Reviewer Report

Title: "Draft genome of the sea cucumber Apostichopus japonicus and genetic polymorphism among color variants"

Version: Original Submission **Date:** 9/22/2016

Reviewer name: Kim Worley

Reviewer Comments to Author:

The genome assembly is listed as 0.67 Gb. The Assemblathon statistics run on the assembly file indicates that the total scaffold size 0.66 Gb and the number of scaffolds is 132,497 (both numbers are similar to the numbers reported in the manuscript). But there are 102,722 contigs in scaffolds and 164,958 contigs greater than 1kb, also according to those statistics. Which sequences were used to calculate the completeness statistics - was it with or without the unscaffolded contigs? Did it include the small contigs (20,922 total <1kb)? Please make it clear the N50 statistics refer to scaffold N50 numbers and also give the contig N50 numbers if the unscaffolded contigs continue to be included in the assembly files. Also, note if the CEGMA and BUSCO analyses are based upon the assembly as in the files or on the scaffolds only.The genome assembly should be submitted to the International Nucleotide Sequence Databases (DDBJ/NCBI/EMBL).

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: Acceptable

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