027827	-1.108406318	0.28173937	-3.9341549	8.35E-05	0.00012545
LOC100644162	4001.24915	-1.108314873	0.11446198	-9.6828209	3.57E-22	1.52E-21
LOC100646259	1126.65956	-1.107910916	0.12672509	-8.7426329	2.28E-18	7.88E-18
LOC100647597	1870.13026	-1.107786346	0.09854245	-11.241717	2.54E-29	1.67E-28
LOC100650905	2460.84602	-1.107785747	0.10672981	-10.379347	3.08E-25	1.58E-24
LOC100651623	469.569727	-1.106595779	0.09219183	-12.003187	3.42E-33	2.83E-32
LOC100642226	991.249428	-1.105917381	0.16907801	-6.5408707	6.12E-11	1.35E-10
LOC100646277	706.865074	-1.104908572	0.10443192	-10.58018	3.68E-26	2.00E-25
LOC100645956	51843.6169	-1.104292672	0.48350008	-2.2839555	0.02237415	0.02769822
LOC105666380	69.3438018	-1.104116073	0.23772487	-4.6445122	3.41E-06	5.61E-06
LOC100651878	496.296988	-1.103550687	0.09285958	-11.884079	1.43E-32	1.14E-31

LOC100643864	559.827778	-1.103459014	0.12414056	-8.8887872	6.18E-19	2.21E-18
LOC100642252	111.431786	-1.103395479	0.23237753	-4.7482881	2.05E-06	3.43E-06
LOC100649018	550.363328	-1.103087395	0.0985336	-11.195038	4.31E-29	2.81E-28
LOC100650262	36.2710227	-1.100495767	0.26490848	-4.1542489	3.26E-05	5.05E-05
LOC100643264	76.0333996	-1.099684402	0.20579151	-5.3436821	9.11E-08	1.66E-07
LOC100644293	3720.16853	-1.099504019	0.07101239	-15.48327	4.50E-54	1.64E-52
LOC100645989	213.671182	-1.09931984	0.13987636	-7.8592256	3.87E-15	1.11E-14
LOC100648101	1221.69432	-1.099238002	0.1262534	-8.7066012	3.13E-18	1.07E-17
LOC100645225	6059.85957	-1.098118886	0.08239307	-13.327806	1.60E-40	2.19E-39
LOC100652075	2463.8575	-1.097774616	0.09563909	-11.478305	1.70E-30	1.21E-29
LOC100651129	4465.31191	-1.097739085	0.28254709	-3.8851544	0.00010226	0.00015245
LOC100649703	308.292825	-1.097652819	0.19063854	-5.7577697	8.52E-09	1.66E-08
LOC100651833	569.203739	-1.097304481	0.27378528	-4.0079017	6.13E-05	9.31E-05
LOC100644369	16326.3773	-1.0964985	0.22752738	-4.8191936	1.44E-06	2.43E-06
LOC100651416	64.463883	-1.096230331	0.18564477	-5.9049891	3.53E-09	7.05E-09
LOC100648934	3603.75365	-1.096059247	0.07632491	-14.360439	9.16E-47	1.95E-45
LOC100646933	70.7287344	-1.095627109	0.24669389	-4.4412414	8.94E-06	1.43E-05
LOC100642392	2157.40855	-1.095437699	0.07486209	-14.632742	1.74E-48	4.34E-47
LOC100649541	5764.55991	-1.095235906	0.08029758	-13.639712	2.32E-42	3.62E-41
LOC100644704	600.948195	-1.094978087	0.08404996	-13.027706	8.51E-39	1.03E-37
LOC100642853	791.020776	-1.094872886	0.10512113	-10.415346	2.11E-25	1.09E-24
LOC100651397	1876.08423	-1.094674153	0.07818894	-14.00037	1.55E-44	2.81E-43
LOC100649174	756.682183	-1.09461505	0.15217048	-7.1933467	6.32E-13	1.59E-12
LOC100651822	857.753199	-1.09457779	0.11992051	-9.1275275	7.01E-20	2.66E-19
LOC100645644	64.8023852	-1.094263696	0.26555186	-4.1207157	3.78E-05	5.82E-05
LOC100648647	301.296829	-1.094034345	0.17567636	-6.2275558	4.74E-10	9.93E-10
LOC100643454	797.597481	-1.094005893	0.11847107	-9.2343719	2.60E-20	1.01E-19
LOC100642803	1626.35508	-1.093517487	0.10565354	-10.350032	4.18E-25	2.12E-24
LOC105667135	1207.71802	-1.093421659	0.06755732	-16.185094	6.43E-59	3.40E-57

LOC100643799	1029.88525	-1.093400147	0.12043632	-9.0786576	1.10E-19	4.12E-19
LOC100643899	1694.10697	-1.092839088	0.08357887	-13.075543	4.54E-39	5.60E-38
LOC100650672	63.9173809	-1.09277723	0.27995904	-3.9033469	9.49E-05	0.00014186
LOC100648541	554.534337	-1.092574212	0.07406818	-14.750927	3.03E-49	7.90E-48
LOC100644077	2150.69204	-1.092243857	0.08885766	-12.292062	9.99E-35	9.26E-34
LOC100648119	1571.89494	-1.09188068	0.07064133	-15.456684	6.80E-54	2.40E-52
LOC100648552	3657.66422	-1.088691275	0.06474789	-16.814313	1.92E-63	1.54E-61
LOC100646589	812.030398	-1.087995568	0.08336405	-13.051136	6.26E-39	7.63E-38
LOC105667208	544.339337	-1.087992378	0.13514832	-8.0503584	8.26E-16	2.46E-15
LOC100652121	489.214607	-1.08765273	0.18437345	-5.8991831	3.65E-09	7.29E-09
LOC100650347	606.899723	-1.087486181	0.08995239	-12.089576	1.20E-33	1.02E-32
LOC100646695	1793.03864	-1.087347147	0.07247581	-15.002898	7.03E-51	2.05E-49
LOC100642672	971.514787	-1.087117152	0.08682009	-12.521493	5.70E-36	5.67E-35
LOC105665823	145.266989	-1.085849103	0.12562067	-8.6438732	5.43E-18	1.84E-17
LOC100647798	365.953434	-1.085697738	0.20812045	-5.2166797	1.82E-07	3.26E-07
LOC100651342	2793.12985	-1.0856043	0.10254833	-10.58627	3.45E-26	1.87E-25
LOC100646969	334.222397	-1.084360384	0.12007742	-9.0305103	1.71E-19	6.33E-19
LOC100648368	329.487111	-1.084096685	0.0905331	-11.97459	4.83E-33	3.96E-32
LOC100651400	655.398585	-1.083415337	0.12841319	-8.4369473	3.26E-17	1.05E-16
LOC100646776	2368.92772	-1.083257307	0.08839718	-12.254432	1.59E-34	1.45E-33
LOC105666296	20.9828664	-1.083063472	0.38325057	-2.8259931	0.00471343	0.00615486
LOC100647719	4513.76324	-1.083060534	0.16621654	-6.5159612	7.22E-11	1.59E-10
LOC105666854	51.4119574	-1.082986844	0.2345633	-4.6170344	3.89E-06	6.38E-06
LOC100647233	550.563903	-1.082607212	0.11703699	-9.2501284	2.24E-20	8.72E-20
LOC100649765	559.131047	-1.081781998	0.18737145	-5.7734623	7.77E-09	1.52E-08
LOC100647377	2816.9895	-1.080808457	0.06510407	-16.601243	6.83E-62	4.71E-60
LOC100649774	982.590212	-1.08076706	0.08660472	-12.479308	9.68E-36	9.53E-35
LOC100647741	968.414222	-1.080746314	0.1121127	-9.6398205	5.43E-22	2.29E-21
LOC105667204	12393.1911	-1.080709132	0.0825362	-13.093759	3.57E-39	4.44E-38

LOC100651235	865.57049	-1.079474604	0.12735797	-8.4759095	2.33E-17	7.60E-17
LOC100645731	22.925427	-1.0789637	0.39753167	-2.7141578	0.00664445	0.0085803
LOC100652072	691.527311	-1.078904497	0.08751312	-12.328488	6.36E-35	5.97E-34
LOC100648245	879.972433	-1.078659698	0.21543488	-5.0068944	5.53E-07	9.64E-07
LOC100648490	16516.4148	-1.078354603	0.23843149	-4.5227021	6.11E-06	9.89E-06
LOC100644031	425.979148	-1.077340512	0.10189474	-10.573073	3.97E-26	2.15E-25
LOC100651788	26.4602928	-1.076391954	0.41478631	-2.5950518	0.00945767	0.01208562
LOC100646517	3950.09203	-1.076275979	0.14180714	-7.5897167	3.21E-14	8.69E-14
LOC105666200	483.866224	-1.075944039	0.10061519	-10.693654	1.09E-26	6.11E-26
LOC100644992	299.381753	-1.075456997	0.09554796	-11.255677	2.17E-29	1.43E-28
LOC100645079	4748.94365	-1.074811583	0.12104714	-8.8792809	6.73E-19	2.40E-18
LOC100649210	823.538443	-1.074485272	0.18969038	-5.6644162	1.48E-08	2.83E-08
LOC100643779	3691.52534	-1.074463712	0.3044141	-3.5296122	0.00041617	0.0005932
LOC100645433	232.474467	-1.073653061	0.2436742	-4.4061006	1.05E-05	1.68E-05
LOC100650536	3296.46577	-1.073381225	0.2145092	-5.0038936	5.62E-07	9.78E-07
LOC100645052	84.971469	-1.072620764	0.40868356	-2.6245753	0.00867571	0.01110959
LOC100649460	53.0259342	-1.072590557	0.17968766	-5.9691944	2.38E-09	4.81E-09
LOC100648102	4428.91835	-1.072483091	0.08118807	-13.209861	7.70E-40	1.01E-38
LOC100648966	1052.07065	-1.072436334	0.08363495	-12.822824	1.22E-37	1.37E-36
LOC100649212	31.6337293	-1.071530722	0.29026214	-3.6915966	0.00022285	0.00032426
LOC105666855	309.761957	-1.070759181	0.12032874	-8.8986152	5.65E-19	2.03E-18
LOC105667035	183.382064	-1.070194131	0.17358704	-6.1651728	7.04E-10	1.46E-09
LOC100645357	9318.15707	-1.070034009	0.09432408	-11.344229	7.92E-30	5.39E-29
LOC100650902	4175.78312	-1.069934997	0.07247267	-14.763289	2.53E-49	6.63E-48
LOC100650338	2356.97789	-1.069717546	0.13897435	-7.6972301	1.39E-14	3.84E-14
LOC105665822	1928.74268	-1.069617634	0.07944748	-13.463204	2.58E-41	3.74E-40
LOC100652275	7210.84924	-1.069010567	0.08544276	-12.511423	6.47E-36	6.41E-35
LOC105666562	62.1091824	-1.068990992	0.25171021	-4.2469116	2.17E-05	3.39E-05
LOC100646049	2145.28029	-1.067882175	0.09410543	-11.347721	7.61E-30	5.19E-29

LOC100644831	637.956603	-1.067029478	0.13005413	-8.2045027	2.32E-16	7.12E-16
LOC100644627	11823.9167	-1.066808432	0.09111075	-11.708919	1.15E-31	8.70E-31
LOC100652304	1033.23243	-1.066113295	0.09560157	-11.151629	7.03E-29	4.53E-28
LOC100649668	1788.49345	-1.065986114	0.09400975	-11.339102	8.40E-30	5.71E-29
LOC100649761	660.911298	-1.06588784	0.15383917	-6.9285856	4.25E-12	1.01E-11
LOC100648877	471.981752	-1.065683897	0.10511704	-10.13807	3.74E-24	1.78E-23
LOC100650854	5468.91199	-1.065578553	0.06354395	-16.769158	4.10E-63	3.19E-61
LOC100646638	76.1599427	-1.065308751	0.2165662	-4.9190905	8.69E-07	1.49E-06
LOC100643797	1368.20113	-1.064926207	0.09955475	-10.69689	1.05E-26	5.91E-26
LOC100651957	11.5007133	-1.064884442	0.45126796	-2.3597608	0.01828672	0.0227967
LOC100650893	979.132469	-1.063729061	0.09173511	-11.595659	4.34E-31	3.18E-30
LOC100644788	1437.65178	-1.063357292	0.0918187	-11.581054	5.14E-31	3.76E-30
LOC105666002	11.24663	-1.063259664	0.49092668	-2.1658217	0.03032481	0.03708133
LOC100643238	2605.37658	-1.062636169	0.07046243	-15.08089	2.16E-51	6.62E-50
LOC100650548	101.439798	-1.062161486	0.21482687	-4.9442674	7.64E-07	1.32E-06
LOC100642957	1068.56148	-1.061893219	0.13644343	-7.7826631	7.10E-15	2.00E-14
LOC100645499	512.263295	-1.061820237	0.10303462	-10.30547	6.66E-25	3.34E-24
LOC100648560	6259.10034	-1.061618031	0.06458361	-16.437887	1.02E-60	6.51E-59
LOC100647064	541.146293	-1.061597609	0.10062152	-10.550404	5.06E-26	2.72E-25
LOC100643568	54.6191083	-1.061043958	0.30580288	-3.469699	0.00052104	0.00073647
LOC100649182	2269.41235	-1.060557282	0.08070683	-13.140862	1.92E-39	2.44E-38
LOC100644354	2489.85313	-1.059883074	0.09309382	-11.385107	4.96E-30	3.44E-29
LOC100650534	401.981911	-1.058413039	0.09131162	-11.59122	4.57E-31	3.35E-30
LOC100650880	2587.57903	-1.058095366	0.12866131	-8.2238813	1.97E-16	6.09E-16
LOC100645566	559.985053	-1.05742739	0.23004002	-4.5967105	4.29E-06	7.01E-06
LOC100642760	8474.17471	-1.057363346	0.1344428	-7.8647822	3.70E-15	1.06E-14
LOC100647840	178.817747	-1.057212964	0.24412299	-4.3306571	1.49E-05	2.35E-05
LOC100651116	403.437054	-1.057115463	0.13407097	-7.8847453	3.15E-15	9.08E-15
LOC100651068	3670.6402	-1.056351202	0.08051523	-13.119893	2.53E-39	3.16E-38

LOC105665646	235.369876	-1.056016918	0.12014588	-8.7894561	1.50E-18	5.25E-18
LOC100644693	28.4637272	-1.055965088	0.51211482	-2.0619694	0.03921065	0.04749029
LOC100643975	86.3530668	-1.055939907	0.18086076	-5.8384134	5.27E-09	1.04E-08
LOC100643816	854.689361	-1.055533327	0.15022987	-7.0261214	2.12E-12	5.16E-12
LOC100643728	541.825368	-1.055053685	0.15608	-6.7596981	1.38E-11	3.20E-11
LOC100650294	930.575474	-1.054130926	0.18383928	-5.733981	9.81E-09	1.91E-08
LOC100644323	895.579041	-1.053659428	0.09484632	-11.109123	1.13E-28	7.21E-28
LOC100650889	12648.2454	-1.053237968	0.10161231	-10.36526	3.57E-25	1.82E-24
LOC100646234	235.414488	-1.053145934	0.12384662	-8.503631	1.84E-17	6.01E-17
LOC100644958	1488.72372	-1.0528402	0.1176394	-8.9497241	3.56E-19	1.30E-18
LOC100646521	62.354127	-1.052546901	0.18959891	-5.5514396	2.83E-08	5.33E-08
LOC100650663	784.197123	-1.051939547	0.32933746	-3.1941084	0.00140263	0.00191483
LOC100650532	5876.98042	-1.051745929	0.06794314	-15.479796	4.75E-54	1.71E-52
LOC100648166	996.089568	-1.051543351	0.14845394	-7.0832971	1.41E-12	3.46E-12
LOC100650045	322.618707	-1.051300776	0.14964889	-7.0251157	2.14E-12	5.20E-12
LOC100646145	52226.9229	-1.05128507	0.17018188	-6.1774208	6.52E-10	1.35E-09
LOC100647346	980.903653	-1.050634413	0.0888307	-11.82738	2.82E-32	2.21E-31
LOC100642544	3343.38451	-1.049745522	0.0888435	-11.815671	3.24E-32	2.53E-31
LOC100647771	2786.64676	-1.049611272	0.102626	-10.227537	1.49E-24	7.30E-24
LOC105666464	33.2760966	-1.049376671	0.28477667	-3.684911	0.00022878	0.00033264
LOC100645388	1754.48457	-1.049205598	0.19982613	-5.2505925	1.52E-07	2.73E-07
LOC100650256	479.788308	-1.049009771	0.11188573	-9.3757244	6.87E-21	2.75E-20
LOC100650748	1071.96571	-1.048611288	0.08144908	-12.874439	6.27E-38	7.17E-37
LOC100647408	986.063262	-1.048311652	0.07700685	-13.613225	3.34E-42	5.18E-41
LOC100643275	17.6976476	-1.04825535	0.50586302	-2.0722119	0.03824569	0.04636745
LOC105666700	126.353063	-1.048207538	0.17531039	-5.9791524	2.24E-09	4.53E-09
LOC100645419	4423.26984	-1.048175857	0.10024018	-10.456644	1.37E-25	7.14E-25
LOC100649738	70.3287039	-1.047862065	0.17132164	-6.116344	9.57E-10	1.98E-09
LOC100650241	471.677825	-1.04612398	0.09472037	-11.04434	2.33E-28	1.45E-27

LOC100651136	134.930965	-1.045953583	0.13960728	-7.4921133	6.78E-14	1.81E-13
LOC100644987	1695.4434	-1.04586019	0.10782319	-9.6997706	3.02E-22	1.29E-21
LOC100652184	5200.30776	-1.045793771	0.07399988	-14.132372	2.40E-45	4.64E-44
LOC105667138	1391.52554	-1.045007452	0.0938307	-11.137159	8.27E-29	5.31E-28
LOC100647219	160.281595	-1.044854734	0.14991459	-6.9696666	3.18E-12	7.63E-12
LOC100652298	2671.79282	-1.044393192	0.08761892	-11.919722	9.34E-33	7.51E-32
LOC100643362	752.799064	-1.044191963	0.08577376	-12.173793	4.29E-34	3.82E-33
LOC100644424	240.411671	-1.04416216	0.20542606	-5.08291	3.72E-07	6.54E-07
LOC100651452	2509.98871	-1.042477318	0.10181067	-10.239372	1.32E-24	6.48E-24
LOC100652058	1171.23917	-1.042250793	0.11638995	-8.954818	3.40E-19	1.24E-18
LOC100648895	264.91581	-1.041919016	0.11393142	-9.1451423	5.96E-20	2.27E-19
LOC100649655	368.709724	-1.038453166	0.09348288	-11.108484	1.14E-28	7.25E-28
LOC100646806	1269.39221	-1.038261978	0.1884368	-5.5098684	3.59E-08	6.71E-08
LOC100651825	11.5027325	-1.037668385	0.47582285	-2.1807872	0.02919916	0.03578085
LOC100652077	479.660284	-1.036763024	0.12738183	-8.1390181	3.98E-16	1.21E-15
LOC100650185	276.712754	-1.03654413	0.20449999	-5.0686756	4.01E-07	7.03E-07
LOC105665873	27.6685407	-1.036203838	0.29373068	-3.5277345	0.00041913	0.00059708
LOC100642446	203.839932	-1.035975011	0.27260234	-3.8003159	0.00014451	0.00021306
LOC100650377	7138.57088	-1.035324608	0.06432267	-16.095796	2.73E-58	1.39E-56
LOC100642521	136.373993	-1.03520975	0.15336781	-6.7498504	1.48E-11	3.41E-11
LOC100646376	37.1296519	-1.034451785	0.2970096	-3.4828901	0.00049603	0.00070315
LOC105665736	2945.38587	-1.034238946	0.08905683	-11.613247	3.53E-31	2.60E-30
LOC100644092	855.993186	-1.034038131	0.10273181	-10.065414	7.86E-24	3.67E-23
LOC100646655	106.947159	-1.033848613	0.18429209	-5.609837	2.03E-08	3.85E-08
LOC100647494	2655.16014	-1.033621845	0.12086686	-8.5517389	1.21E-17	4.02E-17
LOC100649991	21.9562832	-1.03350019	0.37445816	-2.7599884	0.00578034	0.00749905
LOC100647901	286.238732	-1.033484277	0.09344019	-11.060382	1.95E-28	1.22E-27
LOC100646005	10528.824	-1.0327727	0.05961617	-17.3237	3.12E-67	3.39E-65
LOC100646279	128.213793	-1.032394383	0.14792578	-6.9791378	2.97E-12	7.15E-12

LOC100646873	2510.07099	-1.03231157	0.24153379	-4.273984	1.92E-05	3.01E-05
LOC100646153	27.5877604	-1.03140419	0.25286571	-4.0788615	4.53E-05	6.93E-05
LOC100652328	424.030244	-1.031285685	0.15896179	-6.4876327	8.72E-11	1.90E-10
LOC100643041	586.626388	-1.030589903	0.15312136	-6.7305432	1.69E-11	3.88E-11
LOC100650818	1092.81786	-1.029947914	0.11892764	-8.6602907	4.71E-18	1.59E-17
LOC100643627	794.900429	-1.02919831	0.10765804	-9.5598834	1.18E-21	4.90E-21
LOC100647528	1025.07482	-1.028844596	0.37011798	-2.7797747	0.00543966	0.00707771
LOC100648310	2579.48624	-1.02860349	0.12475015	-8.2453089	1.65E-16	5.12E-16
LOC100646746	2417.86245	-1.028211067	0.08168799	-12.587053	2.49E-36	2.55E-35
LOC100650519	2023.11424	-1.027899496	0.08171448	-12.57916	2.75E-36	2.81E-35
LOC100651565	3347.41732	-1.027848982	0.06885017	-14.928779	2.14E-50	5.96E-49
LOC100645686	290.17974	-1.027711391	0.09835631	-10.448861	1.48E-25	7.74E-25
LOC100642538	454.155591	-1.027249846	0.09607225	-10.692472	1.10E-26	6.18E-26
LOC100631066	4356.13369	-1.026476611	0.07141084	-14.37424	7.51E-47	1.61E-45
LOC100649550	428.720812	-1.025525398	0.10222979	-10.031571	1.11E-23	5.13E-23
LOC100643190	1823.18782	-1.025204684	0.08762512	-11.699894	1.28E-31	9.64E-31
LOC100643834	123.490854	-1.024013776	0.28533151	-3.5888562	0.00033213	0.00047696
LOC100649358	120.963211	-1.023834916	0.20135636	-5.0846912	3.68E-07	6.48E-07
LOC100650438	856.407223	-1.023820165	0.0841765	-12.162779	4.91E-34	4.32E-33
LOC100645036	29.9784851	-1.023780932	0.28509815	-3.5909771	0.00032944	0.00047316
LOC100647507	137.27216	-1.023779151	0.18056042	-5.6700086	1.43E-08	2.74E-08
LOC100643332	6017.43607	-1.023692462	0.07544484	-13.568754	6.14E-42	9.36E-41
LOC100642697	618.83172	-1.023685533	0.09267601	-11.045852	2.30E-28	1.43E-27
LOC100650624	277.559315	-1.023496782	0.15659755	-6.5358417	6.33E-11	1.39E-10
LOC100645926	456.10927	-1.023262048	0.14242744	-7.1844447	6.75E-13	1.69E-12
LOC100647002	1004.03261	-1.022274779	0.11864022	-8.6165952	6.90E-18	2.32E-17
LOC100646136	496.802014	-1.021795136	0.20236155	-5.0493541	4.43E-07	7.76E-07
LOC105665817	369.874044	-1.021299765	0.1467835	-6.9578651	3.45E-12	8.29E-12
LOC100645129	2970.73566	-1.021175744	0.07933828	-12.871161	6.54E-38	7.46E-37

LOC100649148	617.300801	-1.020915648	0.10565236	-9.662971	4.33E-22	1.84E-21
LOC100649737	228.676874	-1.020825373	0.19985957	-5.1077132	3.26E-07	5.76E-07
LOC100645691	20.3917747	-1.020700878	0.37268284	-2.7387923	0.00616653	0.00797892
LOC100644464	5700.02022	-1.020583541	0.23284606	-4.3830828	1.17E-05	1.86E-05
LOC100646879	1075.85138	-1.020570937	0.08830707	-11.557069	6.80E-31	4.95E-30
LOC100648689	3663.35988	-1.020422077	0.29822985	-3.4215961	0.00062255	0.00087289
LOC100644505	299.325086	-1.019866996	0.10472684	-9.738354	2.07E-22	8.92E-22
LOC100645654	3072.70772	-1.019813613	0.06290203	-16.212729	4.10E-59	2.22E-57
LOC100643796	270.289899	-1.01950698	0.46785031	-2.1791307	0.02932196	0.03591784
LOC100644568	2083.95581	-1.018989529	0.0973251	-10.469957	1.19E-25	6.24E-25
LOC100651114	170.389132	-1.018708649	0.17995903	-5.6607811	1.51E-08	2.88E-08
LOC100642698	297.875144	-1.018473316	0.13888529	-7.3331977	2.25E-13	5.79E-13
LOC100649341	1141.36721	-1.018456039	0.19942833	-5.1068775	3.28E-07	5.78E-07
LOC100647908	1049.57437	-1.018428303	0.1248075	-8.1599929	3.35E-16	1.02E-15
LOC105666279	65.2225035	-1.017985895	0.18738952	-5.4324591	5.56E-08	1.03E-07
LOC100651225	1495.30605	-1.01789888	0.09510593	-10.702791	9.88E-27	5.55E-26
LOC100643087	6138.11846	-1.017152503	0.06253525	-16.265267	1.74E-59	9.74E-58
LOC100646563	963.504313	-1.017025735	0.09742144	-10.439444	1.64E-25	8.53E-25
LOC100648872	943.919786	-1.016745174	0.09374558	-10.845793	2.09E-27	1.23E-26
LOC100647956	1488.29363	-1.016178445	0.12854608	-7.9051686	2.68E-15	7.73E-15
LOC100646260	2540.39029	-1.015782761	0.08294329	-12.246714	1.75E-34	1.59E-33
LOC100649547	1920.09406	-1.015663476	0.07526363	-13.494744	1.68E-41	2.48E-40
LOC100646205	33.1527574	-1.015122612	0.38702784	-2.6228672	0.00871933	0.01116252
LOC100645789	1246.76544	-1.014884303	0.10367533	-9.7890624	1.25E-22	5.46E-22
LOC100644796	1662.7231	-1.014583233	0.09161987	-11.073834	1.68E-28	1.06E-27
LOC100644083	2836.45162	-1.0140814	0.06967178	-14.555124	5.42E-48	1.29E-46
LOC100650155	36.28213	-1.013738986	0.30965904	-3.2737265	0.00106139	0.00146347
LOC105665670	4347.67873	-1.013568091	0.30115964	-3.3655509	0.00076391	0.00106363
LOC100651072	337.852579	-1.013405274	0.13276531	-7.6330579	2.29E-14	6.26E-14

LOC100645724	133.204985	-1.01339178	0.26765616	-3.7861702	0.00015299	0.00022515
LOC100644718	160.627647	-1.01304762	0.27583159	-3.6727034	0.00024	0.00034817
LOC100645449	54.6775366	-1.012696746	0.3816708	-2.6533252	0.0079703	0.01023708
LOC100648567	74.7747564	-1.012658238	0.28557332	-3.5460534	0.00039105	0.0005585
LOC100649487	636.53319	-1.01255129	0.14010113	-7.2272887	4.93E-13	1.25E-12
LOC100650072	263.103366	-1.011325504	0.13245711	-7.635117	2.26E-14	6.17E-14
LOC100648915	120.473192	-1.011215996	0.19702487	-5.1324282	2.86E-07	5.07E-07
LOC100648263	1611.06476	-1.011150846	0.08977571	-11.263078	2.00E-29	1.32E-28
LOC105666287	16.1277	-1.011020881	0.32972346	-3.0662691	0.00216748	0.0029199
LOC100643934	225.113336	-1.010676577	0.14229627	-7.1026215	1.22E-12	3.02E-12
LOC105666584	81.2897613	-1.01060229	0.20538317	-4.9205701	8.63E-07	1.48E-06
LOC100645561	461.213334	-1.010380288	0.07950949	-12.707669	5.36E-37	5.73E-36
LOC100644442	1311.45655	-1.010340718	0.08712291	-11.596729	4.28E-31	3.15E-30
LOC100650293	317.522232	-1.01027201	0.10702108	-9.4399344	3.73E-21	1.51E-20
LOC100650598	536.073274	-1.010027165	0.09877511	-10.225524	1.52E-24	7.45E-24
LOC100648858	3653.2616	-1.00921776	0.07780459	-12.971185	1.78E-38	2.11E-37
LOC105666360	2224.31951	-1.008927911	0.09205979	-10.959485	5.98E-28	3.64E-27
LOC100644911	275.080751	-1.008642693	0.29715843	-3.3942927	0.00068806	0.0009613
LOC100645067	2097.52456	-1.008529528	0.07214712	-13.978791	2.10E-44	3.77E-43
LOC100651632	357.144468	-1.00820983	0.11095213	-9.08689	1.02E-19	3.82E-19
LOC100644288	735.897654	-1.007563624	0.19730014	-5.1067559	3.28E-07	5.78E-07
LOC105666763	136.200356	-1.007370434	0.14822823	-6.7960769	1.08E-11	2.50E-11
LOC100642893	5254.71646	-1.007210507	0.11662084	-8.636625	5.79E-18	1.95E-17
LOC100650484	14763.933	-1.007205692	0.11510289	-8.7504813	2.12E-18	7.36E-18
LOC100642282	677.671655	-1.006880879	0.07872563	-12.789748	1.87E-37	2.07E-36
LOC105666190	470.707131	-1.006807684	0.08785726	-11.459584	2.11E-30	1.49E-29
LOC100648570	30.7618031	-1.006720648	0.39446543	-2.5521137	0.01070716	0.01361831
LOC100645222	1480.91967	-1.00667505	0.09802412	-10.269667	9.65E-25	4.79E-24
LOC100644842	1015.50926	-1.004302677	0.11203432	-8.9642414	3.12E-19	1.14E-18

LOC100648730	466.232565	-1.004132547	0.09236599	-10.871237	1.58E-27	9.35E-27
LOC105666484	52.9839405	-1.003263129	0.17941376	-5.5918962	2.25E-08	4.26E-08
LOC100649410	7381.88564	-1.003152052	0.08487769	-11.818795	3.12E-32	2.44E-31
LOC100651813	526.597512	-1.002983604	0.12348502	-8.1223099	4.57E-16	1.38E-15
LOC100643710	295.926454	-1.001331854	0.1466478	-6.8281412	8.60E-12	2.01E-11
LOC100646182	2894.89794	-1.000929336	0.08304274	-12.053183	1.87E-33	1.57E-32
LOC100648943	1021.94791	-1.000207136	0.07316241	-13.671052	1.51E-42	2.40E-41
LOC100643995	41.8565808	-0.999949267	0.28461089	-3.5133907	0.00044243	0.00062935
LOC100646945	575.993647	-0.99962028	0.07152836	-13.975161	2.21E-44	3.95E-43
LOC100651783	301.8924	-0.999530102	0.0913756	-10.938698	7.53E-28	4.55E-27
LOC100644136	104.515121	-0.999230199	0.32013822	-3.1212462	0.00180087	0.00243979
LOC105665806	46.7999426	-0.999092867	0.25421231	-3.9301514	8.49E-05	0.00012742
LOC100650630	410.324291	-0.998987687	0.07853317	-12.720583	4.54E-37	4.89E-36
LOC105666285	5899.77744	-0.998360371	0.06640804	-15.033728	4.41E-51	1.31E-49
LOC100646502	403.827111	-0.997820206	0.10649339	-9.3697857	7.27E-21	2.90E-20
LOC100644545	2100.23352	-0.997806075	0.09511091	-10.490973	9.50E-26	5.03E-25
LOC100645941	3919.40471	-0.997512454	0.07834841	-12.731751	3.94E-37	4.26E-36
LOC100652283	655.647944	-0.996655005	0.09290635	-10.727523	7.56E-27	4.29E-26
LOC100643097	267.503448	-0.996606885	0.10615531	-9.388196	6.10E-21	2.45E-20
LOC105666289	463.429317	-0.996086133	0.19181308	-5.1930041	2.07E-07	3.69E-07
LOC100646152	31.4780628	-0.995781985	0.2697685	-3.6912464	0.00022316	0.00032466
LOC100651111	46.4705844	-0.995099602	0.29337571	-3.391895	0.00069411	0.00096934
LOC100644463	21.4603974	-0.994955529	0.34841773	-2.8556398	0.00429502	0.00563934
LOC100648983	1804.85739	-0.99472996	0.11010473	-9.0343982	1.65E-19	6.12E-19
LOC100645658	8035.11173	-0.994106423	0.06869829	-14.470613	1.86E-47	4.19E-46
LOC100644850	578.756101	-0.994083391	0.16959843	-5.8613951	4.59E-09	9.11E-09
LOC100648644	258.57428	-0.991823977	0.12334336	-8.0411626	8.90E-16	2.64E-15
LOC100648238	319.08294	-0.990851322	0.11087959	-8.9362826	4.02E-19	1.46E-18
LOC105666418	428.370013	-0.990198828	0.3076901	-3.2181693	0.00129012	0.00176689

LOC100643752	29.131423	-0.990198167	0.46797184	-2.1159354	0.03435031	0.04182526
LOC100652285	182.324907	-0.990184594	0.18509126	-5.3497103	8.81E-08	1.61E-07
LOC100646958	2837.12333	-0.989163623	0.15088571	-6.5557144	5.54E-11	1.22E-10
LOC100644345	671.996819	-0.989053703	0.1772254	-5.5807673	2.39E-08	4.53E-08
LOC100645491	2149.9996	-0.98878502	0.08081883	-12.234587	2.03E-34	1.84E-33
LOC105665761	934.766899	-0.988311733	0.16422591	-6.0180013	1.77E-09	3.59E-09
LOC105667121	438.855948	-0.988230828	0.1048977	-9.4209007	4.47E-21	1.81E-20
LOC100646865	334.729196	-0.988108316	0.14822817	-6.6661303	2.63E-11	5.95E-11
LOC100648883	1164.06457	-0.987743932	0.20003444	-4.9378694	7.90E-07	1.36E-06
LOC100644677	175.183419	-0.987613777	0.14520177	-6.8016648	1.03E-11	2.41E-11
LOC100647685	929.028564	-0.987400791	0.08759247	-11.272667	1.79E-29	1.19E-28
LOC105665930	33.4768102	-0.986619304	0.28524292	-3.458874	0.00054244	0.00076517
LOC100645556	16.1669185	-0.986516847	0.41416968	-2.3819147	0.01722289	0.02149787
LOC100644341	473.515002	-0.986222792	0.14932695	-6.6044528	3.99E-11	8.93E-11
LOC100647678	674.469876	-0.985906505	0.09671445	-10.193994	2.11E-24	1.02E-23
LOC100645964	252.785821	-0.984246552	0.29399335	-3.3478531	0.0008144	0.001132
LOC100647540	916.535433	-0.983865771	0.29656777	-3.3175073	0.00090825	0.00125887
LOC100643576	576.882723	-0.983488478	0.10510559	-9.3571468	8.19E-21	3.26E-20
LOC100648843	7400.85023	-0.983376658	0.17370943	-5.6610436	1.50E-08	2.88E-08
LOC100651449	365.844491	-0.981511701	0.09583823	-10.241338	1.29E-24	6.36E-24
LOC100644055	666203.111	-0.981267124	0.25053781	-3.9166429	8.98E-05	0.00013453
LOC100651534	360.154093	-0.980905601	0.14335763	-6.8423674	7.79E-12	1.83E-11
LOC100647058	1821.67696	-0.98090142	0.09061399	-10.825055	2.62E-27	1.53E-26
LOC100650857	590.528138	-0.980712677	0.12665637	-7.743098	9.70E-15	2.71E-14
LOC100645888	3495.00553	-0.980577543	0.08551123	-11.467237	1.93E-30	1.37E-29
LOC100642857	1196.32984	-0.980556711	0.09210273	-10.646337	1.81E-26	1.00E-25
LOC100652256	1790.71559	-0.980538395	0.08066182	-12.156165	5.32E-34	4.65E-33
LOC100646931	218.108391	-0.980523349	0.16582128	-5.9131333	3.36E-09	6.72E-09
LOC100646519	34.8576732	-0.980403442	0.31027242	-3.159815	0.00157869	0.0021477

LOC105665880	31.3805872	-0.980361152	0.42640437	-2.2991349	0.02149728	0.02668017
LOC100642358	203.451104	-0.979775807	0.28653461	-3.4193977	0.0006276	0.00087972
LOC100650586	899.098905	-0.979542001	0.09789874	-10.005665	1.44E-23	6.61E-23
LOC100644983	130.510757	-0.97947873	0.14569124	-6.7229761	1.78E-11	4.08E-11
LOC100649096	1912.42319	-0.979129351	0.07551929	-12.965288	1.93E-38	2.27E-37
LOC100649782	974.877055	-0.979026619	0.11248192	-8.7038579	3.21E-18	1.10E-17
LOC100644017	1134.40031	-0.978776903	0.1556556	-6.288093	3.21E-10	6.80E-10
LOC100649398	811.250379	-0.978752353	0.10198682	-9.5968512	8.24E-22	3.45E-21
LOC100647147	115.56401	-0.978413634	0.16992246	-5.7580005	8.51E-09	1.66E-08
LOC100651829	2087.98201	-0.978276881	0.0785555	-12.453322	1.34E-35	1.31E-34
LOC100649710	2595.34955	-0.978151726	0.07452006	-13.12602	2.34E-39	2.94E-38
LOC100644730	446.600172	-0.977827492	0.12166169	-8.037267	9.19E-16	2.73E-15
npve	16090.605	-0.977679153	0.2432437	-4.0193401	5.84E-05	8.88E-05
LOC100652123	601.455672	-0.97740327	0.17640812	-5.5405798	3.01E-08	5.67E-08
LOC100648512	1120.34345	-0.977330059	0.07613522	-12.836766	1.02E-37	1.15E-36
LOC100648382	816.805962	-0.977220822	0.13539854	-7.2173663	5.30E-13	1.34E-12
LOC100647742	1583.26476	-0.976947494	0.09654471	-10.11912	4.54E-24	2.15E-23
LOC100649555	155.619736	-0.97671247	0.1337237	-7.3039593	2.79E-13	7.17E-13
LOC100647966	10.7966229	-0.976178236	0.45491584	-2.1458436	0.03188546	0.03893136
LOC100652269	31.5742075	-0.976011382	0.41346449	-2.3605688	0.01824693	0.02275
LOC100647602	198.302309	-0.975958476	0.12192031	-8.0048882	1.20E-15	3.52E-15
LOC100649997	1696.79761	-0.975843708	0.10910199	-8.9443253	3.74E-19	1.36E-18
LOC100645773	2395.1214	-0.975376258	0.07833531	-12.451297	1.38E-35	1.34E-34
LOC100649119	276.529673	-0.975359457	0.21659061	-4.5032398	6.69E-06	1.08E-05
LOC100644402	170.781743	-0.973921092	0.17087519	-5.699605	1.20E-08	2.32E-08
LOC100651924	810.506708	-0.973025888	0.11728636	-8.2961553	1.08E-16	3.37E-16
LOC100648751	714.176767	-0.97271174	0.15617834	-6.2282114	4.72E-10	9.89E-10
LOC100652115	286.498288	-0.972531614	0.0942648	-10.317018	5.90E-25	2.97E-24
LOC100647832	462.420538	-0.971564806	0.20080632	-4.8383179	1.31E-06	2.22E-06

LOC100651045	71.9077436	-0.971288974	0.28139791	-3.4516567	0.00055716	0.00078497
LOC100645417	263.146922	-0.971090057	0.1865242	-5.2062416	1.93E-07	3.45E-07
LOC100648481	1967.22755	-0.970970535	0.10971209	-8.8501689	8.74E-19	3.10E-18
LOC100650926	423.311938	-0.970741279	0.15005131	-6.4693955	9.84E-11	2.14E-10
LOC100650821	465.937707	-0.970654245	0.08917559	-10.884753	1.36E-27	8.08E-27
LOC100651712	568.315332	-0.970415569	0.08836467	-10.98194	4.67E-28	2.86E-27
LOC105666531	402.547867	-0.970088884	0.07439486	-13.03973	7.27E-39	8.82E-38
LOC100650852	425.036253	-0.969331112	0.1043657	-9.2878321	1.57E-20	6.18E-20
LOC100648714	645.989961	-0.968946078	0.0796462	-12.165629	4.74E-34	4.20E-33
LOC100643290	1072.34624	-0.968929899	0.07720652	-12.549845	3.98E-36	4.01E-35
LOC100649375	4069.48358	-0.968174619	0.10734105	-9.019612	1.89E-19	6.98E-19
LOC100646782	1652.64761	-0.968090997	0.16836091	-5.7500935	8.92E-09	1.74E-08
LOC100646445	1273.71449	-0.967872759	0.09773294	-9.9032401	4.03E-23	1.80E-22
LOC100646986	97.2874013	-0.966465332	0.43971215	-2.19795	0.02795267	0.03430921
LOC100643859	146.184451	-0.966410157	0.3158902	-3.059323	0.00221838	0.00298641
LOC100650028	109.32027	-0.966144694	0.15085335	-6.4045294	1.51E-10	3.24E-10
LOC100645951	34.6001199	-0.965576013	0.26641937	-3.624271	0.00028978	0.00041754
LOC100650108	8810.78409	-0.965372738	0.1308756	-7.3762624	1.63E-13	4.23E-13
LOC100649996	649.225426	-0.964648162	0.18727294	-5.1510281	2.59E-07	4.60E-07
LOC100650416	172.521855	-0.964408487	0.23776904	-4.0560726	4.99E-05	7.63E-05
LOC100645398	658.404341	-0.964343097	0.08934584	-10.793374	3.70E-27	2.15E-26
LOC100645465	3603.80207	-0.963701182	0.06856038	-14.05624	7.05E-45	1.31E-43
LOC100647456	370.684489	-0.962914198	0.12489035	-7.7100768	1.26E-14	3.48E-14
LOC100644410	908.245989	-0.961906976	0.10633771	-9.0457746	1.49E-19	5.53E-19
LOC100649958	2500.98155	-0.96185024	0.05866834	-16.394708	2.09E-60	1.28E-58
LOC100650789	12611.4208	-0.961842367	0.1062365	-9.0537842	1.38E-19	5.15E-19
LOC100648115	24.2564645	-0.961551728	0.34711801	-2.7701004	0.0056039	0.00728173
LOC100648691	483.768785	-0.961357585	0.18293545	-5.2551739	1.48E-07	2.66E-07
LOC100651830	2171.41913	-0.961333204	0.11799121	-8.1474982	3.72E-16	1.13E-15

LOC100642651	1179.29814	-0.960925816	0.11699544	-8.2133613	2.15E-16	6.63E-16
LOC100643501	98.5088375	-0.960787481	0.30983028	-3.1010122	0.0019286	0.0026085
LOC100649990	1192.82842	-0.95989013	0.09538662	-10.063152	8.04E-24	3.76E-23
LOC100645548	574.823748	-0.959793278	0.12340353	-7.777681	7.39E-15	2.07E-14
LOC100648503	670.255335	-0.95871127	0.20795516	-4.6101826	4.02E-06	6.59E-06
LOC100643578	1344.81262	-0.958146568	0.07532477	-12.720205	4.57E-37	4.91E-36
LOC100649029	731.71746	-0.957667166	0.0783771	-12.218712	2.47E-34	2.22E-33
LOC100651152	1292.08761	-0.957276701	0.1123599	-8.5197364	1.60E-17	5.26E-17
LOC100648051	3280.57656	-0.956949071	0.06876797	-13.915622	5.09E-44	8.85E-43
LOC100646194	376.636239	-0.956380892	0.09154561	-10.447043	1.51E-25	7.88E-25
LOC100645249	488.363766	-0.956276046	0.13471357	-7.0985871	1.26E-12	3.11E-12
LOC100649379	249.671326	-0.955856825	0.11154543	-8.5692157	1.04E-17	3.47E-17
LOC100643798	13153.5462	-0.955608162	0.09492742	-10.066724	7.75E-24	3.63E-23
LOC100647805	74.7744764	-0.955388561	0.16277921	-5.8692296	4.38E-09	8.70E-09
LOC100642656	996.102742	-0.955364507	0.15079463	-6.3355341	2.37E-10	5.04E-10
LOC100644187	3356.40249	-0.955326275	0.07082044	-13.489414	1.81E-41	2.65E-40
LOC100646531	2172.94892	-0.95516229	0.11833468	-8.071702	6.93E-16	2.07E-15
LOC100650224	501.688786	-0.954812339	0.14792047	-6.4549033	1.08E-10	2.35E-10
LOC100644303	2461.593	-0.95381423	0.09117532	-10.46132	1.30E-25	6.80E-25
LOC100643588	1394.26926	-0.95338256	0.10242371	-9.308221	1.30E-20	5.13E-20
LOC100646920	368.984837	-0.953215366	0.14649475	-6.5068227	7.68E-11	1.68E-10
LOC100644237	1003.08373	-0.950874989	0.09115591	-10.431304	1.78E-25	9.29E-25
LOC100650101	67.8436497	-0.950417123	0.17861223	-5.32112	1.03E-07	1.87E-07
LOC100645324	39.7143168	-0.949772844	0.31240425	-3.0402047	0.00236417	0.00317657
LOC100649638	11871.2569	-0.94974177	0.05851694	-16.230202	3.08E-59	1.69E-57
LOC100650746	1340.22597	-0.949418865	0.08530023	-11.13032	8.93E-29	5.72E-28
LOC100650404	375.621314	-0.94910495	0.07868331	-12.062342	1.67E-33	1.41E-32
LOC100631060	287.939621	-0.949057652	0.29231888	-3.2466519	0.00116771	0.00160419
LOC105665993	20.4592625	-0.9464823	0.32230123	-2.9366388	0.0033179	0.00440124

LOC100648402	68.9113258	-0.946262666	0.25448123	-3.7183987	0.00020049	0.00029294
LOC100649810	62.9481628	-0.946136889	0.27970821	-3.3825854	0.00071807	0.00100151
LOC100652140	9879.1045	-0.945919541	0.13160756	-7.1874256	6.60E-13	1.66E-12
LOC105666963	11.6593386	-0.944715435	0.40345527	-2.3415618	0.01920325	0.02390579
LOC100643635	371.986738	-0.944183821	0.11829844	-7.981372	1.45E-15	4.24E-15
LOC100647030	304.491029	-0.944149634	0.09328226	-10.121427	4.44E-24	2.10E-23
LOC100644969	132.872632	-0.943955044	0.13775449	-6.8524446	7.26E-12	1.71E-11
LOC100648394	3602.22986	-0.943767728	0.06626786	-14.241712	5.05E-46	1.02E-44
LOC100646534	694.999127	-0.943362441	0.12400416	-7.6075066	2.79E-14	7.60E-14
LOC100642537	5570.04831	-0.943209004	0.07220866	-13.062269	5.41E-39	6.64E-38
LOC100647118	202.272309	-0.94306848	0.22225584	-4.2431663	2.20E-05	3.45E-05
LOC100644413	376.029619	-0.942697783	0.12713275	-7.4150662	1.22E-13	3.18E-13
LOC100649746	1543.61149	-0.942588655	0.17601813	-5.3550657	8.55E-08	1.56E-07
LOC100650810	101.704569	-0.941389778	0.17545453	-5.3654346	8.08E-08	1.48E-07
LOC100650891	2094.17294	-0.940911266	0.12633927	-7.4474964	9.51E-14	2.51E-13
LOC100645695	3708.68062	-0.940460623	0.0701315	-13.409961	5.29E-41	7.50E-40
LOC105665850	138.404999	-0.939948997	0.14354319	-6.5481963	5.82E-11	1.28E-10
LOC100649536	1054.10123	-0.939880128	0.07351239	-12.78533	1.98E-37	2.19E-36
LOC100651797	149.193155	-0.939559282	0.15479539	-6.069685	1.28E-09	2.63E-09
LOC100642450	1479.83544	-0.939533312	0.14618921	-6.4268307	1.30E-10	2.81E-10
LOC100649013	4349.0543	-0.939354927	0.05689116	-16.511439	3.04E-61	2.04E-59
LOC100645239	1782.8886	-0.939046372	0.07358068	-12.762132	2.67E-37	2.92E-36
LOC100644681	3255.00954	-0.939011166	0.09749555	-9.631323	5.90E-22	2.48E-21
LOC100644602	26.3449043	-0.938903044	0.26235873	-3.5786994	0.00034531	0.00049537
LOC100646254	891.831541	-0.938821627	0.06733098	-13.943382	3.45E-44	6.05E-43
LOC100643615	452.071995	-0.938457732	0.17400295	-5.3933438	6.92E-08	1.27E-07
LOC100652287	2732.23898	-0.93816508	0.08534055	-10.993192	4.12E-28	2.53E-27
LOC100651947	1873.46046	-0.937578529	0.11355584	-8.2565417	1.50E-16	4.67E-16
LOC100651968	3511.75461	-0.936500829	0.09500128	-9.8577707	6.34E-23	2.81E-22

LOC100644612	2318.10588	-0.936457271	0.07536259	-12.426023	1.89E-35	1.83E-34
LOC100651940	41.1409519	-0.936218154	0.33905397	-2.7612659	0.00575778	0.00747077
LOC100649299	1695.74672	-0.934673381	0.24737023	-3.7784392	0.00015781	0.00023208
LOC100650162	1331.70477	-0.934012378	0.11584322	-8.0627279	7.46E-16	2.23E-15
LOC100650391	328.256744	-0.933757997	0.11173513	-8.3568883	6.44E-17	2.05E-16
LOC100650032	367.21441	-0.933520838	0.09503657	-9.8227541	8.99E-23	3.94E-22
LOC100644591	479.204727	-0.931888261	0.07850931	-11.86978	1.70E-32	1.34E-31
LOC100648276	4028.55075	-0.931732763	0.0568161	-16.399096	1.94E-60	1.20E-58
LOC100650890	1041.61247	-0.931580799	0.07949211	-11.71916	1.02E-31	7.73E-31
LOC100645894	86.9438244	-0.931174323	0.31437681	-2.9619689	0.00305679	0.00407087
LOC105665827	77.1124978	-0.930922121	0.25669433	-3.6265785	0.0002872	0.00041395
LOC100650780	253.072726	-0.930870792	0.18669618	-4.9860195	6.16E-07	1.07E-06
LOC100649975	800.816195	-0.930684082	0.17856778	-5.2119373	1.87E-07	3.35E-07
LOC100647560	491.275074	-0.930581134	0.08774863	-10.605079	2.82E-26	1.54E-25
LOC100650153	1224.00585	-0.929561044	0.14409356	-6.4510938	1.11E-10	2.41E-10
LOC100648289	475.454381	-0.929269888	0.07075244	-13.134104	2.10E-39	2.65E-38
LOC100643570	1008.45352	-0.929260795	0.09292061	-10.000589	1.51E-23	6.95E-23
LOC100642326	1902.82832	-0.929185425	0.09077369	-10.236285	1.36E-24	6.69E-24
LOC100647496	171.518953	-0.929120166	0.10753184	-8.6404192	5.60E-18	1.89E-17
LOC100648964	320.398335	-0.928694339	0.12577465	-7.3837961	1.54E-13	4.00E-13
LOC100645293	2210.89379	-0.928364086	0.13050986	-7.1133639	1.13E-12	2.80E-12
LOC105665689	204.020113	-0.928341565	0.10605124	-8.7537079	2.06E-18	7.17E-18
LOC100648845	48.9653135	-0.92800202	0.31290472	-2.9657655	0.00301931	0.00402259
LOC100648353	75.0427586	-0.926988702	0.19181858	-4.8326324	1.35E-06	2.28E-06
LOC100644091	1059.34587	-0.926950019	0.08713527	-10.638057	1.98E-26	1.09E-25
LOC100650280	191.371387	-0.926219567	0.11132928	-8.31964	8.82E-17	2.79E-16
LOC100642728	390.731421	-0.925728419	0.10155256	-9.1157566	7.81E-20	2.96E-19
LOC100648548	784.035257	-0.925609615	0.09955143	-9.2978037	1.43E-20	5.65E-20
LOC100643933	67.611919	-0.925467563	0.23026642	-4.0191164	5.84E-05	8.89E-05

LOC105666631	827.752469	-0.924914629	0.13321748	-6.9428923	3.84E-12	9.20E-12
LOC105666332	1505.57275	-0.924745923	0.08392715	-11.018436	3.11E-28	1.93E-27
LOC100646829	731.11783	-0.924555149	0.09582715	-9.6481541	5.00E-22	2.12E-21
LOC100643527	519.716573	-0.924545465	0.0923273	-10.013782	1.33E-23	6.11E-23
LOC100648815	3307.99267	-0.924083607	0.10015974	-9.2260986	2.81E-20	1.09E-19
LOC100650758	2319.90056	-0.923664855	0.08568621	-10.779621	4.30E-27	2.47E-26
LOC100651569	174.312105	-0.923067549	0.11549899	-7.991997	1.33E-15	3.90E-15
LOC100642856	2669.78176	-0.92249377	0.11222257	-8.2202161	2.03E-16	6.28E-16
LOC100646959	904.174002	-0.92067585	0.05936326	-15.509187	3.01E-54	1.11E-52
LOC100650173	271.087883	-0.919798717	0.0916897	-10.031647	1.11E-23	5.13E-23
LOC100644739	334.759839	-0.918993883	0.21908945	-4.1946059	2.73E-05	4.25E-05
LOC100650515	374.234826	-0.918617555	0.11581595	-7.9317015	2.16E-15	6.28E-15
LOC100650998	284.865022	-0.918083922	0.12195739	-7.5279075	5.16E-14	1.38E-13
LOC100650112	97.9863463	-0.917403698	0.185909	-4.9346923	8.03E-07	1.38E-06
LOC100643805	560.881243	-0.917267969	0.11023498	-8.3210247	8.72E-17	2.76E-16
LOC100651206	95.6442401	-0.917203233	0.17412508	-5.2674964	1.38E-07	2.49E-07
LOC100650579	237.199375	-0.916889748	0.10066784	-9.1080705	8.39E-20	3.17E-19
LOC100646620	269.225447	-0.916280576	0.10561399	-8.6757498	4.11E-18	1.40E-17
LOC100643080	1735.54821	-0.91605587	0.12742297	-7.1890955	6.52E-13	1.64E-12
LOC105666320	201.239479	-0.915199723	0.13012547	-7.0332095	2.02E-12	4.91E-12
LOC100650614	1127.76303	-0.913880212	0.12780149	-7.1507788	8.63E-13	2.15E-12
LOC100642895	1488.70947	-0.913861734	0.0928295	-9.8445185	7.24E-23	3.19E-22
LOC100646559	5857.26216	-0.913610271	0.06694167	-13.647856	2.08E-42	3.27E-41
LOC100643034	96.2463966	-0.913397982	0.19761957	-4.6220016	3.80E-06	6.23E-06
LOC100650636	497.190294	-0.913205549	0.15416993	-5.9233702	3.15E-09	6.32E-09
LOC100643495	1965.58518	-0.91278413	0.08527727	-10.703721	9.78E-27	5.50E-26
LOC100652288	726.7401	-0.912329373	0.08374269	-10.894436	1.23E-27	7.29E-27
LOC100645170	3999.9956	-0.912121115	0.07229886	-12.615983	1.72E-36	1.79E-35
LOC100650471	222.199611	-0.912066866	0.24459486	-3.7288881	0.00019233	0.00028143

LOC100645562	288.160527	-0.911074787	0.11230351	-8.1126115	4.95E-16	1.49E-15
LOC100631065	407.508676	-0.911022541	0.11301602	-8.0610034	7.57E-16	2.26E-15
LOC100643788	325.842203	-0.911005495	0.21651072	-4.2076692	2.58E-05	4.02E-05
LOC100646951	643.629439	-0.910885974	0.08924351	-10.206748	1.85E-24	8.99E-24
LOC100631090	1691.73311	-0.910287319	0.06315421	-14.413724	4.24E-47	9.31E-46
LOC105665978	619.320398	-0.910179954	0.11783792	-7.7239987	1.13E-14	3.13E-14
LOC100645532	73.8606237	-0.908921342	0.17620125	-5.1584272	2.49E-07	4.43E-07
LOC100642347	677.384447	-0.908910686	0.08744856	-10.393661	2.65E-25	1.37E-24
LOC100648971	937.618855	-0.908877287	0.09919919	-9.162144	5.09E-20	1.95E-19
LOC100643132	2452.09216	-0.908308583	0.06236981	-14.563273	4.81E-48	1.15E-46
LOC100646056	43.5443708	-0.907917695	0.39145129	-2.3193631	0.02037536	0.0253249
LOC105666952	44.9430102	-0.907746405	0.33481565	-2.7111827	0.00670437	0.00865311
LOC100645175	908.067039	-0.907612375	0.11082334	-8.1897223	2.62E-16	8.02E-16
LOC100649089	446.575939	-0.906839892	0.10278471	-8.8227121	1.12E-18	3.94E-18
LOC100649534	727.857223	-0.906682215	0.17092532	-5.3045519	1.13E-07	2.05E-07
LOC100651442	419.946468	-0.906345438	0.11509248	-7.8749322	3.41E-15	9.80E-15
LOC100646560	71.9937456	-0.906240188	0.20688505	-4.3804043	1.18E-05	1.88E-05
LOC100644259	725.125065	-0.905709665	0.08858433	-10.224265	1.54E-24	7.53E-24
LOC100648705	2097.49986	-0.905213261	0.1445063	-6.2641783	3.75E-10	7.90E-10
LOC100647137	443.364186	-0.904850477	0.10782417	-8.3919073	4.78E-17	1.53E-16
LOC100651923	1627.6685	-0.904743897	0.24592773	-3.6789015	0.00023424	0.00034018
LOC100644255	746.85414	-0.90465426	0.09367843	-9.6570176	4.59E-22	1.94E-21
LOC100642491	207.690619	-0.904607223	0.34175639	-2.6469358	0.00812248	0.01042843
LOC100646583	2174.79963	-0.90459726	0.09135276	-9.9022429	4.07E-23	1.81E-22
LOC100644257	917.825167	-0.904213251	0.41244922	-2.192302	0.02835771	0.03478456
LOC100643359	1035.37208	-0.903616246	0.07395534	-12.218404	2.48E-34	2.23E-33
LOC105667069	23.6490526	-0.902886823	0.3441501	-2.6235263	0.00870247	0.0111424
LOC105666234	86.3847177	-0.902492954	0.18822225	-4.7948262	1.63E-06	2.74E-06
LOC100645673	3744.70718	-0.901769662	0.06588199	-13.68765	1.20E-42	1.92E-41

LOC105666545	13.1158929	-0.901571036	0.34384252	-2.6220464	0.00874035	0.01118797
LOC100649656	717.498623	-0.901294535	0.06936887	-12.992781	1.34E-38	1.60E-37
LOC100650955	2979.57515	-0.901098016	0.10312847	-8.737626	2.38E-18	8.21E-18
LOC100646928	2300.63065	-0.900591388	0.06598808	-13.647788	2.08E-42	3.27E-41
LOC100645929	1431.8389	-0.900361335	0.11086986	-8.1208849	4.63E-16	1.40E-15
LOC100645441	2209.00665	-0.900215038	0.0775933	-11.601711	4.04E-31	2.97E-30
LOC100645330	444.900745	-0.900142134	0.10839823	-8.3040296	1.01E-16	3.16E-16
LOC100647717	16.4767931	-0.899071753	0.39448677	-2.2790923	0.02266158	0.02804696
LOC100650165	482.480206	-0.898980571	0.10562863	-8.5107661	1.73E-17	5.67E-17
LOC100647338	418.422777	-0.898889856	0.10254454	-8.765848	1.85E-18	6.45E-18
LOC105666232	26.3901404	-0.898861222	0.24851616	-3.6169126	0.00029814	0.00042909
LOC100645311	228.939327	-0.898680432	0.10256821	-8.7617834	1.92E-18	6.68E-18
LOC100645849	10201.757	-0.898536137	0.11205233	-8.0188976	1.07E-15	3.15E-15
LOC100643312	600.626438	-0.898394144	0.15282399	-5.87862	4.14E-09	8.23E-09
LOC100643345	670.307486	-0.898345305	0.17134795	-5.2428133	1.58E-07	2.84E-07
LOC100649405	978.454925	-0.898260194	0.22150966	-4.055174	5.01E-05	7.66E-05
LOC100649024	698.716756	-0.898027645	0.08300363	-10.819137	2.79E-27	1.63E-26
LOC100643426	44.4022634	-0.897879372	0.28087969	-3.1966689	0.00139024	0.00189951
LOC100647548	180.436674	-0.897183582	0.1207588	-7.4295501	1.09E-13	2.86E-13
LOC100645639	1687.51839	-0.897040991	0.08813226	-10.17835	2.48E-24	1.19E-23
LOC100650424	334.444033	-0.896181738	0.09138781	-9.8063592	1.06E-22	4.62E-22
LOC100652312	341.801025	-0.896043405	0.09762371	-9.1785432	4.37E-20	1.68E-19
LOC100648613	1708.06433	-0.895972405	0.08676679	-10.326214	5.36E-25	2.71E-24
LOC100651328	599.356679	-0.895564685	0.08136455	-11.006817	3.54E-28	2.18E-27
LOC100643311	203.227458	-0.895480735	0.13449581	-6.6580566	2.77E-11	6.28E-11
LOC100644166	1359.93751	-0.895474412	0.08415527	-10.64074	1.93E-26	1.06E-25
LOC105665963	46.7235564	-0.895043691	0.29636781	-3.0200435	0.00252738	0.00338935
LOC100642939	537.415247	-0.894212368	0.08904175	-10.042619	9.90E-24	4.61E-23
LOC100643954	244.482818	-0.894015991	0.09643276	-9.2708745	1.85E-20	7.21E-20

LOC100643790	327.71211	-0.893616163	0.22939861	-3.8954732	9.80E-05	0.00014637
LOC100651584	1238.33011	-0.893547854	0.05976982	-14.949816	1.56E-50	4.42E-49
LOC100642793	697.163364	-0.893003459	0.09338833	-9.5622597	1.15E-21	4.79E-21
LOC100644359	343.981446	-0.892938046	0.09434368	-9.4647364	2.94E-21	1.20E-20
LOC100649289	2773.34853	-0.892904701	0.07494884	-11.913523	1.01E-32	8.06E-32
LOC100645940	2759.46206	-0.892635571	0.0728296	-12.256494	1.55E-34	1.42E-33
LOC100647801	330.543307	-0.892344665	0.08870709	-10.059452	8.35E-24	3.90E-23
LOC100651641	143.425114	-0.892223608	0.1368727	-6.5186382	7.09E-11	1.56E-10
LOC105666067	159.110902	-0.892084768	0.19393515	-4.5999128	4.23E-06	6.91E-06
LOC100649726	3064.13354	-0.891994407	0.08435593	-10.574175	3.93E-26	2.12E-25
LOC100647930	149.626454	-0.891459739	0.25791555	-3.4564017	0.00054744	0.00077211
LOC105665640	1848.96228	-0.89123487	0.09803866	-9.0906471	9.85E-20	3.70E-19
LOC100642285	674.202125	-0.891040653	0.11463863	-7.7726038	7.69E-15	2.16E-14
LOC100642349	2047.76246	-0.890950845	0.10682934	-8.3399455	7.43E-17	2.36E-16
LOC100650226	150.691422	-0.890752042	0.12594001	-7.072828	1.52E-12	3.72E-12
LOC100642670	191.752842	-0.890495725	0.10649342	-8.3619787	6.17E-17	1.97E-16
LOC100647610	3380.85672	-0.890074448	0.05883353	-15.128693	1.05E-51	3.29E-50
LOC100651017	300.466516	-0.889471613	0.12495782	-7.1181746	1.09E-12	2.71E-12
LOC100645867	381.922838	-0.889246591	0.09929875	-8.9552651	3.39E-19	1.24E-18
LOC105665888	111.588363	-0.888604617	0.14053277	-6.3231132	2.56E-10	5.46E-10
LOC100645725	840.865655	-0.888164189	0.11221797	-7.9146343	2.48E-15	7.18E-15
LOC100646844	216.739604	-0.887634188	0.15513432	-5.7217139	1.05E-08	2.04E-08
LOC100646694	1877.16355	-0.887134125	0.08250378	-10.752648	5.76E-27	3.30E-26
LOC100651603	2169.10819	-0.886922686	0.16551288	-5.3586325	8.39E-08	1.53E-07
LOC100645196	257.84232	-0.886473896	0.23389603	-3.7900339	0.00015063	0.00022184
LOC100647594	1364.02318	-0.886406004	0.08646684	-10.251398	1.17E-24	5.75E-24
LOC100642933	270.306467	-0.885888102	0.11039965	-8.0243744	1.02E-15	3.02E-15
LOC105666118	198.285256	-0.885723612	0.15783307	-5.6117745	2.00E-08	3.81E-08
LOC100642807	50380.8301	-0.885239447	0.06965318	-12.709247	5.25E-37	5.62E-36

LOC100647690	305.302034	-0.885135536	0.09536543	-9.281514	1.67E-20	6.55E-20
LOC100645971	3505.93486	-0.883852	0.11446364	-7.7216836	1.15E-14	3.19E-14
LOC100642401	2669.54116	-0.883592988	0.08584501	-10.292887	7.59E-25	3.80E-24
LOC100651458	473.471923	-0.883491539	0.08585055	-10.291041	7.73E-25	3.87E-24
LOC100643509	4918.70373	-0.883402063	0.06591195	-13.40276	5.83E-41	8.24E-40
LOC100650341	1434.217	-0.883284416	0.12848439	-6.874644	6.21E-12	1.47E-11
LOC100649237	223.736322	-0.883116976	0.13285637	-6.6471556	2.99E-11	6.74E-11
LOC105665816	66.0362878	-0.882975163	0.208122	-4.2425844	2.21E-05	3.45E-05
LOC100645358	1721.44671	-0.882729673	0.11852363	-7.4477105	9.50E-14	2.51E-13
LOC100651403	2564.61782	-0.882607639	0.11647378	-7.5777365	3.52E-14	9.51E-14
LOC100643028	3413.35661	-0.881766291	0.06246629	-14.115875	3.03E-45	5.81E-44
LOC100646821	1223.51944	-0.881416063	0.10738566	-8.207949	2.25E-16	6.93E-16
LOC100650318	1887.02429	-0.881404461	0.30965075	-2.846447	0.00442101	0.00579466
LOC100644276	2970.00602	-0.881254804	0.06437995	-13.688343	1.19E-42	1.90E-41
LOC100646029	50.8891602	-0.880800641	0.32037139	-2.7493112	0.00597207	0.00773446
LOC100651480	985.127272	-0.880501505	0.10790102	-8.1602702	3.34E-16	1.02E-15
LOC100652100	745.398288	-0.879011237	0.08642688	-10.170577	2.68E-24	1.29E-23
LOC100651521	1452.7196	-0.878952234	0.10199706	-8.6174271	6.85E-18	2.30E-17
LOC100650016	588.229707	-0.878573892	0.15902624	-5.5247101	3.30E-08	6.19E-08
LOC100650820	4789.59194	-0.878015336	0.13733977	-6.3930158	1.63E-10	3.49E-10
LOC100645338	3817.04802	-0.877635758	0.12281855	-7.1457916	8.95E-13	2.23E-12
LOC100646963	505.279009	-0.877467251	0.11196996	-7.8366311	4.63E-15	1.32E-14
LOC105666124	44.1625887	-0.877410566	0.21814493	-4.0221452	5.77E-05	8.78E-05
LOC100650726	292.088942	-0.877360892	0.20377647	-4.3055063	1.67E-05	2.62E-05
LOC100650541	733.434205	-0.877067316	0.11407773	-7.6883305	1.49E-14	4.12E-14
LOC100646610	5174.78277	-0.877055303	0.05906198	-14.849745	6.98E-50	1.89E-48
LOC100645516	1561.62559	-0.876351352	0.10920816	-8.0245959	1.02E-15	3.01E-15
LOC100650842	551.845217	-0.875866862	0.07914095	-11.067176	1.81E-28	1.14E-27
LOC100642920	1177.40462	-0.874429796	0.06702542	-13.046241	6.68E-39	8.11E-38

LOC100650708	3742.61475	-0.873462897	0.15676031	-5.5719644	2.52E-08	4.76E-08
LOC100649166	1491.92576	-0.873039722	0.15461732	-5.6464549	1.64E-08	3.13E-08
LOC105666861	39.4020978	-0.872569337	0.25182147	-3.4650316	0.00053017	0.00074894
LOC100651144	349.48651	-0.872186672	0.09706953	-8.9851746	2.58E-19	9.51E-19
LOC105665630	1728.82473	-0.872023978	0.07705817	-11.316438	1.09E-29	7.35E-29
LOC100646747	560.176571	-0.871981295	0.17491672	-4.9851226	6.19E-07	1.08E-06
LOC100647102	718.819975	-0.871765128	0.08577213	-10.163734	2.88E-24	1.38E-23
LOC100651020	1006.09585	-0.871173752	0.10845221	-8.0327892	9.53E-16	2.82E-15
LOC105666811	2332.57333	-0.870377683	0.06696764	-12.996989	1.27E-38	1.52E-37
LOC100642454	3587.96308	-0.870309887	0.13013241	-6.6878796	2.26E-11	5.15E-11
LOC100651694	1564.7704	-0.869733056	0.06800612	-12.789041	1.89E-37	2.09E-36
LOC100642549	748.560309	-0.868193918	0.07910405	-10.97534	5.02E-28	3.07E-27
LOC100650680	1203.96934	-0.868099237	0.15820235	-5.4872713	4.08E-08	7.61E-08
LOC100646734	410.800267	-0.86784831	0.10111894	-8.5824507	9.29E-18	3.10E-17
LOC100646070	1931.50701	-0.867824657	0.137629	-6.3055364	2.87E-10	6.10E-10
LOC100650613	698.520527	-0.867417916	0.0936879	-9.258591	2.07E-20	8.06E-20
LOC100651430	98.0863296	-0.86722444	0.1323766	-6.5511913	5.71E-11	1.26E-10
LOC100649695	787.2674	-0.867116002	0.15571255	-5.5686969	2.57E-08	4.85E-08
LOC100648034	1167.08263	-0.866970437	0.08243988	-10.516397	7.26E-26	3.87E-25
LOC100648104	4722.57447	-0.866243618	0.07918776	-10.93911	7.49E-28	4.53E-27
LOC100648793	3704.66822	-0.86575169	0.09331752	-9.2774827	1.74E-20	6.80E-20
LOC100644576	55.7771024	-0.865698732	0.19022832	-4.5508404	5.34E-06	8.68E-06
LOC100649195	874.64985	-0.864590014	0.10732349	-8.0559255	7.89E-16	2.35E-15
LOC105666230	330.969082	-0.864025979	0.12184981	-7.0909094	1.33E-12	3.28E-12
LOC100650221	1796.80335	-0.8636512	0.1706852	-5.0599068	4.19E-07	7.35E-07
LOC100652198	878.13186	-0.863291302	0.06974083	-12.378564	3.41E-35	3.26E-34
LOC100643536	3500.8254	-0.863275186	0.19219851	-4.491581	7.07E-06	1.14E-05
LOC105665906	1033.57765	-0.863245001	0.07026112	-12.286241	1.07E-34	9.92E-34
LOC100650394	43.1697657	-0.863054049	0.30840382	-2.7984544	0.00513478	0.0066908

LOC100652199	43309.8735	-0.862632049	0.22167457	-3.8914343	9.97E-05	0.00014874
LOC100644996	265.748724	-0.861985798	0.16395463	-5.2574655	1.46E-07	2.63E-07
LOC100650674	914.398134	-0.861259132	0.15777639	-5.4587328	4.80E-08	8.89E-08
LOC100649757	744.831268	-0.861124692	0.09341501	-9.2182685	3.02E-20	1.17E-19
LOC100651018	1520.17349	-0.860730172	0.08018563	-10.73422	7.03E-27	4.00E-26
LOC100643871	49827.2472	-0.860260888	0.41495652	-2.073135	0.03815971	0.04628041
LOC105666291	28.8558848	-0.860208953	0.26751723	-3.2155272	0.00130205	0.00178224
LOC100651027	591.732642	-0.859961009	0.09895472	-8.6904496	3.61E-18	1.23E-17
LOC100648765	2821.9055	-0.8590209	0.11693865	-7.345911	2.04E-13	5.28E-13
LOC100644264	936.245722	-0.858771897	0.11083091	-7.7484873	9.30E-15	2.60E-14
LOC100643026	59.6367095	-0.858707061	0.19975792	-4.2987385	1.72E-05	2.70E-05
LOC100650956	30.7689651	-0.85838856	0.27221309	-3.1533698	0.00161397	0.00219295
LOC100647558	658.36472	-0.857713409	0.06777469	-12.655365	1.04E-36	1.10E-35
LOC100643604	678.336316	-0.857686076	0.08423182	-10.182447	2.38E-24	1.14E-23
LOC100648319	664.914223	-0.857430541	0.10843023	-7.9076709	2.62E-15	7.58E-15
LOC100645320	517.956343	-0.857415516	0.09430508	-9.0919334	9.73E-20	3.66E-19
LOC105666383	16.1646625	-0.856915151	0.31547596	-2.7162613	0.00660238	0.00853047
LOC100647992	558.564197	-0.856849486	0.09313708	-9.1998748	3.58E-20	1.38E-19
LOC100643503	509.749368	-0.856450603	0.19193455	-4.4622014	8.11E-06	1.30E-05
LOC100650345	723.702401	-0.856226237	0.29302679	-2.9220066	0.00347784	0.00459845
LOC100643946	367.471216	-0.855684656	0.12182531	-7.0238658	2.16E-12	5.24E-12
LOC100652236	485.746654	-0.855347194	0.08967618	-9.5381764	1.45E-21	6.01E-21
LOC100648429	334.440156	-0.855101428	0.2409612	-3.5487101	0.00038712	0.00055309
LOC100651172	3906.29642	-0.854781205	0.17767657	-4.8108832	1.50E-06	2.53E-06
LOC100650277	737.926046	-0.853438999	0.17237185	-4.9511508	7.38E-07	1.28E-06
LOC100647487	234.302462	-0.85334404	0.12641289	-6.7504509	1.47E-11	3.40E-11
LOC100644970	2727.04388	-0.853201592	0.06979137	-12.22503	2.28E-34	2.06E-33
LOC100652330	623.281626	-0.852743573	0.10494738	-8.1254393	4.46E-16	1.35E-15
LOC100646020	768.988238	-0.851406731	0.11694576	-7.2803556	3.33E-13	8.51E-13

LOC100646187	12890.6798	-0.85140529	0.08798129	-9.6771177	3.77E-22	1.61E-21
LOC105666365	69.3776348	-0.851137668	0.29020877	-2.9328461	0.0033587	0.00445054
LOC100646257	3270.36437	-0.850889688	0.1021811	-8.3272705	8.27E-17	2.62E-16
LOC100645665	1213.10656	-0.850789399	0.14931766	-5.6978486	1.21E-08	2.34E-08
LOC100646006	547.968412	-0.850388393	0.1082299	-7.8572405	3.93E-15	1.12E-14
LOC100646557	2323.60564	-0.850220187	0.08429529	-10.086213	6.36E-24	2.99E-23
LOC100649049	358.881862	-0.850155834	0.13671301	-6.2185437	5.02E-10	1.05E-09
LOC100648211	874.336916	-0.848572095	0.10977031	-7.7304339	1.07E-14	2.98E-14
LOC100648675	683.698282	-0.848475404	0.11137193	-7.6183951	2.57E-14	7.00E-14
LOC100646700	213.028746	-0.846753525	0.25005978	-3.3862044	0.00070867	0.00098924
LOC100643406	7740.79029	-0.846644753	0.13952384	-6.0681008	1.29E-09	2.65E-09
LOC100649631	251.887034	-0.845317918	0.11055872	-7.6458731	2.08E-14	5.69E-14
LOC100642447	109.268992	-0.844985127	0.24760529	-3.4126296	0.00064339	0.00090101
LOC100642376	1609.98643	-0.84458151	0.09430831	-8.9555364	3.38E-19	1.24E-18
LOC100642459	30.2635149	-0.844239625	0.28751018	-2.9363817	0.00332065	0.0044043
LOC100650239	17.5537064	-0.843852434	0.34663627	-2.4344032	0.01491637	0.01873107
LOC105666621	2066.91732	-0.843322009	0.11447323	-7.3669804	1.75E-13	4.53E-13
LOC105666561	28.1278666	-0.84229351	0.2916327	-2.8881998	0.00387454	0.00510367
LOC105665885	21.121598	-0.841884035	0.32872937	-2.5610247	0.01043639	0.01329985
LOC100646414	205.7919	-0.84091524	0.20151916	-4.1728799	3.01E-05	4.66E-05
LOC100644197	1359.04843	-0.840707289	0.07431646	-11.312532	1.14E-29	7.68E-29
LOC105666036	101.662265	-0.840573373	0.19309236	-4.3532192	1.34E-05	2.13E-05
LOC105665610	541.181646	-0.840435743	0.07095381	-11.844829	2.29E-32	1.80E-31
LOC105666829	293.208543	-0.839925859	0.34194841	-2.4562941	0.01403782	0.01766409
LOC100649054	778.461062	-0.839549536	0.09994251	-8.4003244	4.45E-17	1.43E-16
LOC100651426	398.358914	-0.838890416	0.08898019	-9.4278333	4.19E-21	1.70E-20
LOC100648586	71.6626989	-0.838598947	0.16364392	-5.1245348	2.98E-07	5.28E-07
LOC100643699	230.762802	-0.838597753	0.1714049	-4.8924957	9.96E-07	1.70E-06
LOC100651960	757.101761	-0.838576423	0.12960326	-6.4703344	9.78E-11	2.13E-10

LOC100647302	1102.35509	-0.83851976	0.09207449	-9.1069716	8.47E-20	3.20E-19
LOC100643726	340.405544	-0.838334304	0.10075904	-8.3201895	8.78E-17	2.77E-16
LOC100648329	243.385991	-0.838067423	0.09815774	-8.5379658	1.37E-17	4.52E-17
LOC105665622	508.107123	-0.837773972	0.11668019	-7.1800872	6.97E-13	1.75E-12
LOC100646214	590.525918	-0.837251525	0.15414673	-5.4315231	5.59E-08	1.03E-07
LOC100649622	1729.66389	-0.836698896	0.07399839	-11.306988	1.21E-29	8.17E-29
LOC100648706	702.404492	-0.836604494	0.18352248	-4.5585941	5.15E-06	8.38E-06
LOC100642552	5364.02428	-0.836001431	0.0582477	-14.352523	1.03E-46	2.17E-45
LOC100648334	721.902026	-0.835198249	0.10153298	-8.2258813	1.94E-16	6.00E-16
LOC100643550	57.5769759	-0.835100895	0.22908479	-3.645379	0.000267	0.00038607
LOC100645503	2227.06154	-0.834879487	0.14850167	-5.6220207	1.89E-08	3.59E-08
LOC100650129	451.837664	-0.8347557	0.10611689	-7.8663792	3.65E-15	1.05E-14
LOC100643611	597.870781	-0.834719182	0.09973222	-8.3696037	5.78E-17	1.85E-16
LOC100643224	91.1597113	-0.834567331	0.22544443	-3.701876	0.00021401	0.00031172
LOC100651999	223.245906	-0.834184769	0.1183724	-7.0471223	1.83E-12	4.46E-12
LOC100649924	475.228803	-0.83348227	0.08459121	-9.8530605	6.65E-23	2.94E-22
LOC100649876	532.343918	-0.833478478	0.07918283	-10.526	6.56E-26	3.50E-25
LOC100648700	374.521753	-0.83343048	0.07263026	-11.474975	1.76E-30	1.25E-29
LOC100649100	540.400822	-0.833264851	0.07679105	-10.851067	1.97E-27	1.16E-26
LOC100647924	2998.44951	-0.833211676	0.07945097	-10.487117	9.90E-26	5.23E-25
LOC100644289	764.409075	-0.83306679	0.11362517	-7.33171	2.27E-13	5.85E-13
LOC100648710	1290.72253	-0.832265071	0.06695913	-12.429448	1.81E-35	1.76E-34
LOC100649077	70.3466142	-0.832065148	0.19497261	-4.2676002	1.98E-05	3.10E-05
LOC100645765	1337.74402	-0.831361577	0.09456678	-8.7912646	1.48E-18	5.17E-18
LOC100642256	2141.62442	-0.831311416	0.10671928	-7.789702	6.72E-15	1.89E-14
LOC100648668	626.295318	-0.830928488	0.09769168	-8.5056215	1.81E-17	5.91E-17
LOC100648774	1059.01936	-0.830828898	0.07975048	-10.417854	2.06E-25	1.07E-24
LOC100650837	1187.27354	-0.830434109	0.07878255	-10.540839	5.60E-26	3.00E-25
LOC100644371	872.219048	-0.830050288	0.10053985	-8.2559332	1.51E-16	4.69E-16

LOC100651199	52.2103474	-0.829940795	0.22841196	-3.633526	0.00027957	0.00040344
LOC100645837	1958.00993	-0.829695836	0.12629678	-6.5694143	5.05E-11	1.12E-10
LOC100642445	475.484824	-0.829470721	0.08627545	-9.6142153	6.96E-22	2.92E-21
LOC105666051	56.2488904	-0.829450225	0.27255532	-3.0432363	0.00234048	0.00314689
LOC105666298	215.190689	-0.829306499	0.15606878	-5.3137246	1.07E-07	1.95E-07
LOC100644767	124.306642	-0.828986093	0.25832961	-3.2090246	0.00133186	0.00182228
LOC100652114	54.6505325	-0.827234008	0.19342506	-4.2767675	1.90E-05	2.98E-05
LOC100642457	914.851634	-0.827214783	0.11611791	-7.1239204	1.05E-12	2.60E-12
LOC100652046	457.118792	-0.826866444	0.09659332	-8.5602856	1.13E-17	3.74E-17
LOC100646890	167.205456	-0.825724394	0.11142006	-7.4109134	1.25E-13	3.28E-13
LOC100646392	199.519665	-0.82562879	0.11534148	-7.1581258	8.18E-13	2.04E-12
LOC100646710	640.942864	-0.825455104	0.09960968	-8.286896	1.16E-16	3.64E-16
LOC100648865	1506.68111	-0.824923619	0.0651787	-12.656338	1.03E-36	1.09E-35
LOC100643881	536.794879	-0.824583983	0.0725847	-11.3603	6.59E-30	4.52E-29
LOC100650719	469.564787	-0.824382462	0.08666819	-9.5119381	1.87E-21	7.69E-21
LOC100648305	49819.5086	-0.824155501	0.35398374	-2.3282298	0.01989991	0.02474787
LOC105665653	308.615617	-0.82410447	0.14162877	-5.8187647	5.93E-09	1.17E-08
LOC100643448	4655.7689	-0.823987766	0.08606802	-9.5736814	1.03E-21	4.29E-21
LOC100649444	1195.11405	-0.823953003	0.08447368	-9.7539615	1.77E-22	7.67E-22
LOC100651819	302.343325	-0.823645543	0.09394311	-8.7674929	1.83E-18	6.36E-18
LOC100650192	318.336232	-0.823520127	0.10086816	-8.1643218	3.23E-16	9.84E-16
LOC100644601	622.011009	-0.822693042	0.07669237	-10.727183	7.59E-27	4.30E-26
LOC100647503	529.39251	-0.82205117	0.30858959	-2.6638979	0.0077241	0.0099325
LOC100647941	108.800891	-0.82203099	0.19455028	-4.2252882	2.39E-05	3.72E-05
LOC100651450	78.834867	-0.821948435	0.18608273	-4.417113	1.00E-05	1.60E-05
LOC100644156	212.454907	-0.821757046	0.15253914	-5.387188	7.16E-08	1.31E-07
LOC100651847	28.4287299	-0.821668833	0.2763132	-2.9736865	0.00294246	0.00392341
LOC100647231	791.907401	-0.820981319	0.07317454	-11.219494	3.27E-29	2.14E-28
LOC105666055	80.7022941	-0.820307314	0.18333598	-4.4743389	7.66E-06	1.23E-05

LOC105665884	1225.85209	-0.819891939	0.06184305	-13.257625	4.08E-40	5.43E-39
LOC100649625	2161.52981	-0.819601884	0.08821605	-9.2908474	1.53E-20	6.02E-20
LOC100651113	4946.40813	-0.819105068	0.06235266	-13.13665	2.03E-39	2.56E-38
LOC100649364	1142.38354	-0.818923671	0.20805818	-3.9360321	8.28E-05	0.00012453
LOC100646667	5489.15028	-0.818444281	0.21934218	-3.7313584	0.00019045	0.00027885
LOC100649313	1821.18453	-0.818424745	0.07574328	-10.805245	3.25E-27	1.90E-26
LOC100645594	37.7266659	-0.817868765	0.22649653	-3.610955	0.00030507	0.00043874
LOC100647264	2001.9537	-0.817122553	0.06284803	-13.001561	1.20E-38	1.43E-37
LOC100647894	5594.95818	-0.817122312	0.06221254	-13.134366	2.09E-39	2.64E-38
LOC100647245	1174.05705	-0.817097641	0.11276335	-7.2461279	4.29E-13	1.09E-12
LOC100647815	679.035558	-0.81648603	0.12700277	-6.4288839	1.29E-10	2.77E-10
LOC100642556	373.85677	-0.816460403	0.19893864	-4.1040817	4.06E-05	6.23E-05
LOC100651747	2001.56048	-0.816408835	0.23888059	-3.4176441	0.00063166	0.00088515
LOC100643331	1413.18659	-0.816142908	0.11896247	-6.8605077	6.86E-12	1.62E-11
LOC100650767	438.51946	-0.815933397	0.10180892	-8.0143603	1.11E-15	3.27E-15
LOC105666626	19.1162394	-0.815773413	0.38678681	-2.1091035	0.03493565	0.0424702
LOC105666110	767.80106	-0.815714869	0.1057787	-7.7115231	1.24E-14	3.44E-14
LOC100643956	747.824034	-0.815644705	0.08100215	-10.069421	7.54E-24	3.53E-23
LOC100643373	275.572695	-0.815115242	0.0868232	-9.3882194	6.10E-21	2.45E-20
LOC100651248	1002.41635	-0.814207507	0.10371518	-7.8504181	4.15E-15	1.18E-14
LOC100649147	205.798472	-0.813963749	0.12867197	-6.3258825	2.52E-10	5.36E-10
LOC100652248	67.6525297	-0.813958696	0.19480921	-4.1782352	2.94E-05	4.56E-05
LOC100649635	358.553497	-0.812873365	0.38894116	-2.0899649	0.03662095	0.04448031
LOC105666089	222.642985	-0.812164872	0.11031449	-7.3622683	1.81E-13	4.68E-13
LOC100650963	712.842365	-0.811791076	0.08816369	-9.2077708	3.33E-20	1.28E-19
LOC100643096	566.382159	-0.811516494	0.07633444	-10.631066	2.14E-26	1.18E-25
LOC100648521	2269.28318	-0.811273816	0.12216883	-6.6405957	3.12E-11	7.04E-11
LOC100651246	392.075154	-0.810267771	0.0905229	-8.9509703	3.52E-19	1.29E-18
LOC100647564	59.8621775	-0.810258061	0.2072962	-3.9086971	9.28E-05	0.00013888

LOC100644684	567.737709	-0.8102279	0.07115862	-11.386222	4.90E-30	3.40E-29
LOC100651312	539.921046	-0.810200651	0.1322843	-6.1246923	9.09E-10	1.88E-09
LOC100651572	1870.88403	-0.809516897	0.0810209	-9.9914582	1.66E-23	7.60E-23
LOC100651388	543.648349	-0.808773959	0.09969432	-8.1125379	4.96E-16	1.49E-15
LOC100648897	312.502364	-0.808557155	0.09026767	-8.9573281	3.33E-19	1.22E-18
LOC100643263	247.014456	-0.808398132	0.19898978	-4.0625109	4.85E-05	7.43E-05
LOC100648949	236.107364	-0.808161068	0.10988522	-7.3545928	1.92E-13	4.96E-13
LOC100647440	683.767472	-0.808114684	0.11510051	-7.0209478	2.20E-12	5.35E-12
LOC100651544	3084.34769	-0.807430555	0.06240724	-12.938091	2.74E-38	3.21E-37
LOC100649489	346.304316	-0.807360854	0.12404867	-6.50842	7.59E-11	1.66E-10
LOC100650694	498.919567	-0.807148573	0.10781452	-7.4864552	7.08E-14	1.88E-13
LOC105665798	20.2282371	-0.806360073	0.31016005	-2.5998193	0.00932729	0.01192368
LOC100646656	281.55356	-0.805983912	0.15548138	-5.1837969	2.17E-07	3.88E-07
LOC100651178	716.464706	-0.805788706	0.08855707	-9.0990896	9.11E-20	3.43E-19
LOC100642794	284.674557	-0.805084598	0.10638802	-7.5674363	3.81E-14	1.03E-13
LOC100650785	3068.16873	-0.80502959	0.10709534	-7.5169432	5.61E-14	1.50E-13
LOC100647048	1901.84747	-0.804919478	0.07826673	-10.284312	8.29E-25	4.13E-24
LOC100645582	508.498453	-0.804682472	0.09453721	-8.511807	1.71E-17	5.62E-17
LOC100645953	1259.1277	-0.804665144	0.08829707	-9.1131584	8.00E-20	3.03E-19
LOC100649641	12.9677797	-0.803848541	0.31734281	-2.5330605	0.01130714	0.01434974
LOC100645028	3347.24737	-0.802642905	0.06185503	-12.976195	1.67E-38	1.98E-37
LOC100651842	429.699713	-0.802427696	0.09903416	-8.1025343	5.38E-16	1.62E-15
LOC105666743	118.043611	-0.801441894	0.23385331	-3.4271138	0.00061003	0.00085583
LOC100642942	61.8345789	-0.801396146	0.27123593	-2.954609	0.00313065	0.00416471
LOC100651657	1241.94791	-0.801334029	0.07631047	-10.500971	8.55E-26	4.53E-25
LOC100650418	818.247757	-0.801189149	0.09089744	-8.8142104	1.21E-18	4.24E-18
LOC100645493	506.975239	-0.801174017	0.07415096	-10.804634	3.27E-27	1.91E-26
LOC105665747	860.741468	-0.800540051	0.08536667	-9.3776657	6.74E-21	2.70E-20
LOC100648444	773.723278	-0.800349926	0.09992973	-8.0091273	1.16E-15	3.40E-15

LOC100650983	327.257309	-0.800046687	0.10007082	-7.9948047	1.30E-15	3.81E-15
LOC100646899	998.548389	-0.799008393	0.09385902	-8.5128571	1.70E-17	5.58E-17
LOC105665678	1275.70435	-0.798661663	0.07909635	-10.097326	5.68E-24	2.67E-23
LOC100649471	1750.94975	-0.798640019	0.07477774	-10.680183	1.26E-26	7.04E-26
LOC100644844	3262.58848	-0.798359317	0.09440695	-8.456574	2.75E-17	8.90E-17
LOC100651223	886.756161	-0.798336332	0.0744946	-10.716701	8.50E-27	4.80E-26
LOC100651237	49.4316441	-0.798051305	0.22455379	-3.5539427	0.0003795	0.00054244
LOC100648327	1836.88616	-0.797899081	0.0921243	-8.661114	4.67E-18	1.58E-17
LOC100651962	544.408376	-0.797827601	0.0720966	-11.066092	1.83E-28	1.15E-27
LOC100648186	533.213196	-0.797781606	0.11304334	-7.0573075	1.70E-12	4.15E-12
LOC100643261	417.905844	-0.797672188	0.09040643	-8.8231796	1.11E-18	3.92E-18
LOC100648846	45.7535338	-0.797657261	0.31492724	-2.5328303	0.01131457	0.0143573
LOC100651332	2038.91884	-0.795071438	0.06779812	-11.727042	9.26E-32	7.07E-31
LOC100645332	1347.86272	-0.794618667	0.07123863	-11.154323	6.82E-29	4.40E-28
LOC100642757	1912.82755	-0.794342045	0.07916274	-10.034291	1.08E-23	5.00E-23
LOC100645760	291.442774	-0.79365971	0.11890632	-6.6746637	2.48E-11	5.62E-11
LOC100644277	447.103954	-0.793523574	0.10712684	-7.407327	1.29E-13	3.37E-13
LOC100649862	2158.6999	-0.792523555	0.075106	-10.552067	4.97E-26	2.67E-25
LOC100652060	970.987065	-0.791975521	0.08175824	-9.686797	3.43E-22	1.46E-21
LOC100649510	356.86807	-0.791082446	0.10113818	-7.821798	5.21E-15	1.47E-14
LOC100644506	576.546827	-0.790845994	0.2236148	-3.5366442	0.00040525	0.00057822
LOC100645298	167.315852	-0.790390978	0.38557758	-2.0498883	0.04037533	0.04884652
LOC100651729	229.538779	-0.789683482	0.17962126	-4.396381	1.10E-05	1.76E-05
LOC100649211	2446.14016	-0.78958601	0.14443164	-5.4668493	4.58E-08	8.50E-08
LOC100651643	437.422304	-0.789383172	0.09513955	-8.2971084	1.07E-16	3.35E-16
LOC100646480	1546.28249	-0.789350707	0.06579204	-11.997663	3.65E-33	3.02E-32
LOC100647810	140.593269	-0.788925833	0.17064948	-4.6230779	3.78E-06	6.20E-06
LOC100645547	1804.7187	-0.788663	0.09799661	-8.04786	8.43E-16	2.51E-15
LOC100644609	2446.19522	-0.787018568	0.09465148	-8.3149103	9.18E-17	2.90E-16

LOC100644907	60.3534808	-0.786970082	0.27566511	-2.8548048	0.00430633	0.00565343
LOC100631077	6263.43427	-0.786631063	0.06072865	-12.953213	2.25E-38	2.65E-37
LOC100642566	218.725354	-0.785766058	0.10607176	-7.4078724	1.28E-13	3.35E-13
LOC100643508	372.910284	-0.785401507	0.0922255	-8.5160988	1.65E-17	5.43E-17
LOC105666693	468.687845	-0.785192741	0.11055056	-7.1025666	1.22E-12	3.02E-12
LOC100646256	272.458274	-0.78516938	0.0906801	-8.6586733	4.77E-18	1.62E-17
LOC100651039	318.911346	-0.784412156	0.09215709	-8.5116856	1.71E-17	5.63E-17
LOC100643292	662.252612	-0.784117977	0.09594891	-8.1722445	3.03E-16	9.23E-16
LOC105665771	387.590147	-0.783906337	0.16731963	-4.6850828	2.80E-06	4.63E-06
LOC100651074	2154.59623	-0.78256614	0.08880819	-8.8118687	1.23E-18	4.32E-18
LOC100648544	2108.897	-0.781663351	0.05552147	-14.078577	5.14E-45	9.63E-44
LOC100651316	867.204887	-0.779199999	0.08442913	-9.2290421	2.73E-20	1.06E-19
LOC100652204	5020.83035	-0.778107196	0.16273852	-4.7813339	1.74E-06	2.93E-06
LOC100649312	461.102943	-0.77787155	0.08180519	-9.5088288	1.93E-21	7.92E-21
LOC100651214	138.551164	-0.776885321	0.27941667	-2.7803828	0.00542949	0.0070654
LOC100643583	15.8490628	-0.776518098	0.37268484	-2.0835785	0.03719853	0.04516503
LOC100649993	2673.8002	-0.776158447	0.08062507	-9.6267631	6.16E-22	2.59E-21
LOC100645252	85.7032922	-0.773338851	0.17128018	-4.5150517	6.33E-06	1.02E-05
LOC100644417	833.538371	-0.772890873	0.08044713	-9.6074386	7.44E-22	3.12E-21
LOC100642264	2114.17386	-0.772799527	0.09493419	-8.1403713	3.94E-16	1.19E-15
LOC100643850	1922.2577	-0.772629743	0.11215076	-6.8892065	5.61E-12	1.33E-11
LOC100644383	2846.55632	-0.772456266	0.07379787	-10.467189	1.22E-25	6.41E-25
LOC100643632	327.809138	-0.772088204	0.10771927	-7.1675961	7.63E-13	1.91E-12
LOC100643379	8849.68076	-0.771576334	0.09751265	-7.9125767	2.52E-15	7.29E-15
LOC100646412	338.917054	-0.77139612	0.15795731	-4.8835733	1.04E-06	1.78E-06
LOC105665749	1867.97779	-0.771216064	0.07345496	-10.499169	8.71E-26	4.62E-25
LOC100645341	246.588881	-0.770512652	0.11515435	-6.6911292	2.21E-11	5.04E-11
LOC100645802	43.288021	-0.77017039	0.21142449	-3.642768	0.00026972	0.00038991
LOC100643872	246.464486	-0.769693015	0.10208992	-7.5393634	4.72E-14	1.27E-13

LOC100644279	147.783034	-0.769024667	0.15677311	-4.9053353	9.33E-07	1.60E-06
LOC100647039	3053.60078	-0.768796725	0.1429247	-5.3790333	7.49E-08	1.37E-07
LOC100650245	924.231033	-0.768092681	0.10253367	-7.4911264	6.83E-14	1.82E-13
LOC100651745	477.127581	-0.768087024	0.09077006	-8.4618986	2.63E-17	8.53E-17
LOC100644733	573.934058	-0.767865447	0.08562637	-8.9676279	3.03E-19	1.11E-18
LOC100651701	590.534003	-0.767358581	0.08044679	-9.5387098	1.45E-21	5.98E-21
LOC100648471	257.715208	-0.767291029	0.10095681	-7.6001912	2.96E-14	8.04E-14
LOC100644376	1006.15159	-0.766936477	0.07523746	-10.193546	2.12E-24	1.03E-23
LOC100647423	482.19834	-0.766736491	0.1122499	-6.8306209	8.45E-12	1.98E-11
LOC100646880	757.24306	-0.766118177	0.07380845	-10.379816	3.06E-25	1.57E-24
LOC100643220	1677.72814	-0.765732683	0.06330534	-12.095862	1.11E-33	9.52E-33
LOC100645097	948.432243	-0.765412961	0.13133259	-5.8280507	5.61E-09	1.11E-08
LOC100644000	561.738311	-0.765268904	0.09945987	-7.694248	1.42E-14	3.93E-14
LOC105665663	1979.16063	-0.765180765	0.08155347	-9.3825656	6.44E-21	2.58E-20
LOC100643137	6726.33967	-0.765114308	0.07318089	-10.455111	1.39E-25	7.25E-25
LOC100642848	150.178244	-0.764657673	0.26401773	-2.8962361	0.00377668	0.00497879
LOC100650119	2197.68332	-0.764524356	0.14989557	-5.10038	3.39E-07	5.98E-07
LOC100644043	574.383877	-0.762193051	0.07283824	-10.464189	1.26E-25	6.61E-25
LOC100648083	2532.25027	-0.761719639	0.26768415	-2.8455911	0.00443291	0.00580792
LOC100646135	729.166405	-0.761579163	0.09318712	-8.1725801	3.02E-16	9.21E-16
LOC100642523	528.289742	-0.76133661	0.09233173	-8.2456664	1.64E-16	5.10E-16
LOC100643494	317.323377	-0.761285111	0.10587432	-7.1904604	6.46E-13	1.62E-12
LOC100644669	624.995244	-0.760990454	0.10492346	-7.2528151	4.08E-13	1.04E-12
LOC100648292	80.5218098	-0.760828399	0.20203889	-3.7657521	0.00016605	0.00024389
LOC100648046	5900.34865	-0.760324886	0.09542424	-7.9678383	1.61E-15	4.73E-15
LOC100646227	426.974575	-0.759835705	0.16173365	-4.6980681	2.63E-06	4.35E-06
LOC100651401	1304.62258	-0.759431857	0.09313771	-8.1538602	3.52E-16	1.07E-15
LOC105666159	59.3561115	-0.759383135	0.22836481	-3.3253071	0.00088321	0.00122521
LOC100648145	168.457213	-0.759351564	0.13612185	-5.5784694	2.43E-08	4.59E-08

LOC100642230	565.431088	-0.757573807	0.08964459	-8.4508589	2.89E-17	9.33E-17
LOC100646866	309.70677	-0.757049981	0.11216811	-6.7492441	1.49E-11	3.43E-11
LOC100648874	530.02905	-0.75702234	0.08919075	-8.4876778	2.11E-17	6.88E-17
LOC100648453	5904.80522	-0.756997134	0.11549842	-6.5541774	5.59E-11	1.24E-10
LOC100646838	1055.85215	-0.756796972	0.08489707	-8.9142883	4.91E-19	1.77E-18
LOC100651298	883.870536	-0.756546296	0.0804737	-9.401162	5.40E-21	2.17E-20
LOC100644452	50.1645523	-0.756394006	0.28657593	-2.6394192	0.00830482	0.01065695
LOC100642261	2110.74902	-0.756374633	0.1222701	-6.1860966	6.17E-10	1.28E-09
LOC100631095	5103.19792	-0.756344351	0.25807571	-2.9307072	0.00338191	0.00447887
LOC100650994	238.743261	-0.756197099	0.09476506	-7.9797039	1.47E-15	4.30E-15
LOC100648588	674.044593	-0.756006781	0.09598412	-7.8763736	3.37E-15	9.69E-15
LOC105666047	6320.26203	-0.755679056	0.0749902	-10.077038	6.98E-24	3.27E-23
LOC105667061	2345.04595	-0.75567118	0.1319588	-5.7265691	1.02E-08	1.99E-08
LOC100642514	1848.35393	-0.755390393	0.07767198	-9.7253917	2.35E-22	1.01E-21
LOC100651436	650.561075	-0.755288931	0.08118767	-9.3030008	1.37E-20	5.39E-20
LOC100650919	1374.98206	-0.755035736	0.11353688	-6.6501364	2.93E-11	6.61E-11
LOC100650696	1849.02985	-0.754682996	0.06336842	-11.909449	1.06E-32	8.45E-32
LOC100647516	2763.50441	-0.753313669	0.05459392	-13.798491	2.60E-43	4.37E-42
LOC100645543	2501.26857	-0.752873867	0.1076212	-6.9955907	2.64E-12	6.37E-12
LOC100645583	168.288538	-0.752684687	0.23669608	-3.1799626	0.00147294	0.00200662
LOC100643637	242.864757	-0.752683019	0.16885446	-4.4575845	8.29E-06	1.33E-05
LOC100648143	320.995006	-0.752008358	0.12034619	-6.2487094	4.14E-10	8.70E-10
LOC100646288	441.76038	-0.751048332	0.11629145	-6.458328	1.06E-10	2.30E-10
LOC100643307	14181.7169	-0.751003829	0.15581867	-4.8197293	1.44E-06	2.43E-06
LOC100648123	758.410404	-0.74950265	0.07578874	-9.8893665	4.63E-23	2.06E-22
LOC100651278	1199.93764	-0.749301772	0.09762727	-7.675128	1.65E-14	4.56E-14
LOC100646274	454.364312	-0.749150027	0.08430258	-8.8864424	6.31E-19	2.26E-18
LOC100649603	163.288375	-0.748869993	0.10820728	-6.9206991	4.49E-12	1.07E-11
LOC100650483	1216.54311	-0.748270636	0.0945264	-7.9159963	2.45E-15	7.11E-15

