Reviewer Report

Title: Whole-genome resequencing reveals signatures of selection and timing of duck domestication

Version: Original Submission **Date:** 11 Dec 2017

Reviewer name: Philip Lavretsky

Reviewer Comments to Author:

Zhang et al. sequenced whole genomes of 78 individuals of domesticated and wild mallard populations. The authors find a complex history of domestication, with particular artificial selection of meat and egg production in domesticated lineages. Further, outlier analyses demonstrate that white plumage was the result of selection of MITF transcriptional factors. I believe that the authors are tackling an important question regarding variation between domesticates and wild populations, and with an extensive genomic dataset. However, I think the authors fall short in introducing the subject and discussing their results. Moreover, the manuscript requires editing prior to publication, particularly the introduction.

Introduction
The introduction requires extensive editing. I would also encourage the authors to add another sentence as the relevance (the why) of looking for outliers between domesticated and wild stocks. What exactly are you trying to learn? Instead of results, I would like to see hypotheses regarding what the authors may expect when comparing the genomes of domesticated and wild populations. I think the

The whole first paragraph requires editing.
For example -- Line 50-52: Suggest change sentence to: "Mallards (Anas platyrhynchos) are the world's most widely distributed and agriculturally important waterfowl species, and are especially of economic importance in Asia [1]."

Results
1. Line 79 - is this 535 billion mappable reads per sample or across samples?
2. Lines 115-121- how did the authors pick the optimum K in FRAPPE analyses? Did the authors explore additional K values? Where separate analyses done within wild and domesticated populations? Please explain.
2a. What do the authors make of domesticated admixture in wild populations? Is this hybridization, ancestry, a combination of both…? I would encourage the authors to explore this further as hybridization between domesticated and wild breeds is a serious concern for conservation of wild populations.
2b. The PCA analyses seem to suggest that there is structure within wild populations. Running a FRAPPE analyses on wild populations could help tease out whether they are 1 population and PCA analyses are just separating samples as there is so much variation.
3. Lines 139-141 - consider revising the sentence into a more formal hypothesis. I would also like to see such hypotheses in the introduction.

4. Outside of outlier tests by calculating FST, the authors should consider more formal testing of these putative outliers (e.g., BayeScan).
5. Although I like the idea of RNA-seq data here. I think that this is largely overlooked in the manuscript and may detract from the main (genome) focus. I would encourage the authors to consider taking the RNA-seq out or sufficiently expanding on methods, reasoning, etc. of the RNA-seq data.
6. I would like to see global Fst estimates among breeds, wild locations

Discussion

I have no issues with the discussion and find it the best written. I think that a section on domesticate and wild hybridization may broaden the appeal of this paper.

Methods

Please add additional information regarding FRAPPE analyses, K selection,etc.

Figures

Figure 1: Consider re-moving statistical tests as these are presented in the results.

Methods

Are the methods appropriate to the aims of the study, are they well described, and are necessary controls included? Yes

Conclusions

Are the conclusions adequately supported by the data shown? Yes

Reporting Standards

Does the manuscript adhere to the journal's guidelines on minimum standards of reporting? Yes

Statistics

Are you able to assess all statistics in the manuscript, including the appropriateness of statistical tests used? Yes, and I have assessed the statistics in my report.

Quality of Written English

Please indicate the quality of language in the manuscript: Not suitable for publication unless extensively edited

Declaration of Competing Interests

Please complete a declaration of competing interests, considering the following questions:

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Yes