

## Reviewer Report

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

**Version:** Revision 1      **Date:** 06 Feb 2018

**Reviewer name:** Martin Johnsson

### Reviewer Comments to Author:

In my opinion, this revision adequately answers most of my comments. The manuscript has also improved with the answers to the other reviewer.

I have only a few remaining comments. The most serious one is about data availability and protocols.

The revision comes with better data availability. VCF files of variants are included, plus a couple of perl scripts used to process them. However, full population genetic statistics and sweep locations still seem to be missing. Scripts for running the bioinformatic tools are not included. The description of the PCR follow-up of variants has been expanded. However, the description does not include the full protocol, and neither does the description of any of the other laboratory methods. This level of detail is about the standard in the field, but it does not seem to live up to the policies of the journal.

A couple of times (the justification for the mix of sequence coverages, and the detail about the origin of the ducks), the reply to reviewers contain useful information that was not incorporated in the manuscript. In my opinion, the Methods should include this information, and in particular as much detail as possible about the origin of the animals.

### Minor comments

The reply to reviewers describe the variant filtering as "extremely strict". In fact, it seems to be mostly the default starting criteria suggested by GATK developers in their "best practices" (with a "QUAL" cutoff and a higher "QD" cutoff). How were these filter settings chosen? Are they actually "extremely strict"?

Line 247: What does "completely associated with selection" mean in this context?

Lines 252-253: In what sense did the PCR primer design fail? Were you unable to amplify the region, amplify specifically, or unable to find primers that lived up to your quality criteria? I fully understand that PCR primer design fails occasionally, but I think a more specific description would be useful.

## **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](#)? No

## **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: Acceptable

## **Declaration of Competing Interests**

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

- Have you in the past five years received reimbursements, fees, funding, or salary from an organisation that may in any way gain or lose financially from the publication of this manuscript, either now or in the future?
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Yes