Reviewer Report

Title: The complexity landscape of viral genomes

Version: Revision 1 **Date:** 6/6/2022

Reviewer name: Anne Kupczok

Reviewer Comments to Author:

I thank the authors for taking all my comments into consideration. Unfortunately I find that only a subset of them are addressed in the current version of the manuscript. My main concern is that the main point of the manuscript is not clearly elaborated in the paper. The abstract, Key points, and the main message in the Results and Discussion should be consistent.

1. I previously noted that the paper is very narrative and contains too many background details. As I do not have a version with tracked changes, I do not see if it has been shortened as some points. However, I notice that it still contains textbook knowledge, e.g., in the "Viruses Microbiology" section. I understand that this is an interdisciplinary manuscript, but in this case, reviews or textbooks can be cited for the relevant knowledge, but they do not need to be repeated in the manuscript.
2. For the "Synthetic sequence benchmark" a repeat length of 5,000 has been simulated. Why has this length been chosen, is it representative of inverted repeats in viruses?
3. In the answers, the authors wrote "One of the main goals of our manuscript was to identify and quantify inverted repeats abundance in viral genomes." However this goes is not mentioned under "Key Points" and is also only a minor point in the abstract. It would help the readers of the manuscript if the main goals of the manuscript were clearly described in the abstract and in the "Key points".
4. I previously suggested to analyze the relationship of sequence length and complexity, which would contribute to the first key point ("We provide a comprehensive landscape of the viral genomes complexity"). Although it is possible to browse all this information, this relationship could be more described in the paper.

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