Comments from editor Colum Walsh:

I have completed my evaluation of your manuscript. The reviewers recommend reconsideration of your manuscript following minor revision and modification. I invite you to resubmit your manuscript after addressing the comments below. Please resubmit your revised manuscript by Sep 01, 2022.

When revising your manuscript, please consider all issues mentioned in the reviewers' comments carefully: please outline every change made in response to their comments and provide suitable rebuttals for any comments not addressed. Please note that your revised submission may need to be re-reviewed.

Genomics values your contribution and I look forward to receiving your revised manuscript.

*Author response: Dear Editor Walsh. We appreciate the insightful comments from you and the reviewers and have done our best to address them all in the revised version. Please, find an updated version of the manuscript in the submission portal where all changes have been highlighted for straightforward re-evaluation.*

Reviewer comments:

Reviewer #1: The work by Shipilina et al on a recombination map for a butterfly species was a very well written and articulated the need and results of the research, and the results track previous work in Lepidoptera.

*Author response: We appreciate the overall positive notes on the manuscript and are grateful for the comments. The manuscript improved considerably after taking the comments into account.*

The manuscript would benefit from reworking part of the introduction so the ideas flow better for the generalist audience of Genomics: the second and third paragraphs can be shortened (even though the writing is very high quality) as the purpose of the manuscript is not to educate the reader on the evolutionary significance of gene duplications and TEs but to introduce the research results. Whilst this would replace a couple of the longer sentences in each paragraph, the text savings replaced with knowledge that will help the reader understand why the presented results are important such as value of discussing the TE and gene families. For example, my understanding from the manuscript's results was that the value of TEs here is mainly as markers rather than biological entities: undertaking an analysis of TE evolution across butterflies would be a completely separate endeavour but that's what I thought I was going to learn after reading the introduction!

*Author response: Thank you for the suggestion. The introduction has now been edited to better fit the scope of the journal and the audience. Specifically, the second and third paragraphs have been shortened as suggested and we now focus more on the relevance of the TE annotation and gene duplication analysis in general. Restructured sentences are highlighted in green.*

Further, explaining the holocentric nature of Lepidopteran chromosomes in the introduction would be vital for the reader to understand the constraints butterfly chromosomes face. Indeed, the first part of the results confirms this hypothesis and it would be valuable to the reader to know that these hypotheses have been voiced and are being explored (here and in previous work).

*Author response: We have now added a paragraph outlining the specifics of holocentricity and how that feature can affect genome evolution in general and recombination rate variation in particular. Section starting from “Such spatial variation…”.*

I think the results are very robust but I wonder why GO terms were used to limit the subset (I am not a fan of the approach for non-models generally). One approach is to use sonic inParanoid to do a all vs all proteome comparison and identify gene family expansions regardless of GO terms. Given the results presented, if a grouping classification was necessary, I find the Enzyme classifications more robust as they are less prone to misclassications. However, I would not expect the authors to redo their analyses at this stage, merely to consider it and mention the issue of using GO as a nomenclature rather than a rough grouping.

*Author response: We agree with the reviewer, that using functional annotation for non-model organisms should be interpreted with caution. However, since the GO-term analysis was performed after orthogroup assignment with OrthoFinder, following evolutionary rate estimations with BadiRate, we think we avoided some of the potential biases. Additionally, we curated gene families using domain annotation (InterProScan) before evaluating enriched GO terms. We are also grateful for the suggestion to use the SonicParanoid suite and will consider it for potential future projects (Cosentino, Iwasaki, 2019).*

I'm glad to see the data to be made publicly available.

Minor comments

Placing - and discussing - both of the sex chromosomes in their own section before Gene Family Analysis would help those of us interested in the topic. I would appreciate a line in the discussion highlighting the difficulty of sequencing the W so that the reader is aware.

*Author response: The structure of the discussion has been changed accordingly. We have also added a short piece of text in the discussion where we address the problems with sequencing and assembling highly repetitive sex-limited chromosomes. It can be found in the beginning of the new “Sex-chromosome” section.*

I was not familiar with the argumentation in the sentence "The absence of SINEs on the ...". Is there any support that SINEs hijack replication machinery but either LTRs are more inefficient or the correlation is watered down by the other parts of their biology?

*Author response: Thank you for the feedback. We have now reformulated the section a bit to make our argumentation clearer. The hypothesis that SINEs may hijack the recombination process comes from our observation that the non-recombining W-chromosome has a very low density of SINEs. This is also supported by studies of Alu elements in human (cited in main text; Batzer, M., and Deininger, P. 2002. “Alu repeats and human genomic diversity”. Nat. Rev. Genet. 3, 370–379).*

Please consider

- "General" after discussion is not needed but other subheadings are needed as the info was quite packed.

*Author response: The discussion has now been broken up in smaller sections with sub-headers, as suggested.*

- changing "Additional curation" -> "manual curation"

*Author response: Changed accordingly.*

Reviewer #2: This is a fine piece of genome analysis work. The methodology is state of the art, and the results add considerably to lepidoptera genomics in general and to the painted lady in particular.

Initially I was a bit surprised that the authors based their work on a previously sequenced genome (Lohse et al., 2021), but that publication is basically a genome announcement. The current work goes well beyond a simple reannotation.

*Author response: Thank you. We are grateful for the very positive review of the manuscript.*