Genome assembly and annotation of the cricket *Gryllus bimaculatus*

Guillem Ylla[1], **Taro Nakamura**[2], **Sumihare Noji**[3], **Taro Mito**[4] & **Cass**andra **Extavour**[1]

[1] Department of Organismic and Evolutionary Biology & Department of Molecular and Cellular Biology, Harvard University, Cambridge, USA.
[2] Division of Evolutionary Developmental Biology, National Institute for Basic Biology, Okazaki, Japan.
[3] Tokushima University, Tokushima, Japan.
[4] Division of Bioscience and Bioindustry, Tokushima University, Tokushima, Japan..

Gryllus bimaculatus

Most of the available insect genomes are from **Holometabolan** insects, which are insects that undergo complete metamorphosis like beetles and flies. In contrast, the **Hemimetabolans**, which undergo gradual metamorphosis, and represent the basal branches of the insect tree, have very few genomic resources available **(Figure 1)**.
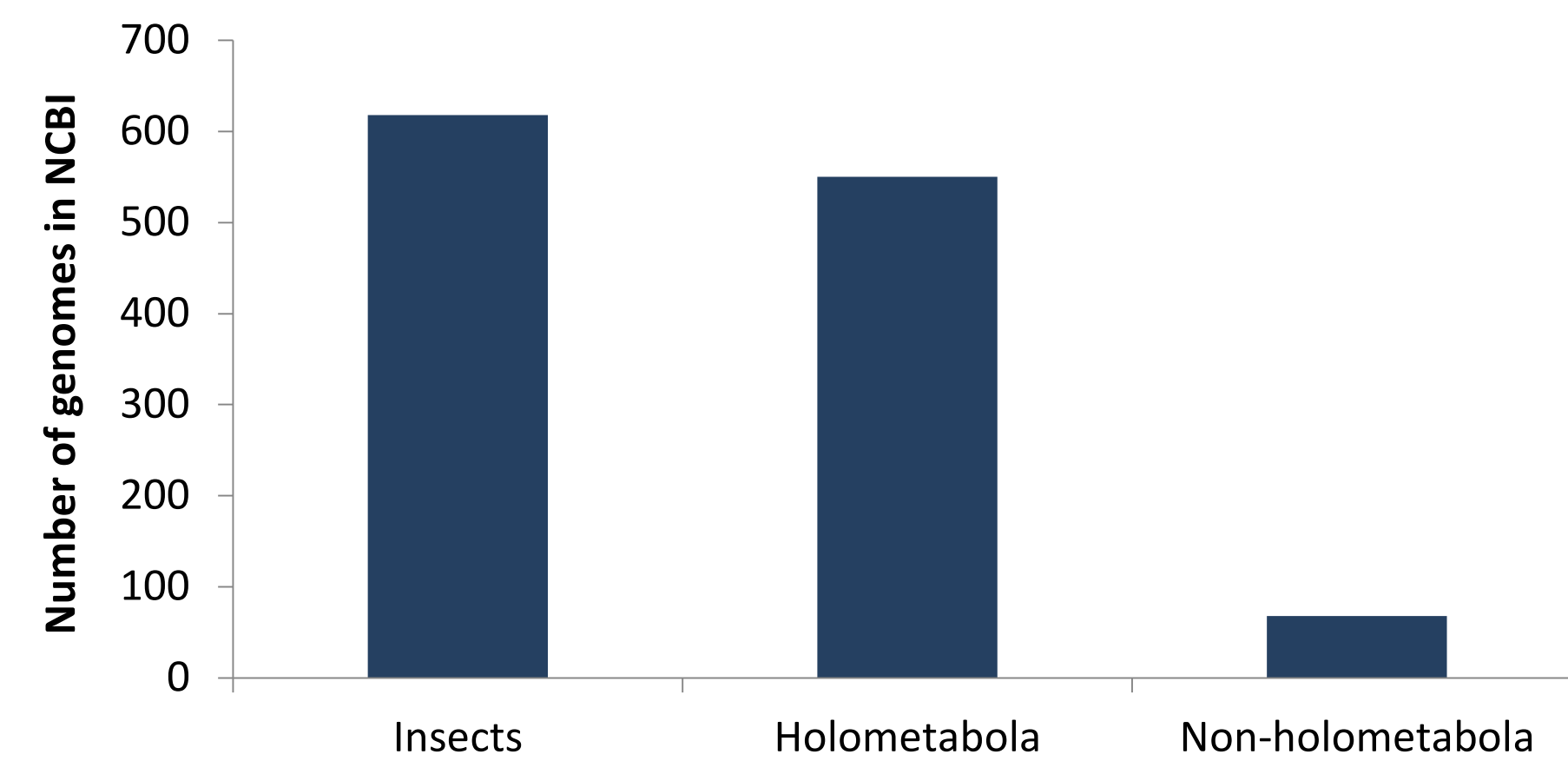
Figure 1: Number of genomes listed in NCBI for all insects, holometabolans ("Endopterygota") and non-holometabolans (insect genomes - holometabolans).

