Reviewer's report

Title: Impacts of Incorporating Personal Genome Sequencing into Graduate Genomics Education: A Longitudinal Study Over Three Course Years

Version: 0 Date: 27 Aug 2017

Reviewer: Philip Empey

Reviewer's report:

Thank you for your paper describing your longitudinal study of the PAPG course. This is interesting work reporting outcomes from the use of personal whole genome sequencing in genomics education for a multi-year cohort of medical and allied health students. After reviewing your manuscript, I have some minor comments described below.

1. Consider discussing more about how much knowledge those in the "IHGS only" group had about the availability of testing. i.e. did they know that if they were part of the PAPG course that they would be able to undergo testing? This may help to better characterize the comparator "ineligible" group.

2. Interpretation of the findings in context of data from similar implementations of classroom participatory genomics education experiences should be incorporated. There are also several integrations of genomic testing in the classroom that reported student perceptions, confidence, engagement, and some outcomes for comparison (e.g. PMID: 27756930, PMID: 26941429, PMID: 27551265, Surofchy et al. Innovations Pharm. 2017;8(1):2., among others). How are the current findings similar? Inconsistent?

3. It is interesting that students themselves were provided a means to incorporate individual exclusions in their analysis. Additional detail beyond the just the % of students that elected to do this would be useful -- both to understand how this was practically accomplished (whether it is can be interpreted as metric of student concern regarding particular types of data) and when done, what regions were excluded (if these data are available).

4. Figures 1-3 are difficult to read. This potentially could be remedied by 1) adjusting the weights of error bars, 2) adjusting the y axis, 3) using another measure of central tendency for ordinal data (e.g. median +/- IQR), which is often favorable to mean +/-
95% CI for ordinal data. As is, the overlap makes it difficult to visualize the data as intended.

5. Clarify legend on Figure 3: Ref Vs Own. Reconciling the "Year" and "Sequence Own Genome" legends is also a bit confusing - though I understand the intention.

6. Suggest including Figure S1 in the main manuscript versus in supplemental information.

**Are the methods appropriate and well described?**
If not, please specify what is required in your comments to the authors.

Yes

**Does the work include the necessary controls?**
If not, please specify which controls are required in your comments to the authors.

Yes

**Are the conclusions drawn adequately supported by the data shown?**
If not, please explain in your comments to the authors.

Yes

**Are you able to assess any statistics in the manuscript or would you recommend an additional statistical review?**
If an additional statistical review is recommended, please specify what aspects require further assessment in your comments to the editors.

I am able to assess the statistics

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