

Reviewer Report

Title: Significantly improving the quality of genome assemblies through curation

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Reviewer name: Alan L Archibald

Reviewer Comments to Author:

The authors provide a concise overview of issues that arise during efforts to establish a reference quality genome sequence assembly, especially for organisms with complex genomes. The relevant published literature and software sources are cited. Whilst the authors' own infrastructure for reviewing and correcting genome assemblies is an in-house bespoke system that is not portable they describe the key processes involved in reviewing and assessing genome assemblies. This brief editorial / review provides a useful checklist for groups generating genome assemblies. Whilst the generation of the primary sequence data from which a first pass contig level assembly can be built is readily within the capacity of well-founded and funded research groups, the conversion of the resulting contigs into a high quality chromosome level assembly requires time and skill. This review provides a useful guide to navigating this transition and those who aspire to contribute to the growing resource of high quality reference genomes would be well served by reading this guide.

This guide is largely set in the context of the current widely adopted paradigm of single pseudo-haploid representations of an organism's genome. As some of the errors that the procedures described in this paper seek to address concern the challenges of resolving an individual's different haplotypes some comment on graph based genome approaches to capture rather than 'resolve' such haplotypic differences would be appropriate.

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