There is only one available annotated genome for the Orthopteran order, that of *Locusta migratoria*, which is the largest insect genome sequenced until this date with ~7Gb.
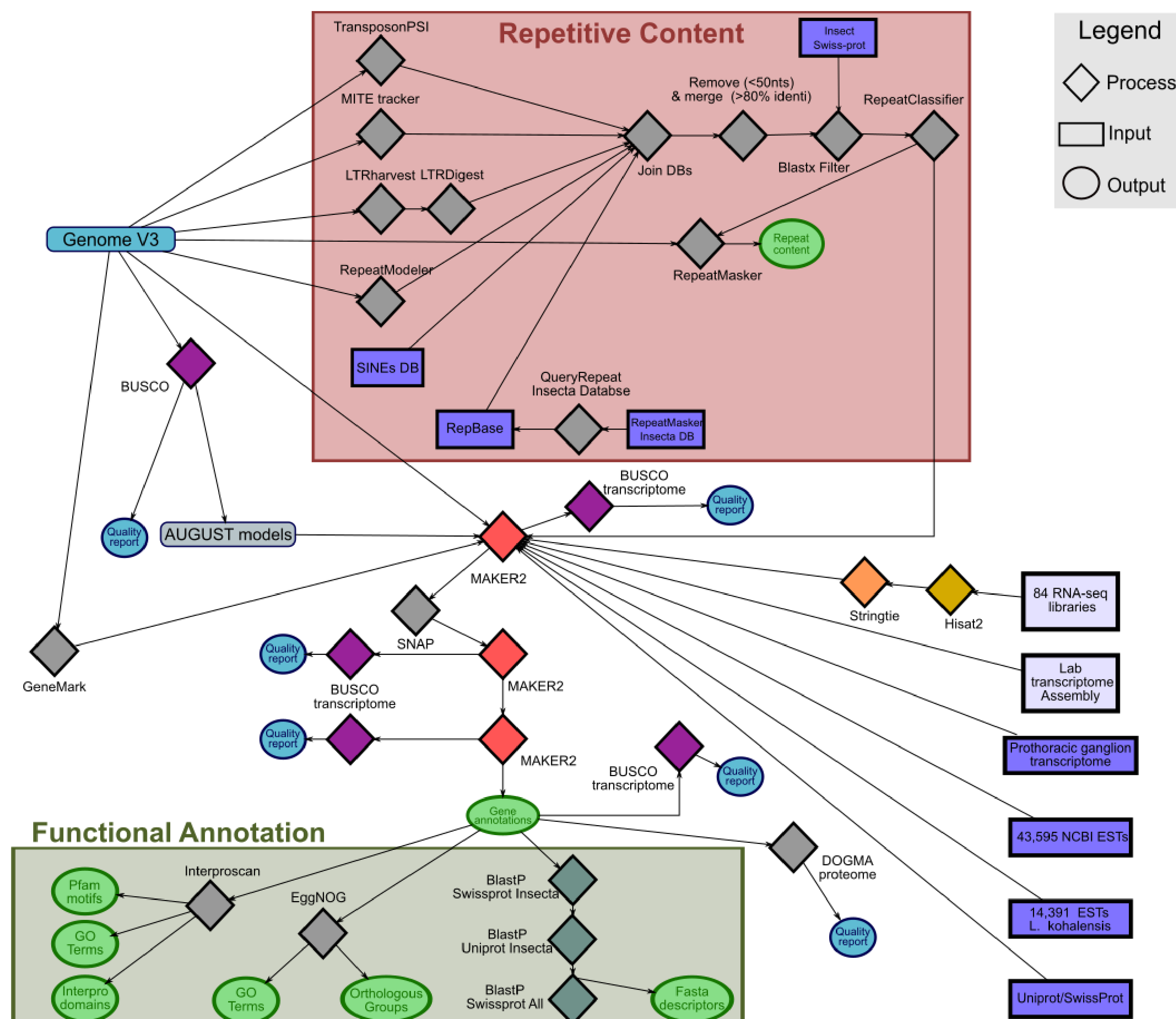
Figure 2: Photo of an adult female of *Gryllus bimaculatus*.

