

## Reviewer Report

**Title:** "Genomic data for 78 chickens from 14 populations"

**Version:** Revision 2      **Date:** 1/27/2017

**Reviewer name:** Martien Groenen

### Reviewer Comments to Author:

In the revised manuscript the authors have sufficiently addressed most of my earlier comments. The only problem I still have is in the choice of the clustering (1-3) as suggested by the authors. In particular the grouping of the animals in cluster two seems odd when one looks at the result of the PCA analyses. I think it would make more sense to split cluster 2 into two clusters. The first dimension of a PCA represents the largest difference seen between the individuals and cluster 2 actually consists of two clusters (2L and 2R) that are equally distant to each other as 2R is to cluster 3. I fail to see the arguments why the authors still group all of these into a single cluster.

A few minor comments:

the term overlapped SNPs seems a bit odd. I suggest to refer to these as "known SNPs". The contrast known vs novel seems more appropriate.

Line 144: (at least in an individual) replace "an" by "one"

I am confused by the "normalized depth" in line 145 (median of normalized depth of 1.14 versus 1.06). The authors state that the novel SNPs also exhibited a comparable sequencing depth with the overlapped SNPs (median of normalized depth of 1.14 versus 1.06). I probably misunderstand this term but could the authors explain what this means (given that the average sequencing depth is 18).

### Level of Interest

Please indicate how interesting you found the manuscript: An article whose findings are important to those with closely related research interests

### Quality of Written English

Please indicate the quality of language in the manuscript: Needs some language corrections before being published

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