LOC100652102	618.372728	-0.74758964	0.0847779	-8.818214	1.16E-18	4.09E-18
LOC100648754	465.851933	-0.747018551	0.08685597	-8.6006583	7.93E-18	2.65E-17
LOC100648792	821.21612	-0.746656494	0.09966687	-7.4915214	6.81E-14	1.81E-13
LOC100650698	1031.08701	-0.746394836	0.10620401	-7.0279347	2.10E-12	5.10E-12
LOC105665927	397.763587	-0.746351761	0.11758668	-6.3472475	2.19E-10	4.68E-10
LOC100644680	1418.46757	-0.746259593	0.06855982	-10.884795	1.36E-27	8.08E-27
LOC100648962	2655.2043	-0.746047198	0.08077323	-9.2363177	2.55E-20	9.89E-20
LOC105665685	124.351098	-0.744073518	0.13714771	-5.4253442	5.78E-08	1.07E-07
LOC100652239	1936.00218	-0.743219724	0.10279318	-7.2302437	4.82E-13	1.22E-12
LOC100648634	20.6309249	-0.742869764	0.27815035	-2.670749	0.00756822	0.00973853
LOC100644759	265.484222	-0.742628005	0.09215435	-8.0585238	7.72E-16	2.30E-15
LOC100644544	626.929633	-0.742147342	0.07898953	-9.3955158	5.69E-21	2.29E-20
LOC100644165	503.356729	-0.741686935	0.0838487	-8.8455392	9.11E-19	3.23E-18
LOC100643599	809.110636	-0.741558987	0.11020699	-6.7287833	1.71E-11	3.92E-11
LOC100648592	31.0007001	-0.741445091	0.35041703	-2.1158934	0.03435387	0.04182526
LOC100647124	1040.46507	-0.740854509	0.06725791	-11.015128	3.23E-28	2.00E-27
LOC100644955	29.3595387	-0.740478285	0.25878472	-2.8613679	0.00421817	0.0055429
LOC100646892	551.445581	-0.739668815	0.12965613	-5.7048502	1.16E-08	2.25E-08
LOC100644859	753.410905	-0.739494354	0.06685786	-11.060695	1.95E-28	1.22E-27
LOC100650811	666.436488	-0.739477332	0.08601797	-8.5967774	8.20E-18	2.74E-17
LOC100647991	593.207153	-0.739172984	0.08662193	-8.5333243	1.42E-17	4.70E-17
LOC100642660	1690.40315	-0.739073344	0.08607872	-8.5860174	9.00E-18	3.01E-17
LOC100647910	791.555906	-0.738257498	0.20297884	-3.6371156	0.00027571	0.00039809
LOC100644347	754.16792	-0.737901857	0.06291704	-11.728171	9.14E-32	6.98E-31
LOC100642361	161.889244	-0.73769071	0.10406909	-7.0884711	1.36E-12	3.33E-12
LOC100648386	306.897739	-0.737665848	0.16925166	-4.3583966	1.31E-05	2.08E-05
LOC100645835	274.080695	-0.73749804	0.10073649	-7.3210618	2.46E-13	6.32E-13
LOC100644170	456.33936	-0.737371979	0.25865823	-2.8507578	0.00436152	0.00572204
LOC105666280	41.0169339	-0.737364959	0.21713991	-3.3958057	0.00068427	0.00095641

LOC100644892	811.264884	-0.737043452	0.12936185	-5.6975334	1.22E-08	2.35E-08
LOC100647392	881.238958	-0.736877494	0.08598688	-8.5696506	1.04E-17	3.45E-17
LOC100646732	1007.44361	-0.736774315	0.10863566	-6.7820667	1.18E-11	2.75E-11
LOC100642388	772.423397	-0.73626191	0.07514387	-9.7980306	1.15E-22	5.01E-22
LOC100651134	1127.80336	-0.736030475	0.22628382	-3.2526871	0.00114319	0.00157205
LOC105667089	160.632515	-0.735853927	0.1871603	-3.9316773	8.44E-05	0.00012664
LOC100631084	46051.4244	-0.735826907	0.07398385	-9.9457768	2.63E-23	1.19E-22
LOC100649854	345.223182	-0.735241633	0.09444593	-7.7847893	6.98E-15	1.96E-14
LOC100645767	197.692511	-0.735151259	0.12514632	-5.874334	4.25E-09	8.44E-09
LOC100649684	1166.11335	-0.735084047	0.06703935	-10.964964	5.63E-28	3.43E-27
LOC100651736	364.632978	-0.734681899	0.11002229	-6.6775734	2.43E-11	5.52E-11
LOC100647314	28.1797132	-0.734173794	0.32972444	-2.2266284	0.02597212	0.03196242
LOC100646007	490.108818	-0.734132001	0.1010919	-7.2620263	3.81E-13	9.73E-13
LOC100642411	175.080917	-0.734090839	0.19116786	-3.8400328	0.00012302	0.00018236
LOC100652139	470.347919	-0.733547362	0.10180026	-7.2057516	5.77E-13	1.46E-12
LOC100648882	791.347068	-0.73324609	0.06693405	-10.954754	6.30E-28	3.82E-27
LOC100647666	376.790571	-0.73246051	0.10318548	-7.0984841	1.26E-12	3.11E-12
LOC105666642	1185.00169	-0.731740748	0.07565774	-9.6717235	3.98E-22	1.69E-21
LOC100647411	102.281	-0.731639395	0.14104971	-5.1871033	2.14E-07	3.81E-07
LOC100644768	1535.05697	-0.731435639	0.06903053	-10.595829	3.12E-26	1.70E-25
LOC100643735	928.443595	-0.731288059	0.08332188	-8.7766627	1.68E-18	5.87E-18
LOC105666217	208.719679	-0.731252035	0.14381545	-5.0846557	3.68E-07	6.48E-07
LOC100650010	3705.06478	-0.731107121	0.10727827	-6.8150535	9.42E-12	2.20E-11
LOC100651624	1558.33905	-0.731062849	0.07676552	-9.5233236	1.68E-21	6.91E-21
LOC100649311	903.688035	-0.73103392	0.09239209	-7.9122994	2.53E-15	7.31E-15
LOC100646744	1224.33355	-0.730839001	0.06879234	-10.623842	2.31E-26	1.27E-25
LOC100650754	1411.10236	-0.730772827	0.08396893	-8.7028955	3.24E-18	1.11E-17
LOC100645089	1526.28328	-0.730684818	0.0780583	-9.3607581	7.92E-21	3.15E-20
LOC100651974	530.201731	-0.730629793	0.08211713	-8.8974099	5.72E-19	2.05E-18

LOC100643412	41.1435383	-0.730463664	0.33757116	-2.1638805	0.03047352	0.03724922
LOC100644337	81117.7329	-0.730450998	0.27242891	-2.6812536	0.00733469	0.00944548
LOC100647980	366.072063	-0.72972766	0.1033757	-7.0589865	1.68E-12	4.10E-12
LOC100650622	717.837047	-0.729519384	0.07236941	-10.080494	6.74E-24	3.16E-23
LOC100644845	1425.94722	-0.729248285	0.06473903	-11.264431	1.97E-29	1.30E-28
LOC100644262	219.58536	-0.728985991	0.12637353	-5.7685022	8.00E-09	1.56E-08
LOC100646221	281.366855	-0.728778658	0.21220795	-3.4342666	0.00059416	0.00083452
LOC100644365	1061.60872	-0.728630692	0.05383644	-13.534154	9.83E-42	1.48E-40
LOC100650402	1258.95521	-0.728340323	0.08184821	-8.898671	5.65E-19	2.03E-18
LOC100649989	1305.488	-0.726480293	0.11250954	-6.4570552	1.07E-10	2.32E-10
LOC100649227	232.600826	-0.726165551	0.08234238	-8.8188553	1.16E-18	4.07E-18
LOC100648018	764.237418	-0.725767113	0.05743581	-12.636143	1.33E-36	1.40E-35
LOC100643111	171.676406	-0.725731559	0.10926382	-6.6420114	3.09E-11	6.97E-11
LOC100644189	280.368928	-0.725222304	0.10445887	-6.9426592	3.85E-12	9.21E-12
LOC100642553	992.394134	-0.725061507	0.16194073	-4.4773265	7.56E-06	1.22E-05
LOC100650973	722.753934	-0.724940193	0.11884362	-6.0999502	1.06E-09	2.18E-09
LOC100647398	947.725037	-0.724760804	0.07939247	-9.1288353	6.92E-20	2.63E-19
LOC100646149	1235.73296	-0.724693225	0.11995752	-6.0412487	1.53E-09	3.12E-09
LOC100645240	839.569332	-0.723960161	0.06679621	-10.838342	2.27E-27	1.33E-26
LOC105666618	23.2392894	-0.723374805	0.29972899	-2.4134295	0.01580318	0.01978884
LOC100646003	1829.48705	-0.722979164	0.14820289	-4.8783068	1.07E-06	1.83E-06
LOC100644738	80.7351081	-0.722034138	0.15203541	-4.7491184	2.04E-06	3.42E-06
LOC100649522	290.791751	-0.721806654	0.09452639	-7.636033	2.24E-14	6.12E-14
LOC100652203	49.9613968	-0.721649564	0.19323804	-3.7345109	0.00018808	0.00027547
LOC100631086	42378.0065	-0.721570024	0.22871296	-3.1549154	0.00160545	0.00218228
LOC100644947	424.57762	-0.721043429	0.08084995	-8.9182911	4.74E-19	1.71E-18
LOC100650125	163.133824	-0.719656597	0.14710766	-4.8920403	9.98E-07	1.71E-06
LOC100644370	231.358016	-0.71935585	0.09454191	-7.6088565	2.77E-14	7.52E-14
LOC100651711	454.339416	-0.719347845	0.08831762	-8.1450096	3.79E-16	1.15E-15

LOC100651786	840.09939	-0.719288365	0.17357438	-4.1439778	3.41E-05	5.27E-05
LOC100646100	202.233896	-0.719259496	0.24463275	-2.9401603	0.00328042	0.00435448
LOC100645203	2506.84485	-0.71886524	0.17037978	-4.2191934	2.45E-05	3.82E-05
LOC100642673	1738.69795	-0.718536654	0.0691523	-10.390639	2.74E-25	1.41E-24
LOC105667170	650.969895	-0.718305952	0.1090314	-6.5880652	4.46E-11	9.94E-11
LOC100651331	1107.89347	-0.718120651	0.1116922	-6.4294608	1.28E-10	2.76E-10
LOC100651759	516.813103	-0.717650058	0.08211212	-8.7398802	2.33E-18	8.06E-18
LOC100646358	519.990876	-0.717103242	0.11086211	-6.468425	9.90E-11	2.15E-10
LOC100642224	2983.10545	-0.716829518	0.07715224	-9.2911047	1.53E-20	6.01E-20
LOC100644094	258.894228	-0.716470066	0.10252209	-6.9884459	2.78E-12	6.70E-12
LOC100643977	291.638045	-0.716152249	0.09385417	-7.6304791	2.34E-14	6.38E-14
LOC100648916	1373.96242	-0.71548902	0.11037889	-6.4821184	9.04E-11	1.97E-10
LOC100647334	459.415205	-0.715273058	0.10622232	-6.7337357	1.65E-11	3.80E-11
LOC100643009	1600.72715	-0.714934988	0.08665724	-8.2501472	1.58E-16	4.92E-16
LOC100647457	3922.23654	-0.713585615	0.10977904	-6.5001991	8.02E-11	1.75E-10
LOC100646723	2013.10892	-0.713396589	0.19457583	-3.6664194	0.00024597	0.00035652
LOC100642949	1049.89935	-0.711976562	0.10158695	-7.0085438	2.41E-12	5.82E-12
LOC105666915	888.884364	-0.711766108	0.10428059	-6.8254901	8.76E-12	2.05E-11
LOC100646154	1909.35276	-0.711354472	0.08205041	-8.6697243	4.33E-18	1.47E-17
LOC100646329	1094.64144	-0.710470989	0.10330939	-6.8771195	6.11E-12	1.45E-11
LOC100651801	29.3709652	-0.710103188	0.32174669	-2.2070256	0.02731227	0.03356105
LOC100646393	84.2626146	-0.709778868	0.1806714	-3.9285624	8.55E-05	0.00012821
LOC105666251	34.6850046	-0.709680526	0.28821818	-2.4623031	0.01380479	0.01738204
LOC100649391	283.601665	-0.709093536	0.14304372	-4.9571803	7.15E-07	1.24E-06
LOC100644298	421.163103	-0.70908349	0.09059551	-7.8269168	5.00E-15	1.42E-14
LOC100645401	285.989807	-0.708680747	0.09589494	-7.3901791	1.47E-13	3.82E-13
LOC100647181	1988.59897	-0.708478314	0.12051275	-5.8788662	4.13E-09	8.22E-09
LOC100643743	4385.51227	-0.708053495	0.06016916	-11.767714	5.73E-32	4.40E-31
LOC100643374	788.126085	-0.707815753	0.10201994	-6.9380137	3.98E-12	9.51E-12

LOC100642303	1751.06242	-0.707230206	0.10195278	-6.9368409	4.01E-12	9.58E-12
LOC105666535	28.478381	-0.706538051	0.26222375	-2.6944091	0.00705136	0.00908897
LOC100648834	59.3364534	-0.706432056	0.18072545	-3.9088688	9.27E-05	0.0001388
LOC100651089	741.574732	-0.706175562	0.1383001	-5.1061102	3.29E-07	5.80E-07
LOC100649187	1174.23573	-0.70593612	0.10291678	-6.8592907	6.92E-12	1.63E-11
LOC100645112	642.559229	-0.705362245	0.17414584	-4.050411	5.11E-05	7.81E-05
LOC100645144	286.594744	-0.704663555	0.10814084	-6.5161647	7.21E-11	1.58E-10
LOC100644993	842.565211	-0.704620753	0.14528846	-4.8498053	1.24E-06	2.10E-06
LOC100643139	202.103394	-0.704470782	0.12953828	-5.4383213	5.38E-08	9.95E-08
LOC100645134	693.721412	-0.704426788	0.11374397	-6.1930914	5.90E-10	1.23E-09
LOC100647971	284.627251	-0.704374368	0.12275973	-5.7378291	9.59E-09	1.86E-08
LOC100651205	1766.67276	-0.703891787	0.07025164	-10.019578	1.25E-23	5.77E-23
LOC100644926	89.1114265	-0.703546631	0.22915759	-3.0701432	0.00213956	0.00288348
LOC100648549	3934.74095	-0.703306486	0.12419707	-5.6628267	1.49E-08	2.85E-08
LOC100644891	1353.55956	-0.70305457	0.07378625	-9.5282595	1.60E-21	6.59E-21
LOC105666721	203.259028	-0.702655406	0.11336988	-6.1979022	5.72E-10	1.19E-09
LOC100631072	1477.03168	-0.702635407	0.07874957	-8.9224029	4.56E-19	1.65E-18
LOC100648055	533.3219	-0.702632121	0.14335871	-4.9012169	9.52E-07	1.63E-06
LOC100645081	2633.34368	-0.702626736	0.070532	-9.9618145	2.24E-23	1.02E-22
LOC100645703	256.778581	-0.702617254	0.16829873	-4.1748222	2.98E-05	4.63E-05
LOC100645279	624.634011	-0.702298733	0.08226273	-8.5372653	1.37E-17	4.55E-17
LOC100644109	638.642858	-0.700918835	0.08137204	-8.6137556	7.07E-18	2.38E-17
LOC100649031	6100.15685	-0.700624936	0.08926661	-7.8486783	4.20E-15	1.20E-14
LOC105665918	83.2341073	-0.699223855	0.15828137	-4.4176005	9.98E-06	1.60E-05
LOC100648608	1367.06399	-0.698224744	0.06669027	-10.469664	1.19E-25	6.25E-25
LOC100644113	512.084371	-0.697791513	0.0924963	-7.543994	4.56E-14	1.23E-13
LOC100648509	300.379731	-0.697479505	0.08128518	-8.5806482	9.43E-18	3.14E-17
LOC100643577	1817.85715	-0.697245202	0.21867927	-3.1884375	0.00143044	0.00195089
LOC105666284	183.562918	-0.697221145	0.19571671	-3.5623996	0.00036748	0.00052587

LOC100650432	223.962107	-0.696827975	0.15327246	-4.5463352	5.46E-06	8.87E-06
LOC100650551	1711.75603	-0.696458491	0.06788136	-10.259936	1.07E-24	5.29E-24
LOC105665805	115.270266	-0.696135537	0.13014774	-5.3488101	8.85E-08	1.62E-07
LOC100647643	703.656316	-0.696098038	0.14799948	-4.7033817	2.56E-06	4.24E-06
LOC105666218	99.4467484	-0.695784974	0.14414506	-4.8269776	1.39E-06	2.35E-06
LOC100651555	486.881684	-0.695111456	0.11294396	-6.1544813	7.53E-10	1.56E-09
LOC100651504	1679.13764	-0.694990911	0.08293281	-8.3801688	5.29E-17	1.69E-16
LOC100642274	158.033992	-0.694885394	0.10780065	-6.4460224	1.15E-10	2.48E-10
LOC105666302	155.869883	-0.694486359	0.13684262	-5.0750735	3.87E-07	6.80E-07
LOC100643821	3723.36386	-0.693600963	0.09072653	-7.6449629	2.09E-14	5.72E-14
LOC100643970	791.294772	-0.693377979	0.07313367	-9.480968	2.52E-21	1.03E-20
LOC100652174	160.393589	-0.693372962	0.12648785	-5.4817357	4.21E-08	7.84E-08
LOC105667005	174.718398	-0.693242228	0.12550296	-5.5237121	3.32E-08	6.22E-08
LOC105666630	334.53453	-0.692898796	0.14588072	-4.7497626	2.04E-06	3.41E-06
LOC100650781	948.366009	-0.692787899	0.06415662	-10.798385	3.50E-27	2.03E-26
LOC100650339	1811.47023	-0.692486821	0.1037195	-6.6765344	2.45E-11	5.56E-11
LOC105666244	1647.95633	-0.692264629	0.08184948	-8.4577772	2.73E-17	8.82E-17
LOC100650489	598.119831	-0.691153675	0.08722596	-7.9237151	2.31E-15	6.69E-15
LOC100649339	351.334572	-0.690699957	0.0877795	-7.8685794	3.59E-15	1.03E-14
LOC100642781	15305.6507	-0.690200713	0.05692856	-12.123981	7.88E-34	6.84E-33
LOC100642917	1004.78063	-0.690114037	0.08038717	-8.5848778	9.09E-18	3.03E-17
LOC100649962	511.636211	-0.690065019	0.0779651	-8.8509476	8.68E-19	3.08E-18
LOC100646138	730.491417	-0.689961062	0.08062568	-8.5575844	1.15E-17	3.83E-17
LOC100642996	418.885221	-0.689846961	0.09991751	-6.9041646	5.05E-12	1.20E-11
LOC100646360	10784.9743	-0.689471832	0.08998144	-7.662378	1.83E-14	5.02E-14
LOC100645832	27.6319623	-0.689412498	0.22306793	-3.0905944	0.00199756	0.00269879
LOC100650740	2227.7586	-0.689231738	0.09287419	-7.4211335	1.16E-13	3.05E-13
LOC100648370	1839.03755	-0.689228246	0.09208564	-7.4846438	7.17E-14	1.91E-13
LOC100642244	143.003929	-0.689081117	0.18605038	-3.703734	0.00021245	0.00030963

LOC100648595	593.031608	-0.688598103	0.13284839	-5.183338	2.18E-07	3.89E-07
LOC100642353	936.683599	-0.688170472	0.10888944	-6.3199009	2.62E-10	5.56E-10
LOC100650283	317.912035	-0.68655329	0.12487649	-5.4978587	3.84E-08	7.17E-08
LOC105666098	95.2561519	-0.686508668	0.14756177	-4.6523479	3.28E-06	5.41E-06
LOC100644076	6250.9556	-0.685954987	0.05019372	-13.666151	1.62E-42	2.55E-41
LOC100644066	303.974507	-0.685756627	0.11161366	-6.1440207	8.05E-10	1.66E-09
LOC100652049	476.895825	-0.685113746	0.08492123	-8.0676384	7.17E-16	2.14E-15
LOC100651913	186.592151	-0.684969757	0.10874042	-6.2991276	2.99E-10	6.34E-10
LOC100647957	379.403569	-0.684882899	0.07836081	-8.7401207	2.33E-18	8.05E-18
LOC100650403	657.786323	-0.684810604	0.10272937	-6.666162	2.63E-11	5.95E-11
LOC100651785	545.227259	-0.684672508	0.08772959	-7.804351	5.98E-15	1.69E-14
LOC100642337	533.066691	-0.684600972	0.08342633	-8.2060539	2.29E-16	7.04E-16
LOC100652125	807.324982	-0.684559825	0.14468905	-4.7312483	2.23E-06	3.72E-06
LOC100650348	944.018706	-0.684296316	0.10710923	-6.3887708	1.67E-10	3.59E-10
LOC100649399	1020.79514	-0.684084665	0.09237239	-7.4057267	1.30E-13	3.40E-13
LOC100644672	556.447121	-0.683885263	0.07692175	-8.8906613	6.07E-19	2.18E-18
LOC100651524	3427.18378	-0.683852951	0.08195503	-8.344246	7.17E-17	2.28E-16
LOC100652249	2066.49692	-0.683478897	0.15852763	-4.3114181	1.62E-05	2.56E-05
LOC100650281	2340.04078	-0.683261621	0.08612137	-7.9337057	2.13E-15	6.18E-15
LOC100651821	761.325645	-0.683051356	0.15016469	-4.5486815	5.40E-06	8.77E-06
LOC100643560	338.888775	-0.682719348	0.10492899	-6.5064893	7.69E-11	1.69E-10
LOC100643586	860.64802	-0.681760407	0.15669526	-4.3508681	1.36E-05	2.15E-05
LOC100651865	271.346242	-0.681596231	0.10766602	-6.3306534	2.44E-10	5.20E-10
LOC100645906	472.339763	-0.681272693	0.09619972	-7.0818574	1.42E-12	3.49E-12
LOC100645033	473.272241	-0.681121799	0.0851329	-8.0006886	1.24E-15	3.64E-15
LOC100649526	479.751455	-0.68085171	0.09792072	-6.9530915	3.57E-12	8.57E-12
LOC100648121	59.5895523	-0.679807506	0.30017356	-2.2647148	0.02353019	0.02909257
LOC100646310	736.542525	-0.679106326	0.12184756	-5.5734094	2.50E-08	4.72E-08
LOC100644326	1167.9496	-0.679080159	0.06842274	-9.9247733	3.25E-23	1.46E-22

LOC100651258	800.42003	-0.678832773	0.06972534	-9.735812	2.12E-22	9.14E-22
LOC100651936	3379.56995	-0.678271931	0.09365797	-7.2420099	4.42E-13	1.12E-12
LOC100645362	335.399561	-0.678219565	0.09663861	-7.0181017	2.25E-12	5.45E-12
LOC100652101	127.32589	-0.678200111	0.19187806	-3.534537	0.00040849	0.0005826
LOC100646409	331.103123	-0.678037499	0.19337737	-3.5062919	0.0004544	0.00064591
LOC100642852	533.633417	-0.67757087	0.07306689	-9.2732959	1.80E-20	7.06E-20
LOC100642602	4342.82876	-0.677325677	0.10313204	-6.567558	5.11E-11	1.13E-10
LOC100646418	835.965155	-0.677250087	0.11802064	-5.7384037	9.56E-09	1.86E-08
LOC100648050	723.323419	-0.677192112	0.07480866	-9.052323	1.40E-19	5.21E-19
LOC100646778	541.761525	-0.676587879	0.09646551	-7.0137805	2.32E-12	5.62E-12
LOC100649769	1585.98514	-0.676556029	0.14853799	-4.5547677	5.24E-06	8.53E-06
LOC100644613	283.714185	-0.676352702	0.12455783	-5.4300295	5.63E-08	1.04E-07
LOC100652282	64.2191157	-0.676307488	0.16658813	-4.0597579	4.91E-05	7.51E-05
LOC100642821	945.392053	-0.67585386	0.10611554	-6.3690374	1.90E-10	4.07E-10
LOC100651763	3617.77134	-0.675514019	0.07385999	-9.1458719	5.92E-20	2.26E-19
LOC100643500	1496.42877	-0.675007719	0.12683213	-5.3220562	1.03E-07	1.86E-07
LOC100649203	745.010739	-0.674941993	0.17006989	-3.9686154	7.23E-05	0.00010911
LOC100644691	405.328394	-0.674681434	0.08782747	-7.6818949	1.57E-14	4.33E-14
LOC100651672	369.358332	-0.674037921	0.09295638	-7.2511208	4.13E-13	1.05E-12
LOC105666164	208.876069	-0.674032145	0.10679512	-6.3114506	2.76E-10	5.87E-10
LOC100650514	129.933973	-0.673786747	0.23035569	-2.9249842	0.00344474	0.00455838
LOC100648219	287.547683	-0.673086639	0.10359072	-6.4975575	8.16E-11	1.78E-10
LOC100644368	882.843559	-0.672533386	0.07050151	-9.5392768	1.44E-21	5.95E-21
LOC100643112	1955.3542	-0.672413636	0.07562651	-8.8912423	6.04E-19	2.17E-18
LOC100649852	130.620901	-0.67240883	0.23067546	-2.9149561	0.00355739	0.00469982
LOC100648116	228.406947	-0.672179803	0.10169959	-6.6094641	3.86E-11	8.63E-11
LOC105665775	282.293295	-0.672069584	0.10453948	-6.4288588	1.29E-10	2.77E-10
LOC100651922	965.442293	-0.671837446	0.12060836	-5.5704051	2.54E-08	4.80E-08
LOC105666547	1314.31938	-0.671813446	0.09853513	-6.8180092	9.23E-12	2.16E-11

LOC100643396	1338.6432	-0.671467194	0.0846245	-7.9346663	2.11E-15	6.14E-15
LOC100644159	3603.93463	-0.670203679	0.07728874	-8.6714276	4.27E-18	1.45E-17
LOC100644678	732.187583	-0.670154367	0.12544717	-5.3421243	9.19E-08	1.67E-07
LOC100644198	786.894218	-0.670129039	0.09804332	-6.8350302	8.20E-12	1.92E-11
LOC100646632	719.042369	-0.669919315	0.10652137	-6.2890603	3.19E-10	6.76E-10
LOC100649062	1565.36176	-0.669825644	0.08493732	-7.8861168	3.12E-15	8.98E-15
LOC100648175	1565.31814	-0.669465523	0.07184071	-9.3187481	1.18E-20	4.66E-20
LOC100647704	2453.63019	-0.669300955	0.08611721	-7.7719771	7.73E-15	2.17E-14
LOC100650494	938.09626	-0.669298373	0.08581746	-7.7990931	6.24E-15	1.76E-14
LOC100647247	281.116602	-0.669117862	0.19417935	-3.4458755	0.00056921	0.0008012
LOC100647783	381.516305	-0.66909254	0.08985769	-7.4461358	9.61E-14	2.53E-13
LOC100647529	2071.19454	-0.668346324	0.05559287	-12.02216	2.72E-33	2.27E-32
LOC100643431	4098.38777	-0.668211509	0.12590968	-5.3070702	1.11E-07	2.02E-07
LOC100644386	359.031964	-0.667818382	0.1438246	-4.6432836	3.43E-06	5.64E-06
LOC100643651	611.898559	-0.667162566	0.08255528	-8.0814038	6.40E-16	1.92E-15
LOC100646608	1831.55728	-0.666990732	0.09307492	-7.1661703	7.71E-13	1.93E-12
LOC100649347	273.962079	-0.666985336	0.11009481	-6.0582811	1.38E-09	2.81E-09
LOC100649969	1326.39636	-0.666922838	0.08952684	-7.4494174	9.38E-14	2.48E-13
LOC100645195	1592.18662	-0.665581421	0.09892678	-6.7280205	1.72E-11	3.94E-11
LOC100647914	4821.87804	-0.665052548	0.10228869	-6.5017215	7.94E-11	1.74E-10
LOC100651739	465.964876	-0.664982474	0.08876851	-7.4911979	6.82E-14	1.82E-13
LOC100651095	1543.13276	-0.664951834	0.13233658	-5.0247016	5.04E-07	8.80E-07
LOC100648727	703.908233	-0.664941519	0.08572982	-7.7562458	8.75E-15	2.45E-14
LOC100643395	337.875405	-0.664893171	0.14622598	-4.5470248	5.44E-06	8.84E-06
LOC100648649	422.745443	-0.664432566	0.07205503	-9.2211827	2.94E-20	1.14E-19
LOC100642309	2057.2163	-0.664306779	0.06464166	-10.276759	8.97E-25	4.47E-24
LOC100651552	1721.3608	-0.663997362	0.1372547	-4.8377021	1.31E-06	2.23E-06
LOC105666419	3209.60764	-0.663924567	0.07846415	-8.4615019	2.64E-17	8.55E-17
LOC100643105	369.011766	-0.663682951	0.08908087	-7.4503418	9.31E-14	2.46E-13

LOC100646091	960.91897	-0.663593338	0.12873302	-5.154803	2.54E-07	4.51E-07
LOC100648922	295.732003	-0.663438812	0.08632641	-7.685236	1.53E-14	4.22E-14
LOC100646627	1079.07342	-0.662717977	0.07292919	-9.0871431	1.02E-19	3.81E-19
LOC100645715	12822.9113	-0.662682543	0.08836062	-7.4997501	6.39E-14	1.71E-13
LOC100642648	473.844476	-0.662670968	0.09453352	-7.009905	2.38E-12	5.77E-12
LOC100648890	2902.13026	-0.662534473	0.07065042	-9.3776432	6.75E-21	2.70E-20
LOC100649457	85.5734516	-0.662452069	0.28864098	-2.2950728	0.02172895	0.0269472
LOC100644236	2046.26702	-0.660907482	0.07457255	-8.8626111	7.82E-19	2.78E-18
LOC100649171	400.882654	-0.660882276	0.2150713	-3.072852	0.00212024	0.00285861
LOC100648244	1013.02254	-0.660457275	0.06996086	-9.4403824	3.71E-21	1.51E-20
LOC100644443	933.793803	-0.659069916	0.07992082	-8.2465356	1.63E-16	5.07E-16
LOC100644967	693.085437	-0.65854854	0.09929103	-6.6325076	3.30E-11	7.41E-11
LOC105665992	152.028952	-0.658393287	0.14345785	-4.5894547	4.44E-06	7.25E-06
LOC100648884	921.146854	-0.658058731	0.13523073	-4.8661921	1.14E-06	1.94E-06
LOC100643923	9956.95407	-0.657750603	0.11312618	-5.8143095	6.09E-09	1.20E-08
LOC100643390	634.411164	-0.65773034	0.08170829	-8.0497384	8.30E-16	2.47E-15
LOC100648341	505.563458	-0.656899125	0.11026	-5.9577282	2.56E-09	5.16E-09
LOC100645655	344.976224	-0.656861543	0.1355771	-4.8449297	1.27E-06	2.15E-06
LOC100645492	1189.11829	-0.65621849	0.0725303	-9.0475081	1.46E-19	5.44E-19
LOC100647559	277.06355	-0.655928547	0.13739403	-4.7740687	1.81E-06	3.03E-06
LOC100646935	569.187361	-0.65540562	0.08006358	-8.1860643	2.70E-16	8.25E-16
LOC100650692	324.62375	-0.655358595	0.2414488	-2.7142757	0.00664209	0.00857838
LOC100642779	848.427895	-0.65475252	0.10656774	-6.1440032	8.05E-10	1.66E-09
LOC105666472	71.2075421	-0.654657143	0.18434091	-3.5513395	0.00038328	0.00054775
LOC100647286	211.797513	-0.654085798	0.12027575	-5.4382183	5.38E-08	9.95E-08
LOC100647959	1396.11707	-0.653595118	0.0500844	-13.049875	6.37E-39	7.75E-38
LOC100647374	882.856454	-0.653167149	0.08147634	-8.0166479	1.09E-15	3.21E-15
LOC100649728	77.8638824	-0.652934241	0.253714	-2.573505	0.01006742	0.01284803
LOC105665908	29.8598167	-0.652812393	0.28377984	-2.3004185	0.02142452	0.02659324

LOC100648703	173.68787	-0.652545962	0.1211041	-5.3883061	7.11E-08	1.31E-07
LOC100652020	4835.76146	-0.652238147	0.06094968	-10.701256	1.00E-26	5.64E-26
LOC100649121	1174.2398	-0.652197871	0.06544221	-9.9660118	2.15E-23	9.78E-23
LOC100648928	3434.06978	-0.652088989	0.07640348	-8.5348076	1.40E-17	4.64E-17
LOC100646400	2285.30915	-0.651922118	0.10009489	-6.5130407	7.36E-11	1.62E-10
LOC100642615	57.0018947	-0.651821745	0.22808739	-2.8577719	0.00426627	0.00560384
LOC100650866	561.64408	-0.651783778	0.07699396	-8.4653887	2.55E-17	8.29E-17
LOC105665987	142.518997	-0.651782654	0.1648668	-3.9533894	7.71E-05	0.00011614
LOC100646316	3473.25533	-0.651297748	0.07353722	-8.8567087	8.24E-19	2.93E-18
LOC100646282	189.844322	-0.651177226	0.12177851	-5.3472262	8.93E-08	1.63E-07
LOC100652278	329.468529	-0.650791461	0.10000103	-6.5078476	7.62E-11	1.67E-10
LOC100649248	586.973189	-0.650711158	0.08720528	-7.4618324	8.53E-14	2.26E-13
LOC100649820	670.48226	-0.65043233	0.09639977	-6.7472397	1.51E-11	3.47E-11
LOC100648165	1052.97485	-0.649788782	0.13283199	-4.8918094	9.99E-07	1.71E-06
LOC100644045	389.545483	-0.649728652	0.11653078	-5.5755967	2.47E-08	4.67E-08
LOC105665631	343.685908	-0.649577435	0.09518545	-6.8243354	8.83E-12	2.07E-11
LOC100644848	1412.37515	-0.6486651	0.12645582	-5.129579	2.90E-07	5.14E-07
LOC105666182	124.513917	-0.648619924	0.13837165	-4.6875205	2.77E-06	4.58E-06
LOC100650411	230.813418	-0.647612603	0.12159069	-5.3261694	1.00E-07	1.82E-07
LOC100646297	130.991463	-0.647207665	0.14111758	-4.5863008	4.51E-06	7.36E-06
LOC100651503	563.567312	-0.64710034	0.08816823	-7.3393821	2.15E-13	5.54E-13
LOC100650664	381.974828	-0.647061256	0.09591175	-6.7464235	1.52E-11	3.49E-11
LOC100644628	177.916903	-0.64705628	0.14998296	-4.3141987	1.60E-05	2.53E-05
LOC100646123	369.788278	-0.646586647	0.1106994	-5.8409229	5.19E-09	1.03E-08
LOC100645476	613.492265	-0.645875093	0.11260927	-5.7355413	9.72E-09	1.89E-08
LOC100646088	139.291168	-0.64429556	0.25223334	-2.5543632	0.01063822	0.01353245
LOC100645380	1696.1842	-0.644000412	0.08536726	-7.5438804	4.56E-14	1.23E-13
LOC100651138	243.723073	-0.643988214	0.10253318	-6.2807785	3.37E-10	7.12E-10
LOC105667042	166.370963	-0.643435678	0.26889701	-2.3928704	0.01671715	0.0208879

LOC100643444	630.007874	-0.64335154	0.08504717	-7.564644	3.89E-14	1.05E-13
LOC100648507	373.105898	-0.64292702	0.08537651	-7.5304905	5.06E-14	1.36E-13
LOC100644754	167.33191	-0.642747014	0.13925868	-4.6154897	3.92E-06	6.43E-06
LOC100644780	857.177579	-0.642335452	0.08480781	-7.5740125	3.62E-14	9.78E-14
LOC105665726	1198.46705	-0.642267145	0.11983014	-5.359813	8.33E-08	1.52E-07
LOC100647343	66849.2926	-0.641753243	0.15352294	-4.1801782	2.91E-05	4.52E-05
LOC100643401	577.866628	-0.641521167	0.10822829	-5.9274815	3.08E-09	6.17E-09
LOC100647141	1296.86474	-0.641331055	0.07834142	-8.1863602	2.69E-16	8.23E-16
LOC100644472	1579.04373	-0.640853443	0.07573345	-8.4619601	2.63E-17	8.52E-17
LOC100651130	2433.39172	-0.639654055	0.06007261	-10.648015	1.78E-26	9.86E-26
LOC100649965	1340.11555	-0.639498571	0.07710457	-8.2939126	1.10E-16	3.43E-16
LOC100648525	152.668707	-0.638912219	0.13740224	-4.6499402	3.32E-06	5.47E-06
LOC105666912	419.658705	-0.638615945	0.09208867	-6.9347938	4.07E-12	9.71E-12
LOC100644874	2490.83501	-0.638100774	0.12173704	-5.2416323	1.59E-07	2.86E-07
LOC100643733	2773.84119	-0.63781096	0.070574	-9.037478	1.60E-19	5.96E-19
LOC100644776	523.651272	-0.637382201	0.19363567	-3.291657	0.00099599	0.00137542
LOC100647868	440.951687	-0.637264042	0.114115	-5.5844022	2.35E-08	4.44E-08
LOC100642733	2430.04219	-0.637193377	0.06413466	-9.9352425	2.92E-23	1.32E-22
LOC100652104	2422.78938	-0.636199831	0.10515422	-6.0501597	1.45E-09	2.96E-09
LOC100643880	1432.65362	-0.63596279	0.0749751	-8.4823197	2.21E-17	7.20E-17
LOC100643320	1631.77702	-0.635716788	0.06094956	-10.430211	1.80E-25	9.39E-25
LOC100651862	1447.58317	-0.635399944	0.09504928	-6.6849527	2.31E-11	5.25E-11
LOC100644275	1191.15762	-0.634840312	0.08225844	-7.7176314	1.19E-14	3.29E-14
LOC105667185	130.398118	-0.6338337	0.14403867	-4.4004413	1.08E-05	1.72E-05
LOC100646306	461.989924	-0.633824623	0.10707657	-5.9193587	3.23E-09	6.47E-09
LOC100649735	383.458353	-0.633668516	0.09823547	-6.4505065	1.11E-10	2.41E-10
LOC100643355	2310.23165	-0.633180371	0.09226106	-6.8629212	6.75E-12	1.59E-11
LOC105667192	376.804228	-0.632770345	0.13244668	-4.7775479	1.77E-06	2.98E-06
LOC100643005	505.628323	-0.632580723	0.08835095	-7.1598633	8.08E-13	2.02E-12

LOC100646004	473.045226	-0.631904924	0.15734146	-4.0161374	5.92E-05	9.00E-05
LOC100648197	650.531226	-0.631270607	0.12959026	-4.8712811	1.11E-06	1.89E-06
LOC100650289	2618.52961	-0.631064407	0.10022903	-6.296224	3.05E-10	6.46E-10
LOC100650448	1069.83681	-0.630611911	0.07285003	-8.6563027	4.87E-18	1.65E-17
LOC100650741	710.062721	-0.629695434	0.10666532	-5.9034695	3.56E-09	7.11E-09
LOC100649866	472.992338	-0.629151979	0.08667724	-7.2585601	3.91E-13	9.97E-13
LOC100644398	966.72166	-0.628514175	0.08522997	-7.3743327	1.65E-13	4.29E-13
LOC100643199	366.934029	-0.628026463	0.10323596	-6.0834081	1.18E-09	2.41E-09
LOC100650962	1059.85942	-0.628001153	0.14221071	-4.4159905	1.01E-05	1.61E-05
LOC100645857	1925.3842	-0.627864441	0.08342081	-7.5264723	5.21E-14	1.40E-13
LOC100648297	3711.10872	-0.627817831	0.05831328	-10.766292	4.97E-27	2.85E-26
LOC105666474	365.11319	-0.627508506	0.09120149	-6.8804634	5.97E-12	1.41E-11
LOC100647789	1140.75586	-0.627468959	0.1110506	-5.6502976	1.60E-08	3.06E-08
LOC100652160	353.613573	-0.62711141	0.22811019	-2.74916	0.00597482	0.007737
LOC100649517	80.3896113	-0.626581042	0.19793639	-3.1655677	0.00154781	0.00210597
LOC100646883	390.742888	-0.626360028	0.09620623	-6.5105973	7.49E-11	1.64E-10
LOC105666987	396.782225	-0.625564389	0.07799458	-8.0206139	1.05E-15	3.11E-15
LOC100652271	345.477267	-0.625548145	0.10819054	-5.7819117	7.39E-09	1.45E-08
LOC100646109	1053.5235	-0.625545869	0.07236488	-8.6443294	5.41E-18	1.83E-17
LOC100642465	7271.10085	-0.625411305	0.09338093	-6.6974198	2.12E-11	4.84E-11
LOC100647764	696.540797	-0.625387516	0.12419836	-5.0353927	4.77E-07	8.33E-07
LOC100644629	491.890616	-0.624882573	0.09336969	-6.6925633	2.19E-11	4.99E-11
LOC100649506	493.022127	-0.624846882	0.07578289	-8.2452236	1.65E-16	5.12E-16
LOC100646195	343.757025	-0.624478665	0.08798704	-7.0973935	1.27E-12	3.13E-12
LOC100647336	474.44097	-0.623986372	0.1130797	-5.5181115	3.43E-08	6.41E-08
LOC100643217	442.090956	-0.623396945	0.21101655	-2.9542561	0.00313424	0.00416891
LOC100643055	1780.923	-0.623381859	0.06776812	-9.198748	3.62E-20	1.39E-19
LOC100645790	714.683858	-0.623249544	0.07203024	-8.6526097	5.03E-18	1.70E-17
LOC100651523	119.865436	-0.622569766	0.15361617	-4.0527619	5.06E-05	7.73E-05

LOC100642551	857.716621	-0.622144746	0.07297759	-8.525148	1.53E-17	5.03E-17
LOC100647725	1908.23742	-0.62202362	0.09178601	-6.7768894	1.23E-11	2.84E-11
LOC100642909	39.6046447	-0.621417979	0.21923907	-2.8344308	0.00459074	0.00600427
LOC100649122	274.581087	-0.620186989	0.12900707	-4.8073877	1.53E-06	2.58E-06
LOC100642461	588.777402	-0.620124862	0.08361602	-7.4163401	1.20E-13	3.16E-13
LOC100650985	1506.01965	-0.619770557	0.08530238	-7.2655716	3.71E-13	9.48E-13
LOC100645003	615.689966	-0.619587797	0.09409914	-6.5844153	4.57E-11	1.02E-10
LOC100648260	314.818704	-0.619408081	0.083151	-7.4491957	9.39E-14	2.48E-13
LOC100645558	227.411228	-0.617784386	0.09872536	-6.2576057	3.91E-10	8.23E-10
LOC100647701	3647.3127	-0.617405352	0.06552309	-9.4227148	4.40E-21	1.78E-20
LOC100646722	642.260205	-0.617029645	0.12795076	-4.8223993	1.42E-06	2.40E-06
LOC100642462	105.492442	-0.617003565	0.19384451	-3.1829819	0.00145767	0.00198636
LOC105666650	113.326251	-0.616795084	0.21684093	-2.8444587	0.0044487	0.00582705
LOC100650265	608.87161	-0.616723463	0.07668995	-8.0417764	8.85E-16	2.63E-15
LOC100651541	1188.79903	-0.615570415	0.07089187	-8.6832302	3.85E-18	1.31E-17
LOC100645578	260.077013	-0.615469568	0.10385259	-5.9263764	3.10E-09	6.21E-09
LOC100650199	600.361803	-0.615462198	0.1132478	-5.4346504	5.49E-08	1.01E-07
LOC100648078	483.914019	-0.614877428	0.08768674	-7.012205	2.35E-12	5.68E-12
LOC100651668	352.681336	-0.614775377	0.11475594	-5.3572422	8.45E-08	1.54E-07
LOC100642621	1085.42692	-0.614763471	0.0919637	-6.6848495	2.31E-11	5.26E-11
LOC100647436	1385.67914	-0.613873449	0.0959248	-6.399528	1.56E-10	3.35E-10
LOC100649057	517.560324	-0.613685569	0.09405268	-6.5249132	6.80E-11	1.50E-10
LOC100642441	305.476776	-0.613416615	0.14499527	-4.2305974	2.33E-05	3.64E-05
LOC100651780	1492.35726	-0.612778483	0.09721285	-6.3034721	2.91E-10	6.18E-10
LOC100650219	9034.53299	-0.612686268	0.17750605	-3.4516359	0.0005572	0.00078497
LOC100647465	2566.84647	-0.612673326	0.12816039	-4.7805203	1.75E-06	2.94E-06
LOC100648405	110.319507	-0.612590766	0.1311342	-4.6714799	2.99E-06	4.94E-06
LOC100631064	568.785054	-0.612153577	0.06475945	-9.4527302	3.30E-21	1.34E-20
LOC100642979	1203.13364	-0.611934001	0.09962354	-6.1424641	8.13E-10	1.68E-09

LOC100648187	978.416473	-0.611830795	0.07583015	-8.0684375	7.12E-16	2.13E-15
LOC100643141	772.403426	-0.610654556	0.10662639	-5.7270488	1.02E-08	1.98E-08
LOC100645950	1819.92985	-0.610221377	0.15516359	-3.9327615	8.40E-05	0.0001261
LOC100643817	196.013486	-0.610165538	0.13248712	-4.6054706	4.12E-06	6.73E-06
LOC100650976	713.406694	-0.609742694	0.13956191	-4.3689764	1.25E-05	1.98E-05
LOC100649222	391.569213	-0.608656509	0.09743672	-6.2466852	4.19E-10	8.81E-10
LOC105666068	82.6474484	-0.607770556	0.28449773	-2.1362932	0.03265553	0.03983681
LOC100649825	3819.13553	-0.607554121	0.05964878	-10.185525	2.30E-24	1.11E-23
LOC100647040	2239.37138	-0.607239869	0.09727184	-6.2427098	4.30E-10	9.03E-10
LOC100648630	316.969662	-0.607149344	0.10949773	-5.5448576	2.94E-08	5.53E-08
LOC100644273	797.366264	-0.606424332	0.06605897	-9.1800451	4.31E-20	1.65E-19
LOC100651080	1712.93197	-0.606106932	0.0685274	-8.8447379	9.17E-19	3.25E-18
LOC100648321	19.2460807	-0.606010659	0.28426658	-2.1318392	0.03302006	0.04025143
LOC100649135	40.5962615	-0.605979118	0.19495121	-3.108363	0.00188127	0.00254659
LOC105666537	133.29093	-0.605727171	0.15044465	-4.0262461	5.67E-05	8.64E-05
LOC100651032	570.98356	-0.605692856	0.0636587	-9.5146913	1.82E-21	7.49E-21
LOC100649784	1494.2401	-0.605621817	0.06733578	-8.9940562	2.38E-19	8.79E-19
LOC100651247	1570.2912	-0.605095689	0.06870139	-8.8076197	1.28E-18	4.48E-18
LOC100642700	838.251325	-0.605060196	0.13743146	-4.4026323	1.07E-05	1.71E-05
LOC100647405	1979.95583	-0.604863661	0.10174338	-5.9449929	2.76E-09	5.56E-09
LOC100647534	551.051707	-0.604142775	0.08703045	-6.9417402	3.87E-12	9.27E-12
LOC100643218	364.490128	-0.603985717	0.17342653	-3.4826604	0.00049646	0.00070365
LOC100647878	486.263474	-0.603617679	0.08027583	-7.5192954	5.51E-14	1.47E-13
LOC100642448	289.060231	-0.603450241	0.1343472	-4.4917217	7.06E-06	1.14E-05
LOC100649704	16697.3746	-0.603272458	0.06659219	-9.0592079	1.31E-19	4.91E-19
LOC100649804	87.2946452	-0.603010101	0.19314735	-3.122021	0.00179614	0.00243371
LOC100642442	664.424899	-0.602990445	0.18934801	-3.1845618	0.00144973	0.00197583
LOC100646040	494.086093	-0.602907011	0.09205738	-6.5492523	5.78E-11	1.28E-10
LOC100645833	275.261817	-0.602436358	0.09137776	-6.5928117	4.32E-11	9.63E-11

LOC100643497	289.286144	-0.602105118	0.09712458	-6.1993075	5.67E-10	1.18E-09
LOC100649164	3289.07847	-0.601760165	0.08910729	-6.7532091	1.45E-11	3.34E-11
LOC100642207	578.480008	-0.601633595	0.08501513	-7.0767829	1.48E-12	3.62E-12
LOC100649038	541.77445	-0.601210643	0.0797918	-7.5347419	4.89E-14	1.31E-13
LOC100649514	99.8952647	-0.60076395	0.25378908	-2.3671781	0.0179243	0.02235629
LOC100646181	5106.12401	-0.600466728	0.0982502	-6.1116081	9.86E-10	2.03E-09
LOC100647641	1539.70074	-0.600441485	0.16795813	-3.5749474	0.0003503	0.00050204
LOC100645603	425.859167	-0.60004533	0.06981395	-8.5949197	8.33E-18	2.79E-17
LOC100647262	1229.83425	-0.599694487	0.06199816	-9.6727785	3.94E-22	1.67E-21
LOC100648864	373.747373	-0.599678014	0.09198031	-6.5196344	7.05E-11	1.55E-10
LOC100646416	1172.07623	-0.599574833	0.06417831	-9.342328	9.42E-21	3.74E-20
LOC100646792	288.801464	-0.599437439	0.09631943	-6.223432	4.86E-10	1.02E-09
LOC105666235	44.64111	-0.598912085	0.25854635	-2.3164593	0.0205332	0.02550629
LOC100648733	163.307299	-0.598818281	0.11969085	-5.0030414	5.64E-07	9.82E-07
LOC100644362	1308.35067	-0.598575414	0.13184937	-4.539843	5.63E-06	9.13E-06
LOC100643035	1408.26291	-0.598524555	0.06491352	-9.2203378	2.96E-20	1.14E-19
LOC105666409	1193.09821	-0.598415104	0.10519814	-5.6884572	1.28E-08	2.47E-08
LOC100643921	41.5961357	-0.597797658	0.24687954	-2.4214143	0.01546024	0.0193842
LOC100650526	376.878602	-0.597666493	0.14413051	-4.1467036	3.37E-05	5.21E-05
LOC100643787	564.965719	-0.59735093	0.08362994	-7.1427876	9.15E-13	2.27E-12
LOC100642201	317.210763	-0.596823738	0.11095906	-5.3787743	7.50E-08	1.37E-07
LOC100648193	6242.3737	-0.596726428	0.04887987	-12.208019	2.82E-34	2.53E-33
LOC100649775	1096.81593	-0.596543624	0.09172471	-6.5036307	7.84E-11	1.72E-10
LOC100642880	645.281492	-0.596191519	0.09084829	-6.5624956	5.29E-11	1.17E-10
LOC100642220	788.329385	-0.596068535	0.067154	-8.876143	6.92E-19	2.47E-18
LOC105665656	68.7827119	-0.595585909	0.17443699	-3.4143326	0.00063938	0.00089572
LOC105665737	602.655943	-0.595499718	0.12906368	-4.6139993	3.95E-06	6.47E-06
LOC100643072	460.673599	-0.595335305	0.07115022	-8.3673005	5.90E-17	1.88E-16
LOC100647097	1490.08461	-0.594636904	0.06483308	-9.1718131	4.65E-20	1.78E-19

LOC105666714	248.892338	-0.594148143	0.26291141	-2.2598797	0.02382872	0.02944059
LOC100650149	1385.54827	-0.592873054	0.06410412	-9.2485952	2.27E-20	8.84E-20
LOC100650159	47.5046824	-0.591857725	0.18845961	-3.1405017	0.00168659	0.00228844
LOC100643819	2034.06233	-0.591776493	0.06536379	-9.0535834	1.38E-19	5.15E-19
LOC100642421	206.974661	-0.591639811	0.19445197	-3.0426012	0.00234543	0.00315268
LOC100649310	3270.35806	-0.591494232	0.06027706	-9.8129244	9.91E-23	4.34E-22
LOC100644562	2828.65932	-0.590751282	0.14303458	-4.1301292	3.63E-05	5.59E-05
LOC100644117	825.05824	-0.590726701	0.09881646	-5.9780192	2.26E-09	4.56E-09
LOC100649424	1696.48548	-0.590158568	0.08790566	-6.7135446	1.90E-11	4.34E-11
LOC100652022	358.078342	-0.588605674	0.10439058	-5.6384942	1.72E-08	3.27E-08
LOC100642884	163.534162	-0.58812618	0.14069083	-4.1802737	2.91E-05	4.52E-05
LOC100651085	3468.24971	-0.588071662	0.07740766	-7.5970737	3.03E-14	8.22E-14
LOC100649707	386.773066	-0.586892546	0.08305596	-7.0662302	1.59E-12	3.89E-12
LOC100643470	465.073673	-0.586798155	0.08311426	-7.060138	1.66E-12	4.07E-12
LOC100650546	413.703547	-0.586765607	0.08842787	-6.6355279	3.23E-11	7.27E-11
LOC100646495	1528.57315	-0.586641678	0.08604156	-6.8181197	9.22E-12	2.15E-11
LOC100642682	60.6224269	-0.58634073	0.16877931	-3.4740083	0.00051275	0.00072516
LOC100648164	440.547477	-0.586041264	0.11476913	-5.1062624	3.29E-07	5.80E-07
LOC105666155	59.9803654	-0.586036937	0.20252941	-2.8935893	0.00380866	0.00501892
LOC100650798	2795.45818	-0.585856961	0.11866186	-4.937197	7.93E-07	1.36E-06
LOC100648157	636.697028	-0.584690621	0.06723127	-8.6967068	3.42E-18	1.17E-17
LOC100645944	269.944095	-0.584634798	0.11055358	-5.2882487	1.23E-07	2.23E-07
LOC100643982	2014.62116	-0.584348876	0.09210999	-6.3440336	2.24E-10	4.78E-10
LOC100651746	208.120235	-0.584245241	0.1433	-4.0770779	4.56E-05	6.98E-05
LOC100649698	736.605989	-0.582948225	0.07890446	-7.3880261	1.49E-13	3.88E-13
LOC100648053	168.049539	-0.582166181	0.12234671	-4.7583314	1.95E-06	3.27E-06
LOC105666135	104.419938	-0.582162888	0.17526028	-3.3217046	0.00089469	0.00124079
LOC100648660	583.552119	-0.581993497	0.07349049	-7.919303	2.39E-15	6.92E-15
LOC100646317	498.691701	-0.581215962	0.08696489	-6.6833403	2.34E-11	5.31E-11

LOC100648308	132.208089	-0.581013516	0.18290145	-3.176648	0.00148988	0.00202941
LOC100647947	1244.07054	-0.580641845	0.07366129	-7.8825916	3.21E-15	9.23E-15
LOC100649180	102.991193	-0.580562218	0.20988563	-2.7660885	0.00567331	0.00736508
LOC105666172	37.824815	-0.579393568	0.20451387	-2.8330282	0.00461093	0.00602826
LOC100643905	1522.5162	-0.57923512	0.08997056	-6.4380519	1.21E-10	2.61E-10
LOC100643652	1012.16268	-0.578953859	0.10184881	-5.6844442	1.31E-08	2.52E-08
LOC100649851	3499.02217	-0.578334785	0.06542348	-8.8398652	9.58E-19	3.39E-18
LOC100645151	70.9040695	-0.578010135	0.18257482	-3.1658808	0.00154614	0.002104
LOC100642211	778.378927	-0.577604489	0.15140273	-3.8150203	0.00013617	0.00020109
LOC100642873	1304.90766	-0.577536149	0.08000635	-7.2186293	5.25E-13	1.33E-12
LOC100645580	635.712183	-0.576933789	0.06933196	-8.3213256	8.70E-17	2.75E-16
LOC100643694	302.210515	-0.576881911	0.11598554	-4.9737401	6.57E-07	1.14E-06
LOC100649719	1276.97501	-0.576320848	0.07155641	-8.0540768	8.01E-16	2.38E-15
LOC105666333	31.4494424	-0.575876167	0.27810315	-2.0707287	0.03838416	0.04652957
LOC100652333	778.499429	-0.574948985	0.16846688	-3.412831	0.00064292	0.00090054
LOC100650011	1013.88094	-0.57457109	0.07046242	-8.1542912	3.51E-16	1.07E-15
LOC100644901	120.719015	-0.574473942	0.20274526	-2.8334766	0.00460447	0.00602142
LOC100652032	934.156988	-0.574272749	0.07312865	-7.8529105	4.06E-15	1.16E-14
LOC100643602	5041.95978	-0.574237836	0.22071232	-2.601748	0.009275	0.01185839
LOC100643961	748.26065	-0.572775265	0.08191208	-6.9925615	2.70E-12	6.51E-12
LOC100646973	366.752882	-0.57268209	0.09818122	-5.8329085	5.45E-09	1.08E-08
LOC100643648	210.326058	-0.572374458	0.13125906	-4.3606471	1.30E-05	2.06E-05
LOC100645632	413.542495	-0.572194955	0.093337	-6.1304196	8.76E-10	1.81E-09
LOC100652230	605.640401	-0.57214535	0.09694475	-5.9017674	3.60E-09	7.18E-09
LOC100643628	564.638318	-0.572028803	0.0969716	-5.8989314	3.66E-09	7.30E-09
LOC100647749	219.089496	-0.571368312	0.0988313	-5.7812484	7.41E-09	1.45E-08
LOC100650096	821.527971	-0.571243931	0.11032066	-5.1780324	2.24E-07	4.00E-07
LOC100642206	1136.20777	-0.570160724	0.06809187	-8.3734033	5.60E-17	1.79E-16
LOC100650826	232.929201	-0.569312475	0.10093359	-5.6404659	1.70E-08	3.24E-08

LOC100649068	69.0277926	-0.568791684	0.20548058	-2.7681043	0.00563834	0.00732453
LOC100650582	3647.68866	-0.568243297	0.11561982	-4.9147569	8.89E-07	1.53E-06
LOC100647296	27488.9049	-0.568156472	0.06339273	-8.9624856	3.17E-19	1.16E-18
LOC100647431	324.708389	-0.568099212	0.08761847	-6.4837835	8.95E-11	1.95E-10
LOC105666585	530.224162	-0.56761623	0.12502997	-4.5398413	5.63E-06	9.13E-06
LOC100651057	948.379686	-0.567607894	0.0723656	-7.8436151	4.38E-15	1.25E-14
LOC100651209	412.784386	-0.566740602	0.09316499	-6.0831928	1.18E-09	2.42E-09
LOC105665935	265.58887	-0.565805457	0.11455418	-4.9391952	7.84E-07	1.35E-06
LOC100649074	499.076339	-0.565130431	0.0665576	-8.4908481	2.05E-17	6.70E-17
LOC100648728	48.4337597	-0.564905322	0.25094042	-2.2511532	0.02437584	0.03008114
LOC100643621	147.882261	-0.563982206	0.12944763	-4.356837	1.32E-05	2.09E-05
LOC100644462	555.044646	-0.563950271	0.17281554	-3.2633075	0.0011012	0.00151601
LOC100649168	656.748624	-0.563662585	0.08164097	-6.9041634	5.05E-12	1.20E-11
LOC100649146	960.242627	-0.563581483	0.07796715	-7.2284475	4.89E-13	1.24E-12
LOC100652056	1157.24784	-0.563535555	0.11894016	-4.7379754	2.16E-06	3.60E-06
LOC100652161	20527.0868	-0.56348761	0.08604454	-6.5487902	5.80E-11	1.28E-10
LOC100645094	932.566179	-0.562801456	0.05563462	-10.11603	4.69E-24	2.21E-23
LOC100651963	803.143043	-0.562467332	0.07516873	-7.4827301	7.28E-14	1.93E-13
LOC100644019	480.088766	-0.562176976	0.09378591	-5.9942582	2.04E-09	4.14E-09
LOC100645805	376.466356	-0.561157395	0.10584826	-5.3015266	1.15E-07	2.08E-07
LOC100650587	1050.79253	-0.561047783	0.06384868	-8.7871472	1.53E-18	5.36E-18
LOC100649176	202.843577	-0.560761443	0.11250401	-4.9843684	6.22E-07	1.08E-06
LOC100642258	417.992677	-0.560599373	0.08418739	-6.6589469	2.76E-11	6.24E-11
LOC100647758	1536.17941	-0.560541708	0.07716527	-7.2641708	3.75E-13	9.58E-13
LOC105667086	127.624896	-0.560357901	0.24901942	-2.2502578	0.02443258	0.03014738
LOC100648461	3029.0574	-0.559844804	0.05842688	-9.5819727	9.52E-22	3.97E-21
LOC100647258	819.996619	-0.55971588	0.07221963	-7.7501906	9.18E-15	2.57E-14
LOC100648920	884.257857	-0.559414975	0.07873718	-7.1048392	1.20E-12	2.97E-12
LOC100648930	3312.63745	-0.558992205	0.05948243	-9.3976027	5.58E-21	2.25E-20

LOC100645201	13332.4498	-0.558277571	0.04837011	-11.541788	8.12E-31	5.88E-30
LOC100649307	1615.54433	-0.557908044	0.22469726	-2.4829321	0.01303059	0.01643893
LOC100644988	1728.12126	-0.557837451	0.07913084	-7.0495584	1.79E-12	4.38E-12
LOC100642360	66.1762368	-0.55658675	0.18853128	-2.952225	0.00315493	0.00419586
LOC100642267	637.7738	-0.556513021	0.10662198	-5.2194961	1.79E-07	3.22E-07
LOC105665841	14131.0524	-0.556346393	0.11275796	-4.9339878	8.06E-07	1.39E-06
LOC100647526	3603.47544	-0.5560761	0.06857671	-8.108819	5.11E-16	1.54E-15
LOC100647688	460.932855	-0.555642849	0.07774812	-7.1467044	8.89E-13	2.21E-12
LOC100650371	2160.2419	-0.55556501	0.07648391	-7.2638152	3.76E-13	9.60E-13
LOC100648977	478.976726	-0.555415388	0.07897208	-7.0330598	2.02E-12	4.92E-12
LOC100643421	3812.6201	-0.555200729	0.08594863	-6.4596813	1.05E-10	2.28E-10
LOC100650440	693.033671	-0.55510428	0.0739112	-7.5104217	5.89E-14	1.58E-13
LOC100644471	712.176638	-0.554933599	0.09287457	-5.9750864	2.30E-09	4.65E-09
LOC100644964	558.434812	-0.554671668	0.0728937	-7.6093223	2.76E-14	7.50E-14
LOC100651762	652.149532	-0.55447897	0.07201905	-7.6990601	1.37E-14	3.79E-14
LOC100648202	239.36325	-0.554070541	0.0876662	-6.32023	2.61E-10	5.55E-10
LOC100642878	6643.30419	-0.553657045	0.08216042	-6.7387323	1.60E-11	3.68E-11
LOC100646758	55.4874524	-0.553214204	0.19926556	-2.776266	0.00549872	0.0071536
LOC100651720	2419.69724	-0.552833428	0.06984115	-7.9155831	2.46E-15	7.13E-15
LOC100643820	349.91808	-0.552650696	0.08602148	-6.4245661	1.32E-10	2.85E-10
LOC100645517	1250.82317	-0.552312993	0.12028473	-4.5917132	4.40E-06	7.18E-06
LOC105665758	1843.05947	-0.552031271	0.15005356	-3.6788949	0.00023425	0.00034018
LOC100651798	1939.43535	-0.551963984	0.10170676	-5.4270136	5.73E-08	1.06E-07
LOC100643659	259.300388	-0.55186953	0.14016986	-3.9371484	8.25E-05	0.00012399
LOC105667124	99.9410123	-0.551567032	0.13626343	-4.0477995	5.17E-05	7.89E-05
LOC100644852	327.621525	-0.551135451	0.08403962	-6.5580428	5.45E-11	1.21E-10
LOC100651058	529.427591	-0.551081232	0.13023355	-4.2314845	2.32E-05	3.63E-05
LOC100646688	48.1092951	-0.550981313	0.2256818	-2.4414078	0.01463012	0.01838577
LOC100646625	1421.15069	-0.550150092	0.13405953	-4.1037746	4.06E-05	6.24E-05

LOC100644096	710.969705	-0.549824708	0.06862844	-8.0116156	1.13E-15	3.34E-15
LOC100648662	7995.69576	-0.549492865	0.14112194	-3.893745	9.87E-05	0.00014737
LOC100648830	23803.8098	-0.549453199	0.09715421	-5.6554752	1.55E-08	2.97E-08
LOC100642752	423.524374	-0.548840517	0.10390263	-5.2822582	1.28E-07	2.30E-07
LOC100646147	370.974593	-0.548443888	0.15544461	-3.5282271	0.00041835	0.00059606
LOC100648951	4397.084	-0.54697268	0.16167869	-3.3830847	0.00071677	0.00099984
LOC100642877	633.925202	-0.545892025	0.07079823	-7.7105325	1.25E-14	3.47E-14
LOC100642802	2373.26461	-0.545542897	0.09706366	-5.6204648	1.90E-08	3.62E-08
LOC100649702	1168.09832	-0.545393606	0.09727775	-5.6065606	2.06E-08	3.92E-08
LOC100649133	844.91379	-0.544742038	0.07987226	-6.8201655	9.09E-12	2.13E-11
LOC100648989	451.173071	-0.54442082	0.07578144	-7.1840919	6.77E-13	1.70E-12
LOC100642780	686.141712	-0.544387384	0.06636511	-8.2029159	2.35E-16	7.21E-16
LOC100651560	364.260766	-0.544357173	0.08560293	-6.3590952	2.03E-10	4.34E-10
LOC100644455	340.420247	-0.543822329	0.09308435	-5.8422528	5.15E-09	1.02E-08
LOC100644878	491.431796	-0.543802395	0.10206293	-5.328109	9.92E-08	1.80E-07
LOC100646630	96.1160502	-0.543516193	0.14001064	-3.8819634	0.00010362	0.00015444
LOC100650134	1815.7478	-0.543062588	0.06756398	-8.0377535	9.15E-16	2.72E-15
LOC100646960	279.98266	-0.542402247	0.14643034	-3.7041658	0.00021209	0.00030915
LOC100646343	7654.96203	-0.542393525	0.10956431	-4.9504582	7.40E-07	1.28E-06
LOC100651266	239.335556	-0.542363475	0.10768084	-5.0367688	4.73E-07	8.28E-07
LOC100644185	1378.03302	-0.542271563	0.19712532	-2.7508975	0.00594322	0.00770322
LOC100649465	2330.17004	-0.542241521	0.08153758	-6.6502034	2.93E-11	6.61E-11
LOC100649705	147.825822	-0.540145342	0.22364575	-2.4151827	0.01572732	0.01969636
LOC100645625	190.805136	-0.540130851	0.13278908	-4.0675848	4.75E-05	7.27E-05
LOC100645295	1083.77299	-0.540085959	0.17212047	-3.1378369	0.001702	0.00230871
LOC100649262	1093.64906	-0.539676029	0.07520111	-7.1764374	7.16E-13	1.79E-12
LOC100645896	267.257233	-0.539369606	0.09742032	-5.5365204	3.09E-08	5.79E-08
LOC100643230	220.565477	-0.53911271	0.13727746	-3.9271759	8.59E-05	0.00012891
LOC100645155	493.727079	-0.538680216	0.13974327	-3.8547846	0.00011583	0.00017202

LOC100642907	379.087636	-0.538236285	0.08972606	-5.9986618	1.99E-09	4.03E-09
LOC100652038	328.591992	-0.536815613	0.10429491	-5.1470932	2.65E-07	4.69E-07
LOC100645274	2082.41654	-0.536663873	0.07454904	-7.1988032	6.07E-13	1.53E-12
LOC100644234	340.886607	-0.535874692	0.08422995	-6.3620448	1.99E-10	4.26E-10
LOC100643136	457.375778	-0.535612916	0.08973442	-5.9688683	2.39E-09	4.82E-09
LOC100646972	933.412452	-0.535494643	0.07156222	-7.4829239	7.27E-14	1.93E-13
LOC100643006	325.742382	-0.535209074	0.08384435	-6.3833646	1.73E-10	3.71E-10
LOC100651859	743.304198	-0.534757512	0.07388973	-7.2372372	4.58E-13	1.16E-12
LOC105665754	707.533657	-0.533642288	0.06787247	-7.8624268	3.77E-15	1.08E-14
LOC100645628	2908.50754	-0.533500788	0.05875496	-9.0800979	1.08E-19	4.06E-19
LOC100648768	425.377374	-0.533269018	0.13979473	-3.8146575	0.00013637	0.00020136
LOC100648938	98.7376732	-0.533070976	0.16129402	-3.3049643	0.00094988	0.00131379
LOC100651453	680.973177	-0.532653529	0.07687935	-6.9284348	4.26E-12	1.01E-11
LOC100648014	2677.60117	-0.532639953	0.07658755	-6.9546548	3.53E-12	8.48E-12
LOC100643029	549.047312	-0.531693824	0.08690527	-6.1180849	9.47E-10	1.96E-09
LOC100647714	162.973203	-0.531251971	0.14794029	-3.590989	0.00032943	0.00047316
LOC100649189	2606.52229	-0.530861873	0.06586969	-8.0592742	7.67E-16	2.29E-15
LOC100646937	335.631399	-0.53069791	0.08913259	-5.954028	2.62E-09	5.27E-09
LOC100647651	45.6082396	-0.529924217	0.20919442	-2.5331661	0.01130374	0.01434727
LOC105665724	4627.09409	-0.529600679	0.07528985	-7.0341575	2.00E-12	4.88E-12
LOC100643926	1918.82988	-0.529589912	0.07467124	-7.092288	1.32E-12	3.25E-12
LOC100649551	910.170216	-0.528912648	0.11073436	-4.7764095	1.78E-06	3.00E-06
LOC100642674	2155.49683	-0.528758354	0.11064949	-4.7786785	1.76E-06	2.96E-06
LOC100650195	729.621326	-0.528090986	0.07126272	-7.4104805	1.26E-13	3.29E-13
LOC100652219	488.848667	-0.527603008	0.07798491	-6.7654503	1.33E-11	3.07E-11
LOC100651854	986.384507	-0.526199184	0.07920223	-6.643742	3.06E-11	6.90E-11
LOC100648397	519.373829	-0.525860574	0.07787914	-6.7522649	1.46E-11	3.36E-11
LOC100652137	1236.31085	-0.52552289	0.09137732	-5.7511305	8.86E-09	1.73E-08
LOC100647209	1026.74975	-0.525506071	0.06636149	-7.9188408	2.40E-15	6.95E-15

LOC100647312	1242.9364	-0.524333601	0.06957586	-7.5361427	4.84E-14	1.30E-13
LOC100649908	412.05726	-0.524173172	0.10069629	-5.2054865	1.93E-07	3.46E-07
LOC100647772	1982.03954	-0.523902199	0.10513836	-4.9829786	6.26E-07	1.09E-06
LOC100649112	159.56786	-0.523544571	0.21913045	-2.3891913	0.01688551	0.02109288
LOC100650228	258.229513	-0.523325353	0.11355352	-4.6086227	4.05E-06	6.63E-06
LOC100650506	872.104439	-0.522160782	0.10909921	-4.7861095	1.70E-06	2.86E-06
LOC100643280	167.433358	-0.521986337	0.1160522	-4.4978584	6.86E-06	1.11E-05
LOC100643456	66.9135767	-0.521677266	0.24465694	-2.1322806	0.03298378	0.0402122
LOC100642885	320.072663	-0.521608001	0.09628557	-5.4173016	6.05E-08	1.12E-07
LOC100642810	350.916143	-0.521439682	0.0787384	-6.6224314	3.53E-11	7.93E-11
LOC100652241	735.05293	-0.52122778	0.07813054	-6.6712428	2.54E-11	5.75E-11
LOC100644805	214.942288	-0.521113074	0.10651905	-4.8922055	9.97E-07	1.70E-06
LOC100648825	739.069311	-0.52078164	0.13241106	-3.9330675	8.39E-05	0.00012596
LOC100652265	599.738224	-0.520752229	0.09979528	-5.2182049	1.81E-07	3.24E-07
LOC100648926	957.344515	-0.520715082	0.06541041	-7.9607369	1.71E-15	4.99E-15
LOC100650083	294.275201	-0.520144568	0.10454707	-4.9752191	6.52E-07	1.13E-06
LOC100650972	379.722967	-0.519726576	0.12509465	-4.1546666	3.26E-05	5.04E-05
LOC100644566	8567.07603	-0.519003319	0.05956797	-8.7127914	2.96E-18	1.02E-17
LOC100649567	499.288466	-0.51813908	0.10585636	-4.8947372	9.84E-07	1.68E-06
LOC100644308	460.978375	-0.518118794	0.09710976	-5.3353939	9.53E-08	1.73E-07
LOC100644752	10506.1286	-0.518067834	0.22604867	-2.291842	0.02191476	0.02716044
LOC100649995	105.616055	-0.517246224	0.12963629	-3.9899802	6.61E-05	0.00010004
LOC100644260	745.910482	-0.51624867	0.06278643	-8.2222964	2.00E-16	6.17E-16
LOC100650252	1501.50088	-0.515915286	0.06584368	-7.8354565	4.67E-15	1.33E-14
LOC100650362	413.285046	-0.515828119	0.138981	-3.7115009	0.00020603	0.00030064
LOC100645118	253.10573	-0.515624183	0.10925097	-4.7196304	2.36E-06	3.93E-06
LOC100649795	165.47759	-0.515587103	0.18064232	-2.8541878	0.0043147	0.00566366
LOC100651946	508.494604	-0.515582386	0.08587086	-6.0041603	1.92E-09	3.90E-09
LOC100650128	548.984462	-0.515509655	0.08414181	-6.1266767	8.97E-10	1.86E-09

LOC100649224	254.787892	-0.514018218	0.13120847	-3.917569	8.94E-05	0.00013403
LOC100645373	1607.63899	-0.513847924	0.07701005	-6.6724792	2.52E-11	5.70E-11
LOC100646841	96.2121435	-0.513817292	0.18546315	-2.7704549	0.00559781	0.00727574
LOC100642892	1498.46545	-0.513144188	0.09433311	-5.4397039	5.34E-08	9.87E-08
LOC100652031	959.939651	-0.512711454	0.079282	-6.4669336	1.00E-10	2.17E-10
LOC100645847	2434.66334	-0.51228324	0.07793153	-6.5735042	4.91E-11	1.09E-10
LOC100646703	3411.82871	-0.512000296	0.09797063	-5.2260593	1.73E-07	3.11E-07
LOC100645404	722.435658	-0.511887917	0.07681768	-6.6636732	2.67E-11	6.05E-11
LOC100642374	415.211285	-0.511791651	0.21049247	-2.4314012	0.01504055	0.01887733
LOC100650910	3586.03807	-0.511713828	0.05000688	-10.232868	1.41E-24	6.92E-24
LOC100649920	643.660802	-0.511607249	0.13148156	-3.8910951	9.98E-05	0.00014892
LOC100647136	370.922528	-0.511461022	0.11712317	-4.3668647	1.26E-05	2.00E-05
LOC100649462	1132.00385	-0.511067305	0.09298064	-5.4964917	3.87E-08	7.23E-08
LOC100642914	482.884959	-0.510708891	0.10962575	-4.6586583	3.18E-06	5.25E-06
LOC100649546	4898.38636	-0.510372395	0.12310053	-4.1459806	3.38E-05	5.23E-05
LOC100644378	303.307449	-0.510313424	0.20712734	-2.4637666	0.01374856	0.01731569
LOC100644525	1423.86956	-0.510111035	0.06618145	-7.707764	1.28E-14	3.54E-14
LOC100647681	176.643822	-0.509392078	0.11141558	-4.5720004	4.83E-06	7.87E-06
LOC100642426	908.128795	-0.509006106	0.06413805	-7.9361015	2.09E-15	6.07E-15
LOC100645633	379.610509	-0.508321597	0.10077983	-5.0438823	4.56E-07	7.98E-07
LOC100644131	2901.19832	-0.508071056	0.12597631	-4.0330682	5.51E-05	8.39E-05
LOC100646613	2539.49708	-0.50794905	0.0834626	-6.0859482	1.16E-09	2.38E-09
LOC100649979	739.243873	-0.507885687	0.08569107	-5.9269382	3.09E-09	6.19E-09
LOC100648994	399.055161	-0.507180048	0.09231456	-5.4940416	3.93E-08	7.32E-08
LOC100642419	645.552305	-0.507110967	0.08415897	-6.0256317	1.68E-09	3.43E-09
LOC100646768	1470.45219	-0.507017676	0.09584172	-5.2901561	1.22E-07	2.21E-07
LOC100651738	690.128865	-0.506933109	0.05643151	-8.9831569	2.63E-19	9.68E-19
LOC100646898	268.368564	-0.506606225	0.12044025	-4.2062868	2.60E-05	4.04E-05
LOC100643814	725.594465	-0.506513507	0.0828179	-6.1159908	9.60E-10	1.98E-09

LOC100647477	329.56191	-0.506346924	0.09980321	-5.0734535	3.91E-07	6.86E-07
LOC105666568	392.473705	-0.506296225	0.10315289	-4.9082118	9.19E-07	1.57E-06
LOC100649616	958.648179	-0.506000422	0.09137986	-5.5373297	3.07E-08	5.77E-08
LOC100643283	262.751642	-0.505325503	0.15578116	-3.2438164	0.0011794	0.00161956
LOC100652224	7173.04595	-0.504392863	0.07185394	-7.0196963	2.22E-12	5.39E-12
LOC100650887	568.058552	-0.503892821	0.116634	-4.3202909	1.56E-05	2.46E-05
LOC100645172	6081.26997	-0.503409964	0.08300349	-6.0649249	1.32E-09	2.70E-09
LOC100646911	203.269696	-0.502747314	0.12091917	-4.157714	3.21E-05	4.97E-05
LOC100645178	1007.34477	-0.502729658	0.06760574	-7.4361979	1.04E-13	2.73E-13
LOC100650030	2968.0514	-0.50234223	0.15612179	-3.2176305	0.00129254	0.00176997
LOC100643237	652.917324	-0.502298952	0.13163792	-3.8157619	0.00013576	0.00020052
LOC100650447	1049.62831	-0.501827243	0.08110034	-6.1877327	6.10E-10	1.27E-09
LOC100648110	536.825691	-0.501419933	0.06775983	-7.3999584	1.36E-13	3.55E-13
LOC100643914	2344.5344	-0.501093681	0.0884732	-5.6637908	1.48E-08	2.84E-08
LOC100651719	2936.06237	-0.50103542	0.067697	-7.4011462	1.35E-13	3.52E-13
LOC105666608	198.784985	-0.500804116	0.10781724	-4.6449356	3.40E-06	5.60E-06
LOC100649238	227.769932	-0.50043272	0.09131573	-5.4802468	4.25E-08	7.90E-08
LOC100642620	195.168186	-0.499876594	0.15410845	-3.2436677	0.00118001	0.00162018
LOC100651227	954.797517	-0.499452183	0.06389449	-7.8168269	5.42E-15	1.53E-14
LOC100651194	2243.21054	-0.498895843	0.10844847	-4.6003031	4.22E-06	6.90E-06
LOC100642623	1766.74473	-0.498823874	0.06123437	-8.1461422	3.76E-16	1.14E-15
LOC100645481	799.699382	-0.498588928	0.13771896	-3.6203361	0.00029422	0.0004237
LOC100646237	712.678894	-0.497906332	0.13448318	-3.7023689	0.0002136	0.00031116
LOC100645827	361.958179	-0.497560657	0.09276608	-5.3636053	8.16E-08	1.49E-07
LOC100642627	1005.49277	-0.497338841	0.07172476	-6.9339906	4.09E-12	9.77E-12
LOC100646529	468.502785	-0.497158301	0.08203538	-6.0602916	1.36E-09	2.78E-09
LOC100649266	2083.41376	-0.496922862	0.08196584	-6.0625608	1.34E-09	2.74E-09
LOC100652220	419.648249	-0.496803382	0.10364974	-4.7930982	1.64E-06	2.76E-06
LOC105667166	338.538684	-0.496657835	0.08602407	-5.7734751	7.77E-09	1.52E-08

LOC100647237	219.999164	-0.496421659	0.10480484	-4.736629	2.17E-06	3.62E-06
LOC100651150	878.686627	-0.496316036	0.09467672	-5.2422183	1.59E-07	2.85E-07
LOC100643993	296.763021	-0.495883614	0.0904608	-5.4817513	4.21E-08	7.84E-08
LOC100650638	1146.24847	-0.494804811	0.08331509	-5.9389582	2.87E-09	5.77E-09
LOC100651251	617.365674	-0.494772857	0.07778424	-6.3608369	2.01E-10	4.29E-10
LOC100649751	177.706863	-0.4946277	0.15170927	-3.2603658	0.00111269	0.00153118
LOC100648849	822.109432	-0.494480457	0.0629915	-7.8499551	4.16E-15	1.19E-14
LOC100643154	1858.30923	-0.493794596	0.06904943	-7.1513205	8.59E-13	2.14E-12
LOC100643844	532.358759	-0.493586468	0.10460012	-4.7187947	2.37E-06	3.95E-06
LOC105665894	1755.62548	-0.492903505	0.08498608	-5.7998144	6.64E-09	1.30E-08
LOC100652329	759.229262	-0.492871045	0.10857999	-4.5392437	5.65E-06	9.16E-06
LOC100646891	271.991708	-0.492743953	0.13058633	-3.7733196	0.00016109	0.00023679
LOC100643808	340.796019	-0.492403906	0.09920383	-4.9635575	6.92E-07	1.20E-06
LOC100647537	565.843	-0.491821003	0.06742802	-7.2940153	3.01E-13	7.70E-13
LOC100649977	2837.21381	-0.491611089	0.12590422	-3.9046434	9.44E-05	0.00014116
LOC100645795	823.468888	-0.491364126	0.07185205	-6.8385538	8.00E-12	1.88E-11
LOC100647395	408.866384	-0.491222637	0.21098023	-2.3282875	0.01989684	0.0247472
LOC100643534	277.203594	-0.490778578	0.18669632	-2.6287533	0.00856985	0.01097977
LOC100643245	237.153954	-0.490750586	0.09752956	-5.0318137	4.86E-07	8.49E-07
LOC100643898	211.324397	-0.490378927	0.12321201	-3.9799606	6.89E-05	0.00010419
LOC100645167	1289.89648	-0.490084233	0.12257137	-3.998358	6.38E-05	9.67E-05
LOC100650610	176.968016	-0.489973679	0.12883983	-3.8029675	0.00014297	0.00021085
LOC100644586	130.590065	-0.489277395	0.1430933	-3.4192893	0.00062785	0.00087994
LOC105665772	739.586898	-0.488948832	0.07296226	-6.7013939	2.06E-11	4.71E-11
LOC100648351	449.546621	-0.488739128	0.07331529	-6.6662647	2.62E-11	5.95E-11
LOC100647433	1719.738	-0.488264188	0.08398994	-5.813365	6.12E-09	1.21E-08
LOC100648000	25347.3297	-0.488076592	0.0991203	-4.9240832	8.48E-07	1.46E-06
LOC100645620	829.693298	-0.487769947	0.06541357	-7.456709	8.87E-14	2.35E-13
LOC100649730	398.618879	-0.487661697	0.11019066	-4.4256172	9.62E-06	1.54E-05

LOC100650269	264.316922	-0.487419502	0.10725843	-4.5443468	5.51E-06	8.95E-06
LOC100652135	1019.99076	-0.48546002	0.06194226	-7.8372995	4.60E-15	1.31E-14
LOC100644804	829.086007	-0.485072638	0.07960612	-6.093409	1.11E-09	2.27E-09
LOC100644280	695.465057	-0.484602707	0.08987723	-5.3918297	6.97E-08	1.28E-07
LOC100648273	2435.38931	-0.484008755	0.06711003	-7.2121676	5.51E-13	1.39E-12
LOC100644183	741.464306	-0.482649054	0.09951307	-4.8501071	1.23E-06	2.10E-06
LOC100643751	1077.67472	-0.482604115	0.07708822	-6.260413	3.84E-10	8.08E-10
LOC100644388	48.2250609	-0.482535501	0.23236427	-2.0766338	0.03783537	0.04590979
LOC100650354	12474.2226	-0.482482984	0.11406338	-4.2299553	2.34E-05	3.65E-05
LOC100647521	4113.8655	-0.481258767	0.09613147	-5.0062559	5.55E-07	9.67E-07
LOC100643239	674.425917	-0.480939233	0.06826985	-7.0446799	1.86E-12	4.53E-12
LOC100650247	577.054089	-0.480804754	0.08072081	-5.9563919	2.58E-09	5.20E-09
LOC100648646	404.150239	-0.479090386	0.16307637	-2.9378285	0.0033052	0.00438558
LOC100642926	161.83104	-0.478996339	0.125509	-3.8164303	0.0001354	0.00020001
LOC100643027	737.909269	-0.478684434	0.07484726	-6.3954835	1.60E-10	3.43E-10
LOC100645066	464.475612	-0.478433244	0.08227864	-5.8147926	6.07E-09	1.20E-08
LOC100649150	699.7443	-0.478125545	0.11885921	-4.0226211	5.76E-05	8.77E-05
LOC100648480	1098.27584	-0.47779023	0.19196335	-2.4889659	0.01281153	0.0161709
LOC100646304	383.92134	-0.477720237	0.10247582	-4.661785	3.13E-06	5.17E-06
LOC100642200	1803.88831	-0.477691693	0.09672175	-4.9388241	7.86E-07	1.35E-06
LOC100631054	2417.39816	-0.477019678	0.0860587	-5.5429572	2.97E-08	5.59E-08
LOC100649082	619.418302	-0.47612629	0.07631179	-6.2392233	4.40E-10	9.23E-10
LOC100651581	72.4825384	-0.476076074	0.15604162	-3.0509557	0.00228114	0.00306921
LOC100650500	1417.38304	-0.475923061	0.09579665	-4.9680554	6.76E-07	1.17E-06
LOC100646704	653.359626	-0.475629241	0.06932921	-6.860445	6.86E-12	1.62E-11
LOC100647982	338.019689	-0.475561742	0.15729207	-3.0234312	0.00249926	0.00335393
LOC100649252	134.686933	-0.475418258	0.13799393	-3.4452115	0.00057061	0.00080306
LOC100643163	84.8419732	-0.474803114	0.18403783	-2.5799212	0.00988229	0.01261834
LOC105666789	264.242949	-0.47461085	0.1205883	-3.9357951	8.29E-05	0.00012464

LOC100642431	314.468656	-0.474482404	0.10033063	-4.7291881	2.25E-06	3.76E-06
LOC100648801	1578.65762	-0.474229376	0.0786051	-6.0330608	1.61E-09	3.28E-09
LOC100642701	979.183084	-0.474186978	0.0636674	-7.4478777	9.49E-14	2.50E-13
LOC100650513	299.080887	-0.4741631	0.10170142	-4.6623055	3.13E-06	5.16E-06
LOC100651508	691.191123	-0.474011836	0.19020959	-2.4920502	0.01270081	0.01603528
LOC100650961	734.670912	-0.473503605	0.07394974	-6.4030466	1.52E-10	3.27E-10
LOC100645405	1640.45476	-0.472967401	0.14752316	-3.2060552	0.00134568	0.00184068
LOC100642635	798.422554	-0.47296334	0.10036057	-4.712641	2.45E-06	4.06E-06
LOC100645458	281.474857	-0.472852784	0.11427994	-4.1376708	3.51E-05	5.41E-05
LOC100645447	919.445774	-0.472563063	0.06743728	-7.0074452	2.43E-12	5.87E-12
LOC100651606	408.806894	-0.471401758	0.08469817	-5.5656665	2.61E-08	4.93E-08
LOC100651339	453.903721	-0.471337513	0.10990152	-4.2887261	1.80E-05	2.83E-05
LOC100644802	748.926183	-0.471050827	0.11461297	-4.1099259	3.96E-05	6.09E-05
LOC100648627	1160.30342	-0.470566102	0.0756228	-6.2225426	4.89E-10	1.02E-09
LOC105665924	175.898862	-0.469928928	0.13688819	-3.4329398	0.00059707	0.00083825
LOC100646396	400.616457	-0.46967426	0.08747161	-5.3694481	7.90E-08	1.44E-07
LOC100642679	674.964361	-0.469598448	0.07675597	-6.1180707	9.47E-10	1.96E-09
LOC105665655	222.382482	-0.469521115	0.12413966	-3.7822006	0.00015545	0.00022873
LOC100645915	1739.40596	-0.469309078	0.11522249	-4.0730682	4.64E-05	7.10E-05
LOC100645643	388.76742	-0.469305363	0.09987163	-4.699086	2.61E-06	4.33E-06
LOC100642899	118.228411	-0.468857266	0.14682324	-3.193345	0.00140635	0.00191937
LOC100651023	7610.43349	-0.468689011	0.08273718	-5.6647928	1.47E-08	2.82E-08
LOC100648686	909.812565	-0.468385326	0.09763339	-4.7973888	1.61E-06	2.71E-06
LOC100645432	636.150191	-0.468174651	0.07754367	-6.0375616	1.56E-09	3.19E-09
LOC100646979	435.138768	-0.468052435	0.11571952	-4.0447145	5.24E-05	7.99E-05
LOC105666381	703.305676	-0.467590576	0.08332169	-5.6118712	2.00E-08	3.81E-08
LOC105666557	563.882765	-0.467434398	0.09816788	-4.7615817	1.92E-06	3.22E-06
LOC100646913	488.587033	-0.465748768	0.09423706	-4.9423099	7.72E-07	1.33E-06
LOC105666622	222.808434	-0.465392593	0.12683389	-3.6693079	0.00024321	0.00035273

LOC100647054	327.859907	-0.465078128	0.09898369	-4.6985329	2.62E-06	4.34E-06
LOC100646171	754.570561	-0.464680255	0.07728092	-6.0128715	1.82E-09	3.70E-09
LOC100647385	1676.97153	-0.46467563	0.09704622	-4.7881891	1.68E-06	2.83E-06
LOC100647642	802.391862	-0.464071123	0.08131558	-5.7070385	1.15E-08	2.22E-08
LOC100645607	516.266957	-0.463874379	0.08123114	-5.7105483	1.13E-08	2.18E-08
LOC100646174	461.607954	-0.463373551	0.16066859	-2.8840331	0.00392617	0.0051696
LOC100645791	208.731872	-0.463256243	0.09375287	-4.9412485	7.76E-07	1.34E-06
LOC100648360	534.565006	-0.46322553	0.10275652	-4.5079915	6.54E-06	1.06E-05
LOC100645955	620.438228	-0.462604219	0.07496762	-6.1707202	6.80E-10	1.41E-09
LOC100646037	757.80578	-0.462238276	0.14422934	-3.2048837	0.00135117	0.00184767
LOC100647551	980.743819	-0.462055207	0.06431997	-7.1836977	6.79E-13	1.70E-12
LOC100650737	3349.90661	-0.462031487	0.08684201	-5.3203684	1.04E-07	1.88E-07
LOC100651793	668.747732	-0.461754588	0.12074487	-3.8242171	0.00013119	0.00019403
LOC100647119	185.763556	-0.461366287	0.20273172	-2.2757478	0.02286111	0.02829033
LOC100642563	178.326559	-0.461301345	0.14671535	-3.1441928	0.00166546	0.00226133
LOC100650619	361.901083	-0.46091696	0.08987031	-5.12869	2.92E-07	5.16E-07
LOC100650063	500.436225	-0.46085084	0.08062581	-5.7159219	1.09E-08	2.11E-08
LOC105666483	1393.74037	-0.460670403	0.0832773	-5.5317645	3.17E-08	5.95E-08
LOC100651753	363.421442	-0.460271861	0.10007496	-4.5992711	4.24E-06	6.93E-06
LOC100646576	894.261632	-0.46026618	0.10583245	-4.3490081	1.37E-05	2.17E-05
LOC100642741	818.953115	-0.460239541	0.07325546	-6.2826653	3.33E-10	7.03E-10
LOC100645575	885.673445	-0.459848497	0.17816077	-2.5810872	0.00984897	0.01257744
LOC100642409	634.005307	-0.459553473	0.05283427	-8.6980195	3.38E-18	1.15E-17
LOC105666825	80.7514553	-0.458692559	0.21084045	-2.1755435	0.02958941	0.03622733
LOC100651781	897.248122	-0.458559847	0.10457781	-4.3848677	1.16E-05	1.85E-05
LOC100648449	460.171978	-0.458404469	0.07952205	-5.7644952	8.19E-09	1.60E-08
LOC100651296	4815.33945	-0.458075645	0.05331841	-8.5913216	8.60E-18	2.87E-17
LOC100650086	146.096939	-0.457539191	0.2027515	-2.2566501	0.02402995	0.02967024
LOC100643665	683.549728	-0.457250436	0.12835383	-3.5624215	0.00036745	0.00052587

LOC100643971	2325.14349	-0.456533657	0.11013847	-4.1450879	3.40E-05	5.25E-05
LOC100642516	141.839616	-0.456020302	0.16796912	-2.7149056	0.00662947	0.00856321
LOC100643250	1026.22395	-0.455984208	0.07558665	-6.0326026	1.61E-09	3.29E-09
Mpk	602.8795	-0.454789342	0.11948841	-3.8061378	0.00014115	0.0002082
LOC100647775	300.915848	-0.454306906	0.08637635	-5.2596214	1.44E-07	2.60E-07
LOC100644865	618.719358	-0.454283913	0.09178324	-4.9495303	7.44E-07	1.29E-06
LOC100643640	490.700156	-0.453794314	0.0920408	-4.9303606	8.21E-07	1.41E-06
LOC100649381	641.451871	-0.452998428	0.08760647	-5.1708329	2.33E-07	4.15E-07
LOC100644432	164.882409	-0.452977077	0.14885266	-3.0431238	0.00234136	0.00314764
LOC100643234	1069.97849	-0.452855694	0.06565586	-6.8974143	5.30E-12	1.26E-11
LOC100646938	446.579042	-0.452567241	0.09041611	-5.0053827	5.58E-07	9.71E-07
LOC100652310	376.701391	-0.451618481	0.11740204	-3.8467687	0.00011969	0.00017763
LOC100643996	1803.04945	-0.451598997	0.09694391	-4.6583535	3.19E-06	5.26E-06
LOC100651365	1490.12705	-0.451503669	0.15306693	-2.949714	0.00318068	0.00422724
LOC100647659	655.08054	-0.449992333	0.09219596	-4.8808251	1.06E-06	1.80E-06
LOC100650679	625.439752	-0.449277313	0.09113359	-4.929876	8.23E-07	1.41E-06
LOC100642528	376.230155	-0.448590814	0.08817745	-5.0873644	3.63E-07	6.39E-07
LOC100644502	1114.47775	-0.447998371	0.07954832	-5.6317765	1.78E-08	3.40E-08
LOC100649886	403.897673	-0.447474601	0.12628504	-3.54337	0.00039505	0.000564
LOC100648824	150.273552	-0.447312651	0.12228281	-3.6580174	0.00025417	0.00036808
LOC100649209	438.432776	-0.447262411	0.07659597	-5.8392424	5.24E-09	1.04E-08
LOC100647356	496.685804	-0.446979825	0.0864309	-5.171528	2.32E-07	4.13E-07
LOC100642451	331.079096	-0.446878492	0.10856768	-4.1161283	3.85E-05	5.93E-05
LOC100651389	657.893335	-0.44660381	0.1118796	-3.9918251	6.56E-05	9.93E-05
LOC100645576	377.114211	-0.44640865	0.08980811	-4.9706943	6.67E-07	1.16E-06
LOC100650768	291.644632	-0.44616843	0.18245585	-2.4453501	0.01447116	0.018193
LOC100650995	1089.46693	-0.445258915	0.1708065	-2.6068032	0.00913919	0.01168933
LOC100646910	19756.8069	-0.445087735	0.08762194	-5.0796381	3.78E-07	6.65E-07
LOC100652176	259.365442	-0.44501392	0.10381566	-4.2865779	1.81E-05	2.85E-05

LOC100645205	2378.03432	-0.443439237	0.05701331	-7.7778196	7.38E-15	2.07E-14
LOC100643818	614.52137	-0.443106772	0.06657989	-6.655264	2.83E-11	6.39E-11
LOC100643893	3667.04137	-0.4430565	0.05697854	-7.7758489	7.49E-15	2.10E-14
LOC105665629	807.793151	-0.442686092	0.08901715	-4.9730428	6.59E-07	1.14E-06
LOC100647428	1381.22782	-0.442620037	0.08107	-5.4597267	4.77E-08	8.84E-08
LOC100647016	240.295891	-0.442235729	0.09075511	-4.8728468	1.10E-06	1.88E-06
LOC100648954	1080.66618	-0.441887375	0.09149517	-4.829625	1.37E-06	2.32E-06
LOC100648206	194.44301	-0.441179051	0.11247264	-3.9225457	8.76E-05	0.00013133
LOC100648113	1070.80877	-0.441153969	0.10621446	-4.1534265	3.28E-05	5.07E-05
LOC100645007	2882.9771	-0.440990153	0.05561516	-7.9293155	2.20E-15	6.40E-15
LOC105666097	3876.47949	-0.440963999	0.08204865	-5.3744209	7.68E-08	1.41E-07
LOC100643949	1088.91836	-0.440779394	0.0861823	-5.1145001	3.15E-07	5.56E-07
LOC100647458	889.627748	-0.4396103	0.1299336	-3.3833457	0.00071608	0.00099903
LOC100648130	788.672261	-0.439478436	0.0906983	-4.845498	1.26E-06	2.15E-06
LOC100649565	656.331913	-0.439466649	0.08484099	-5.179886	2.22E-07	3.96E-07
LOC100649618	431.546316	-0.439401874	0.07720198	-5.691588	1.26E-08	2.42E-08
LOC100648794	399.078618	-0.439074239	0.07963621	-5.5135	3.52E-08	6.58E-08
LOC100648931	715.312518	-0.4387015	0.06696695	-6.5510151	5.71E-11	1.26E-10
LOC100643740	1271.16703	-0.438641795	0.06606861	-6.6391861	3.15E-11	7.10E-11
LOC100643398	235.272256	-0.438571562	0.09287516	-4.722162	2.33E-06	3.89E-06
LOC100651918	2725.65767	-0.43851882	0.06101199	-7.1874204	6.60E-13	1.66E-12
LOC100644134	2281.01123	-0.438247459	0.10993566	-3.9863996	6.71E-05	0.00010152
LOC100651553	1229.52766	-0.437806725	0.06307591	-6.9409493	3.89E-12	9.32E-12
LOC100650158	236.328869	-0.437765651	0.14247795	-3.072515	0.00212263	0.00286145
LOC100649295	1026.85895	-0.437761924	0.06397004	-6.8432338	7.74E-12	1.82E-11
LOC100642515	5959.90707	-0.437563025	0.10823887	-4.0425684	5.29E-05	8.07E-05
LOC100651345	690.710529	-0.437058658	0.06875562	-6.3566972	2.06E-10	4.41E-10
LOC100644740	2208.83935	-0.436309672	0.19352488	-2.2545404	0.02416219	0.02982877
LOC100644380	2991.37854	-0.435711842	0.11290984	-3.8589359	0.00011388	0.00016928

LOC100651656	1032.6345	-0.435593999	0.0832818	-5.2303626	1.69E-07	3.04E-07
LOC105665683	1111.44422	-0.435483759	0.08100906	-5.3757411	7.63E-08	1.40E-07
LOC100644353	933.385719	-0.435271285	0.08760209	-4.9687316	6.74E-07	1.17E-06
LOC100650223	729.042888	-0.434811537	0.07403137	-5.8733416	4.27E-09	8.49E-09
LOC100647744	639.207229	-0.43448165	0.07321685	-5.9341753	2.95E-09	5.93E-09
LOC100642970	701.696636	-0.434299978	0.14541809	-2.986561	0.00282135	0.00376859
LOC100647099	727.231791	-0.434181623	0.06527248	-6.6518326	2.89E-11	6.54E-11
LOC100646380	741.541137	-0.433983267	0.06387426	-6.7943373	1.09E-11	2.53E-11
LOC100645446	1682.04436	-0.43389863	0.13794591	-3.1454257	0.00165845	0.00225214
LOC100642874	4691.91724	-0.433574792	0.0669123	-6.4797476	9.19E-11	2.00E-10
LOC100644266	845.501493	-0.433101246	0.062963	-6.8786632	6.04E-12	1.43E-11
LOC100649276	1467.40228	-0.43303656	0.11576728	-3.7405783	0.0001836	0.00026898
LOC100643867	841.308079	-0.432547883	0.06171403	-7.0089063	2.40E-12	5.81E-12
LOC100650350	439.001749	-0.432341613	0.12154094	-3.5571686	0.00037487	0.00053606
LOC100645434	465.085635	-0.431518587	0.11448012	-3.7693756	0.00016366	0.00024049
LOC100643492	2775.1683	-0.431392808	0.09008243	-4.7888671	1.68E-06	2.82E-06
LOC100642886	356.114327	-0.431373056	0.12643585	-3.4117937	0.00064537	0.00090359
LOC100651383	540.567998	-0.430905925	0.07288893	-5.9118155	3.38E-09	6.77E-09
LOC100646079	418.034521	-0.430116208	0.12491843	-3.4431766	0.00057492	0.00080854
LOC100651434	2227.17544	-0.429893223	0.06262968	-6.8640492	6.69E-12	1.58E-11
LOC100644498	416.794021	-0.429235678	0.08913548	-4.8155425	1.47E-06	2.48E-06
LOC100651600	2815.83157	-0.429068081	0.08088206	-5.3048608	1.13E-07	2.04E-07
LOC100644729	488.237563	-0.429068073	0.07235224	-5.9302667	3.02E-09	6.07E-09
LOC100649142	848.069838	-0.429056573	0.0741007	-5.7901825	7.03E-09	1.38E-08
LOC100642639	557.491606	-0.429029399	0.08511353	-5.0406723	4.64E-07	8.12E-07
LOC100646895	861.222938	-0.428895815	0.0686028	-6.2518705	4.06E-10	8.53E-10
LOC100642342	766.388317	-0.428846833	0.07915709	-5.4176678	6.04E-08	1.11E-07
LOC100651698	368.559191	-0.427947573	0.10667845	-4.0115655	6.03E-05	9.17E-05
LOC100645348	205.861397	-0.4271643	0.19769701	-2.1607019	0.03071838	0.03752669

LOC100648477	983.634557	-0.426741471	0.08110597	-5.2615295	1.43E-07	2.57E-07
LOC100646848	232.024634	-0.426696961	0.08861668	-4.8150865	1.47E-06	2.48E-06
LOC100649732	570.187034	-0.426465671	0.08644461	-4.9333982	8.08E-07	1.39E-06
LOC100645712	610.571104	-0.425530445	0.06231008	-6.8292391	8.54E-12	2.00E-11
LOC100642755	945.248013	-0.425234191	0.08576106	-4.9583599	7.11E-07	1.23E-06
LOC100644311	613.514197	-0.424885157	0.060426	-7.0314955	2.04E-12	4.97E-12
LOC100647530	110.765984	-0.424419442	0.18550594	-2.2879022	0.02214322	0.02743316
LOC100645544	2135.69303	-0.424306523	0.09832371	-4.3154041	1.59E-05	2.51E-05
LOC100648318	1658.21028	-0.424040373	0.18763979	-2.2598638	0.02382971	0.02944059
LOC100651306	1921.04934	-0.423566273	0.05241748	-8.0806297	6.44E-16	1.93E-15
LOC100650110	341.876466	-0.42294126	0.07632039	-5.5416551	3.00E-08	5.63E-08
LOC100651566	596.158216	-0.42262406	0.11995866	-3.523081	0.00042656	0.00060731
LOC100650817	2408.72922	-0.422456734	0.05190486	-8.1390587	3.98E-16	1.21E-15
LOC100643870	754.617082	-0.422244533	0.07595471	-5.5591619	2.71E-08	5.11E-08
LOC100648505	1601.43399	-0.421955577	0.11890393	-3.5487102	0.00038712	0.00055309
LOC100648445	177.68838	-0.421692339	0.13781452	-3.0598543	0.00221445	0.00298153
LOC100643618	340.350247	-0.421514551	0.09311395	-4.5268678	5.99E-06	9.70E-06
LOC100650621	177.867222	-0.420604067	0.11336637	-3.7101307	0.00020715	0.00030218
LOC100647850	685.624598	-0.416924721	0.09914497	-4.205203	2.61E-05	4.06E-05
LOC100649371	2246.59006	-0.416878448	0.06729832	-6.1944848	5.85E-10	1.22E-09
LOC100645709	237.249667	-0.416858208	0.12254147	-3.4017727	0.0006695	0.00093671
LOC100647565	615.191022	-0.416795134	0.07873442	-5.2936839	1.20E-07	2.17E-07
LOC100645636	521.813101	-0.416608184	0.081342	-5.1216861	3.03E-07	5.36E-07
LOC100642931	5045.32006	-0.416462347	0.09902474	-4.2056392	2.60E-05	4.05E-05
LOC100644310	349.541293	-0.416312924	0.15066604	-2.7631504	0.00572464	0.00742875
LOC100649747	162.218355	-0.4156844	0.11761285	-3.534345	0.00040879	0.00058294
LOC105666740	400.244603	-0.415574806	0.0945561	-4.3950081	1.11E-05	1.77E-05
LOC100649959	541.193479	-0.41539949	0.11924262	-3.4836495	0.00049463	0.00070126
LOC100647557	481.070639	-0.413967751	0.08847431	-4.6789602	2.88E-06	4.77E-06

