Reviewer Report

Title: A new mass spectral library for high-coverage and reproducible analysis of the Plasmodium falciparum-infected red blood cell proteome

Version: Original Submission **Date:** 9/21/2021

Reviewer name: Guenther Kahlert

Reviewer Comments to Author:

Siddiqui et al presents new DIA repository library of Plasmodium falciparum in this manuscript, created on-the-fly without using synthetic peptides but solely using the parasitic asexual red blood cell stages. The aim of this survey study is achieved by the authors, covering 87% of the P. falciparum proteome using DDA mass spectrometry to create the presented DIA spectral library.
The by the authors presented DIA spectral library was created by elaborately purifying the parasite. Using their Orbitrap, MaxQuant, and Spectonaut pipeline has lead to a solid, reliable spectral library. And using mutants added biological reliability.
The only thing that the authors did not take into account in the introduction and the discussion is that there are different types of mass spectrometers and their fragmentation pattern has to be noted. DIA methods were first introduced for TOF instruments and using Orbitrap mass spectrometers provides different challenges in fragmentation and dwell times.
Please add more in detail information about this topic to the manuscript.
The statistics and the plots of this manuscript are well done and adequate to the survey. I especially value the volcano plots and the heat maps that show the difference between the red blood cell stages of of the parasite.

Methods

Are the methods appropriate to the aims of the study, are they well described, and are necessary controls included? Choose an item.

Conclusions

Are the conclusions adequately supported by the data shown? Choose an item.

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Statistics

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