

# **Identification of stage specific long non-coding RNAs in the filarial worm, *Brugia malayi***

*A Major Project dissertation submitted  
in partial fulfilment of the requirement for the degree of*

## **Master of Technology In Bioinformatics**

*Submitted by*

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## CERTIFICATE

This is to certify that the dissertation entitled “**Identification of stage specific long non-coding RNAs in the filarial worm, *Brugia malayi***”, submitted by **Deepika Jaggi (2K11/BIO/04)** in partial fulfilment of the requirement for the award of the degree of Master of Technology, Delhi Technological University (Formerly Delhi College of Engineering, University of Delhi), is an authentic record of the candidate’s own work carried out by her under my guidance.

The information and data enclosed in this dissertation is original and has not been submitted elsewhere for honouring of any other degree.

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**Deepika Jaggi**  
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# Identification of stage specific long non-coding RNAs in the filarial worm, *Brugia malayi*

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## 1. ABSTRACT

*Brugia malayi* is one of the filarial nematode other than *Brugia timori* and *Wuchereria bancrofti*, which causes the parasitic infection lymphatic filariasis (LF) and is restricted to South and Southeast Asia including India. Current day anti-filarial drugs like diethylcarbamazine, albendazole, ivermectin etc. are known to cause adverse reactions and require repeated dosage. The optimum drug discovery depends mostly on understanding the lifecycle of the parasite. Recently, several studies have also emphasized on the need for studying the transcriptome profile of the parasite's lifecycle in order to understand the developmental process required for the infectious cycle. But, most of these have mainly focused on the protein-coding genes and there is a dearth in studies on various non-coding RNAs including long non-coding RNAs (lncRNAs). Long non-coding RNAs (lncRNA) are non-protein coding transcripts longer than 200 nucleotides which usually do not code for proteins. These molecules have recently emerged as one of the key regulators in various biological processes that comprise both transcriptional and translational activities. The transcriptome of *B. malayi* has been extensively studied primarily focusing on protein coding genes. In order to study the lncRNAs in the genome of *B. malayi*, we have analyzed 11 publically available RNA-Seq datasets on Sequence Read Archive. Using *in-silico* RNA-Seq analysis tools and an *in-house* pipeline, we identified 997 lncRNAs from 982 genes in *B. malayi*. These lncRNAs were analyzed further and were found to show a sex and stage-specific expression. To the best of our knowledge, this is the first study where lncRNAs in *Brugia* have been identified. We anticipate that this information may be useful for future studies to depict pathogenic lncRNA causing lymphatic filariasis.

## 2. INTRODUCTION

Filarial parasitic nematodes like *Wuchereria bancrofti*, *Brugia malayi* and *Brugia timori* cause an unbearable and disabling neglected tropical disease, Lymphatic filariasis (LF). According to World Health Organization (WHO, 2013), approximately 120 million people have been infected worldwide and more than 1.4 billion people in 73 countries are exposed to acquire this infectious disease. The infection is asymptomatic and causes damage to the lymphatic system of the host with physical manifestations that range from disfigurement due to excessive swelling or edema (referred to as elephantiasis) to permanent disability. LF has been targeted by WHO for elimination by 2020, using mass drug administration (MDA). But the current day treatments used for combating this disease are effective only for short term usage and requires repeated dosage which compromises their effectiveness over long term. Moreover, drugs used for MDA like ivermectin, albendazole and diethylcarbamazine reduce worm burden and disease transmission by clearing only the microfilariae (MF) from the bloodstream and are seen to have no effect on all the life cycle stages of the parasite. We believe that, for the purpose of designing optimum drug therapies, a comprehensive study of the parasite's genome is foremost essential.

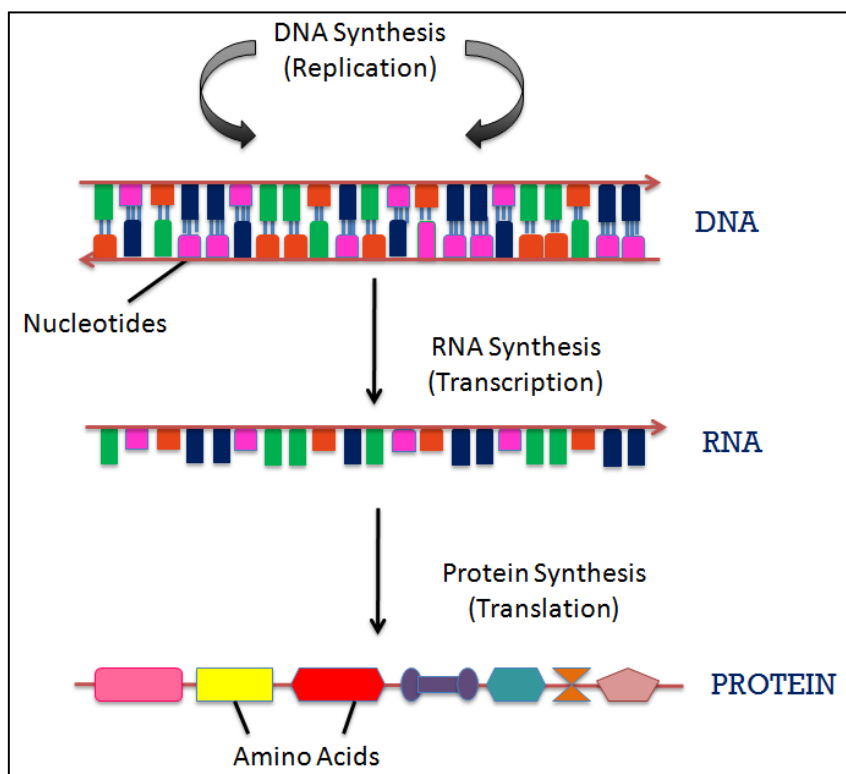
The availability of the draft genome and annotation of the *Brugia malayi* (Ghedin *et al.*, 2007) has facilitated various researches in the recent past which have significantly contributed in comprehending the filarial biology. Global transcriptome and proteome analyses of the genome of *Brugia malayi* have revealed a number of stage-specific pathways and proteins which can be targeted for drug intervention (Choi *et al.*, 2011). Though being informative, these studies have a restrained focus on the protein coding genes and there is an absence of studies on the non-coding regions of the genome. Non-coding RNAs (ncRNAs) have been shown to play both house-keeping and regulatory roles at the transcriptional and translational level. NcRNAs are categorized into small and long non-coding RNAs (sncRNAs and lncRNAs, respectively). LncRNAs are non-protein coding transcripts which are longer than 200 nucleotides and lack an open reading frame (ORF). Though the exact function of lncRNAs is unknown, but the number of publications identifying lncRNAs and characterizing them as a molecule of interest, is continuously growing. Many association studies have found the implication of lncRNAs in diseases like cancer, heart diseases, psoriasis, Alzheimer's disease etc. These findings have increased the cognizance for their potential to cause a certain disease. Identification of lncRNAs in different species, including a closely related homologue *C. elegans* has also solved many intricacies regarding their putative roles in genomic regulation and parasitism. In case of *B. malayi*, even after 5 years of release of its draft genome, the available annotation does not contain a single piece of information on non-coding transcripts which is really vital to realize the full functional potential of its transcriptome.

Using the available RNA-Seq data and an *in-house* pipeline, we have identified 997 lncRNAs from 982 genes in *Brugia malayi* which have a gender and stage dependent expression. We also studied the differential expression of the genes coding for lncRNA. This information can be further used to investigate the function of these lncRNAs and their role in pathogenicity.

### 3. REVIEW OF LITERATURE

#### 3.1 Our Current View of Transcriptome

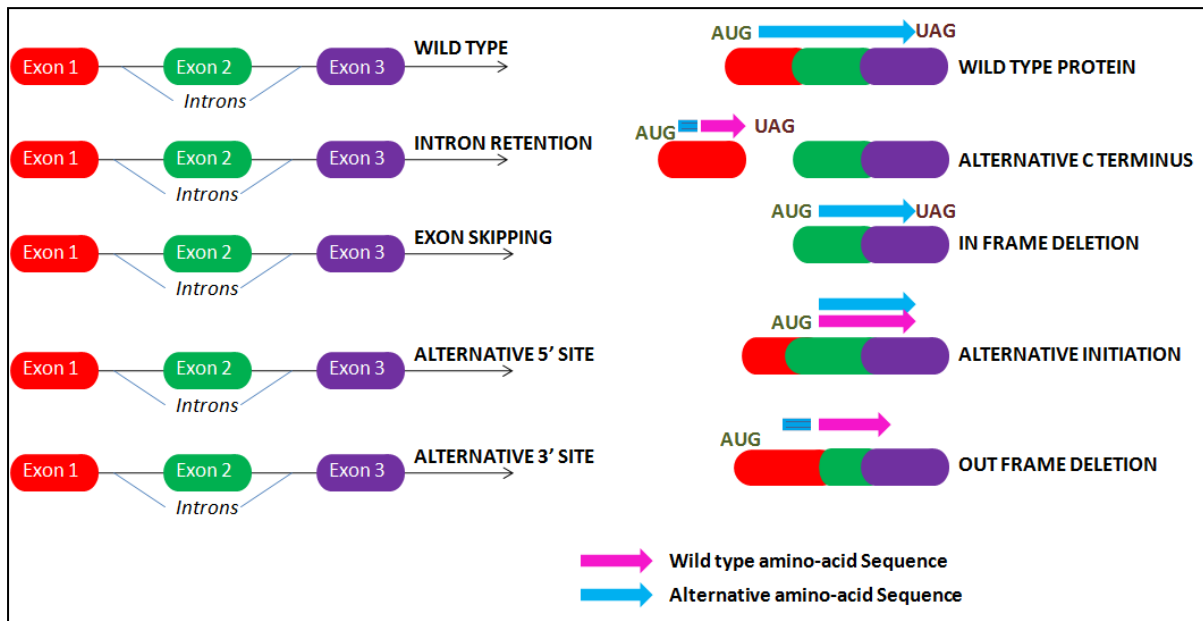
The central dogma of gene expression is that DNA is transcribed into messenger RNAs, which in turn serve as the template for protein synthesis (*Figure 1*). The simplified concept of 'Gene' based on bacterial models which has been followed and worshiped for centuries, is now outdated. It has been replaced that of a transcriptional unit, where the series of transcripts generated from the same region are controlled as one combined unit. ***The transcriptome is the complete set of transcripts in a cell, and their quantity, for a specific developmental stage or physiological condition*** (Snyder *et al.*, 2009).



**Figure 1: Central Dogma of Molecular Biology.**

Ever since the completion of the Human Genome Project, our apprehension of our genome has undergone a remarkable shift. The number of protein coding genes in our genome has been revised downward multiple times, whereas an exponential increment in the number of non-protein coding transcripts has been witnessed (Huttenhofer *et al.*, 2005). In mammalian systems, only about 3% of the complete genome is known to be exonic and the bulk of annotated genes that encode mRNA are multi-exon generating more than one alternative transcript isoform. These isoforms represent both coding and non-coding overlapping RNAs. This heterogeneity in the transcriptional output is contributed by some common events such as alternative splicing, variations in transcription start sites and termination sites (*Figure 2*). Additionally, these multi-exon coding genes can host ncRNAs within their introns, thereby

making these genes multi output (Wang *et al.*, 2008). Though, the characterization of the noncoding RNAs is still in its primitive stages, many of them have been shown to exhibit cell type-specific expression, localization to subcellular compartments, and association with human diseases, thereby challenging the cliché that ncRNAs represents transcriptional *noise*. The discovery of extensive transcription of large RNA transcripts, termed long noncoding RNAs (long ncRNAs, lncRNAs) provides an important new perspective on the centrality of RNA in gene regulation (Rinn *et al.*, 2012).



**Figure 2: Alternative splicing events: causes variation in the canonical transcript.**

LncRNAs represent a major unexplored component of genomes that has a potential biological importance (*described in section 3.2*). With the increase in number of transcriptomics studies being reported, it is believed that analysis of genome-wide differential RNA expression can provide researchers with plausible intuition into biological pathways and molecular mechanisms that regulate cell fate, development, and disease progression (Mortazavi *et al.*, 2008).



## 3.2 Long non-coding RNA

Long non-coding RNAs (lncRNAs) are RNA polymerase II promoted, polyadenylated, and often alternatively spliced non-protein coding transcripts. They are usually longer than 200 nucleotides (nts) and have been proposed to be key regulators of diverse biological processes. One of the first lncRNA genes reported was the imprinted *H19* gene (Bartolomei *et al.*, 1991), followed by the discovery of *XIST*, a long noncoding RNA (lncRNA) involved mammalian X chromosome inactivation (Brown *et al.*, 1991). Since then thousands of other lncRNAs have been reported in mammals and other vertebrates. Although for most lncRNAs, functions have not yet been investigated, few of them are known to play gene-regulatory or other biological roles in cells or during embryonic development. LncRNAs have been depicted as a part of the *dark matter of the genome*, due to the fact that although it is now feasible to detect its presence, but its function and activity remains poorly understood (Sana *et al.*, 2012).

### 3.2.1 Origin of lncRNA

LncRNAs can be originated due to mutations in the protein coding genes, chromosomal rearrangements, duplication events and insertion of transposable elements.

### 3.2.2 Location in Genome

LncRNAs can be categorized according to their proximity to protein coding genes in the genome, using this criteria lncRNAs are generally placed into five categories; sense or antisense (lncRNA overlaps one or more exons of another transcript on the same or opposite strand, respectively), bidirectional (the expression of the lncRNA and neighbouring coding transcript on the opposite strand is initiated in close genomic proximity), intronic (the lncRNA is derived from an intron of a second transcript), and intergenic (the lncRNA is localized between two genes).

### 3.2.3 Conservation of lncRNA

LncRNAs lack strong conservation across diverse species as compared to small RNAs, such as microRNAs or snoRNAs. This lack of conservation is repeatedly quoted as substantiation of its non-functionality. However, some lncRNAs, such as *Air* and *XIST*, are poorly conserved (Nesterova *et al.*, 2001), signifying that lncRNAs may be exposed to different selection pressures (Pang *et al.*, 2006). Despite low conservation of lncRNAs in general, many lncRNAs contain strongly conserved elements.

### 3.2.4 Functional Role of lncRNA

lncRNAs have been found to exhibit a wide range of functions ranging from signalling, serving as molecular decoys, guiding ribonucleic-protein complexes to specific chromatin sites and also participating as scaffolds in the formation of complexes (*Figure 3*). Though the molecular mechanisms of most lncRNAs have yet to be revealed, it is clear that they possibly act by activating or repressing the transcriptional activity of other genes either in *cis* or in *trans*, or by modifying their transcript abundance (Ilott *et al.*, 2013). Activation and repression can be assisted by interactions between lncRNAs and chromatin modifying enzymes. The establishment of repressive chromatin via the recruitment of histone modifying proteins has indeed been described for a number of lncRNAs (Tsai *et al.*, 2010; 2011).

The lncRNAs have regulatory roles in complex molecular processes like regulation of gene transcription, translation repression, gene splicing, chromosomal imprinting, and epigenetic regulation of genes. Examples of their involvement in various biological processes (*Figure 4*) have been provided below.

### 3.2.5 lncRNA in action

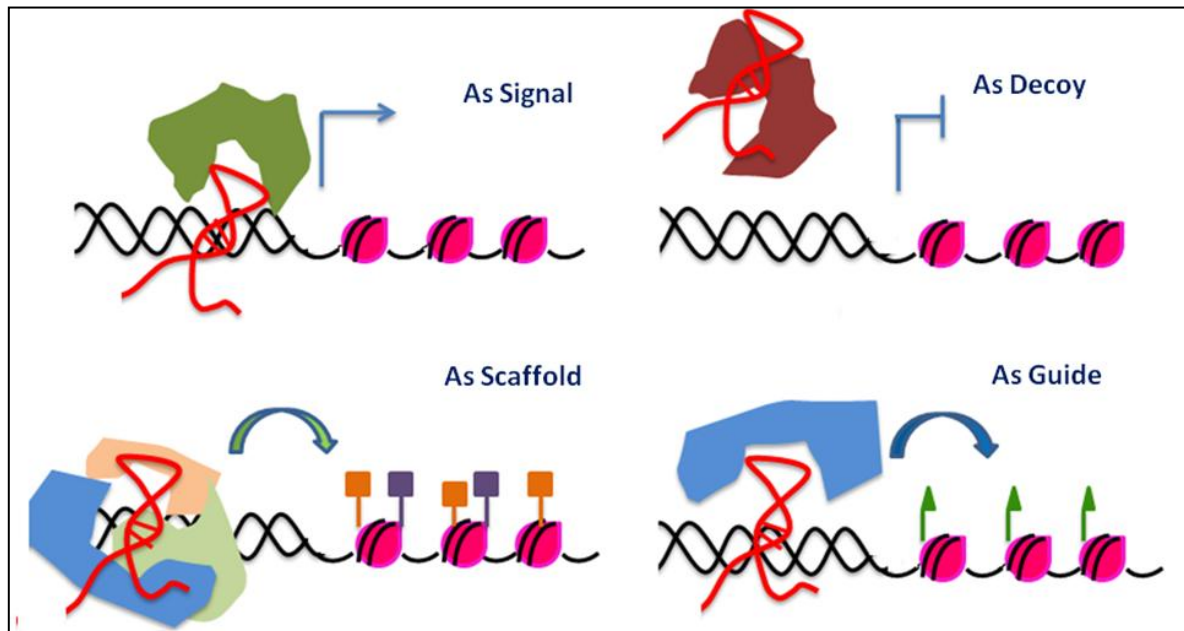
**Transcription:** lncRNAs can target transcriptional activators or repressors, RNA polymerase II and the DNA duplex in order to regulate gene transcription and expression. They can operate as co-regulators and modify transcription factor activity or regulate the association and activity of co-regulators. lncRNAs can also recruit transcriptional programmes to regulate adjacent protein-coding gene expression and can also target components of the initiation complex that assemble on promoters or involved in transcription elongation.

These non-coding molecules usually form complementary base pairing with the target mRNA thereby masking the regions of the mRNA that are required to bind trans-acting factors. This can potentially affect any step in post-transcriptional gene expression including pre-mRNA processing and splicing, transport, translation, and degradation.

**Translation:** lncRNA may apply additional regulatory pressures during translation. Recently, a nuclear-enriched lncRNA has been identified which is antisense to mouse ubiquitin carboxy-terminal hydrolase L1 (*UCHL1*), a gene involved in brain function and neurodegenerative diseases (Carrieri *et al.*, 2012). This lncRNA induces *UCHL1* protein levels, while the mRNA levels remains constant. It specifically promotes the translation of *UCHL1*.

**Epigenetic modification:** RNA is an integral component of chromatin but less is known about their involvement in pathways of chromatin modification. Epigenetic modifications, including histone and DNA methylation, histone acetylation and sumoylation, affect many

aspects of chromosomal biology, primarily including regulation of large numbers of genes by remodelling chromatin domains. Polycomb repressive complex 2 (PRC2), an epigenetic complex responsible for trimethylation of histone H3 at *Lys*, interacts with a 1.6 kb ncRNA (Rep A) within *XIST* and is targeted to the inactive X chromosome. *XIST* is controlled by two other lncRNAs namely *Tsix* (negative) and *Jpx* (positive) (Zao *et al.*, 2008).

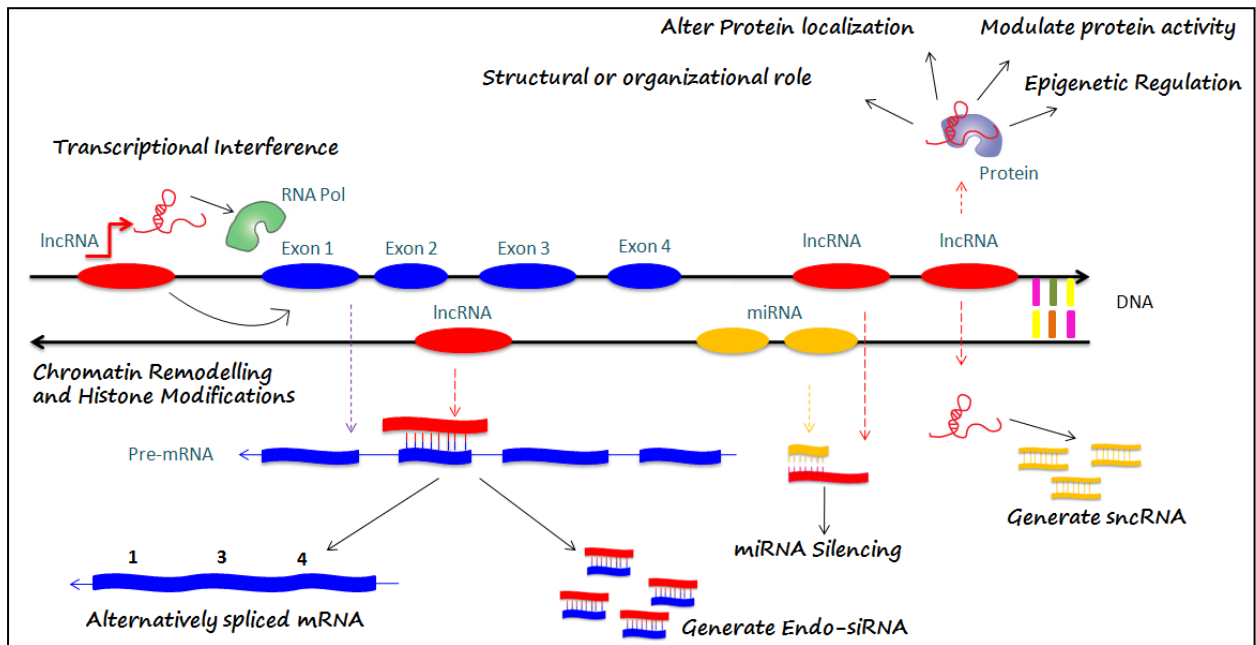


**Figure 3: lncRNAs can function as Signal (in gene activation), Decoy (in gene suppression), Scaffold (for acting on chromatin structure) and Guide (for promoting chromatin modification).**

**Genomic Imprinting:** The phenomenon of imprinting is that only one allele of a gene is expressed from either the maternal or the paternal chromosome. Imprinted genes are generally clustered together on chromosomes, proposing that the imprinting mechanism acts upon local chromosome domains and not on individual genes. These clusters are also frequently associated with long ncRNAs whose expression is associated with the repression of the linked protein-coding gene on the same allele. Two of the best known imprinted genes *H19* and *XIST* are in fact lncRNAs. *H19* encodes a 2.3 kb lncRNA that is expressed from the maternal allele. Loss of imprinting at the *H19* locus results in cancer (Brannan *et al.*, 1990). *XIST* physically coats one of the two X-chromosomes in females and is associated with polycomb-repressor proteins, suggesting a common pathway of including silencing utilized by various lncRNAs (Brown *et al.*, 1991).

**Cell Cycle:** A DNA damage-inducible lncRNA, growth-arrested DNA damage-inducible gene7 (*gadd7*) has been shown to regulate the G1/S checkpoint in response to UV irradiation. UV-induced *gadd7* directly binds to TAR DNA-binding protein (TDP-43) and interferes with

the interaction between TDP-43 and cyclin-dependent kinase 6 (*Cdk6*) mRNA, resulting in *Cdk6* mRNA degradation. These findings demonstrate a role for *gadd7* in controlling cell-cycle progression and define a novel mechanism by which lncRNAs modulate mRNA expression at the post-transcriptional level by altering mRNA stability (Liu *et al.*, 2012).



**Figure 4: Involvement of lncRNAs in various biological processes.**

Involvement of lncRNA in major biological processes and their implication in many diseases has made them gain equal importance as mRNA (protein coding elements) necessitating their identification and characterization. This is essential for understanding the full functional potential of transcriptomes. The technology for sequencing full length transcripts is available and is allowing for the generation of large RNA-Seq data sets. A number of data analysis tools have also been developed that accelerate the pace of lncRNA identification from the sequenced dataset. One such practice is discussed in the next section including the existing sequencing protocols, read mapping and transcript building algorithms, as well as lncRNA categorization using computational methods.

### 3.3 RNA-Seq

Initial transcriptomics studies largely relied on hybridization-based microarray technologies and offered a limited ability to fully catalogue and quantify the diverse RNA molecules that are expressed from genomes over wide ranges of levels. The introduction of high-throughput next-generation DNA sequencing (NGS) technologies transformed transcriptomics by permitting RNA analysis through cDNA sequencing at a considerable scale (RNA-Seq) (Marguerat *et al.*, 2008). RNA-Seq provides an all-inclusive insight into the complexity of eukaryotic transcriptomes by facilitating the identification of exons and introns, transcription start and stop sites, the 5' and 3' ends of genes and the splicing variants. It offers advantages of unbiased transcript discovery and a precise quantification of the expression of exons and splicing variants, along with discriminating highly homologous sequences (Marioni *et al.*, 2008).

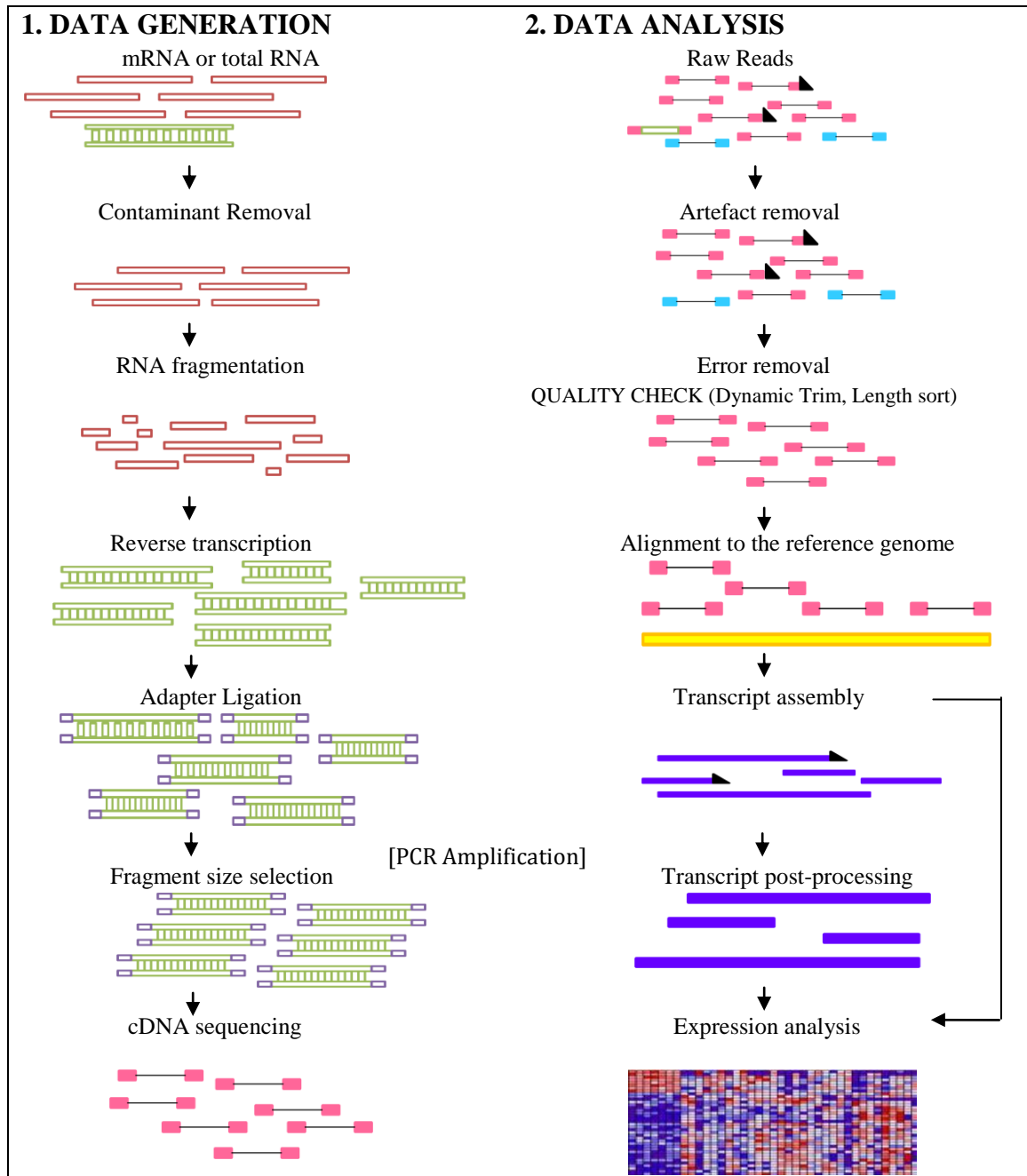
RNA Sequencing (RNA-Seq) involves the reverse transcription of RNA into complementary DNAs (cDNAs) which are then sequenced using high-throughput DNA sequencing technologies (*Figure 5*). NGS platforms used for RNA-Seq are commercially available from four companies namely Illumina, Roche 454, Helicos BioSciences and Life Technologies. (Metzker, M.L. 2010). A brief description of the protocols (*Figure 6*) used by these companies is given below.

#### 3.3.1 Sequencing by ligation

**Applied Biosystems SOLID sequencing technology:** Sequencing by Oligonucleotide Ligation and Detection was developed by Life Technologies. Their protocol involves labelling of all possible oligonucleotides of a fixed length, according to the sequenced position. Oligonucleotides are then annealed and ligated. The favoured ligation by DNA ligase for matching sequences results in a signal revealing the identity of nucleotide at that position. Prior to sequencing, emulsion PCR is used to amplify DNA. The beads containing copies of the same DNA molecule are deposited on a glass slide.

#### 3.3.2 Sequencing by synthesis

**Roche 454:** A template is fragmented and the fragments are end-repaired and ligated to adapters. These are clonally amplified by emulsion PCR inside microscopic "beads". Amplification step is followed by the deposition of the beads into picotiter-plate wells coated with sequencing enzymes, where iterative pyrosequencing is performed. Every time a nucleotide is incorporated a pyrophosphate (PPi) is released and well-localized luminescence is emitted and recorded.



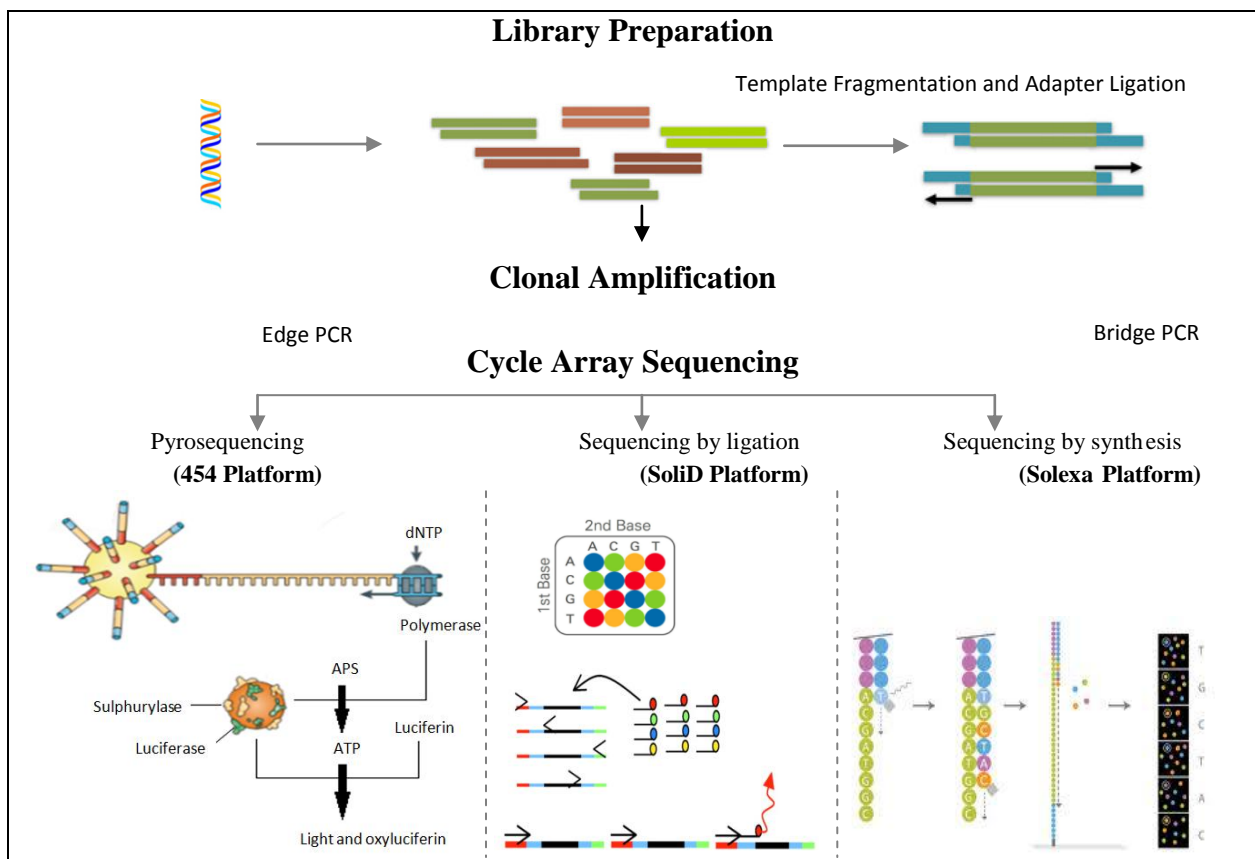
**Figure 5: The data generation and analysis steps of a RNA-Seq experiment.**

**i. Data generation.** RNA is extracted and the DNA contamination is removed using DNase and the RNA is fragmented into short fragments. These fragments are reverse transcribed into cDNA, and adaptors are ligated. Fragments of a particular size are selected. Finally, the cDNAs are sequenced using NGS technologies to produce short reads. Paired-end reads are generated when both ends of the cDNAs are sequenced and Single-end reads are generated when sequencing is performed from one end.

**ii. Data analysis.** Sequencing is followed by pre-processing of reads. Low-quality reads and artefacts like adaptor sequences, contaminant DNA are removed. The sequence errors (black flags) are optionally removed to improve the read quality. This step employs Dynamic trim and Length sort utilities of SolexaQA. The pre-processed reads are then aligned/mapped onto the reference genome and are finally assembled into transcripts. Assembly errors are removed. The transcripts are then post-processed and the expression level of each transcript is then estimated using Cuffdiff or Cuffcompare utility of Cufflinks.

**Illumina Genome Analyzer sequencing:** Adapters are attached to the single stranded template. These modified templates are added to the flow cell and are immobilized by hybridization. They are then subjected to amplification and the clonally amplified clusters are denatured and cleaved. Sequencing is initiated with addition of primer, DNA polymerase and reversible dye terminators. Each nucleotide at incorporation generates fluorescence which is recorded.