LOC100644928	3647.41154	-0.413622163	0.06593026	-6.2736313	3.53E-10	7.45E-10
LOC100645143	693.569157	-0.413402083	0.10059313	-4.1096454	3.96E-05	6.09E-05
LOC100647330	1591.02275	-0.41169616	0.12688106	-3.2447409	0.00117558	0.00161454
LOC100644899	610.252415	-0.411421946	0.12024075	-3.4216517	0.00062242	0.00087283
LOC100652207	223.616165	-0.411251711	0.13176893	-3.1210066	0.00180234	0.00244144
LOC100642434	424.621738	-0.411106118	0.09446391	-4.3519913	1.35E-05	2.14E-05
LOC100650975	3369.98629	-0.411067781	0.05733696	-7.1693331	7.54E-13	1.88E-12
LOC100647899	131.608145	-0.411034244	0.16368346	-2.5111532	0.01203374	0.01522647
LOC100645350	455.203532	-0.41069189	0.1121693	-3.6613573	0.00025088	0.00036337
LOC100649501	372.44337	-0.409869648	0.07884164	-5.1986441	2.01E-07	3.59E-07
LOC100643201	317.298367	-0.409711759	0.13072423	-3.1341684	0.00172342	0.00233615
LOC100649883	563.689582	-0.409630994	0.1368213	-2.9939125	0.00275425	0.00368299
LOC100642378	580.876316	-0.409130914	0.08174211	-5.0051424	5.58E-07	9.72E-07
LOC100649092	84.889528	-0.409082206	0.16537748	-2.4736271	0.01337492	0.01685812
LOC100652159	305.429125	-0.408853458	0.09297014	-4.3976857	1.09E-05	1.75E-05
LOC100650140	1804.32869	-0.408833717	0.06669493	-6.1299067	8.79E-10	1.82E-09
LOC100648837	883.765124	-0.408636771	0.13034276	-3.1350937	0.00171799	0.00232911
LOC100647061	548.162848	-0.408266272	0.07307292	-5.5871073	2.31E-08	4.38E-08
LOC100644317	486.214774	-0.408235492	0.08580458	-4.7577353	1.96E-06	3.28E-06
LOC100649177	294.302264	-0.407923248	0.08625906	-4.7290482	2.26E-06	3.76E-06
LOC100650000	227.69455	-0.407668143	0.12940371	-3.1503591	0.0016307	0.00221506
LOC100649800	1057.88463	-0.406575619	0.06213425	-6.5435027	6.01E-11	1.33E-10
LOC100644485	777.359776	-0.406299203	0.12573207	-3.2314684	0.00123156	0.00168859
LOC100643811	323.060386	-0.406222976	0.10621889	-3.8243948	0.00013109	0.00019392
LOC100643042	340.726778	-0.406081597	0.10299257	-3.9428242	8.05E-05	0.00012122
LOC100649781	586.37947	-0.406035955	0.11031687	-3.6806333	0.00023266	0.00033798
LOC100645372	316.976016	-0.405974118	0.12131536	-3.3464363	0.00081857	0.00113748
LOC100649220	942.093102	-0.405929302	0.09914323	-4.0943723	4.23E-05	6.49E-05
LOC100650328	132.400782	-0.405738596	0.13284859	-3.0541432	0.00225704	0.00303762

LOC100647663	491.876551	-0.404462952	0.09943643	-4.0675529	4.75E-05	7.27E-05
LOC100646961	1167.40483	-0.404428431	0.08230759	-4.9136223	8.94E-07	1.53E-06
LOC100651413	308.650456	-0.404125223	0.11614162	-3.4795899	0.00050218	0.00071115
LOC100649329	1246.53246	-0.403561682	0.10869601	-3.7127554	0.00020501	0.00029937
LOC100644621	1946.06678	-0.40207658	0.05626625	-7.1459634	8.94E-13	2.22E-12
LOC100649073	326.937536	-0.40137924	0.15939258	-2.5181803	0.01179629	0.01493567
LOC100645281	1407.70947	-0.400863712	0.06502618	-6.1646507	7.06E-10	1.47E-09
LOC100642287	1504.4435	-0.400252618	0.05843007	-6.8501136	7.38E-12	1.74E-11
LOC100651197	256.701282	-0.400108065	0.12442469	-3.2156646	0.00130143	0.00178164
LOC100647388	1146.49844	-0.399068393	0.07218029	-5.5287725	3.22E-08	6.05E-08
LOC100651427	1980.41668	-0.399014903	0.06588742	-6.0560104	1.40E-09	2.85E-09
LOC100647020	596.151721	-0.397548389	0.09354825	-4.2496615	2.14E-05	3.35E-05
LOC100650888	521.167847	-0.397150275	0.12006319	-3.3078437	0.00094017	0.00130091
LOC100651362	2028.29428	-0.396375147	0.1176755	-3.3683745	0.00075613	0.00105324
LOC100643253	1816.57582	-0.396239942	0.06835728	-5.796602	6.77E-09	1.33E-08
LOC100643177	1483.56362	-0.395819562	0.05394512	-7.3374493	2.18E-13	5.61E-13
LOC105666197	309.098558	-0.395327483	0.09381931	-4.2137111	2.51E-05	3.92E-05
LOC100646338	191.119238	-0.395255559	0.15646379	-2.5261792	0.01153106	0.01461876
LOC100651250	415.356195	-0.395034925	0.1752693	-2.253874	0.0242041	0.02987674
LOC100644075	453.908931	-0.394881043	0.07712393	-5.1200848	3.05E-07	5.40E-07
LOC100649604	126.861189	-0.394378988	0.1491238	-2.6446414	0.00817775	0.01049802
LOC100648398	873.659857	-0.394200356	0.0632154	-6.2358278	4.49E-10	9.43E-10
LOC100650290	344.400472	-0.394037022	0.15980756	-2.465697	0.0136747	0.01722931
LOC100643207	702.700554	-0.393697537	0.14683066	-2.6813032	0.0073336	0.00944532
LOC100647066	3366.51315	-0.393383702	0.18076211	-2.1762509	0.02953651	0.03616708
LOC100643689	172.514594	-0.392848174	0.16028418	-2.4509478	0.01424806	0.01791943
LOC100647926	326.563127	-0.392653756	0.15437937	-2.5434341	0.01097688	0.01395049
LOC100643504	395.867323	-0.392586172	0.12764265	-3.0756661	0.00210033	0.00283294
LOC100644044	1574.58751	-0.392327693	0.07674545	-5.1120647	3.19E-07	5.63E-07

LOC100646375	201.743244	-0.391900798	0.10011242	-3.9146071	9.06E-05	0.00013563
LOC100647513	354.285252	-0.391746346	0.08194467	-4.7806203	1.75E-06	2.94E-06
LOC100651926	301.173662	-0.391417826	0.09850167	-3.9737177	7.08E-05	0.0001069
LOC100642511	1142.37869	-0.391354878	0.07498231	-5.2192959	1.80E-07	3.22E-07
LOC100648147	602.979869	-0.390711417	0.08780951	-4.4495342	8.61E-06	1.38E-05
LOC100650163	1257.61674	-0.390584815	0.05674333	-6.8833608	5.85E-12	1.39E-11
LOC100644440	1127.07047	-0.389423881	0.06941152	-5.6103638	2.02E-08	3.84E-08
LOC100646022	1684.3238	-0.389226909	0.08009522	-4.8595525	1.18E-06	2.00E-06
LOC100645699	872.72146	-0.389172317	0.07470846	-5.2092132	1.90E-07	3.39E-07
LOC100644699	1209.80406	-0.388694394	0.07284071	-5.3362246	9.49E-08	1.73E-07
LOC100643471	2600.69837	-0.388380437	0.05328393	-7.2888848	3.13E-13	8.00E-13
LOC100646301	4596.12017	-0.387664121	0.08978279	-4.3177997	1.58E-05	2.49E-05
LOC100643584	1728.37554	-0.387646806	0.09641929	-4.0204281	5.81E-05	8.84E-05
LOC100643847	305.123324	-0.387373631	0.10397462	-3.7256558	0.00019481	0.00028485
LOC100649331	882.843223	-0.387173035	0.0909752	-4.2558084	2.08E-05	3.26E-05
LOC100650605	392.409978	-0.384593919	0.16253126	-2.3662766	0.01796801	0.0224051
LOC100644393	690.723852	-0.384528157	0.10770392	-3.5702337	0.00035666	0.00051091
LOC100648038	2213.48275	-0.384397001	0.05841238	-6.5807455	4.68E-11	1.04E-10
LOC100645466	327.130902	-0.384102743	0.08493955	-4.5220718	6.12E-06	9.91E-06
LOC100646749	488.278837	-0.382982341	0.12140923	-3.1544748	0.00160787	0.00218497
LOC100651329	533.274227	-0.382837496	0.08122995	-4.7130092	2.44E-06	4.06E-06
LOC100646425	362.053263	-0.382791815	0.08218569	-4.6576456	3.20E-06	5.27E-06
LOC100649194	122.117882	-0.382494772	0.16495749	-2.3187476	0.02040873	0.0253581
LOC100645439	230.398874	-0.381720307	0.15229711	-2.5064185	0.01219612	0.01541598
LOC100650186	1559.03948	-0.380871891	0.1185791	-3.2119646	0.00131831	0.00180399
LOC100644153	1374.41698	-0.38033156	0.11105621	-3.4246763	0.00061553	0.0008633
LOC100650723	189.430106	-0.380158548	0.10372166	-3.6651799	0.00024716	0.0003582
LOC100651666	495.003	-0.380029593	0.10472233	-3.628926	0.0002846	0.00041027
LOC100646934	395.697054	-0.379412385	0.0910101	-4.1689041	3.06E-05	4.74E-05

LOC100642499	327.5559	-0.379394805	0.11643988	-3.2582893	0.00112086	0.00154199
LOC100649680	633.27825	-0.378975446	0.08348765	-4.5392992	5.64E-06	9.16E-06
LOC100651680	608.175375	-0.3783909	0.09433602	-4.0110966	6.04E-05	9.19E-05
LOC100649576	3999.45739	-0.378387739	0.09532019	-3.9696494	7.20E-05	0.00010866
LOC100646120	628.169413	-0.378327549	0.1117307	-3.3860663	0.00070902	0.0009896
LOC100644050	895.917283	-0.378146602	0.07656336	-4.9390019	7.85E-07	1.35E-06
LOC100645721	785.279886	-0.377870784	0.07958936	-4.7477553	2.06E-06	3.44E-06
LOC100650727	194.148151	-0.377868456	0.10960204	-3.4476407	0.00056551	0.00079621
LOC100647863	269.055224	-0.37692931	0.0977935	-3.8543391	0.00011604	0.0001723
LOC100652209	933.632558	-0.376484448	0.05689753	-6.6168861	3.67E-11	8.23E-11
LOC100649118	1976.63491	-0.373356396	0.07411584	-5.0374709	4.72E-07	8.25E-07
LOC100648407	454.821123	-0.37328942	0.09281726	-4.0217672	5.78E-05	8.80E-05
LOC100642613	1006.19065	-0.373184166	0.08666932	-4.3058393	1.66E-05	2.62E-05
LOC100644898	2867.92126	-0.371424478	0.0697112	-5.3280462	9.93E-08	1.80E-07
LOC100647738	242.594965	-0.371358796	0.13236487	-2.8055691	0.00502278	0.00654834
LOC100642301	327.644945	-0.370639732	0.10919145	-3.3944025	0.00068779	0.00096105
LOC100642263	1879.2388	-0.370389545	0.08818127	-4.2003198	2.67E-05	4.15E-05
LOC100651757	1239.04697	-0.369732241	0.07007564	-5.2761879	1.32E-07	2.38E-07
LOC100647033	140.430799	-0.369511343	0.14019071	-2.6357762	0.00839451	0.01076639
LOC100643114	374.250535	-0.369510609	0.07358379	-5.0216306	5.12E-07	8.94E-07
LOC100648466	435.869697	-0.369260024	0.06877954	-5.3687481	7.93E-08	1.45E-07
LOC100643967	411.545911	-0.368552656	0.09155802	-4.0253453	5.69E-05	8.67E-05
LOC100645099	101.65554	-0.367937654	0.16514895	-2.227914	0.02588625	0.03186877
LOC100651879	462.328332	-0.367572437	0.08928748	-4.1167297	3.84E-05	5.92E-05
LOC100642560	270.954612	-0.367569421	0.1067978	-3.4417321	0.000578	0.00081276
LOC100646590	441.671355	-0.367004594	0.10883972	-3.3719729	0.00074632	0.00104002
LOC100652300	578.544455	-0.366534726	0.08143389	-4.5010096	6.76E-06	1.09E-05
LOC100646374	1713.99558	-0.366415213	0.16636064	-2.2025355	0.02762751	0.03392286
LOC100645810	801.82485	-0.365449792	0.12558898	-2.9098875	0.00361559	0.00477607

LOC100652117	208.790709	-0.365073917	0.14857593	-2.4571538	0.01400427	0.01762414
LOC100647728	257.030197	-0.364074653	0.12818979	-2.8401221	0.00450963	0.0059037
LOC100643046	1063.96032	-0.363861634	0.1015008	-3.5848155	0.00033732	0.00048419
LOC100644590	6860.5492	-0.363762189	0.0640001	-5.6837753	1.32E-08	2.53E-08
LOC100644921	1097.83541	-0.36340911	0.17040438	-2.1326277	0.03295528	0.04019102
LOC100649385	252.94169	-0.363325394	0.10296089	-3.5287709	0.00041749	0.00059501
LOC100648079	468.571527	-0.363028023	0.10513537	-3.452958	0.00055448	0.00078136
LOC100651507	473.583974	-0.362545087	0.0854384	-4.2433506	2.20E-05	3.44E-05
LOC100646284	1883.76761	-0.362340093	0.05625756	-6.440736	1.19E-10	2.57E-10
LOC100651265	469.348424	-0.362294355	0.1102723	-3.2854521	0.00101819	0.00140489
LOC100650052	626.737517	-0.361222423	0.08510568	-4.2443985	2.19E-05	3.43E-05
LOC100644837	815.335788	-0.360612438	0.09277867	-3.8868033	0.00010157	0.00015146
LOC100649198	111.287688	-0.360196142	0.13299279	-2.7083885	0.00676108	0.00872516
LOC100647331	1262.71449	-0.360143	0.12704397	-2.8347902	0.00458558	0.00599832
LOC100646251	1035.60343	-0.357754346	0.08564719	-4.1770703	2.95E-05	4.58E-05
LOC100648465	1265.0365	-0.355737314	0.09024421	-3.9419406	8.08E-05	0.00012164
LOC100645030	422.227276	-0.355339287	0.09557642	-3.7178552	0.00020092	0.00029353
LOC100643015	229.622372	-0.354981339	0.09974984	-3.5587159	0.00037267	0.00053307
LOC100650055	3453.66427	-0.354734767	0.08910812	-3.9809478	6.86E-05	0.00010379
LOC100650409	637.842994	-0.354480433	0.07358712	-4.8171533	1.46E-06	2.46E-06
LOC100645080	539.442912	-0.354078386	0.11877902	-2.9809841	0.00287324	0.00383529
LOC100643538	1784.33348	-0.353715862	0.08673717	-4.0780192	4.54E-05	6.96E-05
LOC100648468	202.978649	-0.352622177	0.10784668	-3.2696619	0.00107676	0.00148342
LOC100647905	271.362796	-0.352463939	0.11165683	-3.1566716	0.00159581	0.00216978
LOC100644577	448.054114	-0.352185039	0.06585352	-5.3480061	8.89E-08	1.62E-07
LOC100646516	388.316424	-0.351894976	0.11704046	-3.0066097	0.00264179	0.00353841
LOC100648619	1537.70841	-0.351392844	0.07028387	-4.9996232	5.74E-07	1.00E-06
LOC100643325	652.125765	-0.351202279	0.1013795	-3.4642339	0.00053174	0.00075073
LOC100650006	412.495688	-0.350508853	0.09676781	-3.6221636	0.00029215	0.00042084

LOC100645886	755.884518	-0.350292764	0.0952375	-3.678097	0.00023498	0.00034115
LOC100644439	1738.42698	-0.349081961	0.06277747	-5.5606247	2.69E-08	5.07E-08
LOC100650176	430.44394	-0.348641122	0.11004082	-3.1682892	0.00153339	0.00208694
LOC100643907	596.241019	-0.348099515	0.07625675	-4.5648355	5.00E-06	8.14E-06
LOC100648188	637.136857	-0.348063168	0.07422734	-4.6891507	2.74E-06	4.54E-06
LOC100648723	327.737067	-0.347057256	0.10724843	-3.2360124	0.00121212	0.00166333
LOC100646800	351.801504	-0.347030076	0.12398958	-2.7988647	0.00512826	0.00668319
LOC100652257	1728.69977	-0.346894428	0.05970475	-5.8101648	6.24E-09	1.23E-08
LOC100642881	621.034923	-0.346248448	0.07750336	-4.4675284	7.91E-06	1.27E-05
LOC100648434	1605.0723	-0.346195637	0.05563883	-6.2221947	4.90E-10	1.03E-09
LOC100646101	646.375604	-0.345926075	0.07002429	-4.9400872	7.81E-07	1.35E-06
LOC100651213	904.240045	-0.345171307	0.07725948	-4.467689	7.91E-06	1.27E-05
LOC100651961	1904.80996	-0.34439469	0.06006258	-5.7339308	9.81E-09	1.91E-08
LOC100644924	217.595207	-0.343713595	0.08998354	-3.8197387	0.00013359	0.00019744
LOC100647196	931.244286	-0.342756865	0.10337028	-3.3158164	0.00091376	0.00126633
LOC100647533	282.52374	-0.34194149	0.10215439	-3.347301	0.00081603	0.0011341
LOC100650041	485.070032	-0.341747275	0.12973483	-2.6341983	0.00843362	0.01081372
LOC100647464	332.585798	-0.341647936	0.0949908	-3.5966424	0.00032235	0.00046325
LOC100645378	476.286241	-0.341548779	0.08579348	-3.9810575	6.86E-05	0.00010376
LOC100644103	810.659498	-0.340216087	0.07002337	-4.8586081	1.18E-06	2.01E-06
LOC100646815	522.163801	-0.340188317	0.07442337	-4.5709876	4.85E-06	7.91E-06
LOC100649072	903.638694	-0.338658884	0.07616477	-4.4463981	8.73E-06	1.40E-05
LOC100651975	1193.50575	-0.337399584	0.07201028	-4.6854365	2.79E-06	4.62E-06
LOC100643376	367.94373	-0.336673843	0.08639574	-3.8968803	9.74E-05	0.00014561
LOC100647640	348.137278	-0.335836696	0.0989178	-3.3951089	0.00068601	0.00095871
LOC100646366	1438.86678	-0.335700254	0.05553169	-6.0452016	1.49E-09	3.05E-09
LOC100649278	810.438161	-0.335393778	0.15311776	-2.1904302	0.02849305	0.03494182
LOC100643991	3299.55653	-0.334942042	0.05652298	-5.9257676	3.11E-09	6.23E-09
LOC100648998	1111.21384	-0.334869159	0.0997919	-3.3556746	0.00079172	0.00110125

LOC100646503	1112.61263	-0.334868213	0.06611543	-5.0649024	4.09E-07	7.17E-07
LOC100652181	549.250357	-0.334507342	0.09020619	-3.7082525	0.00020869	0.00030438
LOC100650939	656.569384	-0.334469412	0.15311111	-2.1844882	0.0289264	0.03545991
LOC100631087	27976.5364	-0.334274714	0.15823423	-2.112531	0.03464093	0.04214854
LOC100642249	357.198076	-0.333983858	0.09421972	-3.5447342	0.00039301	0.00056117
LOC100649577	462.371683	-0.3338471	0.09632801	-3.4657322	0.00052879	0.0007471
LOC100642934	677.309197	-0.333511597	0.12967461	-2.5719114	0.01011388	0.01290564
LOC100647459	479.435689	-0.333293098	0.09464615	-3.5214648	0.00042917	0.00061084
LOC100649521	472.647032	-0.333282575	0.0808518	-4.1221416	3.75E-05	5.79E-05
LOC100643305	310.656956	-0.332800376	0.09437723	-3.5262785	0.00042144	0.00060011
LOC100645046	253.067177	-0.331784372	0.11017889	-3.0113244	0.00260111	0.00348535
LOC100642791	811.392083	-0.331658679	0.08443194	-3.9281188	8.56E-05	0.00012843
LOC100649532	2097.48438	-0.331330311	0.08614113	-3.8463661	0.00011988	0.0001779
LOC100642770	1199.35893	-0.330945023	0.07747978	-4.271373	1.94E-05	3.05E-05
LOC100647017	489.237526	-0.330758252	0.08560461	-3.86379	0.00011164	0.00016612
fem	471.57432	-0.330740224	0.11305484	-2.925485	0.0034392	0.00455228
LOC100645345	788.706941	-0.330268708	0.129105	-2.5581404	0.01052336	0.01340021
LOC100651201	1302.26961	-0.329548808	0.08397753	-3.92425	8.70E-05	0.00013043
LOC100646657	825.466547	-0.329383731	0.06611584	-4.9819182	6.30E-07	1.09E-06
LOC100645617	581.594101	-0.329226971	0.08570022	-3.8416116	0.00012223	0.00018122
LOC100643595	2821.87852	-0.329091142	0.05903901	-5.5741302	2.49E-08	4.70E-08
LOC100649247	532.089236	-0.328638048	0.08507761	-3.8628028	0.00011209	0.00016677
LOC100645191	957.412296	-0.328003004	0.10089184	-3.2510359	0.00114985	0.00158099
LOC100646450	224.254231	-0.327848241	0.1529814	-2.1430595	0.03210832	0.03918881
LOC100643248	621.994249	-0.327694706	0.08542082	-3.8362391	0.00012493	0.00018508
LOC100650791	351.771655	-0.327506804	0.09365345	-3.4970075	0.00047051	0.00066823
LOC100645488	422.113362	-0.326821366	0.09288275	-3.5186445	0.00043376	0.0006172
LOC100642379	381.554363	-0.326804805	0.11471106	-2.848939	0.00438653	0.00575255
LOC100645778	435.119301	-0.326731098	0.14948244	-2.185749	0.02883398	0.03535105

LOC100645722	297.409267	-0.32647418	0.09969827	-3.2746225	0.00105803	0.00145904
LOC100650809	1257.0589	-0.326143368	0.05791922	-5.6310042	1.79E-08	3.42E-08
LOC100651726	336.14256	-0.325459674	0.09636087	-3.3775086	0.00073146	0.00101975
LOC100647226	1041.68327	-0.32515751	0.07398102	-4.3951479	1.11E-05	1.76E-05
LOC100648069	704.112999	-0.324951935	0.10604359	-3.0643241	0.00218162	0.00293774
LOC100645743	363.472432	-0.324765097	0.09534314	-3.4062765	0.00065855	0.00092179
LOC100645227	4457.93091	-0.324520336	0.13111703	-2.4750433	0.013322	0.0167979
LOC100646435	676.726227	-0.324197801	0.07346918	-4.4127048	1.02E-05	1.63E-05
LOC100652280	649.586548	-0.323771582	0.11490261	-2.8177915	0.00483552	0.00630841
LOC100644356	310.233415	-0.32357947	0.10744558	-3.0115661	0.00259904	0.00348305
LOC100643778	1071.38702	-0.323516767	0.05547273	-5.831996	5.48E-09	1.08E-08
LOC100648827	2155.83434	-0.323485583	0.0637744	-5.0723424	3.93E-07	6.90E-07
LOC100647391	818.590974	-0.32282067	0.09359379	-3.4491677	0.00056232	0.00079207
LOC100644580	2513.38844	-0.321790569	0.07266139	-4.428632	9.48E-06	1.52E-05
LOC100650615	1398.59789	-0.321784605	0.07335357	-4.3867611	1.15E-05	1.83E-05
LOC100642646	544.864529	-0.32132286	0.08850448	-3.6305829	0.00028278	0.00040788
LOC100649717	483.450184	-0.320907816	0.10888324	-2.9472656	0.00320598	0.00425912
LOC100631059	2812.22387	-0.320680666	0.12645724	-2.5358822	0.01121644	0.01424202
LOC100652093	355.765203	-0.318153729	0.09080968	-3.5035221	0.00045915	0.00065257
LOC100648132	353.095596	-0.317978012	0.10903176	-2.9163796	0.00354119	0.00467969
LOC100645371	441.150747	-0.317820093	0.06785485	-4.6838225	2.82E-06	4.66E-06
LOC100643603	1985.71474	-0.317612183	0.13880643	-2.2881662	0.02212784	0.02741758
LOC100648707	1121.71572	-0.317336746	0.07035342	-4.5106089	6.46E-06	1.05E-05
LOC100651319	1021.57481	-0.317234784	0.0642934	-4.9341737	8.05E-07	1.38E-06
LOC100648999	360.61337	-0.317194504	0.10550094	-3.0065563	0.00264225	0.00353854
LOC105665756	918.086984	-0.315962681	0.07622476	-4.1451451	3.40E-05	5.25E-05
LOC100648937	220.149506	-0.315021739	0.08118595	-3.8802493	0.00010435	0.00015548
LOC100645621	2766.29233	-0.314706861	0.09690635	-3.2475361	0.00116409	0.00159944
LOC100642541	463.177292	-0.314256531	0.07985785	-3.935199	8.31E-05	0.00012493

LOC100642643	376.199652	-0.313950656	0.08591757	-3.6540916	0.00025809	0.00037343
LOC100647088	333.736541	-0.313894891	0.14601524	-2.1497406	0.03157574	0.03856281
LOC100651468	506.793713	-0.313848084	0.08283449	-3.7888578	0.00015134	0.00022282
LOC100651898	824.596917	-0.313385401	0.06456832	-4.8535474	1.21E-06	2.06E-06
LOC100646289	346.248955	-0.312625913	0.13791058	-2.2668741	0.02339792	0.02893634
LOC105666253	1128.90223	-0.312611852	0.08599495	-3.6352352	0.00027773	0.00040089
LOC100644465	345.03237	-0.311933473	0.13085046	-2.3838928	0.01713059	0.02139084
LOC100647425	503.392534	-0.311502773	0.11112683	-2.8031283	0.00506095	0.00659723
LOC100646336	168.842654	-0.310830507	0.09434661	-3.2945593	0.00098576	0.00136206
LOC100649721	508.767716	-0.310709854	0.08887762	-3.495929	0.00047241	0.00067064
LOC105665620	608.669655	-0.31029188	0.10095203	-3.0736568	0.00211453	0.0028513
LOC100651921	424.392464	-0.309981119	0.12730024	-2.4350395	0.01489016	0.01870056
LOC100642389	3982.54862	-0.30995682	0.10505057	-2.9505488	0.0031721	0.00421755
LOC100651456	1202.1187	-0.309524199	0.05725634	-5.405938	6.45E-08	1.19E-07
LOC100642758	783.868482	-0.309428427	0.09843558	-3.1434612	0.00166963	0.00226605
LOC100651556	457.829915	-0.308846003	0.07922707	-3.8982385	9.69E-05	0.00014484
LOC100649136	505.618089	-0.308728658	0.14665057	-2.1051991	0.03527398	0.04287085
LOC100648828	3309.40432	-0.308646693	0.09783931	-3.1546288	0.00160702	0.00218412
LOC100649763	207.568403	-0.307742751	0.1165274	-2.6409476	0.00826745	0.01061038
LOC100646604	621.540174	-0.307714196	0.07771731	-3.9594038	7.51E-05	0.00011334
LOC100648338	2328.07713	-0.307644423	0.13135547	-2.3420756	0.01917683	0.02387594
LOC100644664	960.755784	-0.306744946	0.07664527	-4.0021378	6.28E-05	9.52E-05
LOC100652168	310.940424	-0.306735201	0.09601097	-3.1947933	0.00139931	0.00191056
LOC100646207	646.400599	-0.306337477	0.14794275	-2.0706488	0.03839163	0.04653286
LOC100642607	1290.34017	-0.30598337	0.12580553	-2.4321933	0.01500769	0.01884092
LOC100643506	415.206092	-0.305621287	0.07613164	-4.0143791	5.96E-05	9.06E-05
LOC100643272	748.392776	-0.305508161	0.11014646	-2.7736539	0.00554306	0.00720841
LOC100650553	3574.62916	-0.305240026	0.11821363	-2.5821052	0.00981996	0.01254367
LOC100645680	507.982254	-0.30478038	0.06897073	-4.4189813	9.92E-06	1.59E-05

LOC100642504	1603.4094	-0.304692965	0.13492183	-2.2582926	0.02392742	0.02955758
LOC100643780	178.13359	-0.304680435	0.12387515	-2.4595766	0.0139101	0.01751238
LOC100648514	394.732588	-0.304269275	0.07853126	-3.8744987	0.00010684	0.0001591
LOC100650589	318.913378	-0.302973586	0.10547594	-2.8724426	0.00407312	0.0053602
LOC100652155	514.262047	-0.302478103	0.06852371	-4.4142111	1.01E-05	1.62E-05
LOC100647383	635.452914	-0.302429704	0.09195459	-3.2889027	0.00100579	0.00138817
LOC100646767	383.280082	-0.301752356	0.08158348	-3.6986943	0.00021671	0.00031561
LOC100644247	505.293451	-0.301554844	0.10246118	-2.943113	0.0032493	0.00431433
LOC100647665	1110.98264	-0.301286651	0.08415217	-3.58026	0.00034325	0.00049249
LOC100643613	370.790925	-0.301271121	0.0807484	-3.7309857	0.00019073	0.00027914
LOC100645675	289.688805	-0.300924571	0.10943427	-2.7498203	0.0059628	0.0077245
LOC100647518	2802.57663	-0.300385851	0.07744216	-3.8788414	0.00010496	0.00015636
LOC100651030	531.34166	-0.30015408	0.13076402	-2.2953873	0.02171094	0.02692827
LOC100643612	934.130407	-0.300124606	0.08980072	-3.3421181	0.00083142	0.00115499
LOC100644401	684.323276	-0.299758364	0.090614	-3.30808	0.00093938	0.0013
LOC100644615	300.041247	-0.298560566	0.11845408	-2.5204751	0.01171965	0.01484439
LOC100649377	1965.48134	-0.298481813	0.118008	-2.5293354	0.01142787	0.01449169
LOC100643437	680.905016	-0.297575292	0.09657796	-3.0811926	0.00206173	0.00278318
LOC100645199	623.403648	-0.29623929	0.11544505	-2.5660632	0.01028601	0.01311674
LOC100646553	708.85127	-0.295986459	0.07579439	-3.9051236	9.42E-05	0.00014091
LOC100647038	128.27649	-0.295971753	0.12039364	-2.458367	0.01395705	0.01756697
LOC100642989	566.383914	-0.295605885	0.07055323	-4.1898281	2.79E-05	4.34E-05
LOC100648467	588.171841	-0.295541095	0.10014291	-2.9511933	0.00316549	0.00420933
LOC100651496	403.550825	-0.295541069	0.08447999	-3.4983561	0.00046814	0.00066495
LOC100650647	487.029107	-0.295465766	0.08437916	-3.5016437	0.0004624	0.00065699
LOC100651133	1220.06977	-0.295321294	0.101023	-2.9233074	0.00346334	0.00458176
LOC100652326	2424.93584	-0.295209792	0.11713318	-2.5202917	0.01172576	0.0148502
LOC100648985	570.910972	-0.29422985	0.09471216	-3.1065689	0.00189272	0.00256174
LOC100646501	723.334699	-0.29387509	0.06795022	-4.3248588	1.53E-05	2.41E-05

LOC100650215	618.441966	-0.29370674	0.13600519	-2.159526	0.03080938	0.03763157
LOC100645570	1132.25612	-0.293648502	0.05335587	-5.5035833	3.72E-08	6.95E-08
LOC100649780	885.043642	-0.29275247	0.13351605	-2.1926387	0.02833342	0.03475912
LOC100648200	427.408107	-0.292384341	0.08014537	-3.6481753	0.00026411	0.00038202
LOC105665738	179.012241	-0.291985325	0.12674193	-2.3037785	0.02123508	0.02636144
LOC100646191	828.231154	-0.291468316	0.09690975	-3.0076263	0.00263297	0.00352707
LOC100651153	1996.43686	-0.291225167	0.06576177	-4.4284876	9.49E-06	1.52E-05
LOC100643089	1691.65007	-0.291084379	0.07035055	-4.1376274	3.51E-05	5.41E-05
LOC100644203	290.648864	-0.290903776	0.10724619	-2.712486	0.00667806	0.00862208
LOC100650157	780.225413	-0.290251547	0.05652261	-5.1351408	2.82E-07	4.99E-07
LOC100648990	1285.70419	-0.290207054	0.06166329	-4.7063184	2.52E-06	4.19E-06
LOC100644252	3643.85405	-0.289587753	0.05636967	-5.1372972	2.79E-07	4.94E-07
LOC100647406	301.460455	-0.289470631	0.09912918	-2.9201354	0.00349879	0.00462553
LOC100647844	559.703473	-0.289224511	0.07229689	-4.0005108	6.32E-05	9.59E-05
LOC100642888	1260.81867	-0.28834174	0.07939264	-3.6318449	0.0002814	0.00040595
LOC100648215	455.708188	-0.288241638	0.12352092	-2.3335451	0.01961955	0.02441162
LOC100643941	393.997937	-0.288219996	0.13327152	-2.1626526	0.03056791	0.03735993
LOC100650061	1790.86878	-0.287831917	0.06427907	-4.477848	7.54E-06	1.21E-05
LOC100647403	212.852506	-0.287741399	0.10387498	-2.7700741	0.00560435	0.00728173
LOC105665953	2338.57625	-0.287730157	0.06575629	-4.3757053	1.21E-05	1.92E-05
LOC100643175	173.344444	-0.287598496	0.14095093	-2.0404157	0.04130894	0.04995132
LOC100645164	194.068974	-0.287560375	0.09106926	-3.157601	0.00159073	0.00216317
LOC100644849	90.9482597	-0.287369199	0.12980934	-2.2137791	0.02684398	0.03300218
LOC100646957	951.19073	-0.287326085	0.06019244	-4.7734576	1.81E-06	3.04E-06
LOC100647909	704.178767	-0.287312286	0.06707434	-4.2834901	1.84E-05	2.89E-05
LOC100648941	276.98321	-0.287164329	0.08120026	-3.5364953	0.00040547	0.00057846
LOC100644227	984.739731	-0.286793694	0.06663304	-4.3040762	1.68E-05	2.64E-05
LOC105666030	726.375885	-0.286161441	0.07830497	-3.6544478	0.00025774	0.00037308
LOC100647238	248.564206	-0.286119075	0.10347864	-2.7650061	0.00569217	0.0073876

LOC100648701	154.538486	-0.285185379	0.12322103	-2.3144212	0.02064463	0.02564145
LOC100648942	1881.7482	-0.284974391	0.1144419	-2.4901229	0.01276989	0.01612043
LOC100649927	4518.25214	-0.284830719	0.06329869	-4.4997884	6.80E-06	1.10E-05
LOC100646178	1049.03536	-0.284021472	0.06901735	-4.1152188	3.87E-05	5.95E-05
LOC100642809	811.305416	-0.283705223	0.05862793	-4.8390793	1.30E-06	2.21E-06
LOC100652242	217.702194	-0.283476834	0.11231175	-2.5240176	0.01160221	0.01469944
LOC105666123	391.003591	-0.283462696	0.10025108	-2.8275275	0.0046909	0.00612708
LOC100649083	330.998146	-0.283451847	0.09698423	-2.9226591	0.00347056	0.00459007
LOC100651784	863.835396	-0.283191342	0.10576128	-2.6776468	0.00741414	0.00954402
LOC100643429	318.713479	-0.282793462	0.12273197	-2.3041548	0.02121396	0.02633856
LOC100645153	638.912146	-0.282757701	0.08210862	-3.4437032	0.00057381	0.00080709
LOC100646626	6813.11281	-0.282647671	0.06141981	-4.6018975	4.19E-06	6.85E-06
LOC100650799	463.217729	-0.281883939	0.07432683	-3.7924923	0.00014914	0.00021975
LOC100648199	685.705771	-0.281582694	0.11114328	-2.5335108	0.01129263	0.01433503
LOC100650711	944.700248	-0.280573716	0.09894983	-2.835515	0.00457519	0.00598632
LOC100651011	434.932167	-0.280523386	0.08672019	-3.2348106	0.00121723	0.00167012
LOC100651971	1008.98134	-0.280004119	0.11467859	-2.4416426	0.01462061	0.01837808
LOC100644090	286.029165	-0.280003368	0.09392474	-2.9811459	0.00287172	0.00383379
LOC100651882	4807.41421	-0.279151556	0.09858018	-2.8317208	0.00462983	0.00605135
LOC100649360	529.937635	-0.277742711	0.08233877	-3.3731703	0.00074308	0.00103566
LOC100649644	1054.97147	-0.277385786	0.05704941	-4.862203	1.16E-06	1.98E-06
LOC100649287	2064.84549	-0.277346554	0.05901277	-4.6997722	2.60E-06	4.32E-06
LOC100650450	706.021881	-0.277061395	0.07613459	-3.6391003	0.00027359	0.00039515
LOC100642707	1500.82187	-0.27651697	0.0836942	-3.3038966	0.00095351	0.00131862
LOC100651285	769.177813	-0.276382547	0.08228931	-3.3586688	0.00078319	0.00108985
LOC100644097	304.850602	-0.276116323	0.11113617	-2.4844866	0.01297384	0.01636944
LOC100644261	396.211422	-0.273890123	0.10718232	-2.5553665	0.0106076	0.01349871
LOC100645331	3402.62396	-0.27357541	0.0575237	-4.7558733	1.98E-06	3.31E-06
LOC100651483	290.365381	-0.272578899	0.0867048	-3.1437578	0.00166793	0.00226407

LOC100651651	361.96361	-0.272540279	0.13176708	-2.0683488	0.03860723	0.0467826
LOC105665618	1163.21552	-0.272140947	0.06998838	-3.888373	0.00010092	0.00015056
LOC100650501	2387.59391	-0.271931314	0.10727791	-2.5348305	0.01125017	0.01428299
LOC100647324	316.425811	-0.271300591	0.09333888	-2.9066192	0.00365358	0.0048243
LOC100642259	254.409452	-0.271020915	0.11526512	-2.3512829	0.0187088	0.023311
LOC100644291	1202.86808	-0.270976214	0.08322884	-3.2557973	0.00113074	0.00155515
LOC100643242	547.754321	-0.270333654	0.06720833	-4.0223234	5.76E-05	8.78E-05
LOC100646150	3406.2593	-0.269940414	0.10234759	-2.6374868	0.00835229	0.01071505
LOC100648422	172.917054	-0.26992708	0.12443492	-2.1692229	0.03006576	0.03677835
LOC100649664	698.639928	-0.269603358	0.06336299	-4.2549025	2.09E-05	3.28E-05
LOC100650966	464.442463	-0.269514643	0.08297458	-3.2481592	0.00116154	0.00159616
LOC100642994	444.392949	-0.268269823	0.0976031	-2.7485789	0.00598542	0.00774971
LOC100649507	646.131619	-0.268107218	0.0939876	-2.8525809	0.00433658	0.00569085
LOC100647106	4191.83723	-0.266646924	0.05894698	-4.5235046	6.08E-06	9.85E-06
LOC100648395	1008.98563	-0.266102038	0.0690095	-3.8560204	0.00011525	0.00017119
LOC100644018	743.977584	-0.265699001	0.10239414	-2.5948653	0.0094628	0.0120906
LOC100650623	400.095947	-0.265285562	0.10373257	-2.5573989	0.01054582	0.01342707
LOC100649404	1236.54912	-0.264385347	0.0565227	-4.6775073	2.90E-06	4.80E-06
LOC100644959	4071.50745	-0.264300227	0.0521602	-5.0670859	4.04E-07	7.09E-07
LOC100644026	1664.85478	-0.264164317	0.08320135	-3.1750003	0.00149836	0.00204068
LOC100642977	881.420218	-0.263770586	0.06783801	-3.888242	0.00010097	0.00015061
LOC100646140	484.113443	-0.263715919	0.09338125	-2.8240778	0.00474169	0.00619012
LOC100644419	438.238043	-0.263681144	0.07879647	-3.3463572	0.00081881	0.00113764
LOC100650116	5332.93327	-0.263660244	0.08548581	-3.0842574	0.00204061	0.00275543
LOC100644025	7284.64263	-0.263352169	0.12357615	-2.1310921	0.03308155	0.04031634
LOC100645838	280.128893	-0.263240336	0.09136317	-2.8812522	0.00396099	0.00521404
LOC100648914	1748.53945	-0.262964093	0.07015815	-3.7481615	0.00017814	0.00026125
LOC100643491	595.528062	-0.262622625	0.10242985	-2.5639266	0.01034954	0.01319432
LOC100650861	2073.20856	-0.262614435	0.07740961	-3.3925302	0.0006925	0.00096723

LOC100649003	370.278513	-0.262118761	0.08653546	-3.029033	0.00245338	0.00329416
LOC100644329	1129.20041	-0.262041216	0.06950339	-3.7701931	0.00016312	0.00023974
LOC100651945	427.863579	-0.261981359	0.07612799	-3.4413275	0.00057887	0.00081386
LOC100646465	701.728962	-0.261748771	0.08726297	-2.9995402	0.00270387	0.0036181
LOC100650190	491.914008	-0.261269182	0.07982682	-3.2729498	0.00106431	0.00146708
LOC100645327	571.791625	-0.261040494	0.06597432	-3.9566983	7.60E-05	0.00011459
LOC100646990	559.284538	-0.2598295	0.08659974	-3.0003496	0.0026967	0.00360899
LOC100647340	344.652975	-0.259569661	0.08520541	-3.046399	0.002316	0.00311441
LOC100647076	541.527248	-0.259211328	0.10616431	-2.4416052	0.01462213	0.01837808
LOC100648822	1091.89399	-0.259059653	0.0673892	-3.8442313	0.00012093	0.00017934
LOC100646474	503.356481	-0.258601954	0.09084733	-2.8465553	0.0044195	0.00579346
LOC100647697	749.34242	-0.258377219	0.08430581	-3.0647618	0.00217843	0.00293425
LOC100651008	420.807743	-0.258333973	0.07927055	-3.2588896	0.00111849	0.00153895
LOC100649396	1148.52025	-0.258330943	0.08342063	-3.0967272	0.0019567	0.00264541
LOC100644722	426.544761	-0.258211345	0.09416537	-2.7421052	0.00610468	0.00790098
LOC100650604	3152.69954	-0.257873693	0.08893211	-2.8996691	0.00373557	0.00492725
LOC100643573	1564.50813	-0.256870291	0.05875441	-4.371932	1.23E-05	1.96E-05
LOC100644833	1069.8107	-0.256714527	0.08236958	-3.1166183	0.00182938	0.00247704
LOC100643725	455.477266	-0.256650924	0.10236748	-2.507153	0.0121708	0.01538597
LOC100647184	719.243132	-0.25471428	0.07550197	-3.3736109	0.00074189	0.00103415
LOC100649483	684.753965	-0.253785473	0.07362383	-3.4470559	0.00056673	0.00079782
LOC100646759	352.455252	-0.253210784	0.10144915	-2.495938	0.01256246	0.01586675
LOC100647746	9202.35403	-0.252383235	0.10297361	-2.4509506	0.01424795	0.01791943
LOC100651704	603.984255	-0.252292121	0.07030748	-3.5884106	0.0003327	0.0004777
LOC100648086	800.066062	-0.252264436	0.06996052	-3.6058115	0.00031118	0.00044746
LOC105665986	2091.86791	-0.252246684	0.05896489	-4.2779134	1.89E-05	2.96E-05
LOC100643634	611.711173	-0.250582193	0.11423874	-2.1934957	0.02827168	0.03468773
LOC100642879	464.047549	-0.250377858	0.08552689	-2.9274754	0.00341726	0.00452385
LOC100644589	704.882216	-0.25026167	0.09314044	-2.6869281	0.00721125	0.0092914

LOC100646982	1151.28575	-0.249846259	0.11205486	-2.2296779	0.02576883	0.0317282
LOC100645834	589.589179	-0.249615297	0.1070133	-2.3325633	0.01967108	0.02446951
LOC100650607	419.38286	-0.248687056	0.08817807	-2.8202825	0.00479814	0.00626131
LOC100644467	509.801286	-0.248144651	0.0839789	-2.9548452	0.00312826	0.00416209
LOC100643061	778.777725	-0.247885193	0.06282256	-3.945799	7.95E-05	0.00011977
LOC100649415	849.842204	-0.246588888	0.06254418	-3.9426349	8.06E-05	0.0001213
LOC100650645	377.634364	-0.246150978	0.07735476	-3.1821051	0.00146209	0.00199211
LOC100642815	2711.81976	-0.245997994	0.05870864	-4.1901496	2.79E-05	4.33E-05
LOC100645207	1230.732	-0.245980698	0.06252854	-3.9338946	8.36E-05	0.00012557
LOC100651996	6822.92398	-0.245979384	0.09249654	-2.6593362	0.00782948	0.0100628
LOC100648709	760.619391	-0.245316895	0.05704486	-4.3004205	1.70E-05	2.68E-05
LOC105666413	829.603253	-0.245201275	0.10178315	-2.4090557	0.01599386	0.02001481
LOC100649113	1844.45549	-0.245196573	0.08320926	-2.9467461	0.00321137	0.0042657
LOC100645533	2678.99165	-0.244899039	0.06344697	-3.8599011	0.00011343	0.00016874
LOC100644127	614.712433	-0.244232899	0.07214671	-3.3852255	0.0007112	0.00099249
LOC100651751	670.000501	-0.243918321	0.10455972	-2.3328135	0.01965794	0.02445627
LOC100649183	441.798194	-0.242285478	0.09386469	-2.5812206	0.00984517	0.01257423
LOC100646837	654.703359	-0.242208126	0.06949261	-3.4853798	0.00049144	0.00069694
LOC100647495	1773.39332	-0.242135309	0.09655226	-2.5078162	0.01214798	0.01536109
LOC100650486	2197.68132	-0.240421035	0.04403759	-5.45945	4.78E-08	8.85E-08
LOC100651980	563.351596	-0.240058372	0.07760962	-3.0931523	0.00198043	0.00267638
LOC100648984	617.373014	-0.239367761	0.05997228	-3.9913065	6.57E-05	9.95E-05
LOC100647591	696.761478	-0.239259926	0.09776815	-2.4472176	0.01439639	0.01810365
LOC100642929	1301.17306	-0.238800491	0.11198365	-2.1324585	0.03296918	0.0401994
LOC100642413	3278.12605	-0.238692766	0.08183767	-2.9166615	0.003538	0.0046761
LOC100644646	2616.72004	-0.237396454	0.07981364	-2.9743844	0.00293577	0.00391609
LOC100644596	1430.01475	-0.235521796	0.06043669	-3.8970003	9.74E-05	0.00014556
LOC100644330	732.457408	-0.235377935	0.07280692	-3.2329061	0.00122538	0.00168035
LOC100645243	1092.07797	-0.23499422	0.06269347	-3.7483047	0.00017803	0.00026114

LOC100642429	864.753873	-0.234651929	0.07540764	-3.1117792	0.00185964	0.00251766
LOC105666410	631.549487	-0.23414639	0.11099138	-2.1095909	0.03489361	0.04242963
LOC100643269	351.547344	-0.234046269	0.0787468	-2.972137	0.00295735	0.00394273
LOC100648180	892.334627	-0.233763559	0.05618182	-4.16084	3.17E-05	4.91E-05
LOC100651949	643.465012	-0.233532413	0.08069239	-2.8941072	0.00380238	0.00501133
LOC100651860	845.422564	-0.233379026	0.08736228	-2.6713935	0.0075537	0.0097224
LOC100642658	1009.24736	-0.233331574	0.06613129	-3.5283081	0.00041823	0.00059596
LOC100649117	585.165443	-0.232964088	0.07858249	-2.96458	0.00303096	0.00403757
LOC100648409	1254.18324	-0.232616755	0.09265993	-2.5104353	0.01205824	0.01525352
LOC100651395	657.042625	-0.232372844	0.08537413	-2.7218181	0.00649239	0.00839279
LOC100650775	503.123704	-0.232206234	0.08087703	-2.8711022	0.00409043	0.00538082
LOC100645720	602.776495	-0.232191231	0.08460694	-2.744352	0.00606305	0.00784918
LOC100644875	672.251138	-0.23196461	0.08602295	-2.6965433	0.00700633	0.00903569
LOC100648420	339.290502	-0.230679618	0.11131771	-2.0722633	0.03824089	0.04636737
LOC100642862	936.094537	-0.23048107	0.0921734	-2.500516	0.01240125	0.01567123
LOC100646549	434.1926	-0.229056734	0.07535742	-3.0396043	0.00236889	0.00318247
LOC100652194	609.090309	-0.22832117	0.08206635	-2.7821535	0.00539995	0.00702977
LOC100651846	444.910178	-0.22750686	0.08213075	-2.7700569	0.00560465	0.00728173
LOC100645797	509.980346	-0.226445369	0.09864544	-2.2955482	0.02170173	0.02692026
LOC100650133	1486.03826	-0.225107782	0.07853736	-2.866251	0.00415365	0.00546156
LOC100644647	1179.43558	-0.220050697	0.06418698	-3.4282763	0.00060743	0.0008523
LOC100651515	518.530678	-0.218836458	0.07985741	-2.7403402	0.00613756	0.00794249
LOC100646671	754.019191	-0.218390779	0.10603136	-2.059681	0.03942905	0.04773709
LOC100646702	641.368772	-0.218150808	0.08094788	-2.694954	0.00703984	0.00907532
LOC100644910	2098.68921	-0.218008314	0.07391812	-2.9493216	0.00318472	0.00423203
LOC100650019	963.617008	-0.217744742	0.07508143	-2.9001145	0.00373026	0.00492095
LOC100648804	937.648718	-0.217321047	0.10266629	-2.1167712	0.03427927	0.04174482
LOC100648389	992.194707	-0.216749565	0.0746468	-2.9036684	0.00368819	0.00486868
LOC100642281	2492.84027	-0.21588004	0.09063089	-2.3819699	0.01722031	0.02149739

LOC100643128	489.172968	-0.215648264	0.07829656	-2.7542494	0.00588269	0.0076288
LOC100644469	651.611546	-0.215455594	0.06957836	-3.0965891	0.00195761	0.00264627
LOC100644971	829.19714	-0.214925086	0.08062112	-2.6658656	0.00767904	0.00987723
LOC100646706	654.581955	-0.214504474	0.09743013	-2.2016235	0.02769191	0.03399768
LOC100651466	797.40223	-0.214270589	0.07149734	-2.9969028	0.00272738	0.00364805
LOC100644872	1246.39083	-0.213969328	0.05937828	-3.603495	0.00031397	0.0004514
LOC100645508	704.579977	-0.213274902	0.05860359	-3.6392805	0.0002734	0.00039493
LOC100650039	304.206033	-0.212403091	0.07896598	-2.6898051	0.00714938	0.0092141
LOC100647486	11323.2553	-0.211905246	0.09440409	-2.2446617	0.02478986	0.03056895
LOC100646033	883.950072	-0.211735209	0.06872062	-3.0811016	0.00206236	0.00278365
LOC100652211	1015.70488	-0.21114528	0.09103696	-2.3193359	0.02037683	0.0253249
LOC100649596	1110.27749	-0.210862495	0.06833219	-3.0858441	0.00202975	0.00274115
LOC100643222	593.695678	-0.210793326	0.07408343	-2.8453504	0.00443626	0.00581154
LOC100650266	824.101265	-0.210039408	0.08682596	-2.4190853	0.01555959	0.01949878
LOC100648806	420.191501	-0.209454586	0.09083099	-2.3059816	0.02111166	0.0262182
LOC100650505	293.969718	-0.20943779	0.09589605	-2.1840086	0.02896162	0.03549865
LOC100651284	303.997976	-0.209351938	0.10055851	-2.0818918	0.03735235	0.04534617
LOC100642381	1380.86385	-0.209156437	0.06179106	-3.3848981	0.00071205	0.00099354
LOC100646659	434.477198	-0.208968669	0.08637524	-2.4193122	0.01554989	0.01948911
LOC100649389	659.985014	-0.208967658	0.06093936	-3.4291084	0.00060557	0.00084981
LOC100642891	1863.75048	-0.208657092	0.07587037	-2.7501787	0.00595628	0.00771809
LOC100652186	346.622948	-0.208626339	0.09292837	-2.2450231	0.02476665	0.03054418
LOC100642217	393.273748	-0.208235366	0.09207754	-2.2615218	0.02372697	0.02932476
LOC100645694	509.857818	-0.208041366	0.09049212	-2.2989998	0.02150495	0.02668631
LOC100642425	886.775971	-0.207370704	0.06595756	-3.1440021	0.00166654	0.0022625
LOC100645902	388.110121	-0.207360027	0.09426509	-2.1997542	0.02782434	0.03415598
LOC100648464	1625.40677	-0.207100296	0.03871604	-5.3492122	8.83E-08	1.61E-07
LOC100644489	337.33002	-0.206022542	0.07761635	-2.6543703	0.00794566	0.01020676
LOC100652188	998.910358	-0.205832489	0.09697788	-2.1224684	0.03379842	0.04116437

LOC100651561	1058.94271	-0.205435359	0.06573957	-3.1249881	0.00177812	0.00240997
LOC100643654	1629.86708	-0.203988811	0.0915849	-2.2273192	0.02592595	0.03191363
LOC100652193	379.648875	-0.198701359	0.08187006	-2.4270334	0.01522286	0.01909145
LOC100646222	405.588082	-0.198406044	0.07263939	-2.7313835	0.0063069	0.00815624
LOC100648616	401.279556	-0.198357791	0.07935886	-2.4995041	0.01243673	0.01571403
LOC100647351	643.947097	-0.196809106	0.06949481	-2.8319971	0.00462583	0.00604692
LOC100652179	1304.30167	-0.19659887	0.05097237	-3.8569692	0.0001148	0.00017059
LOC100644810	2150.33567	-0.196384314	0.09086524	-2.1612699	0.0306745	0.03748084
LOC100647366	962.632466	-0.196110327	0.04995385	-3.9258298	8.64E-05	0.00012961
LOC100643436	4611.06226	-0.195621406	0.06643294	-2.9446447	0.00323326	0.00429361
LOC100645138	654.853799	-0.194347351	0.09213059	-2.109477	0.03490343	0.0424363
LOC100644340	1575.38925	-0.193914885	0.08726475	-2.2221446	0.02627353	0.03231711
LOC100649713	1904.39402	-0.193799206	0.08153663	-2.3768361	0.01746185	0.02179059
LOC100648066	1632.98041	-0.1935526	0.06128802	-3.1580824	0.00158811	0.0021599
LOC100644625	718.170904	-0.193317789	0.08220188	-2.3517441	0.01868562	0.02328509
LOC100646660	1464.74427	-0.193231229	0.06731248	-2.8706596	0.00409616	0.00538763
LOC100644937	974.362078	-0.192880209	0.06691117	-2.882631	0.00394369	0.00519197
LOC100650449	425.568374	-0.192414229	0.09218251	-2.0873183	0.03685937	0.04476434
LOC100643409	1598.20183	-0.191957339	0.06445501	-2.9781601	0.00289984	0.00386923
LOC100645242	555.448371	-0.191890906	0.07137088	-2.6886441	0.00717429	0.00924499
LOC100648581	573.713074	-0.190910938	0.07935368	-2.4058235	0.01613606	0.0201876
LOC100643088	820.037959	-0.189783505	0.06727917	-2.8208362	0.00478987	0.00625218
LOC100646741	1807.95717	-0.188264423	0.05852685	-3.2167191	0.00129665	0.00177535
LOC100649535	756.212548	-0.187976347	0.06727225	-2.7942628	0.00520182	0.00677725
LOC100647669	223.677187	-0.18778085	0.08835824	-2.1252217	0.03356812	0.04088896
LOC105666643	641.536584	-0.187135501	0.08054308	-2.3234212	0.02015654	0.02506065
LOC105666930	473.252872	-0.18662345	0.08608205	-2.1679718	0.03016083	0.03688543
LOC100650750	967.077001	-0.186610599	0.06963835	-2.6797104	0.00736859	0.00948788
LOC100642941	1866.144	-0.186283089	0.05842872	-3.188211	0.00143156	0.00195215

LOC100646378	556.270578	-0.185913135	0.08360824	-2.2236222	0.02617387	0.03219857
LOC100647568	862.710658	-0.185866469	0.07049803	-2.6364775	0.00837718	0.01074557
LOC100645037	304.253343	-0.185550164	0.08312294	-2.2322376	0.02559926	0.03153527
LOC100650625	2845.2892	-0.18477467	0.04996321	-3.6982148	0.00021712	0.00031616
LOC100644818	992.116004	-0.18424486	0.08280405	-2.2250705	0.0260765	0.03208685
LOC100647326	1167.08287	-0.183919732	0.08346933	-2.203441	0.02756368	0.03384874
LOC100647416	510.066173	-0.183639078	0.06744496	-2.7227992	0.00647314	0.00836901
LOC100651582	853.424822	-0.183625906	0.06408646	-2.8652841	0.00416635	0.00547701
LOC100642472	407.50103	-0.182356003	0.08796904	-2.0729565	0.03817633	0.04629483
LOC100650895	1506.66655	-0.182264153	0.07937298	-2.2962996	0.02165876	0.02687036
LOC100647327	1564.98876	-0.180636884	0.05537381	-3.2621359	0.00110576	0.00152186
LOC100646731	876.259183	-0.180242287	0.07431392	-2.4254176	0.01529078	0.01917419
LOC105666160	22430.1653	-0.178134824	0.05508445	-3.2338493	0.00122134	0.00167528
LOC100642502	679.966032	-0.178025791	0.07329605	-2.4288593	0.01514641	0.01900532
LOC100647315	616.773441	-0.175953766	0.07532969	-2.3357826	0.01950258	0.02427533
LOC100645824	299.702896	-0.174687317	0.08069429	-2.1648039	0.03040271	0.0371673
LOC100648643	1325.86284	-0.174558353	0.05776511	-3.0218649	0.00251223	0.00336994
LOC105666351	1010.7635	-0.173920799	0.07985489	-2.1779605	0.02940898	0.03601993
LOC105665872	1390.24856	-0.173328934	0.05724943	-3.0276096	0.00246496	0.00330926
LOC100645574	1064.1321	-0.172650412	0.06752832	-2.5567111	0.01056669	0.01345189
LOC100643085	590.538514	-0.168475008	0.0604472	-2.7871433	0.0053175	0.00692519
LOC100651834	761.967391	-0.168371624	0.07517711	-2.2396662	0.0251126	0.03095914
LOC105666638	859.642507	-0.167968525	0.06691797	-2.5100659	0.01207086	0.01526554
LOC100644541	611.720295	-0.166932385	0.0652267	-2.5592644	0.01048939	0.01336391
LOC100642578	539.344952	-0.166299343	0.07823838	-2.1255469	0.03354101	0.04086102
LOC100648415	467.06324	-0.165673109	0.0758874	-2.1831438	0.02902522	0.03557215
LOC100643836	528.803829	-0.16339629	0.0660228	-2.4748462	0.01332935	0.01680285
LOC100644049	847.256613	-0.162225958	0.05863822	-2.7665568	0.00566517	0.00735548
LOC100649217	912.678591	-0.160105538	0.05383997	-2.97373	0.00294204	0.00392339

LOC100652086	624.371041	-0.159887853	0.07281236	-2.1958889	0.02809989	0.03448127
LOC100651075	1570.5177	-0.159103065	0.06935767	-2.2939506	0.02179334	0.02702363
LOC100642414	656.230639	-0.159076965	0.06099033	-2.6082327	0.00910111	0.01164366
LOC100649012	1830.18094	-0.158908004	0.06536046	-2.4312558	0.01504659	0.01888249
LOC100643381	2989.58692	-0.158529379	0.04553193	-3.481719	0.00049821	0.00070592
LOC100647743	753.803173	-0.156462504	0.05952838	-2.6283681	0.00857956	0.01099078
LOC100648339	1911.77365	-0.156161458	0.04892624	-3.1917732	0.00141402	0.00192931
LOC100643358	671.447556	-0.153572457	0.06755087	-2.2734343	0.02300002	0.02845505
LOC100646696	622.195509	-0.151782091	0.07320813	-2.0732956	0.03814477	0.04626802
LOC105666651	1028.32457	-0.151698919	0.06357842	-2.3860126	0.01703217	0.02127337
LOC105665838	991.936688	-0.148832772	0.06792842	-2.1910235	0.0284501	0.03489351
LOC100650136	2952.52107	-0.144731616	0.06505327	-2.224817	0.02609352	0.03210376
LOC100642464	774.471115	-0.136758396	0.06470272	-2.1136421	0.03454585	0.04204854
LOC100648277	418.261493	-0.136721843	0.06374766	-2.1447351	0.03197404	0.03902977
LOC100647873	1348.72406	-0.131721584	0.05117264	-2.5740629	0.0100512	0.01283068
LOC100646470	1366.03675	-0.127012253	0.05073805	-2.5032937	0.01230434	0.01555076
LOC100645809	1402.22816	-0.114740948	0.05392971	-2.127602	0.0333701	0.04065787
LOC100650997	2396.86261	-0.096782353	0.04658608	-2.0774953	0.03775587	0.045819
LOC100648526	1451.12879	0.12690732	0.05545941	2.28829195	0.02212053	0.02741198
LOC100652131	981.07698	0.139167186	0.06514661	2.13621536	0.03266186	0.03983958
LOC100646314	1172.42353	0.140912516	0.06840942	2.05984074	0.03941377	0.04772449
LOC100651063	978.744951	0.142607004	0.05677838	2.51164271	0.01201707	0.01520733
LOC100644682	497.776621	0.142783957	0.06870267	2.07828846	0.0376828	0.045736
LOC100650695	922.749281	0.145592508	0.06528288	2.23017915	0.02573555	0.03169519
LOC100644595	1085.22712	0.147378632	0.06669906	2.20960595	0.02713252	0.03334855
LOC100651907	1728.71843	0.149069608	0.05665182	2.6313297	0.00850515	0.01090115
LOC100645734	2899.53704	0.152167501	0.05921946	2.56955233	0.010183	0.01299046
LOC100651661	1853.0845	0.15425215	0.04545087	3.39382206	0.00068924	0.00096282
LOC100648697	855.116854	0.154333506	0.06834984	2.25799363	0.02394606	0.02957687

LOC100644051	2043.67447	0.158570359	0.05592088	2.83562	0.00457368	0.00598515
LOC100649056	993.925802	0.158703675	0.05888072	2.69534179	0.00703165	0.00906595
LOC100645090	636.156983	0.159647433	0.06801353	2.34728941	0.01891056	0.0235534
LOC100648576	1098.02356	0.162041918	0.06745043	2.40238518	0.01628855	0.02036536
LOC100648504	1796.16766	0.164801781	0.07599459	2.16859882	0.03011315	0.03683172
LOC100644191	1253.26706	0.165525917	0.07218336	2.29313127	0.02184045	0.02707519
LOC100648911	1087.78564	0.169205608	0.06189249	2.73386329	0.0062596	0.00809614
LOC100643552	1081.59914	0.170878116	0.07588881	2.2516906	0.02434183	0.03004297
LOC100642428	2012.39772	0.173853252	0.06302232	2.75859824	0.00580499	0.00753002
LOC100651646	1159.56948	0.17412005	0.06522042	2.66971699	0.00759152	0.00976722
LOC100647923	820.289638	0.174352052	0.07726188	2.25663741	0.02403074	0.02967024
LOC100646905	1117.74949	0.174729313	0.06280489	2.78209709	0.00540089	0.00703006
LOC100651817	787.816062	0.176762903	0.06555451	2.69642606	0.0070088	0.00903768
LOC100645394	3893.34914	0.177320431	0.05007511	3.54108889	0.00039848	0.00056865
LOC100650560	3341.95767	0.181391278	0.0798322	2.27215689	0.02307704	0.02854672
LOC100647848	1528.89933	0.181892931	0.084183	2.16068491	0.03071969	0.03752669
LOC100642801	1763.14059	0.182449384	0.04587202	3.97735704	6.97E-05	0.00010529
LOC100647009	3293.71438	0.184353195	0.04677588	3.9412021	8.11E-05	0.00012197
LOC100649348	562.927525	0.184435558	0.08941315	2.06273426	0.03913788	0.04740802
LOC100646168	866.340252	0.184874105	0.06473562	2.85583266	0.00429241	0.00563667
LOC100647079	484.963125	0.185041494	0.08525859	2.17035612	0.02997988	0.03667787
LOC100649813	409.742954	0.185103414	0.07510434	2.46461683	0.01371598	0.0172791
LOC100647962	5498.47051	0.185357001	0.07664335	2.41843551	0.01558741	0.01952614
LOC100646681	686.79439	0.186344509	0.06982856	2.66860022	0.00761681	0.00979847
LOC100644786	406.746378	0.186616679	0.08245624	2.26322069	0.02362209	0.02920251
LOC100643059	652.938577	0.186811448	0.07860084	2.37671049	0.01746779	0.02179523
LOC100646545	447.82915	0.187387862	0.08342139	2.24628073	0.02468603	0.03044859
LOC100652057	603.756917	0.188969836	0.07397569	2.55448579	0.01063448	0.01353115
LOC100650504	1040.757	0.189211093	0.07905087	2.39353598	0.01668684	0.0208527

LOC100643555	1104.41704	0.189901597	0.08055152	2.35751713	0.01839761	0.02293201
LOC100649433	1432.50275	0.191383126	0.05751521	3.32752216	0.00087622	0.00121585
LOC100649226	1448.54882	0.192587924	0.06621839	2.90837514	0.00363312	0.00479794
LOC100643346	306.589046	0.192846439	0.08476748	2.27500495	0.02290563	0.02834185
LOC100650126	679.878718	0.193781042	0.08625313	2.24665522	0.02466207	0.03042287
LOC100645247	1650.477	0.193941773	0.05706111	3.39884323	0.00067671	0.0009464
LOC100643416	1182.79953	0.194037942	0.07187624	2.69961167	0.00694205	0.00895515
LOC100642362	698.95981	0.19555674	0.09116835	2.14500697	0.03195229	0.03900809
LOC100652205	1025.64071	0.196056096	0.0599359	3.27109621	0.00107131	0.00147632
LOC100646750	931.929969	0.196135593	0.08444134	2.3227436	0.02019293	0.02510271
LOC100642417	775.240216	0.196913639	0.07461753	2.6389729	0.00831576	0.01066959
LOC100649498	2509.99074	0.198376299	0.05850504	3.39075552	0.000697	0.00097324
LOC100651367	446.778611	0.198416667	0.08868016	2.23744151	0.0252575	0.03112993
LOC100648092	588.637535	0.198491446	0.07787075	2.54898609	0.01080366	0.0137357
LOC100650552	538.323791	0.199401433	0.08953184	2.22715662	0.02593681	0.03192298
LOC100645160	419.388538	0.199671536	0.0969164	2.06024513	0.03937511	0.04768358
LOC100645737	586.185154	0.20033042	0.06723779	2.97943192	0.00288783	0.00385425
LOC100650472	2128.08422	0.200704539	0.09103206	2.20476755	0.02747041	0.03374267
LOC100646352	735.492721	0.201456745	0.06134343	3.28408036	0.00102316	0.00141135
LOC100644163	343.643479	0.202409158	0.07658068	2.64308386	0.00821547	0.01054505
LOC100652185	437.27981	0.202658553	0.09077934	2.23243024	0.02558654	0.03152357
LOC100645370	2360.48148	0.203539455	0.0680097	2.9928002	0.00276431	0.00369593
LOC100649196	328.912313	0.203669899	0.09714522	2.09655084	0.03603335	0.04378833
LOC100648577	1399.56856	0.203798349	0.06952102	2.93146389	0.00337369	0.00446858
LOC100646118	662.928921	0.203965087	0.08257251	2.47013313	0.01350628	0.0170193
LOC100650246	1089.51417	0.204084241	0.06949436	2.9367023	0.00331722	0.00440094
LOC100650395	2341.43359	0.205121005	0.06286415	3.26292485	0.00110269	0.00151784
LOC100646737	652.357489	0.206706647	0.0821654	2.51573823	0.01187834	0.01503566
LOC100645698	863.520943	0.208587315	0.06208005	3.35997364	0.0007795	0.00108487

LOC100647478	444.464925	0.208686594	0.08263088	2.52552785	0.01155246	0.0146402
LOC100647811	356.814647	0.210181112	0.08962139	2.34521157	0.01901629	0.02367906
LOC100652018	735.819925	0.210436223	0.06794791	3.09702297	0.00195475	0.0026435
LOC100652196	2585.37905	0.210484897	0.06284472	3.34928545	0.0008102	0.00112648
LOC100650512	192.324335	0.21069517	0.09591634	2.19665572	0.02804504	0.03441828
LOC100650191	480.699951	0.211360137	0.08866675	2.3837588	0.01713683	0.02139591
LOC100651077	1472.38073	0.21171238	0.08346499	2.53654119	0.01119536	0.01422078
LOC100646321	466.083361	0.212600134	0.10359512	2.05222157	0.04014813	0.04857766
LOC100643636	1204.72461	0.212744398	0.09302872	2.28686783	0.02220354	0.02749745
LOC100651640	1164.30575	0.213044048	0.06865151	3.10326803	0.00191396	0.00258942
LOC100643482	2354.17709	0.213121998	0.07198294	2.96072934	0.00306912	0.00408673
LOC100651415	720.778331	0.213223542	0.05922896	3.5999878	0.00031823	0.00045747
LOC100646788	1493.47684	0.213866391	0.08391394	2.54863965	0.0108144	0.01374757
LOC100642522	889.17832	0.21439156	0.08385858	2.55658454	0.01057054	0.01345504
LOC100645146	330.465177	0.214405989	0.08861942	2.41940189	0.01554605	0.0194868
LOC100651192	274.415504	0.21449659	0.08899415	2.41023237	0.01594236	0.01995547
LOC100643553	904.549414	0.214647687	0.05783309	3.71150315	0.00020603	0.00030064
LOC100648746	1004.54993	0.215657487	0.07540027	2.86016882	0.00423416	0.00556241
LOC100644006	1712.84241	0.215900355	0.05594756	3.85897741	0.00011386	0.00016927
LOC100650401	487.990235	0.218507376	0.08540932	2.55835533	0.01051686	0.01339387
LOC100644930	563.904552	0.219034498	0.07593891	2.88435151	0.00392221	0.00516507
LOC100646653	1421.0575	0.219251447	0.05472379	4.00651086	6.16E-05	9.36E-05
LOC100648817	680.199074	0.219264959	0.07774073	2.82046455	0.00479542	0.00625859
LOC100651506	535.039875	0.220369587	0.0859948	2.56259212	0.0103894	0.01324341
LOC100644944	144.500857	0.220444483	0.10595174	2.08061216	0.03746942	0.04548265
LOC100649236	369.724988	0.220806192	0.09155271	2.41179315	0.01587428	0.0198735
LOC100648388	1031.98747	0.221566209	0.06039492	3.66862356	0.00024386	0.00035362
LOC100646733	394.551084	0.221915643	0.07833044	2.83307024	0.00461033	0.00602826
LOC100648288	498.498889	0.22378689	0.09788787	2.28615541	0.02224517	0.02754552

LOC100646621	393.769969	0.224001008	0.08702602	2.57395446	0.01005435	0.01283303
LOC100647952	751.706257	0.224079203	0.07845818	2.8560338	0.00428969	0.00563386
LOC100646113	309.832554	0.22515726	0.10327187	2.18023809	0.02923982	0.0358217
LOC100643445	321.817734	0.225937538	0.08368364	2.699901	0.00693601	0.00894854
LOC100645264	1048.04768	0.227423125	0.07172025	3.17097502	0.00151928	0.0020686
LOC100650439	657.624061	0.227427714	0.09027747	2.51920776	0.01176192	0.01489408
LOC100647824	514.076398	0.227670868	0.10995478	2.07058635	0.03839747	0.04653418
LOC105666027	1279.54144	0.228042081	0.05763077	3.9569504	7.59E-05	0.00011449
LOC100644830	421.276943	0.228114724	0.09015092	2.53036489	0.0113944	0.01445111
LOC100650422	240.916978	0.228266643	0.10801581	2.11327063	0.03457761	0.04208196
LOC100650064	361.408495	0.228391934	0.09442468	2.41877382	0.01557292	0.01951298
LOC100644622	743.910795	0.228513596	0.09520055	2.40033901	0.01637989	0.02047696
LOC100650026	831.745362	0.229202249	0.08330714	2.75129163	0.00593608	0.00769511
LOC100644141	441.035111	0.229991457	0.09088934	2.5304557	0.01139145	0.01444924
LOC100650414	277.518586	0.230509681	0.09313794	2.47492789	0.01332631	0.01680117
LOC100646369	454.773645	0.231607909	0.09169415	2.52587448	0.01154107	0.01462765
LOC100646654	340.600326	0.234141305	0.0821774	2.84921767	0.00438269	0.00574828
LOC105666558	14498.1349	0.234490076	0.07398083	3.1696059	0.00152646	0.00207808
LOC100650872	2591.61604	0.234712157	0.06198647	3.78650607	0.00015278	0.00022488
LOC100643038	220.242298	0.234745688	0.09217303	2.54679362	0.01087177	0.01381871
LOC100646680	612.717046	0.235185712	0.05630944	4.17666583	2.96E-05	4.59E-05
LOC100648713	590.395537	0.23569669	0.07360008	3.20239732	0.00136289	0.00186291
LOC100650790	383.059379	0.236751643	0.11495297	2.05955222	0.03944137	0.0477461
LOC100650244	642.051111	0.236806121	0.07590895	3.11960757	0.00181092	0.00245238
LOC100651475	615.127102	0.237783179	0.08966223	2.65198824	0.00800193	0.01027635
LOC100645689	426.089677	0.237837216	0.0866898	2.74354341	0.006078	0.00786749
LOC100651944	950.156376	0.237908283	0.06321311	3.76359095	0.00016749	0.00024597
LOC100646824	956.994856	0.238321763	0.06346524	3.75515408	0.00017323	0.00025429
LOC105666216	237.524475	0.238366955	0.10815126	2.20401456	0.02752332	0.03380342

LOC100651410	1502.78439	0.238728358	0.07425362	3.21504019	0.00130426	0.00178502
LOC100648642	266.713808	0.238888831	0.09476298	2.52090871	0.01170522	0.01482803
LOC100644167	420.398963	0.239873388	0.07292675	3.28923728	0.00100459	0.00138671
LOC100649753	401.143041	0.240056195	0.08212006	2.92323468	0.00346415	0.00458221
LOC100652059	1318.79801	0.240112389	0.08275664	2.90142745	0.00371467	0.00490166
LOC100651890	322.815207	0.241101259	0.09587111	2.51484801	0.01190837	0.01507172
LOC100650115	4804.05313	0.241385677	0.06570763	3.67363229	0.00023913	0.00034701
LOC100651853	2378.07915	0.241564447	0.10346844	2.33466801	0.01956077	0.02434467
LOC100645187	686.742217	0.241647822	0.08084639	2.98897492	0.00279915	0.00374048
LOC100652045	416.211346	0.24282676	0.11401728	2.1297364	0.03319338	0.04044759
LOC100644122	601.991628	0.243154147	0.09967442	2.43948405	0.01470825	0.01847921
LOC100644657	1967.98873	0.244628527	0.10696409	2.28701542	0.02219492	0.02749026
LOC100651281	1453.80214	0.244767893	0.05841077	4.19045827	2.78E-05	4.33E-05
LOC100646206	1142.03372	0.245141297	0.06880752	3.56271101	0.00036704	0.0005254
LOC100649542	909.443579	0.245183168	0.10745252	2.28178153	0.02250224	0.02785328
LOC100646131	481.296297	0.245872447	0.11142307	2.20665655	0.02733806	0.03358853
LOC100642271	569.679169	0.246007004	0.07471651	3.2925389	0.00099287	0.00137131
LOC100649895	616.896171	0.246046449	0.07426961	3.31288212	0.0009234	0.00127878
LOC100650731	294.598671	0.246068554	0.09477101	2.59645379	0.00941916	0.01203955
LOC100649214	780.494276	0.246285944	0.06535219	3.76859526	0.00016417	0.0002412
LOC100649246	235.52588	0.246386855	0.11393665	2.16248997	0.03058043	0.03737057
LOC100644543	2204.63564	0.248033132	0.06814626	3.63971769	0.00027294	0.00039436
LOC100646379	880.122705	0.248216416	0.0643714	3.85600468	0.00011526	0.00017119
LOC100642976	873.007831	0.249466709	0.06702534	3.72197611	0.00019767	0.00028895
LOC100642806	606.253337	0.249645543	0.10061456	2.48120686	0.01309384	0.01651659
LOC100648936	423.953096	0.250375005	0.08023669	3.12045536	0.00180572	0.00244567
LOC100642475	683.716862	0.251306304	0.09083406	2.76665272	0.00566351	0.00735429
LOC100647105	513.548542	0.252262988	0.06980263	3.61394656	0.00030157	0.0004339
LOC100643911	883.988565	0.254320102	0.10131901	2.51009262	0.01206995	0.01526554

LOC100651282	500.836207	0.254447909	0.0977895	2.6019962	0.00926829	0.01185135
LOC100647056	346.704437	0.256206138	0.08776563	2.91920795	0.00350922	0.00463869
LOC100645945	1762.52733	0.25653579	0.05816852	4.410217	1.03E-05	1.65E-05
LOC100645383	828.873815	0.257444129	0.07087903	3.63216202	0.00028106	0.00040551
LOC100643750	819.056353	0.258888149	0.08339873	3.10422187	0.0019078	0.00258144
LOC100649976	1937.85619	0.259493007	0.05851724	4.43447117	9.23E-06	1.48E-05
LOC100642496	1624.78134	0.260713464	0.08440612	3.08879805	0.00200968	0.00271441
LOC100646019	330.788296	0.261094274	0.09268228	2.81708948	0.0048461	0.00632137
LOC100648185	7350.14368	0.261487563	0.04015495	6.51196283	7.42E-11	1.63E-10
LOC100650942	3556.1179	0.261533497	0.05079733	5.14856763	2.62E-07	4.66E-07
LOC100647652	294.961832	0.261539675	0.09141009	2.86116864	0.00422082	0.00554564
LOC100650876	392.83147	0.262665452	0.08407698	3.12410663	0.00178346	0.00241686
LOC100631092	599.897357	0.262890671	0.0944804	2.78248902	0.00539437	0.00702344
LOC100649047	2864.36802	0.26297655	0.09677222	2.71747964	0.00657812	0.00850025
LOC100647376	656.23573	0.263392545	0.07844109	3.35783904	0.00078554	0.00109297
LOC100651123	707.860915	0.263566437	0.08225043	3.20443856	0.00135326	0.00185027
LOC100644946	1370.45381	0.265098886	0.07627604	3.47551973	0.00050986	0.0007215
LOC100644124	817.107412	0.265948454	0.12946167	2.05426403	0.03995014	0.04834407
LOC100651081	679.063399	0.266421498	0.12273397	2.17072343	0.02995208	0.03664845
LOC100645684	1307.46434	0.266489966	0.11261765	2.36632511	0.01796566	0.02240502
LOC100651070	451.328875	0.266520502	0.10973622	2.42873774	0.01515149	0.01900925
LOC100643540	1177.99247	0.267226777	0.0769407	3.47315233	0.00051438	0.00072737
LOC100644430	1019.87657	0.267909786	0.09611574	2.7873663	0.00531384	0.00692135
LOC100643730	177.687572	0.269329657	0.12765968	2.10974728	0.03488013	0.0424185
LOC100649002	2437.42315	0.269457423	0.06406954	4.20570275	2.60E-05	4.05E-05
LOC100651290	848.843918	0.270188353	0.10274542	2.62968751	0.00854634	0.01095108
LOC100644991	641.415398	0.270664082	0.06331581	4.27482605	1.91E-05	3.00E-05
LOC100643036	847.983742	0.270998639	0.06587223	4.11400421	3.89E-05	5.98E-05
LOC100651065	963.220033	0.271274889	0.10295152	2.63497713	0.0084143	0.01079036

LOC100649712	445.56081	0.272087765	0.07824125	3.47754892	0.00050602	0.00071648
LOC100642518	498.164644	0.272343933	0.08594822	3.16869794	0.00153123	0.00208429
LOC100652081	1488.75305	0.272573594	0.08262772	3.29881555	0.00097094	0.00134196
LOC100649322	885.886737	0.272597745	0.13241095	2.05872506	0.03952058	0.04783608
LOC100649374	388.845122	0.273043087	0.07809404	3.49633728	0.00047169	0.00066971
LOC100651743	859.808109	0.273445456	0.07882971	3.46881224	0.00052276	0.0007388
LOC100646852	1276.86444	0.274052499	0.08163012	3.35724728	0.00078723	0.00109516
LOC100642681	276.918819	0.274587796	0.08708421	3.15312971	0.0016153	0.00219445
LOC100649234	545.974474	0.274909933	0.07705661	3.56763575	0.00036022	0.00051585
LOC100646112	432.006876	0.275085483	0.08299141	3.31462581	0.00091766	0.00127119
LOC100647613	796.397559	0.275373854	0.06537245	4.21238373	2.53E-05	3.94E-05
LOC105666875	494.65065	0.275483407	0.09417238	2.92531009	0.00344113	0.00455422
LOC100644139	4492.24348	0.275568471	0.10716667	2.5714008	0.0101288	0.012923
LOC100649850	1248.17074	0.275899694	0.096715	2.85270827	0.00433484	0.00568933
LOC100649243	377.899179	0.27717344	0.08466825	3.27364085	0.00106171	0.00146371
LOC100651893	262.188998	0.27722555	0.10081588	2.74982022	0.0059628	0.0077245
LOC100648530	921.14936	0.27723029	0.06787076	4.08467915	4.41E-05	6.76E-05
LOC100646912	309.099653	0.277686077	0.12735852	2.18034936	0.02923157	0.03581609
LOC100651016	1169.94649	0.278074569	0.10945726	2.54048544	0.01106987	0.0140632
LOC100647473	143.010517	0.278196191	0.10891026	2.55436176	0.01063827	0.01353245
LOC100643866	1086.03405	0.278707938	0.06746005	4.13145193	3.60E-05	5.56E-05
LOC100646308	911.36818	0.278932983	0.0707674	3.94154627	8.10E-05	0.00012182
LOC100649888	415.330833	0.279990144	0.10326669	2.71133074	0.00670137	0.00865038
LOC100650091	1060.5765	0.280371697	0.06578902	4.26167893	2.03E-05	3.18E-05
LOC100648141	341.917068	0.280799876	0.09288145	3.02320712	0.00250111	0.00335595
LOC100646902	732.762419	0.280919197	0.09149816	3.07021686	0.00213903	0.00288316
LOC100652171	1933.76775	0.281351378	0.081068	3.47056035	0.00051937	0.00073422
LOC100645751	1231.19691	0.281641076	0.08813161	3.19568741	0.00139498	0.00190545
LOC100649244	5281.38648	0.281872607	0.0846376	3.33034731	0.00086738	0.00120393

LOC100650971	1558.73261	0.282025115	0.04072477	6.92514921	4.36E-12	1.04E-11
LOC100648105	2104.67061	0.282804156	0.0586828	4.81920041	1.44E-06	2.43E-06
LOC100650114	792.886611	0.28327437	0.07238241	3.91358032	9.09E-05	0.00013616
LOC105666536	274.765792	0.283822097	0.09409613	3.01629928	0.00255881	0.00343007
LOC100649600	1057.55865	0.283929036	0.06119616	4.63965444	3.49E-06	5.74E-06
LOC100649192	665.429146	0.28412953	0.07747083	3.6675677	0.00024487	0.00035503
LOC100651857	350.006583	0.284901618	0.09340058	3.05031968	0.00228598	0.00307488
LOC100644747	558.879418	0.285355174	0.09353893	3.05065675	0.00228341	0.00307185
LOC100650088	132.900574	0.286361385	0.11314241	2.53098189	0.01137437	0.01443132
LOC100642260	253.607735	0.286758653	0.10197008	2.81218418	0.00492063	0.00641688
LOC105666636	3618.1194	0.286898347	0.07275898	3.94313322	8.04E-05	0.00012109
LOC100649729	267.217731	0.287360232	0.10757679	2.67121024	0.00755783	0.00972643
LOC100644676	1100.21766	0.28851649	0.0960445	3.0039877	0.00266466	0.00356758
LOC100642363	876.270314	0.289630173	0.07234435	4.00349423	6.24E-05	9.47E-05
LOC100647307	489.698188	0.289678076	0.08293764	3.49272131	0.00047813	0.00067855
LOC100642391	516.689639	0.289808804	0.08448015	3.43049582	0.00060248	0.0008456
LOC100651645	818.300597	0.289960889	0.06529166	4.4410093	8.95E-06	1.44E-05
LOC100647628	1694.32276	0.290942663	0.1144073	2.54304283	0.01098918	0.01396431
LOC100642405	1557.62609	0.291044446	0.06739921	4.31821718	1.57E-05	2.48E-05
LOC100651184	479.677714	0.291105057	0.07842053	3.71210252	0.00020554	0.0003001
LOC100648757	895.162166	0.291513977	0.10853821	2.68581898	0.00723523	0.00932107
LOC100648622	392.140227	0.291570728	0.09436978	3.08966191	0.00200384	0.0027069
LOC100643368	1742.4806	0.29163167	0.06746769	4.32253794	1.54E-05	2.44E-05
LOC100648735	571.255354	0.29167923	0.06738449	4.3285814	1.50E-05	2.37E-05
LOC100643973	570.2649	0.291687549	0.07656049	3.80989667	0.00013902	0.00020518
LOC100642598	201.761723	0.29192396	0.11401695	2.56035573	0.01045651	0.01332375
LOC100646860	539.111394	0.292020937	0.09864239	2.96039992	0.0030724	0.00408999
LOC100642284	1307.30563	0.292395394	0.05102699	5.73021031	1.00E-08	1.95E-08
LOC100643983	761.237926	0.292484591	0.12884764	2.27000345	0.02320737	0.02870432

LOC100650156	1447.36794	0.292814224	0.07928698	3.69309346	0.00022154	0.0003224
LOC100645705	854.965872	0.292994573	0.09834975	2.97910859	0.00289088	0.00385779
LOC100645158	140.844814	0.293483068	0.14034455	2.09116112	0.03651362	0.04435544
LOC100643737	3079.84102	0.293605262	0.11207402	2.61974408	0.00879958	0.01126231
LOC100652027	1740.27874	0.29423531	0.07885066	3.73155177	0.0001903	0.00027868
LOC100646714	166.899093	0.295105535	0.1110445	2.6575429	0.00787126	0.01011384
LOC100649516	5594.2224	0.295789697	0.13997412	2.11317418	0.03458586	0.04208677
LOC100646042	5347.98375	0.29665003	0.05165246	5.7431922	9.29E-09	1.81E-08
LOC100646269	1216.38632	0.296742054	0.10097195	2.93885621	0.00329426	0.00437225
LOC100650583	243.22686	0.297072582	0.09934872	2.99020053	0.00278794	0.00372703
LOC100642519	590.052415	0.298115322	0.07894116	3.77642439	0.0001591	0.00023389
LOC100644435	306.713923	0.298789548	0.08049392	3.71195162	0.00020567	0.00030019
LOC100646200	223.365494	0.299825954	0.14683857	2.04187471	0.04116396	0.04978216
LOC100643795	565.468155	0.300462473	0.07765226	3.86933338	0.00010913	0.00016246
LOC100645666	2553.19053	0.301254044	0.08664735	3.47678312	0.00050747	0.00071842
LOC100648272	312.288604	0.301674886	0.09878551	3.05383737	0.00225935	0.0030403
LOC100647180	623.913551	0.303441674	0.08254801	3.67594173	0.00023697	0.00034399
LOC100652148	2933.55826	0.303528687	0.08386937	3.61906499	0.00029567	0.00042566
LOC100646157	536.866918	0.303707046	0.10348667	2.93474557	0.00333821	0.00442459
LOC100650090	1059.18477	0.304997942	0.06894726	4.42364103	9.71E-06	1.55E-05
LOC100649261	890.823407	0.305135148	0.09266364	3.29293306	0.00099148	0.00136977
LOC100644425	212.625976	0.305364181	0.12954234	2.35725391	0.01841065	0.02294535
LOC100646163	699.581263	0.305462136	0.08020012	3.80874909	0.00013967	0.00020611
LOC100644335	360.762128	0.305759658	0.10125397	3.01973004	0.00253	0.00339239
LOC100642402	186.662665	0.306730876	0.14552298	2.10778311	0.03504975	0.04260362
LOC100642690	836.154618	0.307962246	0.06938916	4.43818958	9.07E-06	1.45E-05
LOC100642534	342.890967	0.308430874	0.09433119	3.26965953	0.00107677	0.00148342
LOC100652037	1260.85445	0.308716233	0.07720654	3.99857641	6.37E-05	9.66E-05
LOC100648929	724.66841	0.309219684	0.08685617	3.56013482	0.00037066	0.00053027

LOC100647619	268.760057	0.309574735	0.12612893	2.45443081	0.01411078	0.01775362
LOC100645270	415.070824	0.31033062	0.12979488	2.39093115	0.0168057	0.02099587
LOC105665890	313.976973	0.310626393	0.105588	2.94187203	0.00326235	0.00433107
LOC100649048	980.249867	0.310800147	0.05840453	5.32150769	1.03E-07	1.87E-07
LOC100649898	415.655914	0.310904852	0.13907914	2.23545276	0.02538764	0.03128245
LOC100646543	559.729842	0.310982949	0.08915368	3.4881672	0.00048634	0.00068991
LOC100643705	564.499065	0.311069851	0.10840496	2.86951678	0.004111	0.00540641
LOC100646203	1788.41052	0.311254503	0.07321262	4.25137785	2.12E-05	3.33E-05
LOC100651112	183.922538	0.311729055	0.11713677	2.66123998	0.00778534	0.01000739
LOC100644016	403.845643	0.312542532	0.08568306	3.64765851	0.00026464	0.00038273
LOC100645354	3370.35701	0.313326492	0.05656873	5.53886368	3.04E-08	5.72E-08
LOC100649980	244.018008	0.313689614	0.10571323	2.96736384	0.00300365	0.00400283
LOC100647091	478.286907	0.314034812	0.0854903	3.67333837	0.0002394	0.00034736
LOC100650089	213.492844	0.314278042	0.13551639	2.31911457	0.02038883	0.02533659
LOC100646132	534.733296	0.314713113	0.07885972	3.99079651	6.59E-05	9.97E-05
LOC100652303	397.978302	0.314961445	0.09447972	3.33364077	0.00085717	0.00119027
LOC100651101	129.740408	0.31505389	0.12285545	2.5644275	0.01033462	0.01317701
LOC100643211	1909.42869	0.315399583	0.05720822	5.5131863	3.52E-08	6.59E-08
LOC100647575	281.964113	0.315654727	0.10754019	2.9352256	0.00333305	0.00441835
LOC100643647	499.882159	0.317141192	0.08505277	3.72875775	0.00019243	0.00028154
LOC100642985	279.061807	0.318302017	0.12885947	2.47014833	0.0135057	0.0170193
LOC100649461	1607.62605	0.319279532	0.0577936	5.52447927	3.30E-08	6.19E-08
LOC100646580	358.412224	0.320084139	0.07830919	4.08744043	4.36E-05	6.69E-05
LOC100650388	170.530816	0.320888185	0.12753986	2.51598346	0.01187008	0.01502714
LOC100649647	532.868036	0.321335419	0.05893112	5.4527285	4.96E-08	9.19E-08
LOC100646924	494.45358	0.3215214	0.10251213	3.13642312	0.00171022	0.00231954
LOC100645546	909.472646	0.321837399	0.08561097	3.759301	0.00017039	0.00025015
LOC100644945	898.824585	0.321989214	0.11096375	2.90175149	0.00371083	0.00489725
LOC100651597	507.831596	0.322579517	0.09266469	3.48114823	0.00049927	0.00070733

LOC100651709	976.649563	0.323414487	0.06208926	5.20886358	1.90E-07	3.40E-07
LOC100631093	600.577096	0.323853533	0.14089704	2.29851196	0.02153267	0.02671732
LOC100650076	2014.07112	0.323970801	0.06760149	4.7923618	1.65E-06	2.77E-06
LOC100645704	694.792561	0.326193651	0.09140425	3.56869254	0.00035877	0.00051385
LOC100642313	1003.24162	0.326438377	0.06880595	4.74433369	2.09E-06	3.49E-06
LOC100651454	1389.32937	0.32706995	0.07264068	4.50257257	6.71E-06	1.08E-05
LOC100643963	655.507917	0.327585978	0.08375437	3.91127042	9.18E-05	0.00013745
LOC100644406	292.100659	0.328203385	0.08503303	3.85971666	0.00011352	0.00016884
LOC105666695	213.171292	0.328213156	0.11130642	2.94873505	0.00319077	0.0042395
LOC100644885	274.153888	0.329097895	0.0870131	3.78216492	0.00015547	0.00022873
LOC100651429	2093.24019	0.329934616	0.12663317	2.60543592	0.00917574	0.01173455
LOC100645127	510.30711	0.330628997	0.08098475	4.082608	4.45E-05	6.82E-05
LOC100650357	530.824852	0.331340371	0.08657829	3.82706061	0.00012968	0.00019197
LOC100651764	883.425625	0.331505734	0.08017444	4.13480581	3.55E-05	5.48E-05
LOC100651455	677.697696	0.331640583	0.09385326	3.53360762	0.00040993	0.00058448
LOC100650721	126.978789	0.331844775	0.13216627	2.51081286	0.01204535	0.01523919
LOC100649972	487.466589	0.331914792	0.11317567	2.93273985	0.00335985	0.00445146
LOC100644490	3400.922	0.332159476	0.05281733	6.28883446	3.20E-10	6.77E-10
LOC100645692	649.100595	0.332961129	0.07910727	4.20898242	2.57E-05	4.00E-05
LOC100645707	98.9050605	0.333533313	0.13049717	2.55586617	0.01059238	0.01348109
LOC100651310	436.182997	0.334800824	0.0975798	3.43104647	0.00060126	0.000844
LOC100646831	507.464066	0.335025349	0.07292453	4.59413813	4.35E-06	7.10E-06
LOC100650593	276.875142	0.33535406	0.09154766	3.66316355	0.00024912	0.00036092
LOC100645206	595.054742	0.335866266	0.13691427	2.45311369	0.01416256	0.01781647
LOC100646216	873.967068	0.336734773	0.11263419	2.98963197	0.00279314	0.00373346
LOC100647998	837.579975	0.336867985	0.09778622	3.44494321	0.00057118	0.00080374
LOC100647853	790.84808	0.337082179	0.10159104	3.31803048	0.00090655	0.00125669
LOC100649143	315.392772	0.337082263	0.11854591	2.8434745	0.00446246	0.00584351
LOC100643164	384.027911	0.337192815	0.09732466	3.46461831	0.00053098	0.00074987

LOC105666259	1615.82719	0.337520202	0.07354645	4.58921143	4.45E-06	7.26E-06
LOC100651096	430.592795	0.33784994	0.14008322	2.41178023	0.01587485	0.0198735
LOC100644500	604.56567	0.337965986	0.09681994	3.49066522	0.00048182	0.0006836
LOC100643424	386.946829	0.337981367	0.08761448	3.85759723	0.00011451	0.00017018
LOC100645889	498.62266	0.339116973	0.11984851	2.82954675	0.0046614	0.00609099
LOC100646481	760.498542	0.339897793	0.07524294	4.51733804	6.26E-06	1.01E-05
LOC100649101	1693.53143	0.34019623	0.05258135	6.46990242	9.81E-11	2.13E-10
LOC100643350	740.641439	0.340538655	0.08786532	3.8756888	0.00010632	0.00015835
LOC100647674	844.309473	0.341696473	0.07872594	4.34032912	1.42E-05	2.25E-05
LOC100650570	391.021581	0.341750985	0.1316618	2.59567299	0.00944059	0.01206537
LOC100650007	564.022631	0.34280739	0.07812454	4.38796048	1.14E-05	1.82E-05
LOC100651845	532.464036	0.343120067	0.08330775	4.11870515	3.81E-05	5.87E-05
LOC100643662	991.374213	0.343231959	0.08108036	4.23323198	2.30E-05	3.60E-05
LOC100650825	241.714123	0.343374752	0.11852578	2.89704706	0.00376693	0.00496661
LOC100650855	1554.12156	0.343395873	0.05360694	6.40581022	1.50E-10	3.22E-10
LOC100649193	805.451434	0.344751161	0.0909125	3.7921206	0.00014937	0.00022005
LOC100648173	558.240392	0.344898283	0.071718	4.80908929	1.52E-06	2.56E-06
LOC100651858	2176.15569	0.345407464	0.06592278	5.23957634	1.61E-07	2.89E-07
LOC100651323	590.790661	0.345524308	0.06506136	5.31074484	1.09E-07	1.98E-07
LOC100645486	237.805021	0.345859633	0.13146066	2.63089843	0.00851595	0.01091357
LOC100650179	577.417446	0.346399719	0.09941346	3.48443496	0.00049318	0.0006993
LOC100645854	319.257431	0.346988491	0.09044348	3.83652295	0.00012479	0.00018493
LOC100646597	2771.61148	0.347024324	0.06270107	5.53458356	3.12E-08	5.86E-08
LOC100646424	2815.06585	0.348188507	0.06118446	5.69079925	1.26E-08	2.43E-08
LOC100644041	87.2005878	0.348738034	0.14290465	2.44035466	0.01467285	0.0184371
LOC100648829	1848.51728	0.349292942	0.07628591	4.57873491	4.68E-06	7.62E-06
LOC100646271	129.556567	0.349315024	0.14727846	2.37179981	0.01770168	0.02208143
LOC100646261	416.290173	0.349663171	0.09009394	3.8810955	0.00010399	0.00015497
LOC105666469	1873.18721	0.350436721	0.06637499	5.27965045	1.29E-07	2.34E-07

LOC100643807	351.938161	0.350737512	0.0963645	3.63969623	0.00027296	0.00039436
LOC100646249	708.575098	0.352212817	0.06951017	5.06706919	4.04E-07	7.09E-07
LOC100648019	433.77421	0.352231696	0.09591022	3.67251462	0.00024018	0.00034838
LOC100642456	651.932881	0.35231008	0.09791747	3.59803094	0.00032064	0.00046085
LOC100650948	126.35242	0.35247969	0.14660304	2.40431361	0.01620287	0.02026859
LOC100646785	192.860693	0.35276309	0.13436757	2.62535885	0.00865577	0.0110855
LOC100645872	477.76948	0.353161127	0.08642995	4.08609661	4.39E-05	6.72E-05
LOC100648111	994.362583	0.353623273	0.08605794	4.10912988	3.97E-05	6.11E-05
LOC100646735	343.22201	0.354314219	0.10237443	3.46096413	0.00053824	0.00075947
LOC105666294	717.689125	0.354438026	0.05861084	6.04731141	1.47E-09	3.01E-09
LOC100650046	1708.29844	0.35456248	0.07781887	4.55625332	5.21E-06	8.47E-06
LOC100643901	760.649973	0.355268511	0.07439284	4.77557424	1.79E-06	3.01E-06
LOC100643822	727.646624	0.355384121	0.10483502	3.3899371	0.00069909	0.00097601
LOC100651347	968.948425	0.355772186	0.07901524	4.50257664	6.71E-06	1.08E-05
LOC100644010	683.061172	0.356452248	0.06880155	5.18087528	2.21E-07	3.94E-07
LOC100652054	1603.03307	0.356550501	0.06590702	5.40990184	6.31E-08	1.16E-07
LOC100648863	235.569702	0.356949781	0.10207727	3.49685845	0.00047077	0.0006685
LOC100651007	1012.56895	0.357352856	0.09040307	3.9528843	7.72E-05	0.00011636
LOC105665938	198.753877	0.358602812	0.10400481	3.44794436	0.00056487	0.00079555
LOC100645474	240.855313	0.358972396	0.09274514	3.87052505	0.0001086	0.0001617
LOC100651723	319.760978	0.359085467	0.08134001	4.41462267	1.01E-05	1.62E-05
LOC100647989	596.567489	0.359668641	0.14601479	2.46323424	0.01376899	0.01733919
LOC100644081	143.353815	0.359811642	0.15021736	2.39527339	0.01660798	0.02075679
LOC100648299	1305.90802	0.360332637	0.06874568	5.24153127	1.59E-07	2.86E-07
LOC100644604	140.085077	0.360623367	0.16846337	2.14066332	0.0323012	0.03941439
LOC100646812	2338.85006	0.360930699	0.06671625	5.40993723	6.30E-08	1.16E-07
LOC100649014	409.999345	0.361087808	0.10452873	3.45443616	0.00055144	0.00077731
LOC100643559	2664.14378	0.361607413	0.1082216	3.34136068	0.00083369	0.00115799
LOC105666384	616.358821	0.361768572	0.09017038	4.01205535	6.02E-05	9.15E-05

LOC100650503	426.50033	0.361854345	0.07596035	4.76372679	1.90E-06	3.19E-06
LOC100650382	290.241297	0.362475122	0.09676675	3.74586428	0.00017977	0.00026358
LOC100651182	961.278689	0.36277312	0.12723177	2.85127782	0.00435439	0.00571346
LOC100649756	226.623975	0.362821695	0.08830479	4.10874315	3.98E-05	6.11E-05
LOC100646766	476.68009	0.363126078	0.0951044	3.81818385	0.00013444	0.00019862
LOC100645123	539.244481	0.363246308	0.07153148	5.0781319	3.81E-07	6.70E-07
LOC100645571	978.289685	0.36336135	0.08860448	4.1009366	4.11E-05	6.31E-05
LOC100648357	533.895268	0.363394516	0.08203831	4.4295712	9.44E-06	1.51E-05
LOC100643943	139.41524	0.363724066	0.13578202	2.67873509	0.00739008	0.00951431
LOC100645377	537.444361	0.363934511	0.07190097	5.06160814	4.16E-07	7.29E-07
LOC100646407	792.697802	0.364579465	0.10009126	3.64247056	0.00027003	0.0003903
LOC105665861	463.747597	0.364744656	0.11450587	3.18537967	0.00144564	0.00197107
LOC100647500	605.460539	0.36542392	0.09147728	3.99469602	6.48E-05	9.81E-05
LOC100646581	666.116637	0.366131896	0.06360468	5.75636753	8.59E-09	1.68E-08
LOC100644282	850.885933	0.366142882	0.07518092	4.87015681	1.12E-06	1.90E-06
LOC100649692	248.406788	0.367153178	0.08615074	4.26175315	2.03E-05	3.18E-05
LOC100647948	8151.29347	0.367322189	0.08789211	4.17923949	2.92E-05	4.54E-05
LOC100646740	304.122438	0.368529244	0.09077553	4.05978605	4.91E-05	7.51E-05
LOC100645265	254.667584	0.36874981	0.12952833	2.84686617	0.00441519	0.00578858
LOC100645071	891.544042	0.368939043	0.08617603	4.28122592	1.86E-05	2.92E-05
LOC100647708	294.556516	0.369000503	0.0860223	4.28959111	1.79E-05	2.82E-05
LOC100644186	584.808493	0.369315892	0.07657044	4.82321746	1.41E-06	2.39E-06
LOC100648745	613.734745	0.369423775	0.09977095	3.70271869	0.0002133	0.00031078
LOC100644851	235.055037	0.369455371	0.12982921	2.84570296	0.00443135	0.00580666
LOC100652233	865.437556	0.369801652	0.08137537	4.54439271	5.51E-06	8.95E-06
LOC100644061	168.045249	0.369984868	0.13429579	2.75499975	0.00586922	0.00761233
LOC100649727	251.336074	0.371306902	0.12454971	2.98119436	0.00287127	0.0038337
LOC100648295	300.215628	0.371444351	0.11217055	3.31142499	0.00092822	0.0012851
LOC100650302	1405.34156	0.371489078	0.07396714	5.02235287	5.10E-07	8.91E-07