Gryllus bimacualtus

- Order: Orthoptera.
- Aka. two-spotted cricket.
- Hemimetabolan insect.
- Experimental model for functional genetics, development and evolution.

Genome annotation Pipeline

Results

Assembly Stats

	Gbi	Lmi	Lko	Bger	Zna
Year	2019	2014	2019	2018	2014
Scaffolds	47,877	564,328	148,784	24,820	31,662
Len. (Gb)	1.66	6.91	1.6	2.04	0.49
Avg.scaff. (Kb)	34.630	12.24	10.72	82.08	15.32
N50 (Kb)	6,287	325	583	1,056	751
N's (Kb)	56,571	1,094,108	31,618	326,821	20,751
L50	71	3,607	753	576	194

Table 1: Descriptive statistics of our newly assembled *Gryllus bimaculatus* genome (Gbi) in comparison with recently published hemimetabolan genomes of *Locusta migratoira* (Lmi), *Blattella germanica* (Bger) and *Zootermopsis nevadensis* (Zna).
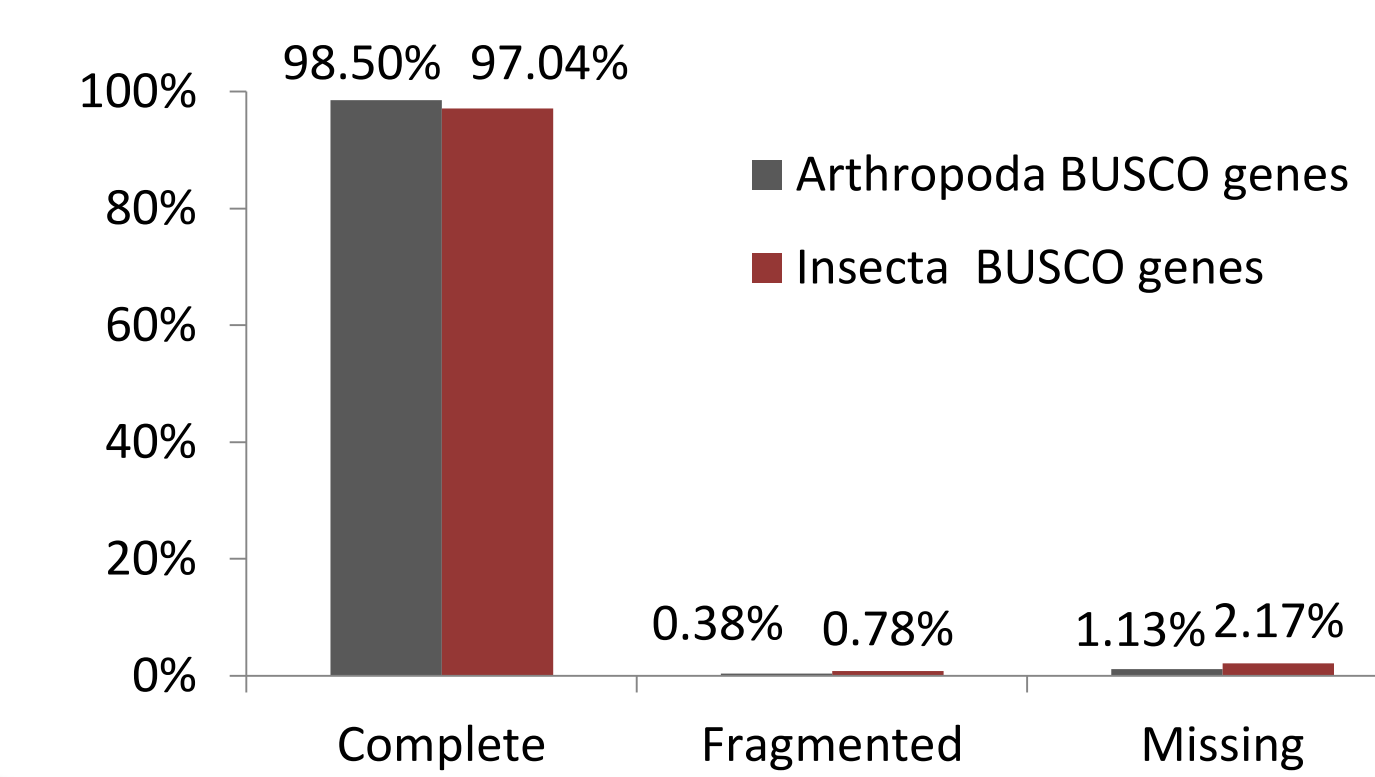
Assembly Completeness

Figure 3: Percentage of complete, fragmented and missing BUSCO genes in the *G. bimaculatus* genome assembly. Analysis performed at arthropod level (1,066 genes) and insect level (1,658 genes).

Gene Annotations

17,871 Protein Coding Genes
28,529 Transcripts

Figure 5: Number of Insect genes that BUSCO found in the genome versus number of insect genes found within the annotated transcripts. The annotation pipeline only failed to annotate 34 genes out of 1,658 (2%) of the BUSCO Insect genes.