**Helicos Biosciences:** A strand of DNA (100-200 bp) is cut into smaller fragments using restriction enzyme and is polyadenylated. These fragments are then hybridized to *polyT* chains that are bound to the surface of Helicos flow cell plate. Each hybridized template is sequenced at once. Labelling is performed in "quads" consisting of 4 cycles, one for each of the 4 nucleotide bases. Fluorescent-labelled bases are added and a laser is used to illuminate the label, taking a read of which strands have taken up that particular labelled base. The label is then cleaved and the next cycle begins with a new base. After the flow cell has been treated with each base (4 cycles) the quad is complete and a new one begins again with the initial nucleotide base.



**Figure 6: Commercially available Sequencing technologies.**

Library preparation involves fragmentation of DNA followed by in vitro adaptor ligation. The fragments are then amplified using PCR: Emulsion PCR or Bridge PCR. Sequencing step consists of an enzymatic reaction which causes emission of light signals corresponding to the nucleotide found in the sequence. These emissions are then recorded in images which are decoded to deduce the sequence.

### 3.4 Transcriptome assembly strategies

Sequencing of the template generates short reads which are subsequently assembled. Depending on whether a reference genome assembly is available, current transcriptome assembly strategies generally fall into one of three categories: a reference-based strategy, a *de novo* strategy or a combined strategy that merges the two (Martin *et al.*, 2011).

#### 3.4.1 Reference-based or *ab initio* based strategy

When a reference genome for the target transcriptome is available, the transcriptome assembly can be built upon it (*Figure 7*). Accurate discovery of novel intron-spanning junctions is important in the discovery of lncRNAs (Illot *et al.*, 2013). RNA-Seq reads are aligned to a reference genome using a splice-aware aligner, such as BLAT (Kent, WZ. 2002), TopHat, MapSplice (Wang *et al.*, 2010) and GSNAP (Wu *et al.*, 2010). The overlapping reads from each locus are then clustered to build a graph representing all possible isoforms. Finally, the graph is traversed to resolve individual isoforms.

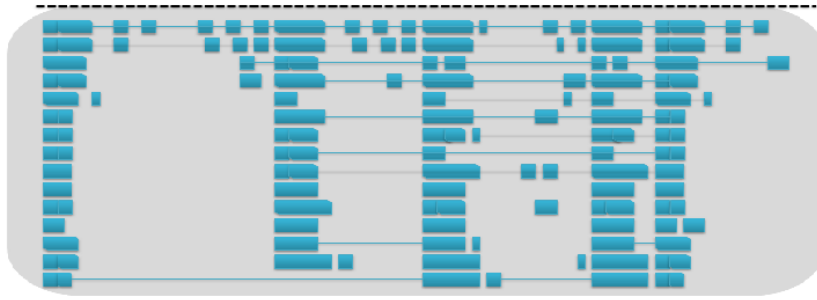
#### *Mapping Algorithms:*

Spliced aware aligners generally use two types of algorithms: seed-and-extend algorithm and Burrows–Wheeler transform (BWT) algorithm. **The seed-and-extend algorithms** rely on finding a 'seed'-a substring of the read-that exactly matches the genome and then locally extending the match using Smith–Waterman alignment algorithms. These aligners shift the gaps in the local alignment to match known splice sites. In **BWT algorithms** a database is created comprising of all possible combinations of splicing junctions within a locus and then the reads that failed to align to the genome are aligned to this database. BWT aligners are optimized to align reads with few errors in them and are therefore generally faster than seed-and-extend aligners (Li *et al.*, 2009).

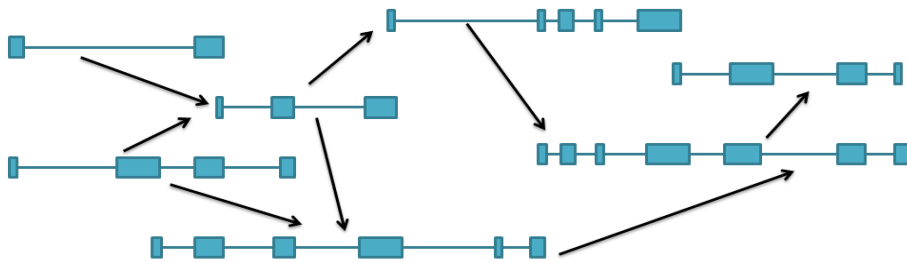
**TopHat** maps reads to the reference and finds junctions in two phases. All the reads are first mapped to the reference genome using Bowtie (Langmead *et al.*, 2009). Bowtie indexes the reference genome using a technique borrowed from data-compression, the Burrows–Wheeler transform. Reads that do not map to the genome are set aside as 'initially unmapped reads', or IUM reads. More than one alignment for a read is reported by Bowtie. The mapped reads are then assembled by TopHat using the assembly module in Maq. For mapping the splice sites, TopHat enumerates all canonical donor and acceptor sites within the island sequences (as well as their reverse complements). It then considers all pairings of these sites that could form canonical (GT–AG) introns between neighbouring islands. Each possible intron is checked against the IUM reads for reads that span the splice junction using seed and extend strategy (Trapnell *et al.*, 2009).



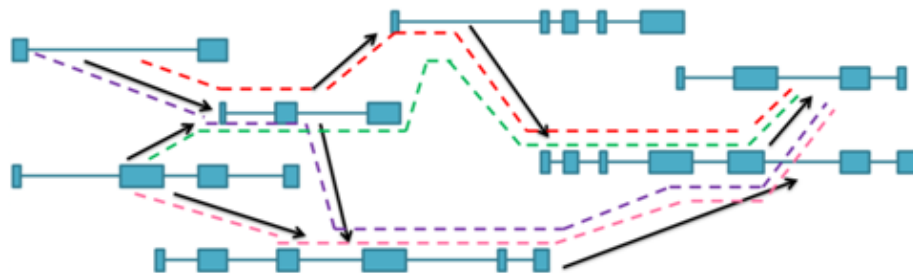
**i. Splice-aligned reads to the reference genome**



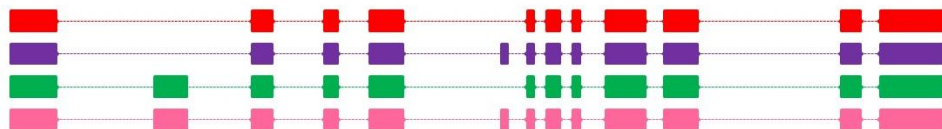
**ii. Graph Construction**



**iii. Traverse the graph**



**iv. Assemble isoforms**



**Figure 7: The reference-based transcriptome assembly strategy.**

**i.** Reads are first splice-aligned to a reference genome. **ii.** A connectivity graph is constructed to symbolize all possible isoforms at a locus. **iii, iv.** Alternative paths through the graph are followed assemble reads together into isoforms.

### ***Transcript Model Reconstruction:***

After alignment to an annotated reference genome, spliced reads are used to reconstruct individual transcripts. Two programs are typically used for graph construction and traversal.

*Cufflinks* is a program that assembles aligned RNA-Seq reads into transcripts, estimates their abundances, and tests for differential expression and regulation transcriptome-wide. It creates an overlap graph from all of the reads that align to a single locus and then traverses this graph to assemble isoforms by finding the minimum set of transcripts that 'explain' the intron junctions within the reads i.e. a minimum path cover of the graph. (Trapnell *et al.*, 2010).

*Scripture* constructs a splice graph containing each base of a chromosome and adds edges (connections) between bases if there is a read that joins the two bases. Scripture then finds all paths through the graph that have a statistically significant read coverage (Guttman *et al.*, 2010).

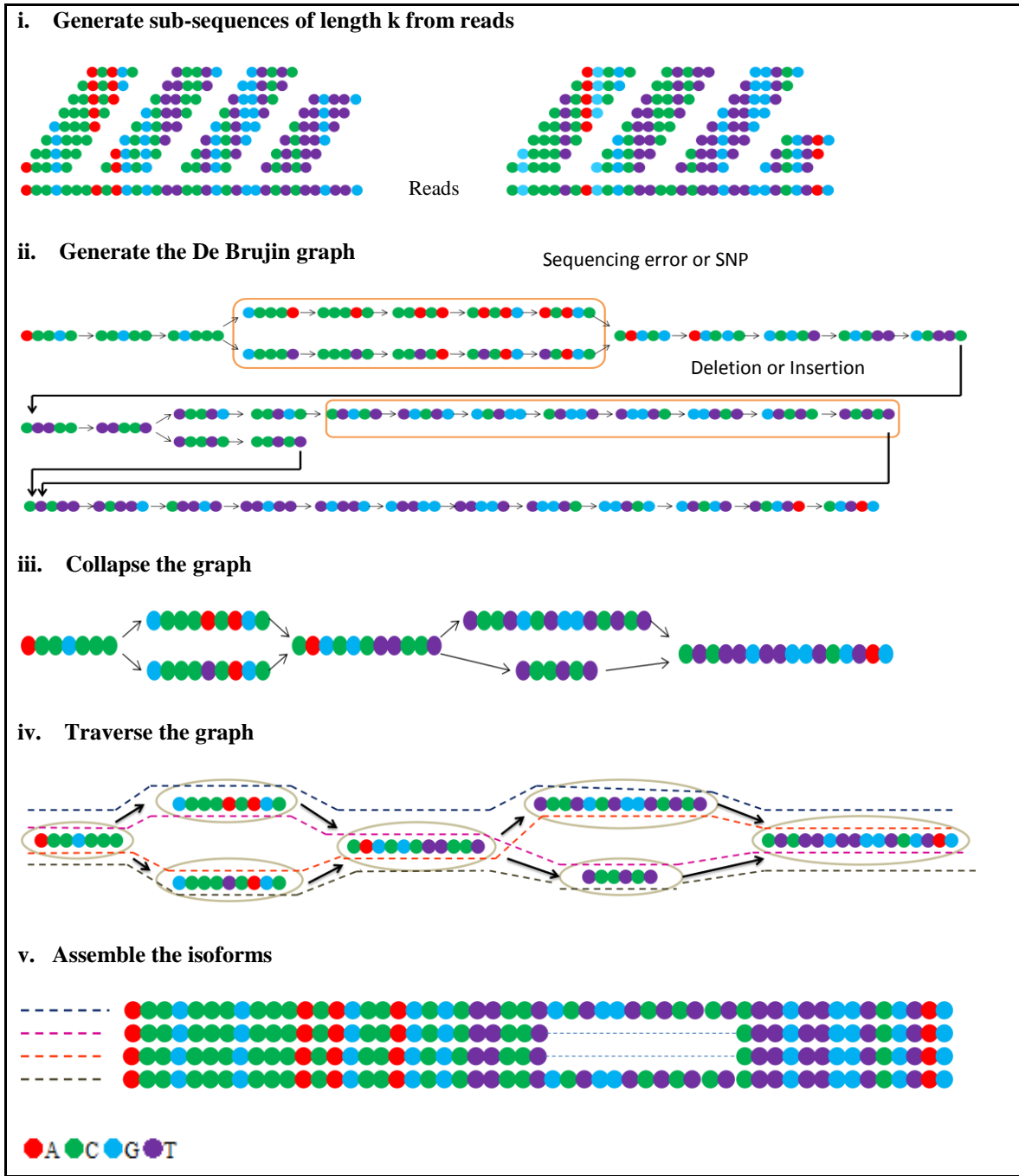
Though both these methods relies on map-first strategy, the differences in graph construction and traversal methods suggest that *Cufflinks is more conservative in its choice of which transcripts to re-construct*, whereas Scripture may produce a larger set of transcripts from a locus.

### **3.4.2 *De novo* strategy**

The *de novo* transcriptome assembly strategy does not use a reference genome: it leverages the redundancy of short-read sequencing to find overlaps between the reads and assembles them into transcripts. These algorithms represent strategies originally used for genome assembly using short read data. Temporarily, short sequences (k-mers) are detected among sequence reads, and those reads that share a particular k-mer are overlapped and assembled into contigs, scaffolds and eventually transcript models (Figure 8).

The *Rnnotator15*, *Multiple-k19* and *Trans-ABYSS18* (Robertson *et al.*, 2010) assemblers assemble the data set multiple times using a *De Bruijn* graph-based approach to reconstruct transcripts from a broad range of expression levels and then post-process the assembly to merge contigs and remove redundancy. *Trinity59* and *Oases* directly traverse the *De Bruijn* graph to assemble each isoform.

***De novo* assemblers are not a preferable choice for studies related to LncRNAs as they do not perform well across the range of low expression values of lncRNA** (Illot *et al.*, 2013).



**Figure 8: The *de novo* transcriptome assembly strategy.**

**i.** Subsequences of length  $k$  (5 mers) are generated from each read. **ii.** Each unique  $k$ -mer is used to represent a node in the De Bruijn graph. If by shifting one character in a  $k$ -mer, an exact  $k-1$  overlap between the two  $k$ -mer is created, the pairs of nodes are connected. SNPs cause 'bubbles' in the De Bruijn graph, whereas introns or deletions generate shorter path in the graph. **iii, iv.** The adjacent nodes in the graph are collapsed into a single node and possible alternative paths through the graph are chosen. **v.** The isoforms are subsequently assembled.

### 3.4.3 Combined strategy

Reference-based and *de novo* strategies can be combined to create a more comprehensive transcriptome. Combine strategy offers advantages of the high sensitivity of reference-based assemblers while leveraging the ability of *de novo* assemblers to detect novel and *trans-spliced* transcripts. Generally, the combined assembly strategy can be carried out by first either aligning the reads to the reference genome or by *de novo* assembling the reads (*Figure 9*).

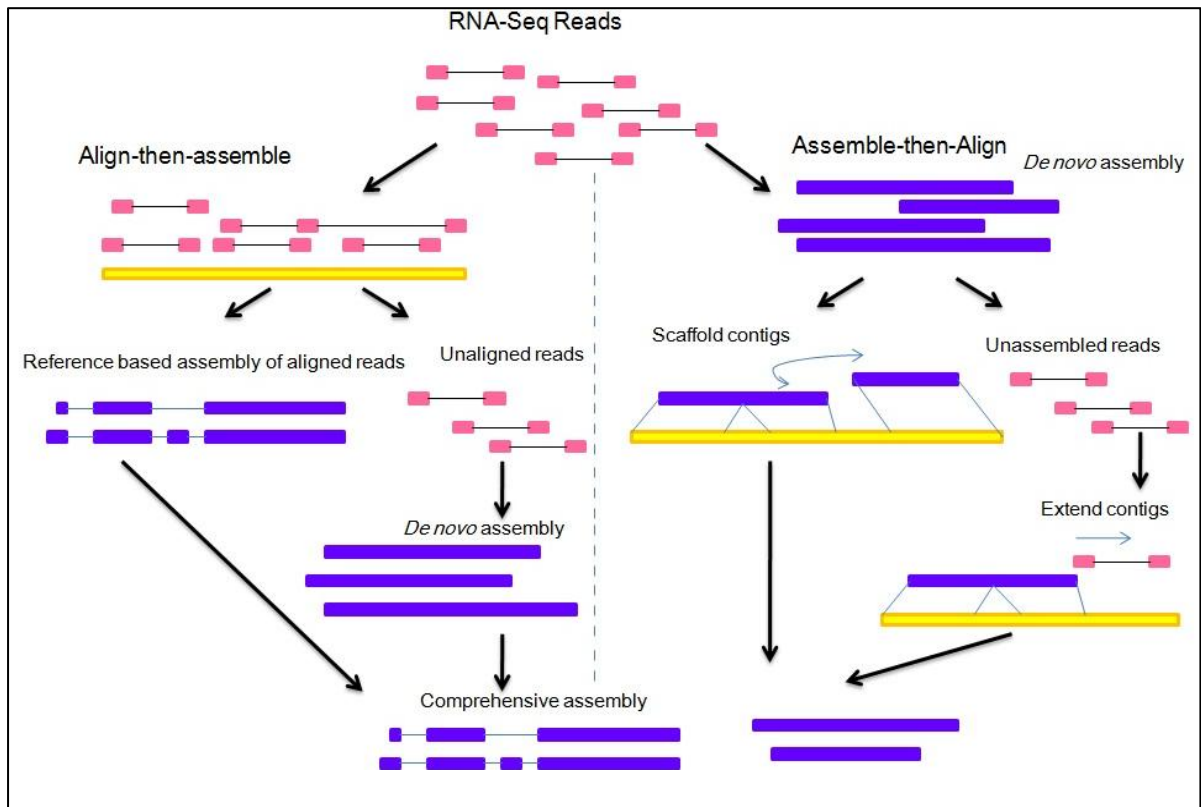
#### *Align-then-assemble:*

Instinctively, when a reference genome is available, the combined approach should start by aligning the data set to the reference genome, followed by *de novo* assembling the reads that failed to align to the genome. Alternatively, the transcripts that result from the reference-based assembly could also serve as input to the *de novo* assembly. This align-then-assemble approach is the preferred method for quickly filtering out unwanted sequences. For example, for pathogen detection, in which reads of human origin are filtered out before assembly.

#### *Assemble-then-align:*

If the quality of the reference genome is called into question or if the reference genome is from a different but closely related species, *de novo* assembly should be performed first, followed by alignment of the contigs to the reference to extend and scaffold contigs.

The main advantage of this approach is that errors in the genome assembly do not get propagated into the assembled transcripts. The *de novo* assembly generates more fragmented transcripts than reference-based assembly. By aligning both the assembled transcripts and the unassembled reads to the reference genome, or to a closely related genome, incomplete transcripts can be merged or extended to form longer, possibly full-length transcripts. Gaps between fragments of the same transcript can also be joined and filled in using the reference genomic sequence. The protein sequences can also be used for the alignment step if the sequence similarity at the RNA level is not sufficient.



**Figure 9: Two approaches for combined transcriptome assembly.**

**Align-then-assemble strategy:** Reference-based assembly is followed by *de novo* assembly of unaligned reads.

**Assemble-then-align strategy:** The reads are first *de novo* assembled and then scaffold are formed and extended using a reference genome. RNA Sequencing (RNA-Seq) reads are colour coded in pink, and assembled transcripts in cobalt blue.

### 3.5 Assessing Protein Coding Potential for characterization of lncRNA

Upon the assembly of a transcript set, two steps are required to separate coding from putatively non-coding transcripts.

- a. The transcripts representing known protein coding genes are required to be removed. This can be achieved by removing transcripts that contain overlapping genomic coordinates with existing protein coding annotations from one or several of currently available sources, such as Ensembl, Broad Institute, RefSeq or UCSC.
- b. The potential for an lncRNA transcript to encode a protein should be calculated. For this purpose methods based on open reading frame (ORF)-based and comparative sequence analysis can be used (Illot *et al.*, 2013).

#### 3.5.1 ORF based analyses

In this method, the putative transcripts are translated into conceptual proteins in all six and a comparison against known protein coding sequences and protein domain families in databases such as PFAM or SwissProt is performed using BLASTX. The length of ORFs is another criterion which can be used for classification of transcripts, as the majority of protein coding genes are considered to have ORFs exceeding 100 amino acids. Alternatively, one can use contemporary tools like the coding potential calculator (CPC) for assessing protein coding potential. CPC uses information from both homology and the presence and integrity of ORFs. Its support vector machine (SVM) framework is trained on known sets of protein coding and non-coding transcripts. It extracts six features from the transcript's nucleotide sequence. When a set of unknown sequences are provided it gives a score based on the distance from the classification hyperplane (see *Appendix III*). A threshold has to be defined to entitle a transcript as non-coding (Kong *et al.*, 2007).

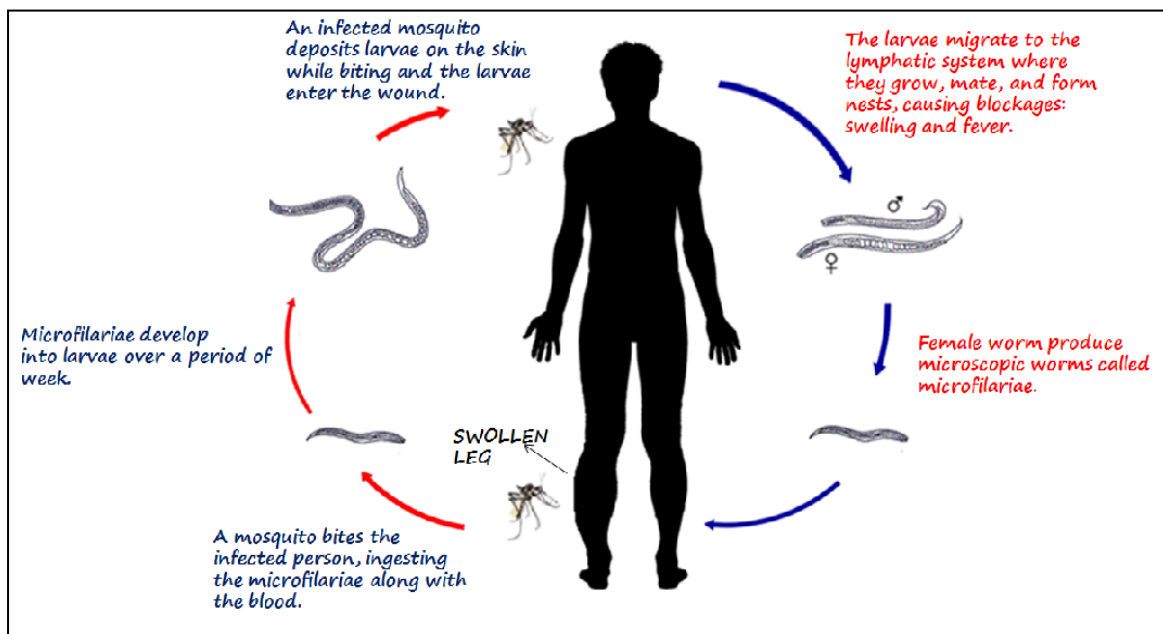
#### 3.5.2 Comparative sequence analysis

It relies on the conservation of amino acid sequence that is evident from multiple species alignments. Codon substitution frequency (CSF) method is based on the expected frequency of nucleotide substitutions at all positions in a codon between a query sequence and homologous sequences. Purifying selection acts differentially on non-synonymous and synonymous sites, and this distinction can be used to deduce the potential of any aligned sequence to encode protein. Another method named phyloCSF (Lin *et al.*, 2011) exploits a statistical model comparison framework to compare two models for each transcript of interest: one with coding model parameters and one with non-coding model parameters. Using maximum likelihood estimation, these models are compared and transcripts are designated as most probably coding or else non-coding.

### 3.6 Choice of Species

Despite their importance globally, both medically and economically, parasitic helminth (worm) research has remained relatively untouched by genomics. Worm infections account for morbidity equivalent to more than 100 million disability-adjusted life years from more than one billion infections globally.

*Brugia malayi* is a parasitic nematode that is one of the causative agents of lymphatic filariasis in humans. Lymphatic filariasis is a chronic, debilitating condition characterized by swelling of the lower limbs, restricted to South and South East Asia. The lifecycle of *B. malayi* involves four life stages in a mosquito host (*Culex*, *Aedes* and *Anopheles*), after which infectious microfilariae are transmitted to human hosts (Figure 10). Elephantiasis (edema with thickening of the skin and underlying tissues) results when the parasites lodge in the lymphatic system of the host leading to physical and sexual disabilities. *Brugia malayi* contains a *Wolbachia* endosymbiont, with horizontal gene transfer occurring. It is believed that *Wolbachia* aids in the embryogenesis of the worm and may be responsible for potent inflammatory responses caused in filarial disease.



**Figure 10: Life Cycle of Nematodes.**

The reproductive cycle of Nematodes begins when a mosquito acquires the sheathed microfilaria (MF) parasite in its blood meal. MF loses their sheath in the gut wall of its intermediate host and migrates to its thorax muscles. After 10 to 20 days, they develop into the infective third larval stage which migrates to the proboscis of the mosquito. During the mosquito's next blood meal, the larvae enter the wound of the human host and migrate from the subcutaneous tissue to the lymphatic vessels. They mature into adults and after reproduction the vicious cycle is repeated.

The available anti-filarial drugs being administered have substantial limitations as they are ineffective against all life cycle stages of worm; require repeated and prolonged treatment

over years. Emergence of drug resistance imposes an additional threat. The 50 Helminth Genomes Initiative is collaborative project that aims to survey the genomes of nematodes and platyhelminths that are either of medical or veterinary importance. Preliminary Illumina sequencing from these helminth species can be used to produce draft genomic assemblies which will create a unique genomic resource.

The draft genome of *Brugia malayi* has already been reported (Ghedini *et al.*, 2007). This genomic information gives us an insight into the importance of various genes in the parasite's life cycle. These genes can be targeted to interrupt *Brugia malayi*'s life cycle. To further understand the host-parasite interactions, various studies have been conducted on *B. malayi* genome including transcriptome profiling of protein coding genes (Choi *et al.*, 2011) and proteomic analysis (Bennuru *et al.*, 2009). But to date, the lncRNAs of *B. malayi* have not been studied. With a belief that as lncRNAs are gaining popularity in the scientific community, an insight into the non-coding content of *Brugia malayi* may solve the intricacies.



## 4. METHODOLOGY

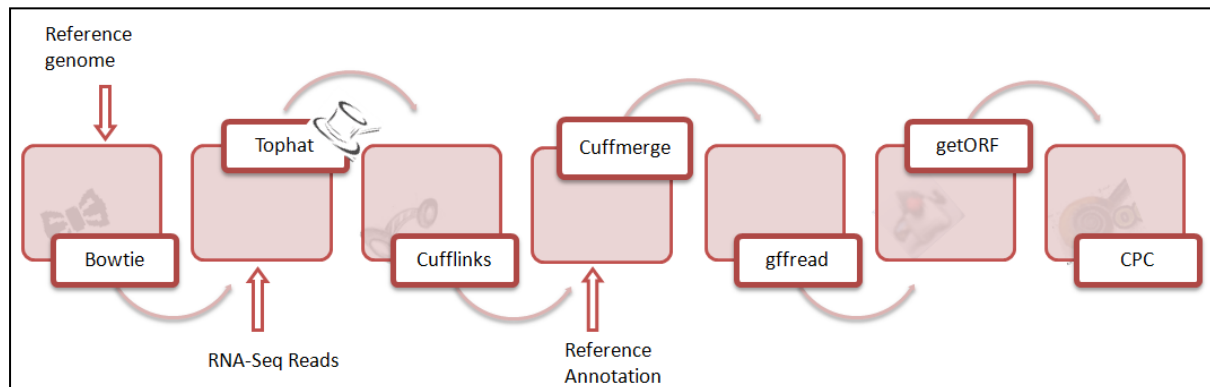


Figure 11: Pipeline used for Identification of lncRNA.

### 4.1 Data Collection

#### 4.1.1 RNA-Seq Reads:

The RNA-Seq data in SRA format was downloaded from DNA-nexus Sequence Read Archive (<http://sra.dnanexus.com/>) [Study: ERP000948].

#### 4.1.2 Reference genome:

The reference genome for *Brugia malayi* was downloaded from NCBI ID 42. Using **Bowtie2-2.1.0** (<https://sourceforge.net/projects/bowtie-bio/files/bowtie2/2.1.0>), an index for the reference genome was created.

#### 4.1.3 Annotation File:

Annotation file for *Brugia malayi* was obtained in the gtf format from the Filarial Worm Database provided by the Broad Institute of MIT and Harvard.

([http://www.broadinstitute.org/annotation/genome/filarial\\_worms/GenomeDescriptions.html#Brugia\\_malayi\\_GB](http://www.broadinstitute.org/annotation/genome/filarial_worms/GenomeDescriptions.html#Brugia_malayi_GB)).

### 4.2 Data Pre-processing

All the reads were converted to Fastq format using **SRA-Toolkit-2.3.2** (<http://ftp-trace.ncbi.nlm.nih.gov/sra/sdk/2.3.2-5/sratoolkit.2.3.2-5-ubuntu64.tar.gz>). Before carrying out the downstream analysis, the data should be checked for quality, as sequencing error rates are high. FastQC, a visualization software can be used to decide a threshold value for the phred quality scores. All the reads were then trimmed and sorted using DynamicTrim and LengthSort

modules of *SolexaQA\_v\_2.1* (<https://sourceforge.net/projects/solexaqa/files/latest/download?source=files>) at a phred quality score of 20 and length of 36, respectively.

DynamicTrim is designed to trim each read to its longest contiguous segment to improve its quality until its quality score exceed user specified quality cutoff. LengthSort separate low quality reads from high quality reads based on length of reads specified by user.

The screenshot shows the SRA homepage with a search bar containing 'Brugia malayi'. Below the search bar, there are two study results listed in a table. The first study is ERP001255, titled 'Transcriptomic analysis of Brugia malayi-elicited alternatively activated macrophages', with organism 'Mus musculus' and type 'RNASeq'. The second study is ERP000948, titled 'Brugia malayi transcriptomics at different life cycle stages', with organism 'Brugia malayi' and type 'RNASeq'. The table includes columns for Accession, Title, Organism(s), Type, Description, Submitter, Submission(s), and Related. There are also filter options on the left for Organism and Type, and navigation buttons like 'Download', 'Related Experiments', 'Related Samples', and 'Related Runs'.

ACCESSION	TITLE	ORGANISM(S)	TYPE	DESCRIPTION	SUBMITTER	SUBMISSION(S)	RELATED
ERP001255	Transcriptomic analysis of Brugia malayi-elicited alternatively activated macrophages	Mus musculus	RNASeq	RNA-Seq expression profiling of flow cytometry sorted macrophages obtained from BALB/c and IL4Ra-/- mice via thioglycollate-elicitation or Brugia m...	The University of Edinburgh	ERA092892	1 1 2
ERP000948	Brugia malayi transcriptomics at different life cycle stages	Brugia malayi	RNASeq	High-throughput sequencing to profile the transcriptome of the human filarial nematode Brugia malayi, the causative agent of lymphatic filariasis, ...	The Sanger Center	ERA063078	14 8 14

Figure 12: Homepage of Sequence Read Archive (SRA): DNA Nexus.

The screenshot shows the ENA homepage with a navigation menu at the top including 'ENA Home', 'Search & Browse', 'Submit & Update', 'About ENA', 'Contact', and 'FAQ'. The main content area features a 'Text search' box with 'Brugia malayi' entered and a 'Search' button. Below it is a 'Sequence Search' box with a placeholder 'Enter or paste a nucleotide sequence or accession number' and a 'Search' button. There is also a 'NEWS AND ANNOUNCEMENTS' section on the left with several news items and a 'View all news' link.

Figure 13: Homepage of European Nucleotide Archive (ENA).

### 4.3 Alignment of Reads

**Tophat-2.0.8** ([http://tophat.cbcb.umd.edu/downloads/tophat-2.0.8b.Linux\\_x86\\_64.tar.gz](http://tophat.cbcb.umd.edu/downloads/tophat-2.0.8b.Linux_x86_64.tar.gz)) was used for aligning the reads onto the reference genome. The \*.paired1 and \*.paired2 files generated after LengthSort was used as input. TopHat can identify exon-exon splice junctions and use Bowtie as an aligner. For reporting alignments across "GT-AG" introns, the --coverage-search option was used. The mate-pair distance (depicted by 'r' in TopHat) for the reads was also provided the dataset was paired-end. The fragment size selected at the time of data generation ranged from 200 to 275 nucleotides and the read length was 54. So, using the below mentioned formula, the mate pair distance was taken to be 141.

$$\text{Mate pair distance (r)} = \text{Fragment size} - 2 * \text{Read length}$$

The aligned data provide information about the mapped and unmapped reads, deletions, insertions and mismatched sequences in the sample. This information can be used to find out the polymorphisms between the sequenced reads and the reference genome. Alignments can also be used to precisely quantify gene and transcript expression, as the no. of reads produced by a transcript is relative to its abundance.

After the alignment, the *accepted\_hits.bam* files containing the mapped reads were converted to SAM format using *samtools-0.1.18* (<http://sourceforge.net/projects/samtools/files/latest/download?source=files>).

### 4.4 Transcriptome Assembly

The individual alignment (SAM) files for the reads were then used as input to **Cufflinks-2.1.1** (<http://cufflinks.cbcb.umd.edu/downloads/>) that generated one transcriptome assembly (*transcripts.gtf*) per read, containing Cufflinks' assembled isoforms. Different isoforms of a given gene produce different expression level which depends on the splice variants of that gene.

**Cuffmerge**, an utility of Cufflinks package, was used to merge all the assemblies along with the reference annotation into a single transcriptome assembly (*merged.gtf*).

### 4.5 Sequence Extraction

The sequences of the transcripts were then extracted using **gffread** utility of the Cufflinks package which gave a multi-fasta file (*transcript.fa*) as output. As lncRNAs have been reported to be longer than 200 nucleotides, transcripts with a length greater than 200 nucleotides were retrieved for downstream analysis using *custom* perl scripts.

## 4.6 Identification of Long Non-Coding RNA

There are 2 main criteria for characterizing a transcript as lncRNA:

1. It should usually lack an open reading frame.
2. It generally should not code for any protein.

This step employed Coding Potential Calculator and ORF prediction tools like Jemboss and ORF Finder.

*getORF* utility of Emboss package was used to find ORFs in the predicted transcripts. The transcripts with ORFs having a length of equal or greater than 30 amino acids in any of the six frames were removed. As, the genes are multi-output and generate both coding and non coding transcripts, so the remaining transcripts were further filtered with a criterion that all transcript isoforms arising out of a locus should be non-coding. The genes with coding transcripts were entirely removed using *custom* perl scripts. The gene ids (*XLOC*) of the coding transcripts (discarded earlier) were retrieved and then all the transcript ids (*TCONS*) of those genes were removed from the Jemboss output.

*Coding Potential Calculator (CPC)* (<http://cpc.cbi.pku.edu.cn/download/cpc-0.9-r2.tar.gz>) was used to calculate the coding potential of the remaining sequences from above in all 6 reading frames and those with cpc score greater than -0.1 were discarded. Sequences for the probable lncRNAs were retrieved.

