Reviewer's report

Title: AGOUTI: improving genome assembly and annotation using transcriptome data

Version: 1 **Date:** 01 May 2016

Reviewer: Pär Engström

Reviewer's report:

I only have a few comments on the revised version:

1. It should be indicated which assembly was used as "truth" in the evaluation on real data (N2/CB), e.g. to compute the error counts for Table 3.

2. I think the following statement, which occurs both in the abstract and main text, could be misleading: "genomes sequenced using short-read, next-generation sequencing technologies are error-filled and fragmented into thousands of small sequences". The term "error-filled" is imprecise and could lead readers to think that sequences are so filled with errors that they are nearly useless, which is certainly not the case. For small genomes the number of contigs can be much less than 1000, so "thousands" should also be changed.

3. Another reason for the worse performance on real data (page 12) could be that actual breakpoints are more common in intergenic regions, e.g. due to enrichment of repeats in those regions. This could easily be checked.

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