Reviewer Report

Title: Chromosome-scale genome assembly of kiwifruit Actinidia eriantha with single-molecule sequencing and chromatin conformation capture

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Reviewer name: Robert Schaffer

Reviewer Comments to Author:

While the paper has been improved I am disappointed by the responses from the authors especially regarding the gene models
Firstly on the genome construction side. it appears that the anomolies that the authors have spotted are in recombination cold spots (Figure s2) and following the lines, the genetic map does not alway correlate with their assembly? There appears to be an inversion in the construction on ch16 and 19. This would be nice to be resolved.
For gene naming I agree if the quality of the genome was to the standard of the arabidopsis, rice or tomato genome then I it would maybe appropriate to name using genome location.
The 3 reasons for NOT giving names by chromosomal location are:
1) Gene names need to be locked for subsequent functional analysis. In Arabidopsis they changed twice and this was a disaster for publications between 2000 and 2003.
2) the genome arrangement will change in the future and therefore it is too early to give a chromosome position in the name. We are not in a position to give gene names based on chromosome location.
3) Chromosome 30 is non existant (I have not managed to find the gene list, but if it is there then it makes the whole gene naming in this paper irrelevant)
I accept that the orthology maybe a challenge to implement.
FOr the 10,000 new genes I am also concerned that the authors are relying on peptide lists from non verified genes.. I have seen many genome locations that have random RNAseq reads aligned (often in a little repetative section that are meaningless and computer generated models are pushed into the creation of a "gene" where there is not a gene, that goes beyond the areas of RNA seq reads. Did the authors check that these genes have good RNA seq reads accross the whole predicted gene? I would be interested to see some validation of the new gene models. Some examples would be nice rather than assertions by the authors, as this would be a significant improvement to our current understanding.

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