Reviewer Report

Title: A chromosome-level genome assembly and annotation of the desert horned lizard, Phrynosoma platyrhinos, provides insight into chromosomal rearrangements among reptiles

Version: Revision 1 **Date:** 10/14/2021

Reviewer name: Tonia Schwartz

Reviewer Comments to Author:

The authors have done a good job with the revision. I only have a few points that I would like to emphasize and suggest they address further.

1. In comparison to BUSCO results from other recent squamate genomes (see Figure 2d in https://www.biorxiv.org/content/10.1101/2021.09.28.462146v1.full for a comparison) the BUSCO results from this genome assembly suggest it is not considerably high quality assembly (relatively). The 16% missing and only 64% complete BUSCOs suggest this assembly is relatively incomplete and is a lower quality assembly (more fragmented) than many of the other squamate genomes. This should be explained and discussed in the text, particularly in how this may affect their conclusions about defining the microchromosomes, their synteny analysis, and their pathway analysis.
2. It should be further emphasized throughout that the microchromosome naming designations are putative (and very possibly may not correspond to the karyotype) due to (1) the incomplete nature of the assembly, (2) the splitting of scaffolds into microchromosomes based on bioinformatic predictions, (3) and their naming based on length when some of their lengths are very similar (many less then 200,000 bp difference, Table S1).
3. Line 181, I think you are missing a number for the upper limit. To define the 14 scaffolds that are > 6mb and < #?
4. Line 193, I think 'm' is supposed to be a number here.

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