We thank the reviewers for their reading of our manuscript and suggestions for improving the clarity and detail. Below, please find our response to the reviewers' comments. We believe we have addressed their concerns and improved the manuscript.

Reviewer #1 (Comments for the Author (Required)):

The authors present a potentially valuable resource. Sequencing reads and assemblies are publicly available.

I suggest the following modifications or clarifications in the manuscript to be considered for publication, while staying near the 500 word count limit:

- Data availability/Table 1: Some of the accession numbers/read counts are mixed up. Please go through every column on each row to ensure the values across columns in this table are correct
We have checked every accession number with the assigned reads in the table. Somehow our read counts with sample numbers 2, 22, 207, 214, 237, 262, 283, and 298 were mixed up during submission to the SRA. We have corrected these errors so the read counts and accession numbers should now be accurate for all samples.

- Please indicate which bead-beater was used and the parameters of the bead-beating step (# cycles, time on/off, speed)
We have added this information to L40-41.

- L49: Please indicate trim/filter parameters such as MaxEE, as well as merging parameters, else state default parameters were used.
This has been corrected to state that default parameters were used (L50).

- L54: Please note which statistical analyses were performed (thinking because some take dispersion into account for beta-diversity, for example).
We have clarified in this sentence which alpha and beta diversity metrics were used (L55-56).

Reviewer #2 (Comments for the Author (Required)):

The authors present a 16S rRNA gene amplicon sequencing (V4 region) of the microbiota from preen oil and the cloaca of chipping sparrows.

I suggest including the statement, "Default parameters were used except where otherwise noted," especially when describing the use of DADA2. They specified the modifications in the trimming and truncation parameters, but it would be helpful to clarify that the parameters were the default for denoising and chimera removal.

We have clarified that default parameters were used unless otherwise specified (L50).

Despite having listed all the sequence read archives, the counts in Table 1 are mixed up. This needs to be addressed and edited.
We have checked every accession number with the assigned reads in the table. Somehow our read counts with sample numbers 2, 22, 207, 214, 237, 262, 283, and 298 were mixed up during submission to the SRA. We have corrected these errors so the read counts and accession numbers should now be accurate for all samples.