The authors have effectively addressed the previous concerns. I have only a few minor concerns to raise.

Minor comments:

I commend the authors on their efforts towards ensuring data reproducibility. However, I suggest depositing the scripts in the Dryad repository or GitHub, and setting the raw sequences in some SRA project from NCBI to enhance data availability.

Regarding Figure 5, I appreciate the authors' utilization of NMDS, but it lacks results on the ANOSIM test. It is important to note that ANOSIM demonstrated significant dissimilarity differences between the Forest and Windwall groups.

In line 189, I recommend replacing "Library preparation" with "Library indexing." Although the indexing of each library using the Nextera XT kit primers (PCR2) was conducted by the company, you were responsible for the initial library preparation. Therefore, I suggest making a change in line 174 to include "For metabarcoding library preparation,..." before "We amplified a 313-base pair."