#### **Reviewer Report**

### Title: An improved pig reference genome sequence to enable pig genetics and genomics research

Version: Original Submission Date: 12/15/2019

Reviewer name: Shanlin Liu

#### **Reviewer Comments to Author:**

The authors present us with two high-quality genome assemblies for the pig. In addition to the regular assembly procedure to obtain the two assemblies, they have made great efforts to check the accuracies of both using lots of other datasets, including FISH, radiation hybrid map, BAC clones. I only have several minor concerns as follows:

The authors annotated both the genomes using full-length transcriptome data from a single individual. I wonder whether you have any specific filtering step to avoid incorrect annotations, as the differential expression (both expression level and alternative splicing) may contribute to their phenotypic variances. Line 180 - 190, the authors may want to explain more on the definition of low quality and low coverage regions, e.g. What're your criteria? Besides, please provide statistics of GC content for those remaining LQLC regions to show your points of view better.

For the assembly of USMARC, the authors mentioned that "The resulting assemblies were compared and the Celera Assembler result was selected based on better agreement with a Dovetail ChicagoÂ<sup>®</sup> library," it is better to explain more on your definition for the "better agreement".

Line 235 - 245, identify heterozygous structure variances using long reads can check whether the incongruencies between the v11.1 and v10.2 derived from innate differences between two haploids.

#### Methods

Are the methods appropriate to the aims of the study, are they well described, and are necessary controls included? Choose an item.

### Conclusions

Are the conclusions adequately supported by the data shown? Choose an item.

### **Reporting Standards**

Does the manuscript adhere to the journal's guidelines on <u>minimum standards of reporting</u>? Choose an item.

Choose an item.

#### **Statistics**

Are you able to assess all statistics in the manuscript, including the appropriateness of statistical tests used? Choose an item.

# **Quality of Written English**

Please indicate the quality of language in the manuscript: Choose an item.

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