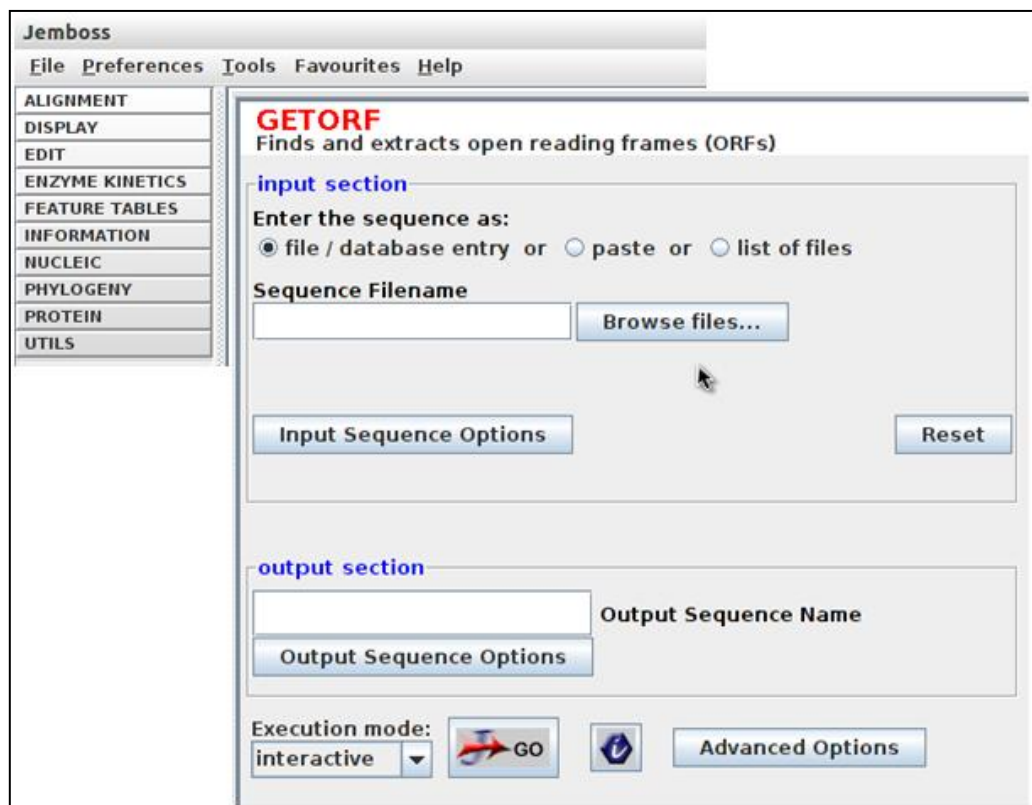


Figure 14: Graphical User Interface of Jemboss.

## 4.7 Differential Expression Analysis

The differential expression of lncRNAs was determined in different development stages using *cuffdiff* utility of cufflinks and various R packages. The binary alignment map (BAM) files from TopHat along with the merged output from Cuffmerge were provided as input to cuffdiff to study the changes in expression levels of transcripts. Cuffdiff calculates expression levels and tests the statistical significance of observed changes. It also identifies the genes that are differentially regulated at the transcriptional or post-transcriptional level, by grouping the transcripts into biological meaningful groups (e.g. transcripts that share the same TSS). *CummeRbund* (<http://www.bioconductor.org/biocLite>) was used to build a database from the cuffdiff output and expression plots such as volcano, scatter and box plots were created.

We also used *DESeq* (<http://www.bioconductor.org/biocLite>) to compare the differential expression patterns. DeSeq uses negative binomial distribution and uses the counts of mapped reads to look for differential expression in genes. Count tables for each read were created from sorted BAM files using *HTSeq* (<http://www-huber.embl.de/users/anders/HTSeq/doc/install.html#installation-on-linux>). Counts for the lncRNAs were retrieved which were then used to create Heat Map and PCA Plots depicting the relative expression of lncRNAs.

## 4.8 Homology Analysis

The sequences of probable lncRNA were mapped onto the genome of *Wolbachia*, *C. elegans* and *Wuchereria bancrofti* using BLAT (Blast like Alignment Tool) at default parameters, with an assumption that if reported lncRNAs are pathogenic:

- i. They should not show any homology with *C. elegans* as it is a non-pathogenic species;
- ii. They should exhibit some level of similarity with the genome of *Wuchereria bancrofti* as it is also a causative agent of Lymphatic filariasis.

We also anticipated a little similarity with *Wolbachia* as an evidence of horizontal gene transfer.

*(See Appendix I and II for the commands and perl scripts used at each step)*

## 5. RESULTS

### 5.1 Data Collection

The transcriptome dataset available at SRA contained 8 samples comprising 14 datasets of different life-cycle stages of *Brugia malayi*. All the reads were paired-end and the sequencing was performed on Illumina genome Analyzer II. The reads obtained in SRA format were converted to fastq using the SRA Toolkit-2.3.2.

The preliminary RNA-Seq experimental data of *Brugia malayi* is given in *Table 1*. The condition and developmental stages were noted against each entry (depending on their availability).

### 5.2 Data Pre-processing

3 reads were discarded (ERR048964, ERR048966 and ERR048968) from the dataset due to poor quality scores and low mapping percentages.

### 5.3 Alignment of Reads

Out of the total 77,300,329 reads in remaining 11 samples, 73,043,519 reads were accepted by TopHat at this step and 62,043,358 were mapped onto the reference genome. The statistics for the individual samples has been provided in *Table 2*.

### 5.4 Transcriptome Assembly

Transcriptome assembly of mapped data produced genomic co-ordinates of all the transcripts. A total of 168,602 transcripts were reported in all the stages. The stages *Adult Female* and *Larvae 3* produced the maximum and minimum number of transcripts, i.e. 52,211 and 10,544, respectively. All the assemblies were then merged using cuffmerge producing a total of 19,059 unique genes with 34,473 unique transcripts.

### 5.5 Sequence Extraction

The sequences for the 34,473 transcripts from the merged assembly were retrieved using gffread and the ones with length greater than 200 nucleotides were removed using *custom perl* scripts. This was done to filter out the probable coding sequences. 29,558 sequences were left for further analysis.

**Table 1: The preliminary RNA-Seq experimental data of *B. Malayi***

Study	Sample	Run	Instrument Model	Library Layout	Run Read Count	Run Base Count	Developmental Stage
ERP000948	ERS067026	ERR048961	Illumina Genome Analyzer II	PAIRED	1,09,87,792	1 Gb	Adult Male
ERP000948	ERS067029	ERR048962	Illumina Genome Analyzer II	PAIRED	1,09,52,058	1 Gb	Adult Female
ERP000948	ERS067030	ERR048963	Illumina Genome Analyzer II	PAIRED	88,36,580	954 Mb	L4 stage
ERP000948	ERS067025	ERR048964	Illumina Genome Analyzer II	PAIRED	56,28,758	607 Mb	L3 stage
ERP000948	ERS067032	ERR048965	Illumina Genome Analyzer II	PAIRED	79,79,044	861 Mb	Microfilariae
ERP000948	ERS067028	ERR048966	Illumina Genome Analyzer II	PAIRED	40,90,544	441 Mb	Immature Female
ERP000948	ERS067031	ERR048967	Illumina Genome Analyzer II	PAIRED	46,98,815	507 Mb	Eggs/embryos
ERP000948	ERS067028	ERR048968	Illumina Genome Analyzer II	PAIRED	77,39,107	835 Mb	Immature Female
ERP000948	ERS067031	ERR048969	Illumina Genome Analyzer II	PAIRED	88,23,462	952 Mb	Eggs/embryos
ERP000948	ERS067029	ERR048970	Illumina Genome Analyzer II	PAIRED	73,93,184	798 Mb	Adult Female
ERP000948	ERS067030	ERR048971	Illumina Genome Analyzer II	PAIRED	56,30,427	608 Mb	L4 stage
ERP000948	ERS067029	ERR048972	Illumina Genome Analyzer II	PAIRED	1,77,84,939	1 Gb	Adult Female
ERP000948	ERS067030	ERR048973	Illumina Genome Analyzer II	PAIRED	91,63,535	989 Mb	L4 stage
ERP000948	ERS067027	ERR048974	Illumina Genome Analyzer II	PAIRED	2,70,21,114	2 Gb	L3 stage

**Table 2: Dataset of different developmental stages of *B. malayi* along with mapping percentages and assembled transcripts.**

STAGE	Accession ID	Total Reads	Reads Mapped	Mapping Percentage	Transcripts
Eggs/Embryos	ERR048967	2,700,478	2,508,143	89.65	17,719
	ERR048969	4,633,606	4,355,394	89.99	18,677
Microfilariae	ERR048965	4,235,847	3,993,945	82.20	14,358
L3 stage	ERR048974	25,611,574	24,117,779	87.11	10,544
L4 stage	ERR048963	3,032,839	2,810,319	82.84	13,648
	ERR048971	3,568,897	3,434,856	72.06	12,775
	ERR048973	5,720,399	5,511,625	73.52	14,175
Adult Male	ERR048961	5,903,617	5,373,019	87.81	14,495
Adult Female	ERR048962	4,595,941	4,310,062	86.14	16,186
	ERR048970	5,668,700	5,476,947	80.41	16,572
	ERR048972	11,628,431	11,151,430	88.70	19,453

## 5.6 Identification of Long Non-Coding RNA

The getorf utility of Jemboss provided the probable open reading frames (ORFs) of all the transcripts. The transcripts having any ORF with length greater than 30 amino acids (aa) were discarded. A total of 28,447 transcripts were discarded from the getorf output which are probably the coding sequences. Any gene with a transcript having ORF length greater than 30 aa was also discarded.

The coding Potential of the remaining 998 sequences was calculated using Coding Potential Calculator (CPC) and transcripts having CPC score less than -0.1 were retained. The CPC output provided 997 transcripts of 982 genes which were denoted as the long non-coding RNA of *B. malayi*.

## 5.7 Differential Expression Analysis

The lncRNAs were analysed for their specific expression in different life-cycle stages of *B. malayi*. The cuffdiff utility of cufflinks was used to get differentially expressed genes. Transcripts abundances were calculated using Fragments Per Kilobase of exon per Million fragments mapped (FPKM) (See Appendix IV). The FPKM values were used to study the sex and stage specific expression.



The cuffdiff results were given as input to CummeRbund which stores the output in SQLite format and analyze it. The stage *Eggs/Embryos* was found to have maximum number of lncRNAs i.e. 855 expressed with a unique number of 58. On the other hand, *Microfilariae* had the minimum number 457 of lncRNAs with a unique number of 1. Various statistical Plots were generated to visualize these results (Figure 15-19). PCA Plot and Heat Map depicting the expression of lncRNAs were generated using DESeq (Figure 20, 21). Sex and Stage specific expression was also accounted (Figure 22, 23).

## 5.8 Homology Analysis

Mapping of probable lncRNA onto the genome of *Wolbachia*, *C. elegans* and *Wuchereria bancrofti* proved all our assumptions to be factual. lncRNAs of *B. malayi* showed significant similarity with *W. bancrofti* whereas with *C. elegans* the conservation was approximately 30 percent.

Only one lncRNA matched with the genome of *Wolbachia* with a conservation of 55, indicating no probable relation of horizontal transfers of lncRNAs.

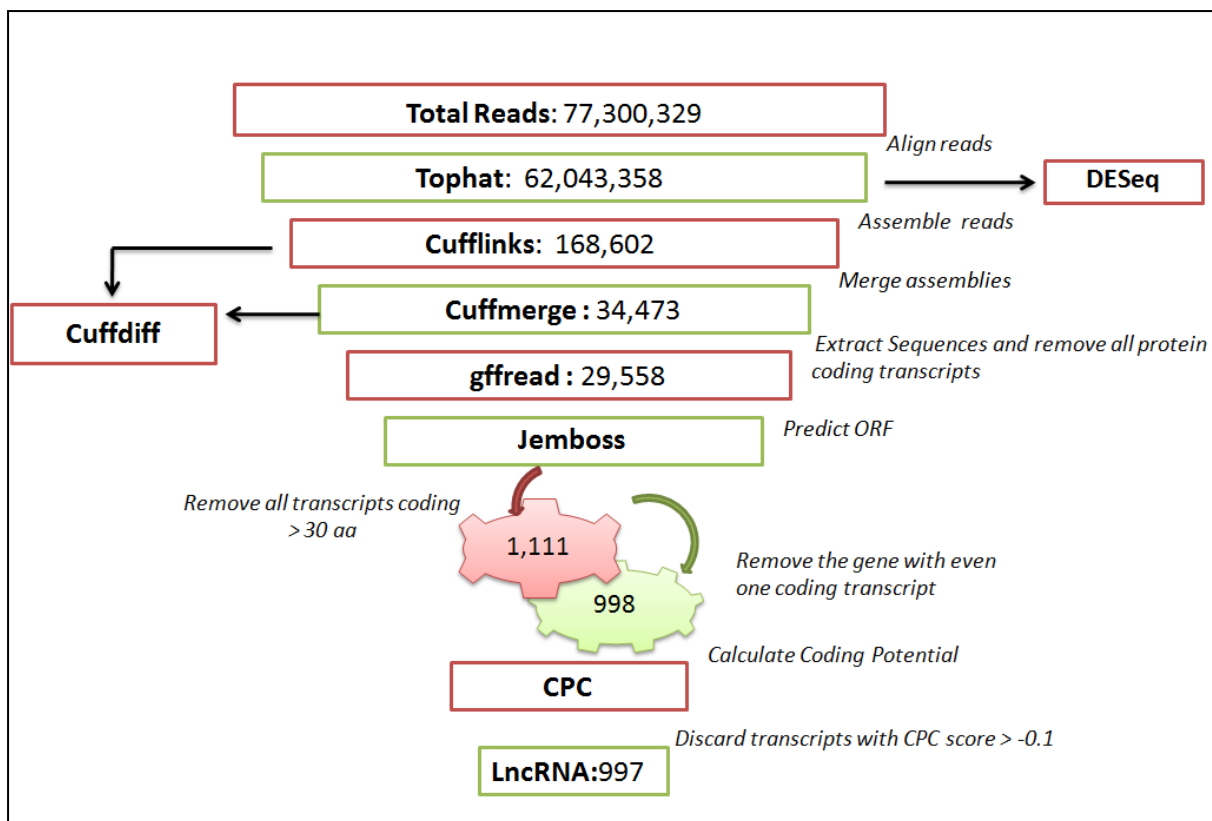
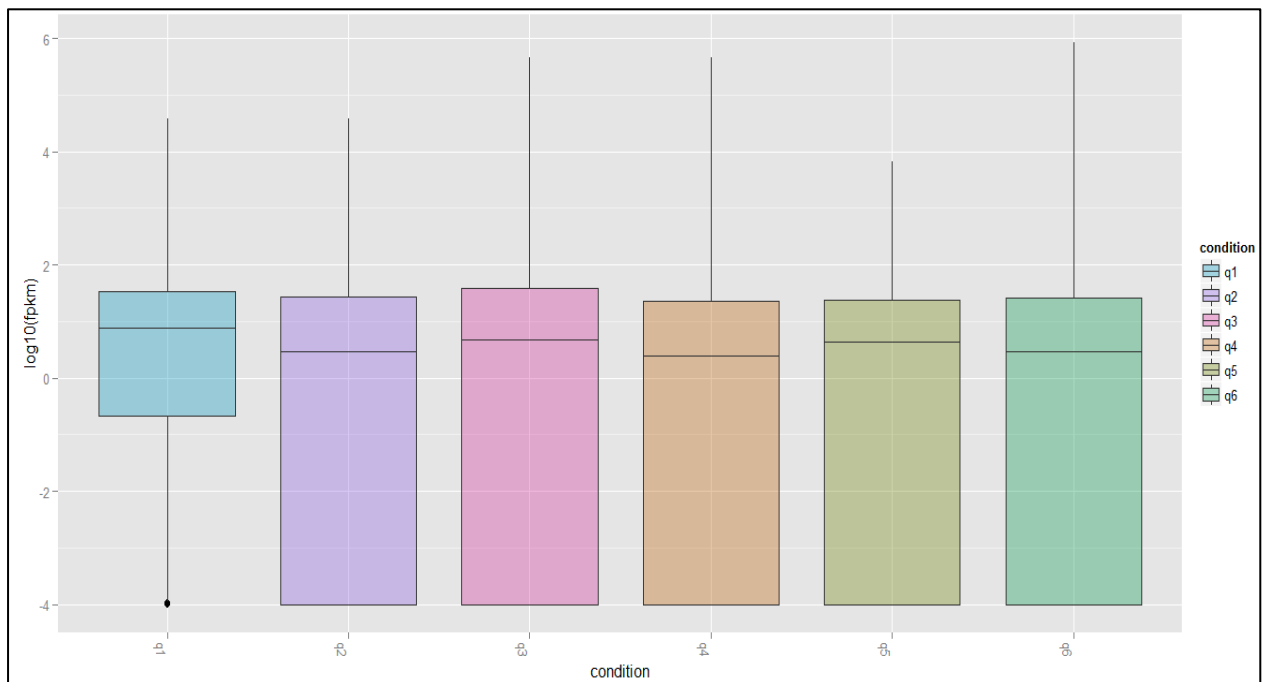


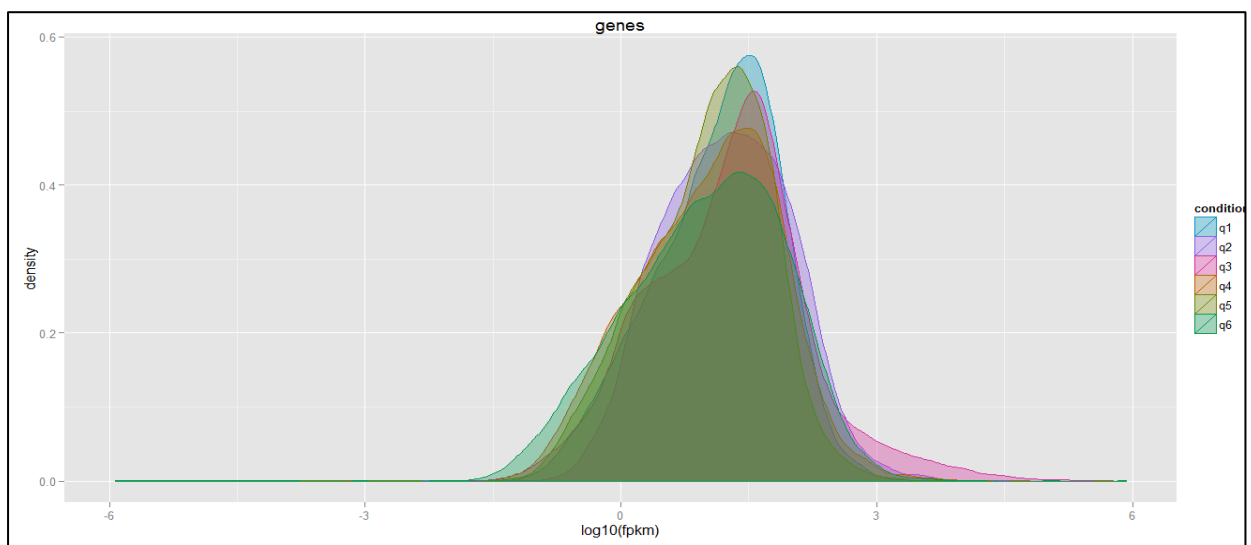
Figure 15: Flowchart representing the *in-house* pipeline adopted for this study.



**Figure 16: Box plot depicting distribution of fpkm in different stages of *B. malayi*.**

The y-axis denotes the log normalized values of FPKM which is Fragments Per Kilobase of exon per Million fragments mapped used to calculate transcript abundances. The x-axis denotes different developmental stages.

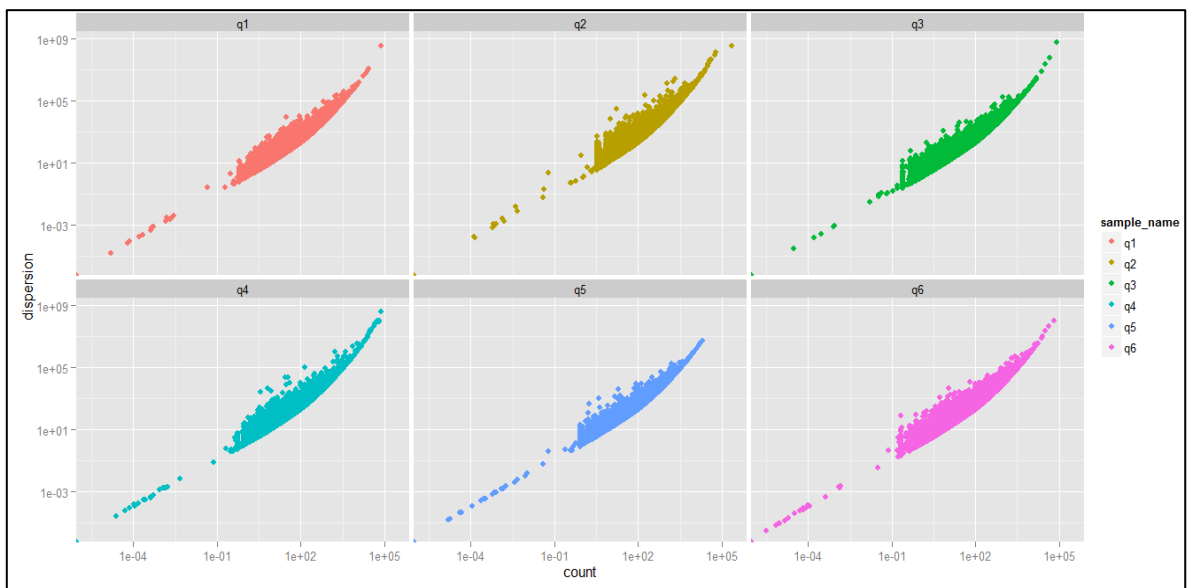
[q1: Eggs/Embryos, q2: Microfilariae, q3: Larvae 3, q4: Larvae 4, q5: Adult male, q6: Adult Female]



**Figure 17: Density plot depicting distribution of fpkm in different stages of *B. malayi*.**

The x-axis denotes the log normalized values of FPKM which is Fragments Per Kilobase of exon per Million fragments mapped used to calculate transcript abundances. The y-axis denotes the density.

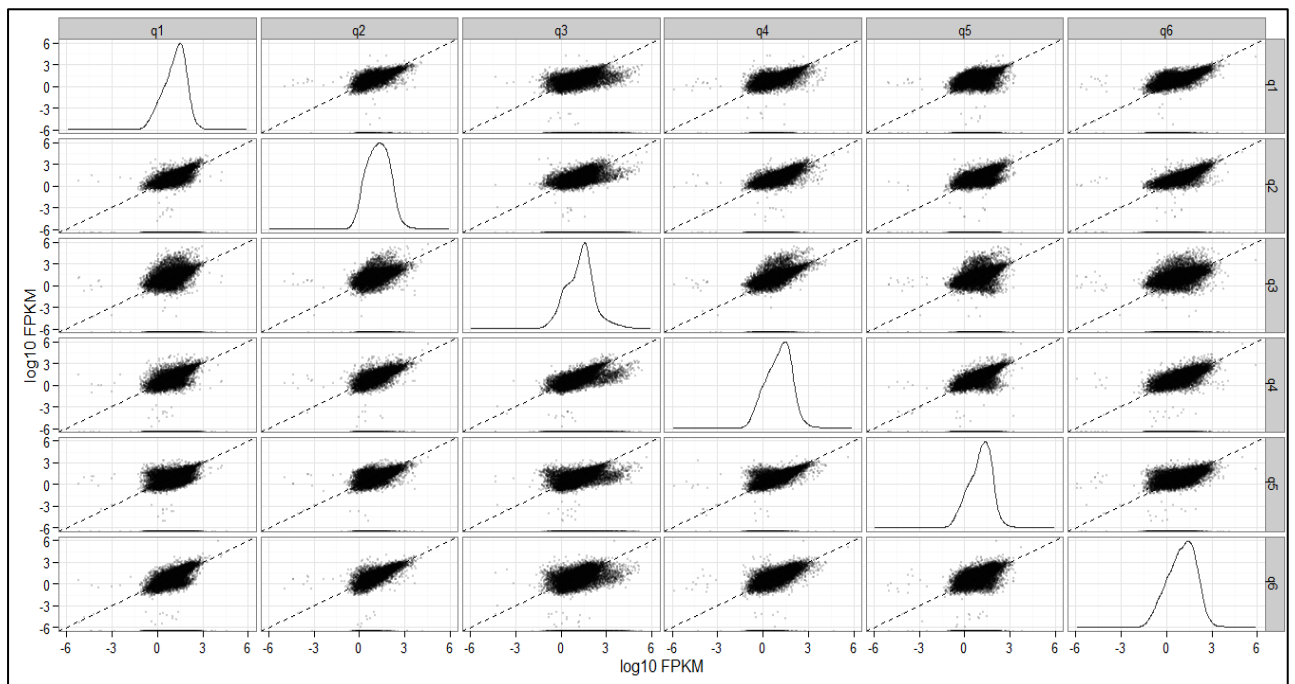
[q1: Eggs/Embryos, q2: Microfilariae, q3: Larvae 3, q4: Larvae 4, q5: Adult male, q6: Adult Female]



**Figure 18: Dispersion plot for different stages of *B. malayi*.**

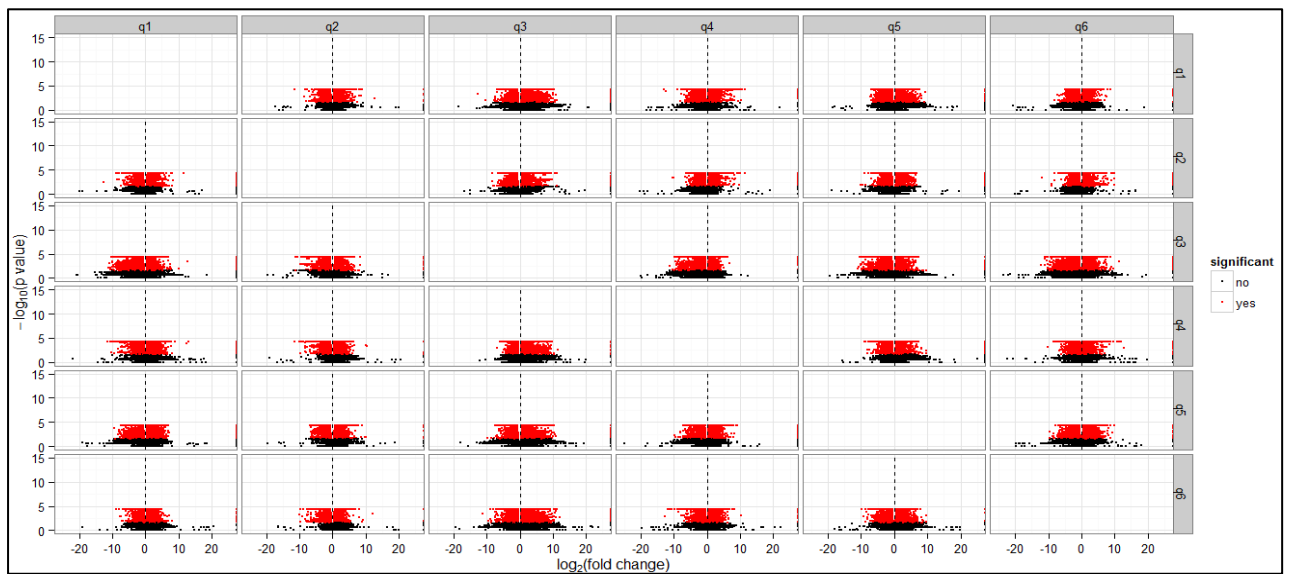
The x-axis denotes the dispersion values and the y axis denotes the counts.

[q1: Eggs/Embryos, q2: Microfilariae, q3: Larvae 3, q4: Larvae 4, q5: Adult male, q6: Adult Female]



**Figure 19: Scatter plot for different stages of *B. malayi*.**

[q1: Eggs/Embryos, q2: Microfilariae, q3: Larvae 3, q4: Larvae 4, q5: Adult male, q6: Adult Female]



**Figure 20: Volcano plot for different stages of *B. malayi*.**

The x-axis denotes the log normalized p values and the y axis denotes the fold change.

[q1: Eggs/Embryos, q2: Microfilariae, q3: Larvae 3, q4: Larvae 4, q5: Adult male, q6: Adult Female]

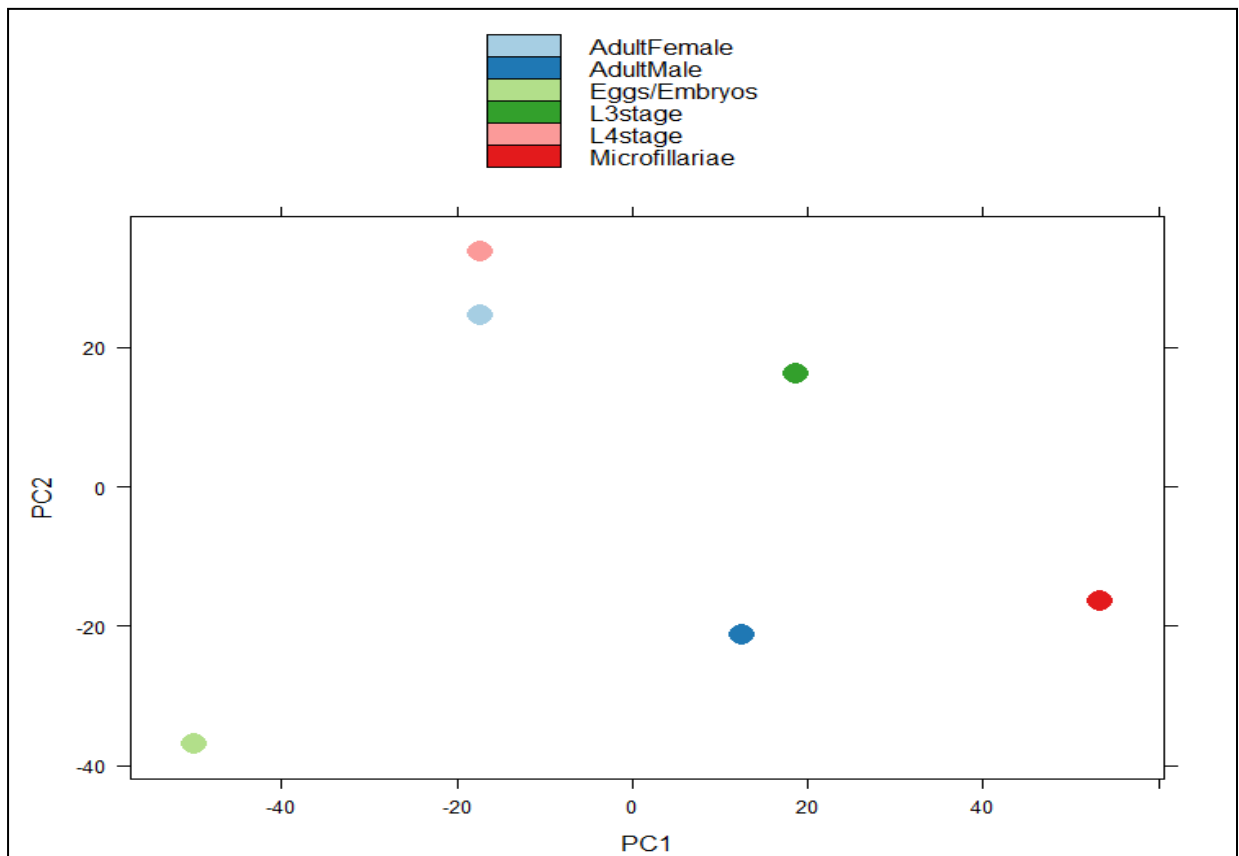
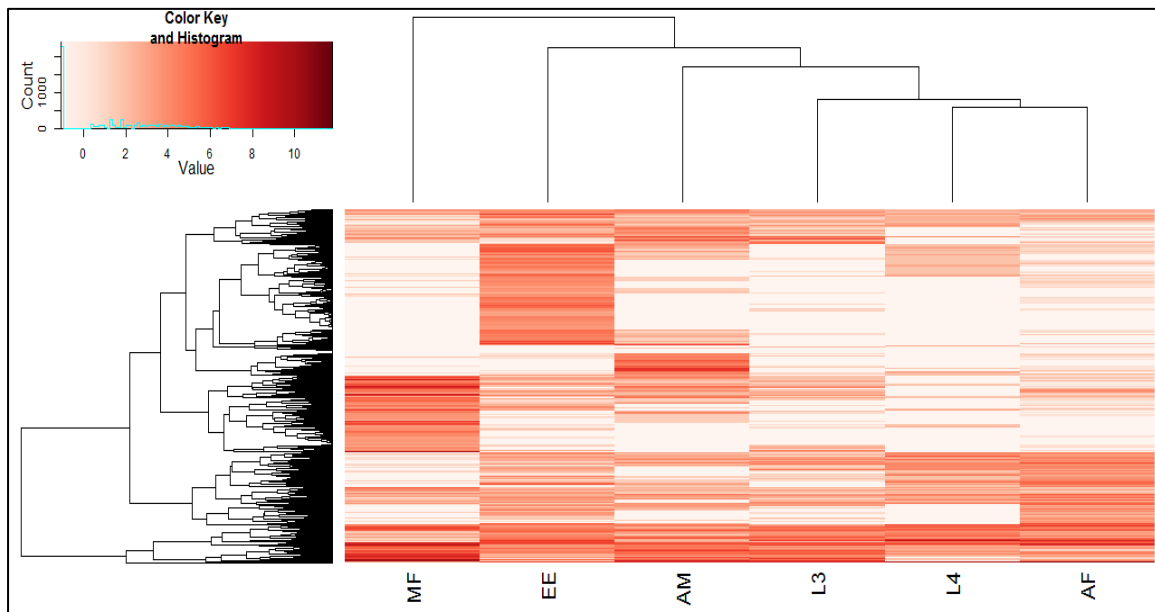


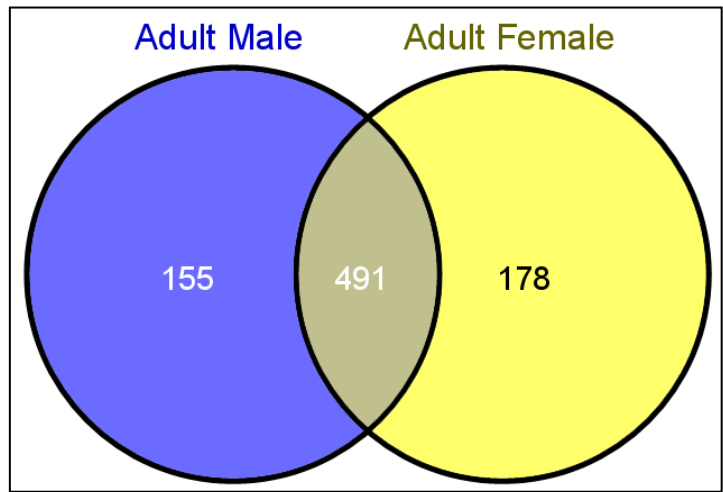
Figure 21: PCA plot for different developmental stages of *B. malayi*.



