Reviewer Report

Title: Chromosome-level genome assemblies of the malaria vectors Anopheles coluzzii and Anopheles arabiensis

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Reviewer name: Jacob Tennessen

Reviewer Comments to Author:

This is a comprehensive description of two new genome assemblies for the important vector species Anopheles coluzzii and Anopheles arabiensis. I have no doubt that these assemblies will be useful to the field. The A. gambiae species complex is unusually diverse and shows complicated patterns of introgression, chromosomal rearrangements, and barriers to gene flow. These Nanopore/Hi-C assemblies will clarify many of these diversity patterns. It is likely that many other third-generation sequencing assemblies will soon be available for Anopheles (e.g. the authors mention the PacBio assembly from A. coluzzii Ngousso), but few have been released yet, and in any case the diversity of these species means that the genomes will not be redundant. Here, the authors have thoroughly assessed the data and compared the genomes to each other and to the A. gambiae genome which is the standard reference for this genus. The methods are robust and well documented.
"Genomics analyses" should be "Genomic analyses"
"scaffold N50s are 99.9 and 95.7" The units here are clearly Mbp but still this should be specifically stated.

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