LOC100646285	194.748401	0.371787585	0.14529064	2.5589232	0.01049969	0.01337529
LOC100650793	526.46155	0.372959639	0.08295691	4.49582357	6.93E-06	1.12E-05
LOC100647169	6652.35525	0.373630187	0.05664072	6.59649394	4.21E-11	9.40E-11
LOC100645218	269.838818	0.373864575	0.11159623	3.35015412	0.00080767	0.00112312
LOC100645623	1180.40925	0.374645469	0.06538383	5.72994035	1.00E-08	1.95E-08
LOC100644128	742.008541	0.374879259	0.11349405	3.3030742	0.00095631	0.0013223
LOC100643417	122.338532	0.375834681	0.14159004	2.65438643	0.00794528	0.01020676
LOC100646303	465.076744	0.376074736	0.08179695	4.5976622	4.27E-06	6.98E-06
LOC100645076	199.459189	0.3760789	0.09813905	3.83210266	0.00012705	0.00018814
LOC100652167	777.973013	0.376913153	0.11369282	3.31518866	0.00091581	0.00126882
LOC100645336	215.972734	0.377330345	0.10418573	3.6217085	0.00029266	0.00042152
LOC100643408	579.352977	0.377429472	0.07871429	4.79492922	1.63E-06	2.74E-06
LOC100650822	904.356242	0.37814966	0.06642191	5.6931461	1.25E-08	2.40E-08
LOC100648885	1180.07451	0.378477781	0.07664422	4.93811248	7.89E-07	1.36E-06
LOC100645801	172.003609	0.378571088	0.17046882	2.22076436	0.02636693	0.03242791
LOC100644372	678.150581	0.378822286	0.06926675	5.46903504	4.52E-08	8.41E-08
LOC100644803	898.637812	0.379956901	0.06508447	5.83790455	5.29E-09	1.04E-08
LOC100648528	191.759732	0.380548209	0.13449715	2.82941472	0.00466332	0.00609269
LOC100649926	3255.9045	0.381068656	0.06176595	6.16955842	6.85E-10	1.42E-09
LOC100647792	648.162215	0.381097771	0.14610577	2.60836903	0.00909748	0.01164054
LOC100648841	1011.99971	0.381417492	0.14888075	2.56189932	0.01041015	0.01326813
LOC100651618	1787.90472	0.381729724	0.05189561	7.35572228	1.90E-13	4.92E-13
LOC100652195	63.0673879	0.382016978	0.17058103	2.23950442	0.02512311	0.0309682
LOC100643241	165.931191	0.382398499	0.13465997	2.83973409	0.00451512	0.00591009
LOC100648343	285.874266	0.382937611	0.09326574	4.1058764	4.03E-05	6.19E-05
LOC100643546	699.492396	0.382956458	0.07813283	4.90135144	9.52E-07	1.63E-06
LOC100651294	465.565299	0.383051318	0.10831685	3.53639627	0.00040563	0.0005786
LOC100643776	917.612839	0.383479293	0.06032858	6.35651136	2.06E-10	4.41E-10
LOC100645379	383.001517	0.383633702	0.10558026	3.6335742	0.00027952	0.00040342

LOC100647350	144.573365	0.383747169	0.15731103	2.43941684	0.01471099	0.01848028
LOC100644207	159.94218	0.383824078	0.12241414	3.13545535	0.00171588	0.00232689
LOC100648474	787.704979	0.384050283	0.06340284	6.05730393	1.38E-09	2.83E-09
LOC100643620	4436.65731	0.38451021	0.08215423	4.68034569	2.86E-06	4.74E-06
LOC100650056	284.709964	0.384565222	0.13535336	2.84119457	0.00449449	0.00588467
LOC100646099	1312.68741	0.384735832	0.06592922	5.83558858	5.36E-09	1.06E-08
LOC100650894	710.928781	0.386611661	0.07932842	4.87355827	1.10E-06	1.87E-06
LOC100643117	1183.5438	0.386900859	0.06138252	6.30311168	2.92E-10	6.19E-10
LOC100642691	551.888102	0.386935636	0.07620024	5.07787979	3.82E-07	6.71E-07
LOC100651802	558.895197	0.387703814	0.08646705	4.48383279	7.33E-06	1.18E-05
LOC100646432	1936.55107	0.388254219	0.10155826	3.82297041	0.00013185	0.00019498
LOC100650675	616.476124	0.388539615	0.06995159	5.55440753	2.79E-08	5.25E-08
LOC100646884	219.428791	0.38884893	0.1046687	3.7150451	0.00020317	0.00029672
LOC100650980	188.52389	0.389420609	0.12986196	2.99872741	0.0027111	0.00362727
LOC100646528	87.5118214	0.390259197	0.17956677	2.17333756	0.02975492	0.0364163
LOC100645965	633.998257	0.39031421	0.09734656	4.00953262	6.08E-05	9.25E-05
LOC100645130	1789.23013	0.391059223	0.06602797	5.92262942	3.17E-09	6.35E-09
LOC100652149	638.579473	0.391235088	0.08481524	4.61279234	3.97E-06	6.51E-06
LOC100650616	552.210855	0.391310512	0.14900331	2.62618675	0.00863474	0.01106002
LOC100642485	441.053419	0.391328461	0.09648826	4.05571052	5.00E-05	7.64E-05
LOC100648248	531.459033	0.391416061	0.07851582	4.98518707	6.19E-07	1.07E-06
LOC100645701	516.805359	0.392272053	0.08262855	4.74741517	2.06E-06	3.44E-06
LOC100647089	320.351594	0.392657621	0.0933786	4.20500671	2.61E-05	4.06E-05
LOC100645054	366.600767	0.392831741	0.12294599	3.19515696	0.00139755	0.00190869
LOC100646499	1080.86748	0.393259814	0.06195149	6.34786737	2.18E-10	4.66E-10
LOC100643925	582.953794	0.393739728	0.07289005	5.40183111	6.60E-08	1.21E-07
LOC100644446	605.575392	0.393975242	0.06626922	5.94507162	2.76E-09	5.56E-09
LOC100647955	251.931352	0.39400846	0.14958126	2.63407636	0.00843665	0.01081619
LOC105666720	67.7291541	0.394627588	0.18692077	2.1112024	0.03475492	0.04227148

LOC100649569	716.283532	0.394995696	0.09537742	4.14139628	3.45E-05	5.33E-05
LOC100642408	381.738445	0.395016	0.13957393	2.83015599	0.00465253	0.00608021
LOC100645770	244.075384	0.395110111	0.11626569	3.3983379	0.00067797	0.00094787
LOC100652286	686.977238	0.395474773	0.10102287	3.91470528	9.05E-05	0.00013559
LOC100648088	721.844133	0.39556444	0.08726019	4.53316039	5.81E-06	9.42E-06
LOC100646361	501.939977	0.395637459	0.12364838	3.19969796	0.00137572	0.00188018
LOC100649716	823.814445	0.396502477	0.07066633	5.61091119	2.01E-08	3.83E-08
LOC100652180	107.422952	0.397126723	0.14663116	2.70833793	0.00676211	0.00872534
LOC100644943	915.130194	0.398968375	0.07893242	5.05455668	4.31E-07	7.56E-07
LOC100647650	799.877184	0.399245092	0.08747697	4.56400233	5.02E-06	8.17E-06
LOC100651336	1725.75082	0.40093405	0.12533513	3.198896	0.00137955	0.00188516
LOC100642473	1225.02794	0.400985244	0.0712452	5.62824232	1.82E-08	3.47E-08
LOC100643091	1409.37766	0.401221457	0.05883451	6.81949192	9.14E-12	2.13E-11
LOC100650853	1348.0609	0.401768258	0.13686839	2.93543506	0.0033308	0.00441656
LOC100644001	254.583769	0.402042242	0.10806824	3.7202628	0.00019902	0.00029083
LOC100649984	622.411042	0.402959743	0.10124023	3.9802335	6.88E-05	0.00010409
LOC100652094	597.840345	0.403874285	0.07870117	5.1317445	2.87E-07	5.08E-07
LOC100650243	81.4281997	0.405028497	0.16875074	2.4001583	0.01638798	0.02048446
LOC100647085	234.723691	0.405439928	0.13409916	3.02343379	0.00249924	0.00335393
LOC100645812	324.257765	0.40555205	0.10408387	3.89639671	9.76E-05	0.00014588
LOC100647928	781.548273	0.405628429	0.05065518	8.00763964	1.17E-15	3.44E-15
LOC100649026	1019.97862	0.406006482	0.0644459	6.2999578	2.98E-10	6.31E-10
LOC100650934	776.03045	0.406016026	0.06541778	6.20650865	5.42E-10	1.13E-09
LOC100646594	2598.00719	0.406784016	0.09441007	4.30869317	1.64E-05	2.59E-05
LOC100650635	572.312388	0.406948357	0.08574928	4.74579331	2.08E-06	3.47E-06
LOC100644390	205.754329	0.407177963	0.18104507	2.24904195	0.02450983	0.03023888
LOC100642943	284.048073	0.407590077	0.09660482	4.21914833	2.45E-05	3.82E-05
LOC100646987	462.909088	0.408917	0.07184061	5.69200373	1.26E-08	2.42E-08
LOC100645754	123.360016	0.409494101	0.12368769	3.31071021	0.0009306	0.00128802

LOC100644760	875.434154	0.409825777	0.07160759	5.72321689	1.05E-08	2.03E-08
LOC100652308	448.501708	0.410763965	0.08875868	4.6278737	3.69E-06	6.06E-06
LOC100643721	434.657098	0.411958227	0.09590333	4.29555697	1.74E-05	2.74E-05
LOC100645874	321.967733	0.412313262	0.0916213	4.50018987	6.79E-06	1.10E-05
LOC100648947	159.210936	0.412609067	0.12561597	3.28468633	0.00102096	0.00140851
LOC100650012	692.285292	0.412887448	0.05993358	6.88908355	5.62E-12	1.33E-11
LOC100644829	770.281385	0.413035895	0.07462983	5.53446137	3.12E-08	5.86E-08
LOC105666249	137.005812	0.413225619	0.1240025	3.33239756	0.00086101	0.00119526
LOC100651097	851.341606	0.413556642	0.10328083	4.00419542	6.22E-05	9.45E-05
LOC100646795	199.516201	0.414263809	0.12581538	3.29263248	0.00099254	0.00137105
LOC100651159	418.030616	0.415058445	0.11275047	3.68121241	0.00023213	0.0003373
LOC100648721	2265.54419	0.415448454	0.06261267	6.63521334	3.24E-11	7.28E-11
LOC100642724	1622.82322	0.416054718	0.10054242	4.13810137	3.50E-05	5.40E-05
LOC100650662	636.489905	0.416627763	0.08386401	4.96789712	6.77E-07	1.17E-06
LOC100652070	174.767787	0.416901097	0.14017399	2.9741688	0.00293783	0.00391831
LOC105666614	580.365497	0.41805186	0.09846704	4.24560208	2.18E-05	3.41E-05
LOC100642736	295.196571	0.419629532	0.14727493	2.84929377	0.00438164	0.00574767
LOC100649590	323.766672	0.420914232	0.10700335	3.93365473	8.37E-05	0.00012568
LOC100649443	795.319786	0.420990356	0.07774969	5.41468885	6.14E-08	1.13E-07
LOC100650181	5010.2142	0.421646392	0.06725883	6.26901173	3.63E-10	7.66E-10
LOC100642606	297.598699	0.422464345	0.08750832	4.82770489	1.38E-06	2.34E-06
LOC100642335	651.242493	0.422740591	0.07159517	5.90459665	3.54E-09	7.07E-09
LOC100649317	980.171047	0.422755423	0.05196439	8.13548299	4.10E-16	1.24E-15
LOC100646774	357.290558	0.423396143	0.11560285	3.66250624	0.00024976	0.0003618
LOC100647028	1905.67748	0.42387476	0.07530226	5.62897789	1.81E-08	3.46E-08
LOC100649156	663.374033	0.42462128	0.08800454	4.82499286	1.40E-06	2.37E-06
LOC100645321	115.450749	0.424947247	0.19258883	2.20649991	0.02734902	0.03359777
LOC100652034	259.896605	0.42694508	0.12244426	3.48685258	0.00048874	0.00069321
LOC100652313	403.607132	0.427022509	0.08888442	4.80424452	1.55E-06	2.62E-06

LOC100646716	680.504961	0.427590899	0.07393702	5.78317737	7.33E-09	1.44E-08
LOC100647499	1113.31339	0.427947753	0.06731512	6.35737927	2.05E-10	4.39E-10
LOC100646454	498.45193	0.428369059	0.06917514	6.19252869	5.92E-10	1.23E-09
LOC100646955	383.123084	0.428756922	0.0838561	5.11300822	3.17E-07	5.60E-07
LOC100650459	761.688085	0.429232858	0.09534861	4.50172138	6.74E-06	1.09E-05
LOC100652132	1335.56455	0.429285441	0.066158	6.48879068	8.65E-11	1.89E-10
LOC100649923	600.31093	0.429363375	0.12020562	3.57190751	0.00035439	0.00050773
LOC100652302	610.142657	0.429850509	0.09053096	4.74810528	2.05E-06	3.43E-06
LOC100650201	2808.24621	0.430531085	0.04800997	8.9675356	3.03E-19	1.11E-18
LOC100643915	372.228265	0.431083026	0.08446275	5.10382401	3.33E-07	5.87E-07
LOC105666264	62.4028218	0.431161314	0.18110685	2.38070133	0.01727972	0.02156605
LOC100647682	455.142863	0.431551675	0.11045675	3.90697438	9.35E-05	0.00013985
LOC100647877	4354.11018	0.431997477	0.08800463	4.90880382	9.16E-07	1.57E-06
LOC100650452	579.237224	0.432946236	0.08576601	5.04799301	4.46E-07	7.82E-07
LOC100644487	664.198085	0.433037538	0.08829843	4.90424933	9.38E-07	1.61E-06
LOC100644024	71.3883563	0.433995298	0.18479101	2.34857369	0.01884547	0.02347532
LOC100650977	169.75382	0.434170887	0.10935845	3.97016311	7.18E-05	0.00010846
LOC100646536	129.208396	0.434642716	0.16626947	2.6140862	0.00894665	0.01144904
LOC100643251	1937.90702	0.435868669	0.09158569	4.75913495	1.94E-06	3.26E-06
LOC100643670	578.998365	0.436122353	0.06010681	7.25578877	3.99E-13	1.02E-12
LOC100649155	396.593915	0.436526052	0.08831394	4.94288974	7.70E-07	1.33E-06
LOC100648023	203.392812	0.436558641	0.11311976	3.85926081	0.00011373	0.00016913
LOC100649906	945.869359	0.436789958	0.06741114	6.47949183	9.20E-11	2.00E-10
LOC100642706	655.95242	0.437020049	0.08450734	5.17138573	2.32E-07	4.14E-07
LOC100647769	325.142975	0.437730902	0.10801693	4.0524288	5.07E-05	7.74E-05
LOC100648452	1154.13733	0.437839145	0.06580429	6.65365616	2.86E-11	6.46E-11
LOC100644948	136.156455	0.43792602	0.11770515	3.72053413	0.0001988	0.00029056
LOC100650073	147.676822	0.438097917	0.13001202	3.36967249	0.00075258	0.00104844
LOC100650900	578.900994	0.439216005	0.1053287	4.16995577	3.05E-05	4.72E-05

LOC100650571	1579.81815	0.439523437	0.0588189	7.47248692	7.87E-14	2.09E-13
LOC100642234	513.525924	0.440748725	0.14914417	2.9551858	0.00312481	0.00415806
LOC100644192	572.831729	0.441306622	0.09909184	4.45351128	8.45E-06	1.36E-05
LOC100650204	543.182731	0.442198391	0.09630533	4.59162933	4.40E-06	7.18E-06
LOC100648635	1323.18737	0.442532133	0.09167423	4.8272249	1.38E-06	2.34E-06
LOC105666213	461.625887	0.442767341	0.07730296	5.72768955	1.02E-08	1.98E-08
LOC100649921	1059.81579	0.443007897	0.06671295	6.64050811	3.13E-11	7.04E-11
LOC100643579	580.539841	0.443731218	0.09078421	4.88775779	1.02E-06	1.74E-06
LOC100645592	948.652652	0.443748575	0.0768205	5.77643405	7.63E-09	1.49E-08
LOC100644181	516.514814	0.443790003	0.07095586	6.25445208	3.99E-10	8.39E-10
LOC100645057	1104.55522	0.444700728	0.07575536	5.87022097	4.35E-09	8.65E-09
LOC100649673	1111.01421	0.4459233	0.05565675	8.01202513	1.13E-15	3.33E-15
LOC100649679	732.936594	0.446320131	0.09096192	4.90667031	9.26E-07	1.59E-06
LOC100650255	420.890319	0.446508006	0.12554505	3.55655595	0.00037575	0.00053715
LOC100648054	1661.63183	0.446529116	0.09404739	4.74791597	2.06E-06	3.44E-06
LOC100645244	965.701773	0.446614045	0.08007509	5.57744077	2.44E-08	4.62E-08
LOC100644774	319.502851	0.447957666	0.11497348	3.89618246	9.77E-05	0.00014598
LOC100648976	1074.59373	0.44864133	0.07210783	6.22181125	4.91E-10	1.03E-09
LOC100650554	332.33691	0.450298927	0.08794861	5.12002331	3.05E-07	5.40E-07
LOC100648062	63.4305938	0.451355271	0.17572593	2.56851836	0.01021343	0.01302758
LOC100652212	383.489285	0.451623593	0.10976365	4.11450947	3.88E-05	5.97E-05
LOC100648008	335.387261	0.452818841	0.11287614	4.01164355	6.03E-05	9.17E-05
LOC100649067	1472.03038	0.452844465	0.12247471	3.69745274	0.00021777	0.00031706
LOC100649968	634.167486	0.452866702	0.07629216	5.93595348	2.92E-09	5.87E-09
LOC100642569	100.385039	0.452956504	0.16450792	2.7534024	0.00589794	0.00764755
LOC100645272	917.751186	0.452998738	0.09417031	4.81041999	1.51E-06	2.54E-06
LOC100647519	384.84067	0.453366738	0.13448342	3.37117189	0.00074849	0.0010429
LOC100651591	243.852125	0.453493344	0.12685353	3.57493678	0.00035031	0.00050204
LOC100650712	935.833187	0.453754443	0.07613804	5.95962864	2.53E-09	5.10E-09

LOC100647074	1251.21564	0.453904913	0.12234131	3.71015259	0.00020713	0.00030218
LOC100647974	1042.4356	0.454052615	0.13502772	3.36266229	0.00077195	0.00107451
LOC100651107	55.8086334	0.454609155	0.18809512	2.41691095	0.01565285	0.01960561
LOC100644418	370.762561	0.454951157	0.09353491	4.8639718	1.15E-06	1.96E-06
LOC100647607	1901.19131	0.455028398	0.08837094	5.14907277	2.62E-07	4.64E-07
LOC100649249	713.611077	0.455207989	0.09112205	4.99558575	5.87E-07	1.02E-06
LOC100648456	675.593629	0.455759262	0.0916916	4.97056734	6.68E-07	1.16E-06
LOC100644213	416.992809	0.455966872	0.1295097	3.52071595	0.00043038	0.00061248
LOC100651440	703.381675	0.45629751	0.08990234	5.07547984	3.87E-07	6.79E-07
LOC105667179	580.87415	0.456403809	0.07489602	6.09383244	1.10E-09	2.27E-09
LOC100642859	913.367505	0.456447715	0.07129063	6.4026324	1.53E-10	3.28E-10
LOC100642612	147.984211	0.456695668	0.1615652	2.82669586	0.0047031	0.00614219
LOC100650788	332.503234	0.456791	0.10121184	4.513217	6.39E-06	1.03E-05
LOC105667209	119.462121	0.45710832	0.15731091	2.90576357	0.00366358	0.00483686
LOC100647615	853.552478	0.458110837	0.0988092	4.63631774	3.55E-06	5.82E-06
LOC100646467	96.0339632	0.460227223	0.14965216	3.07531301	0.00210282	0.00283591
LOC100650617	896.269323	0.46048414	0.07573124	6.08050431	1.20E-09	2.46E-09
LOC100647062	799.836521	0.460607007	0.06821557	6.7522271	1.46E-11	3.36E-11
LOC100648842	508.789756	0.461397717	0.12102463	3.81242825	0.00013761	0.00020315
LOC100644431	329.405924	0.461785904	0.08774291	5.26294275	1.42E-07	2.55E-07
LOC100645072	163.964022	0.461900051	0.1343011	3.4392872	0.00058325	0.00081954
LOC100645626	366.529203	0.462584188	0.09224534	5.0147161	5.31E-07	9.26E-07
LOC105666857	910.707572	0.462726904	0.09895447	4.67615948	2.92E-06	4.83E-06
LOC100643549	373.676813	0.462814498	0.11293104	4.0982044	4.16E-05	6.39E-05
LOC100651639	606.930272	0.463665515	0.0941999	4.92214467	8.56E-07	1.47E-06
LOC100650845	1474.22583	0.463676368	0.06304413	7.3547903	1.91E-13	4.95E-13
LOC100651526	931.911612	0.464172172	0.06503062	7.13774738	9.49E-13	2.36E-12
LOC105666330	58.7820416	0.464272789	0.18840586	2.46421635	0.01373132	0.0172962
LOC100644932	728.569293	0.464275341	0.11299563	4.1087901	3.98E-05	6.11E-05

LOC100643749	4218.69054	0.46446726	0.08305874	5.59203375	2.24E-08	4.26E-08
LOC100642305	1176.68765	0.464588179	0.07864717	5.907246	3.48E-09	6.96E-09
LOC100644196	452.626456	0.464774663	0.09513995	4.88516841	1.03E-06	1.76E-06
LOC100648354	148.239201	0.465439123	0.12856706	3.62020503	0.00029437	0.00042385
LOC100649623	617.762576	0.466133043	0.08952617	5.20666775	1.92E-07	3.44E-07
LOC100643829	319.533948	0.466944095	0.09690522	4.81856472	1.45E-06	2.44E-06
LOC100651855	403.302638	0.467346295	0.07329621	6.37613209	1.82E-10	3.89E-10
LOC100644190	638.784409	0.467414245	0.08456844	5.52705283	3.26E-08	6.11E-08
LOC100642225	346.381176	0.467700147	0.10354768	4.51676123	6.28E-06	1.02E-05
LOC105666954	94.8887765	0.467835145	0.21177278	2.20913729	0.02716509	0.03338439
LOC100645669	348.620514	0.469099788	0.11565145	4.05615147	4.99E-05	7.63E-05
LOC100650542	451.991524	0.469450963	0.08504818	5.51982366	3.39E-08	6.35E-08
LOC100645994	126.343833	0.470127856	0.22533414	2.08635871	0.03694614	0.04486415
LOC100649658	878.179744	0.470542819	0.06909318	6.81026449	9.74E-12	2.27E-11
LOC105666350	801.36573	0.471737913	0.10174406	4.63651541	3.54E-06	5.82E-06
LOC100652178	880.442477	0.472149105	0.08311961	5.68035742	1.34E-08	2.58E-08
LOC100649626	459.443848	0.472337364	0.1201998	3.92960178	8.51E-05	0.00012768
LOC100646715	497.758158	0.472349805	0.07983931	5.916256	3.29E-09	6.60E-09
LOC100643326	556.359673	0.472612726	0.08647498	5.46531201	4.62E-08	8.58E-08
LOC100642626	664.735009	0.472732324	0.08009949	5.90181471	3.60E-09	7.18E-09
LOC100643131	349.047711	0.473011781	0.10305585	4.58985868	4.44E-06	7.24E-06
LOC100646622	370.964885	0.473054184	0.08952158	5.28424734	1.26E-07	2.28E-07
LOC100649131	411.458227	0.474105247	0.11522893	4.11446366	3.88E-05	5.97E-05
LOC100647816	548.405864	0.474155522	0.07916606	5.98937849	2.11E-09	4.26E-09
LOC100646623	2327.38268	0.474408286	0.06535139	7.25934538	3.89E-13	9.92E-13
LOC100652246	186.95083	0.474408731	0.13791747	3.43980151	0.00058214	0.00081811
LOC100646541	1465.4602	0.474593693	0.0539517	8.79664101	1.41E-18	4.93E-18
LOC100649494	910.848332	0.475110507	0.06374563	7.45322439	9.11E-14	2.41E-13
LOC100647490	345.52974	0.475237632	0.12911864	3.68062771	0.00023266	0.00033798

LOC100646977	380.416108	0.475859386	0.10868105	4.3784945	1.20E-05	1.90E-05
LOC105665633	1093.57008	0.47621543	0.06724918	7.08135703	1.43E-12	3.50E-12
LOC100642918	1176.27141	0.476823094	0.10733101	4.44254719	8.89E-06	1.43E-05
LOC100645278	597.084994	0.4769109	0.08877599	5.37207096	7.78E-08	1.42E-07
LOC100651938	351.625276	0.477075555	0.0912904	5.22591135	1.73E-07	3.11E-07
LOC100651664	238.311998	0.478131977	0.11931121	4.00743565	6.14E-05	9.32E-05
LOC100646278	115.142344	0.478209787	0.1308662	3.6541888	0.000258	0.00037334
LOC100646772	486.958207	0.478266647	0.12516643	3.82104579	0.00013289	0.00019642
LOC100646170	324.730411	0.479635547	0.12105543	3.96211499	7.43E-05	0.00011209
LOC100645930	839.216464	0.480024403	0.15590383	3.07897764	0.00207712	0.0028028
LOC100642312	633.188518	0.480137969	0.13053459	3.67824312	0.00023485	0.000341
LOC100647633	995.360942	0.480243344	0.07914691	6.06774621	1.30E-09	2.66E-09
LOC105666528	647.449889	0.481088327	0.10898406	4.41429989	1.01E-05	1.62E-05
LOC100644441	81.2290967	0.481560934	0.17281017	2.78664695	0.00532565	0.00693489
LOC100645133	1640.22238	0.48163374	0.05216997	9.23201194	2.66E-20	1.03E-19
LOC100649649	947.402342	0.482269425	0.07617354	6.33119321	2.43E-10	5.18E-10
LOC100649724	1908.96459	0.482415569	0.070018	6.88987944	5.58E-12	1.32E-11
LOC105666520	97.0212218	0.482424166	0.16663323	2.89512576	0.00379007	0.00499576
LOC100644598	471.85238	0.482726177	0.09675373	4.9892256	6.06E-07	1.05E-06
LOC100643909	6600.00016	0.483261731	0.08210162	5.88614156	3.95E-09	7.88E-09
LOC100645939	2039.18911	0.483405608	0.09312413	5.19098133	2.09E-07	3.73E-07
LOC100651849	1524.29154	0.483436446	0.06833215	7.07480215	1.50E-12	3.67E-12
LOC100651703	1004.67187	0.483795265	0.09862143	4.90557956	9.32E-07	1.60E-06
LOC100642477	192.497568	0.484173043	0.19167557	2.52600288	0.01153685	0.0146242
LOC100644434	750.073679	0.484546808	0.16723459	2.89740784	0.0037626	0.00496157
LOC100644216	950.764806	0.48588652	0.0753223	6.45076614	1.11E-10	2.41E-10
LOC100645022	550.841791	0.486254568	0.07492444	6.48993273	8.59E-11	1.88E-10
LOC100646464	747.195658	0.486351155	0.07150671	6.80147598	1.04E-11	2.41E-11
LOC100651919	161.538137	0.486616256	0.1216062	4.00157439	6.29E-05	9.54E-05

LOC100648683	1065.07017	0.48723294	0.06983521	6.97689548	3.02E-12	7.26E-12
LOC100642243	1097.23049	0.487423935	0.07164813	6.80302363	1.02E-11	2.39E-11
LOC100643084	548.805549	0.487522889	0.0801861	6.07989297	1.20E-09	2.47E-09
LOC100651366	3037.86756	0.490079187	0.08815138	5.5595181	2.71E-08	5.10E-08
LOC100643120	483.903634	0.491167414	0.07312245	6.71705329	1.85E-11	4.24E-11
LOC100643803	2364.21471	0.491649234	0.05428746	9.05640482	1.35E-19	5.03E-19
LOC100647071	788.337319	0.491884907	0.07497187	6.56092589	5.35E-11	1.18E-10
LOC100642561	1581.09663	0.493338253	0.06072592	8.12401431	4.51E-16	1.36E-15
LOC100644697	1162.96101	0.494197169	0.10869231	4.54675392	5.45E-06	8.85E-06
LOC100644214	514.555843	0.49459677	0.09278411	5.33061927	9.79E-08	1.78E-07
LOC105666587	72.5777897	0.495975046	0.18473368	2.68481121	0.00725708	0.00934799
LOC100646437	71.5764778	0.496158064	0.18272552	2.71531889	0.0066212	0.00855365
LOC100646421	231.563737	0.496275087	0.0958845	5.17575911	2.27E-07	4.04E-07
LOC100647212	1366.22276	0.496648224	0.09876272	5.02870124	4.94E-07	8.62E-07
LOC100645851	1525.85282	0.498255673	0.06383805	7.80499556	5.95E-15	1.68E-14
LOC100646068	741.728156	0.499123814	0.08303442	6.01104691	1.84E-09	3.75E-09
LOC100650670	681.362496	0.499198256	0.10939203	4.56338775	5.03E-06	8.19E-06
LOC100650145	181.230344	0.49969579	0.1501275	3.32847616	0.00087322	0.00121187
LOC100645297	508.691432	0.499861954	0.0865535	5.77517895	7.69E-09	1.50E-08
LOC105665751	194.96155	0.50003455	0.11819296	4.23066263	2.33E-05	3.64E-05
LOC100645126	324.453919	0.500038284	0.10323002	4.84392309	1.27E-06	2.16E-06
LOC100648160	579.050006	0.500267729	0.07690976	6.50460647	7.79E-11	1.71E-10
LOC100648778	589.79724	0.500826459	0.0798521	6.27192563	3.57E-10	7.53E-10
LOC100645400	438.330006	0.501688273	0.11542496	4.34644516	1.38E-05	2.19E-05
LOC100644719	254.140534	0.501733971	0.11575872	4.33430835	1.46E-05	2.31E-05
LOC100647622	2485.41367	0.501887436	0.08788419	5.71078201	1.12E-08	2.18E-08
LOC100644779	486.49391	0.502479279	0.17537523	2.86516678	0.0041679	0.0054783
LOC100645145	1924.98996	0.502504202	0.05900162	8.5167864	1.64E-17	5.40E-17
LOC100643835	392.069677	0.503403141	0.09548374	5.27213452	1.35E-07	2.43E-07

LOC100644962	202.878178	0.503520459	0.10351295	4.86432347	1.15E-06	1.96E-06
LOC100645667	533.944445	0.50391731	0.08938756	5.63744351	1.73E-08	3.29E-08
LOC100648315	475.479862	0.504104273	0.14095523	3.57634328	0.00034843	0.00049964
LOC100646334	298.644294	0.504259992	0.10757627	4.68746505	2.77E-06	4.58E-06
LOC100642766	421.339975	0.504799388	0.07231366	6.98069222	2.94E-12	7.07E-12
LOC100651445	1319.71298	0.505585097	0.10349273	4.88522352	1.03E-06	1.76E-06
LOC100651900	843.255576	0.506575652	0.06408354	7.9049258	2.68E-15	7.74E-15
LOC100642696	240.930364	0.506748576	0.10951586	4.62717088	3.71E-06	6.08E-06
LOC100647292	1593.75846	0.506893052	0.06383212	7.94103464	2.01E-15	5.84E-15
LOC100643030	253.669296	0.507604041	0.09431622	5.38193799	7.37E-08	1.35E-07
LOC100642398	495.89507	0.507615145	0.08553834	5.93435847	2.95E-09	5.93E-09
LOC100646479	820.884414	0.507619398	0.07425241	6.83640258	8.12E-12	1.90E-11
LOC100644250	624.281159	0.507834871	0.06921647	7.33690841	2.19E-13	5.63E-13
LOC100650666	768.491454	0.508082694	0.078755	6.45143444	1.11E-10	2.40E-10
LOC105667115	1368.54542	0.508135566	0.06246708	8.13445398	4.14E-16	1.25E-15
LOC100644711	958.408601	0.508401299	0.08935458	5.68970628	1.27E-08	2.45E-08
LOC100651927	426.908774	0.508545993	0.09452365	5.38009257	7.44E-08	1.36E-07
LOC100650925	2139.46337	0.509054883	0.08918024	5.70815809	1.14E-08	2.21E-08
LOC100648064	181.933574	0.509249996	0.12546227	4.05898909	4.93E-05	7.54E-05
LOC100646293	2864.63209	0.509587235	0.1056517	4.82327514	1.41E-06	2.39E-06
LOC100643655	166.868764	0.510852011	0.12244042	4.17224986	3.02E-05	4.68E-05
LOC100642649	432.316022	0.51133338	0.09492923	5.386469	7.19E-08	1.32E-07
LOC100651193	340.609414	0.511745045	0.09784497	5.23016177	1.69E-07	3.04E-07
LOC100642743	592.317401	0.511819309	0.17467932	2.93005096	0.00338906	0.00448713
LOC100647001	137.188798	0.513605007	0.20888238	2.45882394	0.0139393	0.01754688
LOC100645981	629.182067	0.513678219	0.06999358	7.33893313	2.15E-13	5.55E-13
LOC100647726	335.80858	0.513708215	0.09300812	5.52326189	3.33E-08	6.23E-08
LOC100646513	740.855415	0.513733093	0.0856836	5.99569904	2.03E-09	4.10E-09
LOC100646307	349.817654	0.514428634	0.09472414	5.4308083	5.61E-08	1.04E-07

LOC100650321	617.939812	0.515098324	0.08110022	6.35138004	2.13E-10	4.56E-10
LOC100649599	252.18362	0.516111231	0.10919444	4.72653418	2.28E-06	3.81E-06
LOC100652107	691.158845	0.517103308	0.09558122	5.41009316	6.30E-08	1.16E-07
LOC100648656	551.344902	0.51814555	0.17260514	3.00191263	0.00268289	0.00359149
LOC100649172	1377.16254	0.518368163	0.0810481	6.39580901	1.60E-10	3.43E-10
LOC100652172	317.520619	0.519051825	0.10782753	4.81372258	1.48E-06	2.50E-06
LOC100650082	550.836478	0.519538539	0.08828834	5.88456604	3.99E-09	7.95E-09
LOC100645304	164.494733	0.519550385	0.22924829	2.26632174	0.02343169	0.02897445
LOC100645693	220.475052	0.520282659	0.12202767	4.263645	2.01E-05	3.16E-05
LOC100644908	324.15717	0.52028917	0.08924655	5.82979613	5.55E-09	1.10E-08
LOC100645511	3397.72198	0.520641845	0.08313962	6.26225883	3.79E-10	7.99E-10
LOC100642837	511.23597	0.520646516	0.07596445	6.85381847	7.19E-12	1.69E-11
LOC100647008	620.049856	0.521586277	0.09014234	5.78625173	7.20E-09	1.41E-08
LOC100650608	454.851904	0.522888235	0.09230396	5.66485172	1.47E-08	2.82E-08
LOC100645375	667.579136	0.52396043	0.0895122	5.85350827	4.81E-09	9.54E-09
LOC100647874	116.108551	0.524801732	0.20575449	2.55062102	0.01075312	0.01367499
LOC100647820	1545.89083	0.526027989	0.09261228	5.67989487	1.35E-08	2.59E-08
LOC100648285	3606.97933	0.526543558	0.0531598	9.90491977	3.96E-23	1.77E-22
LOC105665723	59.7827157	0.526900533	0.17888177	2.945524	0.00322408	0.00428201
LOC100650392	1967.10385	0.527691748	0.10636681	4.96105658	7.01E-07	1.21E-06
LOC100643287	3435.99941	0.527802467	0.07936064	6.65068335	2.92E-11	6.59E-11
LOC100645552	223.105854	0.527929665	0.13425563	3.93227219	8.41E-05	0.00012634
LOC100645587	202.337391	0.528068691	0.12189781	4.33206045	1.48E-05	2.34E-05
LOC100647337	164.277802	0.529293482	0.1242638	4.25943427	2.05E-05	3.21E-05
LOC100650544	793.969746	0.529443987	0.07466237	7.09117608	1.33E-12	3.27E-12
LOC100648620	1743.61157	0.529936045	0.1807603	2.93170596	0.00337106	0.0044657
LOC100647753	469.954334	0.530067437	0.11355669	4.6678664	3.04E-06	5.02E-06
LOC100646058	2496.8083	0.530608344	0.07808389	6.79536247	1.08E-11	2.51E-11
LOC100651010	471.130476	0.531446666	0.10464227	5.07869962	3.80E-07	6.68E-07

LOC105667038	200.489507	0.5318633	0.16113767	3.30067644	0.00096452	0.00133347
LOC100651308	1785.10727	0.532000132	0.06726391	7.90914661	2.59E-15	7.49E-15
LOC105666032	152.324288	0.532008884	0.12485259	4.2610962	2.03E-05	3.19E-05
LOC100649093	172.548347	0.532200171	0.18714042	2.84385481	0.00445714	0.00583732
LOC100643236	651.434042	0.532913607	0.08667109	6.14868924	7.81E-10	1.62E-09
LOC100651955	813.255802	0.533097082	0.10232935	5.20962059	1.89E-07	3.39E-07
LOC100648446	2753.92091	0.534774309	0.05711686	9.36280991	7.76E-21	3.09E-20
LOC100644764	1107.27499	0.535188158	0.08307743	6.44203998	1.18E-10	2.55E-10
LOC100649901	599.52332	0.536928635	0.12203794	4.39968628	1.08E-05	1.73E-05
LOC100651775	968.236724	0.537056798	0.12534869	4.28450256	1.83E-05	2.88E-05
LOC100644807	761.508356	0.537390407	0.07218035	7.4451065	9.69E-14	2.55E-13
LOC100643683	672.926434	0.537993754	0.09363773	5.7454806	9.17E-09	1.78E-08
LOC100649253	60.1857691	0.53804786	0.25048457	2.14802794	0.03171154	0.03872383
LOC100652042	724.450371	0.538664453	0.16885677	3.19006726	0.0014224	0.00194046
LOC100642542	280.825175	0.538737291	0.11258297	4.78524672	1.71E-06	2.87E-06
LOC100652048	500.910727	0.53900947	0.09322592	5.78175514	7.39E-09	1.45E-08
LOC100644482	688.671509	0.539351353	0.08389578	6.42882596	1.29E-10	2.77E-10
LOC100645025	159.886152	0.539752436	0.14214032	3.79732102	0.00014627	0.00021558
LOC100643679	819.26925	0.5398101	0.07501291	7.19622895	6.19E-13	1.56E-12
LOC100651069	1145.24494	0.540004672	0.06196062	8.71528834	2.90E-18	9.95E-18
LOC100645581	450.885825	0.540481323	0.07799721	6.92949582	4.22E-12	1.01E-11
LOC100643700	162.078643	0.542385163	0.11845492	4.57883198	4.68E-06	7.62E-06
LOC100647182	537.715912	0.542554357	0.08823566	6.14892365	7.80E-10	1.62E-09
LOC100652098	332.336624	0.543170658	0.17195124	3.15886437	0.00158385	0.00215442
LOC105666043	190.556464	0.543590367	0.14706583	3.6962384	0.00021882	0.00031848
LOC100643001	145.871206	0.543807216	0.12962868	4.19511493	2.73E-05	4.24E-05
LOC105666697	443.404289	0.544289444	0.09331169	5.83302498	5.44E-09	1.08E-08
LOC100642373	156.25038	0.544304159	0.12810216	4.24898505	2.15E-05	3.36E-05
LOC100649575	401.443389	0.544672533	0.09491953	5.73825547	9.57E-09	1.86E-08

LOC100650060	611.399567	0.544761826	0.07302707	7.45972462	8.67E-14	2.30E-13
LOC100643318	446.490976	0.546204115	0.11259323	4.85112769	1.23E-06	2.09E-06
LOC100646391	299.529538	0.547044385	0.09554968	5.72523511	1.03E-08	2.00E-08
LOC100649683	448.337229	0.547650523	0.07931416	6.90482679	5.03E-12	1.20E-11
LOC105665866	335.121544	0.547665734	0.08910507	6.14629167	7.93E-10	1.64E-09
LOC100648650	723.676403	0.548763016	0.06671152	8.22591132	1.94E-16	6.00E-16
LOC100651314	384.05506	0.549174347	0.08225327	6.6766263	2.45E-11	5.56E-11
LOC100646030	394.003153	0.549306428	0.0919837	5.97178035	2.35E-09	4.74E-09
LOC100649293	487.540185	0.549564207	0.08091406	6.79194931	1.11E-11	2.57E-11
LOC100642483	2114.99452	0.54994348	0.13121833	4.19105687	2.78E-05	4.32E-05
LOC105666265	92.2383931	0.549957372	0.16627093	3.30759792	0.000941	0.00130187
LOC100645462	334.593592	0.550337392	0.11848186	4.64490843	3.40E-06	5.60E-06
LOC100643846	397.762742	0.550445294	0.07270759	7.57067191	3.71E-14	1.00E-13
LOC100645364	368.093484	0.550512866	0.11560154	4.76215873	1.92E-06	3.21E-06
LOC100644639	275.725157	0.550986791	0.10772679	5.11466831	3.14E-07	5.55E-07
LOC100648760	186.117407	0.551091744	0.15704652	3.50909879	0.00044963	0.00063941
LOC100643706	524.848398	0.551685413	0.08958512	6.15822579	7.36E-10	1.53E-09
LOC100646948	1115.04018	0.552105654	0.06390792	8.63907969	5.67E-18	1.91E-17
LOC100644714	510.443594	0.553861814	0.08393066	6.5990401	4.14E-11	9.25E-11
LOC100643452	269.253792	0.554593313	0.11859569	4.67633611	2.92E-06	4.83E-06
LOC100646927	1538.85213	0.555251676	0.07308675	7.59715889	3.03E-14	8.22E-14
LOC100645573	1104.68845	0.555408969	0.06227352	8.91886253	4.71E-19	1.71E-18
LOC100648716	183.126595	0.555551229	0.11468958	4.84395543	1.27E-06	2.16E-06
LOC100648871	462.531611	0.555649294	0.0845441	6.57230113	4.95E-11	1.10E-10
LOC100648932	780.375648	0.555787227	0.12184278	4.56151126	5.08E-06	8.26E-06
LOC100647373	955.822246	0.556323941	0.08680854	6.4086312	1.47E-10	3.16E-10
LOC100647382	1054.96613	0.556932475	0.09584804	5.81057761	6.23E-09	1.23E-08
LOC100651994	315.575218	0.558317833	0.10529075	5.30262964	1.14E-07	2.07E-07
LOC105667148	139.290666	0.55843805	0.17692993	3.15626676	0.00159803	0.00217249

LOC105666306	449.689473	0.559146705	0.09084186	6.15516557	7.50E-10	1.56E-09
LOC100648910	649.083422	0.55916278	0.08537513	6.54948094	5.77E-11	1.27E-10
LOC100651359	386.270811	0.559578896	0.10226089	5.47207119	4.45E-08	8.27E-08
LOC100643158	1899.7679	0.559986284	0.07742338	7.23278028	4.73E-13	1.20E-12
LOC100650423	2226.98987	0.560633685	0.05774486	9.70880723	2.77E-22	1.18E-21
LOC100646048	16152.178	0.560715044	0.09820316	5.70974538	1.13E-08	2.19E-08
LOC100643653	1084.01924	0.561413368	0.06718462	8.35627764	6.47E-17	2.06E-16
LOC100649397	2416.87692	0.562225851	0.07103052	7.91527124	2.47E-15	7.14E-15
LOC100644663	2618.67991	0.563761218	0.05691271	9.90571767	3.93E-23	1.76E-22
LOC100644283	77.0160059	0.564011591	0.18329178	3.07712432	0.00209008	0.00281951
LOC100643758	66.0558396	0.564127962	0.24659852	2.28763723	0.02215866	0.02744881
LOC100644879	397.123599	0.56541442	0.11169056	5.06232956	4.14E-07	7.26E-07
LOC100651522	1024.55267	0.566481516	0.06121974	9.2532498	2.18E-20	8.47E-20
LOC100645615	747.411103	0.566747949	0.08363102	6.77676689	1.23E-11	2.85E-11
LOC100648862	541.012496	0.566877356	0.0777215	7.29370056	3.02E-13	7.72E-13
LOC100643056	969.901553	0.566947833	0.07858822	7.21415829	5.43E-13	1.37E-12
LOC105665728	552.455469	0.56709808	0.12199738	4.64844484	3.34E-06	5.51E-06
LOC105666205	99.3594826	0.567225506	0.27453184	2.06615563	0.03881379	0.04702707
LOC100650850	1558.71981	0.567958125	0.13163438	4.31466404	1.60E-05	2.52E-05
LOC100645793	1043.72664	0.568721038	0.07521696	7.56107428	4.00E-14	1.08E-13
LOC100649998	458.699683	0.568928469	0.0879055	6.47204635	9.67E-11	2.10E-10
LOC100646083	448.064396	0.570846469	0.10745025	5.31265834	1.08E-07	1.96E-07
LOC100649897	221.597254	0.571062706	0.16596227	3.44091893	0.00057974	0.00081485
LOC100643774	314.917599	0.572085407	0.1324599	4.31893269	1.57E-05	2.47E-05
LOC100643079	485.108194	0.573064908	0.09459591	6.05803058	1.38E-09	2.82E-09
LOC100648061	391.924202	0.573382956	0.11872138	4.82965222	1.37E-06	2.32E-06
LOC100645104	3541.46092	0.573823119	0.07133872	8.04364237	8.72E-16	2.59E-15
LOC100643288	368.484266	0.574315689	0.09902013	5.79998922	6.63E-09	1.30E-08
LOC100651525	110.646063	0.574358464	0.14550694	3.94729251	7.90E-05	0.00011906

LOC100643888	711.644463	0.574660359	0.08069406	7.12147001	1.07E-12	2.65E-12
LOC100649925	184.32081	0.574781401	0.17166642	3.34824594	0.00081325	0.00113056
LOC100644922	505.724006	0.575054674	0.12101252	4.75202616	2.01E-06	3.37E-06
LOC100647636	473.467175	0.575113236	0.09921365	5.79671468	6.76E-09	1.33E-08
LOC100644736	162.197793	0.575264079	0.10420413	5.52054989	3.38E-08	6.33E-08
LOC100650830	262.45938	0.575272788	0.1116919	5.15053284	2.60E-07	4.61E-07
LOC100648485	2364.02242	0.575638813	0.05869041	9.80805618	1.04E-22	4.55E-22
LOC100643860	434.935487	0.576043043	0.12871729	4.47525761	7.63E-06	1.23E-05
LOC100642246	199.981546	0.577086705	0.1037963	5.55980062	2.70E-08	5.09E-08
LOC100644479	485.755353	0.577194044	0.1132281	5.0976221	3.44E-07	6.06E-07
LOC100643432	1622.60334	0.577273664	0.07040097	8.19979648	2.41E-16	7.40E-16
LOC100649789	773.053451	0.577357759	0.0776577	7.43464953	1.05E-13	2.76E-13
LOC105666388	1706.94195	0.577565325	0.13091554	4.41173984	1.03E-05	1.64E-05
LOC100649241	530.499438	0.577598957	0.08900034	6.48985088	8.59E-11	1.88E-10
LOC100645212	482.990059	0.577650144	0.13020927	4.43632107	9.15E-06	1.47E-05
LOC100651490	321.359595	0.577923487	0.11242978	5.14030591	2.74E-07	4.86E-07
LOC105666441	99.1566381	0.579340129	0.14384013	4.0276668	5.63E-05	8.59E-05
LOC105665615	523.788257	0.579403652	0.09058001	6.39659491	1.59E-10	3.41E-10
LOC100645004	1152.31369	0.58021088	0.0950647	6.1033261	1.04E-09	2.14E-09
LOC100644514	566.222075	0.581719331	0.08638789	6.73380656	1.65E-11	3.80E-11
LOC100644504	331.505937	0.582006535	0.08390787	6.9362569	4.03E-12	9.62E-12
LOC105665779	24.3885226	0.582025697	0.25744617	2.26076659	0.02377371	0.02937883
LOC100642308	596.047512	0.5823807	0.09280079	6.2756006	3.48E-10	7.35E-10
LOC100649006	181.847867	0.582845373	0.11798622	4.93994447	7.81E-07	1.35E-06
LOC100649537	600.838412	0.58381103	0.0764	7.64150601	2.15E-14	5.88E-14
LOC100646555	246.878576	0.584244071	0.13419113	4.3538204	1.34E-05	2.12E-05
LOC100643206	174.876029	0.584920993	0.11111343	5.26417905	1.41E-07	2.54E-07
LOC100651384	231.703232	0.585753654	0.14466644	4.0489946	5.14E-05	7.85E-05
LOC100645482	442.169356	0.585807533	0.11396178	5.14038583	2.74E-07	4.86E-07

LOC100644496	683.033011	0.585999211	0.10457508	5.60362176	2.10E-08	3.99E-08
LOC100642432	546.233087	0.586271563	0.0900552	6.51013544	7.51E-11	1.65E-10
LOC100647197	3283.79291	0.587126067	0.06270058	9.36396477	7.68E-21	3.06E-20
LOC100642875	424.796103	0.587431426	0.08932801	6.57611642	4.83E-11	1.07E-10
LOC105667144	196.742458	0.587748394	0.14837942	3.96111799	7.46E-05	0.00011254
LOC100650365	1136.20507	0.587930474	0.06148055	9.56286948	1.15E-21	4.76E-21
LOC100643789	326.571557	0.58801902	0.10562392	5.56710076	2.59E-08	4.89E-08
LOC100646383	778.060653	0.588633936	0.07185024	8.19251126	2.56E-16	7.84E-16
LOC100642792	750.38993	0.589831671	0.07188746	8.20493131	2.31E-16	7.10E-16
LOC100648301	94.6385976	0.590249109	0.27109363	2.17728873	0.02945903	0.03607672
LOC100642396	441.118653	0.59026912	0.10907341	5.41166847	6.24E-08	1.15E-07
LOC100651929	1095.48532	0.591571569	0.08408547	7.0353601	1.99E-12	4.84E-12
LOC100649725	433.794784	0.592240621	0.19468528	3.04204106	0.0023498	0.00315812
LOC100647869	599.087159	0.593375914	0.09050124	6.55654991	5.51E-11	1.22E-10
LOC100648876	449.406381	0.593536714	0.10083599	5.88615962	3.95E-09	7.88E-09
LOC105666959	259.668968	0.594803765	0.14270419	4.16808892	3.07E-05	4.76E-05
LOC100648797	278.07382	0.594927443	0.11328119	5.25177589	1.51E-07	2.71E-07
LOC100651252	3246.1705	0.595141052	0.0815465	7.29818003	2.92E-13	7.47E-13
LOC100643958	760.045113	0.595355522	0.08287779	7.183535	6.79E-13	1.70E-12
LOC100649116	578.583614	0.595389096	0.07530422	7.90645095	2.65E-15	7.65E-15
LOC100646796	524.590642	0.59646015	0.09434214	6.32230897	2.58E-10	5.48E-10
LOC100650275	249.867776	0.596534125	0.13334901	4.47348008	7.70E-06	1.24E-05
LOC100649628	6510.04031	0.596862576	0.08653896	6.89703907	5.31E-12	1.26E-11
LOC100647985	231.036332	0.598893262	0.156324	3.8311024	0.00012757	0.00018888
LOC100644986	139.678349	0.599748554	0.14344729	4.18096827	2.90E-05	4.51E-05
LOC100644536	1017.83518	0.600010639	0.05649936	10.6197781	2.41E-26	1.32E-25
LOC100645463	1205.0066	0.600094169	0.08720146	6.88169874	5.91E-12	1.40E-11
LOC100651236	345.55143	0.600825239	0.1022298	5.8772025	4.17E-09	8.30E-09
LOC100642468	2836.76877	0.601102031	0.05928037	10.1399849	3.67E-24	1.75E-23

LOC100648901	630.47823	0.601219126	0.1875429	3.20576845	0.00134702	0.00184226
LOC100649491	549.851838	0.601331586	0.09367034	6.41965848	1.37E-10	2.94E-10
LOC100648486	388.8741	0.601338305	0.08667256	6.93804697	3.98E-12	9.51E-12
LOC100652327	289.837308	0.601416163	0.13055686	4.6065459	4.09E-06	6.70E-06
LOC100649929	2149.4586	0.601593084	0.07340465	8.19557139	2.49E-16	7.65E-16
LOC100642577	228.352112	0.601859067	0.11401764	5.27864878	1.30E-07	2.35E-07
LOC100651767	216.472353	0.602865431	0.16673005	3.61581746	0.0002994	0.00043084
LOC100647152	208.9275	0.6030157	0.12709811	4.74448996	2.09E-06	3.49E-06
LOC100647724	1014.15756	0.603047799	0.11186302	5.39094863	7.01E-08	1.29E-07
LOC100651750	386.398023	0.603199633	0.14668531	4.11220216	3.92E-05	6.03E-05
LOC100645804	620.969398	0.603226141	0.12977634	4.64819822	3.35E-06	5.51E-06
LOC100645360	508.85283	0.60323312	0.08709614	6.92606007	4.33E-12	1.03E-11
LOC100649021	1224.23832	0.603569879	0.06171566	9.77984961	1.37E-22	5.97E-22
LOC100647834	244.800012	0.604125802	0.11684186	5.17045689	2.34E-07	4.15E-07
LOC100647951	968.817108	0.604356567	0.08979381	6.73049282	1.69E-11	3.88E-11
LOC100644161	2367.53442	0.604560331	0.08979706	6.73251796	1.67E-11	3.83E-11
LOC100651752	665.915809	0.604974537	0.07072333	8.55410115	1.19E-17	3.94E-17
LOC100652130	166.3947	0.605082513	0.13833288	4.37410469	1.22E-05	1.94E-05
LOC100651108	755.502498	0.60551415	0.05907582	10.24978	1.19E-24	5.85E-24
LOC100651527	562.861776	0.606834394	0.08646377	7.01836599	2.24E-12	5.44E-12
LOC105665983	2574.43552	0.606847783	0.07931677	7.65093951	2.00E-14	5.48E-14
LOC100642269	60.0978271	0.60728688	0.28760237	2.11155033	0.03472504	0.04224563
LOC100648017	660.609002	0.607310189	0.07662532	7.92571124	2.27E-15	6.58E-15
LOC100643937	470.001565	0.607670092	0.11689904	5.19824694	2.01E-07	3.59E-07
LOC100645157	337.352757	0.609891932	0.12960683	4.70570827	2.53E-06	4.20E-06
LOC100650733	1433.18474	0.609921298	0.08458854	7.21044805	5.58E-13	1.41E-12
LOC100649216	719.917945	0.610633504	0.09992626	6.11084115	9.91E-10	2.04E-09
LOC100647570	204.783253	0.610822054	0.17823588	3.42704325	0.00061019	0.00085593
LOC100647616	707.99536	0.611111352	0.15685308	3.89607482	9.78E-05	0.00014603

LOC105667060	69.9953116	0.611571604	0.17573581	3.48006257	0.0005013	0.00071
LOC100644357	130.508183	0.611618401	0.18349852	3.33309715	0.00085885	0.00119243
LOC100643581	997.116238	0.611704017	0.06247954	9.79046961	1.24E-22	5.39E-22
LOC100648067	184.766238	0.61184399	0.27684814	2.21003469	0.02710276	0.03331614
LOC100647059	660.534464	0.61186319	0.09309627	6.5723709	4.95E-11	1.10E-10
LOC100643110	75.6044297	0.612611828	0.21107888	2.90228859	0.00370447	0.00488952
LOC100652133	482.591551	0.612794281	0.09476913	6.46618017	1.01E-10	2.18E-10
LOC100652019	453.282361	0.614955526	0.09301654	6.611249	3.81E-11	8.53E-11
LOC100644822	356.690176	0.615146834	0.10669459	5.765492	8.14E-09	1.59E-08
LOC100649931	486.998084	0.616069045	0.08036357	7.66602342	1.77E-14	4.88E-14
LOC100647113	1115.78455	0.616301046	0.09969955	6.18158284	6.35E-10	1.32E-09
LOC100648093	639.990306	0.616750565	0.06046121	10.2007651	1.97E-24	9.54E-24
LOC100647243	452.633903	0.616827987	0.11262226	5.47696334	4.33E-08	8.05E-08
LOC100651875	424.773796	0.61686786	0.07706813	8.00418871	1.20E-15	3.54E-15
LOC100648447	900.283506	0.617302675	0.12364676	4.99246936	5.96E-07	1.04E-06
LOC100650260	788.810635	0.617428373	0.08074153	7.64697414	2.06E-14	5.64E-14
LOC105665886	113.450112	0.6176424	0.2246514	2.74933698	0.0059716	0.00773446
LOC100642558	1020.4722	0.617988786	0.0678414	9.10931667	8.29E-20	3.13E-19
LOC100649564	477.527747	0.618530691	0.11129127	5.55776493	2.73E-08	5.15E-08
LOC100642940	1864.86203	0.6188282	0.21059737	2.9384422	0.00329866	0.0043775
LOC100648496	1080.27493	0.619484273	0.13181694	4.69958023	2.61E-06	4.32E-06
LOC100647776	189.068774	0.620046884	0.14370055	4.31485384	1.60E-05	2.52E-05
LOC100644533	872.651441	0.620532565	0.05317126	11.67045	1.80E-31	1.36E-30
LOC100644263	141.106311	0.62125393	0.16254846	3.82196133	0.00013239	0.00019575
LOC100642984	353.203154	0.621557023	0.09734095	6.38536008	1.71E-10	3.67E-10
LOC100642935	629.171649	0.621935962	0.10194844	6.10049518	1.06E-09	2.18E-09
LOC100648118	546.049474	0.621942411	0.1465235	4.24465977	2.19E-05	3.43E-05
LOC100648772	470.830885	0.622570142	0.09474677	6.57088514	5.00E-11	1.11E-10
LOC100646371	195.218631	0.623053717	0.12576809	4.95398886	7.27E-07	1.26E-06

LOC100643591	96.1435318	0.623057307	0.14386603	4.33081607	1.49E-05	2.35E-05
LOC100650920	981.707051	0.623065098	0.07584506	8.2149732	2.12E-16	6.55E-16
LOC100646584	2278.37141	0.623859033	0.09262886	6.7350392	1.64E-11	3.77E-11
LOC105666292	2655.7488	0.624366436	0.0792775	7.87570799	3.39E-15	9.74E-15
LOC100649690	353.986516	0.624806774	0.09915378	6.30139148	2.95E-10	6.26E-10
LOC100644287	14163.6543	0.625085212	0.09638242	6.48546922	8.85E-11	1.93E-10
LOC100646351	581.913604	0.625631688	0.08074251	7.74847968	9.30E-15	2.60E-14
LOC100644286	252.940737	0.625809095	0.10653114	5.87442392	4.24E-09	8.44E-09
LOC100650118	539.881404	0.62598227	0.08806262	7.10837629	1.17E-12	2.90E-12
LOC100649090	1717.83605	0.626005238	0.13155666	4.75844595	1.95E-06	3.27E-06
LOC100650491	513.90351	0.626265508	0.11859126	5.28087398	1.29E-07	2.32E-07
LOC105666988	147.98823	0.627345775	0.16473809	3.80814049	0.00014002	0.00020658
LOC100645646	37.7220981	0.627362234	0.25845913	2.42731694	0.01521096	0.01908142
LOC100643385	503.566508	0.627581811	0.09320442	6.73339141	1.66E-11	3.81E-11
LOC100649030	987.835484	0.627666706	0.17546978	3.57706446	0.00034747	0.00049841
LOC105666795	35.165146	0.628635891	0.28352447	2.21721914	0.02660812	0.03271633
LOC100646684	370.649631	0.629230075	0.08516725	7.38816951	1.49E-13	3.87E-13
LOC100646046	771.973763	0.629502868	0.0767256	8.20460028	2.31E-16	7.12E-16
LOC100644321	1953.46003	0.630457258	0.10897029	5.7855887	7.23E-09	1.42E-08
LOC100644085	302.817244	0.630861094	0.30167974	2.09116164	0.03651358	0.04435544
LOC100643566	680.99234	0.631751826	0.06813569	9.27196582	1.83E-20	7.14E-20
LOC100642332	3223.41727	0.63218579	0.09462966	6.68063047	2.38E-11	5.41E-11
LOC100648732	1865.71862	0.632357473	0.21538097	2.93599509	0.0033248	0.00440919
LOC100651721	51.6300376	0.632369776	0.27094473	2.33394386	0.01959866	0.02438873
LOC100651570	502.219003	0.632422727	0.09179315	6.88965027	5.59E-12	1.33E-11
LOC100649964	300.43157	0.632466308	0.1099431	5.75266959	8.78E-09	1.71E-08
LOC105665748	94.3089763	0.632611666	0.18792176	3.36635673	0.00076168	0.00106068
LOC100651176	266.674181	0.632824798	0.16455246	3.84573273	0.00012019	0.0001783
LOC100644295	992.801464	0.633401231	0.06495524	9.75134968	1.82E-22	7.86E-22

LOC100648442	1232.85631	0.634085163	0.0620865	10.2129313	1.74E-24	8.45E-24
LOC100647098	4129.17555	0.634253058	0.07125498	8.90117456	5.53E-19	1.99E-18
LOC100643955	1127.54551	0.634260691	0.08278538	7.66150634	1.84E-14	5.05E-14
LOC100651126	493.879804	0.634324474	0.08293773	7.64820181	2.04E-14	5.59E-14
LOC100647078	345.232875	0.635924676	0.09842263	6.46116348	1.04E-10	2.26E-10
LOC100643890	150.616126	0.636163036	0.11751892	5.41328172	6.19E-08	1.14E-07
LOC100651988	181.372256	0.636277576	0.18733933	3.39639086	0.00068281	0.00095451
LOC100643605	712.328514	0.63635557	0.07764497	8.19570913	2.49E-16	7.64E-16
LOC100649484	2375.12678	0.637162711	0.10319495	6.17435935	6.64E-10	1.38E-09
LOC100648163	409.531751	0.63729378	0.16654181	3.82662939	0.00012991	0.00019225
LOC100644979	1804.26555	0.638402367	0.1025165	6.22731351	4.75E-10	9.94E-10
LOC100647349	48.9466874	0.638430035	0.19269149	3.31322389	0.00092227	0.0012774
LOC100651181	516.296706	0.638430822	0.12033345	5.30551424	1.12E-07	2.04E-07
LOC100645572	422.939328	0.638763733	0.09780894	6.53072986	6.54E-11	1.44E-10
LOC100644029	796.970424	0.638809207	0.08998407	7.09913675	1.26E-12	3.09E-12
LOC100649065	95.0552772	0.639240376	0.16224976	3.93985406	8.15E-05	0.00012264
LOC100650523	1599.07972	0.639352058	0.08942905	7.14926612	8.72E-13	2.17E-12
LOC100648664	891.844563	0.639711453	0.06411705	9.97724466	1.92E-23	8.76E-23
LOC100643240	707.120165	0.639799525	0.08462283	7.56060172	4.01E-14	1.08E-13
LOC100652010	128.394042	0.639859353	0.2566962	2.49267172	0.0126786	0.01600931
LOC100644887	1193.68644	0.639978241	0.07010723	9.12856225	6.94E-20	2.64E-19
LOC100644062	829.661096	0.640397812	0.09800398	6.53440641	6.39E-11	1.41E-10
LOC100647538	1248.19582	0.640573688	0.06875287	9.31704701	1.20E-20	4.73E-20
LOC100642975	415.476942	0.640776008	0.09064119	7.06936927	1.56E-12	3.81E-12
LOC100644278	614.343462	0.641624927	0.13836843	4.63707608	3.53E-06	5.81E-06
LOC100649434	3160.33247	0.642518668	0.09826069	6.53891904	6.20E-11	1.37E-10
LOC100643663	1205.92803	0.642815508	0.0759613	8.46240826	2.62E-17	8.49E-17
LOC100647461	684.99409	0.642918398	0.09300255	6.91291171	4.75E-12	1.13E-11
LOC100651772	874.347958	0.643266294	0.08790971	7.31735194	2.53E-13	6.49E-13

LOC100646894	1254.5552	0.643284797	0.07598577	8.46585916	2.54E-17	8.26E-17
LOC100646160	376.492533	0.644446967	0.13872309	4.64556387	3.39E-06	5.58E-06
LOC105665659	429.637608	0.646278826	0.10719491	6.02900683	1.65E-09	3.36E-09
LOC105666314	697.439235	0.64630879	0.10074076	6.41556426	1.40E-10	3.02E-10
LOC105666512	144.009564	0.646797127	0.16760398	3.85907985	0.00011381	0.00016923
LOC100651852	316.221571	0.647632257	0.12851726	5.03926281	4.67E-07	8.18E-07
LOC100647866	103.709461	0.648125646	0.19906206	3.25589749	0.00113035	0.00155482
LOC100646675	2867.38206	0.648247798	0.08137868	7.96581819	1.64E-15	4.80E-15
LOC100649994	2235.00816	0.648386511	0.06182804	10.4869324	9.92E-26	5.24E-25
LOC100646586	622.933034	0.648441169	0.08694846	7.45776489	8.80E-14	2.33E-13
LOC100648687	641.386735	0.649471344	0.09549445	6.801142	1.04E-11	2.42E-11
LOC100644385	251.403128	0.649675739	0.10864786	5.97964589	2.24E-09	4.52E-09
LOC100647977	402.923273	0.65011577	0.19904505	3.26617395	0.00109011	0.00150138
LOC100649159	326.326523	0.650946503	0.13738302	4.73818752	2.16E-06	3.60E-06
LOC100647280	409.123948	0.652025569	0.09300499	7.01065147	2.37E-12	5.74E-12
LOC100648596	440.479767	0.652507513	0.09278674	7.03233587	2.03E-12	4.94E-12
LOC100649448	515.850259	0.653345696	0.10882902	6.00341435	1.93E-09	3.92E-09
LOC100647913	1793.77368	0.654151114	0.0669004	9.77798517	1.40E-22	6.07E-22
LOC100645368	351.249808	0.654202484	0.09444683	6.92667456	4.31E-12	1.03E-11
LOC100643378	703.452807	0.654780444	0.09119234	7.18021309	6.96E-13	1.75E-12
LOC100651958	1199.51729	0.654941751	0.07357057	8.90222459	5.47E-19	1.97E-18
LOC100644405	459.974001	0.65505099	0.10858474	6.03262498	1.61E-09	3.29E-09
LOC100648519	1440.03876	0.65600918	0.0727716	9.01463159	1.98E-19	7.30E-19
LOC100650735	782.998141	0.656143538	0.08385518	7.82472235	5.09E-15	1.44E-14
LOC100644656	419.921649	0.656163099	0.10940827	5.99738122	2.01E-09	4.06E-09
LOC100651276	429.235841	0.656241681	0.08441221	7.77425094	7.59E-15	2.13E-14
LOC105666183	100.398741	0.656410194	0.20564079	3.19202331	0.0014128	0.0019279
LOC100650216	48.9880833	0.656436903	0.2732038	2.40273705	0.01627288	0.02034838
LOC100646573	112.132961	0.656649529	0.19230739	3.41458295	0.0006388	0.00089503

LOC100649190	779.837408	0.657305829	0.1712663	3.83791687	0.00012408	0.00018391
LOC100645946	126.065261	0.657989196	0.24690325	2.66496775	0.00769957	0.00990234
LOC100646244	608.625763	0.658039768	0.09406833	6.99533818	2.65E-12	6.38E-12
LOC100643895	1173.80537	0.658129991	0.0951181	6.9190827	4.55E-12	1.08E-11
LOC100651592	564.722251	0.658378943	0.08762301	7.51376749	5.74E-14	1.54E-13
LOC100645825	913.575558	0.65846446	0.0831227	7.92159626	2.34E-15	6.80E-15
LOC100649061	458.423885	0.659172149	0.07224373	9.1242814	7.22E-20	2.74E-19
LOC100643904	433.432936	0.660579276	0.08755394	7.54482614	4.53E-14	1.22E-13
LOC100647242	606.385437	0.660645195	0.11447619	5.7710271	7.88E-09	1.54E-08
LOC100645051	290.417533	0.661105488	0.15197954	4.34996385	1.36E-05	2.16E-05
LOC100650375	843.943997	0.661408091	0.07135714	9.26898261	1.88E-20	7.33E-20
LOC100651046	192.355121	0.661508055	0.2024756	3.26710007	0.00108655	0.00149668
LOC100646859	2850.68062	0.661671258	0.05390637	12.2744539	1.24E-34	1.14E-33
LOC100646357	655.009539	0.661951431	0.06587355	10.0488202	9.30E-24	4.33E-23
LOC100648307	228.640717	0.661995024	0.11843435	5.58955233	2.28E-08	4.31E-08
LOC100651202	522.681277	0.662368032	0.08443542	7.84467045	4.34E-15	1.24E-14
LOC100645454	208.018071	0.663327561	0.12729161	5.2110861	1.88E-07	3.36E-07
LOC100646568	254.77757	0.663488179	0.16524885	4.01508504	5.94E-05	9.04E-05
LOC100646219	761.587979	0.66391225	0.06427662	10.3289848	5.21E-25	2.63E-24
LOC105667022	206.564761	0.664856516	0.11376775	5.84398041	5.10E-09	1.01E-08
LOC100650841	465.528996	0.665190814	0.08917752	7.45917569	8.71E-14	2.31E-13
LOC100645975	614.03793	0.665838336	0.08053318	8.26787597	1.36E-16	4.26E-16
LOC100647345	2611.20738	0.666269335	0.05543611	12.0186886	2.83E-33	2.36E-32
LOC100650795	905.020066	0.668052643	0.09626231	6.93991902	3.92E-12	9.38E-12
LOC100643197	577.033151	0.668253895	0.101777	6.5658638	5.17E-11	1.15E-10
LOC100645185	532.117438	0.668327083	0.08909563	7.50123343	6.32E-14	1.69E-13
LOC100644858	594.8236	0.668978373	0.08825874	7.57974094	3.46E-14	9.37E-14
LOC100643792	669.910956	0.670023517	0.12898787	5.1944693	2.05E-07	3.67E-07
LOC100644451	511.297784	0.670291302	0.09882305	6.78274252	1.18E-11	2.74E-11

LOC100642900	327.15853	0.670497509	0.08427319	7.95623732	1.77E-15	5.17E-15
LOC100647313	103.69335	0.670984746	0.14901301	4.50286007	6.70E-06	1.08E-05
LOC100645535	306.128239	0.671019149	0.10774217	6.22800847	4.72E-10	9.90E-10
LOC100644785	321.14756	0.671059756	0.32353566	2.07414461	0.03806588	0.04617805
LOC100650584	621.164163	0.671091876	0.13012287	5.15737068	2.50E-07	4.45E-07
LOC100646631	1742.37693	0.671404711	0.04904162	13.6905095	1.16E-42	1.85E-41
LOC100650776	358.079006	0.671658026	0.09066643	7.40801247	1.28E-13	3.35E-13
LOC105666436	1009.93031	0.672531798	0.09398679	7.15559919	8.33E-13	2.08E-12
LOC100652069	291.410585	0.672671139	0.09082976	7.40584542	1.30E-13	3.40E-13
LOC100647418	633.629267	0.673012092	0.11742414	5.73146279	9.96E-09	1.93E-08
LOC100650967	26951.9783	0.674470134	0.09956149	6.77440803	1.25E-11	2.89E-11
LOC100646183	984.92457	0.675051676	0.19856137	3.39971311	0.00067457	0.00094352
LOC100649416	250.456406	0.67617281	0.10160518	6.65490512	2.83E-11	6.41E-11
LOC100647656	212.678759	0.676241079	0.16964524	3.98620713	6.71E-05	0.00010158
LOC100648763	644.345479	0.676478012	0.09849906	6.86786286	6.52E-12	1.54E-11
LOC100643384	2039.44806	0.676608064	0.08916564	7.588215	3.24E-14	8.79E-14
LOC100644853	1015.15989	0.677439831	0.14991943	4.51869273	6.22E-06	1.01E-05
LOC100642486	626.00745	0.677949544	0.08161329	8.30685182	9.83E-17	3.09E-16
LOC100648679	162.851581	0.678040291	0.1423937	4.76172959	1.92E-06	3.22E-06
LOC100648184	104.047369	0.678787884	0.21649884	3.13529572	0.00171681	0.00232783
LOC100651602	625.822136	0.679783343	0.06572434	10.3429474	4.50E-25	2.28E-24
LOC100647535	477.59495	0.679952851	0.10108599	6.72647965	1.74E-11	3.98E-11
LOC100643427	786.17579	0.680104615	0.10815975	6.28796401	3.22E-10	6.80E-10
LOC100647379	823.774797	0.680275293	0.07183871	9.46948059	2.81E-21	1.15E-20
LOC100645232	398.435646	0.680452355	0.09483258	7.17530178	7.21E-13	1.81E-12
LOC100647861	1990.59936	0.680743054	0.08339439	8.16293549	3.27E-16	9.95E-16
LOC100648948	261.11864	0.681324238	0.09918703	6.86908596	6.46E-12	1.53E-11
LOC100645077	130.496252	0.681415669	0.16735815	4.07160124	4.67E-05	7.15E-05
LOC100645957	555.610735	0.681928371	0.09739112	7.00195647	2.52E-12	6.10E-12

LOC100642756	1225.23401	0.681969682	0.0678039	10.0579714	8.47E-24	3.95E-23
LOC100649855	1572.37475	0.682117712	0.15808345	4.31492166	1.60E-05	2.52E-05
LOC100649264	146.223733	0.68260874	0.17753043	3.84502393	0.00012054	0.00017879
LOC100642435	182.353458	0.683598034	0.11027227	6.19918343	5.68E-10	1.18E-09
LOC100644364	538.531059	0.683646767	0.09473839	7.2161539	5.35E-13	1.35E-12
LOC100643936	990.414291	0.683852416	0.08149982	8.39084599	4.83E-17	1.55E-16
LOC100644724	505.317408	0.683930116	0.09367717	7.30092628	2.86E-13	7.33E-13
LOC100647095	242.899604	0.684706818	0.13070731	5.23847375	1.62E-07	2.91E-07
LOC105666248	805.323383	0.684722963	0.07386391	9.27006131	1.86E-20	7.26E-20
LOC100648243	343.164288	0.685037632	0.10140433	6.75550667	1.42E-11	3.29E-11
LOC100642304	264.460638	0.685055024	0.11010897	6.22160932	4.92E-10	1.03E-09
LOC100642383	132.040722	0.685074808	0.21449298	3.19392647	0.00140352	0.00191577
LOC100652229	429.06325	0.685697763	0.09310623	7.36468163	1.78E-13	4.60E-13
LOC100648657	873.287525	0.687521039	0.09421203	7.29759301	2.93E-13	7.50E-13
LOC100651292	2444.1842	0.688158372	0.22891462	3.0061792	0.00264553	0.00354245
LOC100643532	3271.6149	0.688776338	0.09318794	7.39126046	1.45E-13	3.79E-13
LOC100648684	566.324901	0.68931387	0.11415208	6.03855711	1.55E-09	3.17E-09
LOC100643053	105.77898	0.690997725	0.24264018	2.84782899	0.00440186	0.00577187
LOC100646276	86.9323475	0.691306461	0.15817517	4.37051188	1.24E-05	1.97E-05
LOC100651678	598.996047	0.691746511	0.07156362	9.66617554	4.20E-22	1.78E-21
LOC105665913	162.50693	0.692780429	0.13855554	5.00001982	5.73E-07	9.98E-07
LOC100646258	565.861088	0.692890564	0.08060156	8.59649122	8.22E-18	2.75E-17
LOC100650419	803.5118	0.693610367	0.05926714	11.7031178	1.23E-31	9.30E-31
LOC100645742	455.833523	0.694036397	0.08995893	7.71503615	1.21E-14	3.35E-14
LOC100648963	408.381745	0.69479433	0.09804221	7.08668582	1.37E-12	3.37E-12
LOC100647491	419.526471	0.694848837	0.08342731	8.3287934	8.17E-17	2.59E-16
LOC100644888	469.146503	0.695202569	0.08459463	8.21804575	2.07E-16	6.39E-16
LOC100642876	2460.01735	0.695553446	0.06647436	10.4634851	1.27E-25	6.65E-25
LOC100650540	811.036432	0.698663079	0.08089242	8.63694094	5.77E-18	1.95E-17

LOC100645599	328.036149	0.698931911	0.09163009	7.62775518	2.39E-14	6.52E-14
LOC100645630	956.090463	0.699452032	0.14694978	4.75980331	1.94E-06	3.25E-06
LOC100651257	474.056096	0.700201743	0.09494875	7.37452331	1.65E-13	4.28E-13
LOC100645919	482.891897	0.700464483	0.08222585	8.5187871	1.61E-17	5.31E-17
LOC100644423	370.359675	0.701318482	0.21004598	3.33888075	0.00084117	0.00116821
LOC100648191	31.7725001	0.702085391	0.27539613	2.54936549	0.01079191	0.01372255
LOC100643393	162.676862	0.702191102	0.11905693	5.89794392	3.68E-09	7.34E-09
LOC100647424	508.379655	0.702680978	0.08559364	8.20950021	2.22E-16	6.85E-16
LOC100646548	388.008881	0.703933817	0.12037223	5.84797522	4.98E-09	9.86E-09
LOC100651702	402.995768	0.704173985	0.11241031	6.26431853	3.74E-10	7.89E-10
LOC100645220	105.610519	0.704447547	0.15365062	4.58473606	4.55E-06	7.41E-06
LOC100646991	1220.11121	0.705113444	0.09302933	7.5794744	3.47E-14	9.38E-14
LOC100642345	534.847026	0.707136601	0.11647469	6.07116094	1.27E-09	2.60E-09
LOC100650687	498.6203	0.707278476	0.08770604	8.06419376	7.37E-16	2.20E-15
LOC100645735	464.18565	0.70790924	0.07784433	9.09390931	9.55E-20	3.60E-19
LOC100647727	638.973289	0.708038403	0.23933173	2.95839759	0.00309243	0.00411553
LOC100643299	502.012976	0.708200906	0.09159238	7.73209455	1.06E-14	2.95E-14
LOC100643122	579.357616	0.70909446	0.10923387	6.49152539	8.50E-11	1.86E-10
LOC100648559	92.9979572	0.709506594	0.21363043	3.32118696	0.00089635	0.00124291
LOC100643719	1291.87778	0.709606056	0.08004236	8.8653811	7.62E-19	2.72E-18
LOC100646526	279.315874	0.709812337	0.1006898	7.04949617	1.80E-12	4.38E-12
LOC100645342	186.948553	0.709812546	0.14118885	5.02739808	4.97E-07	8.68E-07
LOC100646906	2000.66562	0.709947129	0.06923314	10.2544402	1.13E-24	5.58E-24
LOC100650407	1174.23724	0.711209959	0.0630912	11.2727289	1.79E-29	1.19E-28
LOC100645794	550.302932	0.711369504	0.09870608	7.2069469	5.72E-13	1.44E-12
LOC100647710	936.586174	0.711490917	0.08738543	8.14198573	3.89E-16	1.18E-15
LOC100646770	155.390295	0.711582881	0.14002208	5.08193321	3.74E-07	6.57E-07
LOC105666490	75.0533807	0.711771522	0.21470018	3.31518829	0.00091581	0.00126882
LOC100648908	525.836396	0.712215185	0.08356818	8.52256453	1.56E-17	5.14E-17

LOC100649451	878.988001	0.712222755	0.06748498	10.5537973	4.88E-26	2.62E-25
LOC105666581	550.665589	0.713115828	0.17365021	4.10662243	4.01E-05	6.17E-05
LOC100651488	1536.05329	0.713932609	0.07628552	9.35869106	8.07E-21	3.21E-20
LOC100646146	347.501413	0.714697211	0.1078191	6.62866988	3.39E-11	7.60E-11
LOC105666092	993.821054	0.714699051	0.07585928	9.42137982	4.45E-21	1.80E-20
LOC100648513	580.479008	0.715208556	0.11112049	6.43633357	1.22E-10	2.64E-10
LOC100647195	1148.04503	0.716502485	0.09054758	7.91299449	2.51E-15	7.27E-15
LOC100651141	390.295277	0.71691026	0.10452536	6.85872089	6.95E-12	1.64E-11
LOC100650121	810.997798	0.717295563	0.08241639	8.70331156	3.22E-18	1.10E-17
LOC100645758	220.322632	0.717657157	0.10602337	6.76885827	1.30E-11	3.00E-11
LOC100645116	229.286607	0.71822958	0.12710178	5.65082219	1.60E-08	3.05E-08
LOC100642422	282.199657	0.7190317	0.09837552	7.30905109	2.69E-13	6.90E-13
LOC100645110	746.250136	0.719374248	0.0781771	9.20185431	3.52E-20	1.35E-19
LOC100648722	554.771255	0.719945105	0.11112243	6.47884569	9.24E-11	2.01E-10
LOC100649109	419.739099	0.720740024	0.09563745	7.53616932	4.84E-14	1.30E-13
LOC100651864	203.612754	0.720987513	0.10753743	6.70452631	2.02E-11	4.61E-11
LOC100642716	1149.39988	0.720989688	0.05983279	12.0500766	1.94E-33	1.63E-32
LOC100643757	275.561552	0.721203021	0.11836499	6.09304355	1.11E-09	2.28E-09
LOC100650706	703.75307	0.72199725	0.08248299	8.75328691	2.07E-18	7.19E-18
LOC100651286	290.017304	0.722177627	0.12787834	5.64738035	1.63E-08	3.11E-08
LOC100649748	577.594552	0.722293586	0.07735839	9.33697775	9.91E-21	3.93E-20
LOC100649909	1383.52287	0.722700059	0.06617692	10.9207264	9.18E-28	5.50E-27
LOC100646159	299.924402	0.722811103	0.11687409	6.18452831	6.23E-10	1.30E-09
LOC100649505	291.307854	0.723286956	0.11291282	6.40571156	1.50E-10	3.22E-10
LOC100646839	1133.65634	0.724242	0.08053782	8.99256988	2.42E-19	8.91E-19
LOC100647864	866.36454	0.724638835	0.07470388	9.70014964	3.01E-22	1.29E-21
LOC100644862	968.93002	0.725210251	0.12695061	5.71253855	1.11E-08	2.15E-08
LOC100651983	1150.69636	0.726410984	0.07763795	9.35639104	8.25E-21	3.28E-20
LOC100647606	626.910857	0.726586174	0.10222729	7.10755592	1.18E-12	2.92E-12

LOC100645255	455.355041	0.726610102	0.089628	8.10695471	5.19E-16	1.56E-15
LOC100645286	993.254455	0.726822851	0.06117369	11.881298	1.48E-32	1.17E-31
LOC100651717	520.649559	0.727681416	0.07985835	9.11215164	8.08E-20	3.05E-19
LOC100643688	320.326774	0.728096534	0.09520367	7.64777807	2.04E-14	5.61E-14
LOC100650259	384.252064	0.728669328	0.09076976	8.02766587	9.93E-16	2.94E-15
LOC100642315	702.328034	0.72870042	0.09021848	8.07706346	6.63E-16	1.99E-15
LOC100642638	48.0427273	0.729360777	0.34793539	2.09625349	0.03605971	0.04381492
LOC100643449	314.687033	0.729615937	0.11080419	6.58473238	4.56E-11	1.02E-10
LOC100650907	592.790313	0.729797609	0.08867179	8.23032412	1.87E-16	5.78E-16
LOC100648761	268.0667	0.730333021	0.13535091	5.3958487	6.82E-08	1.25E-07
LOC100651275	342.029743	0.730575806	0.13117067	5.56965807	2.55E-08	4.82E-08
LOC100645102	1134.93453	0.730806302	0.09013375	8.10802049	5.15E-16	1.55E-15
LOC100647206	715.055971	0.731152599	0.08403472	8.70060091	3.30E-18	1.13E-17
LOC100646031	271.420653	0.73192588	0.11464693	6.3841732	1.72E-10	3.69E-10
LOC100649558	1096.86075	0.732760682	0.07987946	9.17333016	4.59E-20	1.76E-19
LOC105666014	694.862805	0.733634287	0.09845555	7.45142641	9.23E-14	2.44E-13
LOC100645882	714.147087	0.73540316	0.09073913	8.10458647	5.29E-16	1.59E-15
LOC100643135	1422.0841	0.73541531	0.11520711	6.38341969	1.73E-10	3.71E-10
LOC100645986	836.246027	0.735993728	0.14068362	5.23155223	1.68E-07	3.02E-07
LOC105666647	50.4422712	0.736422683	0.20568138	3.58040524	0.00034306	0.00049229
LOC100646238	513.064844	0.737514736	0.07685968	9.59560024	8.34E-22	3.49E-21
LOC100648178	1000.2099	0.737703602	0.10873156	6.78463188	1.16E-11	2.70E-11
LOC100645251	777.320117	0.738602756	0.08678654	8.51056775	1.73E-17	5.68E-17
LOC100646826	101.154483	0.738748513	0.15361334	4.80914285	1.52E-06	2.56E-06
LOC100642622	1295.03359	0.739823543	0.07592609	9.74399644	1.96E-22	8.44E-22
LOC100642555	1177.20397	0.739862073	0.14593116	5.06993894	3.98E-07	6.99E-07
LOC100645732	1158.77864	0.739979918	0.09985057	7.41087351	1.25E-13	3.28E-13
LOC100643265	26.0183938	0.74014834	0.2728697	2.71246068	0.00667857	0.00862208
LOC100650521	2857.96384	0.740447618	0.13158066	5.62732847	1.83E-08	3.49E-08

LOC100647831	567.317753	0.740447901	0.0982518	7.53622767	4.84E-14	1.30E-13
LOC100643146	1150.77277	0.741233993	0.16878118	4.39168635	1.12E-05	1.79E-05
LOC100643666	300.829445	0.741273634	0.15626807	4.74360261	2.10E-06	3.50E-06
LOC100649091	134.288806	0.741429915	0.15025138	4.9345965	8.03E-07	1.38E-06
LOC100651340	677.763851	0.742068924	0.09987437	7.43002357	1.09E-13	2.85E-13
LOC100647300	208.08847	0.742341669	0.12147306	6.11116296	9.89E-10	2.04E-09
LOC100646460	335.882188	0.742558924	0.11831305	6.2762218	3.47E-10	7.33E-10
LOC100648362	2267.78339	0.742959948	0.06959373	10.6756731	1.32E-26	7.37E-26
LOC100642870	772.351105	0.744848085	0.09576807	7.77762425	7.39E-15	2.07E-14
LOC100650431	595.250358	0.745403392	0.08627488	8.63986549	5.63E-18	1.90E-17
LOC100644254	1659.17504	0.74560163	0.07774753	9.59003618	8.81E-22	3.67E-21
LOC100648030	1483.91176	0.746013351	0.07056734	10.5716524	4.03E-26	2.18E-25
LOC100643302	715.066141	0.746154001	0.07482807	9.97157862	2.03E-23	9.26E-23
LOC100649539	332.38922	0.746394805	0.13438864	5.55400205	2.79E-08	5.26E-08
LOC100647504	912.002886	0.746604994	0.11680418	6.39193716	1.64E-10	3.51E-10
LOC100651532	521.039668	0.746723463	0.09501484	7.85901907	3.87E-15	1.11E-14
LOC100648633	482.109473	0.747701388	0.09518377	7.85534515	3.99E-15	1.14E-14
LOC100646944	648.67398	0.748014842	0.08230873	9.08791625	1.01E-19	3.79E-19
LOC100642366	1026.82645	0.748305204	0.07762967	9.63942241	5.45E-22	2.30E-21
LOC100649323	437.315139	0.748743125	0.09618507	7.78440105	7.00E-15	1.97E-14
LOC100650774	385.599092	0.749087757	0.08886103	8.4298796	3.46E-17	1.11E-16
LOC100649777	1034.71183	0.750338853	0.07446836	10.0759412	7.06E-24	3.31E-23
LOC100647720	281.127977	0.750811457	0.10581916	7.09523167	1.29E-12	3.18E-12
LOC100649492	915.8721	0.751471599	0.10640142	7.06260886	1.63E-12	4.00E-12
LOC100646871	775.495832	0.75148293	0.0873249	8.60559738	7.59E-18	2.55E-17
LOC100644686	1411.14396	0.751684746	0.10577638	7.10635741	1.19E-12	2.94E-12
LOC100650062	187.038515	0.751919819	0.15068949	4.98986235	6.04E-07	1.05E-06
LOC100645152	103.543131	0.752190659	0.19607343	3.8362703	0.00012492	0.00018508
LOC100646868	981.756126	0.753558831	0.09423059	7.99696631	1.28E-15	3.75E-15

LOC100645870	453.622084	0.753774105	0.09053761	8.32553536	8.39E-17	2.66E-16
LOC100651675	802.614143	0.754139703	0.13982953	5.39327943	6.92E-08	1.27E-07
LOC100647700	381.073142	0.754888988	0.08528318	8.85155796	8.63E-19	3.07E-18
LOC100651909	568.60831	0.754998904	0.11340563	6.65750797	2.79E-11	6.30E-11
LOC100642440	575.246311	0.755262211	0.07708224	9.79813464	1.15E-22	5.01E-22
LOC100649363	137.14421	0.755709929	0.14218527	5.31496655	1.07E-07	1.94E-07
LOC100647586	148.646393	0.757104346	0.10975367	6.89821437	5.27E-12	1.25E-11
LOC100652063	67.1121381	0.75728951	0.31439213	2.40874193	0.01600761	0.02002946
LOC100646300	772.947306	0.757352918	0.06503054	11.6461123	2.40E-31	1.79E-30
LOC100651992	1198.5939	0.757788841	0.06990035	10.8409877	2.20E-27	1.30E-26
LOC100648440	412.576439	0.758215736	0.08684647	8.73053006	2.53E-18	8.72E-18
LOC100648058	551.469681	0.75839459	0.09747846	7.78012502	7.25E-15	2.04E-14
LOC100647173	492.117886	0.760232213	0.09061347	8.38983637	4.87E-17	1.56E-16
LOC100642820	959.633319	0.760297452	0.06388454	11.9011181	1.17E-32	9.32E-32
LOC100647479	1097.46154	0.761091562	0.07085268	10.7418877	6.47E-27	3.69E-26
LOC100650417	1091.10881	0.761836528	0.08014247	9.50602743	1.98E-21	8.12E-21
LOC100651211	2206.66287	0.762538153	0.05914283	12.8931639	4.92E-38	5.65E-37
LOC100652277	1349.15129	0.762784204	0.05984184	12.7466711	3.25E-37	3.53E-36
LOC100647963	574.80337	0.763055433	0.10238602	7.45273081	9.14E-14	2.42E-13
LOC100645060	2250.63893	0.76367166	0.07663638	9.96487165	2.17E-23	9.89E-23
LOC100650097	233.244624	0.763712712	0.16255207	4.698265	2.62E-06	4.35E-06
LOC100643978	462.634351	0.764782465	0.0915889	8.35016512	6.82E-17	2.17E-16
LOC100643849	172.202396	0.764913851	0.14461924	5.28915684	1.23E-07	2.22E-07
LOC105665997	318.321241	0.764956536	0.09449819	8.09493363	5.73E-16	1.72E-15
LOC100645288	273.038808	0.766338178	0.09618094	7.96767175	1.62E-15	4.73E-15
LOC100650253	574.07635	0.767037939	0.08680909	8.83591719	9.93E-19	3.51E-18
LOC100644980	536.104721	0.767135161	0.06864583	11.1752631	5.39E-29	3.50E-28
LOC100642507	223.792878	0.767396603	0.18414912	4.16725648	3.08E-05	4.78E-05
LOC100651562	378.039424	0.768080875	0.15460593	4.96799106	6.77E-07	1.17E-06

LOC100644813	59.4513443	0.768170995	0.24044224	3.19482551	0.00139915	0.00191056
LOC100650627	985.610458	0.768956722	0.07124971	10.7924187	3.74E-27	2.17E-26
LOC100651104	139.086545	0.76976217	0.14240241	5.40554178	6.46E-08	1.19E-07
LOC100652232	599.635729	0.770134456	0.09327493	8.25660708	1.50E-16	4.67E-16
LOC100650212	739.340141	0.770503704	0.07560399	10.1913106	2.17E-24	1.05E-23
LOC100646930	204.106595	0.770904355	0.12984831	5.93696104	2.90E-09	5.84E-09
LOC100642481	188.986109	0.771501201	0.13538026	5.69877181	1.21E-08	2.33E-08
LOC100651351	1677.49607	0.771848455	0.08846804	8.72460176	2.67E-18	9.18E-18
LOC100650703	348.59799	0.772501684	0.10806908	7.14822117	8.79E-13	2.19E-12
LOC100649967	263.202319	0.774111831	0.10355377	7.47545809	7.69E-14	2.04E-13
LOC100649242	1804.27676	0.774978787	0.07317037	10.5914295	3.27E-26	1.78E-25
LOC100649199	489.195403	0.775065458	0.09469608	8.18476777	2.73E-16	8.33E-16
LOC100645390	1284.02207	0.776918262	0.05642559	13.7688999	3.92E-43	6.50E-42
LOC100651230	418.699609	0.778033078	0.0906074	8.58685977	8.94E-18	2.98E-17
LOC100651273	843.007226	0.778063818	0.12646551	6.15237952	7.63E-10	1.58E-09
LOC100650847	308.274636	0.778337961	0.11121986	6.99819202	2.59E-12	6.26E-12
LOC100649449	661.3741	0.778719455	0.10506095	7.41207306	1.24E-13	3.26E-13
LOC100650865	798.629292	0.779045944	0.12574917	6.19523704	5.82E-10	1.21E-09
LOC100648201	851.377013	0.779782651	0.06921925	11.2654015	1.94E-29	1.29E-28
LOC100648484	224.066111	0.780096905	0.12573545	6.20427156	5.50E-10	1.15E-09
LOC100651042	1763.17066	0.780100828	0.0761478	10.2445621	1.25E-24	6.16E-24
LOC100651154	2195.28148	0.780267353	0.11605654	6.72316579	1.78E-11	4.07E-11
LOC100645708	9521.89048	0.780615059	0.10385188	7.51661942	5.62E-14	1.50E-13
LOC100650358	395.092493	0.780759255	0.15082591	5.17655923	2.26E-07	4.03E-07
LOC100645301	7272.72228	0.781071059	0.1430021	5.46195527	4.71E-08	8.73E-08
LOC100649205	548.008469	0.781128636	0.10183474	7.67055149	1.71E-14	4.72E-14
LOC100645477	1294.64539	0.781746799	0.09556925	8.17989898	2.84E-16	8.67E-16
LOC100649320	4757.29014	0.781869212	0.08248062	9.47942932	2.56E-21	1.05E-20
LOC100642300	2395.73429	0.78267963	0.07519586	10.408547	2.27E-25	1.17E-24

LOC100648336	1380.19632	0.782877253	0.06066479	12.9049703	4.22E-38	4.88E-37
LOC100650050	1973.99531	0.784016817	0.08112565	9.66422883	4.28E-22	1.82E-21
LOC100650480	464.747157	0.784369898	0.11547933	6.79229685	1.10E-11	2.56E-11
LOC100645202	48.6643591	0.785075532	0.26517259	2.96062102	0.00307019	0.00408761
LOC100647580	20.0692365	0.785746994	0.32282237	2.43399174	0.01493334	0.01874997
LOC100651161	393.825211	0.785884246	0.11180772	7.02889086	2.08E-12	5.06E-12
LOC100651839	1341.25102	0.786314463	0.06858954	11.4640578	2.00E-30	1.42E-29
LOC100644068	327.858223	0.786364692	0.11961339	6.57421937	4.89E-11	1.09E-10
LOC100649966	100.432527	0.787100037	0.17643626	4.46110132	8.15E-06	1.31E-05
LOC100648873	1125.17094	0.787149923	0.08058215	9.76829143	1.54E-22	6.68E-22
LOC100651361	2266.18054	0.787707039	0.09622142	8.18640005	2.69E-16	8.23E-16
LOC100647463	1494.16287	0.788146085	0.09235866	8.53353754	1.42E-17	4.69E-17
LOC100643677	663.627135	0.788181375	0.08782946	8.97399734	2.86E-19	1.05E-18
LOC100648135	590.145059	0.789480801	0.08036171	9.82409192	8.87E-23	3.89E-22
LOC100646886	728.788083	0.790090247	0.08531672	9.2606727	2.03E-20	7.91E-20
LOC100650325	572.299746	0.790385778	0.12474266	6.3361304	2.36E-10	5.02E-10
LOC100646644	2839.09741	0.790430793	0.08624183	9.16528367	4.94E-20	1.89E-19
LOC100643227	473.995533	0.79144618	0.07961487	9.94093471	2.76E-23	1.25E-22
LOC100652319	259.689468	0.791618089	0.16418746	4.82142858	1.43E-06	2.41E-06
LOC100646535	419.643081	0.792392448	0.23219521	3.41261325	0.00064343	0.00090101
LOC100648060	1682.69137	0.792400686	0.06696478	11.8330957	2.63E-32	2.07E-31
LOC100642629	1167.72533	0.793461218	0.07434968	10.6720195	1.38E-26	7.66E-26
LOC100646802	828.507376	0.793646498	0.09818866	8.0828729	6.33E-16	1.90E-15
LOC100649709	78.7514818	0.794253129	0.18488551	4.29591865	1.74E-05	2.74E-05
LOC100643257	53.5795805	0.794277204	0.21167659	3.75231478	0.00017521	0.00025708
LOC105666873	243.122403	0.796123642	0.14155837	5.62399536	1.87E-08	3.55E-08
LOC100648562	74.1359959	0.796190028	0.19388891	4.10642374	4.02E-05	6.17E-05
LOC100645011	8004.10422	0.796726255	0.07874969	10.1171982	4.63E-24	2.19E-23
LOC100646272	229.083013	0.79840939	0.17872783	4.46717995	7.93E-06	1.27E-05

LOC100647140	306.0551	0.79848018	0.11470253	6.961313	3.37E-12	8.10E-12
LOC100645852	337.912924	0.798694484	0.12235441	6.52771283	6.68E-11	1.47E-10
LOC100645005	13.326954	0.798911097	0.36892328	2.16552096	0.03034781	0.03710482
LOC100646143	240.213428	0.799768145	0.09179193	8.7128371	2.96E-18	1.02E-17
LOC100649107	732.853292	0.799998655	0.21375338	3.74262465	0.00018211	0.00026688
LOC100643862	4686.31118	0.800280445	0.17408503	4.59706654	4.28E-06	7.00E-06
LOC100643854	1156.74351	0.800593107	0.08528258	9.38753382	6.14E-21	2.46E-20
LOC100642536	1809.75958	0.800711538	0.10178937	7.86635682	3.65E-15	1.05E-14
LOC100647333	9652.81486	0.801585647	0.10240914	7.82728622	4.99E-15	1.41E-14
LOC105666214	357.684618	0.801607148	0.10274918	7.80159181	6.11E-15	1.72E-14
LOC100648600	234.061429	0.802280141	0.15740097	5.097047	3.45E-07	6.08E-07
LOC100647316	4176.36157	0.802781033	0.14382084	5.58181284	2.38E-08	4.51E-08
LOC100646018	743.948779	0.803460218	0.08440771	9.5188008	1.75E-21	7.21E-21
LOC100650117	208.221593	0.80354159	0.12004959	6.69341373	2.18E-11	4.97E-11
LOC100650470	313.40771	0.803735773	0.17538714	4.58263788	4.59E-06	7.49E-06
LOC100650734	2038.65957	0.804279068	0.08209812	9.79655847	1.16E-22	5.08E-22
LOC100647318	439.456781	0.804720581	0.07849478	10.2518997	1.16E-24	5.73E-24
LOC100647157	963.874196	0.805220112	0.05886055	13.6801326	1.33E-42	2.12E-41
LOC100644387	62.2470576	0.805423541	0.17251446	4.66873066	3.03E-06	5.00E-06
LOC100642196	1259.0129	0.806441335	0.13277839	6.07358858	1.25E-09	2.56E-09
LOC100649720	762.278631	0.806884929	0.0701652	11.4997879	1.32E-30	9.49E-30
LOC100651498	5775.99703	0.806886418	0.11439138	7.05373444	1.74E-12	4.25E-12
LOC100651547	225.800677	0.807315069	0.10138642	7.96275375	1.68E-15	4.91E-15
LOC100648408	638.850151	0.807865639	0.07688625	10.5072841	8.00E-26	4.25E-25
LOC100649645	429.007537	0.807898474	0.09784508	8.25691499	1.49E-16	4.66E-16
LOC105667128	166.726387	0.807946483	0.17170154	4.70552854	2.53E-06	4.20E-06
LOC100650258	239.01104	0.809666183	0.11362434	7.12581661	1.03E-12	2.57E-12
LOC100647794	521.588837	0.811008653	0.08658639	9.36646834	7.50E-21	2.99E-20
LOC100643375	97.7150363	0.811162614	0.2924751	2.77344157	0.00554668	0.00721216

LOC100643044	420.03923	0.812007971	0.12714567	6.38643851	1.70E-10	3.64E-10
LOC100646974	1844.71262	0.813604155	0.07208987	11.2859713	1.54E-29	1.03E-28
LOC100644120	277.506854	0.814348757	0.10757752	7.56987881	3.74E-14	1.01E-13
LOC100650545	757.315747	0.814573749	0.10532798	7.73368813	1.04E-14	2.91E-14
LOC100650236	645.010384	0.814674413	0.07470022	10.9059173	1.08E-27	6.44E-27
LOC100644193	463.974493	0.815028478	0.09111495	8.94505743	3.72E-19	1.36E-18
LOC100650487	120.795777	0.815372585	0.22819576	3.57312762	0.00035274	0.00050544
LOC100649425	650.831304	0.815448844	0.09290445	8.77728476	1.67E-18	5.84E-18
LOC100651807	63.5985417	0.815606688	0.19657773	4.14902901	3.34E-05	5.16E-05
LOC100649213	202.440929	0.816652778	0.11480711	7.11325956	1.13E-12	2.80E-12
LOC100644642	303.602881	0.816734307	0.09716236	8.40587147	4.25E-17	1.36E-16
LOC100648965	383.870017	0.817323805	0.19595808	4.17091142	3.03E-05	4.70E-05
LOC100642520	161.185014	0.817516816	0.14010666	5.83496039	5.38E-09	1.06E-08
LOC100647389	238.148154	0.817933393	0.12973929	6.30443879	2.89E-10	6.14E-10
LOC100645766	708.868124	0.819172439	0.06830461	11.9929304	3.87E-33	3.19E-32
LOC105665692	367.23425	0.820459131	0.10622055	7.72410956	1.13E-14	3.13E-14
LOC100646225	322.749255	0.821294182	0.10473998	7.84126712	4.46E-15	1.27E-14
LOC100647694	231.897489	0.821808584	0.12526776	6.56041563	5.37E-11	1.19E-10
LOC100647839	47.1964837	0.821897944	0.33604412	2.44580371	0.01445297	0.01817247
LOC100649432	511.989919	0.82250839	0.08587515	9.57795588	9.90E-22	4.12E-21
LOC100644325	802.572546	0.822510408	0.12467987	6.59697822	4.20E-11	9.37E-11
LOC100646808	453.827683	0.822532324	0.22613713	3.63731657	0.00027549	0.00039784
LOC100642868	450.906265	0.823303838	0.09968028	8.25944507	1.46E-16	4.56E-16
LOC100645098	182.144951	0.82370574	0.14319478	5.75234482	8.80E-09	1.71E-08
LOC100648189	78.2970103	0.82397152	0.27256321	3.02304744	0.00250243	0.00335726
LOC100652255	2681.50074	0.824109634	0.07296645	11.2943635	1.40E-29	9.40E-29
LOC100647885	1288.86514	0.824164717	0.1000531	8.23727323	1.76E-16	5.46E-16
LOC100649950	562.458049	0.82483869	0.12430717	6.63548758	3.23E-11	7.27E-11
LOC105667114	60.1343635	0.824893898	0.24193242	3.4096046	0.00065057	0.00091074