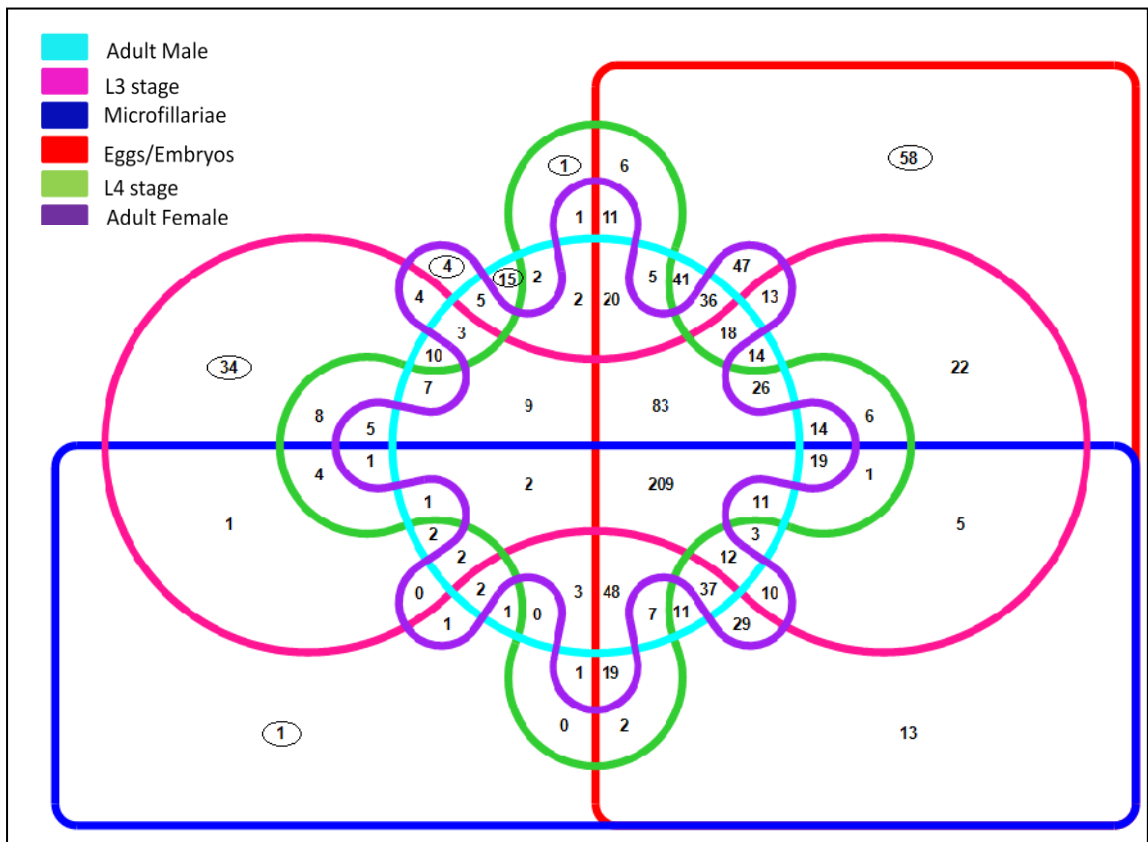
**Figure 22: Heat Map depicting differential expression of putative lncRNAs across different developmental stages of *B. malayi*.**

The x-axis denotes different developmental stages as denoted by: MF: Microfilariae, EE: Eggs/Embryos, AM: Adult male, L3: Larvae 3, L4: Larvae 4, AF: Adult Female. The y-axis depicts 982 lncRNAs genes.





**Figure 23: Sex-specific expression of lncRNA.** (VENNY- Oliveros, J.C., 2007)



**Figure 24: Stage-specific expression of lncRNA** (VENNTURE- Martin *et al.*, 2012).  
Number of unique lncRNA expressed in different stages is encircled in black.

## 6. DISCUSSION

Filarial nematodes populate the lymphatics and subcutaneous tissues of up to 150 million people worldwide and are responsible for prominent morbidity, disability and socio-economic loss. To date the treatment for filariasis relies on conventional drugs like albendazole, ivermectin etc. and there is no prophylactic vaccine available in the market. RNA-Seq has revolutionized the transcriptome study owing to its ability to capture the whole transcriptome of various cell types under different conditions. The study of some nematode genomes has already offered great insights into the genomic structure, biology and evolution of the nematode parasites. The release of the genome of *B. malayi* gave researchers an opportunity to study its transcriptome, the major focus being its protein coding content.

The present study provides the first identification of lncRNAs in *B. malayi* and shows their stage dependent expression. Though the functions of these lncRNAs are not very clear but our study highlights the importance of these lncRNAs in the pathogenicity of the filarial worm. Also, a stage and sex specific expression does indicate an important functional significance of these lncRNAs. Higher order of mapping of identifies lncRNAs in another pathogenic species, *Wuchereria bancrofti* as compared to a non-pathogenic species; *C. elegans* proposes a role of lncRNAs in pathogenicity.

## 7. CONCLUSION AND FUTURE PERSPECTIVE

Our study, to the best of our knowledge, is the first study providing identification and annotation of long non-coding RNAs of *B. malayi*. This study will prove to be a starting landmark for lncRNAs in pathogenic nematodes and help the community to better understand their life cycles. The stage-dependent expression has depicted a much significant role of non-coding RNAs in the life cycle of *B. malayi* as originally anticipated. Moreover, it has also been observed that pathogenicity might be one of the possible roles of these lncRNAs. This information can be of primary interest in search for macrofilaricidal and microfilaricidal drug targets to control and eliminate this important but neglected parasite.

These identified lncRNAs can further be taken into consideration to evaluate their potential functional roles in providing pathogenicity to *B. malayi*. Additionally, the elucidation of common structural features and structure/function relationships will help us understand the role of these lncRNAs in development and disease. At present, the *de novo* annotation of lncRNA is quite difficult due to their low conservation patterns among and across species. Further studies and datasets along with newer tools will definitely help in identification of newer lncRNAs in *B. malayi* and would provide a better annotation to these datasets.

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## 9. APPENDIX

### APPENDIX I: *LIST OF COMMANDS*

#### 1. Build Bowtie Index for reference genome.

```
€ bowtie2-build Reference.faa Reference > Reference.*.bt2, Reference.rev.*.bt2
```

#### 2. Convert sra to fastq format.

##### For Paired-end Reads:

```
€ fastq-dump --split-3 Accession.sra > Accession.fastq
```

##### For Single-end reads:

```
€ fastq-dump Accession.sra > Accession.fastq
```

#### 3. Alignment with Tophat.

```
€ tophat --coverage-search --microexon-search -r 141 -o /path/to/OUTPUT  
/path/to/Reference.faa /path/to/Accession_1.fastq /path/to/Accession_2.fastq >  
accepted_hits.bam  
€ samtools view accepted_hits.bam > accepted_hits.sam
```

#### 4. Transcript Assembly using Cufflinks.

```
€ cufflinks accepted_hits.sam > transcripts.gtf
```

#### 5. Merging assembled transcripts with the Annotation File using Cuffmerge.

```
€ samtools faidx Brugia_malayi.faa > Brugia_malayi.faa.fai  
€ cuffmerge -o /path/to/Cuffmerge/  
-g Annotation.gtf /path/to/Cufflinks/LIST.txt > merged.gtf
```

#### 6. Extracted transcript sequence with gffread.

```
€ gffread -w transcript.fa -g /home/to/Reference.faa /path/to/Reference.faa  
/path/to/Cuffmerge/merged_asm/merged.gtf
```



## 7. Remove the transcripts with nucleotide length less than 200.

€ perl **step1.pl** > *step1.out*

€ perl **step2.pl** > *step2.out*

€ perl **step3.pl** > *step3.out*

## 8. Run Jemboss with the remaining transcripts from step 7.

€ Open the GUI of Jemboss

€ Nucleic > Gene Finding > getorf > *Jemboss.out*

## 9. Remove the transcripts coding for amino acid less than a length of 30 and the protein coding genes.

€ perl **parse\_Jemboss.pl** > *Jemboss\_parse.out*

€ sed 's/\t\n\n/g' *Jemboss\_parse.out* > *Jemboss\_parsed.out*

€ grep -v -w '[3-9][0-9]\|[1-9][0-9][0-9]' *Jemboss\_parsed.out* > *Jemboss\_parsed\_grep.out*

## 10. Remove all the transcripts which have coding isoforms.

### § Retrieve the gene ids of the transcripts removed in step 9.

€ awk '{print \$1}' *Jemboss\_parsed\_grep.out* > *Jemboss\_TCONS*

€ perl **edit1.pl** > *Jemboss\_parsed\_TCONS*

€ grep '>' *Jemboss.out* > *Jemboss\_all\_TCONS\_header*

€ awk '{print \$1}' *Jemboss\_all\_TCONS\_header* > *Jemboss\_all\_TCONS*

€ perl **edit2.pl** > *Jemboss\_all\_TCONS\_1*

€ awk '{print \$1}' *Jemboss\_all\_TCONS\_1* |sort| uniq > *Jemboss\_all\_TCONS\_2*

€ Venny: *Jemboss\_parsed\_TCONS* Vs *Jemboss\_all\_TCONS\_2*

Take the uncommon ids from *Jemboss\_all\_TCONS\_2* > *Jemboss\_DISCARDED\_TCONS*

€ awk '{print \$12 "\t" \$10}' *merged.gtf* > *TCONS\_XLOCS\_from\_merged\_1*

€ sed 's//g' *TCONS\_XLOCS\_from\_merged* > *1*

€ sed 's//g' *1* > *TCONS\_XLOCS\_from\_merged*

€ perl **retrieve\_XLOCS.pl** > *XLOCS\_of\_Discarded\_TCONS*

€ awk '{print \$3}' *XLOCS\_of\_Discarded\_TCONS* |sort|uniq > *XLOCS\_D*

§ **Extract all the transcript ids corresponding to the geneids of discarded TCONS.**

```
€ perl retrieve_all_TCONS_XLOCS_D.pl > All_TCONS_of_Discarded_XLOCS  
€ awk '{print $3}' All_TCONS_of_Discarded_XLOCS |sort |uniq >TCONS_to_be_discarded
```

```
€ Venny: TCONS_to_be_discarded VS Jemboss_parsed_TCONS  
Take the uncommon ids from Jemboss_parsed_TCONS > Jemboss_final_output
```

### **11. Retrieve sequences for these transcript ids from transcript.fa**

```
€ perl Extract_Sequence_for_CPC.pl > Sequences_for_CPC_F
```

### **12. Calculate Coding Potential for the remaining transcripts in both forward and reverse frames.**

```
€ perl ReverseComplement.pl Sequences_for_CPC_F > Sequences_for_CPC_R  
€ sudo bash run_predict.sh /path/to/Sequences_for_CPC_F  
/path/to/CPC_Forward.out  
€ sudo bash run_predict.sh /path/to/ Sequences_for_CPC_R  
/path/to/CPC_Reverse.out
```

### **13. Remove the transcripts with coding potential less than -0.1**

```
€ perl filter_CPC_F.pl > Probable_IncRNAs_forward_ids  
€ perl filter_CPC_R.pl > Probable_IncRNAs_reverse_ids
```

### **14. Extract Sequences for lncRNA**

```
€ perl Extract_Sequence_for_lncRNA_F.pl > Sequences_IncRNAs_forward  
€ perl Extract_Sequence_for_lncRNA_R.pl > Sequences_IncRNAs_reverse
```

### **15. Differential Expression Analysis**

§ **Cuffdiff**

```
€ cuffdiff -o /path/to/Cuffdiff_Results /path/to/merged.gtf  
accepted_hits_67.bam,accepted_hits_69.bam accepted_hits_65.bam accepted_hits_74.bam  
accepted_hits_63.bam,accepted_hits_71.bam, accepted_hits_73.bam accepted_hits_61.bam  
accepted_hits_62.bam,accepted_hits_70.bam, accepted_hits_72.bam
```

## § CummeRbund

€ Open R

```
> library ("cummeRbund")
> setwd ("/path/to/Cuffdiff_Results/")
> cuff <- readCufflinks()
> disp <- dispersionPlot(genes(cuff))
> disp
> genes.scv <- fpkmSCVPlot(genes(cuff))
> isoforms.scv <- fpkmSCVPlot(isoforms(cuff))
> dens <- csDensity(genes(cuff))
> dens
> densRep <- csDensity(genes(cuff),replicates=T)
> densRep
> b <- csBoxplot(genes(cuff))
> b
> brep <- csBoxplot(genes(cuff),replicates=T)
> brep
> s <- csScatterMatrix(genes(cuff))
> s
> dend <- csDendro(genes(cuff))
> dend.rep <- csDendro(genes(cuff),replicates=T)
> v <- csVolcanoMatrix(genes(cuff))
> v
> q()
```

## § DESeq

**Sort all the alignment files generated by tophat (accepted\_hits.sam)**

€ `sort -s -k 1,1 accepted_hits.sam > accepted_hits_sorted.sam`

**Make a count table for all the sorted files**

€ `py htseq-count --no --m intersection-strict -t exon accepted_hits_sorted.sam > /path/to/CountTables/Counts_id.txt`

**Make a text file containing all the counts**

€ *fileofcounts.txt*

€ Open R

```
> library ("DESeq")
> setwd ("/path/to/CountTables/")
> CountTable = read.delim("fileofcounts.txt", row.names="Symbol")
> head (CountTable)
> conditions = c ("Eggs/Embryos", "Microfilariae", "L3stage", "L4stage",
```

```
      "AdultMale", "AdultFemale"))  
> cdsFull = newCountDataSet(CountTable, conditions )  
> cdsFull = estimateSizeFactors( cdsFull )  
> cdsFullBlind = estimateDispersions( cdsFull, method = "blind" )  
> vsdFull = varianceStabilizingTransformation( cdsFullBlind )  
> library ("RColorBrewer")  
> library ("gplots")  
> select = order(rowMeans(counts(cdsFull)), decreasing=TRUE)[1:982]  
> hmcol = colorRampPalette(brewer.pal(9, "Reds"))(100)  
> heatmap.2 (exprs(vsdFull)[select,], col = hmcol, trace="none", margin=c(10, 6))  
> print (plotPCA(vsdFull, intgroup=c("condition")))  
> q ()
```

## 16. Homology Analysis

```
€ ./blat Sequences_IncRNAs_forward target_genome > output.psl
```

## APPENDIX II: *PERL SCRIPTS*

### 1. step1.pl

```
#!/usr/bin/perl -w
@file=<transcript.fa>;
$f="@file";
@all=split '>', $f;
for ($k=1;$k<scalar @all;$k++)
{
    @sp=split '\n', $all[$k];
    $head=shift @sp;
    $seq= join ", @sp;
    $seq=~s/\s+//ig;
    print "$head\t",
    length $seq, "\n";
}
exit;
```

### 2. step2.pl

```
#!/usr/bin/perl -w
open (FILE, "step1.out");
# @file1=<FILE>;
while ($line = <FILE>)
{
    @fields=split('\s', $line);
    if (@fields[2]>=200)
    {
        print $fields[0] . "\n";
    }
}
exit;
```

### 3. step3.pl

```
#!/usr/bin/perl -w
use strict;
my $idsfile = "step2.out";
my $seqfile = "transcripts.fa";
my %ids = ();
open FILE, $idsfile or die $!;
```

```

while(<FILE>)
{
chomp;
$ids{$_} += 1;
}
close FILE;
local $/ = "\n>"; # read by FASTA record
open FASTA, $seqfile or die $!;
while (<FASTA>) {
chomp;
my $seq = $_;
my ($id) = $seq =~ /^>*(\S+)/; # parse ID as first word in FASTA header
if (exists($ids{$id}))
{
print "$seq" . "\n";
}
}
close FASTA;

```

#### 4. parse\_Jembooss.pl

```

#!/usr/bin/perl -w
use Bio::SeqIO;

my $seqio = Bio::SeqIO->new(-file => "Jembooss.out", '-format' => 'Fasta');

while(my $seq = $seqio->next_seq)
{
chomp $seq;
my $string = $seq->seq;
my $id = $seq->display_id;
$string_seq= split ("",$string);
$length_seq= scalar @string_seq;
$id =~ /(.*?)_(\d+)/;
$prefix=$1;
push @all_prefix, $prefix;
push @id_list, $id;
push @seq_list, $string;
push @length_list, $length_seq;
}
@same_id="";
@length_same_ids="";

```

```
for ($i=0; $i< scalar @id_list ; $i++)
{
print "\n";
if ($all_prefix[$i]=~/^$all_prefix[$i+1]$/)
{
print "$id_list[$i]\t$length_list[$i]\t";
}
}
exit;
```

### 5. edit1.pl

```
#!/usr/bin/perl -w
use strict;
open(info1,"<Jembooss_TCONS ") or die "Cant open";
open(info2,">Jembooss_parsed_TCONS");
while($f1=<info1>)
{
$f2=substr($f1,0,14);
print info2 "$f2\n";
}
```

### 6. edit2.pl

```
#!/usr/bin/perl -w
use strict;
open(info1,"<Jembooss_all_TCONS ") or die "Cant open";
open(info2,">Jembooss_all_TCONS_1");
while($f1=<info1>)
{
$f2=substr($f1,0,14);
print info2 "$f2\n";
}
```

### 7. retrieve\_XLOCS.pl

```
#!/usr/bin/perl -w
use strict;
open (FILE1,"< Jembooss_DISCARDED_TCONS ") or die "Cant open File1";
my @a=<FILE1>;
close FILE1;
```

```

open (FILE2, "<TCONS_XLOCS_from_merged " ) or die "Cant open File2";
my @b = <FILE2>;
close FILE2;
for(my $i=0;$i<@a;$i++)
{
chomp $a[$i];
for(my $j=0;$j<@b;$j++)
{
chomp $b[$j];
my @c=split ('\t', $b[$j]);
if ($a[$i]=~/^$c[0]$/)
{
print "$a[$i]\t$c[0]\t$c[1]\n";
}
}
} exit;

```

## 8. retrieve\_all\_TCONS\_XLOCS\_D.pl

```

#!/usr/bin/perl -w
use strict;
open (FILE1,"< XLOCS_D") or die "Cant open File1";
my @a=<FILE1>;
close FILE1;
open (FILE2, "<merged.gtf" ) or die "Cant open File2";
my @b = <FILE2>;
close FILE2;
for(my $i=0;$i<scalar @a;$i++)
{
chomp $a[$i];
my @c=split ('\t', $a[$i]);
    for(my $j=0;$j<scalar @b;$j++)
    {
chomp $b[$j];
my @d=split ('\t', $b[$j]);
$d[8]=~/gene_id \"(XLOC_.*)\"; transcript_id \"(TCONS_.*)\"; exon_/;
my $xloc=$1;
my $tcon=$2;
if ($c[2]=~/^$xloc$/)
{
print "$c[2]\t$xloc\t$tcon\n";
}
} } exit;

```



## 9. Extract\_Sequence\_for\_CPC.pl

```
#!/usr/bin/perl -w
use strict;
my $idsfile = "Jemboss_final_output";
my $seqfile = "transcripts.fa";
my %ids = ();
open FILE, $idsfile or die $!;
while(<FILE>)
{
    chomp;
    $ids{$_} += 1;
}
close FILE;
local $/ = "\n>"; # read by FASTA record
open FASTA, $seqfile or die $!;
while (<FASTA>) {
    chomp;
    my $seq = $_;
    my ($id) = $seq =~ /^>*(\S+)/; # parse ID as first word in FASTA header
    if (exists($ids{$id}))
    {
        print "$seq" . "\n";
    }
}
close FASTA;
```

## 10. ReverseComplement.pl

```
#!/usr/bin/perl -w
use strict;
my $usage = "perl ReverseComplement.pl input_fasta_file
            output_fasta_file\n";
my $inFastaFile = shift or die $usage;
my $outFastaFile = shift or die $usage;
my $unixFile = $inFastaFile.".unix";
my (@seqNames, %nameSeq);
my $flag = my $totalSeq = 0;
my $seqName = "";
ConvertToUnix ($inFastaFile, $unixFile);
open INFASTA, $unixFile or die "couldn't open $unixFile: $!\n";
while (my $line = <INFASTA>)
{
```

```

chomp $line;
next if $line =~ /^s*$/;
if ($line =~ /^>(.*)/)
{
$seqName = $1;
push @seqNames, $seqName;
$totalSeq++;
}
else
{
$nameSeq{$seqName} .= $line;
}
}
close INFASTA;
unlink $unixFile;
open OUTFASTA, ">$outFastaFile" or die "couldn't open $outFastaFile:
$!\n";
foreach my $seqName (@seqNames)
{
my $seq = $nameSeq{$seqName};
$seq =~ tr /ACGTacgt/TGCAtgca/;
print OUTFASTA ">",$seqName, "\n";
print OUTFASTA $seq, "\n";
}
close OUTFASTA;
print "Total $totalSeq sequences in input fasta file. All done!\n";
sub ConvertToUnix
{
my ($infile, $unixFile) = @_ ;
open (IN, $infile) or die "Couldn't open $infile: $!\n";
open (OUT, ">$unixFile") or die "Couldn't open $unixFile:
$!\n";
my @buffer = <IN>;
close IN;
my $line = "";
foreach my $element (@buffer)
{
$line .= $element;
}
if ($line =~ /\r\n/)
{
$line =~ s/\r//g;
}
elsif ($line =~ /\r/)

```

```
{
$line =~ s/\r/\n/g;
}
print OUT $line;
close OUT;
}
```

### 11. filter\_CPC\_F.pl

```
#!/usr/bin/perl -w
use strict;
open (FILE, " CPC_Forward.out ");
while ( my $line = <FILE>)
{
    my @fields=split("\s", $line);
    if (@fields[3]<-0.1)
    {
        print $fields[0] . "\n";
    }
}
exit;
```

### 12. filter\_CPC\_R.pl

```
#!/usr/bin/perl -w
use strict;
open (FILE, " CPC_Reverse.out ");
while ( my $line = <FILE>)
{
    my @fields=split("\s", $line);
    if (@fields[3]<-0.1)
    {
        print $fields[0] . "\n";
    }
}
exit;
```

### 13. Extract\_Sequence\_for\_lncRNA\_F.pl

```
#!/usr/bin/perl -w
use strict;
my $idsfile = "Probable_lncRNAs_forward_ids";
my $seqfile = "Sequences_for_CPC_F";
my %ids = ();
```

```

open FILE, $idsfile or die $!;
while(<FILE>)
{
chomp;
$ids{$_} += 1;
}
close FILE;
local $/ = "\n>"; # read by FASTA record
open FASTA, $seqfile or die $!;
while (<FASTA>) {
chomp;
my $seq = $_;
my ($id) = $seq =~ /^>*(\S+)/; # parse ID as first word in FASTA header
if (exists($ids{$id}))
{
print "$seq" . "\n";
}
}
close FASTA;

```

#### **14. Extract\_Sequence\_for\_lncRNA\_R.pl**

```

#!/usr/bin/perl -w
use strict;
my $idsfile = "Probable_lncRNAs_reverse_ids";
my $seqfile = "Sequences_for_CPC_R";
my %ids = ();
open FILE, $idsfile or die $!;
while(<FILE>)
{
chomp;
$ids{$_} += 1;
}
close FILE;
local $/ = "\n>"; # read by FASTA record
open FASTA, $seqfile or die $!;
while (<FASTA>) {
chomp;
my $seq = $_;
my ($id) = $seq =~ /^>*(\S+)/; # parse ID as first word in FASTA header
if (exists($ids{$id}))
{
print "$seq" . "\n";
}} close FASTA;

```

## **APPENDIX III: KEY TERMINOLOGY**

### **1. RNA Sequencing (RNA-Seq)**

An experimental protocol that uses next-generation sequencing technologies to sequence the RNA molecules within a biological sample in an effort to determine the primary sequence and relative abundance of RNA.

### **2. Sequencing depth**

The average number of reads representing a given nucleotide in the reconstructed sequence. A 10× sequence depth means that each nucleotide of the transcript was sequenced, on average, ten times.

### **3. Paired-end protocol**

A library construction and sequencing strategy in which both ends of a DNA fragment are sequenced to produce pairs of reads (mate pairs). Paired-end sequencing provides long-range positional information.

### **4. Contigs**

An abbreviation for contiguous sequences that is used to indicate a contiguous piece of DNA assembled from shorter overlapping sequence reads.

### **5. k-mer frequency**

The number of times that each k-mer (that is, a short oligonucleotide of length k) appears in a set of DNA sequences.

### **6. Splice-aware aligner**

A program that is designed to align cDNA reads to a genome.

### **7. Traversing**

A method for systematically visiting all nodes in a mathematical graph.

### **8. Seed-and-extend aligners**

An alignment strategy that first builds a hash table containing the location of each k-mer (seed) within the reference genome. These algorithms then extend these seeds in both directions to find the best alignment (or alignments) for each read.

## **9. Burrows–Wheeler transform**

This re-orders the characters within a sequence, which allows for better data compression. Many short-read aligners implement this transform in order to use less memory when aligning reads to a genome.

## **10. Parallel computing**

A computer programming model for distributing data processing across multiple processors, so that multiple tasks can be carried out simultaneously.

## **11. De Bruijn graph**

A directed mathematical graph that uses a sequence of letters of length  $k$  to represent nodes. Pairs of nodes are connected if shifting a sequence by one character creates an exact  $k-1$  overlap between the two sequences.

## **12. Emulsion PCR**

Amplified sequences are embedded in tiny beads jointly with all that is needed for the sequencing process

## **13. Bridge PCR**

Amplified sequences are clustered on an iterative process that collates their extremes to the support (creating a “bridge”) before breaking and duplicating them.

## **14. Read**

It is a raw sequence that comes off a sequencing machine. A read may consist of multiple segments, which are sometimes called subreads.

## **15. ORF**

An open reading frame (ORF) is the part of a reading frame that contains no stop codons. They are used as an evidence to assist in gene prediction. Long ORFs are often considered to identify candidate protein coding regions in a DNA sequence.

## **16. Quality scores**

It is an integer representing the probability that a given base in a nucleic acid sequence is correct.

## 17. Phred Score

Phred quality scores  $Q$  are defined as a property which is logarithmically related to the base-calling error probabilities  $P$ .

$$Q = -\log_{10}P$$

For example, if Phred assigns a quality score of 20 to a base, the chances that this base is called incorrectly are 1 in 100 (99% base call accuracy).

Phred quality scores are used for sequence quality assessment, recognition and removal of low-quality sequence and determination of accurate consensus sequences.

## 18. CPC score

CPC score is derived from six features:

### Log-odd score

An indicator of the quality of a predicted ORF and the higher the score, the higher the quality.

### Coverage of the predicted ORF

An indicator of good ORF quality.

### Integrity of the predicted ORF

Indicates whether an ORF begins with a start codon and ends with an in-frame stop codon.

### Number of Hits

Upon BLASTX search, true protein-coding transcript is likely to have more hits with known proteins than a non-coding transcript does.

### Hit score

For a true protein-coding transcript the hits are also likely to have higher quality i.e. low e-value. The higher the HIT SCORE, the better the overall quality of the hits and the more likely the transcript is protein-coding.

### Frame score

For a true protein-coding transcript most of the hits are likely to reside within one frame: measure the distribution of the HSPs among three reading frames. The higher the FRAME SCORE, the more concentrated the hits are and the more likely the transcript is protein-coding.

## 19. SAM Format

SAM (Sequence Alignment/Map) format is a generic format for storing large nucleotide sequence alignments. It is a TAB-delimited text format consisting of a header section, which is optional, and an alignment section. If present, the header must be prior to the alignments. Header lines start with '@', while alignment lines do not. Each alignment line has 11

mandatory fields for essential alignment information such as mapping position, and variable number of optional fields for flexible or aligner specific information.

## 20. BAM Format

BAM is the compressed binary version of the Sequence Alignment/Map (SAM) format, a compact and index-able representation of nucleotide sequence alignments.

## 21. Fastq Format

FASTQ format stores sequences and Phred qualities in a single file. It is concise and compact. Both the sequence letter and quality score are encoded with a single ASCII character for brevity. It was originally developed at the Wellcome Trust Sanger Institute to bundle a FASTA sequence and its quality data.

A FASTQ file normally uses four lines per sequence.

Line 1 begins with a '@' character and is followed by a sequence identifier and an optional description (like a FASTA title line).

Line 2 is the raw sequence letters.

Line 3 begins with a '+' character and is optionally followed by the same sequence identifier (and any description) again.

Line 4 encodes the quality values for the sequence in Line 2, and must contain the same number of symbols as letters in the sequence.

## 22. GFF Format

General Feature Format (GFF) has nine required fields that must be tab-separated:

<b>Seqname</b>	The name of the sequence. Must be a chromosome or scaffold.
<b>Source</b>	The program that generated this feature
<b>Feature</b>	The name of this type of feature. Some examples of standard feature type are "CDS", "start_codon", "stop_codon", and "exon".
<b>Start</b>	The starting position of the feature in the sequence. The first base is numbered 1.
<b>End</b>	The ending position of the feature (inclusive).
<b>Score</b>	A score between 0 and 1000. If the track line useScore attribute is set to 1
<b>Strand</b>	Valid entries include '+', '-', or '.'
<b>Frame</b>	If the feature is a coding exon, frame should be a number between 0-2 that represents the reading frame of the first base. If the feature is not a coding exon, the value should be '.'.
<b>Group</b>	All lines with the same group are linked together into a single item.

## 23. Scatter Plot

Scatter plots are similar to line graphs in that they use horizontal and vertical axes to plot data points. It uses Cartesian coordinates to display values for two variables for a set of data. Scatter plots show how much one variable is affected by another i.e. their correlation.



## **24. Density Plot**

Density Plots are an effective way to view the distribution of a variable.

## **25. Volcano Plot**

A volcano plot is a type of scatter-plot that is used to quickly identify changes in large datasets composed of replicate data. It plots significance versus fold-change on the y- and x-axes, respectively. A volcano plot combines a statistical test (e.g., p-value, ANOVA) with the magnitude of the change enabling quick visual identification of those data-points.

## **26. Box Plot**

A box plot is a convenient way of graphically depicting groups of numerical data through their quartiles. Box plots may also have lines extending vertically from the boxes (whiskers) indicating variability outside the upper and lower quartiles, hence the terms box-and-whisker plot and box-and-whisker diagram. Outliers may be plotted as individual points.

The bottom and top of the box are always the first and third quartiles, and the band inside the box is always the second quartile (the median).

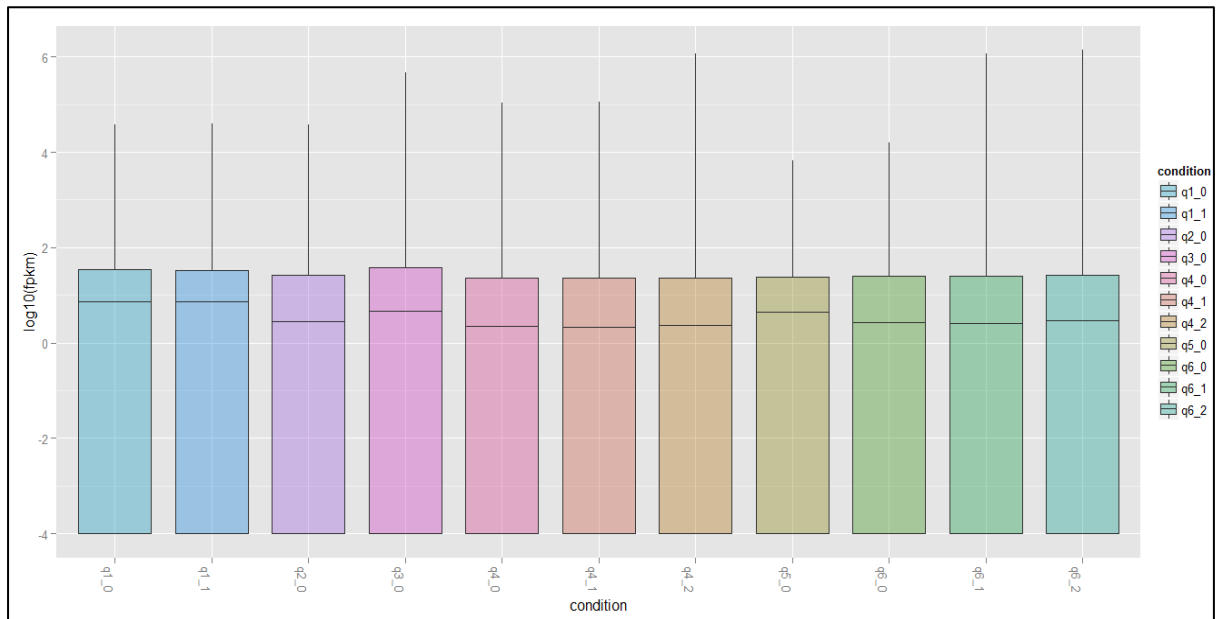
## **27. PCA plot**

Principal component analysis (PCA) is a mathematical procedure that uses an orthogonal transformation to convert a set of observations of possibly correlated variables into a set of values of linearly uncorrelated variables called principal components. It extracts the smallest number components that account for most of the variation in the original multivariate data and summarize the data with little loss of information.

## **28. Heat Map**

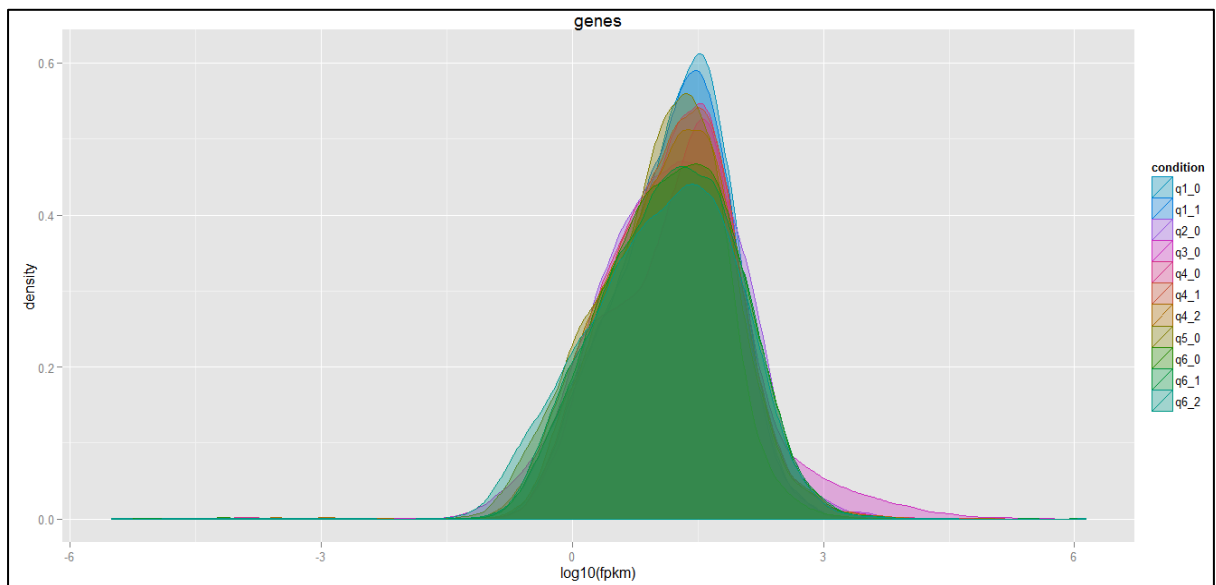
A heat map is a graphical representation of data where the individual values contained in a matrix are represented as colours. It is used to represent the level of expression of many genes across a number of comparable samples.

