

Author's Response To Reviewer Comments

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Dear Editor and Reviewer,

We would like to thank you for helpful suggestions on our manuscript entitled "The chromosome-level draft genome of a diploid plum (*Prunus salicina*)" (GIGA-D-20-00195R1). Following the comments and suggestions, we corrected the numbering of the *P. salicina* pseudochromosomes all over the manuscript. The *P. salicina* pseudo-chromosome names and gene IDs in Figure 1, 3 and 4 were modified in the revised manuscript. We also contacted the staff of GDR (Genome Database for Rosaceae) and GenBank to update our genomic information. We expected that it would meet the publication requirement of GigaScience.

A point by point response to the reviewer' comments and questions and the main corrections in the paper were provided below.

Reviewer #1: I thank the authors for further revising their manuscript and clarifying some outstanding issues in regards of English proofreading and MS layout. Thank you very much for the answers to my previous questions, even if I do not fully agree with soem of them. However, there is still a major revision necessary before the manuscript is ready for publication. I bet I overlooked it in the first version of the manuscript because of the other issues that were since corrected. My main concern relates to the chromosome nomenclature: the chromosome numbering is not in adequation with the *Prunus* genetic map. For exemple, Chromosome 1 in all *Prunus* species is always the largest one and following Figure 1, it appears that it is chromosome 2, here. The same remark applies to the other chromosomes, not only chromosome 2 (see figure 2B, chromosome 1 of *P. salicina* should in fact be chromosome 6 in the *Prunus* genetic map, chr3 should be chr4 and so on), and that's the reason why I was recommending using, even a few, *Prunus* genetic markers, to correct this discrepancy. This major issue is coming from the first release of the *P. mume* genome in 2012 and was reproduced in the *P. armeniaca* genome presented here. If colinearity has to be displayed (Figure 3) then it should be made clear that Chr2 here should be in fact Chr 1 in the genetic map. In fact, I would once again recommend the authors to re-order their chromosomes, according to the general acknowledged genetic map. Since the genetic maps were obtained by using molecular markers which are largely colinear and syntenic in between *Prunus* species (peach, *P. mume*, apricot and plum included) I would strongly recommend to right this issue, both within the *P. salicina* assembly and the following colinearity studies with the other genomes. Since genetic maps were released before genome assembly, the authors are expected to follow the internationally acknowledged nomenclature. Reproducing forever the mistake made initially for the *P. mume* genome would severely limit the interest of this de novo assembled genome and thus the impact of its release. In conclusion, I recommend the authors to correct the numbering of the *P. salicina* chromosome all over the MS (by using a few of plum markers and even better *Prunus* orthologous markers as published in <https://doi.org/10.1371/journal.pone.0208032>, for that they only need to do a ePCR with markers depicted in Table S2F) and the data available online (and therefore Figure 3, accordingly).

Response : Thank you very much for your kindly suggestion. We further carefully read the literatures that you mentioned, and realized that the important role of the *Prunus* genetic maps was ignored in our first version of the manuscript. According to your kind advices, the numbering of the *P. salicina* pseudochromosome was corrected in the revised manuscript, using the markers that you recommended.

The present pseudochromosome numbering is consisted with that in the published *P. salicina* genetic map (Ref 77 in the revised manuscript). The *P. salicina* pseudo-chromosomes names and gene IDs in Figure 1, 3 and 4 were modified in the revised manuscript. The detailed information about the *P. salicina* pseudochromosomes in Table S5 was corrected accordingly. Moreover, we also contacted the staff of GDR (Genome Database for Rosaceae) and GenBank to update our genomic information.

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