Comments to the Author:

The article entitled “Construction of a high-density linkage map and detection of sex-specific markers in *Penaeus japonicus*” by Zhang et al. constructed a high-density genetic linkage map and identified sex QTL for kuruma prawn *P. japonicus*. This study not only provide a reference for further genome assembly and genomic selection for important economic traits, but also lay a research foundation for investigating the molecular mechanism of sex determination and differentiation of *P. japonicus,* which could provide theoretical support for unisexual breeding. The results obtained are beneficial both in theory and application. The tables are sufficiently organized, and the figures are well presented in the manuscript. Overall, the study deserves publication. However, there are still some issues needed to be corrected and clarified.

1. Line 29: “an average inter-marker distance of 0.117 cM”. However, in the text, you presented that “an average inter-locus distance of 0.123 cM” on Line 153. Please clarify which is right?

2. Line 49-52: This sentence is not related to this paper, please delete it or replace it by other contents.

3. Line 73: you used “,” in “9,289” but not in “3610.90”. Please unify them in the manuscript.

4. Line 88: “Sex was determined by observing their sexual characteristics”, this is intricate to readers who are not very professional. Please state how to distinguish the sex of *P. japonicus*. For example, you can explain them by describing, pictures of sexual characteristics, or the references.

5. Line 135-136, I am confused about this sentence “The feasibility of this pair of sex-specific primers was validated using PCR with samples from six females and six males”. I wonder which would you want to validate, primers or SNP markers? Besides, I think six males and six females are too few to validate the SNP markers. What’s more, where did these 12 individuals obtain, from the 200 offspring or from other groups? Please clarify.

6. Line 150-151: “two LGs comprising only three SNPs and nine SNPs, respectively, which are relatively too short for one chromosome, were excluded from the map”. Is it logical and reasonable to remove SNPs and delete chromosomes from the genetic map just because the SNP markers are scarce? Please give the explanation.

7. Line 160-163, you said that six SNPs on LG1 were obviously associated with the sex. However, you only presented one SNP marker in Figure 3. The sex-specific markers are very important for MAS breeding. Please show the detail information of these six SNPs, containing the genotypes of females and males and the picture of Sanger sequencing of every SNP marker.

8. Line 172-174, this sentence is repetitive and useless, please delete it.

9. Line 186-188, “9289 SNP markers” appeared twice in this sentence, please rewrite it.

10. Line 190, “average inter-locus distance was 0.12 cM”, and “0.123 cM” was presented in Line 153. Please unify them in the manuscript.

11. Line 212 and Line 215, “Jones et al., 2020b” and “Jones et al., 2020a” appeared, respectively. But I can’t find these two articles in the reference. Please clarify.

12. Line 218-220, you said “One sex locus was located, supporting that the sex of the black tiger shrimp is determined by a WZ-ZZ chromosomal system”. I wonder that this sex locus was identified by three articles? Why did you give three references in this sentence?

13. Line 220-222, please give the name of the species you described in this sentence.

14. The discussion section is illogical, chaotic and simple. I suggest the authors revising this section carefully.