

## **EDITOR'S SUMMARY REPORT**

### ***From your editor:***

It has been a pleasure to edit your paper on the development of a new genome browser and its applications for comparing and calculating genome complexity. It was engaging and thoughtful, and it is clear that you put a great deal of effort into writing it. I have edited your document, paying careful attention to grammar and phrasing. Please review my edits before accepting or rejecting any changes. In addition, please review this summary report for some of my more general observations about your manuscript.

Thank you for giving me the opportunity to work on your manuscript. I wish you the best of luck throughout the publication process.

Yours sincerely,  
Lisa G., PhD

<b>Overall Summary</b>	
<b>• Content</b>	The length and content are reasonable. Please review the comments, which indicate certain areas where placeholder type or incomplete sentences were identified. Please consider being more precise in your descriptions of minimal and maximal capacity for GCB (rather than dozens and hundreds, which can represent a wide range).
<b>• Grammar and Punctuation</b>	"Fig." is an abbreviation for "Figure" and should include an abbreviating period ("Fig." instead of "Fig")
<b>• Word Choice</b>	The language appears appropriate. Please be sure that program names (especially OrthoFinder) are appropriately capitalized throughout the document.
<b>• Style</b>	Some examples of passive voice and choppy sentences. Active voice as used and some sentences were combined for better flow.
<b>• Formatting</b>	Discussion section had a number in front of it, which was the only place a numbered heading was used. I removed this number. Please review.

Finally, I'd like to share an example of a phrasing convention and how I applied it in your paper: The two sentences below are related and can be easily placed within one single sentence to reduce choppiness.

**Original sentence:** Synteny visualization tools (i.e. Mauve [22], BRIG [36], genePlotR) are often used for genome comparative studies. Such tools allow visual inspection of large and small genome rearrangements.

**Edited sentence:** Synteny visualization tools (e.g., Mauve [22], BRIG [36], and genePlotR) are often used for genome comparative studies and allow the visual inspection of large and small genome rearrangements.