LOC100648076	145.2159	0.825021951	0.16839966	4.8991902	9.62E-07	1.65E-06
LOC100642703	623.005807	0.825245254	0.0802067	10.2889812	7.90E-25	3.95E-24
LOC100646103	150.880041	0.825530158	0.14028384	5.88471305	3.99E-09	7.94E-09
LOC100649103	245.647272	0.825644372	0.17189669	4.80314298	1.56E-06	2.63E-06
LOC100648203	2387.98647	0.825711698	0.07330067	11.2647228	1.96E-29	1.30E-28
LOC100650959	1362.25408	0.825742045	0.09672646	8.53687871	1.38E-17	4.56E-17
LOC100650364	124.746637	0.825932201	0.19028835	4.34042448	1.42E-05	2.25E-05
LOC100642270	2191.23718	0.826553048	0.11774214	7.02002731	2.22E-12	5.38E-12
LOC100644491	1220.92496	0.827083998	0.11684026	7.07875834	1.45E-12	3.57E-12
LOC100644633	631.463992	0.827509238	0.10333568	8.00797231	1.17E-15	3.44E-15
LOC100647446	114.913556	0.828305093	0.20730376	3.99561049	6.45E-05	9.78E-05
LOC100643048	1085.0457	0.828923947	0.08846091	9.37051129	7.22E-21	2.89E-20
LOC100651686	979.517351	0.829895002	0.08201587	10.1187121	4.56E-24	2.16E-23
LOC100642568	600.899846	0.830069855	0.08807086	9.42502313	4.30E-21	1.74E-20
LOC100645931	9399.44826	0.830689726	0.05870203	14.1509534	1.84E-45	3.59E-44
LOC100650520	369.044041	0.832054333	0.08846703	9.40524804	5.19E-21	2.09E-20
LOC100645912	261.23631	0.832409666	0.11239355	7.40620496	1.30E-13	3.39E-13
LOC100649742	564.275462	0.832972656	0.07698373	10.8201127	2.76E-27	1.62E-26
LOC100647770	418.542026	0.833071678	0.09773923	8.52341182	1.55E-17	5.11E-17
LOC100644790	764.773333	0.833274439	0.07653824	10.887034	1.33E-27	7.90E-27
LOC100651676	880.137843	0.835665504	0.06544873	12.7682469	2.47E-37	2.70E-36
LOC100643329	521.172924	0.835916314	0.07817234	10.6932496	1.09E-26	6.14E-26
LOC100651598	788.826619	0.836284307	0.08091359	10.335523	4.87E-25	2.46E-24
LOC100651162	317.08127	0.83694826	0.1283863	6.51898408	7.08E-11	1.55E-10
LOC100643483	591.986241	0.837242535	0.08786887	9.52831797	1.60E-21	6.59E-21
LOC100646874	410.116979	0.837533231	0.09953698	8.41429258	3.95E-17	1.27E-16
LOC100650018	792.99428	0.837671119	0.06725694	12.4547916	1.32E-35	1.29E-34
LOC100645609	809.771243	0.837857196	0.17626806	4.7533126	2.00E-06	3.35E-06
LOC100645253	749.612026	0.837867264	0.08186026	10.2353363	1.38E-24	6.75E-24

LOC100651831	145.189671	0.838097982	0.13552833	6.18393222	6.25E-10	1.30E-09
LOC100651297	467.393715	0.839936483	0.10714672	7.83912428	4.54E-15	1.29E-14
LOC100645525	222.794531	0.840165592	0.11468192	7.32605119	2.37E-13	6.10E-13
LOC100651930	2115.05808	0.84017038	0.06381652	13.1654067	1.39E-39	1.79E-38
LOC100646953	193.042156	0.840623529	0.11263418	7.46330777	8.44E-14	2.24E-13
LOC100649681	1613.11954	0.841175742	0.08106468	10.3766002	3.17E-25	1.62E-24
LOC100642581	2084.614	0.841228037	0.10561149	7.96530818	1.65E-15	4.82E-15
LOC100650914	31.3365598	0.841850856	0.36716824	2.29282045	0.02185834	0.02709394
LOC100649463	112.872258	0.84202559	0.14735323	5.71433408	1.10E-08	2.13E-08
LOC100644667	386.154388	0.842071353	0.09090276	9.26342981	1.98E-20	7.71E-20
LOC100644072	588.290964	0.842143726	0.10145997	8.30025562	1.04E-16	3.26E-16
LOC100647278	782.76495	0.843320091	0.09956705	8.46987095	2.46E-17	7.99E-17
LOC100646262	239.078417	0.843648254	0.14560425	5.79411822	6.87E-09	1.35E-08
LOC100643571	454.319299	0.843821283	0.08774569	9.61666889	6.80E-22	2.86E-21
LOC100647301	256.690229	0.844267825	0.1812481	4.65807831	3.19E-06	5.26E-06
LOC105666125	198.771112	0.844577012	0.15441345	5.46958199	4.51E-08	8.38E-08
LOC100648493	884.927731	0.844632383	0.08463418	9.97980198	1.87E-23	8.54E-23
LOC100652103	215.544661	0.844688633	0.11486355	7.35384397	1.93E-13	4.98E-13
LOC100647050	497.934961	0.844982195	0.10634701	7.9455188	1.93E-15	5.63E-15
LOC100651047	610.536767	0.845098868	0.09369005	9.02015626	1.88E-19	6.94E-19
LOC100652088	388.257321	0.845715536	0.13538272	6.24685014	4.19E-10	8.80E-10
LOC100644927	2664.30496	0.845790363	0.08313829	10.1732948	2.61E-24	1.25E-23
LOC100646661	670.818138	0.846478728	0.07619656	11.1091468	1.13E-28	7.21E-28
LOC100646419	698.683645	0.847799856	0.07901274	10.7299134	7.37E-27	4.18E-26
LOC100648213	204.658507	0.84899489	0.1158594	7.32780328	2.34E-13	6.02E-13
LOC100650877	611.529755	0.849093875	0.08243144	10.3006077	7.00E-25	3.51E-24
LOC100644215	1549.14243	0.849215104	0.12803662	6.63259557	3.30E-11	7.41E-11
LOC100646441	901.762392	0.849901827	0.0726329	11.7013338	1.25E-31	9.49E-31
LOC100644607	1270.552	0.849928637	0.10009222	8.49145575	2.04E-17	6.67E-17

LOC100643281	506.259441	0.850226703	0.08557932	9.93495474	2.93E-23	1.32E-22
LOC100647655	113.185661	0.85033097	0.14449251	5.88494826	3.98E-09	7.93E-09
LOC100650699	3260.30253	0.850693301	0.05242736	16.2261313	3.30E-59	1.79E-57
LOC100643170	1034.4198	0.850808081	0.07758185	10.9665863	5.53E-28	3.38E-27
LOC100650563	793.904326	0.851298325	0.1143173	7.44680225	9.56E-14	2.52E-13
LOC100648905	549.56329	0.851664294	0.10109963	8.42401016	3.64E-17	1.17E-16
LOC100644548	583.549117	0.853019692	0.0933239	9.14042087	6.22E-20	2.37E-19
LOC100649624	598.795812	0.853664702	0.10855342	7.86400593	3.72E-15	1.07E-14
LOC100647250	1229.4073	0.853987424	0.06171993	13.8364931	1.54E-43	2.60E-42
LOC100648431	976.470106	0.854257449	0.11335028	7.53643911	4.83E-14	1.30E-13
LOC100651421	327.585446	0.854413649	0.12389206	6.89643601	5.33E-12	1.27E-11
LOC100647891	638.829552	0.856825255	0.11308045	7.57713003	3.53E-14	9.55E-14
LOC100642452	228.680436	0.857443242	0.15573397	5.5058202	3.67E-08	6.86E-08
LOC100651127	589.702018	0.857656083	0.08110321	10.5748721	3.90E-26	2.11E-25
LOC100644915	819.802278	0.857702596	0.08717488	9.83887362	7.66E-23	3.37E-22
LOC100644801	835.378388	0.858769561	0.08963551	9.58068435	9.64E-22	4.02E-21
LOC100646197	725.454973	0.859594042	0.10802061	7.95768526	1.75E-15	5.12E-15
LOC100642632	1128.50407	0.859999801	0.17717125	4.85405957	1.21E-06	2.06E-06
LOC100651000	342.75051	0.860122902	0.10301475	8.34951182	6.85E-17	2.18E-16
LOC100646298	358.608552	0.861640875	0.08795333	9.79656937	1.16E-22	5.08E-22
LOC100644211	1305.40335	0.861765971	0.07318003	11.7759714	5.19E-32	4.01E-31
LOC100645381	888.92895	0.861970573	0.06953509	12.3961952	2.74E-35	2.63E-34
LOC100652309	1039.7506	0.862144649	0.12219008	7.05576645	1.72E-12	4.19E-12
LOC100649806	1026.30856	0.862935724	0.07429187	11.6154804	3.44E-31	2.54E-30
LOC100645436	101.407089	0.862951971	0.17347122	4.9746117	6.54E-07	1.13E-06
LOC100644426	294.143422	0.863033437	0.08732004	9.88356662	4.91E-23	2.18E-22
LOC100642213	1149.46963	0.863217043	0.08276441	10.4298091	1.81E-25	9.42E-25
LOC100648979	260.390604	0.863346017	0.12033237	7.17467835	7.25E-13	1.81E-12
LOC100651872	188.837911	0.865484852	0.12462832	6.94452805	3.80E-12	9.09E-12

LOC100646836	913.288076	0.865648257	0.11755059	7.36404836	1.78E-13	4.62E-13
LOC100643018	431.861492	0.866195267	0.08913065	9.71826467	2.52E-22	1.08E-21
LOC105665770	391.452905	0.866618478	0.18411024	4.70706298	2.51E-06	4.17E-06
LOC100649458	1493.94321	0.866957814	0.12899426	6.72090241	1.81E-11	4.13E-11
LOC100643321	294.937829	0.867642853	0.10197805	8.5081331	1.77E-17	5.79E-17
LOC100648918	929.360416	0.867904354	0.08702649	9.97287507	2.00E-23	9.15E-23
LOC100642751	642.052781	0.870711618	0.07639475	11.3975316	4.30E-30	2.99E-29
LOC100650577	585.981823	0.872709489	0.08292157	10.5245172	6.66E-26	3.55E-25
LOC100649538	487.915698	0.873473241	0.07992632	10.928481	8.42E-28	5.07E-27
LOC100642245	201.195046	0.873600325	0.12874075	6.78573286	1.15E-11	2.68E-11
LOC100643902	355.241627	0.875183002	0.13020085	6.72179166	1.80E-11	4.11E-11
LOC100644594	606.537421	0.876480101	0.16840844	5.20449026	1.95E-07	3.48E-07
LOC100650047	1984.34631	0.87679059	0.07162	12.2422586	1.85E-34	1.68E-33
LOC100649798	1052.94031	0.876791448	0.08327216	10.5292265	6.34E-26	3.39E-25
LOC100649688	281.740842	0.877197822	0.12181779	7.20090073	5.98E-13	1.51E-12
LOC100648317	259.429553	0.877292571	0.11243913	7.80237755	6.08E-15	1.71E-14
LOC100651838	1072.6009	0.877581316	0.13068764	6.71510556	1.88E-11	4.30E-11
LOC105665730	648.763605	0.877597862	0.10005397	8.77124456	1.77E-18	6.15E-18
LOC100647821	820.115304	0.878062135	0.12117659	7.2461366	4.29E-13	1.09E-12
LOC100645149	301.355006	0.87857229	0.18195801	4.82843432	1.38E-06	2.33E-06
LOC100650875	347.205959	0.87872483	0.09335884	9.41233669	4.85E-21	1.96E-20
LOC100648788	636.688825	0.878789955	0.07914207	11.1039549	1.20E-28	7.61E-28
LOC100644022	234.444209	0.879096342	0.10887456	8.07439606	6.78E-16	2.03E-15
LOC100651660	426.839741	0.880004279	0.08892103	9.89646986	4.31E-23	1.92E-22
LOC100648013	176.818249	0.880430586	0.137482	6.4039699	1.51E-10	3.25E-10
LOC100646900	459.460242	0.880572099	0.07931896	11.1016595	1.23E-28	7.79E-28
LOC100651609	1516.53582	0.881167172	0.06666314	13.2182059	6.89E-40	9.07E-39
LOC105666872	140.890992	0.881205077	0.29268549	3.01075764	0.00260597	0.00349138
LOC100652033	437.035269	0.882573189	0.08710411	10.1323948	3.97E-24	1.88E-23

LOC100647019	122.332315	0.882819552	0.12902438	6.84226938	7.79E-12	1.83E-11
LOC105666346	773.259058	0.88314792	0.10014371	8.81880528	1.16E-18	4.07E-18
LOC100651158	399.95713	0.883154579	0.08967977	9.84786855	7.00E-23	3.09E-22
LOC100647387	954.659893	0.884186324	0.16467625	5.36924021	7.91E-08	1.45E-07
LOC100644154	1088.23761	0.884513795	0.13218032	6.691721	2.21E-11	5.02E-11
LOC100642505	1806.49344	0.88458142	0.06388223	13.8470652	1.33E-43	2.26E-42
LOC100647221	346.657692	0.885290088	0.10434035	8.48463765	2.16E-17	7.06E-17
LOC100647806	458.153396	0.88596206	0.11838422	7.4837851	7.22E-14	1.92E-13
LOC100631094	304.040796	0.886785896	0.09974601	8.8904398	6.09E-19	2.18E-18
LOC100645569	372.734598	0.887208499	0.11553415	7.67918843	1.60E-14	4.42E-14
LOC100646356	532.512218	0.88776347	0.11014792	8.05973893	7.65E-16	2.28E-15
LOC100651277	659.895843	0.888803478	0.08286748	10.725601	7.72E-27	4.37E-26
LOC100648626	631.105193	0.892327676	0.08105726	11.0086083	3.47E-28	2.14E-27
LOC100649127	2703.14408	0.892403525	0.0979048	9.11501257	7.87E-20	2.98E-19
LOC100647192	1151.7969	0.892459049	0.08302848	10.748831	6.00E-27	3.43E-26
LOC100648462	805.305636	0.892460317	0.09813189	9.09449827	9.50E-20	3.58E-19
LOC100651041	543.796236	0.892975014	0.10113075	8.82990606	1.05E-18	3.70E-18
LOC100649776	1127.10554	0.893786494	0.06599812	13.5426045	8.76E-42	1.33E-40
LOC100648899	598.335823	0.895099781	0.06189289	14.462077	2.10E-47	4.72E-46
LOC100645550	1354.67349	0.895468023	0.06550578	13.6700613	1.53E-42	2.42E-41
LOC100651690	896.461801	0.896552393	0.09302785	9.63746229	5.55E-22	2.34E-21
LOC100645880	621.516124	0.897266565	0.2434896	3.68503038	0.00022868	0.00033254
LOC105666446	532.580477	0.898116988	0.13770059	6.52224494	6.93E-11	1.52E-10
LOC100652085	1877.98773	0.898538517	0.1502121	5.98179862	2.21E-09	4.46E-09
LOC100642938	30.2862736	0.898641457	0.43677318	2.05745567	0.03964241	0.04797761
LOC100644567	725.447143	0.899399296	0.08754815	10.2731963	9.31E-25	4.63E-24
LOC105666565	3078.98459	0.899506748	0.12577483	7.15172279	8.57E-13	2.14E-12
LOC100644233	73.609851	0.899667951	0.26303107	3.42038668	0.00062532	0.00087665
LOC100644652	670.9997	0.900215539	0.08436947	10.6699201	1.41E-26	7.83E-26

LOC105666105	23.1849192	0.900771757	0.28238482	3.1898731	0.00142335	0.00194149
LOC100652052	731.180451	0.900936326	0.20768453	4.33800395	1.44E-05	2.28E-05
LOC100642241	153.088192	0.902370898	0.30956062	2.91500544	0.00355682	0.00469971
LOC100648087	857.349648	0.904056406	0.0827498	10.9251791	8.74E-28	5.25E-27
LOC100650013	199.428127	0.904296801	0.2163147	4.18046864	2.91E-05	4.52E-05
LOC100646872	1014.6586	0.90509482	0.07537614	12.0077106	3.24E-33	2.69E-32
LOC100650612	257.072173	0.905307297	0.10874908	8.32473536	8.45E-17	2.68E-16
LOC100645540	191.57143	0.905488822	0.13698197	6.61027747	3.84E-11	8.59E-11
LOC100648640	1143.35775	0.906507661	0.08289781	10.9352426	7.82E-28	4.71E-27
LOC100650851	238.005769	0.907083311	0.11139553	8.14290569	3.86E-16	1.17E-15
LOC100642771	529.082083	0.907925849	0.10224688	8.87974146	6.70E-19	2.39E-18
LOC100652296	169.486543	0.907963665	0.13126076	6.91725152	4.60E-12	1.10E-11
LOC100650024	871.519923	0.908451973	0.08939352	10.1623916	2.92E-24	1.40E-23
LOC100648520	117.709457	0.909305526	0.16048161	5.66610416	1.46E-08	2.80E-08
LOC100647252	1124.57604	0.910047969	0.06829696	13.3248672	1.66E-40	2.28E-39
LOC100645231	1237.89469	0.910110445	0.1785115	5.09832948	3.43E-07	6.04E-07
LOC105667194	206.439289	0.91031613	0.19306193	4.71515095	2.42E-06	4.02E-06
LOC100651088	285.554719	0.910379863	0.18838332	4.83259264	1.35E-06	2.28E-06
LOC100645719	3142.78002	0.91064462	0.08090304	11.2559998	2.16E-29	1.43E-28
LOC100650267	983.41482	0.910650485	0.07513799	12.1197077	8.31E-34	7.17E-33
LOC100647999	392.148673	0.910678604	0.11159	8.16093362	3.32E-16	1.01E-15
LOC100651612	71.3954889	0.91117632	0.40864375	2.22975717	0.02576357	0.03172571
LOC100642463	422.187766	0.912731546	0.1047139	8.71643153	2.87E-18	9.86E-18
LOC100647693	308.070409	0.913134069	0.21986852	4.1530914	3.28E-05	5.07E-05
LOC100644653	685.241004	0.913838847	0.09685993	9.4346433	3.92E-21	1.59E-20
LOC100647353	513.220548	0.913931415	0.13839327	6.60387197	4.01E-11	8.96E-11
LOC100651644	310.775867	0.91428956	0.1152974	7.92983668	2.19E-15	6.37E-15
LOC100650142	619.966015	0.915861466	0.10067039	9.09762528	9.23E-20	3.48E-19
LOC100650066	1557.3119	0.915956584	0.10914295	8.3922652	4.77E-17	1.53E-16

LOC100651760	445.865329	0.918555177	0.08483382	10.8277009	2.54E-27	1.49E-26
LOC100644135	2337.83558	0.91867723	0.06461347	14.2180455	7.08E-46	1.41E-44
LOC100651293	476.549831	0.919579853	0.09114463	10.0892384	6.16E-24	2.90E-23
LOC100643697	368.825765	0.92033277	0.09876445	9.31846186	1.18E-20	4.67E-20
LOC100650792	350.499937	0.920483503	0.20830835	4.41885065	9.92E-06	1.59E-05
LOC100647567	262.056293	0.920779539	0.13934945	6.60770132	3.90E-11	8.73E-11
LOC100646093	1251.36509	0.921086299	0.08399327	10.9661911	5.56E-28	3.39E-27
LOC100647802	712.513123	0.92167673	0.06822057	13.5102476	1.36E-41	2.02E-40
LOC100646210	390.75144	0.921916123	0.11488338	8.02479962	1.02E-15	3.01E-15
LOC100651322	1067.76422	0.922202364	0.12222769	7.54495468	4.52E-14	1.22E-13
LOC100642550	403.107057	0.922442693	0.08122176	11.3570884	6.84E-30	4.68E-29
LOC100647213	791.429215	0.924179398	0.07855339	11.7649844	5.91E-32	4.54E-31
LOC100645179	882.640925	0.924566213	0.13744462	6.72682715	1.73E-11	3.97E-11
LOC100648677	1499.51765	0.925046931	0.13008129	7.11129908	1.15E-12	2.84E-12
LOC100651419	2425.04985	0.927010087	0.07381156	12.5591446	3.54E-36	3.59E-35
LOC100647133	2573.73983	0.928302281	0.13658004	6.79676391	1.07E-11	2.49E-11
LOC100649914	13.5042307	0.928462999	0.38106841	2.43647326	0.01483127	0.01862898
LOC100646554	220.951619	0.929069403	0.14844253	6.25878181	3.88E-10	8.17E-10
LOC100643510	37.2528647	0.929136141	0.32279092	2.87844573	0.0039964	0.00525995
LOC100646524	167.067524	0.92955664	0.15795489	5.88495012	3.98E-09	7.93E-09
LOC100650839	255.273612	0.929640738	0.12508902	7.43183308	1.07E-13	2.82E-13
LOC100648529	850.348657	0.929742502	0.06420225	14.4814627	1.59E-47	3.60E-46
LOC100647342	590.552468	0.930593232	0.13988522	6.65254863	2.88E-11	6.51E-11
LOC100648571	203.470288	0.931337488	0.19227019	4.84389954	1.27E-06	2.16E-06
LOC100646984	791.08917	0.93222909	0.07521811	12.3936794	2.83E-35	2.71E-34
LOC100649318	130.916749	0.932265217	0.3119538	2.98847208	0.00280376	0.00374613
LOC100647617	55.9476298	0.932336855	0.22209914	4.19784095	2.69E-05	4.19E-05
LOC100648367	446.792127	0.933036538	0.10246831	9.10561048	8.58E-20	3.24E-19
LOC100645726	1049.58909	0.93315496	0.0973413	9.58642357	9.12E-22	3.80E-21

LOC100646877	1353.66009	0.933402811	0.07256392	12.8631809	7.25E-38	8.25E-37
LOC105665999	683.442263	0.933430137	0.07895708	11.8219939	3.00E-32	2.35E-31
LOC100642689	1164.2434	0.93468002	0.0741574	12.6040012	2.01E-36	2.07E-35
LOC100652259	1601.20612	0.93478009	0.09344465	10.0035702	1.47E-23	6.74E-23
LOC100645254	1171.88367	0.934903153	0.08118537	11.5156605	1.10E-30	7.92E-30
LOC100645455	372.831547	0.93613946	0.09188733	10.1879057	2.25E-24	1.08E-23
LOC100647823	843.376237	0.937143188	0.14947541	6.2695475	3.62E-10	7.64E-10
LOC100644735	515.146214	0.937169441	0.10030511	9.34318711	9.35E-21	3.71E-20
LOC100646797	119.814442	0.938475577	0.20688795	4.53615378	5.73E-06	9.29E-06
LOC100646305	1877.30535	0.938479262	0.09442735	9.93863778	2.83E-23	1.28E-22
LOC100647282	63.6365411	0.939859829	0.25034254	3.75429536	0.00017383	0.00025513
LOC100644806	430.235896	0.94096058	0.08895479	10.5779637	3.77E-26	2.04E-25
LOC100645876	122.863981	0.941849661	0.27670715	3.40377789	0.00066461	0.00093013
LOC100644133	330.401842	0.94190917	0.09561711	9.85084364	6.80E-23	3.01E-22
LOC100651188	572.205497	0.942355479	0.0780548	12.0729987	1.47E-33	1.24E-32
LOC100646649	562.829053	0.943028585	0.09179035	10.2737228	9.26E-25	4.61E-24
LOC105667205	781.210054	0.943073437	0.07755377	12.1602531	5.06E-34	4.45E-33
LOC100644240	145.372134	0.9435277	0.1595423	5.91396559	3.34E-09	6.69E-09
LOC100645256	913.702794	0.943672331	0.06581218	14.3388711	1.25E-46	2.63E-45
LOC100648847	183.548089	0.944771783	0.13324018	7.09074245	1.33E-12	3.28E-12
LOC100647931	1673.47495	0.946300756	0.06754185	14.0105848	1.34E-44	2.45E-43
LOC105665642	2682.9744	0.946524766	0.10637195	8.89825523	5.67E-19	2.04E-18
LOC100642798	250.059708	0.948306786	0.13270925	7.14574758	8.95E-13	2.23E-12
LOC100651744	792.534545	0.948690729	0.109246	8.6839859	3.82E-18	1.30E-17
LOC100645365	522.241588	0.948720745	0.08881986	10.6814029	1.24E-26	6.95E-26
LOC100649562	406.443041	0.949369623	0.16142482	5.88118751	4.07E-09	8.11E-09
LOC100649380	170.516562	0.950013954	0.15844356	5.99591398	2.02E-09	4.10E-09
LOC100645771	717.202479	0.951169036	0.08351139	11.3896922	4.71E-30	3.27E-29
LOC100652080	395.466169	0.951425394	0.11427858	8.32549189	8.40E-17	2.66E-16

LOC100646427	273.504886	0.952205685	0.14526667	6.5548806	5.57E-11	1.23E-10
LOC100649973	126.303256	0.952863723	0.13907281	6.85154552	7.31E-12	1.72E-11
LOC100646643	153.456155	0.953096439	0.1267063	7.52209201	5.39E-14	1.44E-13
LOC100646538	863.65111	0.953442385	0.08209625	11.6137143	3.51E-31	2.59E-30
LOC100647029	1048.98907	0.953890369	0.07386849	12.9133588	3.78E-38	4.40E-37
LOC100646834	490.84024	0.954054626	0.10087882	9.45743216	3.16E-21	1.29E-20
LOC105666152	115.350535	0.95453489	0.16096323	5.93014259	3.03E-09	6.08E-09
LOC100648316	481.525593	0.955065528	0.08585599	11.1240411	9.58E-29	6.13E-28
LOC100647677	16.2290596	0.955575321	0.44015306	2.17100689	0.02993065	0.0366268
LOC100642530	619.402224	0.956032455	0.16647067	5.74294848	9.30E-09	1.81E-08
LOC100649620	65.3441457	0.956436637	0.26346408	3.63023548	0.00028316	0.00040831
LOC100651439	492.377965	0.957180607	0.11526718	8.30401686	1.01E-16	3.16E-16
LOC105665848	263.455523	0.957919973	0.11799862	8.11806048	4.74E-16	1.43E-15
LOC100650337	1765.10014	0.9579882	0.08773353	10.9192941	9.32E-28	5.59E-27
LOC100649034	1244.61281	0.958003657	0.12863034	7.44772673	9.50E-14	2.51E-13
LOC100651239	151.877839	0.958357057	0.19809142	4.83795336	1.31E-06	2.23E-06
LOC100643473	448.901488	0.958861833	0.1031385	9.29683725	1.45E-20	5.70E-20
LOC100651595	634.190653	0.959349048	0.2782447	3.44786104	0.00056504	0.00079568
LOC100645193	636.480666	0.960072308	0.09130918	10.5145214	7.41E-26	3.94E-25
LOC100645921	847.950388	0.960354606	0.12559672	7.64633482	2.07E-14	5.67E-14
LOC105666758	50.7122145	0.960482299	0.29738948	3.22971178	0.00123915	0.00169828
LOC100643531	509.831704	0.960559397	0.09352814	10.270271	9.59E-25	4.76E-24
LOC100643974	201.739565	0.96065585	0.15505433	6.19560795	5.81E-10	1.21E-09
LOC100648167	714.944076	0.961004294	0.08220295	11.6906303	1.42E-31	1.07E-30
LOC100646323	303.442617	0.961150556	0.09251821	10.3887713	2.79E-25	1.43E-24
LOC100646204	899.367447	0.961412095	0.09474859	10.1469803	3.42E-24	1.63E-23
LOC100649470	251.498154	0.961445799	0.10425769	9.22182174	2.92E-20	1.13E-19
LOC105666897	15.6267079	0.962187977	0.37846544	2.54234036	0.01101129	0.0139906
LOC100646853	41.8355249	0.963290271	0.30038363	3.20686669	0.00134189	0.00183575

LOC100645970	441.118671	0.964601749	0.12062571	7.99665142	1.28E-15	3.76E-15
LOC100646907	481.053021	0.965378061	0.09696256	9.95619355	2.37E-23	1.08E-22
LOC100645473	702.718151	0.966257518	0.08349128	11.5731543	5.64E-31	4.12E-30
LOC100649464	885.19751	0.966427569	0.1041414	9.27995575	1.70E-20	6.65E-20
LOC100644584	25.4092386	0.966502151	0.42713736	2.2627432	0.02365152	0.02923521
LOC100650609	2350.10349	0.966850968	0.0843628	11.4606316	2.08E-30	1.47E-29
LOC100650147	805.414852	0.967506273	0.08220163	11.7699166	5.58E-32	4.29E-31
LOC105665645	21.6927839	0.96789651	0.32601537	2.96886773	0.00298899	0.00398383
LOC100642823	686.420266	0.96803239	0.09356095	10.3465428	4.34E-25	2.20E-24
LOC100649981	190.93314	0.968556659	0.25112215	3.85691445	0.00011483	0.0001706
LOC100650567	952.240046	0.968825304	0.08751401	11.0705163	1.74E-28	1.09E-27
LOC100643525	475.406747	0.968965955	0.08900377	10.8867971	1.33E-27	7.91E-27
LOC100649480	10.9270244	0.9698514	0.45477585	2.13259214	0.0329582	0.04019102
LOC100652183	3937.88886	0.970233975	0.09175306	10.5744049	3.92E-26	2.12E-25
LOC100642299	3552.57539	0.970369678	0.09020466	10.7574224	5.47E-27	3.13E-26
LOC100647514	778.021274	0.971929972	0.08513759	11.415991	3.48E-30	2.43E-29
LOC100642212	31.1484574	0.972512516	0.38348436	2.53599006	0.01121299	0.01424133
LOC105665624	342.838715	0.972556772	0.14772075	6.58375215	4.59E-11	1.02E-10
LOC100644367	1806.7276	0.972767847	0.07299906	13.3257577	1.64E-40	2.25E-39
LOC100650023	114.547222	0.972831745	0.18753874	5.18736423	2.13E-07	3.81E-07
LOC100642763	768.37993	0.972923061	0.09700884	10.0292208	1.13E-23	5.25E-23
LOC100650732	1590.59088	0.974430417	0.11716404	8.31680429	9.04E-17	2.85E-16
LOC100648136	237.928988	0.974630831	0.12741734	7.6491227	2.02E-14	5.56E-14
LOC100645661	646.898391	0.975051637	0.09793952	9.9556501	2.38E-23	1.08E-22
LOC100643315	211.795378	0.975443486	0.09827264	9.92589104	3.21E-23	1.44E-22
LOC100650897	347.124218	0.975749693	0.11537728	8.45703478	2.74E-17	8.87E-17
LOC100644256	284.757488	0.975795363	0.12464658	7.82849685	4.94E-15	1.40E-14
LOC100651622	1352.25417	0.97628138	0.07338114	13.3042545	2.19E-40	2.97E-39
LOC100647680	395.859596	0.97657344	0.10922016	8.94132931	3.85E-19	1.40E-18

LOC100642199	222.618991	0.976625596	0.31103143	3.13995793	0.00168972	0.00229237
LOC100645044	660.935344	0.976970727	0.08546287	11.4315225	2.91E-30	2.04E-29
LOC100649477	49.155754	0.97706429	0.31728446	3.0794584	0.00207377	0.00279866
LOC100649587	125.371174	0.977285863	0.20025002	4.88032851	1.06E-06	1.81E-06
LOC100643686	1329.63672	0.97736054	0.08484707	11.5190847	1.06E-30	7.62E-30
LOC100649105	338.947717	0.977374182	0.32698271	2.98906994	0.00279828	0.00373983
LOC100642722	544.197076	0.977551638	0.08471221	11.5396788	8.32E-31	6.02E-30
LOC100646822	501.163685	0.977781225	0.13388701	7.30303295	2.81E-13	7.21E-13
LOC100647842	2052.86399	0.977800582	0.08193404	11.9339967	7.87E-33	6.37E-32
LOC100644297	263.675364	0.978602965	0.10958725	8.92989812	4.26E-19	1.55E-18
LOC100651190	463.776367	0.978753899	0.11539998	8.48140406	2.22E-17	7.25E-17
LOC100648469	143.699739	0.979502854	0.13243736	7.39597071	1.40E-13	3.66E-13
LOC100650421	2339.3678	0.979618893	0.05979624	16.3826171	2.55E-60	1.55E-58
LOC100642774	3359.04294	0.979729855	0.07247124	13.5188788	1.21E-41	1.80E-40
LOC100646637	1013.4235	0.979749703	0.22442996	4.36550324	1.27E-05	2.01E-05
LOC100649598	1343.66618	0.979786313	0.11560747	8.47511271	2.35E-17	7.64E-17
LOC100643342	174.366755	0.979843711	0.30017699	3.26421987	0.00109766	0.00151135
LOC100643200	96.9726367	0.979912874	0.26311677	3.7242509	0.0001959	0.0002864
LOC100645819	5525.7756	0.980268741	0.29822924	3.28696387	0.00101274	0.00139756
LOC100643268	61.3841471	0.980470861	0.17206655	5.69820709	1.21E-08	2.34E-08
LOC100643786	437.445665	0.981010527	0.10870772	9.02429459	1.81E-19	6.69E-19
LOC105666525	116.591994	0.981022795	0.21118212	4.64538758	3.39E-06	5.58E-06
LOC105666653	65.7952866	0.982084969	0.24881431	3.94705988	7.91E-05	0.00011916
LOC100644176	9.95571123	0.982460522	0.48104041	2.04236589	0.04111525	0.04972939
LOC100647090	612.536406	0.983303832	0.08730462	11.2629072	2.00E-29	1.32E-28
LOC100651998	1098.85289	0.98351825	0.0739071	13.3074926	2.09E-40	2.84E-39
LOC100650717	1056.62685	0.983681078	0.09183519	10.7113736	9.00E-27	5.07E-26
LOC100643472	3257.33846	0.983683645	0.11620669	8.4649486	2.56E-17	8.32E-17
LOC100645877	332.551992	0.984089032	0.11059691	8.89797972	5.69E-19	2.04E-18

LOC100651691	635.000614	0.984258985	0.08873385	11.0922604	1.37E-28	8.63E-28
LOC105667041	1363.44966	0.984936843	0.10673512	9.22786133	2.76E-20	1.07E-19
LOC100650027	446.890771	0.986185262	0.10955547	9.00169765	2.22E-19	8.21E-19
LOC100645911	425.655097	0.988092478	0.09164694	10.7815105	4.21E-27	2.43E-26
LOC100642904	100.518924	0.988252628	0.18020135	5.48415781	4.15E-08	7.74E-08
LOC100645269	456.869814	0.990923072	0.09307724	10.6462446	1.82E-26	1.00E-25
LOC100648412	1018.24541	0.991080035	0.09434252	10.5051261	8.18E-26	4.34E-25
LOC100645223	23.9452793	0.991182782	0.38324796	2.5862702	0.00970208	0.01239472
LOC100649963	3350.77108	0.991212056	0.06143746	16.1336745	1.48E-58	7.62E-57
LOC100647536	410.477848	0.992069954	0.08478747	11.7006666	1.26E-31	9.56E-31
LOC100650771	289.11442	0.993289311	0.13549614	7.33075731	2.29E-13	5.89E-13
LOC100650304	69.404247	0.994378038	0.24208873	4.10749407	4.00E-05	6.15E-05
LOC100642805	360.425942	0.994501536	0.11232597	8.85370944	8.47E-19	3.01E-18
LOC100652119	223.032814	0.99491308	0.14255939	6.97893774	2.97E-12	7.15E-12
LOC100642808	713.063986	0.995432196	0.08897403	11.1878957	4.67E-29	3.04E-28
LOC100642762	603.069673	0.99604924	0.11647733	8.55144321	1.22E-17	4.03E-17
LOC100644095	32.037524	0.996200748	0.28621751	3.48057229	0.00050034	0.00070875
LOC100649368	1077.25856	0.996224175	0.08523581	11.6878599	1.47E-31	1.11E-30
Kr-h1	259.021202	0.996730288	0.27508645	3.62333475	0.00029083	0.000419
LOC100650784	476.327551	0.997029596	0.13623024	7.31870965	2.50E-13	6.43E-13
LOC100650693	577.767089	0.99745888	0.08194913	12.1716838	4.40E-34	3.90E-33
LOC100643464	378.359371	0.999404903	0.12020666	8.31405606	9.25E-17	2.92E-16
LOC100650254	196.43812	1.000105003	0.11142717	8.97541432	2.82E-19	1.04E-18
LOC100642334	24.1991948	1.00111829	0.401525	2.49329006	0.01265654	0.01598351
LOC100650840	776.592214	1.001806361	0.08300919	12.0686204	1.55E-33	1.31E-32
LOC100644475	257.44351	1.001944308	0.12822297	7.81407813	5.54E-15	1.57E-14
LOC100644258	547.307766	1.002967742	0.08915434	11.2497918	2.32E-29	1.53E-28
LOC100647979	109.093481	1.002993035	0.1499022	6.69098258	2.22E-11	5.05E-11
LOC100645008	702.110956	1.003266728	0.09068421	11.0633007	1.89E-28	1.18E-27

LOC100645266	738.851071	1.003492288	0.13710815	7.31898367	2.50E-13	6.42E-13
LOC100646199	375.270867	1.004025905	0.14356946	6.99331123	2.68E-12	6.47E-12
LOC100650764	547.380707	1.004196516	0.21255971	4.72430314	2.31E-06	3.85E-06
LOC105665876	162.483231	1.004532066	0.12608006	7.96741408	1.62E-15	4.74E-15
LOC100647786	692.281832	1.005123384	0.1010518	9.94661517	2.61E-23	1.18E-22
LOC100646345	98.7562896	1.006990141	0.17691531	5.69193335	1.26E-08	2.42E-08
LOC100649343	1237.09185	1.007108316	0.09298852	10.8304588	2.47E-27	1.45E-26
LOC100647123	1509.65823	1.007483168	0.07652957	13.1646266	1.40E-39	1.80E-38
LOC100644773	324.812689	1.007538758	0.10259328	9.82070902	9.17E-23	4.02E-22
LOC100647637	435.123276	1.007634697	0.09048443	11.1360012	8.38E-29	5.38E-28
LOC100651511	1570.12211	1.00812593	0.08646505	11.6593454	2.06E-31	1.54E-30
LOC100644620	659.895422	1.008497899	0.09940732	10.1451065	3.48E-24	1.66E-23
LOC100647210	226.872851	1.008987934	0.24602468	4.10116548	4.11E-05	6.31E-05
LOC100642467	1825.33784	1.009412371	0.10002216	10.0918875	6.00E-24	2.82E-23
LOC100643316	687.07217	1.010146719	0.10713503	9.4287252	4.15E-21	1.68E-20
LOC100652305	688.221637	1.011821254	0.11998312	8.43303005	3.37E-17	1.09E-16
LOC100647736	1207.61951	1.012240212	0.08685653	11.654163	2.19E-31	1.64E-30
LOC100651700	605.714299	1.012241182	0.17921963	5.64804856	1.62E-08	3.10E-08
LOC100646567	862.265	1.012309921	0.08581671	11.7961864	4.08E-32	3.18E-31
LOC100651379	1606.56563	1.013267843	0.09427416	10.7480969	6.05E-27	3.46E-26
LOC100645918	1085.09253	1.013542068	0.09538625	10.6256627	2.26E-26	1.24E-25
LOC100648209	102.251985	1.013582475	0.33333362	3.04074483	0.00235994	0.00317131
LOC100643039	935.970578	1.013803819	0.11667162	8.68937814	3.64E-18	1.24E-17
LOC100643195	301.414048	1.01433241	0.09078999	11.1722939	5.57E-29	3.61E-28
LOC100649085	12.0326987	1.014618229	0.40628683	2.49729541	0.01251447	0.01580817
LOC100650667	1001.35607	1.014827145	0.07674863	13.2227397	6.49E-40	8.55E-39
LOC100647953	807.499887	1.015509825	0.0977147	10.3926003	2.68E-25	1.38E-24
LOC100651119	612.182944	1.016971671	0.07917424	12.8447295	9.21E-38	1.04E-36
LOC100643276	260.878718	1.017452133	0.10550879	9.64329225	5.25E-22	2.22E-21

LOC100642865	612.591291	1.017465678	0.10456649	9.73032234	2.24E-22	9.62E-22
LOC100643425	424.902483	1.018089712	0.11714975	8.69049873	3.61E-18	1.23E-17
LOC100649400	5631.45666	1.019414602	0.09774896	10.4289047	1.83E-25	9.51E-25
LOC100642423	771.051469	1.020024295	0.09854858	10.3504714	4.16E-25	2.12E-24
LOC100644349	192.439721	1.020041495	0.10979974	9.29001736	1.54E-20	6.06E-20
LOC100650022	489.443576	1.02011637	0.08926526	11.4279219	3.03E-30	2.12E-29
LOC100651689	823.395982	1.020769188	0.06811854	14.9851882	9.18E-51	2.65E-49
LOC100642946	2109.70104	1.021410957	0.07267064	14.0553453	7.14E-45	1.32E-43
LOC100650671	240.491421	1.021695912	0.15727766	6.49612873	8.24E-11	1.80E-10
LOC100644511	699.26426	1.021966556	0.08573949	11.9194382	9.37E-33	7.53E-32
LOC100647994	1171.03122	1.024128572	0.07119478	14.3848837	6.44E-47	1.39E-45
LOC100647077	1153.98946	1.024148171	0.07013902	14.6016898	2.74E-48	6.72E-47
LOC100645563	167.124336	1.024244066	0.44031398	2.32616751	0.02000962	0.02488115
LOC100642433	488.774136	1.024818314	0.09204737	11.1335969	8.61E-29	5.52E-28
LOC100644583	757.600837	1.026895219	0.09764604	10.5165069	7.25E-26	3.86E-25
LOC100642197	883.580047	1.026901814	0.08946233	11.478594	1.69E-30	1.20E-29
LOC100645103	430.44525	1.026980048	0.1146087	8.96075112	3.22E-19	1.18E-18
LOC100645820	741.027391	1.027475733	0.09069685	11.3286817	9.46E-30	6.40E-29
LOC100644272	166.170723	1.027769364	0.14677499	7.00234656	2.52E-12	6.08E-12
LOC100649882	1501.20536	1.028024542	0.08027813	12.8057857	1.52E-37	1.69E-36
LOC100650292	479.250385	1.028610896	0.09092534	11.3126976	1.14E-29	7.67E-29
LOC105666336	386.64572	1.02926842	0.10459363	9.84064166	7.52E-23	3.31E-22
LOC100650911	767.550135	1.029301441	0.11633557	8.84769293	8.93E-19	3.17E-18
LOC100650898	335.642266	1.03006336	0.13118311	7.85210382	4.09E-15	1.17E-14
LOC100643099	1412.08008	1.032028423	0.09986579	10.334154	4.94E-25	2.50E-24
LOC100651049	355.14999	1.032920647	0.10759157	9.60038606	7.96E-22	3.33E-21
LOC100650210	79.9958135	1.03348846	0.17353524	5.95549613	2.59E-09	5.22E-09
LOC100642744	136.824753	1.033620629	0.32261957	3.20383737	0.00135609	0.00185388
LOC100644950	508.876088	1.033737491	0.10509804	9.83593457	7.88E-23	3.47E-22

LOC100643127	1835.10142	1.033969821	0.08316518	12.4327256	1.74E-35	1.69E-34
LOC100642482	340.350629	1.034203395	0.15351184	6.73696196	1.62E-11	3.72E-11
LOC100645325	1979.24995	1.034444955	0.08931911	11.5814516	5.12E-31	3.74E-30
LOC100652011	418.915671	1.03446954	0.1239554	8.34549794	7.09E-17	2.25E-16
LOC100649689	398.383744	1.034520357	0.11668365	8.86602685	7.58E-19	2.70E-18
LOC100643701	425.78366	1.034906729	0.07561198	13.6870734	1.21E-42	1.93E-41
LOC100651163	227.552944	1.03544927	0.1431416	7.23374115	4.70E-13	1.19E-12
LOC100650105	738.582998	1.035537824	0.1095411	9.45341787	3.28E-21	1.34E-20
LOC100649563	3170.4757	1.035646496	0.11038543	9.38209392	6.47E-21	2.59E-20
LOC100650640	461.451993	1.036035771	0.11957858	8.66405815	4.55E-18	1.54E-17
LOC100643344	246.025298	1.037606093	0.12952721	8.01071921	1.14E-15	3.36E-15
LOC100643894	815.629102	1.037958074	0.10089687	10.2873167	8.04E-25	4.01E-24
LOC100648348	273.040356	1.038717325	0.07864908	13.2069871	8.00E-40	1.05E-38
LOC100645106	237.10464	1.038946612	0.11007918	9.43817533	3.79E-21	1.54E-20
LOC100649086	341.778307	1.039941303	0.13169325	7.89669411	2.86E-15	8.26E-15
LOC100646550	143.527759	1.039963688	0.18275673	5.6904263	1.27E-08	2.44E-08
LOC100643479	230.506058	1.040479969	0.16135565	6.44836416	1.13E-10	2.45E-10
LOC100642726	2861.3769	1.040538599	0.07915137	13.1461864	1.79E-39	2.28E-38
LOC100650949	82.4975504	1.040562219	0.20836612	4.99391276	5.92E-07	1.03E-06
LOC100646483	974.621537	1.040624762	0.08931015	11.6518089	2.25E-31	1.68E-30
LOC100645515	613.626244	1.041286735	0.08587581	12.1254951	7.74E-34	6.72E-33
LOC100650465	921.53712	1.041698215	0.12315618	8.45835099	2.71E-17	8.78E-17
LOC100650461	1279.20277	1.042440685	0.08740705	11.9262773	8.63E-33	6.96E-32
LOC100652235	276.748198	1.043860899	0.12381825	8.43058977	3.44E-17	1.11E-16
LOC105665812	206.891041	1.044524196	0.15248086	6.85019874	7.37E-12	1.73E-11
LOC100645627	2078.10698	1.044604374	0.09045069	11.5488819	7.48E-31	5.43E-30
LOC100652272	478.39278	1.044650357	0.12116913	8.62142353	6.61E-18	2.23E-17
LOC100649201	1070.76027	1.044900489	0.08682222	12.0349438	2.33E-33	1.95E-32
LOC100649017	930.178642	1.044950439	0.09488698	11.0125803	3.32E-28	2.06E-27

LOC100647271	56.8089935	1.044996838	0.24560755	4.25474239	2.09E-05	3.28E-05
LOC100646189	1318.17719	1.04568783	0.13266532	7.88214893	3.22E-15	9.26E-15
LOC100646346	348.688293	1.046323213	0.13965683	7.4921019	6.78E-14	1.81E-13
LOC100650278	474.607267	1.046751646	0.10421552	10.044105	9.75E-24	4.54E-23
LOC100651951	701.634114	1.047363105	0.08240459	12.7100088	5.20E-37	5.57E-36
LOC100646406	613.270273	1.047768211	0.09355017	11.2000672	4.07E-29	2.66E-28
LOC100646108	347.141306	1.047800716	0.11168051	9.38212679	6.47E-21	2.59E-20
LOC100647036	3696.59117	1.048080865	0.06849815	15.3008648	7.54E-53	2.57E-51
LOC105666049	424.272603	1.048997265	0.09763058	10.7445564	6.29E-27	3.59E-26
LOC100649499	579.505789	1.049135048	0.09803361	10.7017891	9.98E-27	5.61E-26
LOC100645132	483.158958	1.049163925	0.1050766	9.9847535	1.78E-23	8.13E-23
LOC100647590	1062.82942	1.049444254	0.07829809	13.4031915	5.79E-41	8.21E-40
LOC100647938	948.050618	1.049630987	0.08892867	11.8030667	3.76E-32	2.93E-31
LOC100646773	2416.3412	1.050082141	0.09680944	10.8468977	2.06E-27	1.22E-26
LOC100647867	356.700927	1.050118324	0.09314226	11.2743486	1.76E-29	1.17E-28
LOC100642863	1432.56919	1.050184845	0.08134953	12.9095382	3.98E-38	4.61E-37
LOC100648881	522.653182	1.050539838	0.10666478	9.84898513	6.92E-23	3.06E-22
LOC100642412	530.640688	1.051783811	0.080048	13.1394136	1.96E-39	2.48E-38
LOC100649640	511.81187	1.051964245	0.1058078	9.94221836	2.73E-23	1.23E-22
LOC100644028	407.878414	1.052915144	0.14059408	7.48904332	6.94E-14	1.85E-13
LOC100651256	33.4662104	1.054150133	0.3298056	3.19627726	0.00139213	0.00190182
LOC100647903	997.849823	1.055982343	0.12083292	8.73919408	2.35E-18	8.11E-18
LOC100648945	368.479609	1.056351766	0.12154382	8.69111838	3.59E-18	1.22E-17
LOC100642894	551.702664	1.056884278	0.09296773	11.3682918	6.02E-30	4.14E-29
LOC100644957	1440.20605	1.057074457	0.07621047	13.8704627	9.57E-44	1.65E-42
LOC100651303	1226.73131	1.058003092	0.12145854	8.71081669	3.02E-18	1.03E-17
LOC100642720	1206.48855	1.05838477	0.07781657	13.6010204	3.95E-42	6.08E-41
LOC100650040	1062.83012	1.060013205	0.12919299	8.2048817	2.31E-16	7.10E-16
LOC105666519	816.705139	1.060697326	0.09047107	11.7241603	9.58E-32	7.31E-31

LOC100650152	605.164865	1.061097827	0.08631778	12.292923	9.89E-35	9.18E-34
LOC100643161	640.019678	1.061224198	0.09761704	10.8713004	1.58E-27	9.35E-27
LOC100644516	244.164289	1.061463333	0.12015847	8.83386216	1.01E-18	3.57E-18
LOC100647692	160.380289	1.062202723	0.12438964	8.53931857	1.35E-17	4.47E-17
LOC100646397	813.162214	1.062252284	0.09365432	11.3422673	8.10E-30	5.51E-29
LOC105665695	18.7296278	1.062558173	0.30569489	3.47587815	0.00050918	0.00072064
LOC100650714	40.5543878	1.062726725	0.26755959	3.97192542	7.13E-05	0.00010767
LOC100650138	306.206425	1.063447522	0.11447196	9.29002631	1.54E-20	6.06E-20
LOC100651663	140.889654	1.065009304	0.19246601	5.53349305	3.14E-08	5.89E-08
LOC100646339	350.404324	1.066226108	0.30864127	3.45458051	0.00055115	0.00077701
LOC100642357	626.565	1.066934224	0.11340138	9.40847676	5.03E-21	2.03E-20
LOC100650003	256.249319	1.067067286	0.14491328	7.3634887	1.79E-13	4.64E-13
LOC100644690	146.618866	1.067545988	0.18435742	5.79063204	7.01E-09	1.38E-08
LOC100644843	26.8989912	1.067575775	0.26493281	4.02960948	5.59E-05	8.52E-05
LOC100647361	1199.42781	1.068573197	0.10123845	10.5550129	4.82E-26	2.59E-25
LOC100647024	220.933628	1.068773109	0.19297678	5.53835087	3.05E-08	5.74E-08
LOC100645565	697.568556	1.068875835	0.07420062	14.4052146	4.80E-47	1.04E-45
LOC100647862	189.239531	1.070214523	0.12883126	8.30710295	9.81E-17	3.09E-16
LOC100644245	584.757457	1.071019773	0.11547897	9.27458677	1.78E-20	6.98E-20
LOC100646331	1000.39817	1.07106196	0.10528384	10.1730894	2.61E-24	1.26E-23
LOC100651448	1050.7576	1.07122597	0.07366036	14.5427747	6.49E-48	1.53E-46
LOC100650316	1810.55995	1.072002743	0.10103953	10.6097359	2.69E-26	1.47E-25
LOC100647916	47.4190449	1.073002928	0.41941208	2.55835007	0.01051702	0.01339387
LOC100645816	296.045384	1.073127817	0.1090116	9.84416179	7.26E-23	3.20E-22
LOC100646929	285.892613	1.073255411	0.14140747	7.58980692	3.20E-14	8.68E-14
LOC105666969	156.844369	1.075713539	0.33184711	3.2415938	0.00118863	0.00163156
LOC100646857	109.768489	1.075799344	0.2169397	4.95897855	7.09E-07	1.23E-06
LOC100642565	809.715096	1.076137616	0.13173993	8.16865206	3.12E-16	9.50E-16
LOC100650747	1148.34421	1.076964026	0.08059835	13.3621102	1.01E-40	1.41E-39

LOC100645711	203.208317	1.077133304	0.22913584	4.70085045	2.59E-06	4.30E-06
LOC100644294	2262.82577	1.077353081	0.07061614	15.2564714	1.49E-52	4.97E-51
LOC105666942	733.363289	1.077534829	0.08889255	12.1217671	8.10E-34	7.01E-33
LOC100648021	932.965772	1.078827334	0.0744392	14.4927315	1.35E-47	3.07E-46
LOC100643270	328.224565	1.080354439	0.09881238	10.933391	7.98E-28	4.81E-27
LOC100646593	48.9295841	1.081854702	0.39810207	2.71753094	0.0065771	0.00850005
LOC100646436	500.595086	1.082020058	0.1013229	10.6789286	1.28E-26	7.13E-26
LOC100646462	520.474053	1.082351028	0.12947052	8.35982617	6.28E-17	2.00E-16
LOC100646489	285.297831	1.082372325	0.21017187	5.14993918	2.61E-07	4.62E-07
LOC100652284	432.73261	1.082721071	0.08709774	12.4311041	1.77E-35	1.72E-34
LOC100650987	924.014228	1.084716739	0.09782626	11.0881962	1.43E-28	9.03E-28
LOC100650539	565.36544	1.085539093	0.08405637	12.9144177	3.73E-38	4.34E-37
LOC100643831	938.446855	1.086006033	0.08515781	12.7528641	3.00E-37	3.28E-36
LOC100651073	212.663762	1.087166407	0.1615312	6.73038016	1.69E-11	3.88E-11
LOC100645924	476.783014	1.087481479	0.11712107	9.28510502	1.62E-20	6.34E-20
LOC100642529	686.525702	1.089178889	0.0932595	11.6790131	1.63E-31	1.23E-30
LOC100651203	310.962667	1.092338199	0.16514178	6.61454782	3.73E-11	8.36E-11
LOC100643407	367.677818	1.092492822	0.11120131	9.82446037	8.83E-23	3.88E-22
LOC100644493	592.626444	1.092795647	0.08983311	12.1647312	4.79E-34	4.24E-33
LOC100643380	677.946193	1.093071287	0.1736723	6.29387226	3.10E-10	6.55E-10
LOC100642583	241.709255	1.094019668	0.10185808	10.7406271	6.56E-27	3.74E-26
LOC100643988	2180.66181	1.094191639	0.09988883	10.9540937	6.35E-28	3.85E-27
LOC100649632	2324.88563	1.094739651	0.13777166	7.94604402	1.93E-15	5.61E-15
LOC100651098	2229.78632	1.09542129	0.12719707	8.61200089	7.18E-18	2.41E-17
LOC100648347	3171.41219	1.09737243	0.09571555	11.4649338	1.98E-30	1.40E-29
LOC100643935	1289.26156	1.097829107	0.08160682	13.4526645	2.97E-41	4.28E-40
LOC100650603	405.060988	1.098604981	0.11017633	9.97133409	2.03E-23	9.28E-23
LOC100650389	483.165119	1.100775886	0.10012659	10.9938419	4.09E-28	2.52E-27
LOC100647638	123.579288	1.101566875	0.1666954	6.60826197	3.89E-11	8.70E-11

LOC100642330	375.720059	1.103414338	0.1347798	8.18679281	2.68E-16	8.21E-16
LOC100642972	804.875312	1.104254047	0.16759633	6.58877217	4.43E-11	9.89E-11
LOC100651706	856.384075	1.106820973	0.12219739	9.05764818	1.33E-19	4.98E-19
LOC100646867	582.246929	1.107551433	0.07655866	14.4667044	1.97E-47	4.43E-46
LOC100643440	357.60138	1.108258448	0.10127631	10.9429189	7.18E-28	4.35E-27
LOC100643422	1371.0699	1.108619576	0.12696202	8.73189946	2.50E-18	8.62E-18
LOC100643179	463.600387	1.109262145	0.09838639	11.2745486	1.75E-29	1.17E-28
LOC100651906	10.35229	1.10941789	0.39710886	2.79373746	0.00521028	0.00678736
LOC100651179	1050.4133	1.109490908	0.07413062	14.9667014	1.21E-50	3.48E-49
LOC100644708	549.987873	1.110215824	0.07798185	14.2368498	5.41E-46	1.09E-44
LOC100645489	5677.34322	1.110293241	0.13998731	7.93138519	2.17E-15	6.30E-15
LOC100642732	38.3975739	1.110707237	0.31229705	3.55657299	0.00037572	0.00053715
LOC100643718	731.754949	1.110937858	0.09626674	11.5402044	8.27E-31	5.99E-30
LOC100647134	106.339134	1.111564432	0.1921082	5.78613747	7.20E-09	1.41E-08
LOC100652136	402.659345	1.112386105	0.09197677	12.094207	1.13E-33	9.71E-33
LOC100647620	245.241852	1.112993579	0.18587077	5.98799687	2.12E-09	4.30E-09
LOC100647480	487.344801	1.113172447	0.10626988	10.4749577	1.13E-25	5.92E-25
LOC100649734	149.746227	1.113615561	0.19663376	5.66339963	1.48E-08	2.84E-08
LOC100643999	95.114869	1.113790326	0.21684325	5.13638456	2.80E-07	4.96E-07
LOC100650777	1479.87768	1.116155391	0.08173125	13.6564097	1.85E-42	2.91E-41
LOC100648535	1099.89592	1.1172452	0.11307515	9.88055506	5.06E-23	2.24E-22
LOC100645938	104.38747	1.11740135	0.17025795	6.56299093	5.27E-11	1.17E-10
LOC100643226	346.78648	1.117734137	0.09555305	11.697524	1.31E-31	9.91E-31
LOC105666780	384.26374	1.118199791	0.20766205	5.38470946	7.26E-08	1.33E-07
LOC100647976	712.454907	1.11868538	0.16543254	6.76218474	1.36E-11	3.14E-11
LOC100646753	18.8809631	1.119163775	0.39569118	2.82837685	0.00467847	0.00611166
LOC100642365	295.612687	1.119763469	0.10168713	11.0118505	3.35E-28	2.07E-27
LOC100650429	627.733794	1.119844452	0.09806567	11.4193321	3.35E-30	2.34E-29
LOC100646023	754.429903	1.120682468	0.1136157	9.86379957	5.97E-23	2.65E-22

LOC100651590	568.151576	1.121315322	0.18443023	6.07988901	1.20E-09	2.47E-09
LOC100642479	949.238248	1.123096889	0.08950927	12.5472687	4.11E-36	4.14E-35
LOC100645285	456.958258	1.123888473	0.10975831	10.2396659	1.32E-24	6.47E-24
LOC100649764	652.821567	1.123925248	0.10027624	11.2082911	3.71E-29	2.43E-28
LOC100643259	264.320025	1.123992784	0.1236279	9.09174083	9.75E-20	3.66E-19
LOC100645100	433.282787	1.124398912	0.09471485	11.8714104	1.67E-32	1.32E-31
LOC100652260	1576.09088	1.124982489	0.08934541	12.5913849	2.36E-36	2.42E-35
LOC100645962	72.2267871	1.125545082	0.15644031	7.19472531	6.26E-13	1.57E-12
LOC100645659	375.749857	1.12556944	0.10686819	10.5323147	6.13E-26	3.28E-25
LOC100651681	1285.99912	1.126334385	0.07643119	14.736581	3.75E-49	9.67E-48
LOC100646180	636.367077	1.126353826	0.09181319	12.2678867	1.35E-34	1.23E-33
LOC100645948	698.804988	1.126623453	0.1021758	11.0263237	2.85E-28	1.77E-27
LOC100650766	589.189443	1.127846831	0.11734967	9.61099243	7.19E-22	3.01E-21
LOC100642630	291.270186	1.128062948	0.12133352	9.29720812	1.44E-20	5.68E-20
LOC100649291	1006.07982	1.129700276	0.10619584	10.6378956	1.99E-26	1.10E-25
LOC100649202	695.505166	1.130052166	0.32915224	3.43322031	0.00059646	0.0008375
LOC100646000	560.133847	1.130366222	0.10917604	10.3536104	4.03E-25	2.05E-24
LOC100648387	366.208151	1.131706202	0.10360814	10.9229466	8.95E-28	5.38E-27
LOC100649879	425.895863	1.132168645	0.14871822	7.61284418	2.68E-14	7.30E-14
LOC100642712	554.605672	1.13247068	0.11224476	10.0892971	6.16E-24	2.90E-23
LOC100651787	4229.46629	1.132845182	0.17924861	6.31996637	2.62E-10	5.56E-10
LOC100650796	493.75073	1.134630648	0.08692973	13.0522734	6.17E-39	7.54E-38
LOC100649316	426.850335	1.135439599	0.0942621	12.0455579	2.05E-33	1.72E-32
LOC100646634	313.471185	1.136300475	0.10414974	10.910257	1.03E-27	6.15E-27
LOC100642631	1038.08925	1.139571591	0.07624663	14.9458623	1.66E-50	4.68E-49
LOC100650462	410.836704	1.13993274	0.11340852	10.0515621	9.04E-24	4.21E-23
LOC100642842	2979.26838	1.141425464	0.13299501	8.58246806	9.29E-18	3.10E-17
LOC100649027	154.343668	1.142500081	0.16295507	7.01113549	2.36E-12	5.72E-12
LOC100645977	503.649935	1.144133971	0.09854779	11.6099407	3.67E-31	2.70E-30

LOC100645142	1744.587	1.144417968	0.07675	14.9109833	2.80E-50	7.73E-49
LOC100642966	164.421175	1.145225102	0.12819345	8.93356962	4.12E-19	1.50E-18
LOC100648857	1811.63806	1.145543547	0.08310916	13.7836009	3.20E-43	5.32E-42
LOC100648759	1791.73232	1.145656273	0.07835146	14.6220161	2.03E-48	5.04E-47
LOC100652215	2663.63402	1.147541345	0.10082678	11.3813155	5.18E-30	3.59E-29
LOC100648085	778.158082	1.148986032	0.1314899	8.73820744	2.37E-18	8.17E-18
LOC100646678	1669.84687	1.150238169	0.07675893	14.9850734	9.19E-51	2.65E-49
LOC100648270	353.310155	1.15183615	0.13631746	8.44965972	2.92E-17	9.42E-17
LOC100642273	790.004528	1.152451674	0.0941722	12.2377059	1.95E-34	1.77E-33
LOC100642323	409.191933	1.153893317	0.08779444	13.1431249	1.86E-39	2.37E-38
LOC100642424	712.00556	1.154570275	0.08014963	14.4051855	4.80E-47	1.04E-45
LOC100642314	275.815195	1.15512198	0.14742618	7.83525668	4.68E-15	1.33E-14
LOC100646190	2675.2762	1.158930074	0.0768211	15.0860906	2.00E-51	6.16E-50
LOC100642998	688.182057	1.159231102	0.10029425	11.5583009	6.70E-31	4.88E-30
LOC100648906	210.539867	1.159397343	0.15291943	7.58175298	3.41E-14	9.23E-14
LOC100650917	245.361358	1.159765637	0.12385085	9.36421235	7.66E-21	3.06E-20
LOC100650109	985.587596	1.159802853	0.09995652	11.6030741	3.98E-31	2.93E-30
LOC100649699	293.688719	1.160224689	0.12977323	8.94040091	3.88E-19	1.41E-18
LOC100646724	843.054679	1.161096931	0.07994763	14.5232187	8.64E-48	2.01E-46
LOC100649944	752.648116	1.161457198	0.08736051	13.2949907	2.48E-40	3.34E-39
LOC100647546	1340.14688	1.16225634	0.07786849	14.9258881	2.24E-50	6.20E-49
LOC105666676	82.7248685	1.162310047	0.18769824	6.19243961	5.92E-10	1.23E-09
LOC100650559	415.391211	1.162375455	0.08387308	13.8587422	1.13E-43	1.93E-42
LOC105665936	7773.43224	1.162711202	0.51896827	2.2404283	0.02506313	0.03090204
LOC100651264	739.837588	1.16339775	0.08112569	14.340683	1.22E-46	2.57E-45
LOC105666220	61.8280558	1.164903705	0.27280199	4.27014367	1.95E-05	3.07E-05
LOC100643185	204.758949	1.16850213	0.1870572	6.24676385	4.19E-10	8.80E-10
LOC100648523	1194.32596	1.169326538	0.0897859	13.0234991	9.00E-39	1.08E-37
LOC100647244	1199.845	1.169571146	0.08023727	14.5764083	3.97E-48	9.64E-47

LOC100647323	338.700311	1.170489785	0.21937845	5.33548196	9.53E-08	1.73E-07
LOC100642911	713.096532	1.170506834	0.07359768	15.9041274	5.93E-57	2.76E-55
LOC100643924	566.719433	1.171011294	0.10548706	11.1009952	1.24E-28	7.85E-28
LOC100647420	950.522606	1.171328876	0.0943237	12.4181816	2.08E-35	2.02E-34
LOC100651575	838.641582	1.171499699	0.10805974	10.841223	2.20E-27	1.29E-26
LOC100643147	758.646096	1.171616884	0.12046083	9.72612321	2.33E-22	1.00E-21
LOC100647553	1056.19653	1.17167063	0.09089217	12.8907759	5.07E-38	5.82E-37
LOC100648080	916.5694	1.172550535	0.10342785	11.3368941	8.61E-30	5.85E-29
LOC100646756	377.654495	1.174171729	0.34546639	3.39880168	0.00067682	0.0009464
LOC100647987	469.809344	1.174728929	0.11358583	10.3422141	4.54E-25	2.30E-24
LOC100644060	357.816332	1.174835776	0.15004995	7.82963101	4.89E-15	1.39E-14
LOC100646250	624.95439	1.175035641	0.09241819	12.7143328	4.92E-37	5.29E-36
LOC100643917	775.132477	1.175610132	0.08339433	14.0970026	3.96E-45	7.49E-44
LOC100646855	499.021154	1.176742494	0.08724637	13.4875814	1.85E-41	2.72E-40
LOC100646830	224.987544	1.176745777	0.15475971	7.60369589	2.88E-14	7.82E-14
LOC100643340	294.879704	1.177146687	0.0960098	12.2606936	1.47E-34	1.35E-33
LOC100642854	500.720854	1.178784621	0.09113838	12.9340083	2.89E-38	3.38E-37
LOC100643118	1227.69032	1.178807086	0.12035986	9.7940217	1.19E-22	5.21E-22
LOC100649935	265.867957	1.179267417	0.09854132	11.9672378	5.28E-33	4.32E-32
LOC100648808	514.478549	1.17986958	0.11360766	10.3854752	2.89E-25	1.48E-24
LOC100650691	1491.26991	1.179932729	0.07156306	16.4880134	4.47E-61	2.98E-59
LOC100649794	614.166158	1.18071443	0.16154144	7.30904989	2.69E-13	6.90E-13
LOC100642278	424.406987	1.181245063	0.16242662	7.27248445	3.53E-13	9.01E-13
LOC100651346	410.43667	1.181947706	0.21592117	5.47397783	4.40E-08	8.18E-08
LOC100644547	667.251266	1.182013975	0.1017306	11.6190608	3.30E-31	2.44E-30
LOC100651933	96.1687002	1.182505148	0.15527684	7.61546357	2.63E-14	7.16E-14
LOC100649893	2786.20104	1.182767932	0.07031433	16.8211515	1.71E-63	1.38E-61
LOC100645235	580.377682	1.184046855	0.10633944	11.1345969	8.51E-29	5.46E-28
LOC105666674	42.0205696	1.185440718	0.28884126	4.10412523	4.06E-05	6.23E-05

LOC100648489	11.87524	1.186678479	0.45516999	2.60711051	0.00913099	0.01168036
LOC100649422	436.473894	1.188410324	0.1032627	11.5086121	1.19E-30	8.58E-30
LOC100643403	377.22266	1.190884067	0.11204362	10.6287538	2.19E-26	1.20E-25
LOC100650485	66.9773652	1.19188206	0.34710874	3.43374256	0.00059531	0.00083601
LOC100651477	777.413682	1.194206921	0.08436076	14.1559528	1.72E-45	3.35E-44
LOC100643486	64.5299675	1.194558434	0.39531154	3.02181524	0.00251264	0.00337003
LOC105666150	120.145574	1.194816022	0.20784558	5.74857564	9.00E-09	1.75E-08
LOC100651326	2296.64014	1.195144929	0.08170231	14.6280439	1.86E-48	4.64E-47
LOC100651375	2252.25713	1.197653732	0.10755024	11.1357609	8.40E-29	5.39E-28
LOC100650510	1072.44413	1.197890106	0.09149234	13.0927913	3.62E-39	4.49E-38
LOC100642532	462.018484	1.197967273	0.11605429	10.322473	5.58E-25	2.81E-24
LOC100648366	88.1060451	1.198291778	0.27149176	4.41373168	1.02E-05	1.62E-05
LOC100645678	511.361948	1.199956957	0.25641823	4.67968666	2.87E-06	4.75E-06
LOC100650306	818.907954	1.200165627	0.08818663	13.6093836	3.52E-42	5.44E-41
LOC105666801	9.7029125	1.200564819	0.55240458	2.17334337	0.02975448	0.0364163
LOC100649474	887.782945	1.200752051	0.14085651	8.52464689	1.53E-17	5.05E-17
LOC100650829	798.467871	1.2007536	0.11298106	10.6279194	2.21E-26	1.21E-25
LOC100644952	955.887526	1.20083344	0.0699821	17.1591516	5.37E-66	5.31E-64
LOC100644610	408.546212	1.201483142	0.15714952	7.64547746	2.08E-14	5.70E-14
LOC100644005	221.937026	1.202379514	0.1176979	10.2158111	1.68E-24	8.21E-24
LOC100642785	864.023325	1.202530203	0.09470104	12.6981725	6.05E-37	6.44E-36
LOC100652039	617.390049	1.20460046	0.10970464	10.9803962	4.75E-28	2.91E-27
LOC100651514	1267.65533	1.205347787	0.09582179	12.5790571	2.75E-36	2.81E-35
LOC100651885	927.32243	1.206551627	0.08587665	14.0498213	7.72E-45	1.42E-43
LOC100648177	41.0815921	1.208699046	0.30164942	4.00696622	6.15E-05	9.34E-05
LOC100644036	112.756225	1.209033419	0.20569717	5.87773481	4.16E-09	8.27E-09
LOC100643564	978.230313	1.209423891	0.0716852	16.8713182	7.31E-64	6.12E-62
LOC100645514	193.977831	1.210615563	0.1356154	8.92682949	4.38E-19	1.59E-18
LOC100649130	2195.44239	1.21131806	0.10670106	11.3524462	7.21E-30	4.93E-29

LOC100651699	1898.66473	1.212548789	0.0697028	17.3959837	8.85E-68	1.01E-65
LOC100650342	99.401027	1.212757016	0.25103386	4.83104951	1.36E-06	2.30E-06
LOC100646335	498.283472	1.212868114	0.16354961	7.41590339	1.21E-13	3.16E-13
LOC100650881	2150.55282	1.21403343	0.08555394	14.1902687	1.05E-45	2.08E-44
LOC100650912	5991.7227	1.214219284	0.09110081	13.3283044	1.58E-40	2.18E-39
LOC100648241	489.326723	1.214575319	0.11999033	10.1222767	4.40E-24	2.08E-23
LOC100648129	869.577115	1.215444262	0.10256661	11.8502917	2.14E-32	1.69E-31
LOC100647573	738.093041	1.215547359	0.08350095	14.5572871	5.25E-48	1.25E-46
LOC100644328	275.230609	1.216984487	0.10200675	11.9304315	8.21E-33	6.64E-32
LOC100644698	315.578522	1.218488197	0.19018315	6.40691991	1.48E-10	3.20E-10
LOC100647162	295.737859	1.219803822	0.1075588	11.3408096	8.24E-30	5.60E-29
LOC100649853	508.123434	1.221844632	0.09474175	12.8965809	4.71E-38	5.42E-37
LOC100648987	166.318294	1.222198946	0.22990365	5.31613538	1.06E-07	1.92E-07
LOC100643569	30.1598079	1.225279262	0.32177929	3.80782517	0.00014019	0.00020682
LOC100651990	66.9441698	1.225293052	0.37931815	3.23025161	0.00123681	0.00169532
LOC100643337	482.244988	1.225432659	0.09567175	12.8087195	1.47E-37	1.63E-36
LOC100642290	274.068131	1.227218429	0.119297	10.2870858	8.06E-25	4.02E-24
LOC100649847	1201.43608	1.227297651	0.1798783	6.82293344	8.92E-12	2.09E-11
LOC100649043	2191.59604	1.227542204	0.0814882	15.0640485	2.79E-51	8.46E-50
LOC100646981	569.470813	1.22808233	0.1053655	11.6554502	2.15E-31	1.61E-30
LOC100644065	587.521296	1.228576691	0.07339246	16.7398212	6.72E-63	4.95E-61
LOC100643205	867.7351	1.229177733	0.13311138	9.23420461	2.60E-20	1.01E-19
LOC100652142	665.525068	1.229209544	0.08780544	13.9992414	1.58E-44	2.85E-43
LOC100643690	171.096342	1.229654999	0.12657396	9.714913	2.60E-22	1.12E-21
LOC100649568	17.8871859	1.229955192	0.53839931	2.28446652	0.02234413	0.02766456
LOC100647660	364.868873	1.231859113	0.11151245	11.0468306	2.27E-28	1.42E-27
LOC100642527	272.921021	1.232872751	0.1202051	10.25641	1.11E-24	5.47E-24
LOC100644794	688.238878	1.233249269	0.08650788	14.2559183	4.12E-46	8.38E-45
LOC100651533	354.188891	1.233351263	0.14833338	8.31472505	9.20E-17	2.90E-16

LOC100644873	139.168761	1.233534948	0.25818704	4.77767949	1.77E-06	2.98E-06
LOC100645428	528.761984	1.233780452	0.10717359	11.5119822	1.15E-30	8.26E-30
LOC100643282	267.129717	1.234475711	0.14232461	8.67366299	4.18E-18	1.42E-17
LOC100648946	1901.71223	1.234897054	0.07282639	16.956724	1.72E-64	1.51E-62
LOC100648606	401.871209	1.235014773	0.09086201	13.5922016	4.45E-42	6.84E-41
LOC105665619	408.772962	1.235111739	0.11130915	11.0962279	1.31E-28	8.27E-28
LOC100646628	736.048773	1.235309729	0.09387841	13.1586138	1.52E-39	1.94E-38
LOC100652095	1254.97056	1.235461236	0.10011398	12.3405464	5.48E-35	5.15E-34
LOC100642195	384.293954	1.235478875	0.1420705	8.6962382	3.43E-18	1.17E-17
LOC100642800	336.894939	1.235487121	0.11456842	10.7838364	4.10E-27	2.37E-26
LOC100651673	925.910725	1.235801228	0.12796594	9.65726676	4.58E-22	1.94E-21
LOC100648978	449.767883	1.236580623	0.11430263	10.8184788	2.81E-27	1.64E-26
LOC100646322	504.113597	1.237133256	0.10426204	11.865615	1.79E-32	1.41E-31
LOC100650634	271.11748	1.239279368	0.15693949	7.89654251	2.87E-15	8.27E-15
LOC100651914	542.254037	1.239873843	0.08008264	15.4824301	4.56E-54	1.65E-52
LOC100650381	808.423279	1.24031477	0.13160405	9.42459448	4.32E-21	1.75E-20
LOC100649889	111.25132	1.240399741	0.18801985	6.59717434	4.19E-11	9.36E-11
LOC100646707	383.451424	1.240622799	0.11770276	10.5403033	5.63E-26	3.02E-25
LOC105666989	171.807785	1.241050996	0.17433142	7.11891743	1.09E-12	2.69E-12
LOC100648565	644.489285	1.241838956	0.095953	12.9421591	2.60E-38	3.05E-37
LOC100643076	396.561019	1.241982801	0.10833822	11.463939	2.00E-30	1.42E-29
LOC100645140	3022.62377	1.242342209	0.07624765	16.2935157	1.10E-59	6.25E-58
LOC100652044	216.896338	1.242472765	0.15340452	8.09932321	5.53E-16	1.66E-15
LOC105666297	38.1451683	1.243134522	0.26773465	4.64315894	3.43E-06	5.64E-06
LOC100650884	1121.74939	1.243476996	0.16388291	7.58759422	3.26E-14	8.83E-14
LOC100646916	171.686789	1.244377608	0.15216457	8.17784075	2.89E-16	8.82E-16
LOC100651414	1064.69147	1.244438201	0.08585572	14.4945283	1.31E-47	2.99E-46
LOC100646063	971.68525	1.245512544	0.20680604	6.02261201	1.72E-09	3.49E-09
LOC100650683	743.191668	1.246792392	0.09223199	13.5180044	1.22E-41	1.82E-40

LOC100649796	15.6825649	1.250976509	0.52440002	2.38553865	0.01705413	0.02129809
LOC100648907	599.795282	1.252186162	0.13754828	9.10361211	8.74E-20	3.29E-19
LOC100643781	39.5117623	1.253518108	0.4521134	2.77257455	0.00556148	0.00722948
LOC100648614	2302.86642	1.254698834	0.08557694	14.6616457	1.13E-48	2.87E-47
LOC100651380	1052.81926	1.255012488	0.08593237	14.6046529	2.62E-48	6.47E-47
LOC100643467	872.382005	1.255195461	0.10115498	12.4086372	2.35E-35	2.27E-34
LOC100651667	63.4808736	1.256039096	0.26477448	4.74380716	2.10E-06	3.50E-06
LOC100650677	852.22427	1.256704175	0.08726506	14.4010011	5.10E-47	1.11E-45
LOC100650180	412.73232	1.25714183	0.09112435	13.7958931	2.70E-43	4.52E-42
LOC105666550	195.904592	1.257371796	0.20075882	6.26309627	3.77E-10	7.95E-10
LOC100649485	156.362683	1.258636406	0.19621291	6.41464617	1.41E-10	3.04E-10
LOC100651164	562.414999	1.25941203	0.1219865	10.3241922	5.48E-25	2.76E-24
LOC105666877	490.474621	1.260624866	0.13189624	9.5577016	1.20E-21	5.00E-21
LOC105666348	35.237652	1.261609454	0.21908253	5.75860351	8.48E-09	1.65E-08
LOC100650594	695.074201	1.262422894	0.09419312	13.4024956	5.85E-41	8.26E-40
LOC100642254	7360.51995	1.262655951	0.10754898	11.740288	7.92E-32	6.06E-31
LOC100648365	626.588324	1.262680654	0.10454037	12.078402	1.37E-33	1.17E-32
LOC100644745	174.84935	1.266159633	0.12442775	10.1758622	2.54E-24	1.22E-23
LOC100645165	280.785077	1.266474019	0.1327979	9.53685279	1.47E-21	6.08E-21
LOC100644542	990.767585	1.266494642	0.10608259	11.9387602	7.43E-33	6.03E-32
LOC100644560	589.690062	1.268192615	0.08564694	14.8072151	1.32E-49	3.52E-48
LOC100645303	579.082009	1.269824208	0.10069696	12.6103534	1.85E-36	1.92E-35
LOC100650079	1121.473	1.270369267	0.11833083	10.7357425	6.92E-27	3.94E-26
LOC100649701	311.426062	1.271168118	0.1251138	10.1600953	2.99E-24	1.43E-23
LOC100644741	628.967086	1.271497733	0.13316258	9.54846093	1.32E-21	5.45E-21
LOC100647949	961.176302	1.272701282	0.54258715	2.34561635	0.01899565	0.02365637
LOC100651585	255.277228	1.275112057	0.13940015	9.14713549	5.85E-20	2.23E-19
LOC100648742	371.317782	1.276391468	0.10513577	12.1404113	6.45E-34	5.63E-33
LOC100648553	34.4555557	1.276471316	0.23971886	5.32486815	1.01E-07	1.84E-07

LOC100649591	2667.03862	1.276889616	0.08120024	15.7251942	1.02E-55	4.23E-54
LOC100649844	523.27444	1.277095132	0.13527451	9.44076694	3.70E-21	1.50E-20
LOC100642665	1305.68463	1.277959323	0.08916397	14.3326876	1.37E-46	2.87E-45
LOC100650644	900.440823	1.278271418	0.11234522	11.3780666	5.38E-30	3.72E-29
LOC100642986	701.020747	1.278443959	0.1298383	9.84643147	7.10E-23	3.14E-22
LOC100651302	412.322541	1.27860791	0.08548091	14.9578183	1.38E-50	3.94E-49
LOC100650932	628.05038	1.279530911	0.14897409	8.58894959	8.78E-18	2.93E-17
LOC100650356	426.927472	1.279837731	0.12742775	10.0436344	9.80E-24	4.56E-23
LOC100646438	934.56381	1.27983815	0.08216739	15.5759865	1.06E-54	3.98E-53
LOC105667118	14.1550633	1.280872437	0.47473161	2.69809806	0.00697369	0.00899478
LOC100645524	24459.8464	1.282677901	0.42508708	3.01744739	0.00254913	0.00341758
LOC100642788	1696.35673	1.283552339	0.08938076	14.3604994	9.16E-47	1.95E-45
LOC100652214	326.182429	1.283625579	0.100179	12.8133206	1.38E-37	1.54E-36
LOC100648074	1574.60635	1.284472	0.08115305	15.8277719	2.00E-56	8.71E-55
LOC100649561	649.315327	1.284513801	0.14714117	8.72980558	2.55E-18	8.77E-18
LOC100649903	913.32365	1.284985874	0.11677617	11.0038364	3.66E-28	2.26E-27
LOC100649948	1878.34635	1.285035916	0.1156811	11.1084345	1.14E-28	7.25E-28
LOC100651950	760.840034	1.285529686	0.08347107	15.4009012	1.61E-53	5.62E-52
LOC100652290	380.55983	1.285545682	0.14437304	8.90433337	5.37E-19	1.94E-18
LOC100652128	5240.68676	1.287519485	0.07581347	16.9827263	1.10E-64	1.01E-62
LOC105666526	10.0080548	1.28755473	0.45934718	2.80300996	0.00506281	0.00659877
LOC100649987	121.62657	1.287621247	0.1806688	7.1269707	1.03E-12	2.54E-12
LOC100645480	94.9813952	1.288032155	0.21081718	6.10971167	9.98E-10	2.06E-09
LOC100644688	895.525246	1.289106219	0.14378889	8.96527015	3.10E-19	1.13E-18
LOC100644890	99.3750036	1.289211024	0.17992775	7.16515952	7.77E-13	1.94E-12
LOC100651242	380.196344	1.293209162	0.1235086	10.4706002	1.18E-25	6.20E-25
LOC100649849	2032.45653	1.295380998	0.15242719	8.49835899	1.92E-17	6.29E-17
LOC100652299	480.556617	1.295485575	0.09248394	14.0076815	1.40E-44	2.54E-43
LOC100650528	840.644172	1.296657053	0.08215984	15.7821274	4.13E-56	1.76E-54

LOC100644896	331.340287	1.296699682	0.11995874	10.8095474	3.10E-27	1.81E-26
LOC100646520	13.8141232	1.296944823	0.39926445	3.24833535	0.00116082	0.0015954
LOC100643082	18.3854348	1.297947923	0.34176473	3.79778191	0.000146	0.00021521
LOC100651424	501.048653	1.299198937	0.10329394	12.5776879	2.80E-36	2.85E-35
LOC100649511	648.368674	1.299473292	0.11430494	11.3684786	6.00E-30	4.13E-29
LOC100648181	887.076311	1.300220907	0.08265565	15.7305742	9.34E-56	3.91E-54
LOC100646211	485.673712	1.300393694	0.13900355	9.35511121	8.35E-21	3.32E-20
LOC100650960	406.349403	1.300417319	0.12276361	10.5928565	3.22E-26	1.75E-25
LOC100645899	863.45334	1.301855819	0.11334759	11.4855181	1.56E-30	1.11E-29
LOC100650946	625.766897	1.302617395	0.09686279	13.4480686	3.16E-41	4.54E-40
LOC100650531	634.711773	1.303896116	0.10155329	12.8395267	9.85E-38	1.11E-36
LOC100645246	435.810724	1.304106065	0.10472512	12.4526581	1.35E-35	1.32E-34
LOC100644411	672.610813	1.304873971	0.1640447	7.95438039	1.80E-15	5.25E-15
LOC100650008	313.302934	1.305403787	0.12041528	10.8408485	2.20E-27	1.30E-26
LOC100649330	240.539426	1.305534447	0.15059458	8.66919964	4.35E-18	1.48E-17
LOC100647973	864.875701	1.306106819	0.07755161	16.8417757	1.21E-63	9.92E-62
LOC100646635	884.144732	1.306181293	0.10563982	12.3644783	4.07E-35	3.86E-34
LOC100643051	303.350426	1.306249449	0.1360169	9.60358199	7.72E-22	3.23E-21
LOC100646493	578.014385	1.30681992	0.10644576	12.2768623	1.21E-34	1.11E-33
LOC100643987	287.669343	1.306919101	0.16406791	7.96572026	1.64E-15	4.80E-15
LOC100651620	673.540568	1.307267566	0.11710392	11.1633113	6.17E-29	3.98E-28
LOC100647360	826.137542	1.307273006	0.16504858	7.92053475	2.36E-15	6.86E-15
LOC100646185	688.958264	1.307777478	0.12199619	10.7198221	8.22E-27	4.65E-26
LOC100644710	24.1196876	1.310901973	0.32904631	3.98394365	6.78E-05	0.00010254
LOC100651826	248.14663	1.310999148	0.14520652	9.02851422	1.74E-19	6.45E-19
LOC100645746	1093.16277	1.311065782	0.08748803	14.9856593	9.11E-51	2.64E-49
LOC100644157	373.827939	1.311827006	0.12252869	10.7062849	9.51E-27	5.36E-26
LOC100651012	800.762425	1.312659171	0.07759405	16.9170072	3.37E-64	2.90E-62
LOC100647352	13032.9631	1.31285671	0.11445593	11.4704123	1.86E-30	1.32E-29

LOC100645423	35.3448824	1.316485749	0.32869879	4.00514327	6.20E-05	9.41E-05
LOC100648401	877.824849	1.317286088	0.07395352	17.8123505	5.67E-71	8.67E-69
LOC105666648	1229.80853	1.319058934	0.07592756	17.3725977	1.33E-67	1.50E-65
LOC100646869	303.650523	1.319093434	0.11561982	11.4088867	3.78E-30	2.63E-29
LOC100647177	194.888395	1.319922143	0.16846224	7.83512181	4.68E-15	1.33E-14
LOC100644564	872.197285	1.320933678	0.09428277	14.0103401	1.35E-44	2.45E-43
LOC100648411	569.868655	1.321281656	0.10382152	12.7264713	4.21E-37	4.54E-36
LOC100648413	331.33286	1.321313393	0.11877885	11.1241473	9.57E-29	6.13E-28
LOC100649808	1332.52625	1.321805203	0.09872753	13.388415	7.07E-41	9.97E-40
LOC100645728	512.545714	1.32208986	0.1407507	9.39313172	5.82E-21	2.34E-20
LOC100650206	354.489822	1.322890046	0.12708219	10.4097201	2.24E-25	1.16E-24
LOC100650725	225.54657	1.323977756	0.14763829	8.96771266	3.03E-19	1.11E-18
LOC100646137	559.291226	1.325186433	0.13737493	9.64649428	5.09E-22	2.15E-21
LOC100651357	50.1147364	1.32633248	0.24164309	5.48880779	4.05E-08	7.54E-08
LOC100651219	784.677726	1.327535995	0.102872	12.9047363	4.23E-38	4.89E-37
LOC100643064	294.498163	1.32782857	0.12817358	10.3596123	3.78E-25	1.93E-24
LOC100649309	106.603639	1.329035535	0.38266513	3.47310332	0.00051448	0.0007274
LOC100642819	729.871579	1.330893747	0.10631313	12.518621	5.91E-36	5.87E-35
LOC100645871	2698.25956	1.330915259	0.08459413	15.7329512	8.99E-56	3.78E-54
LOC100645313	753.097709	1.331156962	0.09410567	14.1453421	2.00E-45	3.88E-44
LOC100645846	423.326648	1.331233914	0.13784178	9.65769538	4.56E-22	1.93E-21
LOC100648291	13.7212286	1.331542499	0.37945948	3.50905052	0.00044971	0.00063943
LOC100643930	353.364091	1.331657815	0.11737289	11.345531	7.81E-30	5.32E-29
LOC100649495	932.040994	1.332909627	0.07950774	16.7645273	4.44E-63	3.39E-61
LOC100649186	373.118529	1.333322259	0.14290572	9.33008345	1.06E-20	4.19E-20
LOC100646755	195.842306	1.333521706	0.17092972	7.80157894	6.11E-15	1.72E-14
LOC100645844	683.84293	1.33483777	0.11122537	12.0011985	3.50E-33	2.90E-32
LOC100645276	851.023824	1.335799893	0.09561927	13.9699864	2.38E-44	4.24E-43
LOC100644084	132.895047	1.336226275	0.2112185	6.32627476	2.51E-10	5.35E-10

LOC100649873	2288.31619	1.337532587	0.10132471	13.2004577	8.72E-40	1.14E-38
LOC100647884	110.187736	1.338438425	0.46353344	2.887469	0.00388355	0.00511485
LOC100647297	637.244611	1.339199774	0.08870937	15.0964868	1.71E-51	5.28E-50
LOC100651965	1577.10031	1.341107266	0.11023343	12.1660663	4.71E-34	4.18E-33
LOC100646783	691.052021	1.343563101	0.11783831	11.4017509	4.10E-30	2.85E-29
LOC100644003	428.484839	1.348637781	0.20773792	6.49201529	8.47E-11	1.85E-10
LOC100651792	401.899256	1.348791671	0.13219111	10.2033464	1.92E-24	9.30E-24
LOC100643966	291.991139	1.349072736	0.12314619	10.9550502	6.28E-28	3.81E-27
LOC100645267	61.9095756	1.349395922	0.26312366	5.12837167	2.92E-07	5.17E-07
LOC100649165	886.924213	1.350389007	0.12647129	10.6774349	1.30E-26	7.24E-26
LOC105666281	12.867827	1.352132162	0.49440877	2.73484666	0.00624093	0.00807306
LOC100645093	655.116464	1.352393186	0.10263515	13.1767063	1.19E-39	1.55E-38
LOC100651060	691.34091	1.353114965	0.21091293	6.41551451	1.40E-10	3.02E-10
LOC100648045	631.7115	1.353612591	0.0954355	14.1835337	1.16E-45	2.28E-44
LOC100648648	622.46366	1.354234584	0.0994879	13.612053	3.40E-42	5.25E-41
LOC100642601	502.044904	1.356008854	0.12554601	10.800892	3.41E-27	1.98E-26
LOC100652201	1469.41643	1.356778533	0.12176717	11.1424	7.80E-29	5.01E-28
LOC105666672	77.5518888	1.356841318	0.28158524	4.81858106	1.45E-06	2.44E-06
LOC100642406	566.037671	1.357552472	0.10892775	12.462871	1.19E-35	1.17E-34
LOC100645505	183.160902	1.358619573	0.13403808	10.1360716	3.82E-24	1.82E-23
LOC100649099	30.5659702	1.359081873	0.36362064	3.73763681	0.00018576	0.00027211
LOC100646072	370.516184	1.360518565	0.0984775	13.8155273	2.05E-43	3.47E-42
LOC100647145	635.643503	1.360600992	0.10656032	12.768364	2.46E-37	2.70E-36
LOC100647630	1284.10915	1.362853968	0.11801858	11.5477921	7.57E-31	5.49E-30
LOC100648591	4101.62505	1.363239927	0.09261543	14.7193605	4.84E-49	1.24E-47
LOC100643777	11709.9281	1.36340709	0.46530452	2.93013936	0.0033881	0.00448646
LOC100648364	1030.31533	1.36425569	0.1678529	8.1276862	4.38E-16	1.32E-15
LOC100649011	1715.74739	1.366820335	0.10612075	12.8798594	5.84E-38	6.69E-37
LOC100646512	584.089692	1.368118284	0.16678388	8.20294057	2.35E-16	7.21E-16

LOC100649560	700.277495	1.369659185	0.08805859	15.5539526	1.50E-54	5.53E-53
LOC100645753	56.9207889	1.370089061	0.29351045	4.66793964	3.04E-06	5.02E-06
LOC100650870	372.84117	1.371873019	0.11805958	11.6201749	3.25E-31	2.41E-30
LOC100647460	18.7159661	1.372067707	0.34327252	3.99702167	6.41E-05	9.72E-05
LOC100644274	540.101126	1.372458853	0.11952756	11.4823636	1.62E-30	1.15E-29
LOC100651147	142.873674	1.372616927	0.22771654	6.02774364	1.66E-09	3.39E-09
LOC100650940	1272.2266	1.373229889	0.0862582	15.919992	4.60E-57	2.17E-55
LOC100651056	478.430979	1.373814833	0.20641909	6.65546397	2.82E-11	6.39E-11
LOC100650469	2001.984	1.375630118	0.0792253	17.3635206	1.56E-67	1.73E-65
LOC100652043	63.3814733	1.377147058	0.24706403	5.57404927	2.49E-08	4.71E-08
LOC100642927	205.931237	1.377476565	0.15428521	8.92811832	4.33E-19	1.57E-18
LOC100651662	96.8080882	1.377944351	0.1814838	7.59265761	3.13E-14	8.50E-14
LOC100644734	311.819755	1.379022847	0.14721993	9.36709336	7.46E-21	2.98E-20
LOC100645875	513.11118	1.379502853	0.13282058	10.386213	2.87E-25	1.47E-24
LOC105665614	532.567849	1.38033439	0.11270014	12.2478499	1.73E-34	1.57E-33
LOC100646601	1867.47449	1.380808301	0.10232384	13.4944929	1.69E-41	2.49E-40
LOC100649366	266.425199	1.381568178	0.18608185	7.42451854	1.13E-13	2.97E-13
LOC100644059	937.015222	1.381828801	0.07823856	17.6617354	8.27E-70	1.08E-67
LOC100644972	1244.67956	1.382247921	0.09471351	14.5939885	3.07E-48	7.51E-47
LOC100643183	82.7265596	1.382383766	0.2180018	6.34115766	2.28E-10	4.87E-10
LOC100643094	283.864419	1.382911493	0.25513636	5.42028394	5.95E-08	1.10E-07
LOC100644913	704.645656	1.383064528	0.1047053	13.2091164	7.77E-40	1.02E-38
LOC105666661	20.8321178	1.383244794	0.46358598	2.98379343	0.00284699	0.00380181
LOC100651274	1205.76997	1.383329935	0.09794179	14.1240003	2.70E-45	5.21E-44
LOC100644587	575.669317	1.383919113	0.09174443	15.0845028	2.05E-51	6.29E-50
LOC100651469	424.780807	1.384759111	0.14497516	9.55169903	1.28E-21	5.29E-21
LOC105665959	211.607474	1.387748916	0.15271325	9.08728565	1.02E-19	3.81E-19
LOC100649594	42.6342277	1.388202343	0.48331559	2.8722482	0.00407563	0.00536278
LOC100649454	162.714505	1.388406577	0.18001585	7.71269052	1.23E-14	3.42E-14

LOC100648861	731.2708	1.390390334	0.13418943	10.3613995	3.71E-25	1.90E-24
LOC100644953	55.4711904	1.391702053	0.24558928	5.66678661	1.46E-08	2.79E-08
LOC100646295	974.648828	1.392261921	0.08365349	16.6432024	3.39E-62	2.42E-60
LOC100645020	517.770189	1.39230831	0.143533	9.70026626	3.01E-22	1.29E-21
LOC100648690	2966.88575	1.3934587	0.08380164	16.6280601	4.36E-62	3.05E-60
LOC100645865	723.078331	1.395535529	0.08526751	16.3665564	3.31E-60	2.00E-58
LOC100650596	754.58257	1.395698771	0.11251492	12.404566	2.47E-35	2.38E-34
LOC100643889	369.985548	1.396337254	0.15624449	8.93687365	4.00E-19	1.46E-18
LOC100645391	387.989616	1.397062161	0.15843557	8.81785694	1.17E-18	4.11E-18
LOC100649693	3156.14825	1.397307742	0.29748922	4.69700299	2.64E-06	4.37E-06
LOC100644770	633.787654	1.397478164	0.10357696	13.4921716	1.74E-41	2.56E-40
LOC100645672	384.226997	1.39834452	0.11174458	12.5137573	6.28E-36	6.23E-35
LOC100652092	470.23973	1.400389401	0.12623224	11.0937538	1.35E-28	8.50E-28
LOC100648868	1236.15864	1.401528781	0.08757406	16.0039262	1.20E-57	5.93E-56
LOC100647256	175.616727	1.401973065	0.29661287	4.72660899	2.28E-06	3.80E-06
LOC100645817	96.1343283	1.402799867	0.15914097	8.81482551	1.20E-18	4.21E-18
LOC100644550	991.347674	1.403225762	0.09750079	14.391943	5.81E-47	1.26E-45
LOC100646645	955.131159	1.405712259	0.10765285	13.0578269	5.73E-39	7.02E-38
LOC100648561	587.003997	1.40796311	0.11935626	11.796307	4.08E-32	3.17E-31
LOC100651687	238.426371	1.408446728	0.2343299	6.01052918	1.85E-09	3.76E-09
LOC100648532	99.4676009	1.408858617	0.13609346	10.3521405	4.09E-25	2.08E-24
LOC100643443	804.360728	1.412422071	0.08570262	16.4805009	5.07E-61	3.33E-59
LOC100645328	14.2068669	1.412672845	0.40103075	3.52260482	0.00042733	0.00060831
LOC100652084	145.749316	1.412825955	0.16679674	8.47034524	2.45E-17	7.96E-17
LOC100648796	241.734471	1.412983131	0.2222586	6.35738343	2.05E-10	4.39E-10
LOC100651883	952.190409	1.413158133	0.09011792	15.681212	2.03E-55	8.23E-54
LOC100648096	5954.42734	1.413423493	0.12438876	11.3629518	6.39E-30	4.39E-29
LOC105666889	1876.59295	1.413574541	0.08353855	16.9212249	3.14E-64	2.74E-62
LOC100651355	365.71176	1.414833067	0.11101758	12.7442255	3.36E-37	3.64E-36

LOC105666816	128.063668	1.415308226	0.23207374	6.098528	1.07E-09	2.20E-09
LOC100650410	1007.3288	1.416265131	0.14582534	9.71206456	2.68E-22	1.15E-21
LOC100649259	284.617657	1.416758485	0.14251254	9.94129021	2.75E-23	1.24E-22
LOC100646086	529.731497	1.416881707	0.09069787	15.6219957	5.16E-55	1.98E-53
LOC100642333	358.564158	1.41735738	0.14005885	10.1197276	4.52E-24	2.14E-23
LOC100650069	1221.96434	1.418424614	0.11644888	12.180663	3.94E-34	3.52E-33
LOC105665926	65.3595428	1.418687236	0.21171906	6.70080081	2.07E-11	4.73E-11
LOC105667116	148.929197	1.418998867	0.16307871	8.70131293	3.28E-18	1.12E-17
LOC100644645	1482.57673	1.419123579	0.1067878	13.2891922	2.67E-40	3.60E-39
LOC100650805	4332.10447	1.420449731	0.10160742	13.9797841	2.07E-44	3.73E-43
LOC100648374	451.778814	1.42058513	0.15027066	9.45350979	3.28E-21	1.34E-20
LOC100645183	908.372797	1.420836123	0.07510784	18.9172816	8.22E-80	2.44E-77
LOC100647705	395.391142	1.421103213	0.12586899	11.2903359	1.46E-29	9.81E-29
LOC100645829	540.216738	1.421506662	0.09641985	14.7428836	3.42E-49	8.83E-48
LOC100643927	752.149115	1.422110987	0.16137704	8.81235037	1.23E-18	4.30E-18
LOC100644840	801.875721	1.422120765	0.10717573	13.2690564	3.50E-40	4.69E-39
LOC100647207	556.274667	1.4228145	0.13434099	10.5910673	3.28E-26	1.78E-25
LOC100644230	1006.69841	1.423359014	0.09794783	14.5318069	7.62E-48	1.78E-46
LOC100642825	220.302109	1.424194741	0.20303583	7.01449965	2.31E-12	5.59E-12
LOC100646998	276.710273	1.425531287	0.12336436	11.5554552	6.93E-31	5.04E-30
LOC100643741	412.231466	1.426238776	0.15380989	9.2727375	1.81E-20	7.09E-20
LOC100650716	237.318198	1.426542826	0.12630641	11.2943029	1.40E-29	9.40E-29
LOC100644290	820.376961	1.426680144	0.13066307	10.9187714	9.38E-28	5.62E-27
LOC105666542	593.503231	1.427123055	0.16662868	8.56469038	1.08E-17	3.60E-17
LOC100645502	67.0356648	1.429132565	0.2255164	6.33715589	2.34E-10	4.99E-10
LOC100642439	362.394894	1.429354906	0.15550127	9.19191814	3.86E-20	1.48E-19
LOC100648155	765.197238	1.430062123	0.12945652	11.0466598	2.28E-28	1.42E-27
LOC100645393	535.913166	1.432071534	0.10736465	13.3383896	1.38E-40	1.92E-39
LOC105666920	23.1794827	1.432175108	0.53869012	2.65862516	0.00784602	0.01008274

LOC100652151	173.462726	1.432670726	0.22648982	6.32554138	2.52E-10	5.37E-10
LOC100647332	753.781634	1.432874708	0.08726823	16.4192012	1.39E-60	8.75E-59
LOC100649419	613.920968	1.433176815	0.10656804	13.4484669	3.14E-41	4.53E-40
LOC100643430	511.436569	1.434933138	0.10787422	13.3019103	2.26E-40	3.06E-39
LOC100647774	534.710655	1.436240334	0.11639797	12.3390494	5.58E-35	5.24E-34
LOC100648991	116.912622	1.437128183	0.16024696	8.96820863	3.01E-19	1.11E-18
LOC100646856	124.593393	1.437655681	0.21845795	6.5809265	4.68E-11	1.04E-10
LOC100646816	1029.3154	1.437777076	0.08242802	17.4428196	3.90E-68	4.60E-66
LOC100645471	481.85742	1.438304787	0.13192667	10.9023048	1.12E-27	6.70E-27
LOC100650803	565.586458	1.440180202	0.10567406	13.6285117	2.71E-42	4.21E-41
LOC100646081	228.062287	1.441547853	0.21024844	6.85640215	7.06E-12	1.66E-11
LOC100648016	809.156867	1.442468023	0.10418099	13.8457897	1.35E-43	2.29E-42
LOC100650035	2350.532	1.442625702	0.35623951	4.04959485	5.13E-05	7.83E-05
LOC100649619	601.690647	1.443806965	0.10085204	14.3160909	1.74E-46	3.60E-45
LOC105666983	25.4753669	1.445472215	0.2926839	4.93868032	7.87E-07	1.36E-06
LOC100643809	571.309207	1.4455154	0.13882156	10.412759	2.17E-25	1.12E-24
LOC100651877	117.746561	1.446899362	0.16012469	9.03607889	1.62E-19	6.03E-19
LOC100652297	468.970148	1.448148433	0.13980026	10.358696	3.82E-25	1.95E-24
LOC100649388	1243.25413	1.448543435	0.12705997	11.4004707	4.16E-30	2.89E-29
LOC100646686	1641.25472	1.450138633	0.09313409	15.5704386	1.16E-54	4.32E-53
LOC100643980	300.624577	1.450339971	0.14080227	10.3005439	7.01E-25	3.51E-24
LOC100651200	1463.38443	1.450345954	0.11416571	12.7038667	5.63E-37	6.00E-36
LOC100644222	468.482775	1.450932612	0.11120868	13.0469369	6.62E-39	8.05E-38
LOC100651777	2130.43104	1.454286747	0.08384204	17.345556	2.13E-67	2.34E-65
LOC100644799	1373.41576	1.454530513	0.09632455	15.1003098	1.61E-51	4.99E-50
LOC100644020	331.80117	1.454665357	0.12933245	11.2474893	2.38E-29	1.57E-28
LOC100650301	643.611009	1.455211316	0.15092939	9.64166943	5.33E-22	2.25E-21
LOC100647511	455.343923	1.455535556	0.11547335	12.6049473	1.98E-36	2.05E-35
LOC100644869	547.925757	1.457514762	0.20407073	7.14220382	9.18E-13	2.28E-12