tRNA genes
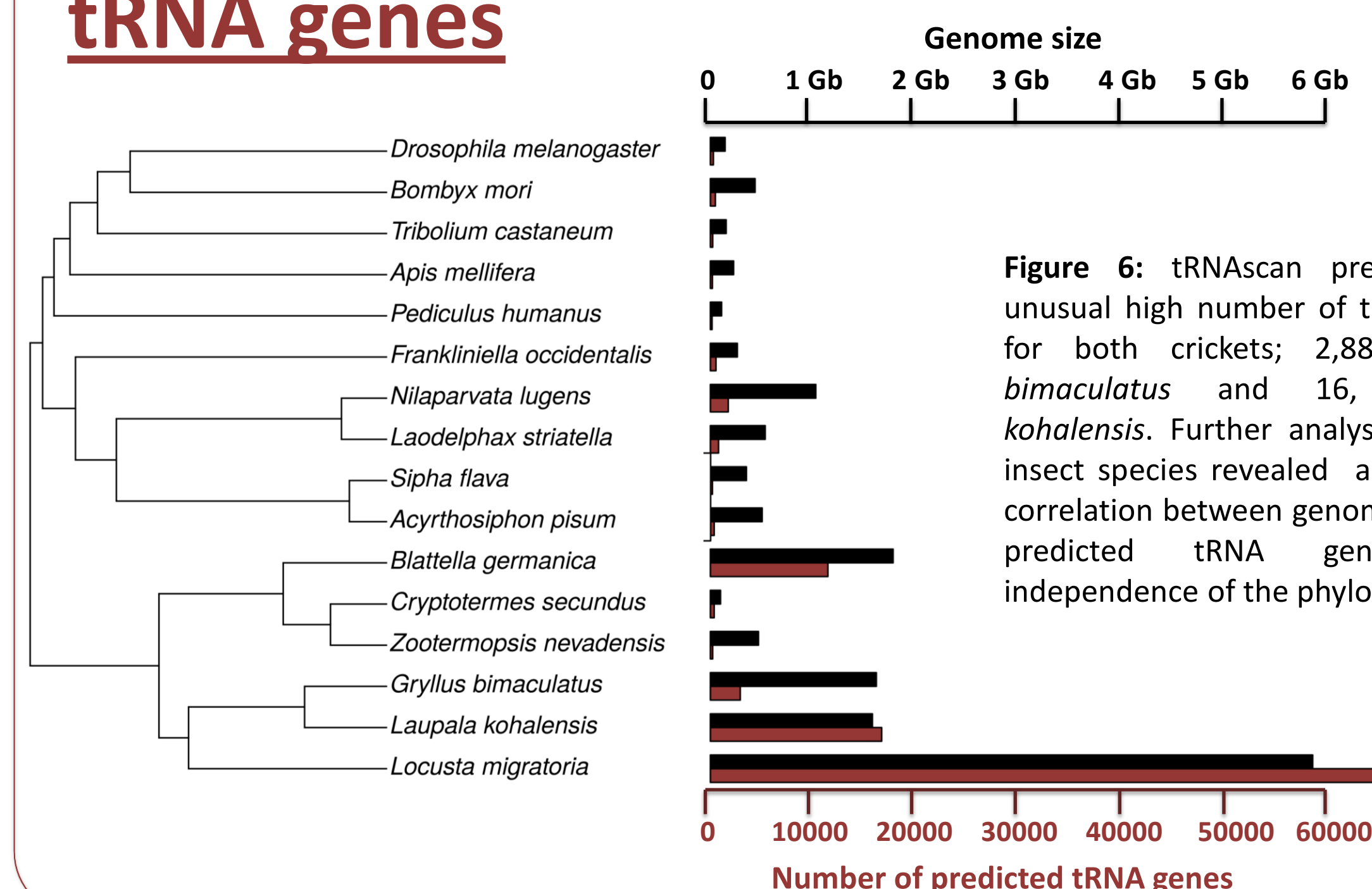
Figure 6: tRNAscan predicted an unusual high number of tRNA genes for both crickets; 2,886 for *G. bimaculatus* and 16, 530 *L. kohalensis*. Further analysis with 16 insect species revealed a significant correlation between genome size and predicted tRNA genes with independence of the phylogeny.

