

Reviewer Report

Title: Multifaceted Hi-C benchmarking: what makes a difference in chromosome-scale genome scaffolding?

Version: Revision 1 **Date: 11/7/2019**

Reviewer name: Derek Bickhart

Reviewer Comments to Author:

Summary: I was impressed with the authors' tests on PCR overamplification and assembly quality. These have addressed many of my concerns with the previous manuscript, so my remaining concerns are minor.

Line 323: The authors' tests of PCR overamplification bias have allayed many of my concerns. I still think that the interpretation of the data in this sentence could be couched in more caution. The Arima libraries had 10% more valid interaction pairs than the Icon-HI-C prep. Why was this?

Line 435: I still believe that this paragraph is gratuitous. I would be satisfied if the authors shortened this by two sentences and made the point that Hi-C scaffolding software does not provide consistent gap lengths for gaps of unknown length.

Supplementary table S8: Please provide captions that explain the difference between libraries "g" and "h" in the table as this is not immediately clear without referring to the main text.

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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Are the conclusions adequately supported by the data shown? Choose an item.

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