LOC100644268	144.094095	1.45794149	0.3075843	4.73997376	2.14E-06	3.57E-06
LOC100652029	160.181212	1.459808813	0.12853007	11.3577225	6.79E-30	4.65E-29
LOC100644634	3311.33852	1.461472009	0.45117748	3.23923969	0.00119849	0.00164486
LOC100649435	633.310586	1.462022502	0.09841427	14.8557977	6.38E-50	1.74E-48
LOC105666998	67.8412749	1.462601598	0.5093369	2.87157986	0.00408426	0.00537341
LOC100651995	1032.7512	1.46300338	0.1354334	10.8023822	3.35E-27	1.95E-26
LOC100649677	983.845109	1.463673417	0.09840888	14.8733877	4.91E-50	1.34E-48
LOC100649887	611.521111	1.464780216	0.11098211	13.1983452	8.97E-40	1.17E-38
LOC100643155	2987.43968	1.465796641	0.12902065	11.3609459	6.54E-30	4.49E-29
LOC100650430	649.038629	1.465888947	0.08989377	16.306902	8.82E-60	5.11E-58
LOC100649827	1017.58571	1.466039868	0.10959949	13.3763379	8.31E-41	1.17E-39
LOC100646498	776.245662	1.466776182	0.08631865	16.9925762	9.32E-65	8.61E-63
LOC100647583	245.750638	1.467226991	0.17243357	8.50894059	1.76E-17	5.76E-17
LOC100649869	141.152733	1.46975455	0.25356831	5.7962865	6.78E-09	1.33E-08
LOC100644938	724.454535	1.471646355	0.09404006	15.6491434	3.37E-55	1.34E-53
LOC100647348	400.290088	1.471889003	0.1282113	11.4801818	1.66E-30	1.18E-29
LOC100644674	1075.4671	1.472806735	0.1471001	10.0122753	1.35E-23	6.19E-23
LOC100645287	19.8720512	1.473651709	0.35913868	4.10329438	4.07E-05	6.25E-05
LOC100642319	675.188823	1.475212586	0.09283479	15.8907308	7.35E-57	3.36E-55
LOC100647595	205.556194	1.475487501	0.11901794	12.3971853	2.71E-35	2.60E-34
LOC100645783	5049.16396	1.475801966	0.09052508	16.3026869	9.44E-60	5.44E-58
LOC100642849	324.778029	1.47584982	0.12008196	12.2903544	1.02E-34	9.45E-34
LOC100646840	246.335376	1.476309204	0.28628526	5.1567769	2.51E-07	4.47E-07
LOC100648032	1648.40861	1.477797239	0.0865471	17.0750639	2.28E-65	2.14E-63
LOC100651216	190.532929	1.479218949	0.15546579	9.51475531	1.82E-21	7.49E-21
LOC100647037	363.328665	1.479960663	0.11128612	13.2986989	2.36E-40	3.19E-39
LOC100647187	317.412414	1.481751256	0.14294482	10.3658969	3.54E-25	1.81E-24
LOC100644218	1176.82841	1.482317832	0.18067834	8.20418137	2.32E-16	7.14E-16
LOC105666826	9.20508936	1.482965567	0.63959906	2.31858622	0.02041748	0.02536576

LOC100650496	232.359206	1.482977406	0.11670152	12.7074388	5.38E-37	5.74E-36
LOC100646172	211.37414	1.483373271	0.14524571	10.2128546	1.74E-24	8.45E-24
LOC105665904	9.82577575	1.485872139	0.52212372	2.84582388	0.00442967	0.00580523
LOC100643806	411.620129	1.486383788	0.11137327	13.3459655	1.25E-40	1.74E-39
LOC100645845	494.392305	1.488161973	0.10318649	14.4220624	3.76E-47	8.27E-46
LOC100646448	76.7704931	1.488825875	0.20538902	7.24880952	4.20E-13	1.07E-12
LOC100644701	123.330441	1.488966124	0.23014458	6.46969872	9.82E-11	2.13E-10
LOC100645282	549.631123	1.48924927	0.09087214	16.3884029	2.31E-60	1.42E-58
LOC100648380	1573.24053	1.491147559	0.15165781	9.83231615	8.17E-23	3.60E-22
LOC100645448	719.293692	1.491631499	0.09809341	15.2062363	3.22E-52	1.06E-50
LOC105666686	214.856241	1.492411255	0.41903133	3.56157443	0.00036864	0.00052745
LOC100642437	1725.48963	1.492425123	0.10917967	13.6694418	1.55E-42	2.44E-41
LOC100649812	107.976392	1.493896413	0.3035213	4.92188334	8.57E-07	1.47E-06
LOC100648225	514.138641	1.494229013	0.09891783	15.1057596	1.48E-51	4.61E-50
LOC100651009	349.189966	1.49511522	0.13928723	10.7340441	7.04E-27	4.00E-26
LOC100651086	2825.4265	1.497279836	0.11834265	12.6520726	1.09E-36	1.14E-35
LOC100650835	264.170387	1.497567822	0.2397291	6.24691725	4.19E-10	8.80E-10
LOC105665946	10.7068786	1.497952648	0.46319204	3.23397753	0.00122079	0.00167476
LOC100646176	22.3840879	1.498048802	0.35443805	4.22654621	2.37E-05	3.70E-05
LOC105667080	94.7142027	1.498091347	0.20695273	7.23880919	4.53E-13	1.15E-12
LOC100645853	191.987323	1.498257448	0.14646317	10.2295849	1.46E-24	7.15E-24
LOC100649639	970.936041	1.499054419	0.09496995	15.7845126	3.98E-56	1.70E-54
LOC100643959	76.6796408	1.50040072	0.22369053	6.70748436	1.98E-11	4.52E-11
LOC100648077	58.788345	1.503159706	0.50329037	2.98666497	0.00282039	0.00376783
LOC100647055	1306.4257	1.503711816	0.0978608	15.3658244	2.77E-53	9.57E-52
LOC100648891	1175.72441	1.504750298	0.09463598	15.9004045	6.30E-57	2.91E-55
LOC105665855	1963.62086	1.505621577	0.1300193	11.5799855	5.21E-31	3.80E-30
LOC100651991	1048.97338	1.505871695	0.09323178	16.1519136	1.10E-58	5.73E-57
LOC100649076	205.835759	1.507169652	0.14549481	10.3589239	3.81E-25	1.94E-24

LOC100646551	832.585873	1.507896956	0.11182949	13.4838942	1.95E-41	2.85E-40
LOC100644138	47.9158618	1.508042071	0.21425513	7.03853431	1.94E-12	4.73E-12
LOC100647745	342.188019	1.509262218	0.13174506	11.45593	2.20E-30	1.55E-29
LOC100650104	369.760926	1.51017443	0.14244279	10.601972	2.92E-26	1.59E-25
LOC100650355	1250.31699	1.510215742	0.09238806	16.3464379	4.61E-60	2.72E-58
LOC100644106	902.412237	1.511425482	0.09454508	15.9862936	1.59E-57	7.76E-56
LOC100650882	1639.44213	1.512781397	0.10433084	14.4998492	1.21E-47	2.78E-46
LOC100645762	4559.51775	1.514701908	0.19270017	7.86040766	3.83E-15	1.10E-14
LOC100646253	2908.69541	1.515560411	0.10590245	14.3109093	1.87E-46	3.87E-45
LOC100650633	152.23691	1.518964362	0.69857326	2.1743809	0.02967654	0.03632946
LOC105665694	199.528051	1.520897055	0.18414757	8.25912108	1.47E-16	4.58E-16
LOC105666129	33.312685	1.522098244	0.37661029	4.0415737	5.31E-05	8.10E-05
LOC100645261	193.926872	1.522845529	0.14657392	10.3896075	2.76E-25	1.42E-24
LOC100648773	393.693088	1.523560103	0.1883016	8.09106313	5.91E-16	1.77E-15
LOC100647365	390.115685	1.524379865	0.17899454	8.51634833	1.65E-17	5.42E-17
LOC100643724	733.053399	1.525973511	0.11432614	13.3475469	1.22E-40	1.70E-39
LOC100649373	44.8719708	1.527656067	0.28613042	5.33902015	9.35E-08	1.70E-07
LOC100646500	145.184481	1.527731338	0.17747554	8.6081235	7.43E-18	2.49E-17
LOC100648583	21.8219608	1.529965432	0.31997842	4.78146446	1.74E-06	2.93E-06
LOC100646842	278.552114	1.530222015	0.13162555	11.6255697	3.06E-31	2.27E-30
LOC100648522	510.696476	1.5314454	0.12800052	11.9643686	5.46E-33	4.46E-32
LOC100648271	267.806062	1.53173	0.14460397	10.5925859	3.23E-26	1.76E-25
LOC105667149	64.7400945	1.533464824	0.24568267	6.24164824	4.33E-10	9.09E-10
LOC100648974	1778.51118	1.533543112	0.09133354	16.7905801	2.86E-63	2.24E-61
LOC100644916	1353.72289	1.533616982	0.12660471	12.1134274	8.97E-34	7.72E-33
LOC100650996	27.5935413	1.534942563	0.35765822	4.29164627	1.77E-05	2.79E-05
LOC100647871	355.177332	1.535871089	0.16849394	9.11528997	7.85E-20	2.97E-19
LOC100643402	792.749179	1.536994067	0.23336211	6.58630525	4.51E-11	1.01E-10
LOC100646574	1071.99403	1.537526887	0.12228756	12.5730444	2.97E-36	3.02E-35

LOC100652090	28.1583766	1.539291771	0.57840269	2.66128044	0.00778441	0.01000739
LOC100651177	50.0505689	1.541642801	0.30630825	5.03297841	4.83E-07	8.44E-07
LOC100643330	199.894294	1.542523517	0.16684867	9.24504533	2.35E-20	9.13E-20
LOC100643294	775.951651	1.544730587	0.09741013	15.858007	1.24E-56	5.46E-55
LOC100642832	2371.49018	1.545977613	0.08655532	17.8611517	2.37E-71	3.74E-69
LOC100645329	1425.0101	1.546358943	0.10042782	15.3977143	1.70E-53	5.89E-52
LOC105665732	22.0746099	1.546695925	0.36599802	4.22596804	2.38E-05	3.71E-05
LOC100643369	7976.808	1.547196312	0.10152313	15.2398402	1.92E-52	6.34E-51
LOC100642384	644.461427	1.548854005	0.1231805	12.5738568	2.94E-36	2.99E-35
LOC105666154	105.067454	1.549331065	0.1566236	9.89206643	4.51E-23	2.01E-22
LOC100643266	1368.60083	1.549733782	0.11241757	13.7855122	3.12E-43	5.19E-42
LOC100648670	11.0098981	1.5521397	0.63946987	2.42722883	0.01521466	0.01908361
LOC100648960	279.063162	1.553279955	0.20303782	7.65020028	2.01E-14	5.51E-14
LOC105665648	42.056028	1.553398578	0.27392362	5.6709188	1.42E-08	2.73E-08
LOC105666245	14.4548757	1.555753335	0.57187483	2.72044381	0.00651944	0.00842664
LOC105666878	44.0618909	1.556343908	0.24523628	6.34630374	2.21E-10	4.71E-10
LOC100648734	596.651956	1.557210192	0.09860986	15.7916272	3.55E-56	1.53E-54
LOC100649615	37.8965367	1.558887118	0.30843044	5.05425837	4.32E-07	7.57E-07
LOC105666947	19.7907277	1.559729875	0.5242413	2.97521366	0.00292785	0.00390605
LOC100642668	1496.0257	1.560614679	0.100235	15.5695584	1.17E-54	4.36E-53
LOC100644421	1155.4141	1.560974274	0.10445954	14.9433392	1.72E-50	4.84E-49
LOC100644912	99.7887656	1.561137012	0.16178273	9.64959028	4.94E-22	2.09E-21
LOC105666048	204.84321	1.565002053	0.18916024	8.27341972	1.30E-16	4.07E-16
LOC100644416	395.404903	1.566076868	0.13211093	11.8542566	2.05E-32	1.61E-31
LOC100645586	984.376282	1.567213555	0.11642805	13.4607902	2.66E-41	3.85E-40
LOC100651451	802.923162	1.568026501	0.0988458	15.8633595	1.14E-56	5.08E-55
LOC100649179	466.841337	1.569307343	0.12013505	13.0628597	5.37E-39	6.59E-38
LOC100644267	929.122945	1.56948033	0.11909876	13.1779741	1.18E-39	1.53E-38
LOC100644206	561.562678	1.569541468	0.09597167	16.3542169	4.06E-60	2.42E-58

LOC100642988	496.406153	1.57027844	0.1496752	10.4912397	9.48E-26	5.02E-25
LOC100644129	1323.02204	1.57182906	0.16125336	9.74757396	1.89E-22	8.16E-22
LOC100651505	117.098523	1.572685821	0.19806083	7.9404182	2.02E-15	5.86E-15
LOC100645942	957.085457	1.573980784	0.09906535	15.8883077	7.64E-57	3.48E-55
LOC100644501	607.810028	1.57455273	0.10175087	15.4745872	5.15E-54	1.84E-52
LOC100645992	971.036514	1.574891064	0.12167789	12.943116	2.57E-38	3.02E-37
LOC100643107	505.212784	1.576161989	0.13780138	11.4379257	2.70E-30	1.90E-29
LOC100651892	1215.55703	1.577905799	0.13229501	11.9271751	8.54E-33	6.90E-32
LOC100651669	131.906693	1.578173501	0.1874421	8.41952512	3.78E-17	1.22E-16
LOC100647402	223.127655	1.578878496	0.14625664	10.7952603	3.62E-27	2.10E-26
LOC100642693	2575.66903	1.580656959	0.08505446	18.5840583	4.33E-77	1.12E-74
LOC100643671	18.972956	1.580778067	0.35507696	4.4519308	8.51E-06	1.37E-05
LOC100650765	437.398974	1.581073846	0.14219078	11.1193836	1.01E-28	6.45E-28
LOC100646605	1497.85943	1.581108755	0.10997869	14.3765013	7.27E-47	1.56E-45
LOC100645113	383.497795	1.581408391	0.12321669	12.8343686	1.05E-37	1.18E-36
LOC100648488	291.216059	1.581760841	0.13597021	11.6331428	2.80E-31	2.08E-30
LOC100650456	440.773523	1.586160256	0.17573557	9.02583488	1.78E-19	6.60E-19
LOC100644123	1436.81211	1.586654013	0.11969077	13.2562772	4.15E-40	5.51E-39
LOC100642416	390.674702	1.587067092	0.10760034	14.749648	3.09E-49	8.01E-48
LOC100646451	570.37422	1.587119844	0.10960111	14.4808736	1.60E-47	3.63E-46
LOC105665877	66.1316427	1.588437527	0.19656823	8.08084581	6.43E-16	1.93E-15
LOC100643496	254.256415	1.590333081	0.18703481	8.50287223	1.85E-17	6.05E-17
LOC100646125	379.326643	1.592944123	0.12276502	12.9755539	1.68E-38	2.00E-37
LOC100649185	963.864025	1.593280047	0.10772092	14.7908136	1.68E-49	4.44E-48
LOC100648853	1042.23094	1.593515966	0.1116245	14.2756827	3.10E-46	6.35E-45
LOC100645593	84.9216907	1.59385198	0.2911814	5.47374239	4.41E-08	8.19E-08
LOC100645663	757.760826	1.595079274	0.11941195	13.357786	1.07E-40	1.49E-39
LOC100644217	30.6283885	1.596175635	0.39876783	4.00276929	6.26E-05	9.50E-05
LOC100648887	627.253036	1.596343017	0.09874568	16.1662053	8.73E-59	4.60E-57

LOC100648836	753.672415	1.596955627	0.13526075	11.8064973	3.61E-32	2.82E-31
LOC100646870	240.865501	1.598397641	0.15088369	10.5935748	3.19E-26	1.74E-25
LOC100649134	353.858665	1.5985937	0.14872536	10.7486286	6.01E-27	3.44E-26
LOC100643101	1042.08457	1.600540564	0.0943518	16.9635405	1.53E-64	1.36E-62
LOC100646726	541.844831	1.604799447	0.16853666	9.52196082	1.70E-21	6.99E-21
LOC105666944	716.371059	1.605215884	0.1051826	15.2612301	1.39E-52	4.63E-51
LOC105667006	117.067875	1.605262288	0.16304802	9.8453343	7.18E-23	3.17E-22
LOC100650915	496.296352	1.605377178	0.08758493	18.3293771	4.82E-75	9.84E-73
LOC100643256	82.7705381	1.606195223	0.35570595	4.51551406	6.32E-06	1.02E-05
LOC100651084	337.501693	1.606618961	0.12244969	13.1206451	2.51E-39	3.14E-38
LOC100652267	178.951321	1.607278739	0.12269935	13.0993255	3.32E-39	4.13E-38
LOC105666064	68.1686821	1.607956007	0.17168153	9.36592307	7.54E-21	3.01E-20
LOC100650868	949.223216	1.608429709	0.11037841	14.5719588	4.24E-48	1.02E-46
LOC100648672	115.200714	1.609222724	0.24648828	6.5285973	6.64E-11	1.46E-10
LOC100648516	412.504411	1.613551359	0.14960073	10.7857185	4.02E-27	2.32E-26
LOC105666946	21.223544	1.614488672	0.47938488	3.36783396	0.00075761	0.00105516
LOC100643876	450.279699	1.614501426	0.11519944	14.0148376	1.26E-44	2.31E-43
LOC100644685	3651.89731	1.614721335	0.09106322	17.7318727	2.38E-70	3.43E-68
LOC100651353	82.5796171	1.614937633	0.29030199	5.56295759	2.65E-08	5.00E-08
LOC100650331	144.779179	1.615552679	0.18185267	8.88385456	6.46E-19	2.31E-18
LOC100647482	338.125266	1.616620204	0.11330048	14.2684316	3.44E-46	7.04E-45
LOC100648005	614.236417	1.617480435	0.12496525	12.9434413	2.56E-38	3.01E-37
LOC100650969	438.089336	1.617566443	0.11457649	14.1177869	2.95E-45	5.67E-44
LOC100649814	247.440609	1.618093823	0.14179167	11.4117691	3.65E-30	2.55E-29
LOC100645685	30.9787574	1.618311852	0.34744322	4.65777355	3.20E-06	5.27E-06
LOC100650685	1043.87393	1.619251476	0.14526707	11.1467206	7.43E-29	4.79E-28
LOC105665862	47.9289075	1.619543954	0.27411961	5.90816535	3.46E-09	6.92E-09
LOC100646440	671.466028	1.620961821	0.09704038	16.7039929	1.23E-62	8.96E-61
LOC100646428	1256.06844	1.621369073	0.13403906	12.0962431	1.11E-33	9.49E-33

LOC100651714	342.654853	1.622152634	0.16348334	9.92243383	3.33E-23	1.49E-22
LOC100648251	426.912696	1.622962463	0.14370827	11.2934517	1.41E-29	9.48E-29
LOC100647968	207.981116	1.624679288	0.26070463	6.23187736	4.61E-10	9.66E-10
LOC100642945	88.0507064	1.625412148	0.30200487	5.38207261	7.36E-08	1.35E-07
LOC100646606	168.137888	1.626301139	0.26244158	6.19681207	5.76E-10	1.20E-09
LOC100644531	1229.72299	1.626658664	0.10178429	15.9814321	1.72E-57	8.34E-56
LOC100646270	4582.67172	1.626998128	0.17939174	9.06952644	1.20E-19	4.47E-19
LOC100646805	231.036934	1.627099544	0.2071826	7.85345638	4.05E-15	1.16E-14
LOC100646011	116.71813	1.630208392	0.40425288	4.0326451	5.52E-05	8.41E-05
LOC100649344	426.224009	1.630858725	0.12381373	13.1718726	1.27E-39	1.65E-38
LOC100642367	16.0082488	1.631226852	0.47356395	3.44457569	0.00057196	0.00080472
LOC100650883	1175.68996	1.63279558	0.15913522	10.2604285	1.06E-24	5.26E-24
LOC100643692	76.8816153	1.634662771	0.31123356	5.25220598	1.50E-07	2.70E-07
LOC100648654	379.527831	1.634962177	0.1281803	12.755175	2.92E-37	3.19E-36
LOC100646718	1632.98459	1.636139156	0.08860599	18.4653331	3.93E-76	8.94E-74
LOC100643343	292.65734	1.636748078	0.18478529	8.85756688	8.18E-19	2.91E-18
LOC100646971	131.965575	1.637897099	0.20256913	8.08562043	6.18E-16	1.85E-15
LOC100646570	2875.54287	1.638289742	0.11842076	13.8344806	1.58E-43	2.67E-42
LOC100644540	177.770587	1.638670477	0.19679622	8.32673748	8.31E-17	2.63E-16
LOC100647311	953.256025	1.63906993	0.15574902	10.5237897	6.71E-26	3.58E-25
LOC100649326	281.030359	1.639413556	0.1450635	11.3013512	1.29E-29	8.69E-29
LOC100645900	99.90724	1.639533158	0.24041506	6.8195943	9.13E-12	2.13E-11
LOC100645596	107.125066	1.640947275	0.28497038	5.75830814	8.50E-09	1.66E-08
LOC100644180	29.4678547	1.641380762	0.42906373	3.82549406	0.00013051	0.00019308
LOC100648001	290.338694	1.642418351	0.41522022	3.95553553	7.64E-05	0.00011513
LOC100650295	3087.87315	1.64248203	0.13815814	11.8884203	1.36E-32	1.08E-31
LOC100646268	537.973623	1.643329616	0.12200306	13.4695768	2.36E-41	3.44E-40
LOC100642787	108.265741	1.64340068	0.35992521	4.56595046	4.97E-06	8.10E-06
LOC100651157	955.339748	1.644790876	0.10755024	15.2932326	8.48E-53	2.87E-51

LOC100649037	222.398082	1.64552451	0.13610905	12.0897507	1.20E-33	1.02E-32
LOC100645437	512.762836	1.645843367	0.13953457	11.7952374	4.13E-32	3.21E-31
LOC100652003	550.535797	1.645995594	0.11186348	14.7143246	5.22E-49	1.33E-47
LOC100646455	411.228597	1.646496126	0.16783959	9.80993898	1.02E-22	4.47E-22
LOC100647075	515.06733	1.646518531	0.12855728	12.8076649	1.49E-37	1.65E-36
LOC100646066	925.827621	1.647857568	0.09406273	17.5187078	1.03E-68	1.25E-66
LOC100645961	79.9340902	1.648973319	0.21725861	7.58991027	3.20E-14	8.68E-14
LOC100649280	568.328575	1.651134602	0.10679269	15.4611197	6.35E-54	2.25E-52
LOC100646265	69.2960755	1.651154286	0.24468977	6.74794987	1.50E-11	3.46E-11
LOC100643938	38.4178124	1.653575541	0.39290414	4.2085979	2.57E-05	4.00E-05
LOC100649651	292.929192	1.654987661	0.15214392	10.8777773	1.47E-27	8.72E-27
LOC100651800	379.667652	1.655601029	0.12290617	13.4704464	2.33E-41	3.41E-40
LOC100646364	1201.19535	1.657443181	0.0903519	18.3443088	3.67E-75	7.64E-73
LOC105666243	965.362559	1.660003583	0.13220249	12.5565227	3.66E-36	3.70E-35
LOC100650952	50.1079327	1.663209391	0.38717361	4.29577154	1.74E-05	2.74E-05
LOC100643856	155.519132	1.663515166	0.15247477	10.9101011	1.03E-27	6.15E-27
LOC105665784	680.581094	1.664380785	0.11445341	14.5419935	6.57E-48	1.55E-46
LOC100645776	79.0143503	1.665675909	0.22082941	7.54281734	4.60E-14	1.24E-13
LOC105666635	48.920534	1.665830481	0.3455536	4.82075859	1.43E-06	2.42E-06
LOC100648731	155.528053	1.666662912	0.2466478	6.75725844	1.41E-11	3.25E-11
LOC100645475	170.610906	1.66711551	0.30012869	5.55466898	2.78E-08	5.24E-08
LOC100651125	527.923149	1.667586517	0.14046454	11.8719399	1.66E-32	1.31E-31
LOC100642950	357.563291	1.668298961	0.13633708	12.2365752	1.98E-34	1.80E-33
LOC100645589	191.246008	1.670268059	0.1689748	9.8847169	4.85E-23	2.15E-22
LOC105665693	104.75179	1.670484657	0.13999968	11.9320606	8.06E-33	6.52E-32
LOC100644033	235.705865	1.671030045	0.16443717	10.1621188	2.93E-24	1.40E-23
LOC100650595	565.022391	1.671496969	0.12189421	13.7126854	8.52E-43	1.39E-41
LOC100650054	108.388665	1.671797319	0.25429427	6.57426265	4.89E-11	1.09E-10
LOC100649267	3050.04959	1.672099544	0.1220285	13.7025328	9.80E-43	1.59E-41

LOC100645413	29.3875974	1.673217404	0.32856852	5.09244587	3.53E-07	6.22E-07
LOC100648099	504.56522	1.673410582	0.22985435	7.28030844	3.33E-13	8.51E-13
LOC100644906	1076.4848	1.673759933	0.13950321	11.9980034	3.64E-33	3.01E-32
LOC100649016	718.470708	1.673951639	0.111675	14.989493	8.60E-51	2.50E-49
LOC100652116	618.473634	1.674932793	0.09864124	16.9800459	1.15E-64	1.04E-62
LOC105665956	17.8972231	1.675339818	0.32509316	5.1534145	2.56E-07	4.54E-07
LOC105666201	495.65644	1.677179896	0.13889855	12.074855	1.43E-33	1.22E-32
LOC105666146	121.107811	1.678516073	0.32666437	5.13835057	2.77E-07	4.91E-07
LOC100649482	2864.1161	1.678983552	0.10735528	15.6395061	3.92E-55	1.55E-53
LOC100648693	604.292067	1.679150485	0.13294587	12.6303321	1.44E-36	1.50E-35
LOC100652153	932.80896	1.679564595	0.15362823	10.9326557	8.05E-28	4.84E-27
LOC100647179	215.582441	1.679717069	0.22610055	7.42907105	1.09E-13	2.87E-13
LOC100650312	1688.96372	1.682315281	0.07475151	22.5054346	3.67E-112	7.19E-109
LOC100642991	1297.29576	1.682477998	0.19206728	8.7598367	1.96E-18	6.79E-18
LOC100651908	154.405134	1.682912363	0.18389354	9.15155794	5.61E-20	2.14E-19
LOC100643541	846.375841	1.684051832	0.11989259	14.0463383	8.11E-45	1.49E-43
LOC100647014	1382.31522	1.684223258	0.12608494	13.3578469	1.07E-40	1.49E-39
LOC100648850	529.620916	1.685469472	0.10130419	16.6377068	3.72E-62	2.62E-60
LOC100645933	105.765605	1.687250921	0.29726576	5.67590057	1.38E-08	2.65E-08
LOC100645363	382.354942	1.687421083	0.11995747	14.0668283	6.07E-45	1.13E-43
LOC100648196	381.198743	1.688747986	0.14003336	12.0596118	1.73E-33	1.45E-32
LOC100648089	822.478289	1.690864044	0.15220837	11.108877	1.14E-28	7.22E-28
LOC100649549	141.774642	1.691549814	0.18923831	8.93872839	3.94E-19	1.43E-18
LOC100644110	657.646714	1.692092756	0.11461689	14.7630312	2.54E-49	6.64E-48
LOC100646395	307.150163	1.692752155	0.1601418	10.5703331	4.09E-26	2.21E-25
LOC100644655	1882.68326	1.693825185	0.10585855	16.0008347	1.26E-57	6.20E-56
LOC100645337	1657.284	1.693943491	0.14553062	11.6397741	2.59E-31	1.93E-30
LOC100644373	270.127078	1.696936428	0.13233859	12.8226879	1.22E-37	1.37E-36
LOC100651654	2383.38073	1.697292742	0.09215574	18.4176559	9.48E-76	2.11E-73

LOC100650344	1560.35134	1.701798612	0.11967949	14.2196347	6.92E-46	1.38E-44
LOC100651279	93.4588234	1.703091828	0.20230582	8.41840237	3.82E-17	1.23E-16
LOC100646141	205.011236	1.703449846	0.24779871	6.87432905	6.23E-12	1.47E-11
LOC100649254	2212.8022	1.703687863	0.08900238	19.1420484	1.13E-81	3.68E-79
LOC100646202	84390.0556	1.705601662	0.30007576	5.68390342	1.32E-08	2.53E-08
LOC105666851	37.2561625	1.706651566	0.40744486	4.18866881	2.81E-05	4.36E-05
LOC105666916	655.705246	1.7080692	0.13995928	12.2040437	2.96E-34	2.65E-33
LOC100643764	513.592673	1.70906484	0.15769657	10.837679	2.28E-27	1.34E-26
LOC100643102	921.560494	1.710554186	0.13049838	13.1078577	2.97E-39	3.70E-38
LOC100651315	669.369874	1.711399165	0.17494438	9.78253297	1.34E-22	5.82E-22
LOC100642240	1501.77163	1.71148255	0.14076441	12.1584893	5.17E-34	4.54E-33
LOC100645438	1377.65013	1.713281428	0.10952126	15.643368	3.69E-55	1.46E-53
LOC100643638	107.126185	1.714079046	0.35369955	4.84614431	1.26E-06	2.14E-06
LOC100648695	436.04319	1.717863757	0.11749077	14.6212659	2.06E-48	5.08E-47
LOC100645974	253.231857	1.722814613	0.19546174	8.81407602	1.21E-18	4.24E-18
LOC100651818	476.029643	1.725959009	0.12254684	14.0840765	4.76E-45	8.94E-44
LOC100650941	76.6738184	1.72726008	0.25445302	6.78812953	1.14E-11	2.64E-11
LOC105666477	117.75654	1.727460804	0.1668855	10.3511739	4.13E-25	2.10E-24
LOC100644121	231.433975	1.728333144	0.14666816	11.7839698	4.72E-32	3.65E-31
LOC100643708	1272.25049	1.729468161	0.11944863	14.4787615	1.65E-47	3.73E-46
LOC105666482	116.163938	1.730213093	0.19243438	8.99118475	2.45E-19	9.01E-19
LOC100647443	446.600351	1.730987803	0.10658778	16.2400208	2.63E-59	1.45E-57
LOC100651594	1867.2777	1.731241942	0.10162346	17.0358495	4.45E-65	4.15E-63
LOC100644205	168.482967	1.735347065	0.20398279	8.5073209	1.78E-17	5.83E-17
LOC100651956	286.094867	1.737117224	0.16383881	10.602599	2.90E-26	1.58E-25
LOC100647260	145.802472	1.738765656	0.29396706	5.91483168	3.32E-09	6.65E-09
LOC100642642	1522.55774	1.740745639	0.15151717	11.4887683	1.50E-30	1.07E-29
LOC100642557	414.461892	1.741686779	0.12726061	13.6859848	1.23E-42	1.96E-41
LOC100651876	743.241389	1.743288985	0.1101101	15.8322348	1.86E-56	8.15E-55

LOC100644777	400.115919	1.743947437	0.16975297	10.2734429	9.28E-25	4.62E-24
LOC100644078	23.8365905	1.744799486	0.7013266	2.48785584	0.01285158	0.01621937
LOC100642571	1614.04119	1.744898755	0.08994623	19.3993544	7.81E-84	3.06E-81
LOC100651370	523.85804	1.746889722	0.1242653	14.0577435	6.91E-45	1.28E-43
LOC100647279	316.296199	1.750085805	0.17330983	10.098018	5.64E-24	2.66E-23
LOC100651022	393.986093	1.750473918	0.13425659	13.0382722	7.41E-39	8.97E-38
LOC100648015	149.235219	1.750878348	0.19788145	8.84811762	8.90E-19	3.16E-18
LOC100642327	521.872487	1.751398965	0.11174798	15.6727567	2.32E-55	9.36E-54
LOC100643883	506.870114	1.752807703	0.10999102	15.9359157	3.57E-57	1.70E-55
LOC105666191	1121.09621	1.75329648	0.14030515	12.4963088	7.82E-36	7.73E-35
LOC100645756	215.899545	1.75419517	0.27079985	6.47782928	9.31E-11	2.03E-10
LOC100651406	4098.64316	1.755886385	0.12144864	14.4578519	2.24E-47	5.00E-46
LOC100648229	945.930938	1.756935726	0.11445985	15.3497987	3.55E-53	1.22E-51
LOC100647703	1727.74529	1.758993832	0.14652554	12.0046908	3.36E-33	2.79E-32
LOC100652250	807.274311	1.759634905	0.12842942	13.7011828	9.99E-43	1.61E-41
LOC100648290	372.053021	1.763800957	0.13900369	12.6888785	6.82E-37	7.22E-36
LOC100650858	577.291957	1.7654033	0.12209446	14.4593235	2.19E-47	4.91E-46
LOC100651471	1625.74709	1.765546568	0.09500487	18.5837484	4.35E-77	1.12E-74
LOC100644712	39.0073275	1.766418716	0.23244629	7.59925546	2.98E-14	8.09E-14
LOC100646509	322.212773	1.766754337	0.15541715	11.3678207	6.05E-30	4.16E-29
LOC100643054	528.805408	1.766926244	0.14570321	12.1268859	7.61E-34	6.61E-33
LOC100651574	491.70857	1.767790315	0.13708231	12.8958312	4.75E-38	5.47E-37
LOC100642487	1188.66122	1.769859057	0.12449574	14.2162218	7.27E-46	1.45E-44
LOC105665795	21.6950776	1.770034649	0.35783286	4.94654028	7.55E-07	1.30E-06
LOC100652292	2247.56166	1.770853264	0.31943079	5.54377757	2.96E-08	5.57E-08
LOC100647080	335.701657	1.772179973	0.09718701	18.2347415	2.74E-74	5.25E-72
LOC100650879	39.4464416	1.773869017	0.27396379	6.4748302	9.49E-11	2.07E-10
LOC100648889	76.3501585	1.777620107	0.36303527	4.89654931	9.75E-07	1.67E-06
LOC100642694	1065.00875	1.779228645	0.10936696	16.2684287	1.65E-59	9.30E-58

LOC100645884	253.140277	1.779814656	0.15383621	11.5695432	5.88E-31	4.29E-30
LOC100648967	530.351725	1.783222502	0.10403026	17.1413824	7.29E-66	7.00E-64
LOC100649951	262.345903	1.78663613	0.17581281	10.1621499	2.93E-24	1.40E-23
LOC105666316	186.929732	1.787174942	0.1783745	10.019229	1.25E-23	5.79E-23
LOC100643539	566.810925	1.791291733	0.24026386	7.45551898	8.95E-14	2.37E-13
LOC100650921	315.053712	1.7924349	0.13977631	12.8235953	1.21E-37	1.36E-36
LOC100647716	469.845103	1.793875795	0.12103902	14.8206405	1.08E-49	2.90E-48
LOC100643033	1901.82531	1.795515011	0.10228942	17.5532811	5.61E-69	6.96E-67
LOC105666261	15.1759774	1.797923519	0.43658098	4.11819022	3.82E-05	5.88E-05
LOC100650433	433.324761	1.798918441	0.1750976	10.273804	9.25E-25	4.60E-24
LOC100651715	531.914924	1.798982716	0.13493493	13.3322238	1.50E-40	2.07E-39
LOC100646275	46.1376354	1.800047194	0.337104	5.3397385	9.31E-08	1.70E-07
LOC100650279	54.2544636	1.802194418	0.40352911	4.46608278	7.97E-06	1.28E-05
LOC100644296	1108.9346	1.803087346	0.12006137	15.0180477	5.59E-51	1.65E-49
LOC100651001	314.129812	1.803770143	0.14116375	12.7778569	2.18E-37	2.40E-36
LOC100643083	480.857474	1.804393508	0.12059801	14.9620509	1.30E-50	3.72E-49
LOC100646085	753.308973	1.805889406	0.10776209	16.7581141	4.94E-63	3.75E-61
LOC100648747	1554.48166	1.805940082	0.12743143	14.1718581	1.37E-45	2.68E-44
LOC100643762	390.94334	1.806430679	0.13978302	12.9231049	3.33E-38	3.89E-37
LOC100644651	203.614382	1.807541478	0.14179972	12.7471444	3.23E-37	3.51E-36
LOC100643704	1510.73833	1.809244213	0.11920665	15.1773764	4.99E-52	1.59E-50
LOC100642386	920.148242	1.812786057	0.14770118	12.2733348	1.26E-34	1.16E-33
LOC100647027	96.9190992	1.814275724	0.17674472	10.26495	1.01E-24	5.03E-24
LOC100652053	477.434532	1.816231209	0.1489302	12.1951839	3.30E-34	2.95E-33
LOC100646648	19.2810773	1.816283968	0.4181266	4.34386135	1.40E-05	2.22E-05
LOC100645978	77.1434237	1.816474563	0.27119194	6.69811406	2.11E-11	4.81E-11
LOC100645176	328.706335	1.817214365	0.11899868	15.2708789	1.20E-52	4.01E-51
LOC100651512	146.726028	1.817387754	0.20943779	8.67745881	4.05E-18	1.37E-17
LOC100645638	460.785319	1.817865799	0.2674964	6.79585152	1.08E-11	2.51E-11

LOC100652006	171.705798	1.818410751	0.25665898	7.08492942	1.39E-12	3.42E-12
LOC100648645	1823.74717	1.818837627	0.12714882	14.3047939	2.04E-46	4.21E-45
LOC100648454	617.539175	1.81982463	0.13722206	13.2618958	3.85E-40	5.14E-39
LOC105666613	12.710392	1.820917789	0.44963258	4.04979056	5.13E-05	7.83E-05
LOC100652111	705.981594	1.821108056	0.12054824	15.1068819	1.46E-51	4.55E-50
LOC100650658	53.8072565	1.824654934	0.24594793	7.41886676	1.18E-13	3.10E-13
LOC105666746	117.529632	1.82515472	0.19382981	9.41627458	4.67E-21	1.89E-20
LOC100648953	764.859769	1.826972707	0.18007537	10.1456002	3.47E-24	1.65E-23
LOC100646111	1019.47198	1.826991764	0.09510358	19.2105457	3.02E-82	1.02E-79
LOC100642320	1547.9603	1.827196078	0.09367838	19.5049916	9.96E-85	4.43E-82
LOC100649955	412.556769	1.827388595	0.14260337	12.8144844	1.36E-37	1.52E-36
LOC100649294	564.088059	1.827601942	0.11101971	16.4619585	6.88E-61	4.49E-59
LOC100642902	122.790328	1.829071852	0.14390817	12.7099932	5.20E-37	5.57E-36
LOC100651238	462.182458	1.829829899	0.10826407	16.9015437	4.38E-64	3.73E-62
LOC100644495	305.621184	1.830648057	0.31933926	5.73261192	9.89E-09	1.92E-08
LOC100645796	675.076283	1.831222407	0.15167439	12.0733787	1.46E-33	1.24E-32
LOC100642905	191.094659	1.834030581	0.35592612	5.15284073	2.57E-07	4.56E-07
LOC100648075	165.945614	1.835681658	0.16666511	11.0141925	3.26E-28	2.02E-27
LOC100646950	211.999911	1.835694081	0.2051529	8.94793146	3.62E-19	1.32E-18
LOC100643271	950.113322	1.837192689	0.146127	12.5725748	2.99E-36	3.04E-35
LOC100642372	330.350972	1.838390474	0.14436766	12.7340876	3.82E-37	4.14E-36
LOC100649114	59.6585914	1.838964169	0.2513727	7.31568776	2.56E-13	6.57E-13
LOC100650816	484.915489	1.83959786	0.13436237	13.6913172	1.14E-42	1.83E-41
LOC100650287	219.815855	1.840292771	0.20839543	8.83077313	1.04E-18	3.67E-18
LOC105666188	21.271342	1.840777125	0.36144675	5.09280311	3.53E-07	6.21E-07
LOC100642350	25.0987073	1.8431877	0.39637664	4.65009161	3.32E-06	5.47E-06
LOC100642727	316.732977	1.84523092	0.15975756	11.550195	7.37E-31	5.35E-30
LOC100643979	20.5005572	1.845242254	0.31316603	5.89221725	3.81E-09	7.60E-09
LOC100651377	452.304051	1.8463758	0.15046597	12.2710522	1.30E-34	1.19E-33

LOC100647711	578.546338	1.851398866	0.17813628	10.3931602	2.66E-25	1.37E-24
LOC100645219	2184.70054	1.852776632	0.09710728	19.0796887	3.72E-81	1.18E-78
LOC100651778	65.265835	1.852854429	0.25722672	7.20319587	5.88E-13	1.48E-12
LOC100644374	180.066651	1.85428737	0.18775852	9.87591619	5.29E-23	2.35E-22
LOC100649659	1178.00595	1.854440708	0.10015529	18.5156535	1.54E-76	3.88E-74
LOC100649283	77.0016073	1.854563021	0.33434311	5.54688565	2.91E-08	5.47E-08
LOC100649552	190.601135	1.855164784	0.27933802	6.64129002	3.11E-11	7.01E-11
LOC105666147	11.7652546	1.857596705	0.4371994	4.24885468	2.15E-05	3.36E-05
LOC105666979	9.50509982	1.859571287	0.57235618	3.24897565	0.00115821	0.00159204
LOC100647689	215.127987	1.861303329	0.28695476	6.48639999	8.79E-11	1.92E-10
LOC100647561	47.8923679	1.861591477	0.3355379	5.54808113	2.89E-08	5.44E-08
LOC100646252	1576.79236	1.862980309	0.09060785	20.5609157	6.15E-94	3.76E-91
LOC100646047	261.112293	1.863443888	0.15974883	11.6648357	1.93E-31	1.45E-30
LOC100645479	38.0801623	1.871455186	0.32514403	5.75577282	8.62E-09	1.68E-08
LOC100642705	453.294455	1.87286986	0.15080885	12.4188327	2.07E-35	2.00E-34
LOC105665773	239.294286	1.874949075	0.23870067	7.85481268	4.00E-15	1.14E-14
LOC100645522	1001.41738	1.876674955	0.099803	18.8037938	7.03E-79	1.91E-76
LOC105665903	50.9448173	1.877173726	0.23175299	8.09988997	5.50E-16	1.65E-15
LOC100644670	2506.24349	1.877175911	0.12005145	15.6364281	4.11E-55	1.62E-53
LOC100648719	288.444346	1.879460681	0.22052959	8.52248764	1.56E-17	5.14E-17
LOC100650659	365.114841	1.879953706	0.21646418	8.68482577	3.79E-18	1.29E-17
LOC100642443	3268.40218	1.881375442	0.83347549	2.25726548	0.02399149	0.02962925
LOC100643212	103.075574	1.884427915	0.31748972	5.93539816	2.93E-09	5.89E-09
LOC100646410	322.29546	1.884851717	0.11667643	16.15452	1.06E-58	5.53E-57
LOC105665917	134.158217	1.884928117	0.34701382	5.43185318	5.58E-08	1.03E-07
LOC100647455	1174.54488	1.885034654	0.10659442	17.6841776	5.55E-70	7.66E-68
LOC105666711	92.385791	1.885590712	0.1706612	11.048737	2.22E-28	1.39E-27
LOC100650651	126.011937	1.885664447	0.22167416	8.50646934	1.79E-17	5.87E-17
LOC100652009	253.254411	1.887138417	0.20562497	9.17757414	4.41E-20	1.69E-19

LOC105666684	46.8040836	1.888730651	0.33601349	5.62099643	1.90E-08	3.61E-08
LOC100644484	154.285064	1.889211844	0.34204427	5.52329624	3.33E-08	6.23E-08
LOC100642997	259.425593	1.894112649	0.13576759	13.9511401	3.10E-44	5.47E-43
LOC100646133	673.567239	1.894508752	0.17572175	10.7812992	4.22E-27	2.43E-26
LOC100646919	353.060074	1.894633669	0.15872972	11.9362248	7.66E-33	6.21E-32
LOC100648249	47.21728	1.895437311	0.36917066	5.1343119	2.83E-07	5.02E-07
LOC100652225	1696.1707	1.897182489	0.1248975	15.189915	4.12E-52	1.34E-50
LOC100643119	425.237742	1.897579807	0.1061913	17.8694464	2.04E-71	3.27E-69
LOC100648044	2098.14797	1.89781981	0.14729	12.88492	5.47E-38	6.27E-37
LOC100650992	552.161574	1.900358414	0.11530265	16.4814811	4.98E-61	3.30E-59
LOC100647375	262.142792	1.901661276	0.14230386	13.3633853	9.90E-41	1.39E-39
LOC100647248	333.831899	1.902358757	0.16053138	11.8503858	2.14E-32	1.69E-31
LOC100643521	290.238397	1.903168168	0.13366934	14.2378809	5.33E-46	1.07E-44
LOC100644765	1252.92883	1.903361323	0.14811445	12.8506124	8.53E-38	9.68E-37
LOC100648323	10.4999872	1.903881361	0.48368797	3.93617675	8.28E-05	0.00012448
LOC100651243	574.781941	1.905834824	0.15916245	11.9741488	4.85E-33	3.98E-32
LOC100647246	116.561588	1.906131424	0.17792409	10.7131723	8.83E-27	4.98E-26
LOC100644312	328.994262	1.908051171	0.17690428	10.785783	4.02E-27	2.32E-26
LOC100645983	1250.49462	1.908355551	0.14713004	12.9705364	1.80E-38	2.13E-37
LOC105665878	462.728241	1.908661102	0.19558791	9.75858404	1.70E-22	7.33E-22
LOC100652118	149.211774	1.910393836	0.17706066	10.7894881	3.86E-27	2.23E-26
LOC100648106	54.3963226	1.911319668	0.26710533	7.15567778	8.33E-13	2.08E-12
LOC100642283	700.846618	1.911600139	0.13887675	13.7647241	4.15E-43	6.86E-42
LOC100649607	655.024491	1.912092507	0.10569901	18.0899764	3.82E-73	6.93E-71
LOC100645914	241.947577	1.912880174	0.14702041	13.010984	1.06E-38	1.27E-37
LOC105666815	30.0932748	1.914195819	0.34731652	5.51138714	3.56E-08	6.65E-08
LOC100645591	97.9033545	1.914956828	0.23759332	8.05980918	7.64E-16	2.28E-15
LOC100647632	3300.4663	1.915437911	0.1714698	11.1707015	5.67E-29	3.67E-28
LOC100650762	631.186532	1.915705008	0.14450819	13.2567226	4.13E-40	5.49E-39

LOC100644614	1391.82088	1.916268199	0.12048937	15.9040441	5.94E-57	2.76E-55
LOC100642216	46.4372836	1.917145826	0.366481	5.23122842	1.68E-07	3.02E-07
LOC100643698	200.515179	1.919810516	0.15573498	12.3274204	6.45E-35	6.05E-34
LOC100646699	57.8729969	1.921437772	0.27153338	7.07624888	1.48E-12	3.63E-12
LOC100651026	1557.1611	1.921899155	0.15331505	12.53562	4.77E-36	4.76E-35
LOC100649191	1760.47831	1.925086304	0.08888594	21.6579399	5.12E-104	6.26E-101
LOC100643742	2220.39454	1.925730521	0.16931773	11.3734727	5.67E-30	3.91E-29
LOC100648090	105.345109	1.926074642	0.25678106	7.50084394	6.34E-14	1.69E-13
LOC100643919	418.244456	1.929007256	0.11738572	16.4330657	1.11E-60	7.01E-59
LOC105665727	23.1986278	1.930077069	0.42624623	4.52808006	5.95E-06	9.64E-06
LOC100642394	464.411374	1.932757079	0.13412951	14.4096339	4.50E-47	9.84E-46
LOC100646996	847.805129	1.933701459	0.13311354	14.5267078	8.21E-48	1.92E-46
LOC100645494	72.8228585	1.93432234	0.26540269	7.28825443	3.14E-13	8.03E-13
LOC100650425	14.6097106	1.936905443	0.3845252	5.0371353	4.73E-07	8.26E-07
LOC100648151	1938.16788	1.938603103	0.10060874	19.2687336	9.83E-83	3.44E-80
LOC100643912	302.702481	1.940944816	0.15289396	12.6947122	6.33E-37	6.72E-36
LOC100646579	1284.78703	1.941643199	0.17062047	11.3798957	5.27E-30	3.64E-29
LOC100643707	44.2866386	1.942336274	0.28053828	6.92360512	4.40E-12	1.05E-11
LOC100645208	660.299254	1.944190485	0.11448572	16.9819474	1.12E-64	1.01E-62
LOC100648378	86.3234899	1.945400945	0.40960727	4.74942974	2.04E-06	3.41E-06
LOC105665833	105.964821	1.946504058	0.2977502	6.53737279	6.26E-11	1.38E-10
LOC100651482	212.159409	1.949590407	0.2158258	9.03316648	1.67E-19	6.19E-19
LOC100642228	194.937653	1.950519828	0.13969602	13.962601	2.64E-44	4.68E-43
LOC100643582	1180.60084	1.951472825	0.13835203	14.1051257	3.53E-45	6.71E-44
LOC100644480	1832.3963	1.95150565	0.13915806	14.023662	1.12E-44	2.05E-43
LOC100649447	870.616286	1.951730929	0.13185643	14.8019396	1.42E-49	3.80E-48
LOC100650139	501.666111	1.955295549	0.13252766	14.7538678	2.91E-49	7.59E-48
LOC100645050	124.814288	1.955456158	0.17804993	10.9826284	4.63E-28	2.84E-27
LOC100651537	313.842418	1.956093771	0.13395036	14.6031247	2.68E-48	6.60E-47

LOC100650804	514.108725	1.958160583	0.33902909	5.77578922	7.66E-09	1.50E-08
LOC100647819	229.240696	1.965150442	0.29995112	6.55156886	5.69E-11	1.26E-10
LOC100651863	83.8283856	1.966621835	0.28877137	6.81030754	9.74E-12	2.27E-11
LOC100644457	273.688673	1.966911948	0.19642212	10.0136988	1.33E-23	6.11E-23
LOC105666991	48.6841524	1.968384465	0.56640448	3.47522758	0.00051042	0.00072208
LOC100642776	296.408149	1.969094513	0.2047295	9.61803006	6.71E-22	2.82E-21
LOC100648097	127.413295	1.971967076	0.15998161	12.3262107	6.55E-35	6.13E-34
LOC100649770	1023.86708	1.972076626	0.14377685	13.7162324	8.12E-43	1.32E-41
LOC100651105	14.6500799	1.972149353	0.46492531	4.24186274	2.22E-05	3.46E-05
LOC100651463	334.555346	1.973811947	0.13783407	14.3202034	1.64E-46	3.40E-45
LOC100649661	38.83606	1.975316679	0.39356763	5.01900193	5.19E-07	9.06E-07
LOC100642625	83.6691174	1.97563472	0.23313	8.47439066	2.36E-17	7.69E-17
LOC100645652	1027.57205	1.976367682	0.13357373	14.7960811	1.55E-49	4.12E-48
LOC100652227	778.874383	1.977363042	0.12277502	16.1055807	2.33E-58	1.19E-56
LOC100652082	2198.91275	1.977642664	0.11493556	17.2065341	2.37E-66	2.42E-64
LOC100647997	1055.4147	1.98073281	0.11204892	17.6773937	6.26E-70	8.52E-68
LOC100646949	415.468037	1.980768577	0.16925064	11.7031674	1.23E-31	9.30E-31
LOC100649584	645.39985	1.981390019	0.15045489	13.1693299	1.32E-39	1.70E-38
LOC100645230	1462.15768	1.982325609	0.19838316	9.9924087	1.65E-23	7.53E-23
LOC100647022	156.587521	1.983030008	0.26373863	7.51892139	5.52E-14	1.48E-13
LOC105666403	32.4598097	1.983367416	0.36047633	5.50207392	3.75E-08	7.00E-08
LOC105666961	16.0867292	1.983622063	0.83557025	2.37397402	0.01759779	0.02195463
LOC100643052	141.527257	1.985508534	0.18445801	10.7640139	5.09E-27	2.92E-26
LOC100648610	375.144706	1.987117322	0.20604954	9.64388116	5.22E-22	2.20E-21
LOC100645811	461.651137	1.990245967	0.13864417	14.3550645	9.90E-47	2.10E-45
LOC105667130	113.735164	1.991705	0.25713076	7.74588385	9.49E-15	2.65E-14
LOC100648755	379.535291	1.992188215	0.14453683	13.7832564	3.21E-43	5.33E-42
LOC100651444	2502.38964	1.994501018	0.11286654	17.6713231	6.97E-70	9.35E-68
LOC100651191	1632.06708	1.996545228	0.14567322	13.7056432	9.39E-43	1.53E-41

LOC100648741	1006.05729	1.999066307	0.2694237	7.41978642	1.17E-13	3.08E-13
LOC100648072	741.453323	2.000356408	0.1132192	17.6679968	7.40E-70	9.79E-68
LOC105666679	26.8943752	2.007924707	0.56150904	3.57594368	0.00034897	0.00050033
LOC100648011	151.806848	2.008958191	0.25033721	8.0250082	1.02E-15	3.00E-15
LOC100650729	908.251408	2.009787042	0.12809877	15.6893552	1.79E-55	7.36E-54
LOC100650068	337.986838	2.010606344	0.15273033	13.1644209	1.41E-39	1.80E-38
LOC100646408	237.451805	2.01096731	0.29558242	6.80340626	1.02E-11	2.38E-11
LOC100650701	232.653587	2.012316708	0.16763916	12.0038584	3.39E-33	2.81E-32
LOC100646669	144.235422	2.013074182	0.21664487	9.29204636	1.51E-20	5.96E-20
LOC100642572	197.715939	2.013893289	0.16241849	12.399409	2.63E-35	2.53E-34
LOC100650442	4224.0386	2.014649459	0.11678865	17.2503879	1.11E-66	1.16E-64
LOC100651412	336.881753	2.018749687	0.14856301	13.5885081	4.69E-42	7.18E-41
LOC100649110	489.744958	2.026839634	0.20866867	9.71319579	2.65E-22	1.14E-21
LOC100647791	2774.01488	2.031100376	0.14726227	13.7924021	2.83E-43	4.72E-42
LOC100652055	793.358159	2.032124691	0.14186178	14.3246804	1.53E-46	3.20E-45
LOC100647430	419.032069	2.032383633	0.12248071	16.5935	7.77E-62	5.28E-60
LOC100643592	962.756443	2.033450884	0.12033143	16.8987516	4.60E-64	3.88E-62
LOC105666860	2475.74895	2.034086009	0.18076366	11.2527374	2.25E-29	1.48E-28
LOC100645053	95.6670773	2.035026185	0.29515582	6.89475194	5.40E-12	1.28E-11
LOC100644900	146.287504	2.037259212	0.29680159	6.8640442	6.69E-12	1.58E-11
LOC105666948	1259.26276	2.040396212	0.1751878	11.6469078	2.38E-31	1.78E-30
LOC100650751	893.41835	2.040977614	0.16416337	12.432601	1.74E-35	1.69E-34
LOC100651372	100.604432	2.041347784	0.30290589	6.73921458	1.59E-11	3.67E-11
LOC100644599	173.169715	2.04334828	0.15109827	13.5233065	1.14E-41	1.71E-40
LOC100643303	1086.73893	2.045105545	0.14324407	14.2770695	3.04E-46	6.24E-45
LOC100643773	183.542812	2.047615382	0.19208446	10.6599742	1.57E-26	8.69E-26
LOC100650098	528.352402	2.048540285	0.20621822	9.93384729	2.97E-23	1.34E-22
LOC100650770	796.600842	2.049464645	0.11512068	17.8027504	6.73E-71	1.01E-68
LOC105665832	158.006944	2.049875294	0.22075892	9.28558301	1.61E-20	6.31E-20

LOC100648448	168.909614	2.051357716	0.29951061	6.84903195	7.44E-12	1.75E-11
LOC100643524	116.307419	2.051388908	0.34793299	5.89593098	3.73E-09	7.43E-09
LOC100643434	476.142587	2.053282994	0.12939013	15.8689305	1.04E-56	4.69E-55
LOC100650786	173.490803	2.054041021	0.30484037	6.73808732	1.60E-11	3.69E-11
LOC105666804	374.212682	2.054654089	0.14595018	14.0777767	5.20E-45	9.72E-44
LOC100642390	3189.67884	2.056177449	0.11373838	18.0781325	4.74E-73	8.44E-71
LOC100644160	176.06667	2.056317979	0.19374285	10.6136458	2.58E-26	1.41E-25
LOC100643775	723.016104	2.056753054	0.1715304	11.990604	3.98E-33	3.28E-32
LOC100642830	23.5579118	2.057928539	0.67102644	3.06683676	0.00216337	0.00291476
LOC100647335	407.15796	2.057973956	0.2023015	10.172806	2.62E-24	1.26E-23
LOC100644047	467.598845	2.05819411	0.1461679	14.0810264	4.97E-45	9.32E-44
LOC100645908	494.590947	2.060052665	0.16658214	12.3665881	3.96E-35	3.77E-34
LOC100644570	1554.14569	2.062147022	0.16096619	12.8110571	1.42E-37	1.59E-36
LOC100645618	1459.83171	2.064603897	0.12989001	15.8950174	6.86E-57	3.15E-55
LOC100650177	507.385245	2.06519901	0.23921294	8.63330819	5.96E-18	2.01E-17
LOC100643639	619.32003	2.068171491	0.31906027	6.48207142	9.05E-11	1.97E-10
LOC100650368	816.481989	2.068176819	0.11961914	17.2896811	5.63E-67	5.99E-65
LOC100646054	986.218146	2.069876901	0.14422296	14.3519232	1.04E-46	2.19E-45
LOC100649860	560.867507	2.070589383	0.15528787	13.3338773	1.47E-40	2.03E-39
LOC100651803	34.9038813	2.075897489	0.47529267	4.3676194	1.26E-05	1.99E-05
LOC100644300	285.712431	2.076512091	0.15412443	13.4729585	2.26E-41	3.30E-40
LOC100651899	185.999618	2.078660791	0.19039751	10.9174789	9.51E-28	5.69E-27
LOC100648680	244.536981	2.079471721	0.16656885	12.4841575	9.11E-36	8.97E-35
LOC100644512	196.815327	2.079522434	0.21723446	9.57270989	1.04E-21	4.33E-21
LOC100652202	156.120434	2.083180495	0.23841384	8.737666	2.38E-18	8.21E-18
LOC100646757	421.687767	2.083238908	0.13323733	15.6355501	4.17E-55	1.63E-53
LOC100648769	167.806552	2.083754821	0.20381189	10.2239117	1.55E-24	7.56E-24
LOC105666541	58.3529407	2.084554315	0.25046655	8.32268545	8.60E-17	2.72E-16
LOC105666950	16.9530774	2.085707999	0.45066656	4.62805143	3.69E-06	6.06E-06

LOC105666461	66.9019328	2.087002949	0.32071176	6.50741014	7.65E-11	1.68E-10
LOC100649009	205.331254	2.091419411	0.28494749	7.33966613	2.14E-13	5.53E-13
LOC100644389	215.940986	2.092698438	0.20425514	10.2455118	1.24E-24	6.10E-24
LOC100644080	427.869144	2.096827023	0.16520543	12.6922407	6.53E-37	6.93E-36
LOC100647721	1014.74591	2.096913722	0.13547363	15.4783904	4.85E-54	1.74E-52
LOC100646144	254.388875	2.098918364	0.22953806	9.14409741	6.01E-20	2.29E-19
LOC100645283	1697.08876	2.09965284	0.16657226	12.6050573	1.98E-36	2.05E-35
LOC100649696	227.453238	2.101233388	0.17261704	12.1728038	4.34E-34	3.86E-33
LOC100645808	206.858887	2.102481966	0.18484103	11.3745413	5.60E-30	3.87E-29
LOC105666006	9.27820299	2.104074189	0.54639641	3.85081994	0.00011772	0.00017475
LOC100651981	20.8071585	2.105141445	0.38691509	5.44083571	5.30E-08	9.81E-08
LOC105665731	899.965792	2.105548608	0.13192585	15.9600915	2.42E-57	1.17E-55
LOC105666428	14.6458094	2.11050918	0.42935179	4.91557097	8.85E-07	1.52E-06
LOC100647115	2170.5936	2.11147781	0.1304436	16.1869021	6.24E-59	3.32E-57
LOC105665767	442.002308	2.111802243	0.39804597	5.30542298	1.12E-07	2.04E-07
LOC100643308	207.326565	2.114165615	0.18018591	11.7332461	8.61E-32	6.58E-31
LOC100631073	457.08505	2.1142867	0.14265113	14.821381	1.07E-49	2.87E-48
LOC100646511	1390.4601	2.116411411	0.11225224	18.8540685	2.72E-79	7.84E-77
LOC100648385	1126.21552	2.117039361	0.1226669	17.2584406	9.67E-67	1.02E-64
LOC100646035	1402.47454	2.118693934	0.12755848	16.6095889	5.94E-62	4.12E-60
LOC100650198	1028.18199	2.12337299	0.12004079	17.6887619	5.12E-70	7.16E-68
LOC100642616	98.7830226	2.124022648	0.24091813	8.81636693	1.18E-18	4.16E-18
LOC100645000	312.786872	2.124157945	0.17036993	12.4679161	1.12E-35	1.10E-34
LOC100651464	233.332567	2.132534758	0.14487103	14.7202295	4.78E-49	1.23E-47
LOC100645590	311.164905	2.132809151	0.15749447	13.5421206	8.82E-42	1.33E-40
LOC100650885	520.963063	2.134925374	0.26675583	8.003294	1.21E-15	3.56E-15
LOC100643361	2719.10586	2.135124668	0.13720257	15.5618414	1.32E-54	4.90E-53
LOC100642817	396.935367	2.13561641	0.205616	10.3864308	2.86E-25	1.47E-24
LOC100648623	693.098324	2.137217508	0.16283295	13.1252149	2.36E-39	2.96E-38

LOC105666396	363.556579	2.138216242	0.24301621	8.79865674	1.38E-18	4.85E-18
LOC100645236	279.263803	2.140913997	0.17720728	12.0814112	1.32E-33	1.13E-32
LOC100645763	348.684498	2.143839369	0.17052452	12.5720296	3.01E-36	3.05E-35
LOC100650463	391.55755	2.143849598	0.22002258	9.74377095	1.96E-22	8.46E-22
LOC100649952	321.587393	2.148231465	0.21267762	10.1008818	5.47E-24	2.58E-23
LOC100644552	392.434275	2.149127808	0.30983482	6.93636627	4.02E-12	9.61E-12
LOC100642338	76.8712275	2.149624049	0.38137686	5.63648258	1.74E-08	3.31E-08
LOC100644155	156.835603	2.150285148	0.20852423	10.3119198	6.22E-25	3.13E-24
LOC100642844	2570.40837	2.156753128	0.17241659	12.5089652	6.67E-36	6.61E-35
LOC105665871	140.700981	2.159089491	0.30729883	7.0260257	2.12E-12	5.16E-12
LOC100647569	408.904003	2.163954396	0.13367384	16.1883162	6.10E-59	3.26E-57
LOC100646532	341.417941	2.167893419	0.12946394	16.7451526	6.14E-63	4.56E-61
LOC100649875	79.4721861	2.171435059	0.26546368	8.17978206	2.84E-16	8.68E-16
LOC100642896	264.737515	2.17385354	0.22254428	9.76818415	1.54E-22	6.68E-22
LOC100649670	1231.01542	2.174345741	0.14127012	15.3914056	1.87E-53	6.47E-52
LOC100650945	50.9419433	2.175436682	0.3154562	6.8961607	5.34E-12	1.27E-11
LOC100649669	449.709319	2.177458756	0.15291151	14.2399924	5.17E-46	1.04E-44
LOC100642688	251.018408	2.18073863	0.14899624	14.6361987	1.65E-48	4.13E-47
LOC105666984	82.3918185	2.183797597	0.26937028	8.1070473	5.19E-16	1.56E-15
LOC100650970	317.017489	2.18757604	0.17183779	12.7304714	4.00E-37	4.32E-36
LOC100649706	38.4467243	2.188619671	0.36371419	6.01741626	1.77E-09	3.60E-09
LOC100650490	232.905063	2.189577977	0.18108738	12.091279	1.17E-33	1.00E-32
LOC100645512	375.111664	2.193338542	0.29478248	7.44053233	1.00E-13	2.64E-13
LOC100642692	1959.97872	2.196338825	0.10556756	20.8050553	3.90E-96	3.18E-93
LOC100646162	540.431235	2.197481622	0.16884488	13.014796	1.01E-38	1.21E-37
LOC105665919	10.0542228	2.198755263	0.63149873	3.48180474	0.00049805	0.0007058
LOC100648919	109.925872	2.19880638	0.3254519	6.7561639	1.42E-11	3.27E-11
LOC100651132	618.583059	2.19937271	0.19299654	11.3959178	4.38E-30	3.04E-29
LOC100649788	673.221118	2.201940208	0.2052626	10.7274304	7.57E-27	4.29E-26

LOC100646381	698.617549	2.203062615	0.12433037	17.7194249	2.97E-70	4.21E-68
LOC100642375	688.956958	2.203494512	0.21608867	10.1971775	2.04E-24	9.88E-24
LOC100648968	893.632355	2.210105757	0.12878723	17.1609074	5.21E-66	5.20E-64
LOC100644224	69.3303115	2.210127479	0.2092955	10.5598421	4.57E-26	2.47E-25
LOC100643439	362.674316	2.214441644	0.16049569	13.7975151	2.64E-43	4.42E-42
LOC100651461	275.283661	2.214546126	0.20472965	10.8169293	2.86E-27	1.67E-26
LOC100645868	1379.01853	2.217278496	0.1547191	14.3309936	1.40E-46	2.93E-45
LOC100643309	394.372046	2.224128112	0.16994185	13.0875834	3.88E-39	4.79E-38
LOC105666688	24.1939209	2.224914904	0.5230475	4.25375302	2.10E-05	3.29E-05
LOC100649762	143.595118	2.229216408	0.16438952	13.5605747	6.86E-42	1.04E-40
LOC100644200	165.486251	2.231630918	0.18071899	12.3486246	4.96E-35	4.67E-34
LOC100650999	3594.7521	2.238471004	0.12114089	18.4782441	3.09E-76	7.21E-74
LOC100650844	368.223915	2.239134194	0.19457321	11.5079263	1.20E-30	8.64E-30
LOC100645916	170367.659	2.241357324	0.33575776	6.67551901	2.46E-11	5.59E-11
LOC100644519	2253.97658	2.242693556	0.19491722	11.5058772	1.23E-30	8.85E-30
LOC105667147	114.740254	2.244714632	0.30847477	7.27681765	3.42E-13	8.73E-13
LOC105666796	104.271712	2.246886932	0.1593505	14.1002819	3.78E-45	7.16E-44
LOC100648161	1941.7248	2.247650378	0.1303236	17.2466867	1.19E-66	1.22E-64
LOC100642730	1166.70516	2.249284368	0.24752019	9.0872764	1.02E-19	3.81E-19
LOC100648566	3111.46623	2.250078727	0.23826028	9.44378446	3.60E-21	1.46E-20
LOC100649334	508.190203	2.252339431	0.12556214	17.9380455	5.95E-72	1.00E-69
LOC100646566	96.5107736	2.254729423	0.25048263	9.00154018	2.23E-19	8.22E-19
LOC100650436	130317.684	2.255441744	0.34390908	6.55825011	5.44E-11	1.20E-10
LOC100647120	624.195509	2.256674074	0.23683125	9.52861634	1.59E-21	6.58E-21
LOC100648674	116.734309	2.256675271	0.23652455	9.54097702	1.41E-21	5.86E-21
LOC100651979	958.341678	2.256925422	0.17175511	13.1403685	1.93E-39	2.45E-38
LOC100650202	48.1819819	2.258802134	0.4026211	5.61024276	2.02E-08	3.84E-08
LOC105666745	43.6700623	2.259183386	0.29206685	7.73515857	1.03E-14	2.88E-14
LOC100645818	5708.11713	2.259495122	0.14452864	15.6335457	4.30E-55	1.67E-53

LOC100647589	16605.7934	2.261675103	0.17938404	12.6080066	1.91E-36	1.98E-35
LOC100645156	1279.51877	2.262956948	0.13764421	16.4406263	9.79E-61	6.27E-59
LOC100643658	572.920169	2.268948194	0.1485595	15.2729925	1.16E-52	3.89E-51
LOC100647917	32.0057346	2.269103121	0.38982048	5.82089251	5.85E-09	1.15E-08
LOC105666005	85.710486	2.271012413	0.1937324	11.7224192	9.78E-32	7.45E-31
LOC100644204	1776.64103	2.271328214	0.12418285	18.2901921	9.91E-75	1.98E-72
LOC100643024	950.692076	2.27503175	0.1985051	11.4608228	2.08E-30	1.47E-29
LOC100642205	15.539373	2.277316025	0.5850612	3.89244069	9.92E-05	0.00014814
LOC100651931	541.206996	2.282645719	0.72464983	3.14999827	0.00163271	0.00221749
LOC105666597	8.83678715	2.283113099	0.90433671	2.52462726	0.01158211	0.01467586
LOC100643194	672.361109	2.283925705	0.26092945	8.75303922	2.08E-18	7.20E-18
LOC100642194	50.8762691	2.285780035	0.37032196	6.17241291	6.73E-10	1.40E-09
LOC100647857	552.828241	2.290363887	0.14442634	15.8583528	1.23E-56	5.45E-55
LOC100650025	103.255462	2.291852013	0.18991354	12.0678705	1.56E-33	1.32E-32
LOC100642497	48.0425386	2.292799447	0.37293236	6.1480303	7.85E-10	1.62E-09
LOC100651404	774.144359	2.294708061	0.13992304	16.3997873	1.92E-60	1.20E-58
LOC105666617	24.7048984	2.298933714	0.39819155	5.77343673	7.77E-09	1.52E-08
LOC100645682	393.421176	2.301456599	0.1817945	12.6596605	9.89E-37	1.04E-35
LOC100643339	69.2349167	2.303219837	0.30161787	7.63621813	2.24E-14	6.12E-14
LOC100645114	643.983457	2.304803266	0.12889787	17.8808482	1.66E-71	2.76E-69
LOC105666312	633.794033	2.304986949	0.15181944	15.1824232	4.62E-52	1.48E-50
LOC100648629	2647.4638	2.305087589	0.14450868	15.9512048	2.79E-57	1.33E-55
LOC100650641	593.719903	2.305339192	0.13479944	17.101994	1.43E-65	1.36E-63
LOC100645045	272.534562	2.307073233	0.15299621	15.0792831	2.22E-51	6.76E-50
LOC100643235	578.064849	2.309030641	0.1630439	14.162018	1.57E-45	3.08E-44
LOC105665623	798.418626	2.317921948	0.19089099	12.142647	6.28E-34	5.49E-33
LOC100643323	472.761825	2.319340323	0.16922141	13.7059511	9.35E-43	1.52E-41
LOC100642513	25.2173438	2.320028397	0.43068236	5.38686649	7.17E-08	1.32E-07
LOC105666399	1311.61521	2.320902278	0.24406357	9.50941708	1.92E-21	7.87E-21

LOC100647781	574.584047	2.322648859	0.22015199	10.5502063	5.07E-26	2.72E-25
LOC100644101	69.8375697	2.323936155	0.8018511	2.89821408	0.00375294	0.0049495
LOC100644320	1125.09212	2.324371251	0.14467917	16.0656937	4.44E-58	2.25E-56
LOC100650270	1570.72407	2.324724903	0.09426704	24.6610563	2.80E-134	9.14E-131
LOC100642453	68.316429	2.32845885	0.26201744	8.88665607	6.30E-19	2.25E-18
LOC100643711	83.3202395	2.329634263	0.54529918	4.272213	1.94E-05	3.04E-05
LOC100650657	841.431149	2.332113602	0.17523573	13.3084369	2.07E-40	2.81E-39
LOC100647139	364.315554	2.336587021	0.16939119	13.7940295	2.77E-43	4.63E-42
LOC105666184	76.0400789	2.337684135	0.23965823	9.75424086	1.77E-22	7.65E-22
LOC100646939	441.91534	2.339553628	0.12820147	18.2490391	2.11E-74	4.12E-72
LOC100648369	686.234416	2.340222489	0.16462002	14.2159048	7.30E-46	1.45E-44
LOC100648659	35.1977636	2.340809365	0.3162558	7.40163302	1.35E-13	3.51E-13
LOC100646692	603.42961	2.342146579	0.12874579	18.1920247	5.97E-74	1.10E-71
LOC100651476	1296.88277	2.346846997	0.14140757	16.5963321	7.41E-62	5.07E-60
LOC100644895	235.830978	2.347030557	0.27501002	8.5343457	1.41E-17	4.66E-17
LOC105666166	107.557274	2.347488162	0.27754963	8.45790406	2.72E-17	8.81E-17
LOC100646728	24.0811683	2.349401871	0.54070362	4.34508257	1.39E-05	2.21E-05
LOC100650196	1677.14183	2.352280818	0.1482649	15.8653925	1.10E-56	4.94E-55
LOC105666075	16.9879807	2.352456051	0.38436657	6.12034504	9.34E-10	1.93E-09
LOC100643951	2209.83898	2.353002822	0.18581631	12.6630589	9.47E-37	1.00E-35
LOC100648037	57.4102867	2.355612622	0.31152809	7.56147754	3.99E-14	1.07E-13
LOC100646717	183.778416	2.357320756	0.40466149	5.82541418	5.70E-09	1.12E-08
LOC100642813	198.575114	2.359213016	0.19878323	11.8682699	1.73E-32	1.37E-31
LOC100644067	1279.64167	2.361022376	0.12843874	18.3824779	1.81E-75	3.86E-73
LOC100647661	5211.10039	2.362193666	0.13214384	17.8759277	1.82E-71	2.96E-69
LOC100644929	11.1604771	2.363280207	0.97168548	2.43214524	0.01500969	0.01884101
LOC100647501	124.653437	2.365259468	0.21032687	11.2456361	2.43E-29	1.60E-28
LOC100643075	852.285695	2.367311406	0.13315897	17.7780847	1.04E-70	1.53E-68
LOC100648439	143.367837	2.369159807	0.2434994	9.72963304	2.25E-22	9.68E-22

LOC100644004	333.580752	2.370997266	0.12246999	19.3598222	1.68E-83	6.34E-81
LOC100643738	379.322316	2.374087737	0.16996781	13.967867	2.45E-44	4.36E-43
LOC100648584	745.358448	2.374270299	0.10810084	21.9634776	6.44E-107	1.05E-103
LOC100650950	1747.573	2.376961181	0.16825663	14.1269983	2.59E-45	5.00E-44
LOC100645674	324.422244	2.380915331	0.16488769	14.4396181	2.91E-47	6.47E-46
LOC100651621	275.547258	2.381689388	0.20220507	11.7785841	5.03E-32	3.89E-31
LOC100643159	558.466025	2.385007073	0.17411642	13.6977722	1.05E-42	1.69E-41
LOC100642981	136.189959	2.385260852	0.25880292	9.21651458	3.07E-20	1.18E-19
LOC100648785	643.13065	2.386528918	0.16407943	14.5449613	6.29E-48	1.49E-46
LOC100647437	208.987759	2.402148476	0.15218339	15.7845645	3.97E-56	1.70E-54
LOC100651630	547.045936	2.402645864	0.20111613	11.9465596	6.77E-33	5.49E-32
LOC100647397	528.253487	2.404211684	0.20605558	11.6677823	1.86E-31	1.40E-30
LOC100645635	53.7670076	2.406545251	0.55543061	4.33275587	1.47E-05	2.33E-05
LOC100647083	69.9333772	2.406795919	0.27333202	8.80539325	1.30E-18	4.57E-18
LOC100644079	357.75187	2.40715775	0.12447131	19.3390571	2.52E-83	9.14E-81
LOC100648332	432.910547	2.410262123	0.18340581	13.1416888	1.90E-39	2.42E-38
LOC100643840	81.2993464	2.410500316	0.26691437	9.03098754	1.70E-19	6.31E-19
LOC100649440	119.650603	2.410543555	0.27518529	8.75971079	1.96E-18	6.80E-18
LOC105666478	189.628694	2.410917694	0.18596105	12.9646383	1.94E-38	2.29E-37
LOC100642982	840.899118	2.414543428	0.33309834	7.24874052	4.21E-13	1.07E-12
LOC100645233	158.282322	2.417182917	0.26710832	9.04944825	1.44E-19	5.35E-19
LOC100642492	637.397957	2.420810183	0.18049502	13.4120605	5.14E-41	7.31E-40
LOC100648320	295.903019	2.426856956	0.18582983	13.0595662	5.60E-39	6.87E-38
LOC100642229	309.936772	2.426931181	0.18082923	13.4211223	4.55E-41	6.49E-40
LOC100651835	844.12603	2.427110881	0.16884556	14.3747393	7.46E-47	1.60E-45
LOC100650346	872.506684	2.427441482	0.85503207	2.83900637	0.00452543	0.0059228
LOC100642838	955.661517	2.4275192	0.19643406	12.3579343	4.41E-35	4.18E-34
LOC105666689	37.1626293	2.435133801	0.61653218	3.949727	7.82E-05	0.00011787
LOC100647151	602.040152	2.436028245	0.11846929	20.5625292	5.95E-94	3.76E-91

LOC100643772	332.84601	2.436273308	0.16213109	15.0265646	4.92E-51	1.46E-49
LOC105665735	67.9106979	2.437421043	0.26578039	9.17080834	4.69E-20	1.80E-19
LOC105666652	32.9314663	2.440458947	0.6918606	3.52738534	0.00041969	0.00059778
LOC100643563	132.590598	2.44188628	0.29643468	8.23751882	1.76E-16	5.45E-16
LOC105667199	287.725916	2.444428764	0.39093185	6.25282587	4.03E-10	8.48E-10
LOC100644132	553.191707	2.446725905	0.26117978	9.36797606	7.39E-21	2.95E-20
LOC100645909	291.71601	2.447819443	0.24098009	10.1577662	3.06E-24	1.46E-23
LOC105666864	9.40203252	2.451700508	0.67412553	3.63686052	0.00027598	0.00039843
LOC100643306	1110.13972	2.454441871	0.17746066	13.8309069	1.66E-43	2.81E-42
LOC100643304	13.2938764	2.455353087	0.63840082	3.8460995	0.00012001	0.00017806
LOC100644827	802.594522	2.457471366	0.17478492	14.0599733	6.69E-45	1.24E-43
LOC100647171	119.279951	2.4586739	0.32490463	7.56737106	3.81E-14	1.03E-13
LOC100649610	42.7518861	2.459666227	0.34774089	7.07327304	1.51E-12	3.71E-12
LOC100644400	1297.50421	2.465077739	0.17713171	13.9166369	5.02E-44	8.75E-43
LOC100650873	343.038221	2.466213598	0.18514983	13.3200963	1.77E-40	2.42E-39
LOC100651028	154.615467	2.478821914	0.2763253	8.97066563	2.95E-19	1.08E-18
LOC100648349	226.311066	2.48063166	0.76871038	3.22700425	0.00125094	0.00171395
LOC100647950	29.444248	2.483466921	0.32423367	7.65949735	1.87E-14	5.13E-14
LOC100651220	122.931249	2.483793771	0.45036165	5.51510945	3.49E-08	6.52E-08
LOC100642354	10.7338323	2.485480606	0.57920018	4.29122902	1.78E-05	2.80E-05
LOC105666042	389.759422	2.489710189	0.16593729	15.003922	6.92E-51	2.03E-49
LOC100631082	1182.20827	2.492733401	0.46860983	5.31942193	1.04E-07	1.89E-07
LOC100644404	256.791549	2.492845316	0.22239389	11.2091449	3.68E-29	2.41E-28
LOC105665984	360.205925	2.495196858	0.15159788	16.4593124	7.19E-61	4.66E-59
LOC100646487	108.212614	2.495251122	0.30063327	8.29998331	1.04E-16	3.27E-16
LOC100651371	1113.55719	2.499901495	0.11659765	21.4404114	5.61E-102	5.49E-99
LOC100647978	256.536912	2.500221895	0.22654949	11.0360959	2.56E-28	1.59E-27
LOC100644427	437.459032	2.501333771	0.20695247	12.0865133	1.24E-33	1.06E-32
LOC100649115	581.586793	2.503413232	0.20043871	12.4896697	8.50E-36	8.38E-35

LOC100642436	171.000757	2.504954464	0.19050206	13.1492251	1.72E-39	2.20E-38
LOC100648771	260.803426	2.506321449	0.21081627	11.8886529	1.36E-32	1.08E-31
LOC100651169	97.4635937	2.508794096	0.24225492	10.3560087	3.93E-25	2.00E-24
LOC100642641	41.7582312	2.509872718	0.37602443	6.67475964	2.48E-11	5.62E-11
LOC100650639	41.2489043	2.512912128	0.37526373	6.69638966	2.14E-11	4.87E-11
LOC100648738	1483.41414	2.515372012	0.15714939	16.0062475	1.16E-57	5.77E-56
LOC100649863	3218.99301	2.516189876	0.12948153	19.4328092	4.07E-84	1.66E-81
LOC100647784	105.447808	2.516531806	0.32401511	7.76671121	8.06E-15	2.26E-14
LOC100651092	133.266628	2.520345553	0.26823945	9.39587955	5.67E-21	2.28E-20
LOC100643228	62.4339228	2.522947347	0.32687472	7.71839226	1.18E-14	3.27E-14
LOC100650718	726.900795	2.523010566	0.22425435	11.2506649	2.30E-29	1.51E-28
LOC100647450	58.697715	2.526436307	0.36933784	6.84044805	7.89E-12	1.85E-11
LOC100647004	311.155512	2.526478601	0.18805299	13.4349293	3.77E-41	5.39E-40
LOC100643812	257.37705	2.52958472	0.21042921	12.0210724	2.75E-33	2.30E-32
LOC105667047	23.5972973	2.531742926	0.5798462	4.36623183	1.26E-05	2.01E-05
LOC100643629	259.059937	2.535720671	0.30566914	8.29563845	1.08E-16	3.39E-16
LOC100645310	51.1090228	2.537503078	0.38928595	6.51835261	7.11E-11	1.56E-10
LOC100647218	98.1969367	2.538976733	0.31563357	8.04406437	8.69E-16	2.58E-15
LOC100647679	1486.91131	2.539177801	0.17718183	14.3309154	1.40E-46	2.93E-45
LOC100643944	109.515842	2.539318872	0.38640725	6.57161283	4.98E-11	1.11E-10
LOC100646561	88.8530891	2.541386481	0.25635524	9.91353429	3.64E-23	1.63E-22
LOC105666145	13.2433208	2.541732603	0.47922946	5.3037904	1.13E-07	2.05E-07
LOC100647294	1184.33315	2.541870279	0.1162976	21.8566009	6.73E-106	9.41E-103
LOC100652113	286.73835	2.546946661	0.15054037	16.9186953	3.28E-64	2.84E-62
LOC100651932	847.614853	2.546947686	0.13044066	19.5257197	6.64E-85	3.09E-82
LOC105666377	651.306551	2.554212724	0.17608642	14.5054496	1.12E-47	2.58E-46
LOC100645723	2093.57948	2.554349088	0.16392736	15.5822014	9.62E-55	3.62E-53
LOC100646901	793.399402	2.555782765	0.24346939	10.4973474	8.88E-26	4.70E-25
LOC100643225	677.194668	2.557843725	0.16063811	15.923019	4.39E-57	2.07E-55

LOC100648098	1185.4468	2.569218259	0.14105389	18.2144449	3.96E-74	7.46E-72
LOC100646092	14.7652244	2.570647716	0.45951891	5.59421525	2.22E-08	4.20E-08
LOC100645068	251.008921	2.574972782	0.31157507	8.2643737	1.40E-16	4.38E-16
LOC100647407	2583.38783	2.57555961	0.14997778	17.1729411	4.23E-66	4.27E-64
LOC100642959	1969.67274	2.577344919	0.12465503	20.675819	5.72E-95	4.00E-92
LOC100644529	491.88461	2.590915341	0.20218088	12.8148385	1.35E-37	1.52E-36
LOC100645839	86.1769134	2.592266268	0.55627349	4.66005714	3.16E-06	5.22E-06
LOC100648501	202.883108	2.593221499	0.22936251	11.3062136	1.22E-29	8.23E-29
LOC100645822	513.328454	2.598358337	0.16989089	15.2942774	8.35E-53	2.84E-51
LOC100648441	244.403503	2.598860469	0.25671044	10.1237039	4.34E-24	2.06E-23
LOC100642745	12.0373979	2.600760402	0.55632417	4.67490097	2.94E-06	4.86E-06
LOC105667058	13.445614	2.60960154	1.08297962	2.40964972	0.01596784	0.01998481
LOC100644961	500.346217	2.610236606	0.16504826	15.8149906	2.45E-56	1.06E-54
LOC100650059	45.0797435	2.610844707	0.37595095	6.94464178	3.79E-12	9.09E-12
LOC100642395	54.2064353	2.611322698	0.36684904	7.1182487	1.09E-12	2.71E-12
LOC100642306	274.099045	2.612268721	0.28145506	9.28129963	1.67E-20	6.56E-20
LOC100649682	439.293451	2.612923029	0.31441998	8.31029571	9.55E-17	3.01E-16
LOC100649079	128.724051	2.614106976	0.33129271	7.89062634	3.01E-15	8.67E-15
LOC100649676	69.7539754	2.614464364	0.32555006	8.03091356	9.67E-16	2.87E-15
LOC100646861	465.923877	2.617086738	0.17227468	15.1913599	4.03E-52	1.31E-50
LOC100647438	564.630398	2.619884333	0.1679922	15.5952732	7.84E-55	2.97E-53
LOC100648330	3215.02569	2.621123279	0.12908282	20.3057484	1.14E-91	6.59E-89
LOC100651110	993.779981	2.622502237	0.28691237	9.14042947	6.22E-20	2.37E-19
LOC100648604	289.101739	2.623455149	0.25021733	10.4847062	1.02E-25	5.36E-25
LOC100649221	148.109045	2.625493015	0.32677363	8.03459264	9.39E-16	2.78E-15
LOC100649864	55.4430255	2.625500029	0.2713974	9.67400579	3.89E-22	1.65E-21
LOC100648790	1005.90503	2.626403721	0.29544807	8.8895613	6.14E-19	2.20E-18
LOC105665961	19.9719972	2.632843856	0.48397018	5.4400952	5.33E-08	9.85E-08
LOC100649614	638.941451	2.633424374	0.47781359	5.51140533	3.56E-08	6.65E-08

LOC100647018	71.0145	2.634562843	0.371085	7.09962099	1.25E-12	3.08E-12
LOC100643681	554.189433	2.636479468	0.17514804	15.0528631	3.31E-51	9.99E-50
LOC100651984	123.012194	2.641641421	0.16231264	16.2750192	1.48E-59	8.40E-58
LOC100644499	238.619313	2.642592269	0.28027776	9.4284766	4.16E-21	1.69E-20
LOC100642548	19.3853968	2.643079794	0.54881228	4.81599973	1.46E-06	2.47E-06
LOC100649835	24.6673735	2.645063928	0.48264902	5.48030517	4.25E-08	7.90E-08
LOC100644559	109.389356	2.648216189	0.37044851	7.14867554	8.76E-13	2.18E-12
LOC100644248	80.9692373	2.648922715	0.95252095	2.78096007	0.00541984	0.00705379
LOC100645624	1508.24321	2.650623278	0.17511305	15.13664	9.28E-52	2.92E-50
LOC100648228	17.7161392	2.653163839	0.441196	6.01357179	1.81E-09	3.69E-09
LOC105666728	15.1355179	2.653849294	0.88923229	2.98442751	0.0028411	0.00379446
LOC100647427	483.551059	2.65460587	0.22188813	11.9637127	5.50E-33	4.49E-32
LOC100643985	705.399818	2.657239254	0.19055851	13.9444795	3.40E-44	5.96E-43
LOC105666084	16.3084209	2.659231381	0.43924705	6.05406772	1.41E-09	2.89E-09
LOC105667120	103.454991	2.663385718	0.24634562	10.8115815	3.03E-27	1.77E-26
LOC100643964	138.952887	2.666813763	0.19641396	13.5775162	5.44E-42	8.32E-41
LOC100649938	1194.6106	2.678404867	0.19393854	13.8105859	2.20E-43	3.70E-42
LOC105665944	44.2814936	2.679442366	0.27920117	9.5968163	8.25E-22	3.45E-21
LOC100646014	12.497606	2.680202359	0.59831935	4.47955154	7.48E-06	1.20E-05
LOC100648743	371.742794	2.683252254	0.17995741	14.9104849	2.82E-50	7.77E-49
LOC100652231	37.5584865	2.68421579	0.31547041	8.50861349	1.76E-17	5.77E-17
LOC100650981	331.898189	2.689249701	0.24204857	11.1103723	1.12E-28	7.12E-28
LOC100645564	552.553319	2.689255954	0.20202849	13.311271	1.99E-40	2.71E-39
LOC100642584	144.839125	2.700578854	0.30567166	8.83490113	1.00E-18	3.54E-18
LOC100646619	273.791624	2.70092113	0.1495995	18.0543455	7.29E-73	1.25E-70
LOC100643643	167.570087	2.704151224	0.23555616	11.479858	1.67E-30	1.19E-29
LOC100650620	19.2014955	2.716816611	0.60701528	4.47569727	7.62E-06	1.23E-05
LOC100647990	139.08238	2.717660307	0.39848079	6.82005358	9.10E-12	2.13E-11
LOC100643498	619.819923	2.718944236	0.19318608	14.0742242	5.47E-45	1.02E-43

LOC100645161	2939.65257	2.721055231	0.1855266	14.6666585	1.05E-48	2.67E-47
LOC100642640	1128.47021	2.727333791	0.20560904	13.2646589	3.71E-40	4.96E-39
LOC100646556	1225.80692	2.737088398	0.16790435	16.3014738	9.63E-60	5.52E-58
LOC100648430	461.049007	2.739250198	0.19422117	14.1037675	3.60E-45	6.83E-44
LOC100647254	43.4899922	2.745551758	0.58227485	4.71521612	2.41E-06	4.02E-06
LOC100647624	20.8597914	2.747566202	0.51442522	5.341041	9.24E-08	1.68E-07
LOC100648744	176.029064	2.747761205	0.18429465	14.9096094	2.85E-50	7.83E-49
LOC100643676	1588.49813	2.748718685	0.13719915	20.0345171	2.75E-89	1.44E-86
LOC105666004	136.821579	2.754066522	0.44296817	6.21730113	5.06E-10	1.06E-09
LOC100643010	909.615665	2.757242559	0.18393461	14.9903414	8.49E-51	2.47E-49
LOC100642718	290.303418	2.76161742	0.27788524	9.93797796	2.85E-23	1.28E-22
LOC100649588	284.447327	2.762179528	0.12981979	21.2770297	1.85E-100	1.65E-97
LOC100646459	27.255395	2.764832854	0.43152469	6.4071255	1.48E-10	3.19E-10
LOC100647988	180.664575	2.768164612	0.22533226	12.2848126	1.09E-34	1.01E-33
LOC100644717	514.146025	2.771345874	0.38758253	7.15033747	8.66E-13	2.16E-12
LOC105667084	45.8121532	2.771748194	0.75797217	3.65679417	0.00025539	0.00036973
LOC100648309	483.266119	2.775764451	0.33286113	8.33910655	7.49E-17	2.38E-16
LOC100648390	34.1470888	2.776640778	0.44039517	6.30488465	2.88E-10	6.12E-10
LOC100642214	193.164486	2.776719139	0.20666517	13.4358353	3.73E-41	5.34E-40
LOC100646478	1153.37991	2.777528119	0.13864201	20.0338128	2.79E-89	1.44E-86
LOC100648082	346.504952	2.783293344	0.23819601	11.6848868	1.52E-31	1.15E-30
LOC100649503	278.387124	2.789892464	0.1995722	13.9793644	2.08E-44	3.74E-43
LOC100651048	154.430717	2.791162922	0.590585	4.72609859	2.29E-06	3.81E-06
LOC100652122	974.523353	2.791278107	0.18302373	15.2509086	1.62E-52	5.37E-51
LOC100646544	5113.06727	2.791434769	0.42089739	6.63210277	3.31E-11	7.43E-11
LOC100645748	182.078338	2.796047356	0.33708312	8.29483065	1.09E-16	3.41E-16
LOC100646208	16.4420479	2.796539343	0.4801072	5.8248227	5.72E-09	1.13E-08
LOC100643103	62.1046342	2.796568751	0.50630885	5.52344439	3.32E-08	6.23E-08
LOC105665869	60.1120483	2.798636686	0.64939092	4.3096332	1.64E-05	2.58E-05

LOC100647734	326.815872	2.805247295	0.24497284	11.4512586	2.32E-30	1.63E-29
LOC100645913	15.0129758	2.805650004	0.56462824	4.96902172	6.73E-07	1.17E-06
LOC100649896	91.4458634	2.808760064	0.40287754	6.97174646	3.13E-12	7.52E-12
LOC105666779	49.8462217	2.808899359	0.29726132	9.4492595	3.41E-21	1.39E-20
LOC100650668	1958.81864	2.812894672	0.19935733	14.1098135	3.30E-45	6.32E-44
LOC100644769	445.620659	2.817910012	0.20206879	13.9453002	3.36E-44	5.91E-43
LOC100643997	2168.64762	2.818522601	0.27056513	10.4171686	2.07E-25	1.07E-24
LOC100651638	446.308223	2.823060365	0.21333553	13.232959	5.66E-40	7.47E-39
LOC100646564	109.639158	2.824046516	0.51691131	5.46330963	4.67E-08	8.67E-08
LOC100643537	1254.2388	2.825002054	0.25780378	10.9579544	6.09E-28	3.70E-27
LOC105667196	44.8900672	2.830591765	0.33503428	8.44866306	2.95E-17	9.50E-17
LOC100649154	314.746927	2.831076943	0.20612707	13.73462	6.30E-43	1.03E-41
LOC100646405	238.684056	2.833095172	0.23392593	12.1110778	9.23E-34	7.94E-33
LOC100648103	3292.73744	2.838126121	0.17729342	16.0080734	1.12E-57	5.64E-56
LOC100642872	234.126244	2.841042298	0.37877573	7.50059228	6.35E-14	1.70E-13
LOC100651625	30.0985058	2.841960017	0.42343987	6.71160231	1.92E-11	4.40E-11
LOC100652021	46.1339942	2.852999789	0.80540963	3.54229661	0.00039666	0.00056614
LOC100648258	979.022105	2.854238007	0.22680645	12.5844657	2.57E-36	2.63E-35
LOC100649826	418.748495	2.855664829	0.24385648	11.7104322	1.13E-31	8.56E-31
LOC100644659	381.381421	2.858722908	0.2276783	12.5559746	3.69E-36	3.72E-35
LOC100645277	103.441198	2.85966724	0.29738432	9.61606605	6.84E-22	2.87E-21
LOC100651499	1193.7352	2.868298745	0.23322739	12.2982928	9.25E-35	8.60E-34
LOC100649586	1142.59917	2.87492744	0.16769283	17.1440089	6.97E-66	6.75E-64
LOC100649643	179.903591	2.879399248	0.2201673	13.0782328	4.39E-39	5.41E-38
LOC100652251	215.440421	2.886189959	0.31337551	9.21000489	3.26E-20	1.26E-19
LOC105666981	26.6235212	2.891203899	0.96471698	2.99694517	0.002727	0.00364804
LOC100643365	233.282438	2.891753773	0.42604856	6.78738065	1.14E-11	2.65E-11
LOC100648234	741.840005	2.892310723	0.22187144	13.0359755	7.64E-39	9.23E-38
LOC100646633	22.6610903	2.892777266	0.81577952	3.54602831	0.00039108	0.0005585

LOC100649430	90.6194717	2.898331172	0.33196705	8.73077973	2.53E-18	8.70E-18
LOC100650213	56.0512293	2.902599543	0.25958967	11.1814908	5.02E-29	3.27E-28
LOC100651330	854.209963	2.90260489	0.17786517	16.3191302	7.22E-60	4.21E-58
LOC100650669	1246.6241	2.905845841	0.14858172	19.5572227	3.58E-85	1.75E-82
LOC105665757	617.198267	2.91150927	0.17497909	16.6391842	3.63E-62	2.57E-60
LOC100646122	509.882108	2.912474356	0.27430178	10.6177742	2.46E-26	1.35E-25
LOC100650367	1089.83707	2.926313634	0.17411448	16.8068367	2.17E-63	1.72E-61
LOC100650070	32.8559453	2.926335581	0.33487118	8.73869054	2.36E-18	8.14E-18
LOC100643769	959.058793	2.927977563	0.16636769	17.5994361	2.49E-69	3.21E-67
LOC105666753	121.994169	2.936984741	0.40295901	7.28854459	3.13E-13	8.01E-13
LOC100646267	3174.55361	2.944709629	0.16492817	17.8544979	2.67E-71	4.14E-69
LOC100650779	1333.46839	2.954033944	0.19051914	15.505182	3.20E-54	1.17E-52
LOC100649512	1939.30904	2.956291444	0.1698077	17.4096426	6.97E-68	8.06E-66
LOC100650161	28.6565945	2.957772592	0.40264696	7.34582124	2.04E-13	5.28E-13
LOC100649450	214.605099	2.959415934	0.5442995	5.43710941	5.42E-08	1.00E-07
LOC105666033	44.4070885	2.960758625	0.70153305	4.2204122	2.44E-05	3.80E-05
LOC100645779	1676.17413	2.968058736	0.29146343	10.1832972	2.35E-24	1.13E-23
LOC100648799	2157.49734	2.968197812	0.21175186	14.0173403	1.22E-44	2.23E-43
LOC100643600	482.689177	2.969376455	0.22466847	13.216703	7.03E-40	9.24E-39
LOC105666500	18.4357687	2.969798757	0.54980327	5.40156624	6.61E-08	1.21E-07
LOC100649070	100.589468	2.974160464	0.27879595	10.6678756	1.44E-26	7.99E-26
LOC105665632	120.776713	2.977351748	0.28709507	10.3706126	3.37E-25	1.72E-24
LOC100645238	125.703815	2.979131189	0.2639615	11.2862336	1.53E-29	1.03E-28
LOC100646833	249.300076	2.984345951	0.29791155	10.0175572	1.28E-23	5.89E-23
LOC100644860	94.4818095	2.985433544	0.31197812	9.56936835	1.08E-21	4.47E-21
LOC100647372	1105.92632	2.986893532	0.14446194	20.6759897	5.70E-95	4.00E-92
LOC100644366	269.380173	2.987540408	0.58878513	5.07407587	3.89E-07	6.84E-07
LOC100647227	434.038903	2.987847563	0.26749208	11.1698543	5.73E-29	3.71E-28
LOC100649272	116.478641	2.993053264	0.9082945	3.2952454	0.00098336	0.00135894

LOC100646547	144.197112	2.993590971	0.30001017	9.97829819	1.90E-23	8.67E-23
LOC100648762	461.017281	3.00118094	0.18465252	16.2531274	2.12E-59	1.18E-57
LOC100643771	288.637079	3.001416665	0.3899176	7.69756647	1.39E-14	3.83E-14
LOC105665916	79.9666623	3.003034251	0.33489602	8.96706464	3.05E-19	1.12E-18
LOC100649613	216.18493	3.003418533	0.9850676	3.04894662	0.00229645	0.00308854
LOC100651224	47.5380499	3.005190165	0.54969596	5.46700428	4.58E-08	8.50E-08
LOC105666142	739.205443	3.005461536	0.39450993	7.61821523	2.57E-14	7.01E-14
LOC100644585	33.3112833	3.009604083	0.87549963	3.43758463	0.00058693	0.00082448
LOC100648492	1472.97414	3.01255907	0.21983206	13.7039113	9.62E-43	1.56E-41
LOC105667063	302.756023	3.014892184	0.19861847	15.1793143	4.85E-52	1.55E-50
LOC100647932	666.92143	3.017647307	0.99676563	3.02743917	0.00246635	0.00331068
LOC105666785	9.74765712	3.023599497	0.72583654	4.16567553	3.10E-05	4.81E-05
LOC105665673	547.057365	3.024806685	0.24108231	12.5467801	4.14E-36	4.16E-35
LOC100651587	600.689177	3.026432094	0.24606331	12.2994039	9.12E-35	8.49E-34
LOC100647898	302.228484	3.031302468	0.29008219	10.4498056	1.47E-25	7.66E-25
LOC100643071	44.7574731	3.03583436	0.44253464	6.86010562	6.88E-12	1.62E-11
LOC100651755	146.547468	3.03680141	0.39372538	7.71299385	1.23E-14	3.41E-14
LOC100646494	404.23695	3.044812771	0.1908534	15.9536734	2.69E-57	1.29E-55
LOC100644412	175.101568	3.050800938	0.27082475	11.2648529	1.96E-29	1.30E-28
LOC100651880	214.465276	3.052825858	0.2711761	11.2577247	2.12E-29	1.40E-28
LOC100649239	389.011114	3.053923537	0.23180408	13.1745891	1.23E-39	1.59E-38
LOC100644725	141.346711	3.05427481	0.28963505	10.5452526	5.34E-26	2.86E-25
LOC100650207	139.797769	3.055441748	0.62020553	4.92649868	8.37E-07	1.44E-06
LOC100643370	470.803567	3.06091901	0.24441296	12.5235547	5.55E-36	5.53E-35
LOC100645309	3528.92326	3.064481089	0.32118409	9.5411982	1.41E-21	5.85E-21
LOC100648605	781.486202	3.085110312	0.22184332	13.9067081	5.77E-44	9.99E-43
LOC100650408	298.807337	3.090514574	0.24483271	12.6229644	1.58E-36	1.64E-35
LOC105666924	86.16888	3.091533095	0.53943229	5.73108647	9.98E-09	1.94E-08
LOC105665651	13.0002444	3.091706609	0.84322397	3.66653072	0.00024586	0.00035642