## APPENDIX IV: SUPPLEMENTARY FIGURES AND TABLES



**Figure representing the Box Plot for all the samples.**

q1\_0: ERR048967, q1\_1: ERR048969, q2\_0: ERR048965, q3\_0: ERR048974, q4\_0: ERR048963, q4\_1: ERR048971, q4\_2: ERR048973, q5\_0: ERR048961, q6\_0: ERR048962, q6\_1: ERR048970, q6\_2: ERR048972



**Figure representing the Density Plot for all the samples.**

q1\_0: ERR048967, q1\_1: ERR048969, q2\_0: ERR048965, q3\_0: ERR048974, q4\_0: ERR048963, q4\_1: ERR048971, q4\_2: ERR048973, q5\_0: ERR048961, q6\_0: ERR048962, q6\_1: ERR048970, q6\_2: ERR048972

**Table indicating genomics location and reference transcripts and gene ids of predicted lncRNAs in *B. Malayi*.**

<b>Transcript Id</b>	<b>Gene Id</b>	<b>Scaffold Id</b>	<b>Start Position</b>	<b>Stop Position</b>	<b>exon number</b>
TCONS_00003273	XLOC_003273	gi 154205141 gb AAQA01029718.1	2	227	1
TCONS_00003276	XLOC_003276	gi 154205183 gb AAQA01029676.1	14	245	1
TCONS_00003286	XLOC_003286	gi 154205311 gb AAQA01029548.1	1	282	1
TCONS_00003289	XLOC_003289	gi 154205345 gb AAQA01029514.1	15	286	1
TCONS_00003290	XLOC_003290	gi 154205347 gb AAQA01029512.1	2	238	1
TCONS_00003291	XLOC_003291	gi 154205351 gb AAQA01029508.1	48	272	1
TCONS_00003300	XLOC_003300	gi 154205400 gb AAQA01029459.1	1	212	1
TCONS_00003305	XLOC_003305	gi 154205419 gb AAQA01029440.1	68	299	1
TCONS_00003310	XLOC_003310	gi 154205444 gb AAQA01029415.1	31	231	1
TCONS_00003316	XLOC_003316	gi 154205500 gb AAQA01029359.1	8	317	1
TCONS_00003321	XLOC_003321	gi 154205551 gb AAQA01029308.1	87	332	1
TCONS_00003326	XLOC_003326	gi 154205602 gb AAQA01029257.1	2	316	1
TCONS_00003333	XLOC_003333	gi 154205710 gb AAQA01029149.1	1	325	1
TCONS_00003334	XLOC_003334	gi 154205722 gb AAQA01029137.1	33	345	1
TCONS_00003337	XLOC_003337	gi 154205734 gb AAQA01029125.1	5	358	1
TCONS_00003338	XLOC_003338	gi 154205745 gb AAQA01029114.1	2	304	1
TCONS_00003342	XLOC_003342	gi 154205768 gb AAQA01029091.1	100	374	1
TCONS_00003348	XLOC_003348	gi 154205801 gb AAQA01029058.1	40	241	1
TCONS_00003360	XLOC_003360	gi 154205863 gb AAQA01028996.1	5	392	1
TCONS_00003366	XLOC_003366	gi 154205937 gb AAQA01028922.1	1	223	1
TCONS_00003375	XLOC_003375	gi 154206071 gb AAQA01028788.1	203	411	1
TCONS_00003384	XLOC_003384	gi 154206167 gb AAQA01028692.1	6	243	1
TCONS_00003386	XLOC_003386	gi 154206169 gb AAQA01028690.1	226	437	1
TCONS_00003402	XLOC_003402	gi 154206299 gb AAQA01028560.1	157	414	1
TCONS_00003408	XLOC_003408	gi 154206328 gb AAQA01028531.1	26	321	1
TCONS_00003410	XLOC_003410	gi 154206335 gb AAQA01028524.1	230	432	1
TCONS_00003411	XLOC_003411	gi 154206336 gb AAQA01028523.1	1	220	1
TCONS_00003412	XLOC_003412	gi 154206340 gb AAQA01028519.1	45	360	1
TCONS_00003423	XLOC_003423	gi 154206400 gb AAQA01028459.1	100	352	1
TCONS_00003427	XLOC_003427	gi 154206417 gb AAQA01028442.1	9	471	1
TCONS_00003439	XLOC_003439	gi 154206492 gb AAQA01028367.1	70	392	1
TCONS_00003440	XLOC_003440	gi 154206496 gb AAQA01028363.1	133	368	1
TCONS_00003444	XLOC_003444	gi 154206518 gb AAQA01028341.1	215	442	1
TCONS_00003451	XLOC_003451	gi 154206594 gb AAQA01028265.1	11	469	1
TCONS_00003452	XLOC_003452	gi 154206596 gb AAQA01028263.1	1	238	1
TCONS_00003464	XLOC_003464	gi 154206679 gb AAQA01028180.1	142	454	1
TCONS_00003485	XLOC_003484	gi 154206825 gb AAQA01028034.1	2	285	1
TCONS_00003487	XLOC_003486	gi 154206846 gb AAQA01028013.1	19	280	1
TCONS_00003500	XLOC_003499	gi 154206947 gb AAQA01027912.1	254	510	1
TCONS_00003501	XLOC_003500	gi 154206956 gb AAQA01027903.1	321	525	1
TCONS_00003507	XLOC_003506	gi 154206975 gb AAQA01027884.1	115	440	1
TCONS_00003510	XLOC_003509	gi 154207000 gb AAQA01027859.1	31	347	1

TCONS_00003510	XLOC_003509	gi 154207000 gb AAQA01027859.1	491	534	2
TCONS_00003511	XLOC_003510	gi 154207015 gb AAQA01027844.1	76	505	1
TCONS_00003527	XLOC_003525	gi 154207149 gb AAQA01027710.1	227	546	1
TCONS_00003536	XLOC_003534	gi 154207191 gb AAQA01027668.1	2	453	1
TCONS_00003540	XLOC_003538	gi 154207203 gb AAQA01027656.1	245	524	1
TCONS_00003553	XLOC_003551	gi 154207249 gb AAQA01027610.1	1	94	1
TCONS_00003553	XLOC_003551	gi 154207249 gb AAQA01027610.1	350	515	2
TCONS_00003556	XLOC_003554	gi 154207259 gb AAQA01027600.1	21	537	1
TCONS_00003567	XLOC_003565	gi 154207353 gb AAQA01027506.1	9	285	1
TCONS_00003583	XLOC_003581	gi 154207463 gb AAQA01027396.1	2	401	1
TCONS_00003586	XLOC_003584	gi 154207474 gb AAQA01027385.1	106	342	1
TCONS_00003586	XLOC_003584	gi 154207474 gb AAQA01027385.1	482	572	2
TCONS_00003590	XLOC_003588	gi 154207491 gb AAQA01027368.1	22	270	1
TCONS_00003601	XLOC_003599	gi 154207544 gb AAQA01027315.1	130	552	1
TCONS_00003610	XLOC_003608	gi 154207599 gb AAQA01027260.1	61	267	1
TCONS_00003614	XLOC_003612	gi 154207617 gb AAQA01027242.1	5	485	1
TCONS_00003618	XLOC_003616	gi 154207649 gb AAQA01027210.1	162	438	1
TCONS_00003620	XLOC_003618	gi 154207665 gb AAQA01027194.1	293	571	1
TCONS_00003625	XLOC_003623	gi 154207712 gb AAQA01027147.1	29	542	1
TCONS_00003628	XLOC_003626	gi 154207719 gb AAQA01027140.1	237	588	1
TCONS_00003631	XLOC_003629	gi 154207743 gb AAQA01027116.1	15	250	1
TCONS_00003631	XLOC_003629	gi 154207743 gb AAQA01027116.1	321	443	2
TCONS_00003632	XLOC_003630	gi 154207749 gb AAQA01027110.1	23	409	1
TCONS_00003633	XLOC_003631	gi 154207751 gb AAQA01027108.1	151	440	1
TCONS_00003641	XLOC_003639	gi 154207811 gb AAQA01027048.1	179	392	1
TCONS_00003642	XLOC_003640	gi 154207826 gb AAQA01027033.1	7	32	1
TCONS_00003642	XLOC_003640	gi 154207826 gb AAQA01027033.1	126	235	2
TCONS_00003642	XLOC_003640	gi 154207826 gb AAQA01027033.1	340	460	3
TCONS_00003648	XLOC_003646	gi 154207854 gb AAQA01027005.1	196	546	1
TCONS_00003650	XLOC_003648	gi 154207859 gb AAQA01027000.1	84	512	1
TCONS_00003651	XLOC_003649	gi 154207860 gb AAQA01026999.1	54	277	1
TCONS_00003651	XLOC_003649	gi 154207860 gb AAQA01026999.1	521	596	2
TCONS_00003654	XLOC_003652	gi 154207875 gb AAQA01026984.1	317	538	1
TCONS_00003659	XLOC_003657	gi 154207905 gb AAQA01026954.1	102	109	1
TCONS_00003659	XLOC_003657	gi 154207905 gb AAQA01026954.1	261	390	2
TCONS_00003659	XLOC_003657	gi 154207905 gb AAQA01026954.1	491	603	3
TCONS_00003660	XLOC_003657	gi 154207905 gb AAQA01026954.1	107	114	1
TCONS_00003660	XLOC_003657	gi 154207905 gb AAQA01026954.1	261	390	2
TCONS_00003660	XLOC_003657	gi 154207905 gb AAQA01026954.1	491	603	3
TCONS_00003661	XLOC_003657	gi 154207905 gb AAQA01026954.1	112	119	1
TCONS_00003661	XLOC_003657	gi 154207905 gb AAQA01026954.1	261	390	2
TCONS_00003661	XLOC_003657	gi 154207905 gb AAQA01026954.1	491	603	3
TCONS_00003696	XLOC_003690	gi 154208145 gb AAQA01026714.1	265	619	1
TCONS_00003697	XLOC_003691	gi 154208148 gb AAQA01026711.1	1	269	1
TCONS_00003697	XLOC_003691	gi 154208148 gb AAQA01026711.1	481	619	2
TCONS_00003698	XLOC_003691	gi 154208148 gb AAQA01026711.1	1	265	1
TCONS_00003698	XLOC_003691	gi 154208148 gb AAQA01026711.1	481	619	2
TCONS_00003699	XLOC_003692	gi 154208152 gb AAQA01026707.1	34	569	1
TCONS_00003702	XLOC_003695	gi 154208167 gb AAQA01026692.1	2	544	1

TCONS_00003717	XLOC_003710	gi 154208299 gb AAQA01026560.1	395	600	1
TCONS_00003725	XLOC_003718	gi 154208346 gb AAQA01026513.1	18	286	1
TCONS_00003732	XLOC_003725	gi 154208443 gb AAQA01026416.1	384	632	1
TCONS_00003733	XLOC_003726	gi 154208448 gb AAQA01026411.1	105	629	1
TCONS_00003756	XLOC_003748	gi 154208585 gb AAQA01026274.1	90	638	1
TCONS_00003757	XLOC_003749	gi 154208593 gb AAQA01026266.1	394	644	1
TCONS_00003785	XLOC_003777	gi 154208872 gb AAQA01025987.1	15	123	1
TCONS_00003785	XLOC_003777	gi 154208872 gb AAQA01025987.1	363	660	2
TCONS_00003786	XLOC_003778	gi 154208874 gb AAQA01025985.1	201	477	1
TCONS_00003786	XLOC_003778	gi 154208874 gb AAQA01025985.1	585	660	2
TCONS_00003790	XLOC_003782	gi 154208905 gb AAQA01025954.1	375	651	1
TCONS_00003796	XLOC_003788	gi 154208934 gb AAQA01025925.1	318	651	1
TCONS_00003799	XLOC_003791	gi 154208956 gb AAQA01025903.1	3	172	1
TCONS_00003799	XLOC_003791	gi 154208956 gb AAQA01025903.1	515	663	2
TCONS_00003827	XLOC_003817	gi 154209130 gb AAQA01025729.1	2	546	1
TCONS_00003852	XLOC_003841	gi 154209331 gb AAQA01025528.1	185	270	1
TCONS_00003852	XLOC_003841	gi 154209331 gb AAQA01025528.1	501	663	2
TCONS_00003853	XLOC_003842	gi 154209332 gb AAQA01025527.1	7	245	1
TCONS_00003858	XLOC_003847	gi 154209348 gb AAQA01025511.1	101	399	1
TCONS_00003859	XLOC_003848	gi 154209353 gb AAQA01025506.1	2	494	1
TCONS_00003876	XLOC_003865	gi 154209485 gb AAQA01025374.1	112	419	1
TCONS_00003878	XLOC_003867	gi 154209490 gb AAQA01025369.1	239	598	1
TCONS_00003882	XLOC_003871	gi 154209531 gb AAQA01025328.1	132	387	1
TCONS_00003889	XLOC_003878	gi 154209569 gb AAQA01025290.1	158	396	1
TCONS_00003890	XLOC_003879	gi 154209589 gb AAQA01025270.1	4	234	1
TCONS_00003890	XLOC_003879	gi 154209589 gb AAQA01025270.1	456	657	2
TCONS_00003909	XLOC_003898	gi 154209687 gb AAQA01025172.1	83	618	1
TCONS_00003910	XLOC_003899	gi 154209701 gb AAQA01025158.1	1	325	1
TCONS_00003918	XLOC_003907	gi 154209754 gb AAQA01025105.1	133	313	1
TCONS_00003918	XLOC_003907	gi 154209754 gb AAQA01025105.1	435	532	2
TCONS_00003921	XLOC_003910	gi 154209763 gb AAQA01025096.1	40	118	1
TCONS_00003921	XLOC_003910	gi 154209763 gb AAQA01025096.1	254	370	2
TCONS_00003921	XLOC_003910	gi 154209763 gb AAQA01025096.1	510	653	3
TCONS_00003922	XLOC_003911	gi 154209773 gb AAQA01025086.1	166	520	1
TCONS_00003944	XLOC_003932	gi 154209922 gb AAQA01024937.1	43	709	1
TCONS_00003955	XLOC_003942	gi 154210021 gb AAQA01024838.1	6	345	1
TCONS_00003970	XLOC_003957	gi 154210192 gb AAQA01024667.1	435	721	1
TCONS_00003973	XLOC_003960	gi 154210210 gb AAQA01024649.1	1	89	1
TCONS_00003973	XLOC_003960	gi 154210210 gb AAQA01024649.1	574	700	2
TCONS_00003981	XLOC_003968	gi 154210288 gb AAQA01024571.1	265	662	1
TCONS_00003989	XLOC_003976	gi 154210349 gb AAQA01024510.1	291	518	1
TCONS_00004003	XLOC_003989	gi 154210472 gb AAQA01024387.1	39	397	1
TCONS_00004003	XLOC_003989	gi 154210472 gb AAQA01024387.1	536	690	2
TCONS_00004009	XLOC_003995	gi 154210505 gb AAQA01024354.1	136	613	1
TCONS_00004013	XLOC_003999	gi 154210540 gb AAQA01024319.1	130	476	1
TCONS_00004022	XLOC_004008	gi 154210626 gb AAQA01024233.1	182	306	1
TCONS_00004022	XLOC_004008	gi 154210626 gb AAQA01024233.1	571	733	2
TCONS_00004031	XLOC_004017	gi 154210772 gb AAQA01024087.1	174	704	1
TCONS_00004032	XLOC_004018	gi 154210789 gb AAQA01024070.1	42	393	1

TCONS_00004061	XLOC_004047	gi 154211066 gb AAQA01023793.1	87	555	1
TCONS_00004067	XLOC_004053	gi 154211109 gb AAQA01023750.1	151	593	1
TCONS_00004076	XLOC_004062	gi 154211176 gb AAQA01023683.1	2	348	1
TCONS_00004088	XLOC_004074	gi 154211284 gb AAQA01023575.1	12	145	1
TCONS_00004088	XLOC_004074	gi 154211284 gb AAQA01023575.1	339	454	2
TCONS_00004088	XLOC_004074	gi 154211284 gb AAQA01023575.1	607	638	3
TCONS_00004091	XLOC_004076	gi 154211322 gb AAQA01023537.1	23	424	1
TCONS_00004092	XLOC_004077	gi 154211338 gb AAQA01023521.1	499	761	1
TCONS_00004095	XLOC_004080	gi 154211379 gb AAQA01023480.1	24	386	1
TCONS_00004095	XLOC_004080	gi 154211379 gb AAQA01023480.1	531	650	2
TCONS_00004096	XLOC_004081	gi 154211400 gb AAQA01023459.1	428	676	1
TCONS_00004126	XLOC_004109	gi 154211738 gb AAQA01023121.1	362	736	1
TCONS_00004139	XLOC_004121	gi 154211943 gb AAQA01022916.1	409	723	1
TCONS_00004156	XLOC_004137	gi 154212081 gb AAQA01022778.1	303	779	1
TCONS_00004157	XLOC_004138	gi 154212083 gb AAQA01022776.1	578	777	1
TCONS_00004165	XLOC_004146	gi 154212145 gb AAQA01022714.1	211	404	1
TCONS_00004165	XLOC_004146	gi 154212145 gb AAQA01022714.1	671	770	2
TCONS_00004176	XLOC_004157	gi 154212246 gb AAQA01022613.1	511	743	1
TCONS_00004216	XLOC_004194	gi 154212544 gb AAQA01022315.1	9	96	1
TCONS_00004216	XLOC_004194	gi 154212544 gb AAQA01022315.1	239	318	2
TCONS_00004216	XLOC_004194	gi 154212544 gb AAQA01022315.1	663	797	3
TCONS_00004221	XLOC_004199	gi 154212581 gb AAQA01022278.1	24	123	1
TCONS_00004221	XLOC_004199	gi 154212581 gb AAQA01022278.1	208	350	2
TCONS_00004221	XLOC_004199	gi 154212581 gb AAQA01022278.1	440	540	3
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TCONS_00004226	XLOC_004204	gi 154212627 gb AAQA01022232.1	435	796	1
TCONS_00004228	XLOC_004206	gi 154212649 gb AAQA01022210.1	1	86	1
TCONS_00004228	XLOC_004206	gi 154212649 gb AAQA01022210.1	491	725	2
TCONS_00004244	XLOC_004222	gi 154212809 gb AAQA01022050.1	7	694	1
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TCONS_00004279	XLOC_004257	gi 154213237 gb AAQA01021622.1	379	697	1
TCONS_00004280	XLOC_004258	gi 154213245 gb AAQA01021614.1	17	100	1
TCONS_00004280	XLOC_004258	gi 154213245 gb AAQA01021614.1	406	543	2
TCONS_00004285	XLOC_004262	gi 154213296 gb AAQA01021563.1	46	575	1
TCONS_00004287	XLOC_004264	gi 154213323 gb AAQA01021536.1	460	779	1
TCONS_00004302	XLOC_004278	gi 154213487 gb AAQA01021372.1	364	822	1
TCONS_00004313	XLOC_004289	gi 154213587 gb AAQA01021272.1	46	826	1
TCONS_00004315	XLOC_004291	gi 154213619 gb AAQA01021240.1	4	361	1
TCONS_00004315	XLOC_004291	gi 154213619 gb AAQA01021240.1	577	608	2
TCONS_00004317	XLOC_004293	gi 154213657 gb AAQA01021202.1	504	805	1
TCONS_00004325	XLOC_004301	gi 154213750 gb AAQA01021109.1	244	493	1
TCONS_00004326	XLOC_004302	gi 154213754 gb AAQA01021105.1	3	425	1
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TCONS_00004336	XLOC_004312	gi 154213896 gb AAQA01020963.1	111	208	1
TCONS_00004336	XLOC_004312	gi 154213896 gb AAQA01020963.1	520	615	2
TCONS_00004336	XLOC_004312	gi 154213896 gb AAQA01020963.1	722	833	3
TCONS_00004351	XLOC_004327	gi 154214058 gb AAQA01020801.1	29	150	1

TCONS_00004351	XLOC_004327	gi 154214058 gb AAQA01020801.1	617	798	2
TCONS_00004353	XLOC_004329	gi 154214080 gb AAQA01020779.1	369	754	1
TCONS_00004370	XLOC_004346	gi 154214302 gb AAQA01020557.1	131	490	1
TCONS_00004380	XLOC_004356	gi 154214376 gb AAQA01020483.1	530	748	1
TCONS_00004384	XLOC_004360	gi 154214411 gb AAQA01020448.1	464	749	1
TCONS_00004417	XLOC_004391	gi 154214910 gb AAQA01019949.1	604	838	1
TCONS_00004421	XLOC_004395	gi 154214939 gb AAQA01019920.1	504	827	1
TCONS_00004422	XLOC_004396	gi 154214966 gb AAQA01019893.1	268	387	1
TCONS_00004422	XLOC_004396	gi 154214966 gb AAQA01019893.1	679	837	2
TCONS_00004435	XLOC_004407	gi 154215078 gb AAQA01019781.1	609	847	1
TCONS_00004438	XLOC_004410	gi 154215131 gb AAQA01019728.1	459	713	1
TCONS_00004440	XLOC_004412	gi 154215204 gb AAQA01019655.1	1	478	1
TCONS_00004459	XLOC_004430	gi 154215387 gb AAQA01019472.1	270	470	1
TCONS_00004460	XLOC_004431	gi 154215395 gb AAQA01019464.1	225	470	1
TCONS_00004473	XLOC_004444	gi 154215681 gb AAQA01019178.1	70	307	1
TCONS_00004486	XLOC_004456	gi 154215877 gb AAQA01018982.1	8	876	1
TCONS_00004491	XLOC_004461	gi 154215941 gb AAQA01018918.1	3	479	1
TCONS_00004493	XLOC_004463	gi 154215978 gb AAQA01018881.1	168	288	1
TCONS_00004493	XLOC_004463	gi 154215978 gb AAQA01018881.1	608	846	2
TCONS_00004510	XLOC_004478	gi 154216125 gb AAQA01018734.1	315	872	1
TCONS_00004516	XLOC_004484	gi 154216169 gb AAQA01018690.1	22	178	1
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TCONS_00004517	XLOC_004485	gi 154216172 gb AAQA01018687.1	78	320	1
TCONS_00004530	XLOC_004498	gi 154216353 gb AAQA01018506.1	630	839	1
TCONS_00004537	XLOC_004505	gi 154216474 gb AAQA01018385.1	242	888	1
TCONS_00004544	XLOC_004512	gi 154216583 gb AAQA01018276.1	170	508	1
TCONS_00004557	XLOC_004525	gi 154216719 gb AAQA01018140.1	55	346	1
TCONS_00004557	XLOC_004525	gi 154216719 gb AAQA01018140.1	770	848	2
TCONS_00004568	XLOC_004535	gi 154216828 gb AAQA01018031.1	361	873	1
TCONS_00004671	XLOC_004634	gi 154218249 gb AAQA01016610.1	398	629	1
TCONS_00004671	XLOC_004634	gi 154218249 gb AAQA01016610.1	897	909	2
TCONS_00004672	XLOC_004634	gi 154218249 gb AAQA01016610.1	398	629	1
TCONS_00004672	XLOC_004634	gi 154218249 gb AAQA01016610.1	900	926	2
TCONS_00004684	XLOC_004644	gi 154218405 gb AAQA01016454.1	81	156	1
TCONS_00004684	XLOC_004644	gi 154218405 gb AAQA01016454.1	727	933	2
TCONS_00004707	XLOC_004665	gi 154218706 gb AAQA01016153.1	4	310	1
TCONS_00004727	XLOC_004685	gi 154218995 gb AAQA01015864.1	6	252	1
TCONS_00004727	XLOC_004685	gi 154218995 gb AAQA01015864.1	447	555	2
TCONS_00004728	XLOC_004685	gi 154218995 gb AAQA01015864.1	6	246	1
TCONS_00004728	XLOC_004685	gi 154218995 gb AAQA01015864.1	447	578	2
TCONS_00004736	XLOC_004693	gi 154219114 gb AAQA01015745.1	120	377	1
TCONS_00004737	XLOC_004694	gi 154219117 gb AAQA01015742.1	617	921	1
TCONS_00004740	XLOC_004697	gi 154219188 gb AAQA01015671.1	84	737	1
TCONS_00004776	XLOC_004733	gi 154219604 gb AAQA01015255.1	60	225	1
TCONS_00004776	XLOC_004733	gi 154219604 gb AAQA01015255.1	599	848	2
TCONS_00004780	XLOC_004737	gi 154219671 gb AAQA01015188.1	98	331	1
TCONS_00004790	XLOC_004747	gi 154219749 gb AAQA01015110.1	3	74	1
TCONS_00004790	XLOC_004747	gi 154219749 gb AAQA01015110.1	491	641	2
TCONS_00004796	XLOC_004752	gi 154219812 gb AAQA01015047.1	1	147	1

TCONS_00004796	XLOC_004752	gi 154219812 gb AAQA01015047.1	416	598	2
TCONS_00004799	XLOC_004755	gi 154219826 gb AAQA01015033.1	25	203	1
TCONS_00004799	XLOC_004755	gi 154219826 gb AAQA01015033.1	459	619	2
TCONS_00004819	XLOC_004774	gi 154220059 gb AAQA01014800.1	286	810	1
TCONS_00004820	XLOC_004775	gi 154220069 gb AAQA01014790.1	2	179	1
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TCONS_00004824	XLOC_004779	gi 154220143 gb AAQA01014716.1	6	341	1
TCONS_00004833	XLOC_004788	gi 154220268 gb AAQA01014591.1	216	295	1
TCONS_00004833	XLOC_004788	gi 154220268 gb AAQA01014591.1	557	680	2
TCONS_00004840	XLOC_004795	gi 154220403 gb AAQA01014456.1	413	681	1
TCONS_00004840	XLOC_004795	gi 154220403 gb AAQA01014456.1	949	972	2
TCONS_00004860	XLOC_004815	gi 154220713 gb AAQA01014146.1	572	923	1
TCONS_00004871	XLOC_004825	gi 154220857 gb AAQA01014002.1	112	399	1
TCONS_00004884	XLOC_004836	gi 154220942 gb AAQA01013917.1	218	266	1
TCONS_00004884	XLOC_004836	gi 154220942 gb AAQA01013917.1	577	710	2
TCONS_00004884	XLOC_004836	gi 154220942 gb AAQA01013917.1	812	949	3
TCONS_00004892	XLOC_004844	gi 154221007 gb AAQA01013852.1	69	294	1
TCONS_00004896	XLOC_004847	gi 154221019 gb AAQA01013840.1	593	858	1
TCONS_00004898	XLOC_004849	gi 154221042 gb AAQA01013817.1	1	1001	1
TCONS_00004900	XLOC_004851	gi 154221078 gb AAQA01013781.1	201	357	1
TCONS_00004900	XLOC_004851	gi 154221078 gb AAQA01013781.1	876	960	2
TCONS_00004927	XLOC_004878	gi 154221397 gb AAQA01013462.1	5	64	1
TCONS_00004927	XLOC_004878	gi 154221397 gb AAQA01013462.1	356	502	2
TCONS_00004927	XLOC_004878	gi 154221397 gb AAQA01013462.1	776	1007	3
TCONS_00004928	XLOC_004878	gi 154221397 gb AAQA01013462.1	5	64	1
TCONS_00004928	XLOC_004878	gi 154221397 gb AAQA01013462.1	405	502	2
TCONS_00004928	XLOC_004878	gi 154221397 gb AAQA01013462.1	776	1007	3
TCONS_00004929	XLOC_004879	gi 154221403 gb AAQA01013456.1	807	1013	1
TCONS_00004944	XLOC_004894	gi 154221554 gb AAQA01013305.1	72	608	1
TCONS_00004945	XLOC_004895	gi 154221577 gb AAQA01013282.1	2	1014	1
TCONS_00004950	XLOC_004900	gi 154221648 gb AAQA01013211.1	151	403	1
TCONS_00004955	XLOC_004905	gi 154221682 gb AAQA01013177.1	714	870	1
TCONS_00004955	XLOC_004905	gi 154221682 gb AAQA01013177.1	982	1030	2
TCONS_00004986	XLOC_004935	gi 154221969 gb AAQA01012890.1	465	1033	1
TCONS_00005003	XLOC_004952	gi 154222137 gb AAQA01012722.1	231	652	1
TCONS_00005017	XLOC_004964	gi 154222280 gb AAQA01012579.1	392	618	1
TCONS_00005025	XLOC_004972	gi 154222365 gb AAQA01012494.1	329	763	1
TCONS_00005076	XLOC_005021	gi 154222923 gb AAQA01011936.1	386	720	1
TCONS_00005083	XLOC_005028	gi 154222991 gb AAQA01011868.1	548	727	1
TCONS_00005083	XLOC_005028	gi 154222991 gb AAQA01011868.1	1032	1089	2
TCONS_00005100	XLOC_005044	gi 154223156 gb AAQA01011703.1	131	354	1
TCONS_00005114	XLOC_005056	gi 154223269 gb AAQA01011590.1	870	1107	1
TCONS_00005130	XLOC_005072	gi 154223378 gb AAQA01011486.1	683	726	1
TCONS_00005130	XLOC_005072	gi 154223378 gb AAQA01011486.1	832	1054	2
TCONS_00005141	XLOC_005082	gi 154223610 gb AAQA01011354.1	638	882	1
TCONS_00005145	XLOC_005086	gi 154223697 gb AAQA01011306.1	1	358	1
TCONS_00005156	XLOC_005096	gi 154223760 gb AAQA01011248.1	578	875	1
TCONS_00005171	XLOC_005111	gi 154224287 gb AAQA01011134.1	1	67	1
TCONS_00005171	XLOC_005111	gi 154224287 gb AAQA01011134.1	374	519	2



TCONS_00005171	XLOC_005111	gi 154224287 gb AAQA01011134.1	658	812	3
TCONS_00005176	XLOC_005116	gi 154224579 gb AAQA01011114.1	141	543	1
TCONS_00005177	XLOC_005117	gi 154224588 gb AAQA01011105.1	482	718	1
TCONS_00005178	XLOC_005118	gi 154224591 gb AAQA01011102.1	334	569	1
TCONS_00005182	XLOC_005122	gi 154224640 gb AAQA01011056.1	821	1083	1
TCONS_00005194	XLOC_005133	gi 154224852 gb AAQA01010927.1	180	231	1
TCONS_00005194	XLOC_005133	gi 154224852 gb AAQA01010927.1	581	702	2
TCONS_00005194	XLOC_005133	gi 154224852 gb AAQA01010927.1	793	977	3
TCONS_00005215	XLOC_005154	gi 154224985 gb AAQA01010831.1	49	168	1
TCONS_00005215	XLOC_005154	gi 154224985 gb AAQA01010831.1	326	428	2
TCONS_00005217	XLOC_005156	gi 154224997 gb AAQA01010819.1	353	608	1
TCONS_00005219	XLOC_005158	gi 154225013 gb AAQA01010803.1	75	1107	1
TCONS_00005224	XLOC_005163	gi 154225041 gb AAQA01010775.1	429	652	1
TCONS_00005228	XLOC_005166	gi 154225048 gb AAQA01010768.1	157	236	1
TCONS_00005228	XLOC_005166	gi 154225048 gb AAQA01010768.1	342	434	2
TCONS_00005228	XLOC_005166	gi 154225048 gb AAQA01010768.1	677	762	3
TCONS_00005250	XLOC_005186	gi 154225164 gb AAQA01010652.1	4	215	1
TCONS_00005250	XLOC_005186	gi 154225164 gb AAQA01010652.1	644	860	2
TCONS_00005262	XLOC_005196	gi 154225236 gb AAQA01010580.1	95	103	1
TCONS_00005262	XLOC_005196	gi 154225236 gb AAQA01010580.1	521	892	2
TCONS_00005273	XLOC_005207	gi 154225306 gb AAQA01010510.1	906	1172	1
TCONS_00005337	XLOC_005269	gi 154225864 gb AAQA01009952.1	970	1201	1
TCONS_00005339	XLOC_005271	gi 154225889 gb AAQA01009927.1	181	1209	1
TCONS_00005343	XLOC_005274	gi 154225914 gb AAQA01009902.1	616	818	1
TCONS_00005360	XLOC_005291	gi 154226055 gb AAQA01009761.1	331	560	1
TCONS_00005364	XLOC_005295	gi 154226098 gb AAQA01009718.1	79	128	1
TCONS_00005364	XLOC_005295	gi 154226098 gb AAQA01009718.1	580	690	2
TCONS_00005364	XLOC_005295	gi 154226098 gb AAQA01009718.1	785	871	3
TCONS_00005365	XLOC_005296	gi 154226109 gb AAQA01009707.1	121	1023	1
TCONS_00005389	XLOC_005318	gi 154226204 gb AAQA01009612.1	44	630	1
TCONS_00005409	XLOC_005335	gi 154226337 gb AAQA01009479.1	216	462	1
TCONS_00005413	XLOC_005339	gi 154226412 gb AAQA01009404.1	138	567	1
TCONS_00005415	XLOC_005341	gi 154226418 gb AAQA01009398.1	248	294	1
TCONS_00005415	XLOC_005341	gi 154226418 gb AAQA01009398.1	776	960	2
TCONS_00005427	XLOC_005351	gi 154226507 gb AAQA01009309.1	257	439	1
TCONS_00005427	XLOC_005351	gi 154226507 gb AAQA01009309.1	839	909	2
TCONS_00005459	XLOC_005383	gi 154226656 gb AAQA01009160.1	626	930	1
TCONS_00005469	XLOC_005392	gi 154226756 gb AAQA01009060.1	556	783	1
TCONS_00005470	XLOC_005393	gi 154226759 gb AAQA01009057.1	801	1001	1
TCONS_00005485	XLOC_005407	gi 154226840 gb AAQA01008976.1	162	297	1
TCONS_00005485	XLOC_005407	gi 154226840 gb AAQA01008976.1	952	1052	2
TCONS_00005491	XLOC_005413	gi 154226871 gb AAQA01008945.1	605	835	1
TCONS_00005504	XLOC_005424	gi 154226944 gb AAQA01008872.1	426	905	1
TCONS_00005506	XLOC_005426	gi 154226948 gb AAQA01008868.1	45	445	1
TCONS_00005521	XLOC_005439	gi 154227045 gb AAQA01008771.1	681	1296	1
TCONS_00005537	XLOC_005454	gi 154227142 gb AAQA01008674.1	153	191	1
TCONS_00005537	XLOC_005454	gi 154227142 gb AAQA01008674.1	681	803	2
TCONS_00005537	XLOC_005454	gi 154227142 gb AAQA01008674.1	1133	1272	3
TCONS_00005538	XLOC_005455	gi 154227150 gb AAQA01008666.1	792	1225	1

