

Reviewer Report

Title: De novo transcriptome assembly: A comprehensive cross-species comparison of short-read RNA-Seq assemblers

Version: Revision 1 **Date: 1/27/2019**

Reviewer name: Brian Haas

Reviewer Comments to Author:

I appreciate the authors response to my and the other reviewer's comments, and I feel that the manuscript has been significantly improved as a result of the revisions. The revised scoring system used by the authors is far superior to the earlier method used. The adjustment to the metrics used to account for correlations along with including the additional metrics also added to the rigor of the work. I commend the authors for all their efforts.

My only final critique of the manuscript refers to page 10, left column, lines 60-61: "but failed on the 23h data set (many small contigs, longest hit: 10,677 nt).", which conflicts with what was written in the response to reviewers and in the main text at right column, lines 12-13: "Trinity built two contigs of similar length that together would cover the entire viral genome."

Methods

Are the methods appropriate to the aims of the study, are they well described, and are necessary controls included? Choose an item.

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I am currently the lead developer of the Trinity software which is one of the tools being assessed in this manuscript.

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