LOC100652040	987.284998	3.093703216	0.21283786	14.5354927	7.22E-48	1.70E-46
LOC105666393	145.14374	3.09448372	0.54600696	5.66748035	1.45E-08	2.78E-08
LOC100642654	1254.6392	3.099444155	0.2710415	11.4353119	2.79E-30	1.95E-29
LOC100651467	199.735565	3.100369843	0.44294286	6.99948032	2.57E-12	6.20E-12
LOC100647915	1376.2264	3.108084756	0.29092314	10.6835254	1.22E-26	6.80E-26
LOC100647543	870.720235	3.11478633	0.21069837	14.7831531	1.88E-49	4.97E-48
LOC105666869	13.3847366	3.116379004	0.7786265	4.00240551	6.27E-05	9.51E-05
LOC105666937	137.712757	3.126481209	0.19534835	16.0046464	1.19E-57	5.89E-56
LOC100649245	289.66629	3.135344016	0.94823054	3.30652083	0.00094462	0.0013067
LOC100652146	353.292904	3.145342824	0.35364333	8.89411032	5.89E-19	2.11E-18
LOC100648870	118.10754	3.146056744	0.2979493	10.5590337	4.61E-26	2.49E-25
LOC100647585	132.701081	3.153318641	0.28021122	11.2533632	2.23E-29	1.47E-28
LOC100649528	83.4744701	3.155102716	0.33478713	9.42420548	4.33E-21	1.75E-20
LOC100643887	1704.59679	3.157301362	0.23798433	13.2668457	3.60E-40	4.83E-39
LOC100647552	438.863315	3.166031906	0.38036434	8.3236823	8.53E-17	2.70E-16
LOC105667071	11.1249974	3.166301178	0.91078041	3.47647043	0.00050806	0.00071916
LOC100645937	464.909457	3.170943013	0.21876482	14.4947575	1.31E-47	2.99E-46
LOC100650400	486.501742	3.170952172	0.29213076	10.8545644	1.90E-27	1.12E-26
LOC105666683	71.1858692	3.173335912	0.42753269	7.42244032	1.15E-13	3.02E-13
LOC100648300	195.792417	3.181491016	0.31904403	9.97194954	2.02E-23	9.23E-23
LOC100649961	166.405034	3.183476193	0.24192683	13.158839	1.51E-39	1.94E-38
LOC105666257	144.75297	3.189886845	0.31776625	10.0384696	1.03E-23	4.80E-23
LOC100651604	951.937006	3.192305539	0.21804349	14.6406828	1.55E-48	3.90E-47
LOC100643804	86.5499193	3.193651756	0.66214409	4.82319753	1.41E-06	2.39E-06
LOC100649367	339.894336	3.196210124	0.26363265	12.1237263	7.91E-34	6.85E-33
LOC100645484	664.025136	3.197146227	0.21402128	14.9384503	1.85E-50	5.18E-49
LOC100648888	138.98523	3.204814351	0.25085106	12.7757657	2.24E-37	2.46E-36
LOC100649354	1011.28958	3.209192147	0.67710277	4.73959388	2.14E-06	3.57E-06
LOC100649509	234.736101	3.214911316	0.31821826	10.10285	5.37E-24	2.53E-23

LOC100651776	572.676616	3.215047012	0.23133305	13.8979149	6.52E-44	1.13E-42
LOC100648539	168.559705	3.222011877	0.36187869	8.90356894	5.41E-19	1.95E-18
LOC100647517	14.141848	3.222624259	0.57545996	5.60008425	2.14E-08	4.07E-08
LOC100644027	879.578856	3.226823119	0.20867581	15.4633311	6.13E-54	2.18E-52
LOC100644474	2198.69642	3.227399611	0.12851126	25.1137505	3.52E-139	1.72E-135
LOC105666792	10.400719	3.228168921	0.64592744	4.99772687	5.80E-07	1.01E-06
LOC105667119	401.903661	3.228893171	0.31327946	10.3067502	6.57E-25	3.30E-24
LOC100644870	446.334072	3.232782289	0.25125445	12.8665671	6.94E-38	7.90E-37
LOC100646468	667.076032	3.238154591	0.30223583	10.7139997	8.75E-27	4.94E-26
LOC100642855	831.776314	3.245716927	0.19268791	16.8444246	1.15E-63	9.57E-62
LOC100649365	377.284533	3.248123236	0.2074618	15.6564879	3.00E-55	1.20E-53
LOC100651124	1428.97703	3.250561038	0.81725681	3.97740464	6.97E-05	0.00010529
LOC100647927	422.594361	3.25314996	0.28523398	11.4051978	3.94E-30	2.74E-29
LOC100645119	579.674112	3.259459021	0.32475103	10.0367936	1.05E-23	4.88E-23
LOC100649881	336.068951	3.26543086	0.32913987	9.92110388	3.37E-23	1.51E-22
LOC100650602	2300.87758	3.269119824	0.23969333	13.6387604	2.36E-42	3.66E-41
LOC105666982	46.4755924	3.270228074	0.41642033	7.8531902	4.06E-15	1.16E-14
LOC105665785	10.2618161	3.270797369	0.80487864	4.06371494	4.83E-05	7.39E-05
LOC100651897	384.735832	3.276540561	0.1862267	17.5943654	2.72E-69	3.46E-67
LOC100646784	555.647581	3.281308242	0.19594245	16.7462854	6.03E-63	4.50E-61
LOC100642619	221.709125	3.286686278	0.28590113	11.4958844	1.38E-30	9.91E-30
LOC105666203	750.667172	3.290002035	0.23647915	13.9124404	5.32E-44	9.24E-43
LOC100643727	389.003869	3.290432447	0.22002456	14.9548417	1.45E-50	4.11E-49
LOC100647896	493.731314	3.294460591	0.36683794	8.98069745	2.69E-19	9.90E-19
LOC100648340	508.286862	3.29719302	0.26951916	12.2336126	2.06E-34	1.86E-33
LOC105666665	474.998646	3.298853752	1.01024652	3.26539482	0.00109312	0.0015053
LOC100646878	544.151936	3.305991967	0.28760656	11.4948418	1.40E-30	1.00E-29
LOC100645241	2225.62724	3.306517023	0.37793616	8.74887711	2.15E-18	7.46E-18
LOC105665668	19.4272148	3.309036865	0.59516987	5.55981918	2.70E-08	5.09E-08

LOC100651180	219.24462	3.309273791	0.24168509	13.6925031	1.13E-42	1.81E-41
LOC100651215	61.1088873	3.319104156	0.39200701	8.46695092	2.52E-17	8.18E-17
LOC100647830	11991.1402	3.337842838	0.27008206	12.3586249	4.38E-35	4.15E-34
LOC100649818	2333.47137	3.339776603	0.43035606	7.76049634	8.46E-15	2.37E-14
LOC105666054	48.4870959	3.342453073	0.51689591	6.4663949	1.00E-10	2.18E-10
LOC100649042	9018.3443	3.344652761	0.50171109	6.66649153	2.62E-11	5.94E-11
LOC100647592	549.850404	3.347051248	0.28404888	11.7833635	4.76E-32	3.68E-31
LOC100645092	740.8852	3.349230106	0.44394287	7.54428186	4.55E-14	1.22E-13
LOC100651432	24.1011634	3.351087269	0.65438266	5.12099028	3.04E-07	5.37E-07
LOC100643533	190.010812	3.353095775	0.30713254	10.9174227	9.52E-28	5.69E-27
LOC100647912	2242.19854	3.355393427	0.31447648	10.6697753	1.41E-26	7.84E-26
LOC100650860	155.698452	3.355409816	0.34896025	9.61544996	6.88E-22	2.89E-21
LOC100650048	72.9048741	3.364576763	0.56061022	6.00163294	1.95E-09	3.96E-09
LOC100642983	4611.56366	3.367233553	0.27512548	12.2389013	1.93E-34	1.75E-33
LOC100651044	1120.61562	3.404406442	0.28738382	11.8462009	2.25E-32	1.77E-31
LOC105666086	559.175141	3.404457115	0.25289625	13.4618727	2.62E-41	3.80E-40
LOC100643875	405.700828	3.405509961	0.7219361	4.71719028	2.39E-06	3.98E-06
LOC100643077	1577.27274	3.409566587	0.26944618	12.65398	1.06E-36	1.12E-35
LOC100648475	1156.24715	3.412458972	0.29334232	11.6330266	2.80E-31	2.08E-30
LOC100645414	404.442901	3.414342847	0.47997189	7.11363078	1.13E-12	2.80E-12
LOC100645784	258.88219	3.415386173	0.48065712	7.10566021	1.20E-12	2.96E-12
LOC100642524	345.360485	3.417582908	0.27106903	12.6077958	1.91E-36	1.98E-35
LOC100645641	70.3403523	3.417670286	0.89308786	3.82680185	0.00012982	0.00019215
LOC100646053	428.360763	3.422721506	0.93892721	3.64535341	0.00026702	0.00038607
LOC105666148	78.1074799	3.425203142	0.53545006	6.39686764	1.59E-10	3.41E-10
LOC100646281	277.628199	3.426318791	0.50864444	6.7361767	1.63E-11	3.74E-11
LOC100651228	137.62183	3.426610079	0.33397685	10.2600228	1.07E-24	5.28E-24
LOC100646506	19.0349516	3.42739478	0.58616702	5.84712998	5.00E-09	9.91E-09
LOC105667074	297.773495	3.429328743	0.23969071	14.3073076	1.97E-46	4.07E-45

LOC100642789	1252.31179	3.430942109	0.23648256	14.5082248	1.07E-47	2.48E-46
LOC100642535	520.498642	3.43295004	0.21374761	16.0607648	4.81E-58	2.43E-56
LOC100650297	2781.63657	3.438279709	0.26459039	12.9947266	1.31E-38	1.56E-37
LOC100650705	474.774963	3.444971952	1.0816724	3.18485705	0.00144826	0.00197409
LOC100647509	305.999351	3.447874027	0.39121276	8.81329644	1.22E-18	4.27E-18
LOC100647587	171.50042	3.453484755	0.28323098	12.1931745	3.38E-34	3.02E-33
LOC100648524	121.29799	3.461213642	0.48744584	7.10071427	1.24E-12	3.06E-12
LOC100645585	23.6390419	3.461790169	0.38722844	8.9399171	3.89E-19	1.42E-18
LOC100642898	3328.40317	3.46849302	0.86752194	3.99816171	6.38E-05	9.68E-05
LOC100650474	172.850962	3.470667243	0.52656936	6.59109231	4.37E-11	9.74E-11
LOC100649141	683.691697	3.471987578	0.33608458	10.3306958	5.12E-25	2.58E-24
LOC100643419	129.134344	3.483716708	1.14986232	3.02968158	0.00244812	0.00328755
LOC100651684	47.7831879	3.48603151	0.42236523	8.25359487	1.54E-16	4.78E-16
LOC105666357	20.5439407	3.496994377	0.63591463	5.499157	3.82E-08	7.12E-08
LOC100646988	194.456241	3.498527114	0.38997922	8.97106045	2.94E-19	1.08E-18
LOC105667159	59.9373084	3.506315612	0.81020943	4.32766578	1.51E-05	2.38E-05
LOC100648437	516.492535	3.508380406	0.29087951	12.0612842	1.69E-33	1.43E-32
LOC100650071	54.9920159	3.512716353	0.37629397	9.33503234	1.01E-20	4.00E-20
LOC100644313	40.546789	3.515715202	0.55803378	6.3001835	2.97E-10	6.30E-10
LOC100642587	45.9703475	3.516004526	0.47208102	7.44788369	9.48E-14	2.50E-13
LOC105667158	19.1252898	3.518437283	0.91333425	3.85229971	0.00011701	0.00017372
LOC105667077	23.9625816	3.520579296	0.35388537	9.94836075	2.56E-23	1.16E-22
LOC100650065	30.355498	3.53665704	0.81636205	4.33221638	1.48E-05	2.34E-05
LOC100650730	175.868481	3.543969024	0.89694453	3.9511574	7.78E-05	0.00011719
LOC100647149	802.855951	3.556659346	0.28787052	12.3550663	4.57E-35	4.32E-34
LOC100644238	659.029904	3.557254952	0.3888158	9.14894658	5.75E-20	2.20E-19
LOC100652273	313.34447	3.558603912	0.41983957	8.47610405	2.33E-17	7.59E-17
LOC100646008	4126.84502	3.562094225	0.42602947	8.36114514	6.21E-17	1.98E-16
LOC100643468	14.3532009	3.564457305	0.80836823	4.40944754	1.04E-05	1.66E-05

LOC105666836	14.7012345	3.569035802	0.65076532	5.48436696	4.15E-08	7.73E-08
LOC100649768	22.0810969	3.56957716	0.38471809	9.27842294	1.72E-20	6.74E-20
LOC100650951	117.964439	3.579381158	0.55160958	6.48897571	8.64E-11	1.89E-10
LOC105666344	15.3160828	3.584463901	0.57260681	6.25990439	3.85E-10	8.11E-10
LOC105666808	569.190758	3.591501964	1.00263767	3.58205369	0.0003409	0.00048927
LOC100651407	1044.7285	3.596038859	0.38035304	9.45447637	3.25E-21	1.32E-20
LOC105667027	497.521652	3.600640428	1.14549289	3.14331102	0.00167048	0.0022669
LOC105667123	554.504219	3.604246346	1.0106414	3.56629595	0.00036206	0.00051842
LOC100642922	130.170999	3.613069078	0.40520469	8.91665177	4.81E-19	1.74E-18
LOC100647970	857.08028	3.615790468	0.38090992	9.49250797	2.26E-21	9.24E-21
LOC100650632	1187.70249	3.615937805	0.23934541	15.1076131	1.44E-51	4.51E-50
LOC100642666	205.389643	3.616546218	1.06320883	3.40153892	0.00067008	0.00093738
LOC100651692	664.995909	3.618029142	0.43382537	8.33982846	7.44E-17	2.36E-16
LOC100642469	146.380022	3.622842314	0.50774983	7.13509316	9.67E-13	2.40E-12
LOC100645198	148.386502	3.629785191	0.60003564	6.04928268	1.45E-09	2.97E-09
LOC100645991	1480.69181	3.630369998	0.16776977	21.6389995	7.72E-104	8.39E-101
LOC100647007	112.903074	3.635863894	0.22884775	15.8876976	7.71E-57	3.50E-55
LOC100647603	1254.34236	3.636174611	0.2607062	13.9474037	3.26E-44	5.75E-43
LOC100651758	453.669717	3.636714962	0.22239457	16.3525352	4.17E-60	2.48E-58
LOC100645932	137.678506	3.638074294	0.36264311	10.0321065	1.10E-23	5.11E-23
LOC105667076	149.898061	3.642478067	0.9250625	3.93754808	8.23E-05	0.00012381
LOC105666439	25.4671217	3.644814193	0.50363117	7.23707026	4.58E-13	1.16E-12
LOC100645468	676.539183	3.64947599	0.7744303	4.71246539	2.45E-06	4.07E-06
LOC100642684	497.967935	3.649505379	1.23705226	2.95016265	0.00317607	0.00422225
LOC100649633	1596.59364	3.657544977	0.26413025	13.8475051	1.32E-43	2.25E-42
LOC100651912	262.485633	3.65970388	0.49827444	7.34475543	2.06E-13	5.32E-13
LOC105666786	56.6690645	3.66513277	0.72196109	5.07663479	3.84E-07	6.75E-07
LOC100646477	736.505842	3.66621944	0.42522484	8.62183747	6.59E-18	2.22E-17
LOC100646218	2180.02767	3.668828096	0.28346846	12.9426325	2.59E-38	3.04E-37

LOC100647709	426.082992	3.674021009	1.23824447	2.96712087	0.00300603	0.00400545
LOC100647683	9.94196728	3.67857154	0.68432822	5.37544914	7.64E-08	1.40E-07
LOC100645091	85.5941865	3.686291802	0.29124478	12.6570228	1.02E-36	1.08E-35
LOC100651327	1711.09735	3.689098781	0.20414585	18.0708975	5.40E-73	9.45E-71
LOC100648231	348.300748	3.699269903	0.31132864	11.8822024	1.46E-32	1.16E-31
LOC100648252	4444.10088	3.700804244	0.5165422	7.16457286	7.80E-13	1.95E-12
LOC100644984	764.635593	3.715512761	0.38306151	9.69952004	3.03E-22	1.29E-21
LOC100643215	23.5694363	3.729744177	0.94910329	3.92975583	8.50E-05	0.00012761
LOC105666315	184.040445	3.732610648	1.04366926	3.57643058	0.00034832	0.00049954
LOC105666137	207.70881	3.746383035	0.56394813	6.64313407	3.07E-11	6.92E-11
LOC100647190	213.742803	3.751584154	0.40183585	9.33611107	9.99E-21	3.96E-20
LOC100647577	45.2171143	3.759162635	0.55210025	6.80884068	9.84E-12	2.29E-11
LOC100648655	38.5603972	3.761491705	0.55488599	6.77885508	1.21E-11	2.81E-11
LOC100642322	124.531639	3.76680929	0.36541873	10.3081998	6.47E-25	3.25E-24
LOC105665839	165.6721	3.769317056	0.86262187	4.36960526	1.24E-05	1.98E-05
LOC100646846	74.3545718	3.770224498	0.29177578	12.9216501	3.40E-38	3.96E-37
LOC100649943	51.8230004	3.770720095	0.4869118	7.74415434	9.62E-15	2.69E-14
LOC105667197	49.6213668	3.771575877	0.71395688	5.28263818	1.27E-07	2.30E-07
LOC105666379	79.8213977	3.786735126	0.38999354	9.70973803	2.74E-22	1.17E-21
LOC100651304	589.868398	3.790220354	0.26268981	14.4285015	3.42E-47	7.55E-46
LOC105666670	624.488541	3.791110858	0.49412919	7.67230705	1.69E-14	4.66E-14
LOC100645258	1350.76204	3.796226806	0.32208944	11.7862506	4.60E-32	3.56E-31
LOC100650555	263.551328	3.797861266	0.21708853	17.4945274	1.58E-68	1.88E-66
LOC100649627	897.938208	3.803371502	0.34478193	11.031238	2.70E-28	1.68E-27
LOC100642897	417.117874	3.803981502	0.24151118	15.7507473	6.79E-56	2.86E-54
LOC100651411	28.6598945	3.818504032	0.55786136	6.84489786	7.65E-12	1.80E-11
LOC105666874	22.0028348	3.822168415	0.47522808	8.04280838	8.78E-16	2.61E-15
LOC100646446	53.8364599	3.822904514	0.38937171	9.81813639	9.41E-23	4.12E-22
LOC105665669	176.980156	3.823256461	0.78958294	4.84212142	1.28E-06	2.18E-06

LOC100650378	9.85789416	3.823348171	0.77436851	4.93737556	7.92E-07	1.36E-06
LOC100642277	397.09979	3.8253564	0.32233553	11.8676225	1.74E-32	1.38E-31
LOC100651390	285.319988	3.827698849	0.57879863	6.6131788	3.76E-11	8.43E-11
LOC100643415	16073.839	3.830705481	0.43387829	8.82898639	1.06E-18	3.73E-18
LOC105667163	176.11143	3.831337664	1.00557652	3.81009062	0.00013892	0.00020505
LOC100648410	541.624027	3.845292593	0.72041984	5.33757179	9.42E-08	1.71E-07
LOC100650982	24.0437679	3.848303623	0.86018427	4.47381305	7.68E-06	1.24E-05
LOC105666934	79.0936508	3.849161105	0.46242878	8.32379232	8.52E-17	2.70E-16
LOC100648880	331.094044	3.859840305	1.05626222	3.65424441	0.00025794	0.00037332
LOC105667010	23.4951703	3.878532188	0.6721056	5.77071841	7.89E-09	1.54E-08
LOC100651578	769.087002	3.881915384	0.4277628	9.07492508	1.14E-19	4.26E-19
LOC100650676	201.164827	3.888163678	0.4335155	8.9689151	2.99E-19	1.10E-18
LOC100649269	2302.5356	3.890409152	0.51324709	7.57999263	3.46E-14	9.35E-14
LOC105667026	44.5534285	3.890807812	1.05423448	3.69064748	0.00022368	0.00032537
LOC100651832	52.4136677	3.893040337	0.40251199	9.67186187	3.97E-22	1.69E-21
LOC100645616	329.810013	3.893464392	0.69560616	5.59722526	2.18E-08	4.13E-08
LOC105666219	22.501716	3.895697461	0.77439454	5.03063651	4.89E-07	8.54E-07
LOC100647600	45.7279096	3.896680551	0.54060816	7.2079573	5.68E-13	1.43E-12
LOC100643231	48.5563104	3.918951057	0.38313836	10.228553	1.48E-24	7.23E-24
LOC100645190	697.699589	3.925782683	0.8271083	4.74639497	2.07E-06	3.46E-06
LOC100648041	1798.95454	3.940209055	0.92678394	4.25148612	2.12E-05	3.33E-05
LOC100647961	29.1237906	3.953097676	0.48403301	8.16700013	3.16E-16	9.63E-16
LOC105667034	68.6480108	3.957833905	1.04653772	3.78183588	0.00015568	0.000229
LOC100648144	3659.09769	3.965547088	0.902952	4.39175846	1.12E-05	1.79E-05
LOC100647341	501.835101	3.965794179	0.3420587	11.5938996	4.43E-31	3.25E-30
LOC105666664	1486.99774	3.979627903	1.11829878	3.55864458	0.00037277	0.00053313
LOC100642906	6499.66918	4.01403197	0.53564345	7.49385055	6.69E-14	1.78E-13
LOC100648042	287.57533	4.015491376	0.67910555	5.912912	3.36E-09	6.73E-09
LOC100645928	86.5364857	4.05848096	0.53779047	7.54658398	4.47E-14	1.20E-13

LOC100645907	875.684615	4.061274728	0.41676816	9.74468579	1.94E-22	8.39E-22
LOC100647205	45.7034258	4.065289222	0.38506894	10.5573024	4.70E-26	2.53E-25
LOC100649260	5980.15877	4.087054206	0.47059584	8.68484986	3.79E-18	1.29E-17
LOC105665847	1104.10956	4.090925769	0.5247563	7.79585828	6.40E-15	1.80E-14
LOC100651255	29.2269674	4.093550291	0.56660994	7.22463551	5.02E-13	1.27E-12
LOC105666060	63.8180598	4.103498862	0.58032895	7.07098766	1.54E-12	3.77E-12
LOC100644702	2088.2021	4.119457367	0.89013874	4.62788234	3.69E-06	6.06E-06
LOC100649667	1744.07764	4.140364653	0.57099841	7.25109669	4.13E-13	1.05E-12
LOC100648379	19.1755888	4.141300218	0.50028262	8.27792147	1.25E-16	3.92E-16
LOC105666010	21.0048776	4.145466971	0.56394958	7.35077584	1.97E-13	5.09E-13
LOC100644703	403.680855	4.148671196	0.50231914	8.25903465	1.47E-16	4.58E-16
LOC100651364	2517.72835	4.150521309	0.81326991	5.10349795	3.33E-07	5.88E-07
LOC100647257	485.298004	4.151184022	0.6239399	6.65317931	2.87E-11	6.48E-11
LOC100643382	242.224963	4.156121694	0.29855457	13.9208107	4.74E-44	8.28E-43
LOC100646668	435.609702	4.156725904	0.3751826	11.0792076	1.58E-28	9.96E-28
LOC100652112	9.98590223	4.166691761	0.7314902	5.69616896	1.23E-08	2.36E-08
LOC100650170	277.084438	4.171847416	0.69454242	6.00661283	1.89E-09	3.85E-09
LOC100645038	14.5313155	4.182076803	0.8289373	5.04510633	4.53E-07	7.93E-07
LOC105667146	758.597563	4.186320387	0.57798466	7.2429611	4.39E-13	1.12E-12
LOC105667030	22.095288	4.190314943	0.73220036	5.72290755	1.05E-08	2.03E-08
LOC105666913	54.3769905	4.190423994	1.01682542	4.12108502	3.77E-05	5.81E-05
LOC105666706	490.844467	4.194177713	0.92676042	4.52563321	6.02E-06	9.75E-06
LOC100650406	89.4742821	4.197616424	0.32673302	12.8472367	8.91E-38	1.01E-36
LOC105666694	89.5472976	4.208000094	1.05942723	3.97195764	7.13E-05	0.00010767
LOC105667168	26.2236297	4.231597529	0.40430015	10.4664754	1.23E-25	6.45E-25
LOC100650678	1627.13338	4.233789336	0.28431639	14.8911194	3.76E-50	1.03E-48
LOC100645920	3736.4188	4.234580485	0.3820822	11.0829042	1.52E-28	9.57E-28
LOC105667083	23.3997036	4.238163706	0.90506875	4.68269809	2.83E-06	4.68E-06
LOC100650968	901.867271	4.247564192	0.4221589	10.0615294	8.17E-24	3.82E-23

LOC105666577	22.4905949	4.265395133	0.55778925	7.64696548	2.06E-14	5.64E-14
LOC100650916	1297.13477	4.276856905	0.54778884	7.80749186	5.83E-15	1.65E-14
LOC100645647	1227.55827	4.279398045	0.58627561	7.29929401	2.89E-13	7.41E-13
LOC100644997	10.060958	4.282679406	0.75899991	5.64252953	1.68E-08	3.20E-08
LOC100648033	1196.902	4.286607175	0.94380815	4.54182047	5.58E-06	9.05E-06
LOC100642325	468.611412	4.312509231	0.52117766	8.27454741	1.29E-16	4.03E-16
LOC105666892	654.425831	4.317822473	1.47102346	2.93525058	0.00333278	0.00441835
LOC105666866	9.81409873	4.346529585	0.84300115	5.15601855	2.52E-07	4.48E-07
LOC100642387	757.150475	4.358530191	0.99434714	4.38330844	1.17E-05	1.86E-05
LOC100647879	365.479256	4.364299664	0.50732053	8.60264745	7.79E-18	2.61E-17
LOC100647135	90.5367506	4.367386319	0.47909114	9.11598222	7.80E-20	2.95E-19
LOC100648612	20.6395972	4.373088987	0.57228599	7.64143987	2.15E-14	5.88E-14
LOC105666761	221.572909	4.377211755	1.30451098	3.35544262	0.00079238	0.00110202
LOC100650238	553.830073	4.380778113	0.62686541	6.988387	2.78E-12	6.70E-12
LOC105667057	94.5465526	4.384430939	1.58415194	2.76768335	0.00564563	0.00733303
LOC100652120	686.711138	4.396051878	0.64085141	6.8597054	6.90E-12	1.63E-11
LOC100648782	4244.9876	4.402786973	0.37887889	11.6205657	3.24E-31	2.40E-30
LOC105665990	1867.3778	4.409915219	0.89806579	4.91045898	9.09E-07	1.56E-06
LOC100648226	2735.90045	4.410998218	0.39371815	11.2034413	3.92E-29	2.56E-28
LOC100645988	582.26528	4.427938417	0.33701618	13.1386522	1.98E-39	2.50E-38
LOC105666716	13.1436413	4.433370783	0.68798939	6.44395228	1.16E-10	2.52E-10
LOC100646102	1444.47169	4.436722222	0.3847648	11.5309983	9.21E-31	6.65E-30
LOC100644009	3435.84573	4.453431623	0.78705677	5.65833598	1.53E-08	2.92E-08
LOC100643900	1564.40742	4.458580136	0.96600665	4.61547564	3.92E-06	6.43E-06
LOC105666783	19.0468647	4.46318718	0.53830301	8.2912172	1.12E-16	3.51E-16
LOC100643031	11.6402205	4.467587804	0.81527959	5.47982294	4.26E-08	7.92E-08
LOC105666914	237.097378	4.468935533	1.54507937	2.89236632	0.00382352	0.00503782
LOC100643069	1747.84896	4.470899759	0.42836365	10.4371595	1.68E-25	8.74E-25
LOC105666179	227.078954	4.483529081	0.86481263	5.18439362	2.17E-07	3.87E-07

LOC105665667	12.6020649	4.496005144	0.69187788	6.49826405	8.13E-11	1.78E-10
LOC105666673	35.8268775	4.502262096	0.9537522	4.72057846	2.35E-06	3.92E-06
LOC100644737	218.504014	4.503975392	1.30368971	3.45479092	0.00055072	0.00077651
LOC100651771	60.083785	4.521092907	0.41858632	10.8008615	3.41E-27	1.98E-26
LOC100647114	19.382099	4.533250532	0.63197512	7.17314716	7.33E-13	1.83E-12
LOC100651557	95.017832	4.542525156	0.73314439	6.19594889	5.79E-10	1.21E-09
LOC100644798	20.8662454	4.547426073	0.58628625	7.75632399	8.74E-15	2.45E-14
LOC105667025	16.1360779	4.565653561	0.86193216	5.29699875	1.18E-07	2.13E-07
LOC100645738	288.661438	4.627101852	0.84494372	5.4762249	4.34E-08	8.08E-08
LOC100645642	50.2256576	4.628590483	0.6169335	7.50257599	6.26E-14	1.67E-13
LOC100642203	462.990376	4.639735758	0.56451046	8.21904297	2.05E-16	6.34E-16
LOC100645197	376.107246	4.641867852	0.46755522	9.92795642	3.15E-23	1.42E-22
LOC105667000	428.66448	4.645854652	1.08403619	4.28570069	1.82E-05	2.86E-05
LOC105666013	12.8611376	4.645906374	0.67187855	6.91480082	4.69E-12	1.11E-11
LOC105666968	10.6932361	4.650677101	0.79874436	5.82248503	5.80E-09	1.14E-08
LOC100649557	1803.10389	4.65184885	0.52440243	8.87076149	7.26E-19	2.59E-18
LOC105666733	1062.85689	4.653258613	0.56195073	8.28054557	1.23E-16	3.84E-16
LOC100650954	112.240548	4.666803082	0.50977719	9.1545938	5.46E-20	2.09E-19
LOC105666241	145.100806	4.686210048	0.87595017	5.34985916	8.80E-08	1.61E-07
LOC100644539	385.374115	4.688895908	1.20146045	3.90266355	9.51E-05	0.00014224
LOC100648607	1618.87633	4.693192293	0.52955478	8.86252467	7.82E-19	2.79E-18
LOC105666559	32.6024626	4.703731115	0.83078523	5.66178955	1.50E-08	2.87E-08
LOC100643188	144.042302	4.718706221	0.2869033	16.4470264	8.81E-61	5.67E-59
LOC100650989	582.659909	4.724280107	0.42528954	11.1083854	1.14E-28	7.25E-28
LOC100645237	1149.86563	4.724680508	0.67889418	6.95937695	3.42E-12	8.21E-12
LOC100645424	2753.3164	4.725236811	1.01769617	4.64307222	3.43E-06	5.64E-06
LOC105666730	727.068006	4.728557313	1.29906343	3.63997416	0.00027267	0.00039405
LOC100650188	39.5178433	4.733919527	1.25650734	3.76752238	0.00016488	0.00024221
LOC105667009	380.737198	4.74036499	0.6230293	7.60857477	2.77E-14	7.54E-14

LOC105666122	87.4217387	4.747220534	0.47925322	9.90545354	3.94E-23	1.76E-22
LOC105666668	339.976236	4.759260014	0.94691209	5.02608431	5.01E-07	8.74E-07
LOC100643258	84.7528165	4.777969574	0.59426317	8.04015768	8.97E-16	2.66E-15
LOC100646518	35.4222432	4.791685391	0.58514086	8.18894343	2.64E-16	8.07E-16
LOC105666656	8023.74929	4.805759143	1.02079412	4.70786328	2.50E-06	4.16E-06
LOC100644116	458.921606	4.806051095	0.88424725	5.43518917	5.47E-08	1.01E-07
LOC100647121	85.7613566	4.806077977	0.62030896	7.74787772	9.34E-15	2.61E-14
LOC100652332	224.312472	4.810064756	1.54862473	3.10602348	0.00189622	0.00256612
LOC100644618	245.833318	4.819208928	0.99435336	4.8465758	1.26E-06	2.13E-06
LOC100645399	26.4298954	4.83938778	1.00190484	4.83018707	1.36E-06	2.31E-06
LOC105665905	23.115524	4.854925427	0.97657755	4.97136704	6.65E-07	1.15E-06
LOC100651260	12.1415638	4.855490837	0.68288611	7.11024983	1.16E-12	2.86E-12
LOC100643610	30.9896586	4.885706422	0.47783383	10.2246977	1.54E-24	7.51E-24
LOC100646863	305.437409	4.888490286	1.20615441	4.0529556	5.06E-05	7.73E-05
LOC100649711	2578.49667	4.911606843	1.13577585	4.32445086	1.53E-05	2.42E-05
LOC100645781	395.245829	4.914470071	0.46479146	10.5734947	3.95E-26	2.14E-25
LOC105666750	205.646072	4.91718762	1.59762416	3.07781251	0.00208526	0.00281339
LOC100647275	26.4275826	4.924458749	0.59414396	8.28832586	1.15E-16	3.60E-16
LOC105665828	156.218038	4.968710299	1.4086489	3.52728795	0.00041984	0.00059791
LOC100650067	31.1478874	4.971790176	0.94594753	5.25588369	1.47E-07	2.65E-07
LOC100645177	85.538529	5.002965023	0.79486718	6.29408933	3.09E-10	6.55E-10
LOC105666751	45.5626884	5.003058855	1.36562726	3.66356107	0.00024873	0.00036042
LOC105667177	158.678475	5.010958678	1.3632811	3.67566062	0.00023723	0.00034432
LOC105666729	14.8099777	5.023510899	0.94574862	5.31167667	1.09E-07	1.97E-07
LOC105666669	380.780841	5.027074587	1.28765655	3.90404924	9.46E-05	0.00014147
LOC105666061	130.211197	5.028497696	0.73259572	6.86394635	6.70E-12	1.58E-11
LOC100645169	22.4569793	5.032080074	0.80942278	6.21687477	5.07E-10	1.06E-09
LOC100651895	11.3794466	5.099052235	0.74948861	6.80337522	1.02E-11	2.38E-11
LOC100644792	16.3562976	5.128522531	0.61599792	8.32555165	8.39E-17	2.66E-16

LOC100649007	69.3256842	5.15839041	0.32888132	15.6846561	1.93E-55	7.86E-54
LOC100642209	857.16164	5.167900674	0.7123682	7.25453589	4.03E-13	1.03E-12
LOC100645023	682.570213	5.174407567	0.93021791	5.56257572	2.66E-08	5.01E-08
LOC105666899	52.9382005	5.196852521	1.17927217	4.40683044	1.05E-05	1.67E-05
LOC100644497	394.140692	5.212573764	1.16502044	4.47423376	7.67E-06	1.23E-05
LOC105666791	737.269431	5.221624198	0.83107001	6.28301359	3.32E-10	7.02E-10
LOC100644377	593.301671	5.228779123	0.90697969	5.76504541	8.16E-09	1.59E-08
LOC105666087	43.9382149	5.23171014	0.7525212	6.95224285	3.60E-12	8.62E-12
LOC105666144	412.667557	5.264054927	1.22161661	4.30908919	1.64E-05	2.58E-05
LOC105667200	20.7279836	5.280128356	0.99899561	5.285437	1.25E-07	2.27E-07
LOC105666734	1146.66082	5.28375407	1.1204134	4.71589689	2.41E-06	4.00E-06
LOC105666020	339.118231	5.305211472	1.38838124	3.82114892	0.00013283	0.00019637
LOC105666295	66.2495298	5.311335463	1.2899289	4.11754127	3.83E-05	5.90E-05
LOC100644914	767.479713	5.327189988	1.18283176	4.50375968	6.68E-06	1.08E-05
LOC105665680	774.622903	5.339696763	0.99327303	5.37586004	7.62E-08	1.40E-07
LOC100643057	97.1966197	5.353882419	1.09041826	4.90993468	9.11E-07	1.56E-06
LOC105666847	182.990939	5.437233701	1.57865282	3.44422385	0.0005727	0.00080565
LOC105666712	70.1365596	5.456336644	0.93197426	5.85460013	4.78E-09	9.48E-09
LOC105666678	81.4748451	5.463088953	0.67828658	8.05424893	8.00E-16	2.38E-15
LOC100650225	9.6230026	5.463362858	0.84397468	6.47337293	9.58E-11	2.09E-10
LOC100647295	919.99109	5.503342292	0.61929338	8.88648657	6.31E-19	2.26E-18
LOC105666282	97.9965198	5.533677967	1.4847043	3.72712464	0.00019368	0.00028324
LOC105666845	11.2171122	5.570212206	1.12830585	4.93679279	7.94E-07	1.37E-06
LOC100644883	18.3647894	5.635330011	0.68733178	8.1988498	2.43E-16	7.45E-16
LOC105667039	70.841275	5.647891843	1.56384193	3.61154905	0.00030437	0.00043787
LOC100645510	242.852782	5.672776489	1.49230969	3.80133998	0.00014392	0.00021221
LOC100645406	494.686119	5.712417815	0.71466606	7.9931287	1.32E-15	3.86E-15
LOC100648786	63.1575524	5.713816552	1.09422771	5.22178015	1.77E-07	3.18E-07
LOC105666986	34.8088112	5.745428821	1.32890472	4.32343173	1.54E-05	2.43E-05

LOC100644146	242.439068	5.790016817	0.9755687	5.93501698	2.94E-09	5.90E-09
LOC105666666	77.061406	5.832363934	1.52748618	3.81827608	0.00013439	0.00019858
LOC100651405	34.5800479	5.862891489	0.47363144	12.3785943	3.41E-35	3.26E-34
LOC105666667	131.979394	5.894158417	1.28969469	4.5701967	4.87E-06	7.94E-06
LOC100648039	71.3560476	5.90088453	0.62341607	9.4654033	2.92E-21	1.19E-20
LOC105667142	62.863778	5.993763331	1.10745836	5.41217942	6.23E-08	1.15E-07
LOC105666449	153.148431	6.038656519	2.82325134	2.13890149	0.03244365	0.03958327
LOC100651546	704.815523	6.083996337	0.7793446	7.80655485	5.88E-15	1.66E-14
LOC100651748	32.0860803	6.105231953	0.53680076	11.3733669	5.68E-30	3.91E-29
LOC100645869	127.076394	6.134423781	0.94608062	6.48403914	8.93E-11	1.95E-10
LOC100651964	217.520532	6.141233796	0.59355375	10.3465504	4.34E-25	2.20E-24
LOC100644098	185.621968	6.142155179	2.25133343	2.7282299	0.00636752	0.00823354
LOC105665967	15.2271841	6.19275688	0.8270498	7.48776778	7.01E-14	1.86E-13
LOC100648399	519.613819	6.252935853	0.35543485	17.5923546	2.82E-69	3.54E-67
LOC100646611	23.6203295	6.283574764	0.94774112	6.63005394	3.36E-11	7.53E-11
LOC105666901	19.0268007	6.401527407	0.88690848	7.21779928	5.28E-13	1.34E-12
LOC105666886	608.749325	6.537707405	3.0675146	2.13127181	0.03306676	0.04030332
LOC100647204	768.794382	6.574928459	0.99613858	6.60041544	4.10E-11	9.17E-11
LOC100643523	323.365727	6.657163806	1.17375641	5.67167406	1.41E-08	2.71E-08
LOC105666993	233.380971	6.662578097	1.43662259	4.63766763	3.52E-06	5.79E-06
LOC105666774	43.1988062	6.76579865	0.90247874	7.49690637	6.53E-14	1.74E-13
LOC100647400	9.13789275	6.851356054	0.93083053	7.36047633	1.83E-13	4.75E-13
LOC105666457	35.5870144	7.181340548	1.34021381	5.35835438	8.40E-08	1.53E-07
LOC100651036	22.8949096	7.259978211	0.69619713	10.4280495	1.85E-25	9.59E-25
LOC100646104	231.587901	7.391259264	0.7503464	9.85046277	6.82E-23	3.02E-22
LOC105666222	447.774083	7.475236709	3.65284911	2.04641267	0.04071579	0.04925232
LOC100644582	519.735809	7.51277926	0.64160634	11.7093282	1.14E-31	8.67E-31
LOC105666024	161.558089	7.6469673	0.70002204	10.923895	8.86E-28	5.32E-27
LOC100642575	27.2465257	7.737140302	0.74414656	10.397334	2.55E-25	1.32E-24

LOC100648658	122.574998	8.27721649	0.70251434	11.7822741	4.82E-32	3.72E-31
LOC100648421	5417.40915	8.801250747	0.27386629	32.137036	1.34E-226	1.31E-222
LOC100647081	168.969675	10.19292846	0.7100417	14.3553942	9.86E-47	2.09E-45
LOC100646065	56.2872046	10.23734997	0.75590627	13.5431474	8.70E-42	1.32E-40
LOC100646845	517.835464	10.48888891	0.5672512	18.4907303	2.45E-76	5.86E-74
LOC100648536	9934.46732	10.8470013	0.44127231	24.5811966	2.01E-133	4.91E-130
LOC105665921	2751.3922	11.61484475	0.61706784	18.8226382	4.93E-79	1.38E-76
LOC100648898	273.32358	12.26397219	1.18580203	10.3423437	4.53E-25	2.29E-24
LOC100649020	315.078164	12.70589757	1.18708813	10.7034156	9.81E-27	5.52E-26

Supplementary 4.0.9: enriched GO terms for the differentially expressed genes identified in the abdomen tissue between reproductive and sterile workers.

term_ID	description	frequency	log10 p-value
GO:0000003	reproduction	0.77%	-1.9293
GO:0002377	immunoglobulin production	0.02%	-1.75
GO:0016447	somatic recombination of immunoglobulin gene segments	0.01%	-1.3517
GO:0009161	ribonucleoside monophosphate metabolic process	2.27%	-4.8011
GO:0046128	purine ribonucleoside metabolic process	2.00%	-1.8216
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	0.49%	-1.6418
GO:0034404	nucleobase-containing small molecule biosynthetic process	1.41%	-2.3195
GO:0009259	ribonucleotide metabolic process	2.75%	-2.3893
GO:0006119	oxidative phosphorylation	0.25%	-1.9451
GO:0009116	nucleoside metabolic process	2.92%	-2.5041
GO:0009124	nucleoside monophosphate biosynthetic process	1.49%	-2.3862
GO:0009126	purine nucleoside monophosphate metabolic process	1.92%	-4.7371
GO:0006163	purine nucleotide metabolic process	2.44%	-2.4425
GO:0009144	purine nucleoside triphosphate metabolic process	1.40%	-3.5224
GO:0009142	nucleoside triphosphate biosynthetic process	0.65%	-1.7311
GO:0009168	purine ribonucleoside monophosphate biosynthetic process	1.04%	-2.7261
GO:0006753	nucleoside phosphate metabolic process	4.21%	-3.223
GO:0046034	ATP metabolic process	1.26%	-2.5418
GO:0015986	ATP synthesis coupled proton transport	0.41%	-1.3517
GO:0009199	ribonucleoside triphosphate metabolic process	1.46%	-3.6311
GO:0010212	response to ionizing radiation	0.04%	-2.0714
GO:0009056	catabolic process	4.82%	-1.8709
GO:0051276	chromosome organization	1.48%	-3.8739
GO:0010605	negative regulation of macromolecule metabolic process	1.17%	-3.4332
GO:1902679	negative regulation of RNA biosynthetic process	0.61%	-3.5167
GO:0031327	negative regulation of cellular biosynthetic process	0.77%	-1.4527

GO:0045934	negative regulation of nucleobase-containing compound metabolic process	0.70%	-3.3137
GO:0045892	negative regulation of transcription, DNA-templated	0.59%	-2.0687
GO:0000122	negative regulation of transcription from RNA polymerase II promoter	0.20%	-1.3903
GO:0001935	endothelial cell proliferation	0.02%	-1.8297
GO:0008285	negative regulation of cell proliferation	0.13%	-1.438
GO:0061351	neural precursor cell proliferation	0.03%	-1.3506
GO:0009108	coenzyme biosynthetic process	1.98%	-1.4521
GO:0051186	cofactor metabolic process	3.99%	-1.8198
GO:1902600	hydrogen ion transmembrane transport	1.02%	-3.0119
GO:0015991	ATP hydrolysis coupled proton transport	0.16%	-1.3517
GO:0018205	peptidyl-lysine modification	0.36%	-1.6909
GO:0007293	germarium-derived egg chamber formation	0.01%	-2.3689
GO:0048515	spermatid differentiation	0.04%	-1.5432
GO:0009566	fertilization	0.04%	-1.5748
GO:0051321	meiotic cell cycle	0.18%	-1.8027
GO:0048232	male gamete generation	0.09%	-1.9447
GO:0051402	neuron apoptotic process	0.04%	-1.3044
GO:0006360	transcription from RNA polymerase I promoter	0.05%	-1.5397
GO:0042440	pigment metabolic process	0.49%	-1.3077
GO:0022904	respiratory electron transport chain	0.37%	-2.0714
GO:0042775	mitochondrial ATP synthesis coupled electron transport	0.07%	-1.3364
GO:0015980	energy derivation by oxidation of organic compounds	1.18%	-1.8065
GO:0044272	sulfur compound biosynthetic process	1.24%	-1.3985
GO:0007059	chromosome segregation	0.48%	-1.7766
GO:0032107	regulation of response to nutrient levels	0.01%	-1.8824
GO:0042445	hormone metabolic process	0.09%	-1.5474
GO:0042770	signal transduction in response to DNA damage	0.02%	-1.5397
GO:0051301	cell division	1.23%	-3.3661
GO:0007049	cell cycle	1.89%	-1.6761

GO:0006403	RNA localization	0.12%	-2.3773
GO:0006260	DNA replication	1.58%	-2.6129
GO:0048545	response to steroid hormone	0.12%	-1.8065
GO:0009755	hormone-mediated signaling pathway	0.18%	-1.4044
GO:0071559	response to transforming growth factor beta	0.05%	-1.3044
GO:0071396	cellular response to lipid	0.17%	-1.4389
GO:0007179	transforming growth factor beta receptor signaling pathway	0.04%	-1.3506
GO:0015931	nucleobase-containing compound transport	0.20%	-2.3212
GO:0043085	positive regulation of catalytic activity	0.82%	-1.7722
GO:0048008	platelet-derived growth factor receptor signaling pathway	0.01%	-1.4314
GO:0048024	regulation of mRNA splicing, via spliceosome	0.03%	-1.9818
GO:1901576	organic substance biosynthetic process	30.37%	-1.3457
GO:0006508	proteolysis	5.22%	-1.5038
GO:0098732	macromolecule deacylation	0.09%	-1.3364
GO:0006139	nucleobase-containing compound metabolic process	26.55%	-2.7307
GO:0006730	one-carbon metabolic process	0.33%	-1.3517
GO:0040029	regulation of gene expression, epigenetic	0.13%	-2.7668
GO:1901606	alpha-amino acid catabolic process	0.57%	-2.9397
GO:0006026	aminoglycan catabolic process	0.17%	-1.5397
GO:0046395	carboxylic acid catabolic process	0.95%	-1.3038
GO:0044282	small molecule catabolic process	1.27%	-1.7321
GO:0019318	hexose metabolic process	0.64%	-1.4421
GO:0007419	ventral cord development	0.00%	-1.4163
GO:0006954	inflammatory response	0.11%	-1.3149
GO:0042737	drug catabolic process	0.00%	-2.1496
GO:0050954	sensory perception of mechanical stimulus	0.04%	-1.4008
GO:0032268	regulation of cellular protein metabolic process	1.47%	-1.7328
GO:0006090	pyruvate metabolic process	0.82%	-1.3086
GO:0034502	protein localization to chromosome	0.03%	-1.8297

GO:0000018	regulation of DNA recombination	0.05%	-2.0688
GO:0051053	negative regulation of DNA metabolic process	0.08%	-1.5259
GO:0007596	blood coagulation	0.05%	-1.3953
GO:0090662	ATP hydrolysis coupled transmembrane transport	1.00%	-1.5906
GO:0016444	somatic cell DNA recombination	0.01%	-1.5906
GO:0016569	covalent chromatin modification	0.42%	-3.2321
GO:0031056	regulation of histone modification	0.05%	-1.4709
GO:0060968	regulation of gene silencing	0.03%	-2.2984
GO:0035194	posttranscriptional gene silencing by RNA	0.03%	-1.6938
GO:0016574	histone ubiquitination	0.02%	-1.8297
GO:0006333	chromatin assembly or disassembly	0.12%	-2.1989
GO:0006334	nucleosome assembly	0.09%	-2.6271
GO:0006342	chromatin silencing	0.09%	-2.6543
GO:0030866	cortical actin cytoskeleton organization	0.03%	-1.5397
GO:0034654	nucleobase-containing compound biosynthetic process	14.53%	-2.1448
GO:0097659	nucleic acid-templated transcription	10.72%	-1.302
GO:1905037	autophagosome organization	0.04%	-1.3086
GO:0051169	nuclear transport	0.24%	-1.438
GO:0046434	organophosphate catabolic process	0.37%	-1.5301
GO:0014013	regulation of gliogenesis	0.02%	-1.3517
GO:0006536	glutamate metabolic process	0.20%	-1.8297
GO:0051306	mitotic sister chromatid separation	0.08%	-1.675
GO:0030071	regulation of mitotic metaphase/anaphase transition	0.07%	-1.4059
GO:0007127	meiosis I	0.08%	-1.3622
GO:0044784	metaphase/anaphase transition of cell cycle	0.08%	-1.4726
GO:0000819	sister chromatid segregation	0.24%	-1.4296
GO:1903047	mitotic cell cycle process	0.51%	-1.3421
GO:0006520	cellular amino acid metabolic process	5.59%	-1.4972
GO:0044275	cellular carbohydrate catabolic process	0.20%	-1.4726

GO:0051171	regulation of nitrogen compound metabolic process	10.93%	-3.1038
GO:0080090	regulation of primary metabolic process	11.68%	-3.095
GO:0031323	regulation of cellular metabolic process	11.66%	-1.8079
GO:0051252	regulation of RNA metabolic process	10.03%	-1.8322
GO:2000112	regulation of cellular macromolecule biosynthetic process	10.68%	-1.6762
GO:1903506	regulation of nucleic acid-templated transcription	9.97%	-1.5369
GO:0009889	regulation of biosynthetic process	10.83%	-1.3913
GO:0002200	somatic diversification of immune receptors	0.01%	-1.75
GO:0051028	mRNA transport	0.08%	-1.3077
GO:0050658	RNA transport	0.10%	-1.4067
GO:0090304	nucleic acid metabolic process	21.45%	-1.4177
GO:0080134	regulation of response to stress	0.34%	-1.4725
GO:0002706	regulation of lymphocyte mediated immunity	0.02%	-1.4314
GO:0050776	regulation of immune response	0.15%	-1.438
GO:0002822	regulation of adaptive immune response based on somatic recombination of immune recept	0.02%	-1.3517
GO:0051225	spindle assembly	0.05%	-1.3506
GO:1901565	organonitrogen compound catabolic process	1.20%	-2.108
GO:0032465	regulation of cytokinesis	0.06%	-1.4059
GO:0051100	negative regulation of binding	0.03%	-1.4059
GO:0006323	DNA packaging	0.23%	-1.5419
GO:0009112	nucleobase metabolic process	0.48%	-2.2282
GO:0044764	multi-organism cellular process	0.33%	-1.3483
GO:0071824	protein-DNA complex subunit organization	0.24%	-1.6551
GO:0051168	nuclear export	0.12%	-1.3295
GO:0009066	aspartate family amino acid metabolic process	0.83%	-1.8116
GO:0006378	mRNA polyadenylation	0.04%	-1.4059
GO:0019941	modification-dependent protein catabolic process	0.61%	-1.9061
GO:0030163	protein catabolic process	1.00%	-1.4855
GO:0044265	cellular macromolecule catabolic process	1.27%	-1.556

GO:2001251	negative regulation of chromosome organization	0.06%	-1.7506
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	0.04%	-1.3396
GO:0097305	response to alcohol	0.06%	-1.5285
GO:0046661	male sex differentiation	0.03%	-1.5028
GO:0034655	nucleobase-containing compound catabolic process	0.76%	-1.3515
GO:0048285	organelle fission	0.46%	-2.2138
GO:0033043	regulation of organelle organization	0.50%	-1.4405
GO:0007417	central nervous system development	0.19%	-1.3165
GO:0006281	DNA repair	2.23%	-1.7677
GO:2001020	regulation of response to DNA damage stimulus	0.08%	-1.4516
GO:2000779	regulation of double-strand break repair	0.02%	-1.3517
GO:0007291	sperm individualization	0.00%	-1.3517
GO:2000058	regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process	0.01%	-1.828
GO:1903322	positive regulation of protein modification by small protein conjugation or removal	0.05%	-1.4163
GO:1903052	positive regulation of proteolysis involved in cellular protein catabolic process	0.03%	-1.5814
GO:0032436	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	0.02%	-1.5748
GO:0043280	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	0.02%	-1.5397
GO:0051443	positive regulation of ubiquitin-protein transferase activity	0.03%	-1.3517

Supplementary 4.1.0: enriched GO terms for the up-regulated genes in the abdomen of reproductive workers compared to sterile workers.

term_ID	description	frequency	log10 p-value
GO:0000003	reproduction	0.77%	-8.7361
GO:0006913	nucleocytoplasmic transport	0.24%	-12.1533
GO:0070727	cellular macromolecule localization	1.56%	-8.7512
GO:0006886	intracellular protein transport	1.20%	-2.3926
GO:0008104	protein localization	2.63%	-6.553
GO:0006606	protein import into nucleus	0.10%	-4.2038
GO:0006406	mRNA export from nucleus	0.06%	-6.1803
GO:0071426	ribonucleoprotein complex export from nucleus	0.10%	-7.7729
GO:0071428	rRNA-containing ribonucleoprotein complex export from nucleus	0.04%	-3.0577
GO:0051649	establishment of localization in cell	1.68%	-3.9729
GO:0045184	establishment of protein localization	2.41%	-2.1248
GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	0.10%	-2.2912
GO:0016339	calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules	0.00%	-2.1932
GO:0009987	cellular process	63.78%	-2.1568
GO:0032501	multicellular organismal process	2.37%	-3.1423
GO:0065007	biological regulation	20.50%	-35.6978
GO:0070647	protein modification by small protein conjugation or removal	0.82%	-17.6233
GO:0071840	cellular component organization or biogenesis	8.57%	-31.2272
GO:0051173	positive regulation of nitrogen compound metabolic process	0.69%	-15.9015
GO:0048522	positive regulation of cellular process	1.59%	-3.6811
GO:0045860	positive regulation of protein kinase activity	0.13%	-3.3324
GO:0001932	regulation of protein phosphorylation	0.43%	-2.4487
GO:1902680	positive regulation of RNA biosynthetic process	0.52%	-11.4956
GO:0031325	positive regulation of cellular metabolic process	1.00%	-9.4354
GO:0019220	regulation of phosphate metabolic process	0.58%	-2.7419
GO:0051254	positive regulation of RNA metabolic process	0.54%	-3.7981

GO:0010628	positive regulation of gene expression	0.65%	-2.7464
GO:0045893	positive regulation of transcription, DNA-templated	0.52%	-7.4697
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	0.37%	-4.4752
GO:0008156	negative regulation of DNA replication	0.03%	-2.2475
GO:0010562	positive regulation of phosphorus metabolic process	0.28%	-2.4431
GO:0043549	regulation of kinase activity	0.32%	-2.8933
GO:0031401	positive regulation of protein modification process	0.30%	-2.9502
GO:0042327	positive regulation of phosphorylation	0.25%	-3.0448
GO:0051054	positive regulation of DNA metabolic process	0.05%	-2.6137
GO:0045740	positive regulation of DNA replication	0.01%	-2.0903
GO:0032259	methylation	3.10%	-6.4015
GO:0051301	cell division	1.23%	-16.8606
GO:0043933	macromolecular complex subunit organization	2.37%	-15.5129
GO:0033554	cellular response to stress	2.97%	-12.1206
GO:0006281	DNA repair	2.23%	-6.5956
GO:1901360	organic cyclic compound metabolic process	30.32%	-33.862
GO:0009790	embryo development	0.31%	-4.8114
GO:2000026	regulation of multicellular organismal development	0.42%	-2.0576
GO:0030154	cell differentiation	1.13%	-2.0811
GO:0048856	anatomical structure development	2.54%	-2.1364
GO:0006725	cellular aromatic compound metabolic process	29.63%	-33.6587
GO:0009057	macromolecule catabolic process	1.95%	-4.1385
GO:0000375	RNA splicing, via transesterification reactions	0.32%	-16.2258
GO:0048024	regulation of mRNA splicing, via spliceosome	0.03%	-2.2681
GO:0000245	spliceosomal complex assembly	0.04%	-3.3658
GO:0006376	mRNA splice site selection	0.02%	-2.29
GO:0031442	positive regulation of mRNA 3'-end processing	0.00%	-2.2878
GO:0000387	spliceosomal snRNP assembly	0.05%	-2.7547
GO:0000381	regulation of alternative mRNA splicing, via spliceosome	0.02%	-4.6518

GO:0000398	mRNA splicing, via spliceosome	0.32%	-4.0962
GO:0045292	mRNA cis splicing, via spliceosome	0.03%	-2.1932
GO:0030010	establishment of cell polarity	0.05%	-2.0373
GO:0051321	meiotic cell cycle	0.18%	-15.5343
GO:0044703	multi-organism reproductive process	0.34%	-6.1312
GO:0003006	developmental process involved in reproduction	0.30%	-2.8809
GO:0044764	multi-organism cellular process	0.33%	-2.7818
GO:0048608	reproductive structure development	0.16%	-2.2414
GO:0007283	spermatogenesis	0.09%	-3.2483
GO:0007276	gamete generation	0.16%	-3.75
GO:0048477	oogenesis	0.05%	-4.0749
GO:0022412	cellular process involved in reproduction in multicellular organism	0.11%	-2.5558
GO:0043412	macromolecule modification	9.79%	-2.1847
GO:1902579	multi-organism localization	0.01%	-3.2694
GO:0012501	programmed cell death	0.43%	-2.1065
GO:0007059	chromosome segregation	0.48%	-2.174
GO:2000177	regulation of neural precursor cell proliferation	0.02%	-2.4077
GO:0006928	movement of cell or subcellular component	0.97%	-2.4606
GO:0051302	regulation of cell division	0.08%	-4.5241
GO:0051236	establishment of RNA localization	0.10%	-12.032
GO:0051028	mRNA transport	0.08%	-4.6502
GO:0016973	poly(A)+ mRNA export from nucleus	0.02%	-2.2878
GO:0010501	RNA secondary structure unwinding	0.03%	-2.5969
GO:0050657	nucleic acid transport	0.10%	-12.032
GO:0007049	cell cycle	1.89%	-9.0215
GO:0060249	anatomical structure homeostasis	0.19%	-2.9012
GO:0016073	snRNA metabolic process	0.04%	-4.853
GO:0040008	regulation of growth	0.17%	-2.0909
GO:0046483	heterocycle metabolic process	29.66%	-32.0009

GO:0006310	DNA recombination	1.64%	-11.8715
GO:0090503	RNA phosphodiester bond hydrolysis, exonucleolytic	0.15%	-3.5968
GO:0044093	positive regulation of molecular function	0.89%	-6.4589
GO:0050790	regulation of catalytic activity	1.58%	-3.2536
GO:0051347	positive regulation of transferase activity	0.19%	-5.2662
GO:1904029	regulation of cyclin-dependent protein kinase activity	0.07%	-2.8669
GO:0045737	positive regulation of cyclin-dependent protein serine/threonine kinase activity	0.02%	-3.5968
GO:0033238	regulation of cellular amine metabolic process	0.02%	-2.2771
GO:0048519	negative regulation of biological process	1.98%	-2.4065
GO:0090305	nucleic acid phosphodiester bond hydrolysis	2.27%	-5.3871
GO:1903311	regulation of mRNA metabolic process	0.04%	-13.0804
GO:0097711	ciliary basal body docking	0.00%	-2.7627
GO:0040029	regulation of gene expression, epigenetic	0.13%	-6.8576
GO:0009411	response to UV	0.05%	-2.4418
GO:0010332	response to gamma radiation	0.01%	-2.2475
GO:0030397	membrane disassembly	0.00%	-2.6149
GO:0034660	ncRNA metabolic process	3.41%	-2.9344
GO:0035329	hippo signaling	0.01%	-2.1932
GO:0032784	regulation of DNA-templated transcription, elongation	0.15%	-6.1642
GO:0032968	positive regulation of transcription elongation from RNA polymerase II promoter	0.03%	-2.7627
GO:0010827	regulation of glucose transport	0.01%	-2.322
GO:0010586	miRNA metabolic process	0.00%	-2.9421
GO:0010608	posttranscriptional regulation of gene expression	0.72%	-7.3482
GO:1902679	negative regulation of RNA biosynthetic process	0.61%	-12.8437
GO:0048523	negative regulation of cellular process	1.83%	-9.7043
GO:0060964	regulation of gene silencing by miRNA	0.01%	-3.8386
GO:0060968	regulation of gene silencing	0.03%	-6.1437
GO:0031327	negative regulation of cellular biosynthetic process	0.77%	-7.9226
GO:0051253	negative regulation of RNA metabolic process	0.63%	-2.3203

GO:0045934	negative regulation of nucleobase-containing compound metabolic process	0.70%	-2.0129
GO:0045892	negative regulation of transcription, DNA-templated	0.59%	-2.1097
GO:0010629	negative regulation of gene expression	0.78%	-2.2798
GO:0006342	chromatin silencing	0.09%	-2.7211
GO:0010605	negative regulation of macromolecule metabolic process	1.17%	-2.4743
GO:0010558	negative regulation of macromolecule biosynthetic process	0.74%	-10.4331
GO:0017148	negative regulation of translation	0.09%	-4.6381
GO:0031047	gene silencing by RNA	0.09%	-9.0317
GO:0035195	gene silencing by miRNA	0.02%	-3.0236
GO:0000122	negative regulation of transcription from RNA polymerase II promoter	0.20%	-7.5986
GO:0016441	posttranscriptional gene silencing	0.03%	-6.1917
GO:0006352	DNA-templated transcription, initiation	0.77%	-2.2661
GO:0090304	nucleic acid metabolic process	21.45%	-68.7938
GO:0030522	intracellular receptor signaling pathway	0.08%	-2.1105
GO:0034248	regulation of cellular amide metabolic process	0.70%	-6.5792
GO:0032268	regulation of cellular protein metabolic process	1.47%	-5.4243
GO:0051248	negative regulation of protein metabolic process	0.44%	-4.3786
GO:0031399	regulation of protein modification process	0.57%	-2.1508
GO:1901699	cellular response to nitrogen compound	0.12%	-3.2009
GO:0030422	production of siRNA involved in RNA interference	0.01%	-2.9421
GO:0031050	dsRNA fragmentation	0.02%	-3.001
GO:0043331	response to dsRNA	0.03%	-3.0069
GO:0016579	protein deubiquitination	0.20%	-6.2123
GO:0000338	protein deneddylation	0.02%	-2.6149
GO:0016578	histone deubiquitination	0.01%	-3.355
GO:0016567	protein ubiquitination	0.52%	-2.9745
GO:0000209	protein polyubiquitination	0.07%	-3.271
GO:0070536	protein K63-linked deubiquitination	0.01%	-2.2878
GO:0044260	cellular macromolecule metabolic process	34.28%	-26.9345

GO:0043488	regulation of mRNA stability	0.02%	-2.7546
GO:0006259	DNA metabolic process	5.61%	-3.7233
GO:0006357	regulation of transcription from RNA polymerase II promoter	1.27%	-5.1308
GO:0006367	transcription initiation from RNA polymerase II promoter	0.11%	-2.3036
GO:0034641	cellular nitrogen compound metabolic process	34.14%	-25.4177
GO:0006479	protein methylation	0.34%	-4.5052
GO:0006306	DNA methylation	0.19%	-3.9554
GO:0034968	histone lysine methylation	0.10%	-3.4926
GO:0031060	regulation of histone methylation	0.02%	-3.6022
GO:0031058	positive regulation of histone modification	0.02%	-3.4768
GO:0051571	positive regulation of histone H3-K4 methylation	0.00%	-3.2694
GO:0018205	peptidyl-lysine modification	0.36%	-9.625
GO:0006396	RNA processing	3.21%	-2.8603
GO:0006333	chromatin assembly or disassembly	0.12%	-10.2176
GO:0006338	chromatin remodeling	0.14%	-3.4509
GO:0006336	DNA replication-independent nucleosome assembly	0.01%	-3.0577
GO:0006334	nucleosome assembly	0.09%	-4.1376
GO:1902275	regulation of chromatin organization	0.07%	-7.4539
GO:0030261	chromosome condensation	0.11%	-2.7696
GO:0016570	histone modification	0.37%	-9.6851
GO:0016569	covalent chromatin modification	0.42%	-7.2751
GO:0050821	protein stabilization	0.05%	-2.5317
GO:0044271	cellular nitrogen compound biosynthetic process	22.50%	-16.8278
GO:0031145	anaphase-promoting complex-dependent catabolic process	0.02%	-4.4094
GO:0007077	mitotic nuclear envelope disassembly	0.00%	-2.6149
GO:0035186	syncytial blastoderm mitotic cell cycle	0.00%	-2.4705
GO:0000731	DNA synthesis involved in DNA repair	0.02%	-3.0577
GO:0098727	maintenance of cell number	0.04%	-3.1701
GO:0006270	DNA replication initiation	0.14%	-3.2679

GO:0033260	nuclear DNA replication	0.04%	-2.7279
GO:1901362	organic cyclic compound biosynthetic process	17.87%	-22.2944
GO:0009966	regulation of signal transduction	0.86%	-2.6824
GO:0048584	positive regulation of response to stimulus	0.46%	-2.1993
GO:0051056	regulation of small GTPase mediated signal transduction	0.22%	-2.0164
GO:0030177	positive regulation of Wnt signaling pathway	0.03%	-2.479
GO:0030178	negative regulation of Wnt signaling pathway	0.04%	-2.8112
GO:0090263	positive regulation of canonical Wnt signaling pathway	0.02%	-2.322
GO:0019438	aromatic compound biosynthetic process	16.95%	-26.733
GO:0018130	heterocycle biosynthetic process	17.39%	-25.6065
GO:0075733	intracellular transport of virus	0.01%	-3.2694
GO:0016032	viral process	0.13%	-2.891
GO:1902583	multi-organism intracellular transport	0.01%	-3.2694
GO:0000280	nuclear division	0.42%	-12.9151
GO:0051225	spindle assembly	0.05%	-3.5627
GO:0070192	chromosome organization involved in meiotic cell cycle	0.03%	-2.1899
GO:0051784	negative regulation of nuclear division	0.06%	-2.7999
GO:0051306	mitotic sister chromatid separation	0.08%	-6.3067
GO:0007143	female meiotic division	0.01%	-2.1008
GO:0090307	mitotic spindle assembly	0.02%	-4.7037
GO:0045143	homologous chromosome segregation	0.03%	-3.6543
GO:0045132	meiotic chromosome segregation	0.05%	-2.3345
GO:0007080	mitotic metaphase plate congression	0.02%	-2.6181
GO:0000070	mitotic sister chromatid segregation	0.19%	-3.4095
GO:0007062	sister chromatid cohesion	0.10%	-3.0213
GO:0007052	mitotic spindle organization	0.05%	-3.5849
GO:0031329	regulation of cellular catabolic process	0.09%	-3.9839
GO:1903050	regulation of proteolysis involved in cellular protein catabolic process	0.06%	-2.8231
GO:0008356	asymmetric cell division	0.01%	-2.7585

GO:0031098	stress-activated protein kinase signaling cascade	0.06%	-2.1706
GO:0050000	chromosome localization	0.03%	-5.5732
GO:0033750	ribosome localization	0.04%	-3.5968
GO:0051656	establishment of organelle localization	0.18%	-2.1211
GO:0034629	cellular protein complex localization	0.03%	-2.6149
GO:0031123	RNA 3'-end processing	0.15%	-2.2833
GO:0030030	cell projection organization	0.61%	-3.4343
GO:0032774	RNA biosynthetic process	10.93%	-5.5815
GO:0002562	somatic diversification of immune receptors via germline recombination within a single locu	0.01%	-2.322
GO:0030097	hemopoiesis	0.17%	-2.3213
GO:0016445	somatic diversification of immunoglobulins	0.01%	-2.2509
GO:0006323	DNA packaging	0.23%	-9.2852
GO:0032508	DNA duplex unwinding	0.59%	-2.811
GO:0071103	DNA conformation change	1.08%	-2.983
GO:0006304	DNA modification	0.34%	-4.0614
GO:0038083	peptidyl-tyrosine autophosphorylation	0.01%	-2.4705
GO:0032507	maintenance of protein location in cell	0.06%	-2.1523
GO:0000226	microtubule cytoskeleton organization	0.29%	-7.5727
GO:0070507	regulation of microtubule cytoskeleton organization	0.06%	-4.1207
GO:0007098	centrosome cycle	0.04%	-6.1163
GO:0007099	centriole replication	0.02%	-3.2774
GO:0031122	cytoplasmic microtubule organization	0.03%	-2.0903
GO:0046785	microtubule polymerization	0.06%	-2.2846
GO:0022613	ribonucleoprotein complex biogenesis	1.61%	-11.1652
GO:0022607	cellular component assembly	2.48%	-7.6674
GO:0048749	compound eye development	0.02%	-2.3671
GO:0000724	double-strand break repair via homologous recombination	0.12%	-5.3876
GO:0009889	regulation of biosynthetic process	10.83%	-41.341
GO:0080090	regulation of primary metabolic process	11.68%	-7.6808

GO:2001141	regulation of RNA biosynthetic process	9.97%	-17.355
GO:0019219	regulation of nucleobase-containing compound metabolic process	10.26%	-33.9788
GO:0006355	regulation of transcription, DNA-templated	9.92%	-14.3067
GO:0006351	transcription, DNA-templated	10.66%	-2.7906
GO:0010468	regulation of gene expression	10.82%	-5.8806
GO:2000112	regulation of cellular macromolecule biosynthetic process	10.68%	-7.2246
GO:0060255	regulation of macromolecule metabolic process	11.72%	-2.5661
GO:0006468	protein phosphorylation	4.14%	-4.4222
GO:0036211	protein modification process	7.73%	-18.0206
GO:0048729	tissue morphogenesis	0.18%	-4.7047
GO:0060429	epithelium development	0.30%	-3.6885
GO:0016331	morphogenesis of embryonic epithelium	0.04%	-2.6714
GO:0061053	somite development	0.02%	-2.2475
GO:0001843	neural tube closure	0.02%	-3.2679
GO:0001841	neural tube formation	0.02%	-2.1822
GO:0072175	epithelial tube formation	0.03%	-2.0167
GO:0009792	embryo development ending in birth or egg hatching	0.16%	-2.748
GO:0001738	morphogenesis of a polarized epithelium	0.02%	-2.0368
GO:0048138	germ-line cyst encapsulation	0.00%	-2.2878
GO:0008380	RNA splicing	0.41%	-3.4399
GO:1900034	regulation of cellular response to heat	0.00%	-2.4705
GO:0071826	ribonucleoprotein complex subunit organization	0.38%	-6.7199
GO:0006325	chromatin organization	0.67%	-2.0142
GO:0034622	cellular macromolecular complex assembly	1.21%	-2.0822
GO:0071897	DNA biosynthetic process	0.68%	-4.7055
GO:0035282	segmentation	0.04%	-3.4456
GO:0007350	blastoderm segmentation	0.01%	-2.9324
GO:0008595	anterior/posterior axis specification, embryo	0.01%	-2.2667
GO:0009798	axis specification	0.03%	-2.3574

GO:0009952	anterior/posterior pattern specification	0.06%	-2.4805
GO:0034504	protein localization to nucleus	0.13%	-2.5486
GO:0006302	double-strand break repair	0.21%	-3.3174
GO:0051128	regulation of cellular component organization	1.59%	-6.8547
GO:0016482	cytosolic transport	0.08%	-5.2003
GO:0006378	mRNA polyadenylation	0.04%	-6.1074
GO:0034475	U4 snRNA 3'-end processing	0.01%	-2.2878
GO:0031124	mRNA 3'-end processing	0.07%	-2.7885
GO:0042795	snRNA transcription from RNA polymerase II promoter	0.00%	-2.1814
GO:0051716	cellular response to stimulus	9.56%	-2.7992
GO:0006289	nucleotide-excision repair	0.31%	-3.8588
GO:0006284	base-excision repair	0.27%	-2.322
GO:0006369	termination of RNA polymerase II transcription	0.02%	-2.6149
GO:0006513	protein monoubiquitination	0.02%	-2.0955
GO:0098813	nuclear chromosome segregation	0.29%	-10.5346
GO:0000278	mitotic cell cycle	0.56%	-5.1631
GO:2001251	negative regulation of chromosome organization	0.06%	-4.9023
GO:2001252	positive regulation of chromosome organization	0.03%	-5.2519
GO:0051726	regulation of cell cycle	0.55%	-5.3598
GO:0045841	negative regulation of mitotic metaphase/anaphase transition	0.05%	-3.355
GO:0044772	mitotic cell cycle phase transition	0.20%	-5.5398
GO:0044784	metaphase/anaphase transition of cell cycle	0.08%	-6.4615
GO:0045931	positive regulation of mitotic cell cycle	0.05%	-2.9578
GO:0007346	regulation of mitotic cell cycle	0.27%	-5.0874
GO:0051304	chromosome separation	0.12%	-3.6193
GO:1900087	positive regulation of G1/S transition of mitotic cell cycle	0.01%	-2.7279
GO:0032465	regulation of cytokinesis	0.06%	-3.3659
GO:0032467	positive regulation of cytokinesis	0.02%	-3.0577
GO:0030071	regulation of mitotic metaphase/anaphase transition	0.07%	-3.0686

GO:1901987	regulation of cell cycle phase transition	0.16%	-4.4425
GO:1901988	negative regulation of cell cycle phase transition	0.09%	-8.4954
GO:0033047	regulation of mitotic sister chromatid segregation	0.08%	-3.6693
GO:0010972	negative regulation of G2/M transition of mitotic cell cycle	0.03%	-2.6966
GO:0033048	negative regulation of mitotic sister chromatid segregation	0.05%	-3.9554
GO:1901989	positive regulation of cell cycle phase transition	0.03%	-5.1215
GO:0007093	mitotic cell cycle checkpoint	0.10%	-5.6005
GO:0000076	DNA replication checkpoint	0.02%	-2.1932
GO:0000075	cell cycle checkpoint	0.14%	-4.7601
GO:0000082	G1/S transition of mitotic cell cycle	0.06%	-3.0418
GO:0000077	DNA damage checkpoint	0.07%	-2.2154
GO:0031577	spindle checkpoint	0.05%	-3.001
GO:0000086	G2/M transition of mitotic cell cycle	0.05%	-4.3582
GO:1903047	mitotic cell cycle process	0.51%	-3.067
GO:0022402	cell cycle process	1.05%	-3.6343
GO:0033044	regulation of chromosome organization	0.12%	-4.3236
GO:0010638	positive regulation of organelle organization	0.21%	-2.764
GO:0016574	histone ubiquitination	0.02%	-2.2535
GO:0000904	cell morphogenesis involved in differentiation	0.19%	-2.8695
GO:0007409	axonogenesis	0.12%	-2.0198
GO:0032990	cell part morphogenesis	0.17%	-2.2434
GO:0031175	neuron projection development	0.22%	-2.6652
GO:0018105	peptidyl-serine phosphorylation	0.09%	-2.8317
GO:0032200	telomere organization	0.13%	-4.4213
GO:0006260	DNA replication	1.58%	-3.9833
GO:0007144	female meiosis I	0.00%	-2.2878
GO:0051276	chromosome organization	1.48%	-4.3332
GO:1903747	regulation of establishment of protein localization to mitochondrion	0.02%	-2.021
GO:0034453	microtubule anchoring	0.01%	-2.7279

GO:0030038	contractile actin filament bundle assembly	0.02%	-2.2846
GO:0032231	regulation of actin filament bundle assembly	0.02%	-2.2846
GO:0045886	negative regulation of synaptic growth at neuromuscular junction	0.00%	-2.1932
GO:0046621	negative regulation of organ growth	0.01%	-2.1814
GO:0043124	negative regulation of I-kappaB kinase/NF-kappaB signaling	0.01%	-2.2878
GO:0018393	internal peptidyl-lysine acetylation	0.14%	-9.7465
GO:0043984	histone H4-K16 acetylation	0.01%	-3.2694
GO:0043981	histone H4-K5 acetylation	0.00%	-2.9421
GO:0043982	histone H4-K8 acetylation	0.00%	-2.9421
GO:0043968	histone H2A acetylation	0.01%	-2.4705
GO:0043967	histone H4 acetylation	0.03%	-3.2915
GO:0043966	histone H3 acetylation	0.03%	-5.173
GO:0016925	protein sumoylation	0.05%	-3.7994
GO:0006473	protein acetylation	0.18%	-9.3279
GO:0002520	immune system development	0.19%	-3.4948
GO:0046649	lymphocyte activation	0.12%	-2.7469
GO:0009887	animal organ morphogenesis	0.26%	-2.4369
GO:0050794	regulation of cellular process	18.84%	-13.5434
GO:0006996	organelle organization	3.60%	-3.8393
GO:0000469	cleavage involved in rRNA processing	0.05%	-3.0069
GO:0043044	ATP-dependent chromatin remodeling	0.05%	-4.2593
GO:0006402	mRNA catabolic process	0.23%	-5.7384
GO:0016075	rRNA catabolic process	0.06%	-2.29
GO:0043632	modification-dependent macromolecule catabolic process	0.63%	-4.4969
GO:0034427	nuclear-transcribed mRNA catabolic process, exonucleolytic, 3'-5'	0.01%	-2.9421
GO:0071028	nuclear mRNA surveillance	0.01%	-2.9421
GO:0071025	RNA surveillance	0.02%	-3.2694
GO:0006401	RNA catabolic process	0.40%	-2.2896
GO:0006397	mRNA processing	0.56%	-5.4109

GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	0.03%	-2.0742
GO:0006511	ubiquitin-dependent protein catabolic process	0.58%	-3.0422
GO:0071407	cellular response to organic cyclic compound	0.17%	-2.8103
GO:0006261	DNA-dependent DNA replication	0.58%	-2.9043
GO:0006379	mRNA cleavage	0.05%	-2.2475

Supplementary 4.1.1: enriched GO terms for the up-regulated genes in the abdomen of sterile workers compared to reproductive workers.

term_ID	description	frequency	log10 p-value
GO:0009126	purine nucleoside monophosphate metabolic process	1.92%	-13.5623
GO:0046390	ribose phosphate biosynthetic process	1.78%	-5.7025
GO:0006165	nucleoside diphosphate phosphorylation	0.60%	-2.7731
GO:0006189	'de novo' IMP biosynthetic process	0.40%	-1.3851
GO:0009116	nucleoside metabolic process	2.92%	-3.6447
GO:0009117	nucleotide metabolic process	4.17%	-2.2816
GO:0009124	nucleoside monophosphate biosynthetic process	1.49%	-6.6318
GO:0009135	purine nucleoside diphosphate metabolic process	0.60%	-4.5139
GO:0006163	purine nucleotide metabolic process	2.44%	-13.3096
GO:0090407	organophosphate biosynthetic process	4.11%	-2.0607
GO:0009141	nucleoside triphosphate metabolic process	1.61%	-5.4441
GO:0009152	purine ribonucleotide biosynthetic process	1.34%	-5.9605
GO:0046040	IMP metabolic process	0.42%	-1.9396
GO:0009163	nucleoside biosynthetic process	1.44%	-1.6839
GO:0009161	ribonucleoside monophosphate metabolic process	2.27%	-11.6783
GO:0009168	purine ribonucleoside monophosphate biosynthetic process	1.04%	-7.1702
GO:0009165	nucleotide biosynthetic process	2.56%	-2.5954
GO:0009185	ribonucleoside diphosphate metabolic process	0.60%	-4.5139
GO:0046034	ATP metabolic process	1.26%	-6.6644
GO:0046031	ADP metabolic process	0.55%	-4.098
GO:0046128	purine ribonucleoside metabolic process	2.00%	-2.8348
GO:0046129	purine ribonucleoside biosynthetic process	0.92%	-2.8391
GO:0009205	purine ribonucleoside triphosphate metabolic process	1.37%	-1.5697
GO:0009259	ribonucleotide metabolic process	2.75%	-12.1256
GO:0006096	glycolytic process	0.55%	-3.2921
GO:0072522	purine-containing compound biosynthetic process	1.50%	-6.3972

GO:0010038	response to metal ion	0.13%	-2.7359
GO:0048878	chemical homeostasis	0.54%	-4.4566
GO:0055081	anion homeostasis	0.05%	-1.517
GO:0055080	cation homeostasis	0.38%	-3.7245
GO:0019725	cellular homeostasis	1.25%	-3.8732
GO:0006879	cellular iron ion homeostasis	0.11%	-1.9455
GO:0006873	cellular ion homeostasis	0.32%	-4.5553
GO:0006875	cellular metal ion homeostasis	0.25%	-2.0661
GO:0006885	regulation of pH	0.07%	-3.3142
GO:0051453	regulation of intracellular pH	0.03%	-1.9512
GO:0051452	intracellular pH reduction	0.02%	-1.7289
GO:0030004	cellular monovalent inorganic cation homeostasis	0.04%	-3.1111
GO:0098771	inorganic ion homeostasis	0.41%	-3.964
GO:0098660	inorganic ion transmembrane transport	2.32%	-10.0188
GO:0015991	ATP hydrolysis coupled proton transport	0.16%	-4.7159
GO:0006820	anion transport	1.96%	-1.5683
GO:0006813	potassium ion transport	0.48%	-1.7987
GO:1902600	hydrogen ion transmembrane transport	1.02%	-6.9175
GO:0098656	anion transmembrane transport	1.01%	-7.2629
GO:0098655	cation transmembrane transport	2.29%	-6.0668
GO:0030001	metal ion transport	1.68%	-1.3907
GO:0015698	inorganic anion transport	0.87%	-4.4375
GO:0015711	organic anion transport	1.19%	-4.7651
GO:0034975	protein folding in endoplasmic reticulum	0.01%	-1.6623
GO:0032981	mitochondrial respiratory chain complex I assembly	0.01%	-3.0494
GO:0034551	mitochondrial respiratory chain complex III assembly	0.02%	-1.3851
GO:0042737	drug catabolic process	0.00%	-3.3455
GO:0017001	antibiotic catabolic process	0.02%	-1.7272
GO:0016999	antibiotic metabolic process	0.06%	-3.1186

GO:0042157	lipoprotein metabolic process	0.21%	-2.23
GO:0017144	drug metabolic process	0.06%	-6.0275
GO:0072593	reactive oxygen species metabolic process	0.28%	-2.6142
GO:1901137	carbohydrate derivative biosynthetic process	3.65%	-4.4379
GO:0001935	endothelial cell proliferation	0.02%	-1.4861
GO:0006733	oxidoreduction coenzyme metabolic process	1.27%	-9.3729
GO:0009108	coenzyme biosynthetic process	1.98%	-5.2736
GO:0051188	cofactor biosynthetic process	2.76%	-2.0475
GO:1901135	carbohydrate derivative metabolic process	6.32%	-8.256
GO:0006790	sulfur compound metabolic process	1.82%	-2.8841
GO:0043112	receptor metabolic process	0.04%	-1.7674
GO:0051186	cofactor metabolic process	3.99%	-5.04
GO:0006091	generation of precursor metabolites and energy	1.94%	-4.4226
GO:0005975	carbohydrate metabolic process	5.26%	-9.6826
GO:0018298	protein-chromophore linkage	0.10%	-1.6623
GO:0007311	maternal specification of dorsal/ventral axis, oocyte, germ-line encoded	0.00%	-2.4944
GO:1901568	fatty acid derivative metabolic process	0.02%	-2.5056
GO:0045199	maintenance of epithelial cell apical/basal polarity	0.00%	-1.3851
GO:1903409	reactive oxygen species biosynthetic process	0.02%	-1.7289
GO:0002274	myeloid leukocyte activation	0.03%	-1.3737
GO:0070085	glycosylation	0.42%	-3.3977
GO:0046148	pigment biosynthetic process	0.45%	-2.8768
GO:0042168	heme metabolic process	0.27%	-1.3846
GO:0035384	thioester biosynthetic process	0.15%	-3.6046
GO:0044272	sulfur compound biosynthetic process	1.24%	-3.1644
GO:0046949	fatty-acyl-CoA biosynthetic process	0.00%	-1.3851
GO:0006749	glutathione metabolic process	0.15%	-1.6489
GO:0016226	iron-sulfur cluster assembly	0.22%	-1.3416
GO:0006637	acyl-CoA metabolic process	0.25%	-1.4018

GO:0006085	acetyl-CoA biosynthetic process	0.11%	-2.217
GO:0006084	acetyl-CoA metabolic process	0.17%	-3.055
GO:0032781	positive regulation of ATPase activity	0.03%	-2.7718
GO:0097428	protein maturation by iron-sulfur cluster transfer	0.07%	-1.3851
GO:0008592	regulation of Toll signaling pathway	0.00%	-1.5379
GO:0072524	pyridine-containing compound metabolic process	1.35%	-8.3729
GO:0006081	cellular aldehyde metabolic process	0.75%	-4.0075
GO:0016051	carbohydrate biosynthetic process	1.08%	-2.5063
GO:0009311	oligosaccharide metabolic process	0.34%	-1.4336
GO:0043603	cellular amide metabolic process	6.88%	-1.8659
GO:0015980	energy derivation by oxidation of organic compounds	1.18%	-9.4343
GO:0009060	aerobic respiration	0.62%	-3.0931
GO:0006112	energy reserve metabolic process	0.17%	-1.3881
GO:0006099	tricarboxylic acid cycle	0.47%	-2.1407
GO:0022900	electron transport chain	0.56%	-1.3972
GO:0022904	respiratory electron transport chain	0.37%	-3.1679
GO:0042775	mitochondrial ATP synthesis coupled electron transport	0.07%	-2.7663
GO:0009268	response to pH	0.01%	-1.3851
GO:0048678	response to axon injury	0.01%	-1.5317
GO:0002181	cytoplasmic translation	0.06%	-2.659
GO:0006103	2-oxoglutarate metabolic process	0.02%	-3.0494
GO:0009581	detection of external stimulus	0.06%	-1.9986
GO:0009582	detection of abiotic stimulus	0.06%	-1.6747
GO:0009584	detection of visible light	0.02%	-1.4861
GO:0007632	visual behavior	0.01%	-1.7289
GO:0007602	phototransduction	0.02%	-1.8597
GO:0055114	oxidation-reduction process	15.06%	-19.3167
GO:0006836	neurotransmitter transport	0.11%	-2.1084
GO:0006888	ER to Golgi vesicle-mediated transport	0.13%	-3.37

GO:0034440	lipid oxidation	0.09%	-9.0194
GO:0006576	cellular biogenic amine metabolic process	0.42%	-1.8828
GO:0006575	cellular modified amino acid metabolic process	0.79%	-2.5322
GO:0033013	tetrapyrrole metabolic process	0.83%	-1.9351
GO:0007186	G-protein coupled receptor signaling pathway	0.88%	-2.4759
GO:0098739	import across plasma membrane	0.01%	-1.9276
GO:0098712	L-glutamate import across plasma membrane	0.00%	-1.3851
GO:0006066	alcohol metabolic process	0.42%	-3.7711
GO:1902652	secondary alcohol metabolic process	0.10%	-1.365
GO:0034308	primary alcohol metabolic process	0.05%	-1.5317
GO:0019400	alditol metabolic process	0.13%	-1.5317
GO:1901617	organic hydroxy compound biosynthetic process	0.38%	-3.5802
GO:0006089	lactate metabolic process	0.04%	-1.9396
GO:0046164	alcohol catabolic process	0.14%	-2.0257
GO:0072350	tricarboxylic acid metabolic process	0.50%	-2.519
GO:0044550	secondary metabolite biosynthetic process	0.10%	-1.6069
GO:0043455	regulation of secondary metabolic process	0.01%	-1.3851
GO:0046271	phenylpropanoid catabolic process	0.01%	-1.3851
GO:0018065	protein-cofactor linkage	0.13%	-1.5379
GO:0051182	coenzyme transport	0.02%	-1.3851
GO:1902221	erythrose 4-phosphate/phosphoenolpyruvate family amino acid metabolic proce	0.08%	-1.6623
GO:0006497	protein lipidation	0.13%	-1.4369
GO:0016255	attachment of GPI anchor to protein	0.03%	-1.3851
GO:0003197	endocardial cushion development	0.01%	-2.0143
GO:2000826	regulation of heart morphogenesis	0.01%	-1.5379
GO:0072132	mesenchyme morphogenesis	0.01%	-1.5379
GO:0003205	cardiac chamber development	0.03%	-1.4481
GO:0006954	inflammatory response	0.11%	-1.3787
GO:0006767	water-soluble vitamin metabolic process	1.22%	-1.563

GO:0044282	small molecule catabolic process	1.27%	-13.246
GO:0072329	monocarboxylic acid catabolic process	0.29%	-7.0013
GO:0016042	lipid catabolic process	0.40%	-1.5399
GO:0046395	carboxylic acid catabolic process	0.95%	-8.0883
GO:1901606	alpha-amino acid catabolic process	0.57%	-3.3358
GO:0015858	nucleoside transport	0.08%	-1.5379
GO:0006862	nucleotide transport	0.03%	-1.3867
GO:1901679	nucleotide transmembrane transport	0.01%	-1.3851
GO:0097066	response to thyroid hormone	0.00%	-2.217
GO:0051181	cofactor transport	0.11%	-1.6642
GO:0051180	vitamin transport	0.11%	-1.5379
GO:0046339	diacylglycerol metabolic process	0.00%	-2.217
GO:0019722	calcium-mediated signaling	0.04%	-1.5682
GO:0010575	positive regulation of vascular endothelial growth factor production	0.01%	-1.3851
GO:0035149	lumen formation, open tracheal system	0.00%	-1.6623
GO:0044281	small molecule metabolic process	15.14%	-2.0635
GO:0007218	neuropeptide signaling pathway	0.06%	-2.1956
GO:0010677	negative regulation of cellular carbohydrate metabolic process	0.02%	-1.5379
GO:2001046	positive regulation of integrin-mediated signaling pathway	0.00%	-1.3851
GO:0019369	arachidonic acid metabolic process	0.01%	-1.9396
GO:0072348	sulfur compound transport	0.25%	-1.7467
GO:0061668	mitochondrial ribosome assembly	0.00%	-1.3851
GO:0015748	organophosphate ester transport	0.14%	-1.3905
GO:0042133	neurotransmitter metabolic process	0.01%	-1.6775
GO:0051146	striated muscle cell differentiation	0.06%	-2.2326
GO:0030239	myofibril assembly	0.02%	-1.8251
GO:0055001	muscle cell development	0.04%	-1.56
GO:0007520	myoblast fusion	0.01%	-1.6489
GO:0006414	translational elongation	0.78%	-2.3081

GO:0007005	mitochondrion organization	0.42%	-1.5505
GO:0016101	diterpenoid metabolic process	0.02%	-1.3846
GO:0006591	ornithine metabolic process	0.09%	-1.3851
GO:1901566	organonitrogen compound biosynthetic process	14.06%	-7.3257
GO:0006490	oligosaccharide-lipid intermediate biosynthetic process	0.02%	-1.7743
GO:0060037	pharyngeal system development	0.01%	-1.7743
GO:0051851	modification by host of symbiont morphology or physiology	0.01%	-1.517
GO:0055086	nucleobase-containing small molecule metabolic process	4.92%	-7.3051
GO:0055085	transmembrane transport	8.92%	-10.2803
GO:2001170	negative regulation of ATP biosynthetic process	0.00%	-1.3851
GO:0006694	steroid biosynthetic process	0.12%	-2.6072
GO:0016125	sterol metabolic process	0.11%	-1.7478
GO:0006695	cholesterol biosynthetic process	0.01%	-1.7289
GO:0006638	neutral lipid metabolic process	0.04%	-1.9062
GO:0046348	amino sugar catabolic process	0.04%	-3.5054
GO:0006048	UDP-N-acetylglucosamine biosynthetic process	0.03%	-1.3851
GO:0006030	chitin metabolic process	0.08%	-2.1236
GO:0006032	chitin catabolic process	0.02%	-2.5029
GO:0006027	glycosaminoglycan catabolic process	0.15%	-1.7272
GO:0051193	regulation of cofactor metabolic process	0.02%	-1.3416
GO:0071466	cellular response to xenobiotic stimulus	0.05%	-1.7467
GO:0010745	negative regulation of macrophage derived foam cell differentiation	0.00%	-1.3851
GO:1904293	negative regulation of ERAD pathway	0.00%	-1.3851
GO:1904152	regulation of retrograde protein transport, ER to cytosol	0.00%	-1.3851
GO:1903069	regulation of ER-associated ubiquitin-dependent protein catabolic process	0.00%	-1.3851
GO:1903825	organic acid transmembrane transport	0.55%	-3.9379
GO:0046942	carboxylic acid transport	1.02%	-3.8958
GO:0003333	amino acid transmembrane transport	0.48%	-1.9406
GO:0015718	monocarboxylic acid transport	0.16%	-2.8768

GO:0032787	monocarboxylic acid metabolic process	2.49%	-2.0133
GO:0006487	protein N-linked glycosylation	0.08%	-3.0858
GO:0030166	proteoglycan biosynthetic process	0.02%	-2.5529
GO:0006486	protein glycosylation	0.32%	-1.4246
GO:0050880	regulation of blood vessel size	0.03%	-3.2522
GO:0035296	regulation of tube diameter	0.03%	-1.7272
GO:0042310	vasoconstriction	0.02%	-1.3851
GO:0008217	regulation of blood pressure	0.03%	-1.4861
GO:1901264	carbohydrate derivative transport	0.21%	-3.3221
GO:0006995	cellular response to nitrogen starvation	0.01%	-1.6623
GO:0001101	response to acid chemical	0.12%	-1.363
GO:0045297	post-mating behavior	0.00%	-1.3851
GO:0046068	cGMP metabolic process	0.04%	-1.9351
GO:0006869	lipid transport	0.27%	-3.9314
GO:0033344	cholesterol efflux	0.01%	-1.9276
GO:0032376	positive regulation of cholesterol transport	0.00%	-1.6623
GO:0015918	sterol transport	0.03%	-1.6979
GO:0015909	long-chain fatty acid transport	0.04%	-3.327
GO:0010888	negative regulation of lipid storage	0.00%	-1.3851
GO:0009072	aromatic amino acid family metabolic process	0.72%	-1.9276
GO:0045899	positive regulation of RNA polymerase II transcriptional preinitiation complex a	0.01%	-1.6623
GO:0019637	organophosphate metabolic process	6.15%	-6.1797
GO:0006796	phosphate-containing compound metabolic process	13.11%	-1.516
GO:1903513	endoplasmic reticulum to cytosol transport	0.01%	-2.4944
GO:0006855	drug transmembrane transport	0.19%	-2.5029
GO:0015893	drug transport	0.22%	-1.9663
GO:0032527	protein exit from endoplasmic reticulum	0.01%	-2.5029
GO:0090662	ATP hydrolysis coupled transmembrane transport	1.00%	-4.2726
GO:0021885	forebrain cell migration	0.01%	-1.9396

GO:0021795	cerebral cortex cell migration	0.01%	-1.6623
GO:0006949	syncytium formation	0.02%	-1.5963
GO:0043648	dicarboxylic acid metabolic process	1.02%	-1.787
GO:0042445	hormone metabolic process	0.09%	-1.8762
GO:0006811	ion transport	5.34%	-6.3324
GO:0032940	secretion by cell	0.76%	-1.4062
GO:0045055	regulated exocytosis	0.05%	-1.4007
GO:0090317	negative regulation of intracellular protein transport	0.02%	-2.1661
GO:1903959	regulation of anion transmembrane transport	0.08%	-1.6623
GO:0043269	regulation of ion transport	0.24%	-1.698
GO:2000574	regulation of microtubule motor activity	0.01%	-1.3851
GO:0034698	response to gonadotropin	0.00%	-1.3851
GO:0044283	small molecule biosynthetic process	5.68%	-9.9642
GO:0035924	cellular response to vascular endothelial growth factor stimulus	0.01%	-1.3851
GO:0043174	nucleoside salvage	0.15%	-2.217
GO:0043173	nucleotide salvage	0.13%	-1.9396
GO:0006040	amino sugar metabolic process	0.24%	-3.3423
GO:0009225	nucleotide-sugar metabolic process	0.25%	-2.7508
GO:0042026	protein refolding	0.07%	-1.3851
GO:0019228	neuronal action potential	0.01%	-2.4944
GO:0051881	regulation of mitochondrial membrane potential	0.01%	-1.3416
GO:0043277	apoptotic cell clearance	0.01%	-2.0143
GO:0006911	phagocytosis, engulfment	0.01%	-1.3851
GO:1902476	chloride transmembrane transport	0.05%	-3.0802
GO:0000272	polysaccharide catabolic process	0.29%	-2.3409
GO:0044275	cellular carbohydrate catabolic process	0.20%	-1.8597
GO:0006073	cellular glucan metabolic process	0.32%	-1.3881
GO:0034637	cellular carbohydrate biosynthetic process	0.48%	-1.6489
GO:0031102	neuron projection regeneration	0.01%	-1.3416

GO:0009100	glycoprotein metabolic process	0.36%	-4.3678
GO:0046434	organophosphate catabolic process	0.37%	-6.2803
GO:0009083	branched-chain amino acid catabolic process	0.03%	-2.4944
GO:0051384	response to glucocorticoid	0.01%	-1.3679
GO:0070972	protein localization to endoplasmic reticulum	0.19%	-1.6979
GO:0033540	fatty acid beta-oxidation using acyl-CoA oxidase	0.00%	-2.217
GO:1901136	carbohydrate derivative catabolic process	0.42%	-3.9913
GO:0051189	prosthetic group metabolic process	0.23%	-1.3851
GO:0006120	mitochondrial electron transport, NADH to ubiquinone	0.02%	-3.0494
GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c	0.04%	-2.4944
GO:0019233	sensory perception of pain	0.02%	-1.3416
GO:0006631	fatty acid metabolic process	0.88%	-6.612
GO:0072330	monocarboxylic acid biosynthetic process	0.94%	-3.8957
GO:0046394	carboxylic acid biosynthetic process	4.16%	-2.528
GO:0044255	cellular lipid metabolic process	2.70%	-2.0349
GO:0045017	glycerolipid biosynthetic process	0.30%	-2.0382
GO:0006650	glycerophospholipid metabolic process	0.54%	-2.0929
GO:0006661	phosphatidylinositol biosynthetic process	0.12%	-1.5682
GO:1901607	alpha-amino acid biosynthetic process	2.56%	-2.4752
GO:0008654	phospholipid biosynthetic process	0.89%	-4.2196
GO:0043436	oxoacid metabolic process	9.01%	-13.572
GO:0006090	pyruvate metabolic process	0.82%	-4.9371
GO:0006633	fatty acid biosynthetic process	0.62%	-3.37
GO:1901661	quinone metabolic process	0.25%	-2.7508
GO:0070189	kynurenine metabolic process	0.07%	-1.6623
GO:0006744	ubiquinone biosynthetic process	0.14%	-2.0143
GO:0005976	polysaccharide metabolic process	0.91%	-1.6124
GO:0098869	cellular oxidant detoxification	0.78%	-1.6033
GO:0098754	detoxification	0.80%	-1.6489

GO:0006538	glutamate catabolic process	0.02%	-1.6623
GO:0006024	glycosaminoglycan biosynthetic process	0.56%	-1.9351
GO:0001561	fatty acid alpha-oxidation	0.00%	-1.3851
GO:0006536	glutamate metabolic process	0.20%	-1.3882
GO:0002092	positive regulation of receptor internalization	0.00%	-1.7743
GO:0043090	amino acid import	0.01%	-1.5379
GO:0006777	Mo-molybdopterin cofactor biosynthetic process	0.20%	-1.3851
GO:0032324	molybdopterin cofactor biosynthetic process	0.05%	-1.3851
GO:0006022	aminoglycan metabolic process	0.88%	-2.7812
GO:0019321	pentose metabolic process	0.13%	-1.9396
GO:0046364	monosaccharide biosynthetic process	0.28%	-1.6033
GO:0046365	monosaccharide catabolic process	0.12%	-1.5317
GO:0019318	hexose metabolic process	0.64%	-1.8647
GO:0006094	gluconeogenesis	0.26%	-1.7272
GO:0006775	fat-soluble vitamin metabolic process	0.01%	-1.3851
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	0.49%	-5.3439
GO:0009142	nucleoside triphosphate biosynthetic process	0.65%	-4.8324
GO:0015986	ATP synthesis coupled proton transport	0.41%	-3.5054
GO:0006119	oxidative phosphorylation	0.25%	-4.8784
GO:0017004	cytochrome complex assembly	0.21%	-1.517
GO:0043248	proteasome assembly	0.05%	-1.3416
GO:0009166	nucleotide catabolic process	0.14%	-1.9429
GO:0009154	purine ribonucleotide catabolic process	0.01%	-1.7743
GO:1901565	organonitrogen compound catabolic process	1.20%	-1.8151
GO:0009068	aspartate family amino acid catabolic process	0.07%	-1.6646
GO:0019363	pyridine nucleotide biosynthetic process	0.31%	-4.2653
GO:0046496	nicotinamide nucleotide metabolic process	1.14%	-3.7556
GO:0006739	NADP metabolic process	0.36%	-1.388
GO:0006098	pentose-phosphate shunt	0.29%	-2.4944

Chapter 5: supplementary

Supplementary 5.0.0: data for each worker sample selected for WGBS along with ovary score, age and colony queen-status.

Colony	Worker ID	Weight (mg)	Ovary Score	Age at Sampling (days)	Born before or after queen
08	78	281	4.0	17	Before
08	76	270	4.0	16	Before
08	75	283	3.0	16	Before
19	blue	198	4.0	16	Before
19	68	306	4.0	16	Before
19	67	223	2.0	16	Before
23	20	266	3.5	17	Before
23	22	326	4.0	16	Before
23	23	312	4.0	16	Before
37	77	339	4.0	17	Before
37	76	291	4.0	16	Before
37	75	285	4.0	16	Before

Supplementary 5.0.1: Quantity and quality values for all extracted samples. 260/280 and 260/230 values were determined using a Nanodrop 2000 and quantity was determined using a Qubit fluorometer.

Sample	QUBIT Concentration (ng/µl)	Final Volume (µl)	Total DNA (µg)	260/280	260/230
W08	23.0	50.0	1.2	0.8	1.0
W19	26.6	50.0	1.3	1.8	1.1
W23	26.8	50.0	1.3	1.7	0.9
W37	26.0	50.0	1.3	1.8	1.1
Q08	43.8	50.0	2.2	1.8	1.2
Q19	29.8	50.0	1.5	1.8	1.1
Q23	39.8	50.0	2.0	1.8	1.5
Q37	31.6	50.0	1.6	1.8	1.0
M08	39.6	50.0	2.0	1.8	1.0
M19	37.6	50.0	1.9	1.8	1.2
M23	26.4	50.0	1.3	1.8	1.2
M37	42.4	50.0	2.1	1.8	1.0

Supplementary 5.0.2: Alignment data for each sample against the reference genome (Bter_1.0) using Bismark software. Alignment rate shows the percentage of reads that make a unique alignment. Duplicated sequences represents the percentage of sequences removed as they were identified as PCR duplicates.

Sample	Alignment Rate (%)	Duplicated Sequences (%)	Final Coverage
W08	54.6	36.3	12.0
W19	59.4	37.5	14.2
W23	56.1	38.4	13.5
W37	62.8	35.4	12.1
Q08	60.1	37.1	11.6
Q19	56.3	39.7	16.3
Q23	61.9	37.7	15.8
Q37	62.1	41.1	12.3
M08	64.7	25.6	14.1
M19	61.3	27.3	14.7
M23	60.3	27.7	15.0
M37	61.8	27.2	14.4

Supplementary 5.0.3: methylation percentages calculated by the total number of methylated C's divided by the sum of all methylated and unmethylated C's, times by 100. As the lambda genome is unmethylated a 99.5% bisulfite conversion efficiency is assumed.

