Apr 1, 2020

Dear Robert VanBuren,

We're thankful for your valuable comments on our manuscript entitled 'A de novo assembly of the sweet cherry *(Prunus avium* cv. Tieton) genome using linked-read sequencing technology'.

We've re-looked at the manuscript and changed in line with your comments. All of them have been accepted and incorporated into the revised version of this manuscript.

For your comments:

➤ 1. You are reporting a newly-assembled genome. To meet the PeerJ data sharing policy, you must deposit the raw reads **and** the assembled sequence in the appropriate databases. (e.g. <https://www.ncbi.nlm.nih.gov/guide/howto/submit-sequence-data/>.Since your raw reads are already in the NCBI SRA database, we suggest you use https://www.ncbi.nlm.nih.gov/genbank/eukaryotic_genome_submission/ however if you prefer, an alternative in China is https://bigd.big.ac.cn/gwh/.Another great alternative would be rosaceae.org: https://www.rosaceae.org/.The files are available on Figshare, but they are difficult to find and submitting them to the appropriate database will help improve the impact and accessibility of this manuscript.

Response: Accepted and the assembled sequence has deposited in NCBI under Accession number VTVB00000000. The section summarized the information was also changed in the manuscript.

Thank you very much for considering our manuscript for potential publication. I'm looking forward to hearing from you soon.

Sincerely yours

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