

Improving transcriptome assembly through error correction of high-throughput sequence reads

Matthew D MacManes^{1*} and Michael B. Eisen^{1,2}

1 UC Berkeley. California Institute of Quantitative Biology, Berkeley, CA, USA

2 Howard Hughes Medical Institute

* Corresponding author: macmanes@gmail.com, Twitter: [@PeroMHC](https://twitter.com/PeroMHC)

Response to Editor Comments

Please find the attached paper, which is a revision of manuscript number 2013:04:462:0:0. The manuscript has undergone the recommended changes, except what has been noted below.

Best, Matt MacManes

1. About centralizing data and resources.

This

2. The dashes have been removed.

3. There are 2 supplementary figures, or at least I hope there are.. I did upload as such.

I am happy to make them part of the main document, but I figured that 7 figures for a short MS is too much, and these are important only in that they characterize the simulated datasets, but do speak to findings.

4. I have moved the fastQ files to Dryad. Link included in paper

5. I added some text about what made Reptile laborious. In the not included README file, some instructions about how to select parameters if included. Still the best resource for this is the Reptile paper and download.

6. I moved all the 'gist' scripts to a single folder on github, thus centralizing all those resources.