Reviewer Report

Title: "A high-coverage draft genome of the mycalesine butterfly Bicyclus anynana"

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Reviewer name: Evgeny Zdobnov

Reviewer Comments to Author:

Nowell et al present their manuscript describing the generation of a high-coverage and relatively high-quality draft genome of the butterfly, Bicyclus anynana. The sequencing data included both Illumina and PacBio, which were combined (also transcriptome data) to build the assembly, with appropriate contaminant filtering steps. Genome annotation produced a larger-than-average gene set, but the retained models do appear to be well supported. The data and methods descriptions are clear and concise, and the supporting evidence is convincing. I agree that this draft genome sequence for B. anynana will serve as a key genomics resource for current and future studies of this important model species.Minor points:P9, line 160: 'smaller than the longest', perhaps 'smaller than the largest' or 'shorter than the longest'P9, line 164: 'that' => 'than'P13, line 247: 'divergent', perhaps 'different' Table 5: please check - it seems that there are fewer CDSs than genes for Hmel2 and MelCinx1.0, unless I have misunderstood this could be an error as protein-coding genes can have one or more CDS, so surely the numbers of CDSs should always be greater than or equal to the number of (protein-coding) genes?

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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