Reviewer Report

Title: **Improving the annotation of the Heterorhabditis bacteriophora genome**

Version: **Original Submission** **Date:** 12/15/2017

Reviewer name: **Bruce A Rosa**

Reviewer Comments to Author:

The manuscript "Improving the annotation of the Heterorhabditis bacteriophora genome" presents the re-annotation of an existing high-quality genome assembly which previously had low-quality gene annotation with many issues. By utilizing RNA-Seq datasets and using the latest high-quality annotation tool (BRAKER1), significant improvements were made in completeness, unique protein counts and secretion predictions. This annotation improvement represents a very significant improvement in how results from Heterorhabditis bacteriophora genome studies will be interpreted.

- The supporting data files are thorough and complete, and support the findings. One suggestion: Although not part of the study, a text file could be added within Supp Tables 2 and 3 which provides the WormBase assembly version used, and accession IDs / web links to the genome assembly, so that readers can have all the information they need to work with the new annotation within the single files.

- Tables 1 and 2 in the main text should also be reformatted. Shading is not permitted by Gigascience. Also, removing vertical lines (both tables) and centering the numbers on table 1 would help to improve their look.

- Please ensure that SRA and INSDC accessions are added, since they are currently referenced as "XXXXXXX"

- Since InterProScan was ran, it would be interesting to look at the statistics in regards to the identification of InterPro domains. For example, compare the number of proteins with any annotated IPR domains, the total number of IPR domains identified, and the number of unique IPR domains identified. The previous publication also performed this comparison with other species using KEGG, so it may be interesting to repeat that similar analysis with the current annotation, although there are many updated ways to run KEGG so the re-analysis of the previous annotation may not match wha was previously found.

Methods

Are the methods appropriate to the aims of the study, are they well described, and are necessary controls included? Yes

Conclusions

Are the conclusions adequately supported by the data shown? Yes

Reporting Standards

Does the manuscript adhere to the journal's guidelines on minimum standards of reporting? Yes

Choose an item.

Statistics

Are you able to assess all statistics in the manuscript, including the appropriateness of statistical tests used? Yes, and I have assessed the statistics in my report.

Quality of Written English

Please indicate the quality of language in the manuscript: Acceptable

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