TCONS_00005566	XLOC_005481	gi 154227319 gb AAQA01008497.1	18	82	1
TCONS_00005566	XLOC_005481	gi 154227319 gb AAQA01008497.1	304	566	2
TCONS_00005596	XLOC_005511	gi 154227489 gb AAQA01008327.1	4	132	1
TCONS_00005596	XLOC_005511	gi 154227489 gb AAQA01008327.1	432	562	2
TCONS_00005625	XLOC_005538	gi 154227634 gb AAQA01008182.1	752	961	1
TCONS_00005642	XLOC_005555	gi 154227780 gb AAQA01008036.1	670	851	1
TCONS_00005642	XLOC_005555	gi 154227780 gb AAQA01008036.1	1161	1183	2
TCONS_00005670	XLOC_005583	gi 154227959 gb AAQA01007857.1	326	531	1
TCONS_00005684	XLOC_005595	gi 154228045 gb AAQA01007771.1	222	312	1
TCONS_00005684	XLOC_005595	gi 154228045 gb AAQA01007771.1	1177	1301	2
TCONS_00005686	XLOC_005597	gi 154228058 gb AAQA01007758.1	460	615	1
TCONS_00005686	XLOC_005597	gi 154228058 gb AAQA01007758.1	1268	1359	2
TCONS_00005700	XLOC_005611	gi 154228175 gb AAQA01007641.1	26	1305	1
TCONS_00005701	XLOC_005611	gi 154228175 gb AAQA01007641.1	26	426	1
TCONS_00005701	XLOC_005611	gi 154228175 gb AAQA01007641.1	706	1305	2
TCONS_00005702	XLOC_005612	gi 154228186 gb AAQA01007630.1	63	352	1
TCONS_00005708	XLOC_005618	gi 154228211 gb AAQA01007605.1	749	1260	1
TCONS_00005720	XLOC_005629	gi 154228268 gb AAQA01007548.1	673	1125	1
TCONS_00005729	XLOC_005638	gi 154228323 gb AAQA01007493.1	22	233	1
TCONS_00005737	XLOC_005646	gi 154228351 gb AAQA01007465.1	998	1389	1
TCONS_00005739	XLOC_005648	gi 154228360 gb AAQA01007456.1	442	544	1
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TCONS_00005746	XLOC_005654	gi 154228389 gb AAQA01007427.1	1193	1423	1
TCONS_00005749	XLOC_005657	gi 154228405 gb AAQA01007411.1	437	721	1
TCONS_00005759	XLOC_005667	gi 154228447 gb AAQA01007369.1	321	588	1
TCONS_00005795	XLOC_005702	gi 154228615 gb AAQA01007201.1	359	657	1
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TCONS_00005834	XLOC_005740	gi 154228905 gb AAQA01006911.1	544	750	1
TCONS_00005849	XLOC_005753	gi 154228973 gb AAQA01006843.1	583	919	1
TCONS_00005856	XLOC_005758	gi 154228995 gb AAQA01006821.1	19	224	1
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TCONS_00005890	XLOC_005790	gi 154229175 gb AAQA01006641.1	888	1143	1
TCONS_00005897	XLOC_005795	gi 154229200 gb AAQA01006616.1	119	515	1
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TCONS_00005965	XLOC_005857	gi 154229445 gb AAQA01006371.1	296	897	1
TCONS_00005966	XLOC_005858	gi 154229447 gb AAQA01006369.1	457	589	1
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TCONS_00005974	XLOC_005865	gi 154229489 gb AAQA01006327.1	35	246	1
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TCONS_00005994	XLOC_005884	gi 154229584 gb AAQA01006232.1	838	1043	1
TCONS_00006016	XLOC_005901	gi 154229650 gb AAQA01006166.1	380	502	1
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TCONS_00006169	XLOC_006036	gi 154230088 gb AAQA01005728.1	872	1088	1
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TCONS_00007095	XLOC_006820	gi 154231783 gb AAQA01004033.1	1577	2371	1
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TCONS_00007353	XLOC_007019	gi 154232105 gb AAQA01003711.1	1615	1829	1
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TCONS_00007398	XLOC_007059	gi 154232162 gb AAQA01003654.1	1222	1453	1

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TCONS_00007444	XLOC_007089	gi 154232199 gb AAQA01003617.1	220	1434	1
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TCONS_00007566	XLOC_007187	gi 154232327 gb AAQA01003489.1	229	337	1
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TCONS_00007655	XLOC_007254	gi 154232431 gb AAQA01003385.1	1626	2007	1
TCONS_00007738	XLOC_007319	gi 154232518 gb AAQA01003298.1	2938	3230	1
TCONS_00007800	XLOC_007366	gi 154232585 gb AAQA01003231.1	2621	2936	1
TCONS_00007814	XLOC_007376	gi 154232596 gb AAQA01003220.1	518	761	1
TCONS_00007821	XLOC_007382	gi 154232601 gb AAQA01003215.1	202	626	1
TCONS_00007841	XLOC_007398	gi 154232623 gb AAQA01003193.1	2937	3317	1
TCONS_00007852	XLOC_007407	gi 154232635 gb AAQA01003181.1	28	505	1
TCONS_00007857	XLOC_007412	gi 154232640 gb AAQA01003176.1	3057	3408	1
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TCONS_00007942	XLOC_007478	gi 154232724 gb AAQA01003092.1	1933	2065	1
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TCONS_00007984	XLOC_007503	gi 154232755 gb AAQA01003061.1	24	463	1
TCONS_00008006	XLOC_007519	gi 154232771 gb AAQA01003045.1	3002	3220	1
TCONS_00008009	XLOC_007522	gi 154232776 gb AAQA01003040.1	752	1674	1
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TCONS_00008097	XLOC_007589	gi 154232850 gb AAQA01002966.1	1977	2256	1
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TCONS_00008117	XLOC_007603	gi 154232863 gb AAQA01002953.1	1978	2208	1
TCONS_00008121	XLOC_007607	gi 154232866 gb AAQA01002950.1	3339	3539	1
TCONS_00008221	XLOC_007676	gi 154232944 gb AAQA01002872.1	4	286	1
TCONS_00008224	XLOC_007679	gi 154232947 gb AAQA01002869.1	1159	1201	1
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TCONS_00008236	XLOC_007690	gi 154232955 gb AAQA01002861.1	1395	1682	1
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TCONS_00008254	XLOC_007705	gi 154232967 gb AAQA01002849.1	263	491	1
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TCONS_00008263	XLOC_007711	gi 154232972 gb AAQA01002844.1	2716	2999	1
TCONS_00008264	XLOC_007712	gi 154232978 gb AAQA01002838.1	3196	3459	1
TCONS_00008265	XLOC_007713	gi 154232979 gb AAQA01002837.1	740	818	1
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TCONS_00008296	XLOC_007734	gi 154232999 gb AAQA01002817.1	18	355	1
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TCONS_00008327	XLOC_007757	gi 154233029 gb AAQA01002787.1	33	485	1
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TCONS_00008371	XLOC_007791	gi 154233071 gb AAQA01002745.1	1862	1919	1
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TCONS_00008381	XLOC_007798	gi 154233078 gb AAQA01002738.1	263	535	1
TCONS_00008393	XLOC_007809	gi 154233086 gb AAQA01002730.1	1018	1590	1
TCONS_00008397	XLOC_007813	gi 154233091 gb AAQA01002725.1	2703	3062	1
TCONS_00008414	XLOC_007823	gi 154233099 gb AAQA01002717.1	2421	2636	1
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TCONS_00008500	XLOC_007891	gi 154233175 gb AAQA01002641.1	1831	2018	1
TCONS_00008500	XLOC_007891	gi 154233175 gb AAQA01002641.1	2410	2544	2
TCONS_00008500	XLOC_007891	gi 154233175 gb AAQA01002641.1	4031	4049	3
TCONS_00008501	XLOC_007891	gi 154233175 gb AAQA01002641.1	1831	2544	1
TCONS_00008501	XLOC_007891	gi 154233175 gb AAQA01002641.1	3462	3601	2
TCONS_00008501	XLOC_007891	gi 154233175 gb AAQA01002641.1	4031	4077	3
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TCONS_00008502	XLOC_007891	gi 154233175 gb AAQA01002641.1	2410	2544	2
TCONS_00008502	XLOC_007891	gi 154233175 gb AAQA01002641.1	3462	3601	3
TCONS_00008502	XLOC_007891	gi 154233175 gb AAQA01002641.1	4031	4077	4
TCONS_00008506	XLOC_007895	gi 154233179 gb AAQA01002637.1	2459	2900	1
TCONS_00008520	XLOC_007902	gi 154233185 gb AAQA01002631.1	186	613	1
TCONS_00008557	XLOC_007923	gi 154233214 gb AAQA01002602.1	1993	2285	1
TCONS_00008561	XLOC_007926	gi 154233216 gb AAQA01002600.1	1714	1986	1
TCONS_00008563	XLOC_007928	gi 154233217 gb AAQA01002599.1	1984	2296	1
TCONS_00008564	XLOC_007929	gi 154233217 gb AAQA01002599.1	3165	3404	1
TCONS_00008572	XLOC_007935	gi 154233225 gb AAQA01002591.1	1127	1605	1
TCONS_00008573	XLOC_007936	gi 154233226 gb AAQA01002590.1	1850	2181	1
TCONS_00008573	XLOC_007936	gi 154233226 gb AAQA01002590.1	2613	2701	2
TCONS_00008592	XLOC_007951	gi 154233237 gb AAQA01002579.1	1596	1855	1
TCONS_00008593	XLOC_007952	gi 154233237 gb AAQA01002579.1	2224	2614	1
TCONS_00008594	XLOC_007953	gi 154233237 gb AAQA01002579.1	2677	2939	1
TCONS_00008597	XLOC_007956	gi 154233241 gb AAQA01002575.1	1625	2104	1
TCONS_00008630	XLOC_007983	gi 154233268 gb AAQA01002548.1	3185	3479	1
TCONS_00008679	XLOC_008017	gi 154233319 gb AAQA01002497.1	2149	2370	1
TCONS_00008687	XLOC_008023	gi 154233325 gb AAQA01002491.1	2918	3126	1

TCONS_00008734	XLOC_008056	gi 154233353 gb AAQA01002463.1	935	1141	1
TCONS_00008758	XLOC_008072	gi 154233363 gb AAQA01002453.1	2	248	1
TCONS_00008800	XLOC_008101	gi 154233388 gb AAQA01002428.1	1241	1441	1
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TCONS_00008818	XLOC_008113	gi 154233404 gb AAQA01002412.1	3886	4195	1
TCONS_00008851	XLOC_008138	gi 154233428 gb AAQA01002388.1	1062	1301	1
TCONS_00008885	XLOC_008167	gi 154233454 gb AAQA01002362.1	263	623	1
TCONS_00008912	XLOC_008186	gi 154233475 gb AAQA01002341.1	27	246	1
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TCONS_00009027	XLOC_008265	gi 154233550 gb AAQA01002266.1	1861	1924	1
TCONS_00009027	XLOC_008265	gi 154233550 gb AAQA01002266.1	2223	2303	2
TCONS_00009027	XLOC_008265	gi 154233550 gb AAQA01002266.1	2459	2560	3
TCONS_00009057	XLOC_008282	gi 154233563 gb AAQA01002253.1	2492	2710	1
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TCONS_00009162	XLOC_008356	gi 154233636 gb AAQA01002180.1	1055	1262	1
TCONS_00009182	XLOC_008371	gi 154233648 gb AAQA01002168.1	1537	1842	1
TCONS_00009196	XLOC_008379	gi 154233653 gb AAQA01002163.1	1353	1599	1
TCONS_00009197	XLOC_008380	gi 154233653 gb AAQA01002163.1	1935	2440	1
TCONS_00009287	XLOC_008450	gi 154233714 gb AAQA01002102.1	977	1078	1
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TCONS_00009332	XLOC_008479	gi 154233737 gb AAQA01002079.1	4112	4181	1
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TCONS_00009360	XLOC_008498	gi 154233753 gb AAQA01002063.1	2801	2972	1
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TCONS_00009580	XLOC_008635	gi 154233862 gb AAQA01001954.1	1350	1595	2
TCONS_00009682	XLOC_008695	gi 154233901 gb AAQA01001915.1	4814	5039	1
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TCONS_00009721	XLOC_008721	gi 154233917 gb AAQA01001899.1	591	1361	1
TCONS_00009729	XLOC_008729	gi 154233925 gb AAQA01001891.1	1546	1795	1
TCONS_00009765	XLOC_008752	gi 154233941 gb AAQA01001875.1	4084	4256	1
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TCONS_00009778	XLOC_008763	gi 154233947 gb AAQA01001869.1	64	745	1
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TCONS_00009916	XLOC_008847	gi 154234005 gb AAQA01001811.1	3669	4218	1
TCONS_00009939	XLOC_008862	gi 154234015 gb AAQA01001801.1	2339	2606	1
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TCONS_00010034	XLOC_008926	gi 154234057 gb AAQA01001759.1	1	55	1

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TCONS_00010117	XLOC_008981	gi 154234089 gb AAQA01001727.1	3390	3576	1
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TCONS_00010470	XLOC_009173	gi 154234220 gb AAQA01001596.1	761	1163	1
TCONS_00010539	XLOC_009215	gi 154234250 gb AAQA01001566.1	7033	7267	1
TCONS_00010576	XLOC_009238	gi 154234261 gb AAQA01001555.1	5975	6290	1
TCONS_00010588	XLOC_009249	gi 154234268 gb AAQA01001548.1	5281	5374	1
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TCONS_00010669	XLOC_009296	gi 154234296 gb AAQA01001520.1	6202	6468	1
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TCONS_00010820	XLOC_009378	gi 154234345 gb AAQA01001471.1	1123	1248	1
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TCONS_00011904	XLOC_009944	gi 154234653 gb AAQA01001163.1	10504	10760	1
TCONS_00011927	XLOC_009961	gi 154234657 gb AAQA01001159.1	8225	8451	1
TCONS_00011956	XLOC_009979	gi 154234665 gb AAQA01001151.1	1721	2027	1
TCONS_00012081	XLOC_010042	gi 154234696 gb AAQA01001120.1	856	1189	1
TCONS_00012082	XLOC_010043	gi 154234696 gb AAQA01001120.1	8150	8454	1
TCONS_00012117	XLOC_010057	gi 154234702 gb AAQA01001114.1	1436	2022	1
TCONS_00012150	XLOC_010080	gi 154234710 gb AAQA01001106.1	2539	2945	1
TCONS_00012171	XLOC_010088	gi 154234712 gb AAQA01001104.1	3132	3404	1
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TCONS_00012246	XLOC_010131	gi 154234728 gb AAQA01001088.1	4313	4533	1
TCONS_00012254	XLOC_010136	gi 154234729 gb AAQA01001087.1	630	879	1
TCONS_00012346	XLOC_010180	gi 154234746 gb AAQA01001070.1	10062	10339	1
TCONS_00012394	XLOC_010207	gi 154234756 gb AAQA01001060.1	5469	5716	1
TCONS_00012402	XLOC_010214	gi 154234757 gb AAQA01001059.1	1069	1423	1
TCONS_00012417	XLOC_010224	gi 154234761 gb AAQA01001055.1	69	489	1
TCONS_00012450	XLOC_010248	gi 154234767 gb AAQA01001049.1	6275	6289	1
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TCONS_00012451	XLOC_010249	gi 154234767 gb AAQA01001049.1	12335	12587	1
TCONS_00012458	XLOC_010254	gi 154234768 gb AAQA01001048.1	8997	9213	1
TCONS_00012490	XLOC_010273	gi 154234774 gb AAQA01001042.1	12758	13006	1
TCONS_00012552	XLOC_010308	gi 154234786 gb AAQA01001030.1	12300	12660	1
TCONS_00012568	XLOC_010318	gi 154234792 gb AAQA01001024.1	830	1164	1
TCONS_00012669	XLOC_010373	gi 154234818 gb AAQA01000998.1	13097	13314	1
TCONS_00012669	XLOC_010373	gi 154234818 gb AAQA01000998.1	13621	13722	2
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TCONS_00012681	XLOC_010377	gi 154234820 gb AAQA01000996.1	13264	13535	1
TCONS_00012703	XLOC_010387	gi 154234823 gb AAQA01000993.1	13833	14068	1
TCONS_00012728	XLOC_010398	gi 154234827 gb AAQA01000989.1	1181	1442	1
TCONS_00012744	XLOC_010406	gi 154234831 gb AAQA01000985.1	2804	3057	1
TCONS_00012885	XLOC_010482	gi 154234861 gb AAQA01000955.1	11919	12346	1
TCONS_00012964	XLOC_010517	gi 154234873 gb AAQA01000943.1	11868	11940	1
TCONS_00012964	XLOC_010517	gi 154234873 gb AAQA01000943.1	12198	12336	2
TCONS_00012966	XLOC_010519	gi 154234874 gb AAQA01000942.1	439	447	1
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TCONS_00013046	XLOC_010561	gi 154234885 gb AAQA01000931.1	12456	12657	1

TCONS_00013235	XLOC_010649	gi 154234914 gb AAQA01000902.1	4503	4743	1
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TCONS_00013270	XLOC_010663	gi 154234918 gb AAQA01000898.1	14481	14966	1
TCONS_00013305	XLOC_010681	gi 154234924 gb AAQA01000892.1	374	756	1
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TCONS_00013326	XLOC_010689	gi 154234928 gb AAQA01000888.1	187	266	1
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TCONS_00013714	XLOC_010869	gi 154234983 gb AAQA01000833.1	12436	12635	1
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TCONS_00013731	XLOC_010880	gi 154234986 gb AAQA01000830.1	3153	3387	1
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TCONS_00013851	XLOC_010937	gi 154235004 gb AAQA01000812.1	2310	2332	1
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TCONS_00013881	XLOC_010948	gi 154235007 gb AAQA01000809.1	9114	9344	1
TCONS_00013972	XLOC_010986	gi 154235018 gb AAQA01000798.1	17490	17758	1
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TCONS_00014103	XLOC_011062	gi 154235038 gb AAQA01000778.1	14874	14992	1
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TCONS_00014198	XLOC_011098	gi 154235046 gb AAQA01000770.1	14869	15599	1
TCONS_00014206	XLOC_011101	gi 154235048 gb AAQA01000768.1	1125	1300	1
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TCONS_00014237	XLOC_011114	gi 154235050 gb AAQA01000766.1	311	612	1
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TCONS_00014280	XLOC_011139	gi 154235056 gb AAQA01000760.1	7988	8009	1
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TCONS_00014309	XLOC_011151	gi 154235061 gb AAQA01000755.1	38	331	1
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TCONS_00014402	XLOC_011196	gi 154235070 gb AAQA01000746.1	10734	10975	1
TCONS_00014429	XLOC_011210	gi 154235074 gb AAQA01000742.1	19144	19398	1
TCONS_00014452	XLOC_011221	gi 154235079 gb AAQA01000737.1	8305	8529	1
TCONS_00014465	XLOC_011231	gi 154235081 gb AAQA01000735.1	10446	10665	1
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TCONS_00014514	XLOC_011254	gi 154235085 gb AAQA01000731.1	8851	9095	1
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TCONS_00014663	XLOC_011320	gi 154235108 gb AAQA01000708.1	18914	19115	1
TCONS_00014805	XLOC_011387	gi 154235126 gb AAQA01000690.1	1196	1546	1
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TCONS_00014855	XLOC_011408	gi 154235132 gb AAQA01000684.1	12279	12513	1

TCONS_00014876	XLOC_011419	gi 154235134 gb AAQA01000682.1	18921	19151	1
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TCONS_00014930	XLOC_011445	gi 154235142 gb AAQA01000674.1	7477	7755	1
TCONS_00014975	XLOC_011466	gi 154235147 gb AAQA01000669.1	277	478	1
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TCONS_00015001	XLOC_011477	gi 154235149 gb AAQA01000667.1	231	445	1
TCONS_00015039	XLOC_011497	gi 154235154 gb AAQA01000662.1	12091	12375	1
TCONS_00015049	XLOC_011503	gi 154235155 gb AAQA01000661.1	10107	10415	1
TCONS_00015127	XLOC_011539	gi 154235164 gb AAQA01000652.1	2532	2848	1
TCONS_00015340	XLOC_011630	gi 154235192 gb AAQA01000624.1	5566	5804	1
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TCONS_00015350	XLOC_011636	gi 154235193 gb AAQA01000623.1	2571	2961	1
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TCONS_00015502	XLOC_011706	gi 154235208 gb AAQA01000608.1	17174	17379	1
TCONS_00015570	XLOC_011743	gi 154235217 gb AAQA01000599.1	10795	10980	1
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TCONS_00015612	XLOC_011766	gi 154235221 gb AAQA01000595.1	19152	19840	1
TCONS_00015631	XLOC_011773	gi 154235223 gb AAQA01000593.1	1089	1418	1
TCONS_00015719	XLOC_011812	gi 154235232 gb AAQA01000584.1	2093	2838	1
TCONS_00015748	XLOC_011830	gi 154235235 gb AAQA01000581.1	17474	17754	1
TCONS_00015774	XLOC_011845	gi 154235240 gb AAQA01000576.1	4589	4849	1
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TCONS_00015893	XLOC_011899	gi 154235252 gb AAQA01000564.1	12605	12849	1
TCONS_00015922	XLOC_011916	gi 154235255 gb AAQA01000561.1	16808	17177	1
TCONS_00015920	XLOC_011914	gi 154235255 gb AAQA01000561.1	23983	24346	1
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TCONS_00016007	XLOC_011960	gi 154235266 gb AAQA01000550.1	2689	3231	1
TCONS_00016020	XLOC_011969	gi 154235268 gb AAQA01000548.1	1747	1886	1
TCONS_00016020	XLOC_011969	gi 154235268 gb AAQA01000548.1	2236	2490	2
TCONS_00016082	XLOC_012003	gi 154235275 gb AAQA01000541.1	14773	14868	1
TCONS_00016082	XLOC_012003	gi 154235275 gb AAQA01000541.1	14960	15067	2
TCONS_00016082	XLOC_012003	gi 154235275 gb AAQA01000541.1	15191	15315	3
TCONS_00016151	XLOC_012032	gi 154235280 gb AAQA01000536.1	7224	7502	1
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TCONS_00016168	XLOC_012040	gi 154235282 gb AAQA01000534.1	18606	18817	1
TCONS_00016176	XLOC_012045	gi 154235286 gb AAQA01000530.1	2443	2453	1
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TCONS_00016516	XLOC_012185	gi 154235316 gb AAQA01000500.1	1415	1620	1
TCONS_00016599	XLOC_012228	gi 154235323 gb AAQA01000493.1	26837	27058	1
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TCONS_00018638	XLOC_013134	gi 154235476 gb AAQA01000340.1	2768	3065	1
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TCONS_00020812	XLOC_014103	gi 154235593 gb AAQA01000223.1	8625	8891	1
TCONS_00020855	XLOC_014119	gi 154235595 gb AAQA01000221.1	49684	50267	1
TCONS_00020890	XLOC_014129	gi 154235596 gb AAQA01000220.1	46894	47151	1
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TCONS_00021076	XLOC_014206	gi 154235604 gb AAQA01000212.1	1222	1459	1
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TCONS_00021172	XLOC_014242	gi 154235608 gb AAQA01000208.1	2754	3027	1
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TCONS_00022172	XLOC_014640	gi 154235643 gb AAQA01000173.1	45018	45222	1
TCONS_00022264	XLOC_014685	gi 154235647 gb AAQA01000169.1	12940	13222	1
TCONS_00022255	XLOC_014678	gi 154235647 gb AAQA01000169.1	24193	24344	1
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TCONS_00022348	XLOC_014718	gi 154235650 gb AAQA01000166.1	52556	52819	1
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TCONS_00022655	XLOC_014839	gi 154235659 gb AAQA01000157.1	32636	32838	1
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TCONS_00022889	XLOC_014931	gi 154235666 gb AAQA01000150.1	30135	30537	1
TCONS_00022918	XLOC_014943	gi 154235667 gb AAQA01000149.1	26974	27253	1
TCONS_00022890	XLOC_014932	gi 154235667 gb AAQA01000149.1	53541	53701	1
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TCONS_00022978	XLOC_014967	gi 154235669 gb AAQA01000147.1	70818	71153	1
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TCONS_00023366	XLOC_015117	gi 154235680 gb AAQA01000136.1	72723	72751	1
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TCONS_00023650	XLOC_015211	gi 154235687 gb AAQA01000129.1	75429	75666	1
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TCONS_00025033	XLOC_015754	gi 154235719 gb AAQA01000097.1	93705	93808	2
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TCONS_00025427	XLOC_015886	gi 154235726 gb AAQA01000090.1	29557	29917	1
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TCONS_00025515	XLOC_015919	gi 154235728 gb AAQA01000088.1	104746	104835	1



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TCONS_00025634	XLOC_015960	gi 154235730 gb AAQA01000086.1	10376	10643	1
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TCONS_00026446	XLOC_016255	gi 154235743 gb AAQA01000073.1	1838	2111	1
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TCONS_00027016	XLOC_016437	gi 154235751 gb AAQA01000065.1	97124	97414	1
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TCONS_00028568	XLOC_017015	gi 154235772 gb AAQA01000044.1	30270	30514	1
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TCONS_00028933	XLOC_017164	gi 154235777 gb AAQA01000039.1	61075	61274	1
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TCONS_00029079	XLOC_017207	gi 154235778 gb AAQA01000038.1	54949	55237	1
TCONS_00029149	XLOC_017234	gi 154235779 gb AAQA01000037.1	62040	62063	1
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TCONS_00029647	XLOC_017414	gi 154235784 gb AAQA01000032.1	152847	153169	1
TCONS_00029651	XLOC_017418	gi 154235785 gb AAQA01000031.1	11451	11700	1
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TCONS_00030143	XLOC_017592	gi 154235789 gb AAQA01000027.1	169556	169755	1
TCONS_00030272	XLOC_017635	gi 154235790 gb AAQA01000026.1	216044	216615	1
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TCONS_00030821	XLOC_017787	gi 154235794 gb AAQA01000022.1	95351	95742	1
TCONS_00030959	XLOC_017824	gi 154235795 gb AAQA01000021.1	117033	117240	1
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TCONS_00031276	XLOC_017922	gi 154235797 gb AAQA01000019.1	88484	88716	1
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TCONS_00031385	XLOC_017965	gi 154235798 gb AAQA01000018.1	25087	25410	1
TCONS_00031387	XLOC_017967	gi 154235798 gb AAQA01000018.1	72408	72700	1
TCONS_00031358	XLOC_017952	gi 154235798 gb AAQA01000018.1	85157	85424	1
TCONS_00031358	XLOC_017952	gi 154235798 gb AAQA01000018.1	85643	85678	2
TCONS_00031391	XLOC_017971	gi 154235798 gb AAQA01000018.1	137133	137694	1
TCONS_00031395	XLOC_017975	gi 154235798 gb AAQA01000018.1	238260	239462	1
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TCONS_00031403	XLOC_017983	gi 154235798 gb AAQA01000018.1	259447	259679	1
TCONS_00031660	XLOC_018075	gi 154235800 gb AAQA01000016.1	54536	54759	1
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TCONS_00031777	XLOC_018130	gi 154235801 gb AAQA01000015.1	162013	162305	1
TCONS_00031951	XLOC_018175	gi 154235802 gb AAQA01000014.1	40946	41150	1
TCONS_00031952	XLOC_018176	gi 154235802 gb AAQA01000014.1	62242	62508	1
TCONS_00031954	XLOC_018178	gi 154235802 gb AAQA01000014.1	80348	80618	1
TCONS_00031966	XLOC_018190	gi 154235802 gb AAQA01000014.1	283822	284034	1
TCONS_00031967	XLOC_018191	gi 154235802 gb AAQA01000014.1	284258	284486	1
TCONS_00032065	XLOC_018227	gi 154235803 gb AAQA01000013.1	26581	26851	1
TCONS_00031981	XLOC_018198	gi 154235803 gb AAQA01000013.1	63887	63914	1
TCONS_00031981	XLOC_018198	gi 154235803 gb AAQA01000013.1	64141	64357	2
TCONS_00032070	XLOC_018232	gi 154235803 gb AAQA01000013.1	98468	98834	1
TCONS_00032079	XLOC_018241	gi 154235803 gb AAQA01000013.1	204425	204669	1
TCONS_00032233	XLOC_018287	gi 154235804 gb AAQA01000012.1	29923	30168	1
TCONS_00032237	XLOC_018291	gi 154235804 gb AAQA01000012.1	63916	64203	1
TCONS_00032240	XLOC_018294	gi 154235804 gb AAQA01000012.1	127721	128204	1

TCONS_00032241	XLOC_018295	gi 154235804 gb AAQA01000012.1	132791	132998	1
TCONS_00032248	XLOC_018302	gi 154235804 gb AAQA01000012.1	281331	281853	1
TCONS_00032559	XLOC_018395	gi 154235806 gb AAQA01000010.1	13977	14308	1
TCONS_00032434	XLOC_018357	gi 154235806 gb AAQA01000010.1	49039	49187	1
TCONS_00032434	XLOC_018357	gi 154235806 gb AAQA01000010.1	49335	49754	2
TCONS_00032563	XLOC_018399	gi 154235806 gb AAQA01000010.1	245302	245563	1
TCONS_00032566	XLOC_018402	gi 154235806 gb AAQA01000010.1	261725	262152	1
TCONS_00032767	XLOC_018454	gi 154235807 gb AAQA01000009.1	140273	140663	1
TCONS_00032886	XLOC_018495	gi 154235808 gb AAQA01000008.1	36913	37026	1
TCONS_00032886	XLOC_018495	gi 154235808 gb AAQA01000008.1	37256	37442	2
TCONS_00032944	XLOC_018517	gi 154235808 gb AAQA01000008.1	118714	119030	1
TCONS_00033107	XLOC_018562	gi 154235809 gb AAQA01000007.1	4102	4420	1
TCONS_00033111	XLOC_018566	gi 154235809 gb AAQA01000007.1	47165	47541	1
TCONS_00033112	XLOC_018567	gi 154235809 gb AAQA01000007.1	50208	50507	1
TCONS_00033113	XLOC_018568	gi 154235809 gb AAQA01000007.1	79151	79539	1
TCONS_00033119	XLOC_018574	gi 154235809 gb AAQA01000007.1	146065	146317	1
TCONS_00033123	XLOC_018578	gi 154235809 gb AAQA01000007.1	173014	173338	1
TCONS_00033314	XLOC_018636	gi 154235810 gb AAQA01000006.1	48999	49508	1
TCONS_00033318	XLOC_018640	gi 154235810 gb AAQA01000006.1	86858	87423	1
TCONS_00033325	XLOC_018647	gi 154235810 gb AAQA01000006.1	150154	150470	1
TCONS_00033328	XLOC_018650	gi 154235810 gb AAQA01000006.1	195706	196057	1
TCONS_00033333	XLOC_018655	gi 154235810 gb AAQA01000006.1	239021	239299	1
TCONS_00033283	XLOC_018628	gi 154235810 gb AAQA01000006.1	306536	306675	1
TCONS_00033283	XLOC_018628	gi 154235810 gb AAQA01000006.1	306905	307014	2
TCONS_00033499	XLOC_018714	gi 154235811 gb AAQA01000005.1	15806	16027	1
TCONS_00033500	XLOC_018715	gi 154235811 gb AAQA01000005.1	70560	70963	1
TCONS_00033508	XLOC_018723	gi 154235811 gb AAQA01000005.1	355700	355944	1
TCONS_00033712	XLOC_018790	gi 154235812 gb AAQA01000004.1	29794	30368	1
TCONS_00033533	XLOC_018733	gi 154235812 gb AAQA01000004.1	108123	108278	1
TCONS_00033533	XLOC_018733	gi 154235812 gb AAQA01000004.1	108480	108568	2
TCONS_00033909	XLOC_018853	gi 154235813 gb AAQA01000003.1	18212	18578	1
TCONS_00033923	XLOC_018867	gi 154235813 gb AAQA01000003.1	363821	364122	1
TCONS_00034148	XLOC_018924	gi 154235814 gb AAQA01000002.1	62961	63324	1
TCONS_00034167	XLOC_018943	gi 154235814 gb AAQA01000002.1	442756	442972	1
TCONS_00034170	XLOC_018946	gi 154235814 gb AAQA01000002.1	449023	449228	1
TCONS_00034447	XLOC_019033	gi 154235815 gb AAQA01000001.1	76139	76466	1
TCONS_00034452	XLOC_019038	gi 154235815 gb AAQA01000001.1	173354	173561	1
TCONS_00034456	XLOC_019042	gi 154235815 gb AAQA01000001.1	222202	222454	1
TCONS_00034457	XLOC_019043	gi 154235815 gb AAQA01000001.1	236405	236702	1
TCONS_00034464	XLOC_019050	gi 154235815 gb AAQA01000001.1	458613	459005	1
TCONS_00034465	XLOC_019051	gi 154235815 gb AAQA01000001.1	478838	479103	1
TCONS_00034469	XLOC_019055	gi 154235815 gb AAQA01000001.1	507178	507412	1
TCONS_00034471	XLOC_019057	gi 154235815 gb AAQA01000001.1	594537	594763	1
TCONS_00034473	XLOC_019059	gi 154235815 gb AAQA01000001.1	595894	596149	1
TCONS_00010182	XLOC_009019	gi 154234117 gb AAQA01001699.1	473	540	1
TCONS_00010182	XLOC_009019	gi 154234117 gb AAQA01001699.1	2760	2942	2
TCONS_00010182	XLOC_009019	gi 154234117 gb AAQA01001699.1	3178	3567	3

**Table indicating FPKM values and counts of the genes coding for lncRNA, showing their relative expression in developmental stages of *B. Malayi* (produced using Cuffdiff and HTSeq respectively).**

