

Reviewer Report

Title: Significantly improving the quality of genome assemblies through curation

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Reviewer name: Benjamin D Rosen

Reviewer Comments to Author:

The authors provide much welcome guidelines and recommendations for genome assembly curation derived from their experience curating hundreds of assemblies. Their recommendations are clear but the manuscript could benefit from more examples of what misassembly signals look like in different technologies. The authors mention that gEVAL is tied into their local infrastructure and not portable, but the original gEVAL manuscript mentions that it is downloadable for use with any organism. It should be made more clear why gEVAL cannot be used. If gEVAL indeed cannot be used outside of their group, it would be nice to see how similar views could be generated with publicly available tools. Finally, I think that it would be hugely beneficial for readers to have a workflow figure with their recommendations incorporated from the initial coherence check to final ordering and orientation.

Specific comments:

line 100 - extra period at end of sentence

line 106 - spell out Segmental Duplication Assembler.

line 113 - comma after "For polishing"

line 117 - clarify that they can be assembled independently from the raw reads used for genome assembly.

line 118-119 - This is confusing, it was just stated above that the organelle genome must be included for polishing and now this says to process it independently.

line 208 - typo "gata"

line 223 - provide a link to a public code repository with the nextflow pipeline

Figure 1: This example is a little confusing. It looks like some of the bionano maps agree with the join and span the drop in pacbio read coverage.

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