Transposable Elements

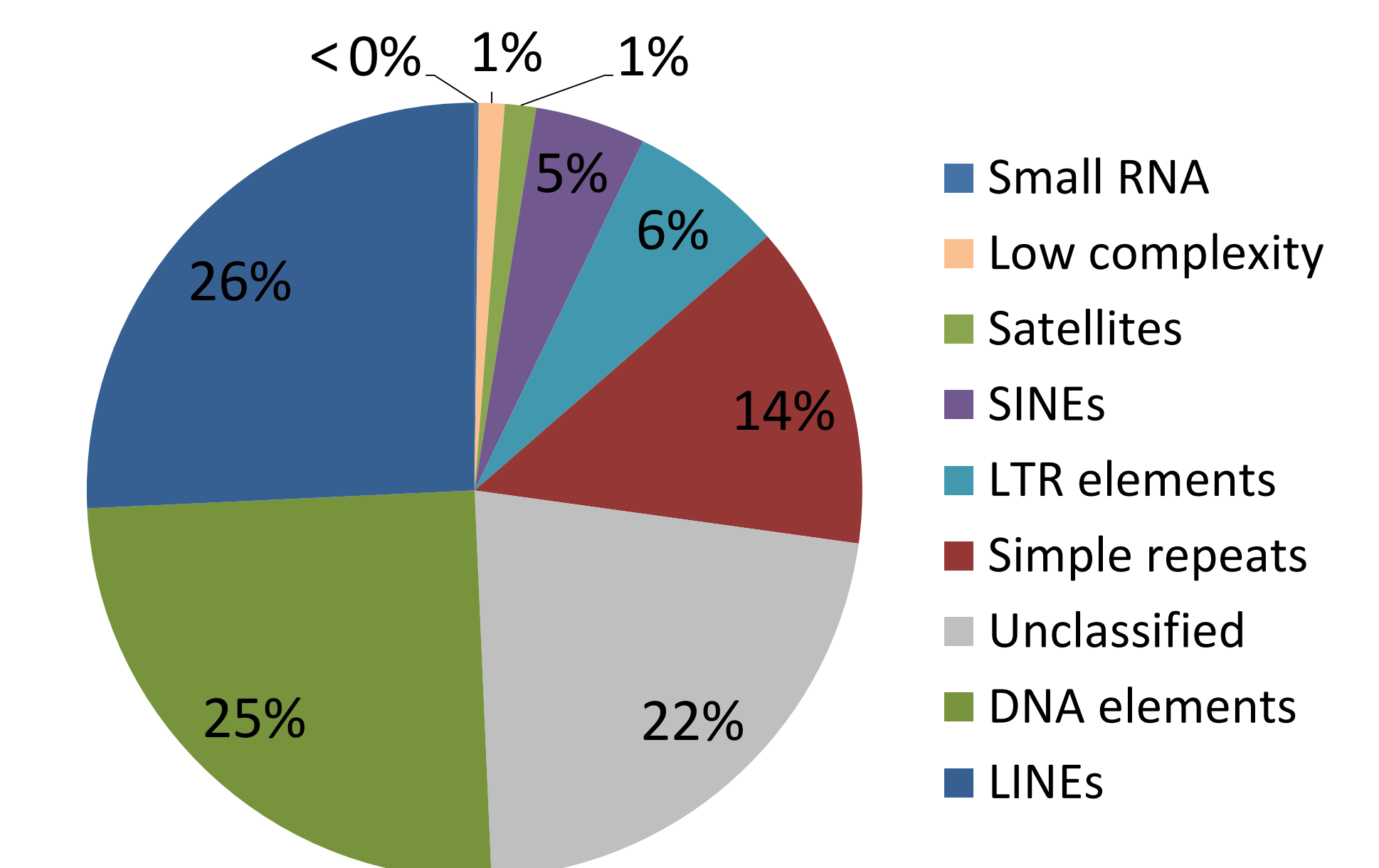**Represent the 34% of the Genome**

Figure 4: The ~34% of the *G. bimaculatus* genome is composed of transposable elements (TEs). The RepeatMasker software using a custom repeat library reported the percentage of genome accounted for each of the main TE families.