GENE_Id	Eggs/Embryos		Microfilariae		Larvae 3		Larvae 4		Adult Male		Adult Female	
	FPKM value	Count	FPKM value	Count	FPKM value	Count	FPKM value	Count	FPKM value	Count	FPKM value	Count
XLOC_003273	1	1	0	13	269.09	0	0	0	0	0	0	0
XLOC_003276	50.57	37	0	24	458.19	0	0	0	0	0	0.39	1
XLOC_003286	5.12	6	0	143	1295.53	5	3.66	0	0.88	1	0.27	1
XLOC_003289	0	0	0	21	230.7	1	1.01	0	0	0	0.68	1
XLOC_003290	3.38	3	0	13	232.23	0	0	0	0	0	0	0
XLOC_003291	0	0	0	21	440.65	6	6.5	0	50.79	41	0	0
XLOC_003300	1.12	1	5.79	93	2342.38	0	0	1	0	0	0	0
XLOC_003305	0	0	0	47	897.3	0	0	0	0	0	0	0
XLOC_003310	0	0	6.35	5	148.43	0	0	1	61.28	41	4.3	5
XLOC_003316	2.23	3	0	135	540.73	8	4.74	0	0	0	1.61	7
XLOC_003321	6.35	6	13.65	73	1158.61	4	4.23	3	5.39	5	5.05	10
XLOC_003326	2.77	4	6.34	53	180.52	4	2.32	2	0.75	1	0.45	2
XLOC_003333	0.94	1	3.04	34	84.8	4	2.23	1	7.23	10	0	0
XLOC_003334	4.39	6	0	12	43.6	0	0	0	0	0	2.67	6
XLOC_003337	0	0	0	21	24.72	0	0	0	0	0	0	0
XLOC_003338	15.48	18	40.18	206	1036.1	13	9.24	12	5.57	7	27.27	72
XLOC_003342	38.23	42	11.54	27	281.45	18	14.79	3	20.08	22	0.56	2
XLOC_003348	2.04	1	0	58	1695.5	1	1.59	0	1.48	1	0.53	1
XLOC_003360	3.11	5	9.61	64	42.39	5	2.65	4	1.72	3	0.65	4
XLOC_003366	3.4	2	0	103	2221.35	0	0	0	7.54	6	5.42	7
XLOC_003375	42.87	28	35.58	134	3526.16	38	44.54	6	36.36	26	22.75	27
XLOC_003384	0	0	0	20	352.59	0	0	0	1.13	1	0	0
XLOC_003386	4.84	3	0	23	579.3	1	0.9	0	0	0	0	0
XLOC_003402	5.61	5	0	990	13398.8	102	90.37	0	174.46	174	3.87	6
XLOC_003408	5.42	7	10.38	4	25.05	0	0	3	0	0	8.32	20
XLOC_003410	0	0	0	11	316.68	0	0	0	0	0	0	0
XLOC_003411	3.84	3	0	31	696.92	7	7.57	0	2.57	2	1.3	3
XLOC_003412	4.92	7	6.32	14	46.18	8	4.93	2	9.01	12	22.39	72
XLOC_003423	0	0	0	1200	17368.6	7	6.55	0	0	0	0	0
XLOC_003427	7.2	17	1.92	253	84.35	12	4.24	1	8.26	18	0.3	1
XLOC_003439	7.83	11	0	151	400.09	3	1.77	0	11.66	16	2.84	6
XLOC_003440	0	0	0	49	886.99	0	0	0	0	0	0	0
XLOC_003444	0	0	0	10	201.46	0	0	0	0	0	0	0
XLOC_003451	29.72	65	110.77	2	0.68	35	14.74	57	1.85	4	24.89	112
XLOC_003452	0	0	0	22	387.85	0	0	0	0	0	0	0
XLOC_003464	16.36	20	12.8	59	214.35	16	11.68	4	17.5	23	7.77	18
XLOC_003484	0	0	0	13	112.54	0	0	0	0	0	0	0
XLOC_003486	1.57	2	4.13	1	12.8	0	0	1	78.4	80	1.45	2
XLOC_003499	12.39	14	0	37	507.61	1	0.67	0	2.02	2	0	0
XLOC_003500	19.49	15	6.13	1	27.93	0	0	1	18.78	13	0.51	1
XLOC_003506	0.94	1	33.28	4506	10907.2	39	24.74	11	9.36	13	7.71	21
XLOC_003509	20.27	31	0	225	230.55	13	7.29	0	3.77	6	2.83	6
XLOC_003510	0	0	0	39	16.64	0	0	0	0	0	0	0
XLOC_003525	0	0	0	123	357.52	0	0	0	0	0	0	0
XLOC_003534	0.37	1	0	14	5.03	0	0	0	0	0	0	0
XLOC_003538	20.96	25	26.23	57	539.06	32	24.56	7	49.81	56	55.98	132
XLOC_003551	49.37	47	175.61	580	7637.27	92	81.11	40	10.9	11	85.69	171
XLOC_003554	0	0	3.36	285	69.97	2	0.71	2	0	0	0	0
XLOC_003565	62.68	66	0	1	10.04	1	0.99	0	3.61	4	0	0
XLOC_003581	4.7	9	27.72	1	0.57	19	9.03	12	6.61	12	5.7	23
XLOC_003584	107.39	157	48.01	325	741.65	102	61.74	16	29.26	41	26.98	82
XLOC_003588	0.85	1	0	11	167.85	0	0	0	1.06	1	0	0

XLOC_003599	3.98	8	2.15	33	14.97	0	0	1	0	0	1.52	5
XLOC_003608	4.29	3	0	0	0	29	36.88	0	8.53	6	1.26	1
XLOC_003612	0	0	0	25	7.45	3	1.25	0	0.88	2	0	0
XLOC_003616	11.73	13	3.81	10	100.42	5	4.15	1	16.26	18	6.29	13
XLOC_003618	0	0	3.77	29	279.95	1	0.98	1	0	0	0	0
XLOC_003623	0.31	1	1.69	97	24.17	1	0.27	1	0	0	0	0
XLOC_003626	0	0	0	11	13.53	0	0	0	0	0	0	0
XLOC_003629	17.63	27	13.29	45	47.75	9	5.14	5	5.7	8	64.27	209
XLOC_003630	0	0	0	10	6.71	1	0.38	0	0	0	0	0
XLOC_003631	44.2	50	35.63	41	304.89	20	15.57	10	2.54	3	84.28	191
XLOC_003639	33.34	21	0	0	0	0	0	0	0	0	0	0
XLOC_003640	5.92	6	0	4	54.88	0	0	0	10.08	9	6.25	15
XLOC_003646	12.57	20	5.48	128	160.97	11	7.02	2	8.48	13	3.5	12
XLOC_003648	16.52	33	6.34	104	44.76	9	4.11	3	13.11	26	11.68	46
XLOC_003649	1.7	2	0	45	249.05	3	2.31	0	6.45	8	0.24	1
XLOC_003652	51.24	43	26.79	14	306.12	74	84.49	5	40.51	32	8.74	12
XLOC_003657	19.57	20	8.82	282	4235.66	8	8.45	1	19.85	19	6.95	16
XLOC_003690	0.5	1	0	14	16.13	0	0	0	0.64	1	0.5	1
XLOC_003691	40.87	74	2.28	1512	832.65	34	16.73	1	16.85	31	4.54	17
XLOC_003692	45.01	123	75.66	322	72.34	64	22.01	47	18.84	49	119.42	705
XLOC_003695	0	0	0	166	36.16	0	0	0	0	0	0.1	1
XLOC_003710	5.51	4	0	29	797.88	2	2.51	0	0	0	0	0
XLOC_003718	23.53	24	0	0	0	0	0	0	0	0	0.29	1
XLOC_003725	5.67	6	13.4	23	350.95	0	0	3	0	0	0.68	2
XLOC_003726	0.81	2	1.65	20	4.73	0	0	1	0	0	0	0
XLOC_003748	1.72	4	0	11	2.34	1	0.42	0	0	0	0	0
XLOC_003749	19.84	19	35.29	52	772.82	5	5.7	8	44.93	43	9.16	14
XLOC_003777	10.59	19	0	198	104.94	8	3.8	0	19.93	37	6.77	24
XLOC_003778	65.59	107	13.59	269	326.05	49	29.31	5	1.29	2	119.53	393
XLOC_003782	0	0	0	28	281.17	0	0	0	9.03	10	0	0
XLOC_003788	16.01	22	2.93	1	1.92	0	0	1	0.7	1	0	0
XLOC_003791	103.49	75	112.76	179	3340.63	121	185.59	17	212.15	129	60.5	71
XLOC_003817	1.35	4	0	30	6.48	8	2.65	0	0.75	2	1.27	7
XLOC_003841	7.35	6	0	67	1022.34	2	2.31	0	1.06	1	3.49	6
XLOC_003842	0	0	9.52	12	208.78	1	1.23	2	0	0	0	0
XLOC_003847	7.04	9	20.47	1	5.71	4	3.21	6	0	0	32.6	87
XLOC_003848	88.09	211	0	2	0.56	0	0	0	0.43	1	51.05	278
XLOC_003865	16.54	19	0	0	0	0	0	0	56.78	73	0.23	1
XLOC_003867	12.14	18	0	24	24.97	7	4.56	0	1.89	3	2.58	10
XLOC_003871	0	0	4.28	0	0	0	0	1	109.55	108	0.75	1
XLOC_003878	4.84	4	0	435	7568.36	12	11.34	0	28.16	25	1.72	2
XLOC_003879	108.27	226	16.72	90	37.45	26	10.99	8	7.97	16	181.66	805
XLOC_003898	0.89	3	0	6	1.35	5	1.77	0	0	0	0.25	1
XLOC_003899	3.59	5	39.5	37	92.28	8	5.06	13	5.06	7	12.65	31
XLOC_003907	6.39	7	86.64	26	250.99	7	4.9	23	0.89	1	12.81	30
XLOC_003910	9.06	15	0	0	0	0	0	0	1.36	2	0	0
XLOC_003911	18.73	26	0	0	0	0	0	0	0	0	0	0
XLOC_003932	1.21	4	0	21	2.97	0	0	0	0	0	0.08	1
XLOC_003942	27	42	28.58	170	278.79	47	29.1	10	19.73	29	4.28	12
XLOC_003957	2.5	3	3.62	16	128.74	0	0	1	0	0	0.26	1
XLOC_003960	12.28	9	0	43	1022.66	13	15.32	0	3.97	3	0.91	2
XLOC_003968	0	0	0	11	6.44	0	0	0	0.55	1	0	0
XLOC_003976	6.23	5	0	12	241.75	0	0	0	0	0	0	0
XLOC_003989	2.28	6	0	58	14.7	9	3.11	0	6.87	17	1.69	10
XLOC_003995	0.98	1	0	384	50.96	14	0	0	1.57	22	0	2
XLOC_003999	10.18	15	0	0	0	0	0	0	0	0	0.46	1
XLOC_004008	1.13	1	0	421	3607.38	7	6.38	0	4.27	5	0	0
XLOC_004017	1	2	0	50	11.49	2	0.51	0	6.22	16	0.11	1
XLOC_004018	17.27	28	0	24	29.52	6	3.68	0	0.65	1	2.41	10
XLOC_004047	2.67	7	1.89	388	124.42	16	6.16	1	3.16	7	3.77	21
XLOC_004053	3.5	8	0	1	0.38	0	0	0	0.48	1	0.27	2

XLOC_004062	2.59	5	0	7	9.65	6	3.21	0	1.32	2	2.87	6
XLOC_004074	15.37	18	0	7	63.42	3	2.12	0	3.52	5	8.75	19
XLOC_004076	0	0	0	14	7.83	2	0.96	0	0	0	0	0
XLOC_004077	3.37	3	0	56	706.93	2	1.71	0	7.8	8	0.81	1
XLOC_004080	2.8	7	16.43	256	75.66	60	23.93	9	29.2	67	4.95	25
XLOC_004081	30.85	29	44.65	8	122.07	69	63.16	10	44.42	42	6.95	13
XLOC_004109	6.52	12	0	0	0	0	0	0	0	0	0	0
XLOC_004121	10.88	15	0	1	3.41	0	0	0	0	0	4.52	11
XLOC_004137	0	0	0	11	3.36	17	5.94	0	0.44	1	0.12	1
XLOC_004138	0	0	0	31	934.64	0	0	0	0	0	0	0
XLOC_004146	0	0	0	1	6.64	0	0	0	10.79	13	0	0
XLOC_004157	21.49	18	0	4	75.35	29	29.43	0	49.22	42	0.39	1
XLOC_004194	6.7	10	10.04	1	5.03	8	6.97	3	3.18	4	12.6	35
XLOC_004199	4.36	10	0	811	251.71	29	11.48	0	3.12	7	0.54	3
XLOC_004204	1.79	3	0	38	37.02	3	1.51	0	2.5	4	7.74	26
XLOC_004206	5.58	7	6.18	215	614.26	15	10.77	2	7.35	10	2.55	9
XLOC_004222	1.1	3	0	155	20.72	8	2.15	0	0.86	3	0.54	7
XLOC_004242	2.36	8	1.29	210	31.61	6	1.62	1	1.55	5	2.15	12
XLOC_004245	18.64	29	5.42	0	0	0	0	2	0	0	0.95	2
XLOC_004257	7	10	0	95	284.92	8	4.87	0	2.22	3	0	0
XLOC_004258	3.43	2	0	51	1115.17	2	2.75	0	1.27	1	1.52	2
XLOC_004262	0	0	0	6	1.39	1	0.26	0	0	0	0.59	2
XLOC_004264	6.96	10	6.21	52	151.15	14	8.45	2	11.81	16	0.22	1
XLOC_004278	37.84	83	23.32	393	134.6	205	87.96	12	15.3	33	23.94	123
XLOC_004289	0	0	0	20	2.14	4	0.89	0	0.25	1	0	0
XLOC_004291	8.4	17	2.39	1	0.65	16	7.99	1	1.14	2	5.53	20
XLOC_004293	2.31	3	10.09	0	0	10	7.01	3	7.19	9	0	0
XLOC_004301	0	0	0	13	195.77	1	0.69	0	0	0	0	0
XLOC_004302	11.13	20	2.15	17	7.71	2	1.13	1	2.57	5	5.24	21
XLOC_004308	4.84	6	0	0	0	0	0	0	0	0	3.47	6
XLOC_004311	30.25	35	0	0	0	0	0	0	1.73	2	0	0
XLOC_004312	5.57	7	56.14	2	9.13	6	4.83	17	3.92	5	68.13	176
XLOC_004327	2.29	2	3.33	34	160.71	2	1.38	1	0.79	1	5.27	11
XLOC_004329	14.64	26	9.67	107	72.78	90	49.21	4	17.86	31	3.84	12
XLOC_004346	0	0	2.65	17	17.69	0	0	1	6.31	10	0	0
XLOC_004356	26	16	0	0	0	0	0	0	0	0	0	0
XLOC_004360	5.92	6	7.27	53	437.26	2	1.51	2	3.45	4	4.13	8
XLOC_004391	9.66	9	0	0	0	0	0	0	0	0	0	0
XLOC_004395	45.23	66	0	0	0	6	3.5	0	0.73	1	16.05	45
XLOC_004396	13.02	14	0	60	579.21	4	4.49	0	7.15	7	2.38	3
XLOC_004407	12.71	10	0	1	17.4	5	4.2	0	5.63	5	4.01	8
XLOC_004410	0	0	4.31	23	324.15	0	0	1	0	0	0	0
XLOC_004412	7.6	19	0	0	0	0	0	0	33.98	77	0	0
XLOC_004430	35.85	23	0	0	0	0	0	0	1.49	1	0	0
XLOC_004431	0	0	0	0	0	0	0	0	9.7	9	0	0
XLOC_004444	1.52	1	0	17	299.7	0	0	0	0	0	0	0
XLOC_004456	2.97	13	2.77	187	16.86	0	0	3	0	0	0.33	2
XLOC_004461	0	0	0	27	8.24	1	0.29	0	0	0	0	0
XLOC_004463	10.99	17	45.03	17	17.69	174	96.96	17	24.6	39	39.28	146
XLOC_004478	0	0	0	4	0.82	0	0	0	0.37	1	0	0
XLOC_004484	0	0	0	295	2962.37	20	15.06	0	13.55	15	0.66	1
XLOC_004485	2.36	2	0	28	462.22	0	0	0	3.29	3	0	0
XLOC_004498	0	0	29.41	0	0	6	7.25	5	2.77	2	20.12	28
XLOC_004505	2.91	9	10.33	263	39.47	74	20.72	8	7.41	24	4.26	35
XLOC_004512	4.64	8	0	0	0	1	0.74	0	0.68	1	0	0
XLOC_004525	3.63	7	15.28	6	5.11	14	7.21	6	4.25	7	11.35	40
XLOC_004535	0.52	1	0	14	3.51	3	1.33	0	0	0	0.11	1
XLOC_004634	40.26	0	50.47	0	0	0	45	0	57.45	0	60.7	0
XLOC_004644	44.91	1	10.9	0	56.99	0	12.74	0	7.88	0	6.84	0
XLOC_004665	1.03	1	0	11	48.59	0	0	0	0	0	0	0
XLOC_004685	9.65	14	32.26	17	14.01	10	5.14	11	8.43	14	9.54	34

XLOC_004693	34.45	29	0	0	0	0	0	0	0	0	0	0
XLOC_004694	2.69	3	3.32	14	66	6	3.81	1	2.37	3	1.43	3
XLOC_004697	0	0	0	15	2.2	0	0	0	0	0	0	0
XLOC_004733	5.55	9	4.39	2	0.97	4	1.83	2	2.62	5	0	0
XLOC_004737	60.86	50	0	0	0	0	0	0	1.16	1	1.28	2
XLOC_004747	19.75	14	10.64	179	3860.4	50	56.98	2	5.03	4	4.79	10
XLOC_004752	28.52	42	47.61	243	523.35	70	46	16	5.66	7	45.01	133
XLOC_004755	15.09	21	5.72	2	3.28	0	0	1	1.36	1	33.73	106
XLOC_004774	6.77	17	0	0	0	0	0	0	0	0	0	0
XLOC_004775	8.43	18	1.91	1	0.33	21	8.5	1	2.28	5	1.06	7
XLOC_004779	52.52	73	2.9	0	0	0	0	1	0.69	1	0.41	2
XLOC_004788	8.03	6	0	2	56.71	52	65.43	0	16.03	11	2.06	4
XLOC_004795	11.66	15	3.51	7	47.87	1	0.92	1	0.83	1	0.93	2
XLOC_004815	0	0	0	19	23.37	0	0	0	1.3	2	1.78	5
XLOC_004825	0.68	1	3.6	142	1113.58	6	5.23	1	4.27	5	0	0
XLOC_004836	8.47	12	18.54	0	0	8	4.2	6	6.61	9	24.67	77
XLOC_004844	13.66	11	0	0	0	1	0.81	0	0	0	0.41	1
XLOC_004847	8.15	8	0	1	12.08	2	1.26	0	1.92	2	0.6	2
XLOC_004849	2.06	11	0	27	1.97	29	5.32	0	0	0	0.19	2
XLOC_004851	10.36	7	0	2	33.45	1	1.2	0	29.83	27	17.57	25
XLOC_004878	0.89	2	0	27	14.17	7	3.86	0	0.57	1	0.39	1
XLOC_004879	1.17	1	30.14	0	0	0	0	5	0	0	1.5	3
XLOC_004894	0	0	0	17	3.8	0	0	0	0	0	0.29	1
XLOC_004895	0.28	2	0	2	0.14	0	0	0	4.3	24	0.19	2
XLOC_004900	71.98	67	0	0	0	1	1.13	0	0	0	0	0
XLOC_004905	4.33	3	0	1480	40856.7	222	284.76	0	279.45	195	33.91	45
XLOC_004935	1.01	3	0	51	9.98	19	6.23	0	6.45	18	0.2	2
XLOC_004952	21.26	38	2.16	0	0	0	0	1	0	0	0	0
XLOC_004964	66	44	0	0	0	0	0	0	1.22	1	0.95	1
XLOC_004972	11.5	24	8.31	4	1.64	18	7.63	4	0.5	1	4.96	19
XLOC_005021	24.47	35	2.92	0	0	0	0	1	0	0	0	0
XLOC_005028	52.16	46	148.51	27	476	7	6.21	31	20.41	17	64.9	96
XLOC_005044	22.68	19	0	0	0	0	0	0	2.5	2	0	0
XLOC_005056	0	0	0	86	1516.14	0	0	0	0	0	0	0
XLOC_005072	3.81	5	0	0	0	1	1.04	0	5.72	6	0.3	1
XLOC_005082	19.76	18	0	0	0	0	0	0	0	0	49.18	78
XLOC_005086	0	0	0	31	33.57	1	0.42	0	6.99	11	0.18	1
XLOC_005096	28.51	33	6.86	0	0	0	0	2	0	0	0	0
XLOC_005111	4.3	7	5.15	0	0	0	0	2	3.06	5	33.06	121
XLOC_005116	11.71	21	2.29	0	0	1	0.61	1	1.09	2	0.15	1
XLOC_005117	90.31	80	0	0	0	0	0	0	3.42	3	0.87	1
XLOC_005118	21.64	18	29.13	1	18.1	9	9.28	6	2.3	2	7.82	12
XLOC_005122	22.02	19	0	1	12.62	0	0	0	0	0	0	0
XLOC_005133	8.91	18	0	0	0	0	0	0	0.63	1	0.5	0
XLOC_005154	34.43	26	5.32	6	129.4	8	10.4	1	5.03	4	55.92	81
XLOC_005156	6.77	7	21.4	2	27.81	9	9.08	5	13.19	13	0.84	1
XLOC_005158	0.42	3	6.88	26	1.81	1	0.12	9	0	0	1.57	15
XLOC_005163	0	0	0	0	0	0	0	0	9.98	8	0	0
XLOC_005166	11.94	9	0	0	0	0	0	0	0	0	0	0
XLOC_005186	3.25	5	2.11	7	3.01	12	5.11	1	1.01	2	0.62	3
XLOC_005196	1.52	2	0	43	35.01	123	74.96	0	14.06	20	9.08	28
XLOC_005207	0	0	0	24	285.63	0	0	0	0.95	1	0	0
XLOC_005269	1.91	2	0	17	324.55	0	0	0	1.18	1	0	0
XLOC_005271	1.07	6	0	33	2.17	1	0	0	0	1	0.36	6
XLOC_005274	33.1	18	0	0	0	0	0	0	0	0	0	0
XLOC_005291	1.61	1	0	0	0	0	0	0	13.16	11	0	0
XLOC_005295	2.84	2	0	0	0	0	0	0	0	0	3.75	11
XLOC_005296	7.9	39	0	16	1.36	0	0	0	0.21	1	0.06	1
XLOC_005318	0.71	2	0	19	3.48	0	0	0	0	0	0	0
XLOC_005335	57.92	52	4.52	0	0	0	0	1	22.48	21	0	0
XLOC_005339	1.04	2	0	0	0	3	1.43	0	0	0	7.06	24



XLOC_005341	6.7	7	14.97	0	0	11	12.08	3	11.8	10	44.79	68
XLOC_005351	16.17	15	25.99	4	57.13	6	5.39	6	9.24	9	6.76	11
XLOC_005383	12.65	17	9.95	0	0	6	4.16	3	3.94	5	6.34	16
XLOC_005392	48.51	36	0	0	0	0	0	0	0	0	0.81	2
XLOC_005393	0	0	0	0	0	0	0	0	28.4	19	0.53	1
XLOC_005407	12.28	10	0	175	3126.19	0	0	0	53.56	32	0.99	1
XLOC_005413	52.91	43	5.02	0	0	0	0	1	0	0	0	0
XLOC_005424	4.85	9	0	41	12.29	3	1.46	0	0.44	1	0.33	1
XLOC_005426	0	0	0	16	9.05	1	0.6	0	4.94	9	0	0
XLOC_005439	0	0	0	7	1.16	0	0	0	0	0	0	0
XLOC_005454	0	0	0	11	57.13	0	0	0	0	0	0	0
XLOC_005455	0	0	0	39	15.27	1	0	0	0	1	0	0
XLOC_005481	34.53	43	6	0	0	0	0	2	2.86	4	0.21	1
XLOC_005511	29.28	24	0	65	869.07	4	3.89	0	6.94	7	1.76	4
XLOC_005538	11.75	7	0	2	51.86	2	2.41	0	11.1	8	0	0
XLOC_005555	40.86	24	6.13	18	530.65	1	1.58	1	4.33	3	1.02	2
XLOC_005583	55.09	38	0	0	0	0	0	0	4.3	3	0	0
XLOC_005595	2.17	2	0	41	975.09	2	2.86	0	17.21	13	24.6	37
XLOC_005597	0	0	0	0	0	0	0	0	36.18	34	0	0
XLOC_005611	0	0	0	126	8.88	1	0.21	0	0.19	1	0	0
XLOC_005612	8.93	10	7.13	1	7.44	13	10.9	2	5.08	6	16.79	42
XLOC_005618	7.08	18	0	0	0	0	0	0	0	0	0	0
XLOC_005629	3.89	10	3.95	0	0	3	0.93	2	0.47	1	5.22	22
XLOC_005638	17.54	13	0	2	50.37	5	5.65	0	13.65	10	11.99	15
XLOC_005646	4.97	8	0	29	18.25	18	8.94	0	11.86	21	0.44	1
XLOC_005648	0	0	7.02	3	20.52	1	0.55	2	59.21	72	0	0
XLOC_005651	60.28	91	10.83	0	0	0	0	4	3.22	5	18.59	56
XLOC_005652	23.51	16	3.71	21	199.31	1	1.54	1	0.88	1	6.54	9
XLOC_005654	166.12	136	5606.52	6	116.09	153	163.13	1116	218.58	184	107.81	147
XLOC_005657	0	0	0	13	109.9	3	2.86	0	0	0	0	0
XLOC_005667	27.69	28	0	0	0	10	8.3	0	6.63	7	4.3	8
XLOC_005702	25.6	30	0	0	0	0	0	0	0	0	0	0
XLOC_005716	0	0	0	0	57.58	0	0	0	13.23	9	1.32	1
XLOC_005726	4.66	16	6.58	56	8.69	24	7.09	5	0	0	1.45	9
XLOC_005740	22.96	13	0	0	0	0	0	0	0	0	0	0
XLOC_005753	8.82	15	5.78	0	0	6	3.62	2	2.06	3	7.95	21
XLOC_005758	6.1	11	7.58	10	8.24	14	7.4	3	10.84	18	0.64	3
XLOC_005763	20.02	32	0	0	0	0	0	0	0	0	0.49	1
XLOC_005780	57.58	38	30.66	2	55.86	30	39.04	5	54.91	38	64.39	74
XLOC_005790	3.79	4	0	38	528.41	2	2.21	0	4.06	4	25.33	41
XLOC_005795	3.45	6	4.66	14	8.29	3	1.6	2	3.34	6	1.71	6
XLOC_005832	12.7	17	0	1	0.84	0	0	0	0	0	0	0
XLOC_005857	1.8	5	1.4	79	13.7	3	1.11	1	0.67	2	0	0
XLOC_005858	15.97	19	0	33	404.64	3	3.12	0	13.34	14	13.58	31
XLOC_005865	20.56	17	0	3	75.56	0	0	0	0	0	0	0
XLOC_005876	17.12	18	0	0	0	0	0	0	2.92	3	30.84	60
XLOC_005884	94.06	65	6.08	0	0	0	0	1	10.03	7	1.51	3
XLOC_005901	1	1	98.89	2	41.4	4	5.37	19	1.23	1	13.34	23
XLOC_005920	22.46	16	0	0	0	0	0	0	0	0	0	0
XLOC_005940	144.93	134	1231.9	12	176	281	275.42	278	141.25	136	2422.9	3960
XLOC_005944	78	107	5.9	0	0	2	1.54	2	3.51	5	1.11	4
XLOC_005977	9.33	10	8.66	3	42.85	32	26.53	2	26.68	26	4.67	13
XLOC_005979	24.61	26	0	2	13.68	0	0	0	0.83	1	0.93	2
XLOC_005981	31.33	28	8.99	0	0	0	0	2	0	0	0.8	1
XLOC_005992	12.74	14	4.04	61	737.01	22	20.11	1	15.33	16	9.05	15
XLOC_005998	3.73	7	0	10	3.5	0	0	0	0	0	0.13	1
XLOC_006036	48.63	34	0	0	0	1	1.43	0	0	0	0	0
XLOC_006068	10.52	14	16.82	0	0	19	14.54	5	5.6	7	3.86	10
XLOC_006077	0	0	0	0	0	0	0	0	0	0	14.15	21
XLOC_006126	8.85	0	0	0	0	0	20.71	0	63.26	1	93.3	0
XLOC_006130	4.07	2	81.78	2	58.47	2	2.57	13	1.48	1	31.25	36

XLOC_006134	0.36	1	0	118	40.97	0	0	0	0.47	1	0	0
XLOC_006137	24.74	26	0	0	0	2	1.52	0	1.73	2	1.41	2
XLOC_006194	23.77	29	0	0	0	0	0	0	0	0	0.6	1
XLOC_006196	21.24	21	0	0	0	0	0	0	0	0	0.34	1
XLOC_006218	27.11	34	0	0	0	1	0.78	0	0	0	0.5	1
XLOC_006232	54.96	49	0	0	0	0	0	0	0	0	1.37	3
XLOC_006248	85.81	60	5.44	0	0	0	0	1	0	0	1.12	1
XLOC_006260	47.76	49	0	945	10589.3	2789	2307.04	0	36.37	39	8.41	16
XLOC_006264	1.19	1	0	12	335.15	0	0	0	4.33	3	0	0
XLOC_006273	4.4	13	1.6	1	0.22	9	3.11	1	1.91	5	0.46	3
XLOC_006280	2.38	4	0	15	18.86	10	5.72	0	5.87	9	0	0
XLOC_006302	33.52	23	0	0	0	0	0	0	0	0	0	0
XLOC_006304	0.45	1	0	0	0	0	0	0	42.34	72	0	0
XLOC_006321	4.85	11	0	46	12.45	7	2.69	0	0.42	1	0	0
XLOC_006339	35.2	38	3.69	0	0	0	0	1	0	0	0	0
XLOC_006340	15.08	30	2.08	2	0.82	0	0	1	0	0	0	0
XLOC_006358	76.55	151	2.08	1	0.41	0	0	1	0	0	0.47	2
XLOC_006367	3.43	5	0	0	0	1	0.46	0	1.38	2	15.06	46
XLOC_006387	0	0	33.24	0	0	0	0.48	0	0.55	0	14.9	0
XLOC_006400	3.33	8	3.62	44	12.73	19	7.52	2	40.22	93	3.52	19
XLOC_006411	54.68	59	0	0	0	1	0.56	0	1.69	2	0.26	1
XLOC_006429	11.18	28	1.75	112	30.15	4	1.49	1	2.93	7	0.28	1
XLOC_006456	0	0	0	18	10.42	0	0	0	0	0	0	0
XLOC_006488	1.16	1	0	1	26.71	28	33.83	0	2.82	2	25.67	32
XLOC_006498	0	0	0	52	561.7	0	0	0	0	0	0	0
XLOC_006524	16.49	22	13.52	2	10.72	2	1.06	4	0.8	1	8.41	21
XLOC_006531	27.01	30	0	0	0	0	0	0	0.88	1	0	0
XLOC_006582	16.42	31	12.61	3228	1365.85	127	58.34	6	19.05	38	3.29	14
XLOC_006593	21.34	32	0	0	0	0	0	0	0	0	0	0
XLOC_006600	0	0	0	26	318.83	0	0	0	0	0	0.71	1
XLOC_006613	60.19	41	102.49	1637	45542.7	121	155.95	17	1.51	1	20.44	28
XLOC_006622	43.75	45	20.66	5	30.37	12	7.18	6	11.45	14	347.01	807
XLOC_006646	0.77	2	0	42	17.05	2	1.09	0	1.48	3	0	0
XLOC_006687	28.81	18	26.79	1	21.87	1	0.84	5	1.27	1	1.85	3
XLOC_006724	5.91	7	0	0	0	0	0	0	0.83	1	36.94	89
XLOC_006790	2.42	8	0	0	0	0	0	0	0	0	0	0
XLOC_006794	1.15	1	0	0	0	0	0	0	86.29	99	1.77	5
XLOC_006810	34.19	21	6.08	0	0	0	0	1	0	0	0	0
XLOC_006816	1.72	4	0	24	4.19	0	0	0	0	0	0	0
XLOC_006820	0	0	0	29	3.02	2	0.53	0	0	0	0.31	3
XLOC_006823	8.47	5	0	4	74.36	38	39.66	0	0	0	0	0
XLOC_006846	6.82	5	0	8	226.84	5	4.81	0	5.83	4	4.67	6
XLOC_006855	23.08	48	12.5	5	2.06	5	2.29	6	0.5	1	61.46	260
XLOC_006863	2.2	5	0	49	15.61	3	1.3	0	0.9	2	0.72	4
XLOC_006876	0	0	0	20	10.83	5	2.51	0	0	0	0.73	2
XLOC_006879	19.49	39	0	0	0	0	0	0	0	0	0.41	1
XLOC_006884	14.72	32	89.01	56	26.11	26	13.04	41	6.73	13	31.4	112
XLOC_006934	0	0	0	10	3	0	0	0	0.88	2	0	0
XLOC_006961	3.09	8	0	45	8.67	0	0	0	2.13	6	0	0
XLOC_006969	11.95	11	0	0	0	0	0	0	0	0	0	0
XLOC_006978	29.22	185	2.78	17	1.05	5	0.69	4	0.67	4	0.36	5
XLOC_006994	11.18	6	13.59	0	4.22	12	31.7	0	16.52	0	21.64	41
XLOC_007004	15.91	16	0	0	0	0	0	0	0	0	0	0
XLOC_007006	0.61	1	0	15	5.47	3	1.16	0	0.48	1	4.47	16
XLOC_007019	6.91	5	11.3	0	0	1	1.46	2	1.33	1	103.91	133
XLOC_007027	31.74	47	39.67	54	138.8	65	42.21	13	26.85	37	35.22	104
XLOC_007031	28.31	40	0	0	0	0	0	0	2.56	4	0	0
XLOC_007059	42.97	35	4.99	0	0	0	0	1	1.18	1	1.01	1
XLOC_007069	41.52	44	0	16	27.65	1	0.45	0	3.43	5	0.74	2
XLOC_007084	0.81	1	0	276	265.96	0	0	0	0	0	0	0
XLOC_007089	1.12	8	0	36	1.89	1	0.1	0	0	0	0.18	3



