Reviewer Report

Title: The first near-complete assembly of the hexaploid bread wheat genome, Triticum aestivum

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Reviewer name: Hikmet Budak

Reviewer Comments to Author:

The manuscript by Zimin et al. describes the whole genome sequencing of bread wheat Triticum aestivum genotype Chinese Spring and the construction of the genome assembly, using a combination of substantially long PacBio and relatively accurate high-depth Illumina reads. The manuscript thoroughly describes the assembly procedure, which is computation intensive as is the case for such genomes. I do appreciate repeated steps to polish the assembly, however, the final assembly is still quite fragmented, made up of >279K contigs. Although this assembly may represent the best near-complete bread wheat genome assembly achieved so far, I doubt that it will be of immediate use to the wheat community. One of the major shortcomings of this approach, in my opinion, is that the contigs are not readily assigned to individual chromosomes, which I believe make an assembly really useful. Although the authors identified the contigs likely belonging to the D-genome, I did not see any indication of how successful this assembly is in distinguishing homeologous sequences from the sub-genomes.Additionally, the manuscript is mostly focused on describing the assembly procedure which is, in my opinion, quite conventional, and very few biological assessments on the genome content and organization (repeat elements, gene content etc.) are provided.As it stands I recommend its rejection.

Level of Interest

Please indicate how interesting you found the manuscript: An article of limited interest

Quality of Written English

Please indicate the quality of language in the manuscript: Acceptable

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