Genome Methylation

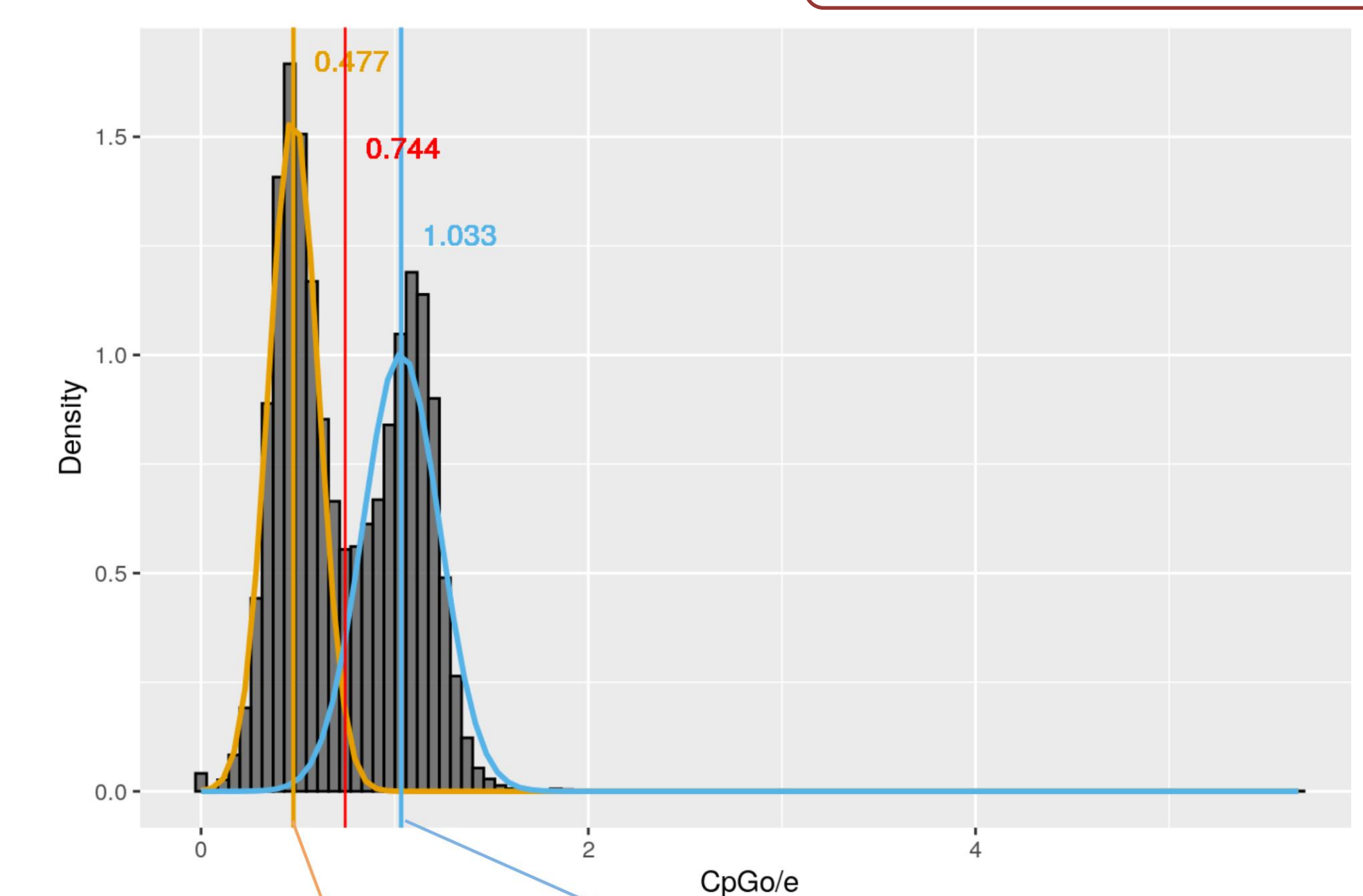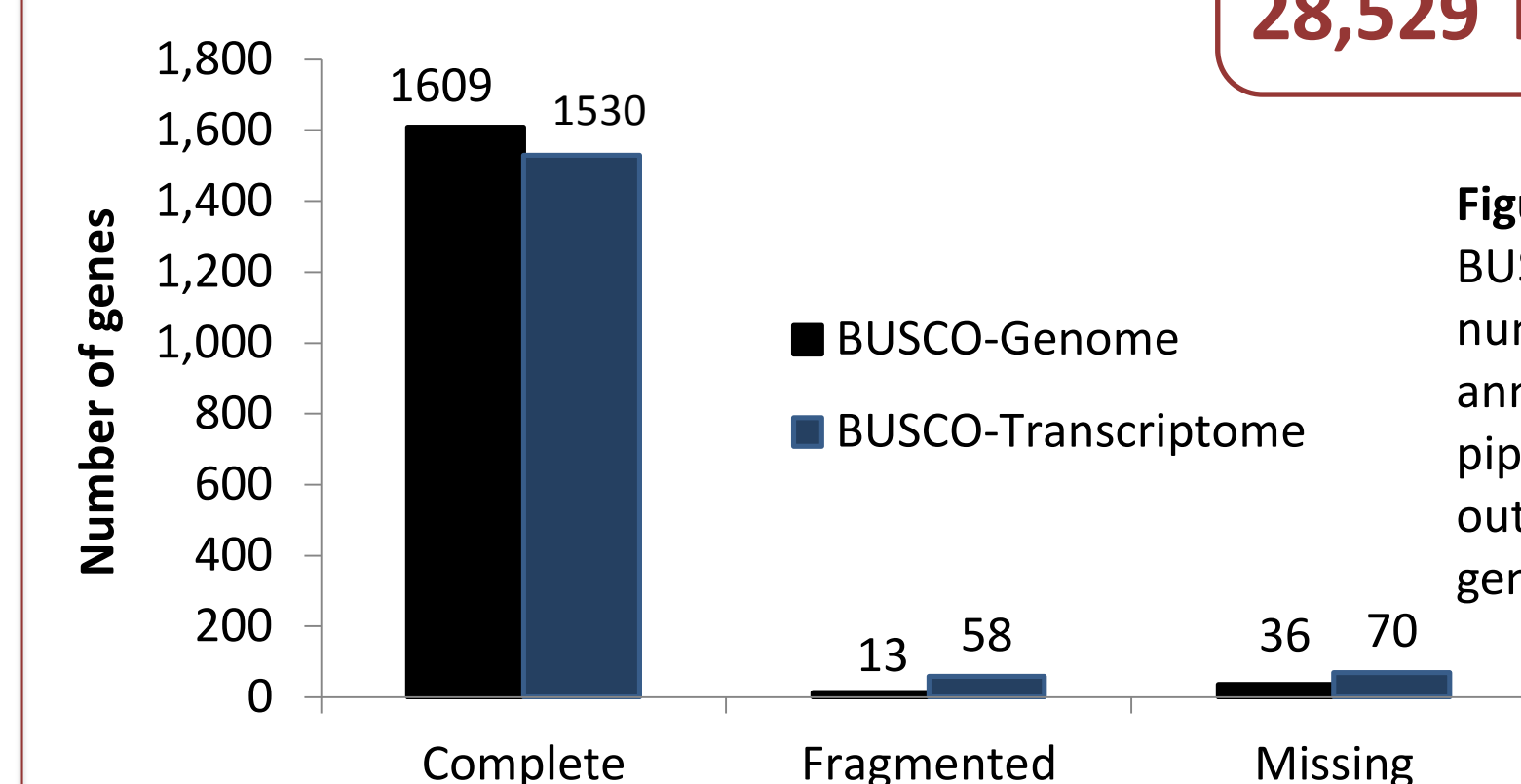**Identification of DNMT1 & DNMT3 genes**

Figure 7: The bimodality on the ratio of observed CpGs to excepted CpGs within the CDS ($CpG_{o/e}$) is an indictor of DNA methylation events. As in other hemimetabolan insect genomes, *G. bimaculatus* genome contains two groups of genes, one with low $CpG_{o/e}$ corresponding to highly methylated genes and another with high $CpG_{o/e}$ corresponding to non methylated genes. The GO-enrichment analysis reveals that high and low methylated genes perform different biological processes.