XLOC_007952	33.04	57	0	0	0	0	0	0	0.57	1	0.38	1
XLOC_007953	31.35	27	0	0	0	0	0	0	0	0	0	0
XLOC_007956	9.59	19	3.68	17	5.09	2	0.98	2	0.44	1	2.07	9
XLOC_007983	17.83	18	0	1	6.45	0	0	0	0	0	0	0
XLOC_008017	4.46	3	5.36	0	0	4	3.89	1	1.27	1	33.51	48
XLOC_008023	136.98	86	5.93	0	0	0	0	1	1.4	1	0.98	2
XLOC_008056	104.1	71	0	0	0	0	0	0	0	0	0	0
XLOC_008072	28.07	22	0	29	454.28	0	0	0	0	0	0	0
XLOC_008101	0	0	0	0	0	4	21.37	0	0.82	0	4.61	2
XLOC_008113	33.38	39	0	0	0	0	0	0	0.77	1	0	0
XLOC_008138	37.57	31	0	0	0	0	0	0	0	0	0	0
XLOC_008167	33.68	56	10.56	29	29.58	8	4.15	4	1.89	3	8.26	29
XLOC_008186	13.98	12	10.88	0	0	6	5.09	2	2.57	2	4.99	7
XLOC_008206	48.15	32	0	0	0	0	0	0	1.38	1	1.43	3
XLOC_008265	3.16	3	0	0	0	1	0.71	0	11.78	11	2.18	5
XLOC_008282	65.75	45	5.48	0	0	4	5.06	1	0	0	0	0
XLOC_008303	3.46	5	0	382	405.38	5	2.93	0	1.27	2	0.68	2
XLOC_008320	0	0	0	55	9.88	3	1.13	0	0	0	0	0
XLOC_008336	0	0	19.13	0	0	2	1.59	5	0	0	13.64	32
XLOC_008345	6.27	9	3.05	0	0	0	0	1	0	0	4.81	16
XLOC_008356	25.85	15	0	0	0	0	0	0	1.41	1	0	0
XLOC_008371	49.9	58	0	0	0	0	0	0	0	0	0.79	2
XLOC_008379	16.05	14	9.04	2	31.33	2	1.41	2	0	0	11.59	20
XLOC_008380	10.89	29	10.35	0	0	1	0.46	6	1.65	4	9.43	44
XLOC_008450	0	0	0	0	0	0	0	0	9.77	12	0.25	1
XLOC_008479	0	0	0	0	0	0	0	0	37.75	36	0	0
XLOC_008498	3.92	5	3.67	3	25.97	0	0	1	10.46	12	0.97	2
XLOC_008508	53.77	42	0	0	0	0	0	0	4.85	4	1.21	3
XLOC_008533	40.36	32	5.09	0	0	0	0	1	0	0	0	0
XLOC_008567	8.05	10	3.77	0	0	0	0	1	0	0	0.92	2
XLOC_008575	51.82	79	0	0	0	0	0	0	2.66	4	0.19	1
XLOC_008627	0	0	0	21	86.9	0	0	0	0	0	0	0
XLOC_008635	4.2	7	0	0	0	0	0	0	0	0	2.63	11
XLOC_008695	17.32	14	5.2	0	0	0	0	1	7.38	6	1.37	2
XLOC_008706	65.67	69	3.83	1	10.23	1	0.6	1	2.72	3	0	0
XLOC_008721	0.19	1	0	10	1.09	0	0	0	0	0	0.07	1
XLOC_008729	34.02	31	0	0	0	0	0	0	0	0	0.34	1
XLOC_008752	8.1	11	17.47	2	13.29	7	6.54	5	8.3	10	13.66	28
XLOC_008757	1.8	4	0	27	8	22	7.29	0	6.12	14	0.33	1
XLOC_008763	2.44	9	1.21	1	0.14	2	0.38	1	0	0	4.02	35
XLOC_008808	22.78	23	3.97	0	0	0	0	1	0	0	0	0
XLOC_008847	12.98	36	12.49	5	1.06	19	6.81	8	2.24	6	8.4	44
XLOC_008862	111.82	120	4	0	0	0	0	1	5.69	6	1.18	4
XLOC_008901	16.3	29	0	0	0	0	0	0	0.54	1	0.98	3
XLOC_008922	5.55	12	0	157	55.28	23	8.95	0	0.94	2	3.37	14
XLOC_008926	9.25	14	19.95	925	715.89	117	59.91	8	11.29	19	76.9	274
XLOC_008979	10.35	10	0	0	0	0	0	0	1.02	1	10.67	23
XLOC_008981	21.57	31	16.14	8	31.02	2	1.52	5	9.21	12	17.59	52
XLOC_008983	60.04	36	6.18	0	0	1	0.96	1	1.46	1	0	0
XLOC_008991	33.86	19	0	1	27.11	1	1.53	0	0	0	2.82	3
XLOC_009006	2.13	14	0	379	23.69	2	0.29	0	0.34	2	0	0
XLOC_009008	4.05	3	4.89	24	440.24	4	4.54	1	5.78	5	5.29	7
XLOC_009011	152.61	146	54.35	1	13.17	3	2.82	13	5.95	5	80.72	156
XLOC_009019	0.87	3	11.74	14	2.14	13	3.49	9	2.5	8	12.76	82
XLOC_009041	19.67	17	4.16	0	0	0	0	1	1.97	2	0.73	1
XLOC_009066	6.9	22	1.32	218	33.83	8	2.27	1	2.2	6	0	0
XLOC_009173	2.26	4	0	278	153.81	1	0.61	0	4.36	8	0	0
XLOC_009215	18.07	16	0	7	128.4	0	0	0	0	0	0	0
XLOC_009238	10.83	15	0	0	0	4	2.63	0	0	0	3.9	10
XLOC_009249	170.87	0	309.98	1	304.48	1	222.18	0	85.3	0	119.2	16
XLOC_009253	2.93	2	39.88	0	0	0	0	7	21.51	16	6.37	6

XLOC_009260	4.61	4	0	0	26.31	1	1.51	0	13.98	9	1.62	2
XLOC_009262	53.67	45	4.44	0	0	0	0	1	2.1	2	1.21	2
XLOC_009281	0.57	2	0	12	1.55	0	0	0	0.28	1	0	0
XLOC_009296	11.17	1	2.41	0	0	4	4.8	0	12.97	1	2.5	2
XLOC_009321	1.27	0	0	0	0	3	5.22	0	51.8	21	0.24	0
XLOC_009343	0	0	0	14	35.98	0	0	0	0	0	0	0
XLOC_009348	230.43	224	0	0	0	0	0	0	4.08	4	0	0
XLOC_009359	2.12	2	0	0	0	3	3.12	0	12.94	10	1.13	1
XLOC_009378	0.98	3	0	81	15.03	0	0	0	4.53	13	1.99	14
XLOC_009382	1.11	1	3.56	0	0	0	0	1	1.69	2	12.47	27
XLOC_009402	1.59	0	0	0	42.33	0	6.84	0	1.5	0	1.51	0
XLOC_009417	83.96	80	12.47	0	0	0	0	3	0.99	1	0	0
XLOC_009467	0	0	0	0	0	0	0	0	22.69	28	0	0
XLOC_009505	81.02	55	0	0	0	0	0	0	0	0	0	0
XLOC_009553	19.85	15	0	2	57.58	6	8.94	0	27.92	19	2.36	3
XLOC_009558	59.43	58	4.06	0	0	0	0	1	0	0	2.3	3
XLOC_009616	29.93	19	0	0	0	0	0	0	0	0	0	0
XLOC_009617	9.19	13	2.52	0	0	0	0	1	1.2	2	0	0
XLOC_009651	90.25	84	0	0	0	0	0	0	0	0	0.31	1
XLOC_009656	16	14	10.41	0	0	5	6.69	2	2.46	2	1.88	3
XLOC_009669	38.06	25	6.18	0	0	1	1.57	1	0	0	1.82	2
XLOC_009705	2.92	8	0	22	5.56	0	0	0	0	0	0.87	5
XLOC_009756	10.46	17	8.03	0	0	2	0.84	3	1.91	3	0.68	2
XLOC_009787	28.88	43	5.48	0	0	0	0	2	1.96	3	1.28	3
XLOC_009800	3.19	4	3.63	0	0	0	0	1	14.67	17	0.53	2
XLOC_009807	29.34	0	0.99	0	20.91	0	32.1	0	36.55	0	7.02	1
XLOC_009819	75.34	45	5.93	0	0	0	0	1	6.99	5	2.76	3
XLOC_009866	33.44	70	0	10	3.62	2	0.84	0	3.32	7	1.12	5
XLOC_009880	62.43	31	6.29	0	0	2	1.96	1	1.48	1	19.58	19
XLOC_009926	11.67	14	0	6	45.83	8	7.08	0	8.5	10	0.69	1
XLOC_009944	22.61	24	25.53	7	96.03	10	10.56	6	8.07	8	6.45	14
XLOC_009961	19.18	16	0	0	0	0	0	0	0	0	0	0
XLOC_009979	22.37	27	0	0	0	0	0	0	0	0	0	0
XLOC_010042	30.56	38	0	0	0	0	0	0	0	0	0	0
XLOC_010043	31.71	39	0	0	0	1	0.87	0	1.58	2	0	0
XLOC_010057	0	0	0	12	2.19	0	0	0	0	0	0.09	1
XLOC_010080	2.37	5	2.26	26	13.78	3	1.55	1	0	0	4.28	17
XLOC_010088	0.74	1	0	4	43.2	6	4.45	0	11.07	12	0	0
XLOC_010106	28.68	26	0	0	0	0	0	0	1	1	0	0
XLOC_010131	27.34	19	0	0	0	0	0	0	0	0	0.43	1
XLOC_010136	0	0	0	0	0	0	0	0	30.49	29	0	0
XLOC_010180	15.47	17	0	0	0	0	0	0	0	0	0	0
XLOC_010207	20.81	21	0	1	15.46	0	0	0	0	0	0	0
XLOC_010214	0	0	0	12	13.83	0	0	0	0	0	0	0
XLOC_010224	0	0	0	13	6.01	0	0	0	0	0	0	0
XLOC_010248	7.93	23	0	10	1.98	0	1.5	0	2.16	1	0.23	1
XLOC_010249	20.96	20	4.36	12	173.69	8	7.67	1	21.68	21	2.29	4
XLOC_010254	24.3	16	0	0	0	0	0	0	0	0	0	0
XLOC_010273	0	0	0	28	427.25	0	0	0	1.06	1	0	0
XLOC_010308	11.61	19	0	0	0	0	0	0	0.63	1	0.18	1
XLOC_010318	35.33	49	0	0	0	0	0	0	2.78	4	0.2	1
XLOC_010373	8.14	11	0	512	231.44	2	0.9	0	1.53	3	0.34	1
XLOC_010377	21.16	22	7.82	25	274.64	22	18.28	2	37.1	40	0.96	2
XLOC_010387	0	0	0	1	18.1	1	1.25	0	47.09	41	0.38	1
XLOC_010398	15.66	16	0	0	0	0	0	0	0.98	1	0	0
XLOC_010406	72.08	69	0	0	0	0	0	0	1.03	1	0	0
XLOC_010482	17.35	31	0	41	17.8	0	0	0	0	0	0	0
XLOC_010517	21.65	16	0	0	0	0	0	0	0	0	18.54	24
XLOC_010519	37.87	3	47.56	0	0	2	14.79	0	16.63	0	79.06	3
XLOC_010561	44.88	28	0	0	0	0	0	0	1.48	1	0	0
XLOC_010649	8.73	14	0	72	72.27	16	9.59	0	18.03	28	1.03	3









XLOC_014010	19.03	16	0	0	0	0	0	0	0	0	0	0
XLOC_014037	17.69	12	0	0	0	0	0	0	0	0	0	0
XLOC_014048	51.8	40	5.13	3	60.44	0	0	1	0	0	2.08	2
XLOC_014051	19.78	50	39.4	112	38	37	14.72	22	4.27	17	14.7	74
XLOC_014103	27.61	29	0	0	0	0	0	0	3.81	4	0	0
XLOC_014119	0.8	3	0	25	4.62	1	0.38	0	1.04	3	0	0
XLOC_014129	90.88	88	0	0	0	0	0	0	0	0	1.26	4
XLOC_014140	7.25	12	12.73	4	3.41	8	3.46	5	4.85	8	24.38	78
XLOC_014170	2	1	6.18	0	0	0	0	1	0	0	23.78	25
XLOC_014206	8.23	7	0	6	105.78	2	1.98	0	12.47	11	0.37	1
XLOC_014207	6.79	17	4.69	169	35.88	36	12.65	3	9.72	26	0.31	3
XLOC_014220	57.97	4	33.94	0	0	0	2.33	0	0	2	42.45	2
XLOC_014233	25.45	87	10.04	150	21.48	123	34.96	8	6.3	21	1.79	13
XLOC_014242	21.15	19	3.87	0	0	0	0	1	0	0	0	0
XLOC_014243	5.26	12	2.25	0	0	1	0.6	1	0	0	0.15	1
XLOC_014244	42.89	29	11.96	0	0	0	0	2	2.82	2	0	0
XLOC_014245	39.12	29	5.4	0	0	0	0	1	5.1	4	0	0
XLOC_014294	12.54	17	0	9	61.55	10	8.75	0	3.34	4	1.1	3
XLOC_014341	180.57	155	4.99	0	0	0	0	1	3.54	3	4.81	7
XLOC_014363	0.81	1	0	0	0	0	0	0	14.2	14	1.81	4
XLOC_014366	21.15	26	3.2	0	0	0	0	1	0	0	0	0
XLOC_014379	32.54	22	5.74	13	322.73	15	15.7	1	6.77	5	7.05	8
XLOC_014405	2.59	10	9.45	9	1.17	4	1.13	8	0	0	29.97	232
XLOC_014406	8.62	19	8.87	1	0.5	9	4.31	4	1.59	3	8.33	35
XLOC_014438	1.7	3	0	0	0	0	0	0	0	0	4.49	15
XLOC_014463	12.92	7	31.1	0	0	0	0	2	0	0	132.84	198
XLOC_014464	0	0	0	11	68.88	0	0	0	0	0	0	0
XLOC_014484	7.08	6	0	1	11.9	7	6.47	0	3.81	4	19.51	39
XLOC_014538	16.73	16	14.09	2	33.89	8	8.26	3	11.12	10	8.96	16
XLOC_014560	296.24	698	966.18	3020	964.28	1172	461.63	525	277.82	622	728.92	3344
XLOC_014567	16.42	30	9.84	33	24.07	0	0	4	2.34	4	8.23	26
XLOC_014570	16.53	16	0	0	0	0	0	0	0	0	0.95	2
XLOC_014571	139.43	115	0	0	0	0	0	0	1.21	1	0	0
XLOC_014573	0	0	0	89	40.74	0	0	0	0.51	1	0	0
XLOC_014599	16.05	67	3.16	61	6.63	9	2.17	3	3.27	13	2.57	24
XLOC_014600	2.46	5	1.91	14	4.58	0	0	1	0	0	0.13	1
XLOC_014625	47.17	40	0	0	0	0	0	0	0	0	0.36	1
XLOC_014626	34.68	29	0	0	0	0	0	0	1.07	1	0	0
XLOC_014640	25.84	19	0	0	0	0	0	0	1.44	1	0	0
XLOC_014678	0.96	1	0	2	38.7	3	3.88	0	65.34	55	0	0
XLOC_014685	38.21	41	0	0	0	0	0	0	0	0	0.63	1
XLOC_014686	22.54	22	0	0	0	0	0	0	0	0	0.79	1
XLOC_014718	1.29	1	4.09	0	0	4	3.4	1	11.63	12	0	0
XLOC_014736	104.05	64	0	0	0	0	0	0	0	0	0	0
XLOC_014827	47.94	33	5.61	2	47.57	0	0	1	0	0	0	0
XLOC_014839	76.77	46	0	0	0	0	0	0	0	0	1.32	1
XLOC_014868	28.74	36	3.58	6	45.83	14	10.07	1	1.7	2	4.32	9
XLOC_014874	2.6	3	7.53	9	86.88	4	4.12	2	2.68	2	9.64	12
XLOC_014878	0.91	3	1.65	68	16.14	2	0.69	1	2.77	7	0	0
XLOC_014880	16.27	23	2.94	2	3.96	4	2.16	1	2.1	3	0.41	2
XLOC_014931	0	0	11.44	46	25.45	9	4.91	5	1.09	2	9.68	37
XLOC_014932	0	0	0	0	0	0	0	0	14.45	13	0	0
XLOC_014943	20.95	23	0	0	0	2	1.56	0	0	0	0.27	1
XLOC_014967	1.44	2	0	29	52.85	7	4.09	0	6.91	10	3.48	10
XLOC_014992	20.34	1	53.99	0	0	2	12.5	0	8.91	3	3.6	0
XLOC_014994	3.87	9	2.03	10	3.84	3	1.17	1	0	0	2.3	9
XLOC_015033	82.7	77	4.09	0	0	0	0	1	1.94	2	1.02	2
XLOC_015036	39.24	30	0	0	0	0	0	0	1.35	1	1.09	1
XLOC_015117	0	0	0	0	0	0	7.44	0	28.39	0	0	0
XLOC_015125	0.87	2	0	121	21.22	2	0.72	0	4.68	13	0	1
XLOC_015164	35.83	119	26.77	83	13.25	27	7.68	20	7.36	23	26.33	191

XLOC_015187	6.29	4	36.48	0	0	1	1.56	6	1.43	1	41.14	44
XLOC_015211	8.25	0	20.42	0	11.86	0	1.52	2	3.12	0	4.06	0
XLOC_015245	1.07	0	3.43	0	0	0	0.54	3	15.47	19	1.39	1
XLOC_015251	6.43	7	3.79	0	0	1	0.59	1	0.9	1	12.42	22
XLOC_015261	44.46	26	0	0	0	0	0	0	0	0	3.72	3
XLOC_015262	15.97	24	6.1	77	197.92	12	7.33	2	11.61	16	0.51	1
XLOC_015280	1.55	3	0	5	2.74	2	1.2	0	0.54	1	0.42	1
XLOC_015281	76.65	93	6.52	0	0	0	0	2	1.55	2	0	0
XLOC_015286	11.51	18	2.73	8	9.84	9	5.02	1	21.44	33	4.94	18
XLOC_015295	6.02	12	9.61	1	0.33	2	0.6	5	0	0	6.7	30
XLOC_015303	31.91	21	5.36	0	0	0	0	1	0	0	1.99	2
XLOC_015318	1.39	3	0	0	0	0	0	0	2.93	6	2.95	17
XLOC_015333	1.6	2	0	31	116.34	15	10.53	0	8.4	11	0	0
XLOC_015345	29.59	23	14.97	0	0	4	4.13	3	1.18	1	0.91	1
XLOC_015359	3.83	6	11.21	1	2.63	5	3.12	4	2.37	3	6.89	20
XLOC_015406	21.33	16	4.67	0	0	0	0	1	1.1	1	0	0
XLOC_015420	46.5	28	0	0	0	2	1.96	0	0	0	1.33	1
XLOC_015476	40.85	27	0	0	0	0	0	0	1.47	1	1.21	1
XLOC_015497	31.65	22	0	1	30.15	1	1.65	0	0	0	0	0
XLOC_015498	15.8	22	51.89	7	28.04	60	42.29	16	10.02	13	25.02	61
XLOC_015499	0.43	1	1.43	13	2.32	0	0	1	2.04	6	3.69	21
XLOC_015524	7.46	9	3.83	0	0	7	5.77	1	2.72	3	18.87	40
XLOC_015566	19.97	26	0	0	0	0	0	0	0.86	1	0.26	1
XLOC_015568	4.7	4	26.21	0	0	2	2.68	5	2.48	2	7.56	14
XLOC_015625	0	0	4.47	3	45.78	1	1.15	1	0	0	8.18	18
XLOC_015635	9.19	18	10.26	19	11.82	7	3.78	4	1.51	3	4.61	16
XLOC_015647	0.62	2	0	21	3.06	1	0.2	0	0	0	0.08	1
XLOC_015649	2.5	2	38.41	1	30.15	1	1.65	6	0	0	63.67	70
XLOC_015664	3.23	14	0	38	4.46	7	1.47	0	0.79	3	2.83	21
XLOC_015668	0	0	2.16	71	32.8	7	3.76	1	10.32	20	1.18	5
XLOC_015670	104.83	66	12.8	0	0	0	0	2	1.51	1	1.8	2
XLOC_015673	220.27	159	5.52	0	0	0	0	1	1.3	1	2.02	3
XLOC_015726	1.81	3	0	0	0	0	0	0	4.58	6	6.4	22
XLOC_015745	5.27	7	6.26	0	0	11	7	2	0.74	1	20.93	58
XLOC_015754	16.62	12	0	1	40.14	14	30.91	0	36.2	22	2.82	3
XLOC_015808	2.52	3	3.65	0	0	0	0	1	0.87	1	21.47	46
XLOC_015810	26.74	21	0	0	0	1	1.22	0	0	0	1.31	2
XLOC_015860	38.83	28	5.32	0	0	0	0	1	0	0	1.09	1
XLOC_015886	0	0	0	0	0	0	0	0	0.63	1	3.06	11
XLOC_015887	40.45	29	0	0	0	0	0	0	0	0	0	0
XLOC_015900	5.72	18	3.22	10	2.25	6	2.2	2	0.38	1	1.53	10
XLOC_015919	50.87	0	18.88	0	62.44	0	20.56	0	9.07	0	36.19	0
XLOC_015940	73.53	50	0	0	0	0	0	0	1.32	1	0	0
XLOC_015960	15.37	17	31.97	2	23.44	2	1.66	8	0	0	14.52	29
XLOC_015964	80.78	71	14.47	0	0	0	0	3	11.41	10	1.34	2
XLOC_015972	3.8	4	0	0	0	0	0	0	0	0	19.77	32
XLOC_015980	19.47	13	5.17	0	0	0	0	1	0	0	0.95	1
XLOC_015983	21.52	21	0	0	0	0	0	0	1.1	1	0	0
XLOC_015985	4.35	8	18.78	7	4.25	9	4.3	8	7.27	13	28	99
XLOC_016007	3.31	9	4.64	92	19.13	18	6.36	3	10.72	29	2.93	15
XLOC_016039	0	0	0	0	0	3	4.38	0	11.96	7	0	0
XLOC_016072	42.95	32	9.52	0	0	0	0	2	1.13	1	0.73	2
XLOC_016074	30.55	26	0	0	0	1	0.7	0	0	0	0.79	1
XLOC_016144	17.1	13	0	0	0	2	2.51	0	0	0	0	0
XLOC_016145	0.89	1	0	1	16.73	1	0.73	0	0	0	13.43	22
XLOC_016189	16.62	13	0	2	57.58	0	0	0	0	0	1.04	2
XLOC_016255	8.76	10	7.74	0	0	1	0.61	2	0	0	23.55	48
XLOC_016258	0	3	4.77	0	0	0	0	2	0	0	12.66	32
XLOC_016273	3.77	0	0	0	0	0	0	0	0.1	0	0	0
XLOC_016347	59.77	52	9.58	0	0	2	1.5	2	0	0	0.87	1
XLOC_016350	35.43	48	6.18	0	0	0	0	2	0	0	1.54	4

XLOC_016352	11.95	11	0	0	0	1	1.36	0	0	0	0.42	1
XLOC_016374	23.65	31	16.74	6	30.22	12	9.75	5	1.59	2	0	0
XLOC_016437	15.76	17	0	1	7.24	0	0	0	1.68	2	0.26	1
XLOC_016439	15.29	26	14.56	1	0.69	1	0.38	6	0	0	17.05	53
XLOC_016473	19.96	12	6.4	0	0	4	3.98	1	0	0	16.33	26
XLOC_016491	3.75	3	0	0	0	0	0	0	0	0	39.78	55
XLOC_016515	4.7	9	0	50	28.61	3	1.82	0	7.16	13	0.31	2
XLOC_016516	16.66	30	2.25	3	1.58	15	7.92	1	1.07	2	3.45	13
XLOC_016548	10.27	20	0	0	0	0	0	0	0	0	0.96	3
XLOC_016590	0	0	0	13	254.93	1	0.79	0	15.55	13	1.42	2
XLOC_016613	13.63	16	0	0	0	0	0	0	0.92	1	1.5	2
XLOC_016617	50.77	61	3.32	0	0	0	0	1	6.31	8	16.31	39
XLOC_016663	73.64	106	11.95	3	6.65	3	2.04	4	1.42	2	4.8	13
XLOC_016690	0	0	3.36	0	0	0	0	1	14.39	16	0	0
XLOC_016711	0.98	1	0	1	0.36	0	0.31	0	20.85	44	0.13	1
XLOC_016716	5.83	9	2.69	6	6.77	7	4.35	1	12.8	20	0.44	1
XLOC_016775	14.03	16	0	1	3.75	0	0	0	0	0	0	0
XLOC_016798	1.11	7	0.63	23	1.26	2	0.2	1	0.3	2	0.42	5
XLOC_016801	2.2	5	0	16	4.09	0	0	0	0	0	0	0
XLOC_016818	10.17	16	10.52	3	18.22	1	1.36	4	9.29	11	2.94	8
XLOC_016860	3.19	5	3.01	1	2.35	5	3.3	1	0.72	1	3.54	14
XLOC_016883	47.98	87	60.45	467	77.7	77	42.58	12	24.29	73	55.06	168
XLOC_016895	2.92	7	0	0	0	0	0	0	0	0	1.9	7
XLOC_016897	18.12	29	20.37	135	114.99	29	16.91	8	2.43	4	12.33	34
XLOC_016899	22.1	19	0	0	0	2	1.97	0	0	0	0	0
XLOC_016926	19.92	37	22.13	12	8.75	11	6.56	9	4.1	7	36.93	118
XLOC_016927	16.4	25	2.78	0	0	0	0	1	0	0	0.19	1
XLOC_016928	22.97	17	0	4	102.22	2	2.98	0	4.13	3	0	0
XLOC_016956	28.18	19	0	0	0	0	0	0	0	0	1.06	2
XLOC_016958	14.1	22	2.77	1	1.35	0	0	1	0.66	1	18.42	55
XLOC_016961	0.61	1	3.23	0	0	2	1.01	1	9.98	13	3.46	9
XLOC_017008	6.78	0	0	0	0	0	0	0	0	0	27.87	9
XLOC_017015	20.93	20	0	0	0	0	0	0	0	0	0	0
XLOC_017022	10.82	9	18.43	0	0	6	5.72	4	2.18	2	23.15	40
XLOC_017054	47.78	42	4.44	0	0	1	0.69	1	0	0	3.68	8
XLOC_017081	4.21	3	0	0	0	0	0	0	13.98	10	1.46	3
XLOC_017082	45.68	37	10.56	1	21.28	2	2.17	2	0	0	2.16	2
XLOC_017111	7.49	9	12.26	1	12.44	0	0	3	10.66	11	0	0
XLOC_017113	42.24	42	0	0	0	0	0	0	1	1	9.09	16
XLOC_017115	38.56	29	4.92	0	0	0	0	1	0	0	0.76	2
XLOC_017128	9.26	22	6.7	1	0.26	5	3.48	2	2.39	3	19.98	85
XLOC_017164	29.05	50	0	0	0	9	0.52	1	0.97	1	0.65	3
XLOC_017207	47.57	54	7.16	0	0	1	0.93	2	0.85	1	0	0
XLOC_017234	0	0	0	0	0	0	0	0	0	0	16.37	0
XLOC_017235	39.74	0	23.41	0	0	2	67.19	0	68.47	26	128.85	1
XLOC_017340	51.47	31	0	0	0	0	0	0	0	0	1.24	1
XLOC_017371	0	0	1.49	14	2.72	0	0	1	0.71	2	0	0
XLOC_017411	40.25	77	10.86	4	1.86	20	9.61	5	4.66	9	2.9	14
XLOC_017412	27.34	31	3.49	0	0	0	0	1	0.83	1	14.04	33
XLOC_017414	10.12	15	3.06	13	34.45	6	4.17	1	8.02	11	5.74	12
XLOC_017418	0	2	6.06	0	0	21	14.08	2	1.63	4	8.77	24
XLOC_017456	0	0	0	0	0	0	0	0	38.31	36	0	0
XLOC_017464	25.17	33	21.91	2	6.19	11	7.02	7	3.72	5	8.4	18
XLOC_017497	17.93	31	0	0	0	0	0	0	0.55	1	0	0
XLOC_017499	32.14	59	84.92	25	13.99	35	16.73	37	6.57	12	63.99	255
XLOC_017518	8.6	8	63.83	0	0	1	0.67	15	0	0	33.83	68
XLOC_017551	70.92	46	0	0	0	1	0.94	0	0	0	0	0
XLOC_017592	35.8	24	38.41	4	120.6	6	8.52	6	4.52	3	145.74	162
XLOC_017635	17.02	45	0	0	0	0	0	0	0	0	0	0
XLOC_017683	80.67	71	4.44	0	0	0	0	1	5.26	5	2.55	3
XLOC_017685	35.62	27	0	1	20.7	0	0	0	2.46	2	0	0

XLOC_017709	3.43	3	29.33	0	0	1	1.26	6	2.31	2	4.54	12
XLOC_017711	1.4	4	0	90	20.68	0	0	0	0.78	2	0.21	2
XLOC_017750	4.4	7	0	22	22.01	0	0	0	6.26	10	0.86	2
XLOC_017757	6.78	16	0	5	1.77	3	1.33	0	1.88	4	0.58	3
XLOC_017787	21.07	36	0	0	0	0	0	0	0	0	0.71	3
XLOC_017824	1.16	1	0	0	0	1	1.52	0	21.15	15	21.07	24
XLOC_017825	9.13	12	0	0	0	2	1.52	0	2.59	3	6.09	13
XLOC_017866	52.1	42	10.56	2	42.62	5	4.65	2	1.25	1	13.53	18
XLOC_017922	70.13	56	0	0	0	0	0	0	0	0	0.9	1
XLOC_017923	3.06	4	0	5	33.22	1	0.91	0	14.11	17	0.25	1
XLOC_017924	9.27	6	5.98	2	53.41	3	4.01	1	2.82	2	42	51
XLOC_017928	17.45	16	9.46	0	0	5	4.65	2	2.24	2	2.52	4
XLOC_017952	0.63	1	0	0	0	1	0.87	0	11.88	15	1.11	3
XLOC_017965	3.99	5	6.1	17	43.7	12	7.64	2	13.06	18	3.75	10
XLOC_017967	21.99	26	10.53	0	0	3	2.37	3	0	0	1.77	7
XLOC_017971	61.19	174	3.04	5	1.01	2	0.8	2	4	11	0.2	2
XLOC_017975	0	0	0	10	0.56	1	0.18	0	0.16	1	0.25	3
XLOC_017976	10.19	10	92.94	0	0	4	2.53	23	0.96	1	21.03	36
XLOC_017983	66.01	51	0	0	0	0	0	0	1.17	1	1.16	3
XLOC_018070	0	0	0	0	0	0	0	0	12.32	26	0	0
XLOC_018075	6.43	5	10.56	1	21.27	1	1.36	2	2.5	2	16.49	28
XLOC_018078	19.4	18	0	0	0	1	1.03	0	0	0	6.31	14
XLOC_018081	15.73	17	0	1	12.44	0	0	0	0	0	20.6	41
XLOC_018130	0	0	0	4	27.36	38	30	0	2.5	3	3.81	9
XLOC_018175	31.4	23	0	1	27.93	5	5.99	0	1.44	1	0.51	1
XLOC_018176	22.29	24	12.06	5	59.51	21	17.72	3	0	0	19.98	40
XLOC_018178	34.64	36	11.79	2	22.34	11	10	3	4.66	5	44.42	85
XLOC_018190	24.78	17	11.48	11	273.08	6	8.82	2	6.77	5	18.31	29
XLOC_018191	44.92	36	45.85	3	59.63	20	22.07	9	7.23	6	8.73	11
XLOC_018198	12.48	3	65.64	0	0	1	9.53	9	0	0	0	0
XLOC_018227	19.31	22	0	0	0	0	0	0	0	0	1.05	2
XLOC_018232	12.47	20	0	0	0	0	0	0	0.62	1	0.48	1
XLOC_018241	50.27	45	32.05	3	48.24	24	22.29	7	33.61	31	18.88	28
XLOC_018287	17.6	15	31.85	0	0	5	4.94	7	0	0	14.55	31
XLOC_018291	25.49	29	7.2	16	125.47	18	13.88	2	15.38	18	6.25	16
XLOC_018294	0.56	1	0	15	4.39	0	0	0	0.43	1	1.19	5
XLOC_018295	10.43	7	5.98	6	160.24	22	25.86	1	2.82	2	0	0
XLOC_018302	9.95	28	4.97	21	5.01	6	2.45	3	7.13	18	2.22	11
XLOC_018357	1.38	5	0	14	2.74	1	0.39	0	0	0	0.33	2
XLOC_018395	19.27	27	0	0	0	0	0	0	0	0	1.66	5
XLOC_018399	27.12	26	4.13	4	51.22	12	11.15	1	9.8	10	6.69	15
XLOC_018402	4.83	11	0	2	0.87	2	0.88	0	0	0	22.84	100
XLOC_018454	32.01	54	7.13	1	0.64	3	1.62	3	0.57	1	2.46	9
XLOC_018495	1.65	0	0	0	0	0	0	0	0	0	26.5	57
XLOC_018517	5.69	9	12.58	3	9.59	1	0.49	4	0.75	1	23.2	63
XLOC_018562	16.3	18	0	31	92.97	5	3.08	0	10.38	14	7.07	25
XLOC_018566	19.43	36	2.49	0	0	0	0	1	0	0	0.17	1
XLOC_018567	0.64	1	20.37	2	11.07	4	2.83	6	4.03	5	7.07	18
XLOC_018568	0.44	1	4.79	1	0.65	1	0.38	2	5.71	10	0	0
XLOC_018574	37.5	34	4.36	0	0	0	0	1	0	0	0.86	1
XLOC_018578	9.28	15	9.12	0	0	2	0.95	3	0	0	26.9	63
XLOC_018628	0.85	1	0	0	0	1	1.15	0	11.56	9	0.67	2
XLOC_018636	4.61	14	13.67	5	1.27	7	2.79	8	0	0	23.06	119
XLOC_018640	8.67	24	0	0	0	0	0	0	0	0	0.74	4
XLOC_018647	20.39	28	18.86	2	6.39	15	10.68	6	1.5	2	10.28	26
XLOC_018650	10.33	17	2.73	102	125.45	52	29.29	1	7.15	11	2.41	8
XLOC_018655	58.19	58	0	0	0	0	0	0	0.89	1	0.55	2
XLOC_018714	29.19	21	0	0	0	0	0	0	0	0	0	0
XLOC_018715	0	0	0	0	0	3	1.57	0	0.54	1	4.15	20
XLOC_018723	3.2	3	0	3	48.24	4	2.86	0	11.92	11	1.73	2
XLOC_018733	17.74	17	0	1	16.08	4	5.44	0	19.51	15	120.86	214

XLOC_018790	11.49	33	1.48	7	1.34	10	2.95	1	3.89	11	1.51	9
XLOC_018853	32.78	57	80.05	4	3.66	14	7.85	31	5.54	9	37.98	122
XLOC_018867	12.41	17	23.55	1	10.39	35	26.78	7	1.6	2	19.07	47
XLOC_018924	2.26	4	2.61	8	7.71	2	1.37	1	9.32	15	2.48	9
XLOC_018943	47.58	35	5.57	0	0	0	0	1	0	0	0	0
XLOC_018946	28.34	20	6.08	1	27.51	2	2.51	1	1.43	1	93.3	117
XLOC_019033	0	0	0	1	2.28	2	1.58	0	0	0	8.9	25
XLOC_019038	44.41	29	0	0	0	0	0	0	0	0	0	0
XLOC_019042	140.39	133	4.36	0	0	1	1.13	1	5.16	5	5.32	7
XLOC_019043	9.01	12	0	6	35.34	4	2.86	0	19.54	24	0	0
XLOC_019050	11.23	17	4.73	3	1.86	3	1.35	2	0.56	1	1.14	4
XLOC_019051	0.77	1	16.16	4	48.33	14	11.34	4	0	0	67.49	123
XLOC_019055	4.98	4	0	0	0	1	1.26	0	15.03	13	0	0
XLOC_019057	152.03	122	0	0	0	0	0	0	2.44	2	0.81	2
XLOC_019059	0	0	4.28	0	0	0	0	1	1.01	1	20.63	40