Sample	CpG Methylation	CHG Methylation	CHH Methylation	Lambda Methylation	Corrected CpG Methylation	Corrected CHG Methylation	Corrected CHH Methylation
M08	0.8	0.5	0.5	0.5	0.3	0	0
M19	0.7	0.5	0.5	0.5	0.2	0	0
M23	0.7	0.5	0.5	0.5	0.2	0	0
M37	0.7	0.5	0.5	0.5	0.2	0	0
Q08	0.7	0.5	0.5	0.5	0.2	0	0
Q19	0.7	0.5	0.5	0.5	0.2	0	0
Q23	0.8	0.5	0.6	0.5	0.3	0	0.1
Q37	0.8	0.5	0.5	0.5	0.3	0	0
W08	0.8	0.5	0.5	0.5	0.3	0	0
W19	0.7	0.5	0.5	0.5	0.2	0	0
W23	0.8	0.5	0.5	0.5	0.3	0	0
W37	0.8	0.5	0.5	0.5	0.3	0	0

Supplementary 5.0.4: differentially methylated CpGs located in genes, found between queens and males and the corresponding geneIDs

chr	position	pvalue	qvalue	meth_diff	geneID
NC_015762.1	437594	0.00634747	0.02641839	25.9259259	LOC100645110
NC_015762.1	906199	0.00037848	0.00349221	-37.300435	LOC100651113
NC_015762.1	2010137	3.68E-05	0.00052536	-31.587057	LOC100651629
NC_015762.1	3653998	0.00062856	0.00521975	-26.358974	LOC100650140
NC_015762.1	4120492	0.0003221	0.00310334	-26.351555	LOC100643434
NC_015762.1	4120492	0.0003221	0.00310334	-26.351555	LOC100643874
NC_015762.1	4212542	0.01981546	0.04121175	-18.981481	LOC100645359
NC_015762.1	4212542	0.01981546	0.04121175	-18.981481	LOC100645477
NC_015762.1	4435199	0.00043181	0.0038663	27.3574561	LOC100647009
NC_015762.1	4469008	0.00321238	0.01716227	18.8804554	LOC100647685
NC_015762.1	5082139	0.02623809	0.04430185	-14.191729	LOC100649952
NC_015762.1	5082178	0.00079137	0.0063161	31.6146881	LOC100649952
NC_015762.1	5112279	0.01314479	0.03737492	-13.939394	LOC100645819
NC_015762.1	7098299	0.00586385	0.0252181	12.4365997	LOC100646331
NC_015762.1	7326658	0.0016967	0.01117536	-18.725172	LOC100643721
NC_015762.1	7345004	0.00513557	0.02356814	15.0829563	LOC100643517
NC_015762.1	11932684	0.00061374	0.00513334	20.8547009	LOC100648926
NC_015762.1	12583435	7.09E-05	0.00091294	24.2924976	LOC100650873
NC_015762.1	16452052	0.00378403	0.01926701	20.7339173	LOC100651946
NC_015763.1	2420285	0.01157307	0.03567824	-18.878074	LOC100644837
NC_015763.1	2465556	5.11E-07	1.44E-05	32.5480154	LOC105665624
NC_015763.1	2465625	3.63E-05	0.00052103	-34.5	LOC105665624
NC_015763.1	8385770	0.00039843	0.00363776	-12.698413	LOC100648426
NC_015763.1	8385770	0.00039843	0.00363776	-12.698413	LOC100644712
NC_015763.1	8385770	0.00039843	0.00363776	-12.698413	LOC105667022
NC_015763.1	8387776	6.63E-07	1.79E-05	-47.740113	LOC100648426

NC_015763.1	10275663	0.01208184	0.03645511	13.4943182	LOC100647720
NC_015764.1	1081801	0.02558354	0.04407771	20.0319872	LOC100645437
NC_015764.1	1198900	0.0016982	0.01117536	17.0160727	LOC100642319
NC_015764.1	1199184	0.00596463	0.02544179	-15.546218	LOC100642319
NC_015764.1	1209507	0.00060672	0.00508678	-16.421569	LOC100652224
NC_015764.1	1209554	0.00244006	0.01442102	18.9083821	LOC100652224
NC_015764.1	3890212	0.02284711	0.042727	22.4537037	LOC100644633
NC_015764.1	8407913	0.00136091	0.00980016	-26.801802	LOC100643758
NC_015764.1	10414346	0.00291073	0.01621726	18.0245133	LOC100645866
NC_015764.1	11166249	0.00035669	0.00334425	-20.885312	LOC105667180
NC_015764.1	12413617	0.00337384	0.01774455	21.1904762	LOC100648741
NC_015764.1	13583819	0.02927822	0.04584883	17.3486088	LOC100642798
NC_015765.1	522953	0.00025152	0.00250637	20.7010711	LOC100649804
NC_015765.1	1839159	1.59E-05	0.00026136	34.5486111	LOC100642683
NC_015765.1	1962016	0.01623795	0.03944691	-12.610169	LOC100643035
NC_015765.1	2412671	3.93E-11	3.05E-09	36.9230769	LOC100643605
NC_015765.1	2412737	1.26E-06	3.19E-05	-42.307692	LOC100643605
NC_015765.1	7438731	0.03118578	0.04668658	11.1111111	LOC100644516
NC_015765.1	11101656	0.01677185	0.03971259	11.8357488	LOC100650920
NC_015765.1	11512508	3.23E-05	0.00047662	30.4156909	LOC100648856
NC_015765.1	11591702	0.00020936	0.00219895	-24.731935	LOC100647893
NC_015766.1	96458	0.00096846	0.0074895	28.3333333	LOC100642364
NC_015766.1	96461	0.01992715	0.04137005	20.6117353	LOC100642364
NC_015766.1	268540	0.02821869	0.04516787	19.9472403	LOC100643402
NC_015766.1	538782	0.00828154	0.03034789	-10.548579	LOC100642803
NC_015766.1	538846	0.0305687	0.04668658	-14.313222	LOC100642803
NC_015766.1	538850	0.02005095	0.04157757	-16.03252	LOC100642803
NC_015766.1	959031	0.00116398	0.00874938	24.002574	LOC100643117
NC_015766.1	998913	0.01201391	0.03637323	20.9090909	LOC105665773

NC_015766.1	1088727	0.01120755	0.03506878	10.1761252	LOC100649840
NC_015766.1	5717695	0.00302696	0.0166258	-14.89888	LOC100644519
NC_015766.1	6190062	0.0042095	0.02053404	22.4561404	LOC100651600
NC_015766.1	7427819	0.00966952	0.0326163	17.948718	LOC100649448
NC_015767.1	2374568	0.00165096	0.010968	-19.047619	LOC100642366
NC_015767.1	4640738	0.01430865	0.03843848	21.2019231	LOC100644252
NC_015767.1	8817997	4.19E-07	1.21E-05	31.6818984	LOC100651639
NC_015767.1	8818024	1.54E-06	3.74E-05	21.028481	LOC100651639
NC_015767.1	8818177	2.58E-06	5.62E-05	30.6034483	LOC100651639
NC_015767.1	8832975	0.00858488	0.03095004	-18.650218	LOC100651680
NC_015767.1	9019658	0.01246644	0.03663041	14.0350877	LOC100642568
NC_015767.1	10937638	0.00232393	0.01399642	22.6293103	LOC100649090
NC_015767.1	11850206	5.42E-05	0.00072877	34.3939394	LOC100648674
NC_015768.1	1536473	0.00550669	0.02425022	25.4755435	LOC100647970
NC_015768.1	2167851	0.00046594	0.00410376	31.714472	LOC100648978
NC_015768.1	4817773	2.21E-09	1.26E-07	23.4375	LOC100647298
NC_015768.1	4817959	1.68E-06	4.00E-05	38.2045539	LOC100647298
NC_015768.1	4818022	1.72E-05	0.00027992	18.792517	LOC100647298
NC_015768.1	4818193	2.17E-10	1.51E-08	40.2794485	LOC100647298
NC_015768.1	7709613	3.40E-05	0.00049174	10.7142857	LOC100645875
NC_015768.1	7709662	0.00135895	0.00980016	-22.5	LOC100645875
NC_015768.1	7709691	0.00218659	0.01337959	13.548282	LOC100645875
NC_015768.1	9064646	9.99E-09	4.98E-07	47.0985155	LOC100646741
NC_015768.1	14817313	3.91E-06	7.87E-05	-27.317968	LOC100645524
NC_015768.1	16109814	0.00010644	0.00128013	13.3333333	LOC100650962
NC_015768.1	17491275	0.0207056	0.04160601	-15.899123	LOC100644607
NC_015768.1	17491314	0.0155768	0.03919596	-19.577206	LOC100644607
NC_015768.1	17491335	0.00466521	0.02225893	-22.364369	LOC100644607
NC_015768.1	17492171	0.00010508	0.00127258	-26.669316	LOC100644607

NC_015768.1	17584947	0.01321651	0.03737492	17.6623377	LOC100646785
NC_015768.1	17584967	0.00282413	0.01581578	31.25	LOC100646785
NC_015769.1	245054	0.01974168	0.0410828	23.3752621	LOC100648677
NC_015769.1	1438431	0.00936669	0.03212295	18.9153439	LOC100643120
NC_015769.1	2933048	0.0091039	0.03155287	11.1681887	LOC100650204
NC_015769.1	3478553	0.0127422	0.03700711	10.962963	LOC100643205
NC_015769.1	3499957	0.02181317	0.04219598	15.9442725	LOC100649260
NC_015769.1	3530563	0.01967631	0.04099983	17.8006776	LOC100649261
NC_015769.1	3530623	0.00075596	0.00604735	15.8974359	LOC100649261
NC_015769.1	3587972	3.65E-07	1.08E-05	13.7931035	LOC100650041
NC_015769.1	4965580	0.00011128	0.00132019	29.0914067	LOC100651406
NC_015769.1	4972748	3.59E-05	0.00051717	22.6857888	LOC100651406
NC_015769.1	5958525	3.36E-06	6.96E-05	-31.410256	LOC100647735
NC_015769.1	8426511	4.91E-05	0.00066952	-26.182432	LOC100648096
NC_015769.1	8426524	0.00010757	0.00128282	-22.202899	LOC100648096
NC_015769.1	8492648	0.00187461	0.01197482	21.9469542	LOC100644808
NC_015770.1	1554528	4.33E-05	0.00060832	-32.058824	LOC100648442
NC_015770.1	4710445	8.06E-08	2.93E-06	26.3372093	LOC100646868
NC_015770.1	7668506	0.00219797	0.01342568	20.0167973	LOC100643207
NC_015770.1	8129365	0.00892381	0.03134375	14.5974576	LOC100652124
NC_015770.1	9671757	0.00444002	0.02138929	24.3478261	LOC100643288
NC_015770.1	9672260	0.02521582	0.04383722	-17.03026	LOC100643288
NC_015770.1	11438053	0.00365777	0.01884418	-26.115978	LOC100649538
NC_015770.1	11528863	0.02770713	0.04496817	16.9811321	LOC100647859
NC_015770.1	11778706	0.02189798	0.04219598	18.9364689	LOC100646064
NC_015770.1	12154972	1.79E-09	1.06E-07	-37.702703	LOC100652317
NC_015770.1	12156521	0.00017497	0.00191908	-27.267312	LOC100652317
NC_015770.1	13470175	5.82E-05	0.00077159	11.6666667	LOC100645380
NC_015770.1	13483097	2.09E-05	0.00032331	36.3502359	LOC100645253

NC_015770.1	13639329	0.0133587	0.03746538	15.3905417	LOC100644811
NC_015770.1	13639329	0.0133587	0.03746538	15.3905417	LOC100644932
NC_015770.1	13639485	0.00315722	0.01696718	-17.353918	LOC100644811
NC_015770.1	13639485	0.00315722	0.01696718	-17.353918	LOC100644932
NC_015771.1	231	0.02402414	0.0433487	14.0873016	LOC100651450
NC_015771.1	1590783	0.00432652	0.02095831	21.5686275	LOC100650567
NC_015771.1	1684253	0.00886745	0.0312299	24.1054001	LOC100650894
NC_015771.1	1977319	2.75E-07	8.73E-06	34.3529412	LOC100646187
NC_015771.1	1977352	0.0204881	0.04160601	21.5130024	LOC100646187
NC_015771.1	2366626	3.22E-07	9.85E-06	25	LOC100643491
NC_015771.1	5825159	0.02684127	0.04455346	-15.043828	LOC100651889
NC_015771.1	11965970	0.00658095	0.02694008	-10.11734	LOC100648288
NC_015771.1	13468464	0.00253524	0.01468833	-26.406926	LOC105666191
NC_015771.1	13468486	0.00052739	0.00453057	-19.472292	LOC105666191
NC_015771.1	13468637	0.00046453	0.00410176	-22.992126	LOC105666191
NC_015772.1	974018	0.02227773	0.04226031	-10.491228	LOC100652166
NC_015772.1	2178531	3.39E-05	0.00049174	29.6187683	LOC100645089
NC_015772.1	2199659	0.00177618	0.01153165	17.2969188	LOC100644970
NC_015772.1	6851729	0.0056201	0.02459439	14.5454546	LOC100647192
NC_015772.1	7171809	0.03446479	0.04847963	15.3146853	LOC100643776
NC_015772.1	7496775	3.51E-10	2.31E-08	48.4848485	LOC100650735
NC_015772.1	7600850	0.00463323	0.02219743	18.579235	LOC100648873
NC_015772.1	7972706	0.00417888	0.02047057	-17.019231	LOC100645844
NC_015772.1	8077648	0.0181297	0.04045219	11.4814815	LOC100644215
NC_015772.1	8077668	0.00019816	0.00210926	10.6060606	LOC100644215
NC_015772.1	8168896	0.00516277	0.02365787	19.5804196	LOC100651892
NC_015772.1	8224590	0.00202759	0.01258329	21.9892473	LOC100650121
NC_015772.1	9553212	2.59E-06	5.62E-05	23.2193732	LOC100651494
NC_015772.1	10067910	0.02119299	0.04170592	18.1003584	LOC100650570

NC_015772.1	12134144	0.01227706	0.03648541	-20.527671	LOC100652318
NC_015772.1	12134156	0.02909428	0.04584883	-15.346386	LOC100652318
NC_015772.1	12211756	0.00148404	0.01031077	22.5259705	LOC100642856
NC_015772.1	14627241	0.00144007	0.0101468	10.1243159	LOC100652132
NC_015772.1	14627951	9.65E-06	0.00016918	14.2329098	LOC100652132
NC_015772.1	14827262	0.00923636	0.03180106	14.633616	LOC100649781
NC_015772.1	15686171	0.00016739	0.00185929	31.5865385	LOC100648221
NC_015772.1	15939990	0.0100292	0.03343986	12.5287356	LOC100643777
NC_015772.1	15940129	1.42E-06	3.51E-05	19.7550492	LOC100643777
NC_015772.1	15940159	0.00263053	0.01506521	11.7835103	LOC100643777
NC_015772.1	15990295	0.00024465	0.00245201	22.542658	LOC100642736
NC_015772.1	16385907	0.01840222	0.04045219	-19.414484	LOC100651216
NC_015772.1	16516255	0.01654617	0.03955417	-22.044025	LOC100642465
NC_015773.1	4243504	2.88E-08	1.13E-06	34.8096348	LOC100642413
NC_015773.1	4334598	5.47E-05	0.00073073	32.7272727	LOC100644186
NC_015773.1	4334866	2.22E-13	2.98E-11	-56.076389	LOC100644186
NC_015773.1	4361543	2.37E-05	0.00036062	32.9044118	LOC100644532
NC_015773.1	4361555	1.04E-05	0.0001797	29.9836601	LOC100644532
NC_015773.1	5754212	0.02932945	0.04584883	-20.721358	LOC100644222
NC_015773.1	5754235	0.00022048	0.00227516	18.8348531	LOC100644222
NC_015773.1	5897430	0.02755694	0.0448847	-16.235151	LOC100643904
NC_015773.1	6718560	1.21E-06	3.08E-05	-45.351823	LOC100652208
NC_015773.1	8693061	0.02230896	0.04226031	13.4272301	LOC100643255
NC_015773.1	8693095	6.97E-05	0.00090378	31.5317036	LOC100643255
NC_015773.1	8708578	0.00010419	0.0012662	-24.871795	LOC100643706
NC_015773.1	8949127	0.0019193	0.012149	19.3910256	LOC100649108
NC_015773.1	8949127	0.0019193	0.012149	19.3910256	LOC100649820
NC_015773.1	8984921	1.73E-07	5.79E-06	39.2307692	LOC105666347
NC_015773.1	8984930	3.42E-07	1.02E-05	37.1551334	LOC105666347

NC_015773.1	9373421	0.00419496	0.02050875	13.1811488	LOC100649591
NC_015773.1	9373660	0.00056427	0.00478844	24.8484849	LOC100649591
NC_015773.1	11566051	4.58E-05	0.00063936	-30.122655	LOC100647938
NC_015773.1	12068871	0.01028937	0.03357074	15.4509804	LOC100647474
NC_015773.1	12093948	0.02116083	0.04170592	12.6988011	LOC100645297
NC_015774.1	6848319	0.00247586	0.01449627	26.9819574	LOC100646601
NC_015774.1	7109145	0.02578154	0.04407771	17.4491393	LOC100644533
NC_015774.1	9413091	0.00038242	0.00351084	-20.238095	LOC100644576
NC_015775.1	734138	7.27E-05	0.00093233	32.0366133	LOC100649470
NC_015775.1	2991731	0.01053015	0.0341964	21.5781871	LOC100647078
NC_015775.1	7869420	0.00015289	0.00172573	13.8461539	LOC100642940
NC_015775.1	7967432	0.00087177	0.00686353	28.062954	LOC100651896
NC_015775.1	8154532	0.00858987	0.03095004	21.9936709	LOC100652055
NC_015775.1	8154538	0.00115075	0.0086686	22.115942	LOC100652055
NC_015775.1	8154550	0.03569658	0.04898219	17.7408177	LOC100652055
NC_015776.1	2420366	0.02485352	0.04380997	-21.801263	LOC100650096
NC_015776.1	3127394	0.03297242	0.04751128	-15.757042	LOC100643060
NC_015776.1	4888188	3.91E-06	7.87E-05	13.559322	LOC100652059
NC_015776.1	4894342	9.40E-07	2.45E-05	32.3684211	LOC100652059
NC_015776.1	4894907	2.61E-08	1.06E-06	22.8627741	LOC100652059
NC_015776.1	4897390	3.13E-07	9.65E-06	35.5018315	LOC100652059
NC_015776.1	4897403	1.33E-11	1.13E-09	42.910102	LOC100652059
NC_015776.1	5120237	6.32E-05	0.00083192	23.5599078	LOC100647824
NC_015776.1	5120244	0.01931609	0.04099983	16.9313525	LOC100647824
NC_015776.1	6037748	0.02233753	0.04226031	16.6666667	LOC100650461
NC_015776.1	7176583	0.0169295	0.03998325	-11.910057	LOC100646364
NC_015776.1	7598074	0.00049733	0.00431487	11.7647059	LOC100643988
NC_015776.1	7598077	0.01245875	0.03663041	11.9929763	LOC100643988
NC_015776.1	9252799	3.31E-07	1.00E-05	46.4393939	LOC100644347

NC_015776.1	9281804	0.0244273	0.04349017	20.952381	LOC100643302
NC_015777.1	3175534	4.03E-10	2.61E-08	-54.631604	LOC100650421
NC_015777.1	3686912	1.15E-09	7.01E-08	16.6632591	LOC100643786
NC_015777.1	3686912	1.15E-09	7.01E-08	16.6632591	LOC100644503
NC_015777.1	4739584	0.00166342	0.01102978	-32.56338	LOC100648726
NC_015777.1	5135893	0.01728451	0.04021731	-16.730524	LOC100651226
NC_015778.1	2814306	0.03636038	0.04942216	10.6086957	LOC100646928
NC_015778.1	3023525	8.16E-08	2.93E-06	-28.548644	LOC100643102
NC_015778.1	3227444	0.01136506	0.03545519	-18.589393	LOC100650381
NC_015778.1	3243961	0.00152478	0.01050713	20.4301075	LOC100650018
NC_015778.1	3255631	0.01504167	0.03880337	-24.636175	LOC100651507
NC_015778.1	3385627	0.00031426	0.0030509	23.3618234	LOC100648492
NC_015778.1	3468190	0.02618166	0.04426373	14.2165052	LOC100648695
NC_015778.1	3468294	0.02893937	0.0456545	-14.466801	LOC100648695
NC_015779.1	2136776	0.00247896	0.01449627	10.6382979	LOC100650940
NC_015779.1	2309544	0.00042339	0.00381572	14.1975309	LOC100646759
NC_015779.1	2309559	4.99E-07	1.42E-05	15.2777778	LOC100646759
NC_015779.1	2716444	2.25E-06	5.12E-05	30.6014151	LOC100649039
NW_0035654(	148623	0.02150066	0.04201107	-27.698864	LOC100647279
NW_0035654(	174439	0.01270403	0.03698579	-27.118644	LOC100647710
NW_0035654(	174497	6.25E-12	5.89E-10	56.5979626	LOC100647710
NW_0035654:	774283	0.00852608	0.0308157	-15.52381	LOC100648347
NW_0035654:	798943	1.52E-05	0.00025129	-26.758621	LOC100648920
NW_0035654!	8967	0.01867491	0.04065801	14.4540456	LOC100647205
NW_0035654!	9018	0.00142715	0.01008552	20	LOC100647205
NW_0035654!	9519	1.90E-05	0.00030139	29.0423862	LOC100647205
NW_0035655!	559711	0.00037678	0.00349221	-14.516129	LOC100642668
NW_0035655!	1461045	0.00521891	0.023659	-21.341772	LOC100647711
NW_0035655(	1905	0.00100148	0.00772777	21.5658136	LOC100643266

NW_0035655	2211	0.02542223	0.04407435	-13.986575	LOC100643266
NW_0035655	2681	0.00885484	0.0312299	-16.680373	LOC100643266
NW_0035655	2755	0.01794908	0.04045219	10.3309353	LOC100643266
NW_0035655	2781	3.28E-05	0.00048005	21.7089284	LOC100643266
NW_0035655	2797	0.00095901	0.00743297	17.2359433	LOC100643266
NW_0035655	2810	0.00152736	0.01050713	12.201087	LOC100643266
NW_0035659	260652	1.76E-07	5.84E-06	17.1381307	LOC100650829
NW_0035659	780953	0.00199205	0.01249613	17.0678864	LOC100648151
NW_0035660	1053131	0.00031491	0.0030509	11.5205725	LOC100651147
NW_0035663	129646	5.17E-05	0.00070122	17.8571429	LOC105666928
NW_0035663	129734	0.00139939	0.0099811	11.5384615	LOC105666928
NW_0035663	389308	0.01107661	0.03493508	12.8503437	LOC100651429
NW_0035663	469406	0.0072465	0.028271	-20.939697	LOC100646328
NW_0035663	900729	0.00025142	0.00250637	29.8076923	LOC100644870
NW_0035663	1609399	0.01884362	0.04094863	20.2068966	LOC100650022
NW_0035663	1638243	0.03015599	0.04651151	16.8125	LOC100650627
NW_0035663	1770848	0.03041112	0.04652086	-19.5	LOC100651511
NW_0035663	1777769	4.21E-07	1.21E-05	23.0908153	LOC100651743
NW_0035663	2082761	1.22E-08	5.64E-07	52.4697581	LOC100643718
NW_0035663	2082761	1.22E-08	5.64E-07	52.4697581	LOC105666950
NW_0035664	1095	0.02456623	0.04369291	-20.797011	LOC100649043
NW_0035664	3239	0.00037765	0.00349221	19.0750213	LOC100649244
NW_0035664	3668	0.00612069	0.02565827	-16.580903	LOC100649244
NW_0035664	3679	7.97E-05	0.00100752	-21.904762	LOC100649244
NW_0035665	395664	0.00021099	0.0022033	21.4912281	LOC100651907
NW_0035665	829844	0.01531541	0.03897564	-16.391941	LOC100645276
NW_0035665	909560	0.00906564	0.03155287	10.0639449	LOC100649523
NW_0035669	300	0.02100084	0.04160601	10.4188526	LOC105667016
NW_0035671	684	2.86E-05	0.00042865	11.4035088	LOC100647326

NW_0035685	576	0.00136278	0.00980016	18.716094	LOC105667038
NW_0035685	582	0.00947141	0.03225805	12.8228944	LOC105667038
NW_0035692	875	0.00244362	0.01442102	-23.835203	LOC100642477
NW_0035703	196	0.00229614	0.01387948	-14.088251	LOC100644791
NW_0035705	500	0.00309669	0.0167972	-12.845538	LOC100645358
NW_0035707	1161	0.00154712	0.01055977	17.8313024	LOC105667080
NC_015762.1	2065589	1.30E-05	0.00022088	19.0476191	LOC100642674
NC_015762.1	4114345	0.0357853	0.04898219	23.2173913	LOC100643434
NC_015762.1	7415101	2.46E-06	5.46E-05	-41.788376	LOC100644474
NC_015763.1	2465457	8.39E-09	4.24E-07	-50.056338	LOC105665624
NC_015763.1	3553787	0.00400934	0.02000913	12.1717962	LOC100651983
NC_015763.1	8805900	0.00072606	0.0058755	12.549221	LOC105667088
NC_015763.1	8805900	0.00072606	0.0058755	12.549221	LOC100650553
NC_015764.1	970138	0.02943775	0.04585647	-11.544012	LOC100646018
NC_015764.1	1081792	5.43E-05	0.00072877	35.0858819	LOC100645437
NC_015764.1	1113051	0.00145001	0.01017572	-13.257278	LOC100644752
NC_015764.1	1211619	0.02599614	0.04407771	-11.733556	LOC100652224
NC_015764.1	6357210	0.00095834	0.00743297	-18.740686	LOC100650717
NC_015764.1	8436131	0.02804991	0.04498033	-17.647059	LOC100651714
NC_015764.1	9050306	0.00094991	0.00739527	-22.410412	LOC100642720
NC_015764.1	9927459	4.75E-05	0.00065273	-35.784314	LOC100646219
NC_015764.1	10828316	0.00600425	0.02544179	13.2519616	LOC100645045
NC_015764.1	14244592	0.0161824	0.03944691	25	LOC100646137
NC_015765.1	2545606	0.00284216	0.01586058	10.1694915	LOC100645187
NC_015765.1	2857541	5.15E-06	0.00010101	-14.440249	LOC100645627
NC_015765.1	11512477	0.01284012	0.03707253	17.2904707	LOC100648856
NC_015766.1	4198359	0.01846519	0.04045219	-25.521822	LOC100645592
NC_015766.1	5135206	0.00132124	0.00960042	-16.24053	LOC100648359
NC_015766.1	7412856	1.60E-06	3.88E-05	-32.532833	LOC105665731

NC_015766.1	9390985	2.41E-07	7.94E-06	-37.04596	LOC100647181
NC_015767.1	4640639	0.03514376	0.04898219	-21.825397	LOC100644252
NC_015767.1	4688149	1.64E-06	3.95E-05	21.1538462	LOC100650925
NC_015767.1	11501218	0.00058183	0.00491355	13.1147541	LOC100647968
NC_015767.1	12496919	0.0001906	0.00205812	22.8110599	LOC100650845
NC_015768.1	322153	0.00060426	0.00507838	13.559322	LOC100647848
NC_015768.1	4818157	0.0069337	0.02757998	17.3930795	LOC100647298
NC_015768.1	5053203	4.93E-06	9.71E-05	13.5135135	LOC100646110
NC_015768.1	11161750	0.00932142	0.03199914	14.1258318	LOC100644135
NC_015768.1	11161772	0.00248546	0.01449627	15.5980861	LOC100644135
NC_015768.1	16109837	0.00034458	0.00324815	16.25	LOC100650962
NC_015768.1	16158542	1.10E-08	5.42E-07	40.2028986	LOC100651805
NC_015769.1	3039777	0.00142848	0.01008552	18.3333333	LOC100651603
NC_015769.1	3545167	0.01449391	0.03843848	-17.352941	LOC100649628
NC_015769.1	4975089	0.00605331	0.02546762	-11.631016	LOC100651406
NC_015769.1	7958155	0.00022501	0.0023082	32.1382429	LOC100645450
NC_015770.1	1065008	0.00419844	0.02050875	-20.21045	LOC100644764
NC_015770.1	1189379	0.00051854	0.00447661	13.4615385	LOC100651720
NC_015770.1	1567391	8.07E-05	0.00101617	-29.666667	LOC100648211
NC_015770.1	9671707	0.00644894	0.02669567	12.3809524	LOC100643288
NC_015770.1	9671713	0.00036302	0.00339443	15.4261705	LOC100643288
NC_015770.1	11517942	0.00399887	0.02000913	22.4969475	LOC100648328
NC_015770.1	11528076	0.03233662	0.04751128	12.6291619	LOC100647859
NC_015771.1	1545563	0.01818902	0.04045219	-12.189055	LOC100650691
NC_015771.1	1977325	0.00019836	0.00210926	14.893617	LOC100646187
NC_015771.1	2351582	2.69E-07	8.65E-06	28.6111111	LOC100648946
NC_015771.1	3823558	0.02551109	0.04407771	-17.601683	LOC100649418
NC_015771.1	9262093	0.00155028	0.01056065	-25.168919	LOC100646066
NC_015771.1	9994075	0.00067009	0.00553823	34.7021944	LOC100652128

NC_015772.1	7968523	0.00246513	0.01449627	-12.155388	LOC100646190
NC_015772.1	7968705	0.0037571	0.01915785	-10.501567	LOC100646190
NC_015772.1	7972717	0.00369241	0.0189946	-16.017316	LOC100645844
NC_015772.1	9386870	0.01020163	0.0334409	15.473109	LOC100643819
NC_015772.1	15939714	0.00021335	0.0022213	-13.218729	LOC100643777
NC_015773.1	222643	8.09E-06	0.0001509	25.3508772	LOC100646479
NC_015773.1	8815633	0.01461766	0.03861444	12.6642772	LOC100648529
NC_015773.1	8815640	0.0143326	0.03843848	11.1488398	LOC100648529
NC_015773.1	9373593	0.00071924	0.00583386	-26.034858	LOC100649591
NC_015774.1	5274066	0.01193053	0.03623397	12.652207	LOC100643708
NC_015775.1	6963860	1.64E-07	5.54E-06	37.4521597	LOC100651419
NC_015775.1	6964102	0.00033805	0.00321267	10.1010101	LOC100651419
NC_015775.1	7264142	0.00566742	0.02470144	-19.49114	LOC100649670
NC_015775.1	7264142	0.00566742	0.02470144	-19.49114	LOC100643014
NC_015776.1	2934377	0.0025282	0.01467189	21.4214047	LOC100651618
NC_015776.1	7176541	0.00674449	0.02728927	18.798151	LOC100646364
NC_015776.1	8637605	0.03198528	0.04739078	-15.95912	LOC100647913
NC_015776.1	9252329	0.02320417	0.04297993	-11.755486	LOC100644347
NC_015776.1	10615520	0.02289456	0.04274748	12.1890547	LOC100642227
NC_015777.1	3146230	0.00085025	0.00670981	18.7739464	LOC100649277
NC_015777.1	3678224	0.0331199	0.04751128	-17.008929	LOC100643786
NC_015778.1	2421210	0.00014476	0.00165001	18.0327869	LOC100645543
NC_015778.1	3023455	0.00012606	0.00147049	-26.645963	LOC100643102
NC_015778.1	3227490	0.00034056	0.00322775	-23.579545	LOC100650381
NC_015778.1	3255647	0.01957116	0.04099983	-21.235103	LOC100651507
NC_015779.1	364097	0.0012295	0.00912392	18.9666137	LOC100652178
NC_015779.1	2203742	1.68E-14	2.66E-12	51.602057	LOC100644154
NW_0035654(	174401	0.00030473	0.00296883	-38.888889	LOC100647710
NW_0035654(	174406	6.73E-05	0.00087919	-37.335526	LOC100647710

NW_0035655(	1851	0.00225137	0.0137278	14.5982906	LOC100643266
NW_0035659(	814370	0.0032132	0.01716227	12.8449281	LOC100649280
NW_0035659(	814375	0.01170828	0.03575832	19.0690078	LOC100649280
NW_0035661(	1286667	0.00011584	0.00136492	15.530303	LOC100645305
NW_0035663(	411475	0.00138485	0.00989766	20.2380952	LOC100645663
NW_0035663(	1474510	2.01E-11	1.67E-09	50.4459309	LOC100646812
NW_0035663(	2217062	0.00155914	0.01060026	-23.817568	LOC100646692
NW_0035663(	2648103	0.02348329	0.04316101	22.1875	LOC100650711
NW_0035664(	503258	0.00174522	0.01139401	-23.848238	LOC100650671
NW_0035664(	506303	0.00020157	0.0021304	18.8679245	LOC100650671
NW_0035665(	392802	0.00185542	0.01187809	-17.171717	LOC100651907
NW_0035665(	393751	8.43E-12	7.35E-10	48.1395349	LOC100651907
NW_0035665(	393923	2.38E-05	0.00036062	21.9889699	LOC100651907
NW_0035692(	954	1.10E-06	2.82E-05	-39.800995	LOC100642477
NC_015762.1	2029630	3.72E-06	7.63E-05	10.4477612	LOC100642191
NC_015762.1	2043196	3.36E-07	1.01E-05	-40.645161	LOC100642314
NC_015762.1	2064183	0.00049615	0.00431487	12.0689655	LOC100642674
NC_015762.1	4435121	1.76E-06	4.14E-05	27.1022727	LOC100647009
NC_015762.1	7326506	0.03461994	0.0486099	-10.615809	LOC100643721
NC_015763.1	10599375	0.01917591	0.04099983	-12.138365	LOC100648009
NC_015763.1	10605796	2.85E-06	6.03E-05	25.1112857	LOC100650355
NC_015764.1	1112964	0.00043608	0.00387234	-21.20743	LOC100644752
NC_015764.1	1211467	0.00140451	0.00999724	-19.047619	LOC100652224
NC_015764.1	1212959	9.30E-06	0.00016458	17.1052632	LOC100652224
NC_015764.1	5505101	0.01554628	0.03919596	11.7661692	LOC100647721
NC_015765.1	11208019	0.00881008	0.03122731	11.3871636	LOC100649652
NC_015766.1	4198517	0.0007375	0.00592682	-26.792453	LOC100645592
NC_015766.1	7427777	0.00070599	0.0057397	-16.887492	LOC100649448
NC_015766.1	7427857	0.00402516	0.02001845	13.5059932	LOC100649448

NC_015768.1	7742569	0.03277529	0.04751128	10.6101695	LOC100647098
NC_015769.1	3036640	4.09E-05	0.00057752	14.5454546	LOC100651603
NC_015769.1	3039331	0.00711417	0.02805323	10.1478768	LOC100651603
NC_015770.1	14498902	0.01165538	0.03575832	11.9230769	LOC100648868
NC_015771.1	1592578	0.00375262	0.01915785	11.5384615	LOC100650567
NC_015771.1	2349371	0.00018937	0.00205752	32.6739795	LOC100648946
NC_015772.1	7910653	0.00734417	0.02842943	16.9158361	LOC105666257
NC_015772.1	8169584	0.00038251	0.00351084	12.6582279	LOC100651892
NC_015772.1	9434904	5.35E-07	1.49E-05	38.3058471	LOC100642412
NC_015773.1	5750560	4.46E-05	0.00062518	15.2941177	LOC100644222
NC_015773.1	8703383	0.00021668	0.00224257	17.5	LOC100643011
NC_015773.1	9373694	0.00851828	0.0308157	-14.802632	LOC100649591
NC_015773.1	11566046	7.06E-05	0.00091148	-27.564103	LOC100647938
NC_015773.1	12093747	0.00072888	0.00588465	16.1290323	LOC100645297
NC_015775.1	915660	0.00109211	0.00832587	10.5947027	LOC100651852
NC_015776.1	4890830	0.00012056	0.00141279	18.7353286	LOC100652059
NC_015777.1	3686978	2.07E-06	4.74E-05	16.4179105	LOC100643786
NC_015777.1	3686978	2.07E-06	4.74E-05	16.4179105	LOC100644503
NC_015777.1	4559878	0.026864	0.04455346	13.7782805	LOC100645391
NC_015778.1	354716	5.47E-08	2.03E-06	-34.451595	LOC100647323
NC_015778.1	1985761	0.00049234	0.00430371	14.8648649	LOC100645779
NC_015779.1	1929622	0.00016954	0.00187717	14.7058824	LOC100650582
NW_0035659	706693	1.24E-08	5.64E-07	32.3529412	LOC100644423
NW_0035659	706723	0.00162229	0.01087669	20.4248366	LOC100644423
NW_0035661	87340	0.00028301	0.0027884	29.0273556	LOC100648119
NW_0035661	87408	1.42E-05	0.00023571	-32.682638	LOC100648119
NW_0035663	2285429	2.32E-06	5.21E-05	23.4126984	LOC100648040
NW_0035663	2298010	0.0136217	0.03782697	-22.612086	LOC100648382
NW_0035665	812021	0.00031733	0.00306584	17.3489279	LOC100645152

NW_0035665	393779	0.0002999	0.00293046	18.2432432	LOC100651907
NW_0035665	459603	0.00579146	0.0250302	12.7674258	LOC100642868
NW_0035665	909236	0.00381068	0.01934618	12.4839125	LOC100649523
NC_015762.1	6229363	1.32E-05	0.00022289	-34.722222	LOC100650429
NC_015762.1	7415056	0.00013079	0.00152055	12.244898	LOC100644474
NC_015763.1	3435203	0.0016768	0.01109736	13.5560676	LOC100651274
NC_015763.1	10600069	1.28E-07	4.42E-06	11.3043478	LOC100648009
NC_015764.1	4369139	0.00044622	0.00395001	15.7932264	LOC100651791
NC_015766.1	96500	0.00128553	0.00939748	11.6425658	LOC100642364
NC_015766.1	3649685	1.81E-05	0.00029057	19.1489362	LOC100649806
NC_015766.1	8460383	0.02731112	0.0448847	-15.6917	LOC100646060
NC_015766.1	8460383	0.02731112	0.0448847	-15.6917	LOC100646177
NC_015767.1	1279262	0.00137612	0.0098555	10.9575013	LOC100642689
NC_015767.1	10937695	0.01558322	0.03919596	-21.794872	LOC100649090
NC_015767.1	11850196	0.00024262	0.00244571	22.5806452	LOC100648674
NC_015768.1	16008517	0.0038251	0.01939117	11.3207547	LOC100650528
NC_015769.1	961217	0.01561755	0.03920651	10.5	LOC105665983
NC_015769.1	3035131	1.26E-07	4.39E-06	16.8405797	LOC100651603
NC_015769.1	3587894	0.00312261	0.01683309	15.3356482	LOC100650041
NC_015769.1	5031790	0.00877075	0.03118149	-16.885031	LOC100651956
NC_015769.1	9255531	6.77E-05	0.00088082	15.4771452	LOC100645525
NC_015770.1	2256080	0.0171282	0.04021731	-15.775401	LOC100642571
NC_015771.1	1711191	0.00055233	0.00472161	12.8205128	LOC100649967
NC_015771.1	7057365	0.001257	0.00922976	19.5701358	LOC100644025
NC_015771.1	7089080	8.97E-05	0.00111288	-18.75	LOC100643659
NC_015772.1	2147964	0.02542517	0.04407435	-15.277778	LOC100644490
NC_015772.1	16728299	3.75E-06	7.64E-05	26.0869565	LOC100647430
NC_015773.1	4334855	3.11E-13	4.02E-11	-59.510442	LOC100644186
NC_015776.1	3617183	6.00E-06	0.0001156	20	LOC100644659

NC_015776.1	7180846	9.00E-07	2.36E-05	25.3521127	LOC100646364
NC_015777.1	2606809	0.00240631	0.01432202	10.4477612	LOC100646203
NW_0035656	5666	0.03152104	0.04684223	18.3876812	LOC100647245
NW_0035663	2080197	3.07E-07	9.58E-06	27.8481013	LOC100643718
NW_0035665	705924	0.02156787	0.04207168	10.1241438	LOC100643677
NC_015762.1	2043047	4.09E-05	0.00057752	-15.09434	LOC100642314
NC_015762.1	11030157	0.00611865	0.02565827	-10.638298	LOC100642436
NC_015762.1	14704509	0.01358386	0.03778121	-16.343883	LOC100646168
NC_015764.1	1191590	2.05E-06	4.74E-05	-23.728814	LOC100642440
NC_015764.1	1191590	2.05E-06	4.74E-05	-23.728814	LOC100646404
NC_015764.1	1209483	6.42E-13	7.35E-11	-43.589744	LOC100652224
NC_015764.1	2293818	3.27E-08	1.27E-06	-31.020769	LOC100648591
NC_015764.1	9050066	6.85E-11	5.19E-09	-38.890057	LOC100642720
NC_015764.1	11042555	2.08E-09	1.21E-07	-31.260504	LOC100651673
NC_015764.1	11042558	0.00014668	0.00166635	-16.259427	LOC100651673
NC_015764.1	11118723	0.01448706	0.03843848	-12.014372	LOC100650635
NC_015765.1	2857448	2.67E-08	1.06E-06	-17.749003	LOC100645627
NC_015766.1	307268	7.13E-12	6.55E-10	-43.079443	LOC100647455
NC_015766.1	538814	0.00336737	0.01774119	-17.054598	LOC100642803
NC_015766.1	4824127	1.75E-05	0.0002838	-20.726571	LOC105665753
NC_015766.1	5765098	6.11E-07	1.68E-05	-25.862069	LOC100644128
NC_015766.1	6173603	0.02327694	0.04309184	-10.204082	LOC100651952
NC_015766.1	6865066	0.00017074	0.00188448	-14.084507	LOC100651599
NC_015766.1	7425065	4.19E-06	8.35E-05	-29.090909	LOC100649448
NC_015766.1	7680025	0.00188031	0.01197778	-10.344828	LOC100649088
NC_015766.1	8068946	2.04E-24	6.71E-22	-25.700209	LOC100647333
NC_015766.1	8068946	2.04E-24	6.71E-22	-25.700209	LOC105665725
NC_015766.1	8068987	7.57E-11	5.62E-09	-11.742416	LOC100647333
NC_015766.1	8068987	7.57E-11	5.62E-09	-11.742416	LOC105665725

NC_015768.1	348954	2.46E-06	5.46E-05	-22.689076	LOC100650560
NC_015768.1	7709850	0.00252373	0.01467041	-13.801958	LOC100645875
NC_015769.1	1438456	0.00027784	0.00274518	-15.407925	LOC100643120
NC_015769.1	2701057	0.00011438	0.00135227	-14.084507	LOC100647538
NC_015769.1	3545179	0.00309358	0.0167972	-17.362637	LOC100649628
NC_015769.1	5230198	0.0008386	0.00664741	-14.885057	LOC100649141
NC_015769.1	9255610	0.00413327	0.02027561	-16.481481	LOC100645525
NC_015770.1	2256190	4.69E-16	8.61E-14	-55.909352	LOC100642571
NC_015770.1	8996649	4.15E-08	1.57E-06	-32.075472	LOC100648640
NC_015770.1	12073667	0.00038712	0.0035438	-13.924051	LOC100644211
NC_015770.1	13318498	3.38E-17	7.36E-15	-32.522819	LOC100643941
NC_015770.1	13319203	2.65E-12	2.72E-10	-17.891374	LOC100643941
NC_015770.1	13319703	1.63E-13	2.27E-11	-24.627584	LOC100643941
NC_015771.1	1545884	0.00653753	0.02682533	-11.901961	LOC100650691
NC_015771.1	5621158	0.00581836	0.02508429	-22.415459	LOC100652130
NC_015771.1	7062694	0.00020841	0.00219604	-25.398048	LOC100644333
NC_015771.1	9260304	3.24E-05	0.00047662	-15.517241	LOC100646066
NC_015771.1	13468667	0.0005003	0.00432991	-14.045699	LOC105666191
NC_015772.1	6372703	0.00036726	0.00342496	-17.180763	LOC100651215
NC_015772.1	7177318	0.00152211	0.01050713	-11.842105	LOC100643457
NC_015772.1	7968508	1.33E-07	4.55E-06	-24.217555	LOC100646190
NC_015772.1	12136189	0.00175343	0.01140969	-23.402256	LOC100652318
NC_015772.1	14827199	9.60E-06	0.00016918	-17.557932	LOC100649781
NC_015772.1	14827210	2.16E-08	9.08E-07	-20	LOC100649781
NC_015772.1	14830311	0.00041062	0.00371409	-16.071429	LOC100649781
NC_015773.1	4335041	0.00032636	0.00311857	-17.886417	LOC100644186
NC_015773.1	5753668	0.00020022	0.00212257	-12.631579	LOC100644222
NC_015773.1	5754605	8.67E-06	0.00015827	-11.881188	LOC100644222
NC_015773.1	7266483	1.46E-08	6.43E-07	-36	LOC100645772

NC_015773.1	8751641	0.00392807	0.01976952	-11.570593	LOC100652133
NC_015773.1	8751656	0.00403493	0.02001845	-10.9375	LOC100652133
NC_015773.1	8752193	1.73E-06	4.10E-05	-26.164875	LOC100652133
NC_015773.1	9384895	0.000617	0.00514821	-20.446669	LOC100649591
NC_015773.1	11566182	0.00207946	0.01288229	-10.294118	LOC100647938
NC_015773.1	12019588	0.00872353	0.031174	-12.334614	LOC100643091
NC_015773.1	12019596	0.00029345	0.0028831	-11.940299	LOC100643091
NC_015773.1	12030767	0.00226303	0.0137591	-10.447761	LOC100644817
NC_015774.1	7190976	0.01287246	0.03713517	-11.654135	LOC100643381
NC_015775.1	7782433	1.33E-05	0.0002238	-23.172669	LOC100643422
NC_015775.1	11078682	0.00019666	0.00210926	-16	LOC100646998
NC_015776.1	4893967	8.36E-06	0.00015509	-18.085106	LOC100652059
NC_015776.1	4894655	1.26E-08	5.64E-07	-28.042929	LOC100652059
NC_015776.1	5279838	1.33E-06	3.34E-05	-21.191756	LOC100644825
NC_015777.1	756923	0.00310771	0.0168047	-21.666667	LOC100649861
NC_015777.1	828175	0.01344641	0.03754862	-10.45584	LOC100650666
NC_015777.1	828175	0.01344641	0.03754862	-10.45584	LOC100651702
NC_015777.1	2641323	0.02648068	0.04447315	-11.565934	LOC100649192
NC_015777.1	3224615	6.46E-06	0.00012383	-28.189117	LOC100651858
NC_015777.1	3791654	0.03633751	0.04941034	-10.25641	LOC100645542
NC_015777.1	4559909	0.00178496	0.01153165	-13.442266	LOC100645391
NC_015778.1	2734887	0.00687883	0.02754522	-17.454545	LOC100631084
NC_015778.1	2828750	0.00162517	0.01087669	-24.514768	LOC100646608
NC_015779.1	2138061	1.22E-16	2.51E-14	-49.056604	LOC100650940
NC_015779.1	2477834	2.13E-12	2.25E-10	-25.806452	LOC105666711
NC_015779.1	2477834	2.13E-12	2.25E-10	-25.806452	LOC105666703
NC_015779.1	2477834	2.13E-12	2.25E-10	-25.806452	LOC105666702
NC_015779.1	2716374	7.46E-06	0.00014148	-26.963563	LOC100649039
NW_0035654(	149751	0.00340177	0.01774455	-19.449847	LOC100647279

NW_0035654	772661	0.0047723	0.02241685	-14.181818	LOC100648347
NW_0035660	1053837	4.70E-06	9.32E-05	-18.085106	LOC100651147
NW_0035660	1219380	4.71E-35	2.35E-32	-42.143405	LOC105666827
NW_0035660	1220116	3.73E-15	6.19E-13	-28.571429	LOC105666827
NW_0035660	1220616	6.24E-18	1.45E-15	-43.75	LOC105666827
NW_0035660	1221555	1.07E-18	2.66E-16	-32.160804	LOC105666827
NW_0035661	26607	0.01010599	0.03343986	-13.943028	LOC100644543
NW_0035661	2135	7.88E-06	0.00014849	-11.16453	LOC105666889
NW_0035661	2197	1.13E-08	5.49E-07	-16.934656	LOC105666889
NW_0035663	1330862	0.00020995	0.00219895	-13.114754	LOC100645179
NW_0035664	505536	1.36E-05	0.00022769	-29.452626	LOC100650671
NW_0035664	505725	3.12E-14	4.54E-12	-55.077805	LOC100650671
NC_015762.1	3654065	5.26E-06	0.00010243	-19.354839	LOC100650140
NC_015762.1	3654075	0.00056049	0.00476795	-11.666667	LOC100650140
NC_015762.1	4741999	0.00142278	0.01008552	-19.221311	LOC100651475
NC_015762.1	5112401	0.00227711	0.01378832	-14.583333	LOC100645819
NC_015762.1	10772775	0.0098889	0.03316385	-10.344828	LOC100649487
NC_015763.1	2590217	3.97E-07	1.16E-05	-35.087719	LOC100645977
NC_015763.1	11720456	2.28E-06	5.17E-05	-13.386613	LOC100642318
NC_015764.1	1213012	7.38E-05	0.00093992	-21.428571	LOC100652224
NC_015764.1	6388930	2.04E-05	0.00031852	-18.181818	LOC100643236
NC_015764.1	6416158	0.00034458	0.00324815	-14.772727	LOC100642991
NC_015764.1	6546721	0.00128154	0.0093902	-20.261438	LOC100651317
NC_015764.1	9050132	6.91E-20	2.01E-17	-61.728395	LOC100642720
NC_015764.1	9050267	0.00063534	0.00526348	-13.258186	LOC100642720
NC_015765.1	7466315	0.00073219	0.00589775	-24.835681	LOC100643926
NC_015765.1	13563109	7.62E-05	0.00096643	-18.644068	LOC100645750
NC_015766.1	5765387	2.68E-06	5.69E-05	-20	LOC100644128
NC_015767.1	4969615	0.00024451	0.00245201	-16.071429	LOC100646021

NC_015767.1	8818237	9.14E-05	0.0011279	-17.924894	LOC100651639
NC_015767.1	8818408	0.00729622	0.02833817	-15.962294	LOC100651639
NC_015767.1	9020359	8.52E-06	0.00015716	-22.413793	LOC100642568
NC_015768.1	455620	0.00763811	0.02917865	-12.763799	LOC100643080
NC_015768.1	455620	0.00763811	0.02917865	-12.763799	LOC100649377
NC_015768.1	455633	8.95E-05	0.00111288	-15.151515	LOC100643080
NC_015768.1	455633	8.95E-05	0.00111288	-15.151515	LOC100649377
NC_015768.1	576668	1.92E-06	4.48E-05	-17.857143	LOC100648438
NC_015768.1	576668	1.92E-06	4.48E-05	-17.857143	LOC105665864
NC_015768.1	2836089	1.89E-05	0.00030139	-15.714286	LOC100642726
NC_015768.1	9065050	1.21E-05	0.0002076	-24.193548	LOC100646741
NC_015769.1	588141	0.00412624	0.02026962	-13.51953	LOC100647101
NC_015769.1	8426544	0.00041043	0.00371409	-14.464565	LOC100648096
NC_015770.1	13482057	0.00010777	0.00128282	-17.647059	LOC100645253
NC_015771.1	1533205	0.00059978	0.00505294	-13.043478	LOC100642495
NC_015771.1	7089071	6.43E-07	1.75E-05	-23.361823	LOC100643659
NC_015771.1	7089077	0.00087635	0.00688407	-15.574549	LOC100643659
NC_015771.1	9262045	0.00809045	0.03001892	-14.181818	LOC100646066
NC_015771.1	13468678	6.60E-08	2.42E-06	-18.421053	LOC105666191
NC_015772.1	1897790	0.00015617	0.00175559	-19.574402	LOC100647155
NC_015772.1	1897828	0.0015208	0.01050713	-17.849462	LOC100647155
NC_015772.1	7177211	0.00560534	0.02456059	-10.144928	LOC100643457
NC_015772.1	10721112	0.01080194	0.03448103	-12.527281	LOC100647867
NC_015772.1	12134464	0.03013297	0.04651151	-13.888889	LOC100652318
NC_015773.1	4372610	0.00042943	0.00386016	-17.1875	LOC100644652
NC_015774.1	5050073	0.00034962	0.0032868	-19.638868	LOC100645808
NC_015774.1	7190955	0.03201803	0.04739902	-10.004675	LOC100643381
NC_015775.1	2454600	7.30E-05	0.00093275	-15.384615	LOC100643907
NC_015775.1	2993779	0.00013481	0.00155686	-17.460317	LOC100647078

NC_015775.1	6320989	0.00439428	0.02125419	-11.47541	LOC100648298
NC_015775.1	7908188	1.40E-06	3.48E-05	-26.666667	LOC100650786
NC_015775.1	8149859	0.02758191	0.0448847	-10.431373	LOC100647437
NC_015775.1	8547490	0.00062549	0.00520658	-16.666667	LOC100651463
NC_015775.1	8547490	0.00062549	0.00520658	-16.666667	LOC105666490
NC_015775.1	8935701	0.02664709	0.04455346	-12.822014	LOC100643058
NC_015776.1	4890425	0.00089683	0.00702907	-11.25	LOC100652059
NC_015776.1	4890602	0.00340212	0.01774455	-13.043478	LOC100652059
NC_015776.1	5279811	6.62E-05	0.00086755	-17.032475	LOC100644825
NC_015776.1	7176423	2.94E-06	6.17E-05	-21.872104	LOC100646364
NC_015776.1	7176437	0.00043233	0.0038663	-10.909091	LOC100646364
NC_015776.1	7897245	0.03646557	0.04949087	-17.185762	LOC100651857
NC_015778.1	3355045	1.27E-05	0.0002158	-26.945003	LOC100648918
NC_015779.1	2477885	4.01E-08	1.54E-06	-18.58762	LOC105666711
NC_015779.1	2477885	4.01E-08	1.54E-06	-18.58762	LOC105666703
NC_015779.1	2477885	4.01E-08	1.54E-06	-18.58762	LOC105666702
NW_0035654	772664	0.00109331	0.00832587	-16.736318	LOC100648347
NW_0035654	772674	5.78E-06	0.00011194	-19.444444	LOC100648347
NW_0035660	1053861	0.00603988	0.02544179	-14.945055	LOC100651147
NW_0035660	93900	9.15E-06	0.00016366	-24.615385	LOC100650586
NW_0035661	759169	8.23E-07	2.18E-05	-27.777778	LOC100650987
NW_0035661	87406	2.74E-05	0.00041226	-21.188406	LOC100648119
NW_0035661	2314	0.00057114	0.00483498	-14.922169	LOC105666889
NW_0035663	1330866	0.00041105	0.00371409	-13.114754	LOC100645179
NW_0035663	2151113	0.01157199	0.03567824	-10.168599	LOC100645971
NW_0035663	2240735	0.00081446	0.0064708	-15.584416	LOC100646571
NW_0035671	815	8.63E-10	5.47E-08	-24.817518	LOC100647326
NC_015762.1	564570	0.00325993	0.01738521	-14.243697	LOC100642190
NC_015762.1	564572	0.00464599	0.02222803	-12.857143	LOC100642190

NC_015762.1	4429997	0.00026057	0.00258917	-16.326531	LOC100647009
NC_015762.1	6978461	2.44E-10	1.67E-08	-27.941176	LOC100644873
NC_015763.1	2491414	0.00114171	0.00861916	-15.789474	LOC100646616
NC_015764.1	959515	0.00307239	0.01671739	-14.274322	LOC100646218
NC_015764.1	6355560	0.03324005	0.04751128	-10.705731	LOC100650717
NC_015764.1	9050155	0.00708519	0.02798598	-12.51634	LOC100642720
NC_015765.1	2464228	0.03304364	0.04751128	-14.411765	LOC100644840
NC_015765.1	7484838	0.00043633	0.00387234	-13.114754	LOC100643799
NC_015768.1	2408268	0.00047501	0.00417315	-13.235294	LOC100648475
NC_015768.1	6648282	0.02735305	0.0448847	-14.039855	LOC100648322
NC_015769.1	588018	0.00148376	0.01031077	-12.940452	LOC100647101
NC_015769.1	588213	0.00048868	0.00428248	-12.150785	LOC100647101
NC_015770.1	13318619	4.27E-09	2.29E-07	-24.719101	LOC100643941
NC_015770.1	13318637	0.00015159	0.00171658	-14.666667	LOC100643941
NC_015770.1	14498831	0.02096048	0.04160601	-12.446074	LOC100648868
NC_015770.1	15302465	0.00796963	0.02992074	-15.249663	LOC100652165
NC_015771.1	169171	0.01792214	0.04045219	-11.111111	LOC100650410
NC_015771.1	6804697	0.00119428	0.00892879	-16.612554	LOC100645763
NC_015772.1	7968454	0.00037542	0.00349167	-14.285714	LOC100646190
NC_015772.1	7968757	2.05E-05	0.00031852	-19.69697	LOC100646190
NC_015773.1	8700597	2.00E-08	8.51E-07	-17.44186	LOC100643011
NC_015773.1	8701719	0.00014189	0.00163009	-18.26368	LOC100643011
NC_015774.1	4999343	0.00350511	0.01813811	-11.594203	LOC100647115
NC_015774.1	5105363	1.91E-05	0.00030193	-18.055556	LOC100643340
NC_015775.1	127859	0.00529526	0.02375013	-14.95042	LOC100646678
NC_015776.1	4894609	3.06E-05	0.00045682	-12.790698	LOC100652059
NC_015776.1	4894615	9.32E-08	3.29E-06	-19.101124	LOC100652059
NC_015777.1	4798261	8.94E-06	0.00016158	-14.457831	LOC100648957
NW_0035656	38807	0.00263889	0.01508835	-12	LOC100646761

NW_0035657(	1559	2.62E-05	0.00039609	-13.157895	LOC100649789
NW_0035659(	707457	1.90E-05	0.00030139	-20.338983	LOC100644423
NW_0035661(	759206	3.37E-06	6.96E-05	-21.538462	LOC100650987
NW_0035665(	392737	5.53E-13	6.89E-11	-33.501471	LOC100651907
NC_015766.1	448264	0.00428707	0.02082503	-11.111111	LOC100647063
NC_015766.1	4824129	9.25E-06	0.00016458	-15.789474	LOC105665753
NC_015767.1	10892454	2.57E-07	8.37E-06	-14.705882	LOC100647967
NC_015767.1	10892650	0.00056031	0.00476795	-19.047619	LOC100647967
NC_015768.1	2408270	0.00013259	0.00153639	-15.942029	LOC100648475
NC_015768.1	7712465	0.00162786	0.01087669	-11.764706	LOC100645875
NC_015768.1	7712468	0.016581	0.03955955	-13.636364	LOC100645875
NC_015769.1	2721821	0.01052344	0.0341964	-10.416667	LOC100647777
NC_015769.1	3113048	0.00255444	0.01472621	-10.416667	LOC100642211
NC_015769.1	3631961	0.00312261	0.01683309	-22.3093	LOC100651604
NC_015769.1	7947731	0.00147427	0.01030446	-12.676056	LOC100645250
NC_015771.1	169241	0.00019836	0.00210926	-10.769231	LOC100650410
NC_015772.1	2280891	0.00024057	0.00244359	-15.517241	LOC100651455
NC_015772.1	7514961	0.00010722	0.00128282	-16.666667	LOC100650368
NC_015772.1	7519398	2.54E-06	5.61E-05	-14.285714	LOC100650491
NC_015775.1	130102	0.00294293	0.01629255	-11.25	LOC100646678
NC_015775.1	8149940	0.00412328	0.02026962	-10.465116	LOC100647437
NC_015779.1	2203814	0.00029995	0.00293046	-15.189873	LOC100644154
NC_015779.1	2203823	0.00157953	0.01069719	-11.688312	LOC100644154
NW_0035655(	625653	1.93E-06	4.48E-05	-18.461538	LOC100631054
NW_0035657(	1670	1.80E-05	0.00029016	-13.513514	LOC100649789

Supplementary 5.0.5: genes with at least one differentially methylated CpG between males and queens and a minimum weighted methylation difference of at least 10%.

geneID	males	queens	percentage diff	hypermethylated
LOC100631084	0.06666667	0.19358974	-65.56291391	queen
LOC100642190	0.04294418	0.17452627	-75.39385774	queen
LOC100642191	0.10637398	0.05815848	82.90364568	male
LOC100642211	0.02631579	0.04733547	-44.4057725	queen
LOC100642227	0.16372549	0.04679803	249.8555212	male
LOC100642314	0.11554622	0.26028574	-55.6079334	queen
LOC100642318	0.00588235	0.08039032	-92.68275957	queen
LOC100642364	0.53848977	0.23741889	126.8099904	male
LOC100642366	0.31594902	0.52314815	-39.60620431	queen
LOC100642412	0.10208333	0.04651163	119.4791667	male
LOC100642413	0.87016603	0.43143143	101.6927754	male
LOC100642436	0.00914634	0.05645625	-83.79923974	queen
LOC100642440	0.14833333	0.24232712	-38.78797595	queen
LOC100642477	0.31352502	0.56918768	-44.91711076	queen
LOC100642495	0	0.13283057	-100	queen
LOC100642568	0.08342603	0.13252197	-37.04739961	queen
LOC100642571	0.0773528	0.24475123	-68.39533841	queen
LOC100642674	0.02668064	0.02232461	19.51226267	male
LOC100642683	0.58130146	0.42667357	36.240326	male
LOC100642689	0.62215321	0.50998161	21.99522365	male
LOC100642720	0.10084409	0.21323103	-52.70665467	queen
LOC100642726	0.08483285	0.11206546	-24.30063401	queen
LOC100642736	0.56570107	0.41499026	36.31670976	male
LOC100642803	0.41055327	0.50445501	-18.61449285	queen
LOC100642856	0.60694444	0.50729271	19.64383397	male
LOC100642868	0.16465246	0.06666667	146.9786899	male

LOC100642940	0.06290236	0	100	male
LOC100642991	0.01973684	0.12937105	-84.74400369	queen
LOC100643014	0.20004112	0.35482679	-43.62288244	queen
LOC100643058	0.10084034	0.15434272	-34.66466434	queen
LOC100643060	0.50784196	0.58839871	-13.69084487	queen
LOC100643080	0.00170068	0.04901961	-96.53061224	queen
LOC100643091	0.01315789	0.16693548	-92.1179761	queen
LOC100643102	0.50825207	0.83456486	-39.09975188	queen
LOC100643117	0.3178219	0.16809117	89.07709708	male
LOC100643205	0.05961538	0	100	male
LOC100643236	0.02308007	0.08622482	-73.23268984	queen
LOC100643255	0.55597868	0.28935249	92.14581278	male
LOC100643288	0.32282945	0.22543784	43.20109261	male
LOC100643340	0	0.125	-100	queen
LOC100643381	0.03709479	0.12557397	-70.45980437	queen
LOC100643402	0.4156259	0.46430026	-10.4833792	queen
LOC100643422	0.04788702	0.14471778	-66.91006289	queen
LOC100643434	0.18885359	0.23492272	-19.61033538	queen
LOC100643457	0.0601972	0.12664231	-52.46675625	queen
LOC100643491	0.2625	0	100	male
LOC100643605	0.54670761	0.45678177	19.68682807	male
LOC100643659	0.11431713	0.21440153	-46.68082187	queen
LOC100643677	0.265625	0	100	male
LOC100643706	0.65037879	0.86896437	-25.15472313	queen
LOC100643708	0.40024281	0.34968072	14.45950416	male
LOC100643718	0.17077503	0.13301131	28.39136511	male
LOC100643721	0.11727964	0.1935532	-39.40702715	queen
LOC100643758	0.20514496	0.276711	-25.86309923	queen
LOC100643799	0	0.11111111	-100	queen

LOC100643819	0.34961089	0.1857066	88.2598088	male
LOC100643874	0.12418696	0.2385595	-47.94298226	queen
LOC100643904	0.68123543	0.79292929	-14.08623224	queen
LOC100643907	0.03070175	0.1049348	-70.74206527	queen
LOC100643926	0.04058442	0.14583333	-72.17068646	queen
LOC100643941	0.01054865	0.10058662	-89.51286813	queen
LOC100644025	0.21390374	0.09259259	131.0160428	male
LOC100644128	0.02157738	0.17391304	-87.59300595	queen
LOC100644135	0.18727615	0.14226289	31.64090484	male
LOC100644154	0.08959172	0.02207977	305.7637978	male
LOC100644186	0.45314195	0.57902878	-21.74103064	queen
LOC100644211	0.09253717	0.18916982	-51.08248701	queen
LOC100644215	0.15845221	0.10374636	52.73038624	male
LOC100644222	0.24206409	0.19984302	21.12711483	male
LOC100644333	0.03571429	0.28162393	-87.31844786	queen
LOC100644347	0.44666086	0.3968599	12.54874974	male
LOC100644423	0.1702183	0.08696928	95.72232437	male
LOC100644474	0.33620275	0.42231135	-20.38983856	queen
LOC100644490	0.11458333	0.1959707	-41.53037383	queen
LOC100644503	0.20888482	0.15018375	39.08616357	male
LOC100644519	0.56058976	0.65531612	-14.45506397	queen
LOC100644532	0.77540486	0.35870418	116.168338	male
LOC100644533	0.55575403	0.40625	36.80099165	male
LOC100644543	0.03571429	0.14444444	-75.27472527	queen
LOC100644576	0.62920594	0.74409053	-15.43959807	queen
LOC100644633	0.26664223	0.19930502	33.78600783	male
LOC100644652	0.08487805	0.10758998	-21.10971175	queen
LOC100644659	0.07482803	0	100	male
LOC100644712	0.86767399	1	-13.23260073	queen

LOC100644752	0.30640562	0.41873121	-26.8252268	queen
LOC100644764	0.42454436	0.54273772	-21.77725274	queen
LOC100644791	0.07332292	0.1397648	-47.53834676	queen
LOC100644808	0.17125636	0.0850502	101.3591568	male
LOC100644817	0.30698563	0.34123906	-10.03795609	queen
LOC100644825	0.01388889	0.28153174	-95.06667033	queen
LOC100644840	0.05	0.16666667	-70	queen
LOC100644870	0.42044326	0.33269476	26.37507504	male
LOC100644873	0	0.11666667	-100	queen
LOC100645089	0.11169837	0.05324446	109.7840373	male
LOC100645110	0.38247648	0.27762923	37.76520349	male
LOC100645152	0.15524566	0.05050505	207.3863971	male
LOC100645179	0.0793749	0.20992104	-62.1882106	queen
LOC100645187	0.1	0	100	male
LOC100645250	0	0.05833333	-100	queen
LOC100645253	0.13933572	0.11382895	22.40797545	male
LOC100645276	0.81370192	0.94411765	-13.81350347	queen
LOC100645297	0.12769089	0.08893319	43.5807011	male
LOC100645305	0.12940368	0.07217474	79.29221031	male
LOC100645358	0.32996099	0.37131192	-11.13644079	queen
LOC100645359	0.10213877	0.18706691	-45.39987079	queen
LOC100645380	0.11961538	0.01666667	617.6923077	male
LOC100645437	0.55143415	0.3132249	76.05054775	male
LOC100645450	0.33035714	0.15238095	116.796875	male
LOC100645477	0.10213877	0.18706691	-45.39987079	queen
LOC100645524	0.76254181	0.93833944	-18.73497214	queen
LOC100645525	0.11111111	0.06891162	61.2371134	male
LOC100645542	0.03485577	0.18333333	-80.98776224	queen
LOC100645543	0.15277778	0	100	male

LOC100645592	0.28524913	0.39593503	-27.9555715	queen
LOC100645627	0.24543457	0.31031254	-20.90729856	queen
LOC100645750	0.06175595	0.15838804	-61.00971296	queen
LOC100645763	0.04166667	0.13888889	-70	queen
LOC100645772	0	0.42407407	-100	queen
LOC100645779	0.125	0	100	male
LOC100645808	0.07682494	0.11174735	-31.25122086	queen
LOC100645819	0.58384767	0.64890009	-10.02502857	queen
LOC100645866	0.14385577	0.17937421	-19.80130679	queen
LOC100645971	0.05828408	0.03594718	62.13811563	male
LOC100645977	0.19031788	0.3391286	-43.88032116	queen
LOC100646018	0.0588411	0.14018379	-58.0257475	queen
LOC100646021	0	0.14285714	-100	queen
LOC100646064	0.51455939	0.36800644	39.82347342	male
LOC100646066	0.12575758	0.26473471	-52.49675559	queen
LOC100646110	0.17261905	0	100	male
LOC100646137	0.61750801	0.53285799	15.88603764	male
LOC100646168	0.13011842	0.20230399	-35.6817302	queen
LOC100646187	0.44834798	0.19305743	132.2355456	male
LOC100646190	0.07973838	0.15633357	-48.99471371	queen
LOC100646203	0.07608696	0	100	male
LOC100646219	0.38181818	0.71367521	-46.49972782	queen
LOC100646328	0.29433761	0.52361111	-43.78698225	queen
LOC100646364	0.11661633	0.14308329	-18.49759254	queen
LOC100646404	0.14833333	0.24232712	-38.78797595	queen
LOC100646479	0.17470665	0.00980392	1682.007823	male
LOC100646571	0.04556452	0.08495852	-46.36851495	queen
LOC100646601	0.67579629	0.54012912	25.11754225	male
LOC100646608	0.03846154	0.24033438	-83.99665552	queen

LOC100646616	0	0.13752914	-100	queen
LOC100646678	0.12928304	0.1525666	-15.2612406	queen
LOC100646692	0.32993421	0.59961168	-44.97535272	queen
LOC100646741	0.20898067	0.12036901	73.61667243	male
LOC100646761	0	0.14141414	-100	queen
LOC100646785	0.68292749	0.45845721	48.96210182	male
LOC100646812	0.18718539	0.0448654	317.2154317	male
LOC100646868	0.20196078	0.08632479	133.9545719	male
LOC100646928	0.12717326	0.07205806	76.48721776	male
LOC100646998	0	0.21367521	-100	queen
LOC100647009	0.21224449	0.09375516	126.3816563	male
LOC100647098	0.13461538	0.04647436	189.6551724	male
LOC100647101	0.03941735	0.15144662	-73.97277703	queen
LOC100647155	0.02272727	0.20496894	-88.91184573	queen
LOC100647181	0.64807708	0.72944526	-11.15480298	queen
LOC100647192	0.46163511	0.41683389	10.74797902	male
LOC100647205	0.38998492	0.23629563	65.04110398	male
LOC100647245	0.14655172	0.1025641	42.88793103	male
LOC100647279	0.37835852	0.51673998	-26.77970918	queen
LOC100647298	0.22633451	0.12258836	84.62969353	male
LOC100647323	0.16228884	0.3214436	-49.51249938	queen
LOC100647326	0.09662399	0.1206742	-19.92986704	queen
LOC100647333	0.00699373	0.13443829	-94.79781248	queen
LOC100647430	0.07539683	0.05691057	32.4829932	male
LOC100647437	0.05216863	0.08076663	-35.40818856	queen
LOC100647455	0.0125	0.54282766	-97.69724335	queen
LOC100647474	0.44026759	0.33258493	32.37749339	male
LOC100647538	0.06471107	0.20391796	-68.26612311	queen
LOC100647685	0.83240117	0.73293293	13.57126015	male

LOC100647710	0.5529281	0.62268002	-11.20188739	queen
LOC100647711	0.27570551	0.31455851	-12.3515983	queen
LOC100647720	0.63298277	0.55605005	13.83557562	male
LOC100647721	0.13235294	0.02380952	455.8823529	male
LOC100647735	0.54122807	0.88550625	-38.87924895	queen
LOC100647777	0	0.05401235	-100	queen
LOC100647824	0.8210433	0.72073579	13.91737605	male
LOC100647848	0.14354067	0	100	male
LOC100647859	0.31274704	0.09571346	226.7534688	male
LOC100647867	0.01041667	0.07575758	-86.25	queen
LOC100647893	0.61500548	0.7194017	-14.51153371	queen
LOC100647913	0.12401848	0.15417978	-19.56242444	queen
LOC100647938	0.13624063	0.28512585	-52.21736944	queen
LOC100647968	0.0311899	0.04233871	-26.33241758	queen
LOC100647970	0.73461538	0.48962121	50.03749152	male
LOC100648040	0.22004608	0.02777778	692.1658986	male
LOC100648096	0.07682042	0.15138006	-49.2532783	queen
LOC100648221	0.47689316	0.34622426	37.74111821	male
LOC100648298	0	0.07832254	-100	queen
LOC100648322	0.08764629	0.11386995	-23.029478	queen
LOC100648328	0.25769231	0.1	157.6923077	male
LOC100648347	0.30604973	0.40106595	-23.69092259	queen
LOC100648359	0.12248168	0.26818182	-54.32886323	queen
LOC100648382	0.09090909	0.33333333	-72.72727273	queen
LOC100648426	0.65219913	0.92735043	-29.67069296	queen
LOC100648438	0.01837336	0.04649115	-60.4798716	queen
LOC100648442	0.27824755	0.52162411	-46.65745995	queen
LOC100648475	0.28451303	0.25722024	10.61067272	male
LOC100648492	0.22632162	0.0955501	136.8617407	male

LOC100648529	0.13905162	0.02502769	455.5912099	male
LOC100648591	0.02380952	0.32467532	-92.66666667	queen
LOC100648640	0	0.25925926	-100	queen
LOC100648674	0.24757241	0.05692289	334.9259139	male
LOC100648677	0.61858974	0.3364899	83.83605138	male
LOC100648726	0.4552032	0.61554119	-26.04829522	queen
LOC100648741	0.87330044	0.6468254	35.01331934	male
LOC100648856	0.32933083	0.12171717	170.5705589	male
LOC100648868	0.13792957	0.16104295	-14.35231044	queen
LOC100648873	0.1526585	0.06451613	136.620671	male
LOC100648918	0.35478453	0.41616328	-14.74871941	queen
LOC100648920	0.18475702	0.37236722	-50.38311399	queen
LOC100648926	0.57722222	0.50261233	14.84442134	male
LOC100648946	0.23639956	0.09000338	162.6563205	male
LOC100648957	0.03658537	0.08148148	-55.09977827	queen
LOC100648978	0.64166667	0.34032634	88.54452055	male
LOC100649039	0.21474516	0.2809229	-23.55726025	queen
LOC100649088	0	0.04731638	-100	queen
LOC100649108	0.3025641	0.09259259	226.7692308	male
LOC100649141	0.03645833	0.2793481	-86.94878077	queen
LOC100649244	0.31663475	0.37201358	-14.88623902	queen
LOC100649260	0.246875	0.11111111	122.1875	male
LOC100649261	0.78564099	0.60154062	30.60481113	male
LOC100649277	0.10576151	0.01129944	835.9893338	male
LOC100649280	0.39336537	0.33984935	15.74698067	male
LOC100649377	0.00170068	0.04901961	-96.53061224	queen
LOC100649418	0.14826303	0.23976024	-38.16196237	queen
LOC100649448	0.22780825	0.20493184	11.16293818	male
LOC100649470	0.44514547	0.31596036	40.88649243	male

LOC100649487	0	0.06944444	-100	queen
LOC100649523	0.0876289	0.02559556	242.359728	male
LOC100649538	0.2	0.42962963	-53.44827586	queen
LOC100649628	0.24901258	0.47355711	-47.41656899	queen
LOC100649652	0.14311497	0.02298851	522.5501337	male
LOC100649670	0.30336681	0.35035842	-13.41243907	queen
LOC100649781	0.0581769	0.13027211	-55.34201571	queen
LOC100649789	0.00543542	0.08070882	-93.26538949	queen
LOC100649820	0.3025641	0.09259259	226.7692308	male
LOC100649861	0.36590235	0.47545455	-23.04157007	queen
LOC100649967	0.21043019	0.08380952	151.0814824	male
LOC100650022	0.84752747	0.6468254	31.02878716	male
LOC100650041	0.16124461	0.03795877	324.7887906	male
LOC100650096	0.42321429	0.66258741	-36.12702601	queen
LOC100650121	0.90527009	0.68888889	31.41017468	male
LOC100650140	0.1852081	0.32861683	-43.64010434	queen
LOC100650204	0.15598739	0.04691358	232.4994471	male
LOC100650355	0.18472222	0.05012531	268.5208333	male
LOC100650368	0	0.10128205	-100	queen
LOC100650381	0.46382447	0.58210781	-20.31983349	queen
LOC100650410	0	0.04487179	-100	queen
LOC100650421	0.14642857	0.52380952	-72.04545455	queen
LOC100650461	0.35530303	0.14285714	148.7121212	male
LOC100650491	0	0.03205128	-100	queen
LOC100650528	0.06108877	0	100	male
LOC100650553	0.12079832	0.01041667	1059.663866	male
LOC100650560	0.06489469	0.0970747	-33.14973843	queen
LOC100650567	0.48314591	0.25520095	89.31979627	male
LOC100650570	0.48616895	0.32195647	51.0045575	male

LOC100650582	0.14895833	0	100	male
LOC100650586	0	0.21302521	-100	queen
LOC100650627	0.7106489	0.64556678	10.08139295	male
LOC100650635	0.01058378	0.12222222	-91.34054448	queen
LOC100650671	0.42157819	0.56536795	-25.43295166	queen
LOC100650691	0.05945323	0.14782448	-59.78120312	queen
LOC100650711	0.42965368	0.26587302	61.60108548	male
LOC100650717	0.22864248	0.33363871	-31.47003831	queen
LOC100650735	0.44395877	0.19644101	126.0010671	male
LOC100650786	0	0.15315315	-100	queen
LOC100650829	0.195924	0.1512091	29.57156427	male
LOC100650845	0.38146147	0.14954052	155.0890363	male
LOC100650873	0.58579637	0.43342912	35.15390214	male
LOC100650894	0.21625881	0.08421053	156.8073322	male
LOC100650920	0.20995447	0.12946128	62.17549522	male
LOC100650925	0.19642857	0	100	male
LOC100650940	0.02272727	0.14333333	-84.14376321	queen
LOC100650962	0.05563226	0.0137457	304.7246953	male
LOC100650987	0	0.21679438	-100	queen
LOC100651113	0.45265152	0.76111111	-40.52753816	queen
LOC100651147	0.0665333	0.09320264	-28.61435464	queen
LOC100651215	0.025	0.30727273	-91.86390533	queen
LOC100651216	0.63977273	0.84126984	-23.95154374	queen
LOC100651226	0.62642983	0.55559215	12.74994293	male
LOC100651274	0.10436329	0.16444444	-36.5358355	queen
LOC100651317	0.01666667	0.25	-93.33333333	queen
LOC100651406	0.27107185	0.246174	10.11392109	male
LOC100651429	0.06344246	0.04416667	43.64330638	male
LOC100651450	0.45054368	0.37339603	20.66107986	male

LOC100651455	0.0661582	0.0998053	-33.71273731	queen
LOC100651463	0.03125	0.07317073	-57.29166667	queen
LOC100651475	0.14138379	0.11063218	27.79625366	male
LOC100651494	0.29370629	0.02083333	1309.79021	male
LOC100651507	0.24975581	0.42246642	-40.88150036	queen
LOC100651511	0.59839768	0.7465812	-19.84827824	queen
LOC100651600	0.83581933	0.57121212	46.32380804	male
LOC100651603	0.17039947	0.10658076	59.87825656	male
LOC100651604	0.03846154	0.07692308	-50	queen
LOC100651618	0.21997247	0.28919468	-23.936196	queen
LOC100651629	0.50660752	0.74007937	-31.54686647	queen
LOC100651639	0.45529052	0.3602362	26.38666507	male
LOC100651673	0.12396064	0.19583227	-36.70060586	queen
LOC100651714	0.61875624	0.83116883	-25.55588942	queen
LOC100651720	0.12548642	0.09470846	32.49758465	male
LOC100651743	0.30075758	0	100	male
LOC100651791	0.14931465	0.10996676	35.7816236	male
LOC100651805	0.44871795	0.05882353	662.8205128	male
LOC100651852	0.20211039	0.08058853	150.7929926	male
LOC100651857	0.11948378	0.18562092	-35.63021448	queen
LOC100651858	0.05555556	0.15458333	-64.06109614	queen
LOC100651889	0.3825493	0.51578947	-25.83227792	queen
LOC100651892	0.11458773	0.09011308	27.15993144	male
LOC100651907	0.26220737	0.1953125	34.25017484	male
LOC100651946	0.89468144	0.80924534	10.55750384	male
LOC100651952	0.04166667	0.25	-83.33333333	queen
LOC100651956	0.1467803	0.25967742	-43.47590815	queen
LOC100652055	0.46455189	0.26719114	73.86500278	male
LOC100652128	0.38894952	0.283126	37.37683086	male

LOC100652130	0.1	0.33809524	-70.42253521	queen
LOC100652133	0.01498014	0.16949545	-91.16192265	queen
LOC100652165	0.04864253	0.1506734	-67.71657524	queen
LOC100652178	0.33164902	0.28951481	14.55338938	male
LOC100652208	0.1875	0.67624521	-72.2733711	queen
LOC100652317	0.42789767	0.56989538	-24.91645221	queen
LOC100652318	0.34953257	0.40853909	-14.44329858	queen
LOC105665725	0.0033843	0.16403758	-97.93687219	queen
LOC105665731	0.33193915	0.39351852	-15.64840368	queen
LOC105665753	0.05507606	0.16657648	-66.93647356	queen
LOC105665773	0.61005472	0.53009334	15.0843958	male
LOC105665864	0.00347222	0.09023001	-96.15181002	queen
LOC105665983	0.0824793	0.04166667	97.95031056	male
LOC105666191	0.29056984	0.47160345	-38.38682802	queen
LOC105666257	0.41739986	0.33073073	26.20534523	male
LOC105666347	0.35481449	0.12039234	194.7151618	male
LOC105666490	0	0.16666667	-100	queen
LOC105666702	0.01526914	0.15359443	-90.05879427	queen
LOC105666703	0.01526914	0.15359443	-90.05879427	queen
LOC105666711	0.02015623	0.08170842	-75.33151448	queen
LOC105666827	0.00491565	0.21512371	-97.71496754	queen
LOC105666889	0.04944567	0.16615929	-70.24200779	queen
LOC105666928	0.21476834	0.1016926	111.1936721	male
LOC105666950	0.33892611	0.28547062	18.72538938	male
LOC105667022	0.86767399	1	-13.23260073	queen
LOC105667038	0.40120419	0.26430838	51.79397146	male
LOC105667088	0.12079832	0.01041667	1059.663866	male
LOC105667180	0.27928216	0.32425268	-13.86897209	queen

Supplementary 5.0.6: list of enriched GO terms associated with differentially methylated genes between queens and males, q<0.05.

term_ID	description	frequency	log10 p-value
GO:0006891	intra-Golgi vesicle-mediated transport	0.06%	-2.3271
GO:0036098	male germ-line stem cell population maintenance	0.00%	-2.0132
GO:0019827	stem cell population maintenance	0.04%	-1.6074
GO:0043933	macromolecular complex subunit organization	2.37%	-3.8876
GO:0071704	organic substance metabolic process	58.36%	-2.2068
GO:0007023	post-chaperonin tubulin folding pathway	0.02%	-2.0132
GO:0016032	viral process	0.13%	-2.3362
GO:0044419	interspecies interaction between organisms	0.26%	-2.0298
GO:0044764	multi-organism cellular process	0.33%	-1.9835
GO:0007283	spermatogenesis	0.09%	-1.5221
GO:1902680	positive regulation of RNA biosynthetic process	0.52%	-2.6523
GO:0045935	positive regulation of nucleobase-containing compound metabolic process	0.60%	-2.2441
GO:0045899	positive regulation of RNA polymerase II transcriptional preinitiation complex assembly	0.01%	-1.5655
GO:0045893	positive regulation of transcription, DNA-templated	0.52%	-1.6932
GO:0060260	regulation of transcription initiation from RNA polymerase II promoter	0.02%	-1.4372
GO:2000144	positive regulation of DNA-templated transcription, initiation	0.02%	-1.8195
GO:0009891	positive regulation of biosynthetic process	0.67%	-2.2298
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	0.37%	-1.4712
GO:0006457	protein folding	0.90%	-1.4345
GO:0061351	neural precursor cell proliferation	0.03%	-1.4844
GO:0006807	nitrogen compound metabolic process	38.74%	-1.9465
GO:0044238	primary metabolic process	53.74%	-1.376
GO:0043543	protein acylation	0.20%	-2.2041
GO:0055069	zinc ion homeostasis	0.01%	-1.5655
GO:0034260	negative regulation of GTPase activity	0.01%	-1.5655
GO:0043547	positive regulation of GTPase activity	0.47%	-1.341

GO:0072594	establishment of protein localization to organelle	0.49%	-2.0876
GO:0070727	cellular macromolecule localization	1.56%	-1.4661
GO:0006626	protein targeting to mitochondrion	0.11%	-1.4903
GO:0034502	protein localization to chromosome	0.03%	-1.609
GO:0008104	protein localization	2.63%	-1.7514
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	0.03%	-1.6856
GO:0006397	mRNA processing	0.56%	-1.4461
GO:0000375	RNA splicing, via transesterification reactions	0.32%	-1.4782
GO:0000398	mRNA splicing, via spliceosome	0.32%	-1.5164
GO:0071044	histone mRNA catabolic process	0.00%	-1.5655
GO:0009048	dosage compensation by inactivation of X chromosome	0.00%	-2.0132
GO:0009059	macromolecule biosynthetic process	19.55%	-2.4136
GO:0002805	regulation of antimicrobial peptide biosynthetic process	0.00%	-2.0878
GO:0002775	antimicrobial peptide production	0.00%	-1.8195
GO:0006974	cellular response to DNA damage stimulus	2.36%	-1.713
GO:0015833	peptide transport	0.30%	-2.0737
GO:0090277	positive regulation of peptide hormone secretion	0.01%	-1.9193
GO:0006310	DNA recombination	1.64%	-1.5034
GO:0002183	cytoplasmic translational initiation	0.03%	-1.3782
GO:0090502	RNA phosphodiester bond hydrolysis, endonucleolytic	0.50%	-2.2345
GO:0000479	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA	0.03%	-1.609
GO:0000469	cleavage involved in rRNA processing	0.05%	-1.4372
GO:0071705	nitrogen compound transport	1.77%	-1.5847
GO:0090305	nucleic acid phosphodiester bond hydrolysis	2.27%	-1.4877
GO:0006368	transcription elongation from RNA polymerase II promoter	0.08%	-2.4078
GO:0032785	negative regulation of DNA-templated transcription, elongation	0.01%	-1.5655
GO:0033135	regulation of peptidyl-serine phosphorylation	0.02%	-1.3782
GO:0044267	cellular protein metabolic process	14.29%	-1.6732
GO:0007362	terminal region determination	0.00%	-1.609

GO:0008286	insulin receptor signaling pathway	0.02%	-1.629
GO:0048167	regulation of synaptic plasticity	0.03%	-1.4177
GO:0070983	dendrite guidance	0.00%	-1.8195
GO:0000462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRI	0.07%	-1.6158
GO:0044260	cellular macromolecule metabolic process	34.28%	-1.6721
GO:0010467	gene expression	19.67%	-1.3446
GO:0035904	aorta development	0.01%	-1.4372
GO:0043044	ATP-dependent chromatin remodeling	0.05%	-4.2662
GO:0043486	histone exchange	0.02%	-1.8195
GO:0034728	nucleosome organization	0.13%	-1.7161
GO:0016573	histone acetylation	0.14%	-2.3535
GO:0016569	covalent chromatin modification	0.42%	-2.7009
GO:0006333	chromatin assembly or disassembly	0.12%	-1.3597
GO:0042766	nucleosome mobilization	0.01%	-2.0878
GO:0006475	internal protein amino acid acetylation	0.15%	-2.2627
GO:0018394	peptidyl-lysine acetylation	0.14%	-2.2627
GO:0016070	RNA metabolic process	15.95%	-2.8145
GO:0008586	imaginal disc-derived wing vein morphogenesis	0.00%	-1.3928
GO:0035222	wing disc pattern formation	0.00%	-1.3928
GO:0007474	imaginal disc-derived wing vein specification	0.00%	-1.3782
GO:0007021	tubulin complex assembly	0.02%	-2.0132
GO:0018193	peptidyl-amino acid modification	1.50%	-1.3925
GO:0032200	telomere organization	0.13%	-1.9711
GO:0042789	mRNA transcription from RNA polymerase II promoter	0.00%	-2.0132
GO:0046604	positive regulation of mitotic centrosome separation	0.00%	-2.0132
GO:0051299	centrosome separation	0.01%	-1.8195
GO:0043974	histone H3-K27 acetylation	0.00%	-2.0132
GO:0034654	nucleobase-containing compound biosynthetic process	14.53%	-1.6575
GO:2000112	regulation of cellular macromolecule biosynthetic process	10.68%	-1.7524

GO:0010468	regulation of gene expression	10.82%	-1.5923
GO:0031323	regulation of cellular metabolic process	11.66%	-1.3196
GO:0051252	regulation of RNA metabolic process	10.03%	-1.3448
GO:1903506	regulation of nucleic acid-templated transcription	9.97%	-1.4702
GO:0051171	regulation of nitrogen compound metabolic process	10.93%	-1.378
GO:0006139	nucleobase-containing compound metabolic process	26.55%	-2.0545
GO:0008154	actin polymerization or depolymerization	0.15%	-1.3632
GO:0032984	macromolecular complex disassembly	0.37%	-2.1302
GO:0043244	regulation of protein complex disassembly	0.16%	-1.4825
GO:0006415	translational termination	0.20%	-1.5655
GO:0065003	macromolecular complex assembly	1.50%	-2.0094
GO:0032204	regulation of telomere maintenance	0.02%	-1.3782
GO:0070827	chromatin maintenance	0.00%	-2.0132
GO:1903524	positive regulation of blood circulation	0.01%	-2.0132
GO:0044249	cellular biosynthetic process	30.05%	-1.6801
GO:0007406	negative regulation of neuroblast proliferation	0.00%	-1.4372
GO:0030433	ER-associated ubiquitin-dependent protein catabolic process	0.05%	-1.3928
GO:0006367	transcription initiation from RNA polymerase II promoter	0.11%	-1.5014
GO:0051276	chromosome organization	1.48%	-3.4233
GO:0006955	immune response	0.34%	-1.4591
GO:0032481	positive regulation of type I interferon production	0.01%	-1.5655
GO:0040018	positive regulation of multicellular organism growth	0.01%	-1.9282
GO:0017038	protein import	0.26%	-1.8655
GO:0022618	ribonucleoprotein complex assembly	0.36%	-2.0893
GO:0008293	torso signaling pathway	0.00%	-1.609
GO:0006607	NLS-bearing protein import into nucleus	0.01%	-2.0878
GO:0034501	protein localization to kinetochore	0.01%	-1.5655

Supplementary 5.0.7: enriched GO terms associated with hypermethylated genes in males and queens compared to all differentially methylated genes, q<0.05.

Male Terms

term_ID	description	frequency	log10 p-value
GO:0001568	blood vessel development	0.14%	-1.4096
GO:0072358	cardiovascular system development	0.15%	-1.4096
GO:0009987	cellular process	63.78%	-1.4488
GO:0044248	cellular catabolic process	3.27%	-1.3988
GO:0043009	chordate embryonic development	0.14%	-1.3431
GO:0048568	embryonic organ development	0.11%	-1.3431

Queen Terms

term_ID	description	frequency	log10 p-value
GO:0010563	negative regulation of phosphorus metabolic process	0.18%	-1.5634
GO:0042326	negative regulation of phosphorylation	0.12%	-1.5634
GO:0016049	cell growth	0.15%	-1.4245
GO:0043604	amide biosynthetic process	6.37%	-1.3302
GO:0031400	negative regulation of protein modification process	0.15%	-1.5634

Supplementary 5.0.8: coverage and aligment statistics for the worker samples aligned to their parental genomes.

ref genome	alignment	number alignments	alignments no mismatch	percent lost	bases_left	coverage	original_bases	coverage	CpGs identified	CpGs with 10 coverage
m08	64.8	12131230	9436654	22.2	2642263120	10.61	3396744400	13.64	3079288	3076201
m19	61.3	12653928	9949163	21.4	2785765640	11.19	3543099840	14.23	5174853	5169665
m23	60.3	12914084	10215217	20.9	2860260760	11.49	3615943520	14.52	3539651	3536105
m37	61.8	12378420	9764004	21.1	2733921120	10.98	3465957600	13.92	3448788	3445338
q08	64.7	12129818	9386969	22.6	2628351320	10.56	3396349040	13.64	3030654	3027618
q19	61.3	12654402	9948178	21.4	2785489840	11.19	3543232560	14.23	5160772	5155610
q23	60.3	12914285	10202390	21.0	2856669200	11.47	3615999800	14.52	3509695	3506176
q37	61.8	12378003	9731659	21.4	2724864520	10.94	3465840840	13.92	3394553	3391153

genome bp:
249000000

Supplementary 5.0.9: enriched FO terms for the genes containing a CpG with parent of origin methylation, compared to all methylated genes as a background.

term_ID	description	frequency	log10 p-value
GO:0010977	negative regulation of neuron projection development	0.02%	-3.0857
GO:0048699	generation of neurons	0.37%	-1.465
GO:0051960	regulation of nervous system development	0.17%	-1.3666
GO:0060284	regulation of cell development	0.17%	-1.3384
GO:0048666	neuron development	0.27%	-1.7378
GO:0050768	negative regulation of neurogenesis	0.05%	-2.3389
GO:0045664	regulation of neuron differentiation	0.12%	-1.7073
GO:0045596	negative regulation of cell differentiation	0.13%	-1.6354
GO:0042147	retrograde transport, endosome to Golgi	0.06%	-3.3137
GO:0048511	rhythmic process	0.08%	-2.0388
GO:0050982	detection of mechanical stimulus	0.01%	-4.121
GO:0018298	protein-chromophore linkage	0.10%	-2.2047
GO:0036315	cellular response to sterol	0.00%	-1.9048
GO:0035075	response to ecdysone	0.00%	-1.9048
GO:0035076	ecdysone receptor-mediated signaling pathway	0.00%	-2.0802
GO:0035063	nuclear speck organization	0.00%	-2.6811
GO:0051606	detection of stimulus	0.35%	-2.7578
GO:0016584	nucleosome positioning	0.01%	-2.2047
GO:0042766	nucleosome mobilization	0.01%	-1.9836
GO:0043044	ATP-dependent chromatin remodeling	0.05%	-1.5103
GO:0006334	nucleosome assembly	0.09%	-1.4826
GO:0035601	protein deacylation	0.08%	-1.4826
GO:0016575	histone deacetylation	0.05%	-1.5103
GO:0009628	response to abiotic stimulus	0.57%	-2.4954
GO:0030030	cell projection organization	0.61%	-1.5739

GO:0060325	face morphogenesis	0.01%	-1.9836
GO:0036211	protein modification process	7.73%	-1.6224
GO:0010171	body morphogenesis	0.02%	-1.5399
GO:0009649	entrainment of circadian clock	0.01%	-1.8383
GO:0042752	regulation of circadian rhythm	0.03%	-1.3518
GO:0061024	membrane organization	0.76%	-1.4641
GO:0010224	response to UV-B	0.01%	-2.6811
GO:0051129	negative regulation of cellular component organization	0.24%	-1.6998
GO:0097306	cellular response to alcohol	0.02%	-1.5717
GO:0035041	sperm chromatin decondensation	0.00%	-2.3804
GO:0007338	single fertilization	0.03%	-1.5717
GO:1901655	cellular response to ketone	0.02%	-1.5717
GO:0035092	sperm chromatin condensation	0.00%	-2.3804
GO:0007286	spermatid development	0.03%	-1.3277
GO:0051241	negative regulation of multicellular organismal process	0.21%	-1.4863

Chapter 6: supplementary

Supplementary 6.0.0: metadata for the samples selected for whole genome bisulfite sequencing. Year was determined via radiometric dating as described in Cuenca-Cambronero et al. (2018).

Lake Phase	Core	Sample_ID	Year	Culturing Batch
Recovery	LRV	0_1	2004	1
Recovery	LRV	0_2	2004	3
Recovery	LRV	0_4	2004	2
Recovery	LRV	1_2	2002	1
Recovery	LRV	2_1	1999	4
Recovery	LRV	2.5_9	1999	3
Recovery	LRV	2.5_11	1999	4
Recovery	LRV	3_6	1998	3
Recovery	LRV	3.5_1	1997	2
Recovery	LRV	3.5_2	1997	4
Recovery	LRV	3.5_15	1997	1
Pesticide	LRV	6_2	1991	1
Pesticide	LRV	6_3	1991	3
Pesticide	LRV	7_3	1988	2
Pesticide	LRV	7_5	1988	4
Pesticide	LRV	7.5_4	1987	3
Pesticide	LRV	8.5_3	1984	1
Pesticide	LRV	9_6	1983	4
Pesticide	LRV	9_20	1983	2
Pesticide	LRV	9.5_1	1981	1
Pesticide	LRV	9.5_3	1981	3
Eutrohpicatic	LRV	12_3	1971	3
Eutrohpicatic	LRV	12_4	1971	1
Eutrohpicatic	LRV	12.5_1	1971	4
Eutrohpicatic	LRV	13_1	1969	2

Eutrohpicatic	LRV	13_2	1969	4
Eutrohpicatic	LRV	13_3	1969	3
Eutrohpicatic	LRV	13.5_1	1968	2
Eutrohpicatic	LRV	14.5_1	1964	1
Eutrohpicatic	LRV	15.5_1	1959	2
Pristine	LR2	48_01	1931	3
Pristine	LR2	48_02	1931	2
Pristine	LR2	54_01	1919	4
Pristine	LR2	54_02	1919	1
Pristine	LR2	36_01	1949	3
Pristine	LR2	36_02	1949	2
Pristine	LR3	74_01	1919	1
Pristine	LR3	77_01	1914	4
Pristine	LR3	53_01	1948	2
Pristine	LR3	88_01	1873	4

Supplementary 6.0.1: quantity of DNA obtained for each sample, determined via Qubit.

Sample_ID	Quantity (µg)
0_1	29.1
0_2	53.7
0_4	4.4
1_2	22.8
2_1	4.5
2.5_9	8.0
2.5_11	39.6
3_6	23.1
3.5_1	17.3
3.5_2	24.6
3.5_15	9.2
6_2	58.2
6_3	3.4
7_3	11.9
7_5	28.5
7.5_4	2.1
8.5_3	27.3
9_6	50.9
9_20	19.1
9.5_1	12.7
9.5_3	15.4
12_3	16.9
12_4	18.4
12.5_1	60.4
13_1	18.1

13_2	16.1
13_3	13.4
13.5_1	12.7
14.5_1	24.6
15.5_1	25.0
48_01	20.0
48_02	20.0
54_01	22.0
54_02	24.7
36_01	62.7
36_02	17.8
74_01	54.0
77_01	51.5
53_01	56.2
88_01	14.3

Supplementary 6.0.2: alignment rates and methylation levels for all samples algined to the daphmag2.4 genome using Bismark.

Sample ID	Alignment Rate (%)	Aligned Paired Reads	Duplicated Sequences (%)	Total Reads	Final Coverage	Methylation in a CpG Context	Methylation in a CHG Context	Methylation in a CHH Context	Lambda Conversion Efficiency: CpG
0_1	47.5	7610140	22.71	5860597	11.8	0.8	0.4	0.4	0.4
0_2	47.5	9367537	22.89	7196066	14.4	1	0.5	0.5	0.5
0_4	49.9	8408422	23	6450016	12.9	1	0.5	0.6	0.5
1_2	50	7971156	22.58	6149445	12.3	0.9	0.5	0.6	0.5
2_1	47.7	8554298	22	6645834	13.3	1	0.6	0.6	0.5
2.5_9	45.9	8388263	23.53	6390709	12.8	1.1	0.6	0.6	0.5
2.5_11	51.2	10547194	24.96	7883548	15.8	1	0.5	0.6	0.5
3_6	51.8	7326954	23.36	5596713	11.2	0.9	0.5	0.6	0.5
3.5_1	48.6	7257046	23.92	5498788	11.0	1	0.5	0.5	0.5
3.5_2	49.2	8890826	23.7	6756529	13.6	1	0.5	0.6	0.5
3.5_15	44.8	9841418	31.46	6690255	13.4	1.8	0.7	0.8	0.7
6_2	51.7	8998636	25.19	6705983	13.5	0.9	0.5	0.6	0.5
6_3	54.2	7255236	27.17	5267335	10.6	1	0.6	0.7	0.5
7_3	49.7	10056204	27.44	7271250	14.6	1	0.6	0.7	0.5
7_5	52.6	8551478	25.15	6374027	12.8	1	0.6	0.6	0.5
7.5_4	47.8	8198926	25.63	6074592	12.2	1	0.5	0.5	0.4
8.5_3	51.3	10032670	26.9	7305836	14.7	0.9	0.4	0.5	0.4
9_6	50.9	11932998	27.19	8654701	17.4	0.9	0.4	0.5	0.4
9_20	49.8	11607502	28.47	8263696	16.6	0.9	0.4	0.4	0.4
9.5_1	49.4	8679700	25.99	6394464	12.8	0.9	0.4	0.4	0.4
9.5_3	48.8	9252413	28.26	6604672	13.3	1	0.4	0.5	0.4
12_3	43.2	7366515	25.89	5435668	10.9	0.7	0.2	0.2	0.2
12_4	47.9	8944670	26.53	6537858	13.1	0.7	0.2	0.2	0.2
12.5_1	46.7	7577944	26.38	5546279	11.1	0.8	0.2	0.2	0.2

13_1	48.7	8023828	27.73	5763553	11.6	0.8	0.2	0.2	0.2
13_2	48.4	7612691	25.41	5650256	11.3	0.7	0.2	0.2	0.2
13_3	47.8	9181782	26.62	6700216	13.4	0.8	0.2	0.2	0.2
13.5_1	47.1	8198320	29.36	5757068	11.6	0.8	0.2	0.2	0.2
14.5_1	48.3	8649508	26.7	6302083	12.6	0.8	0.2	0.2	0.2
15.5_1	46.2	6379634	24.73	4775962	9.6	0.8	0.2	0.2	0.2
48_01	43	7788826	27.12	5638081	11.3	0.8	0.2	0.2	0.2
48_02	46.1	6795169	25.65	5023545	10.1	0.7	0.2	0.2	0.2
54_01	46.4	8999090	25.51	6663806	13.4	0.8	0.2	0.2	0.2
54_02	44.4	7206425	28.11	5141656	10.3	0.8	0.2	0.2	0.2
36_01	48.2	10930230	28.35	7788003	15.6	0.8	0.2	0.2	0.2
36_02	47.9	8177494	25.6	6051829	12.1	0.8	0.2	0.2	0.2
74_01	47.4	11008910	26.16	8087015	16.2	1	0.4	0.4	0.4
77_01	49.1	9987442	26.42	7316008	14.7	0.9	0.4	0.4	0.4
53_01	43.6	8368038	26.31	6130612	12.3	0.8	0.2	0.2	0.2
88_01	42.2	8706333	24.78	6518030	13.1	0.9	0.4	0.4	0.4
MEAN:	**48.1**	**8715797**	**25.87**	**6421565**	**12.9**	**0.9**	**0.4**	**0.4**	**0.4**
SD:	**2.67**	**1301722**	**2.02**	**910148**	**1.8**	**0.18**	**0.16**	**0.19**	**0.14**

Lambda Conversion Efficiency: CHG	Lambda Conversion Efficiency: CHH	Corrected Methylation in a CpG Context	Corrected Methylation in a CHG Context	Corrected Methylation in a CHH Context
0.4	0.4	0.4	0	0
0.5	0.5	0.5	0	0
0.5	0.6	0.5	0	0
0.5	0.6	0.4	0	0
0.5	0.6	0.5	0.1	0
0.5	0.6	0.6	0.1	0
0.5	0.6	0.5	0	0
0.5	0.5	0.4	0	0.1
0.5	0.5	0.5	0	0
0.5	0.6	0.5	0	0
0.7	0.7	1.1	0	0.1
0.5	0.5	0.4	0	0.1
0.5	0.6	0.5	0.1	0.1
0.5	0.6	0.5	0	0
0.5	0.5	0.5	0.1	0.1
0.4	0.5	0.6	0.1	0
0.4	0.4	0.5	0	0.1
0.4	0.4	0.5	0	0.1
0.4	0.4	0.5	0	0
0.4	0.4	0.5	0	0
0.4	0.5	0.6	0	0
0.2	0.2	0.5	0	0
0.2	0.2	0.5	0	0
0.2	0.2	0.6	0	0

read length:	130
genome size	129,543,483

0.2	0.2	0.6	0	0
0.2	0.2	0.5	0	0
0.2	0.2	0.6	0	0
0.2	0.2	0.6	0	0
0.2	0.2	0.6	0	0
0.2	0.2	0.6	0	0
0.2	0.2	0.6	0	0
0.2	0.2	0.5	0	0
0.2	0.2	0.6	0	0
0.2	0.2	0.6	0	0
0.2	0.2	0.6	0	0
0.2	0.2	0.6	0	0
0.4	0.4	0.6	0	0
0.4	0.4	0.5	0	0
0.2	0.2	0.6	0	0
0.4	0.4	0.5	0	0
0.4	**0.4**	**0.5**	**0.0**	**0.0**
0.14	**0.17**	**0.11**	**0.03**	**0.04**