

## Reviewer Report

**Title: A Chromosomal-Level Genome Assembly for the insect vector for Chagas disease, *Triatoma rubrofasciata***

**Version: Revision 1**      **Date: 5/13/2019**

**Reviewer name: Ben Mans**

### Reviewer Comments to Author:

Most reviewer issues were addressed satisfactorily. Some minor issues is suggested below.

Page 4, line 2: ... distribution/ratio is showed in Figure 2.

Figure 3: Unit of X-axes? How does this relate to estimated genome size?

Page 5, line 28: Please note that the last sentence of this paragraph still refer to the difficulty of the mollusk genome assembly. This paragraph also contain numerous small errors. Please see suggested modified paragraph below:

First of all, we compared the contig/scaffold number and N50 length of contigs for *T. rubrofasciata* with insect species with sequenced genomes and found that our assembly has much improved quality over other insects (Figure 5). We attributed the improvement to the application of the PacBio long reads for genome assembly. With Hi-C data analysis, we successfully assembled the *T. rubrofasciata* genome to chromosome-level with just one individual. Like previous studies, insect genome heterozygosity was one of the biggest challenges for genome assembly, both in terms of contig and scaffold assembly. Traditional chromosomal genome assembly requires physical maps and genetic maps, which is time- and labor-consuming. Our work illustrated that the genome assembly using PacBio long sequencing data was not only affordable but also effective for overcoming the difficulties presented by insect genome assembly.

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