

## Reviewer Report

**Title: Developing best practices for genotyping-by-sequencing analysis in the construction of linkage maps**

**Version: Revision 1**      **Date: 8/9/2023**

**Reviewer name: Ramil Mauleon**

### Reviewer Comments to Author:

I'm satisfied with your responses to my comments, thanks for addressing this and congratulations to your team for building this workflow. The major re-write you did on focusing on the software components of the workflow made it an easier read for me, as a bioinformatician. My minor comment is still on the title of your paper, "Developing best practices for genotyping-by-sequencing analysis using linkage maps as benchmarks". Your paper primarily presents the application of Reads2map in the construction of genetic linkage map(s). As I've mentioned, I come from a team where GBS is also extensively applied for population diversity analysis, which means constructing genetic linkage maps is not an endpoint target, and the only benefit from Reads2map for population diversity analysis is the automation of SNP calling using several methods (thanks for adding the other methods, by the way), which you mentioned very briefly when you addressed my comment on this. The title of your paper is also a bit confusing since the use of GBS in population genetic applications cannot be benchmarked by linkage map construction, for obvious reasons. I'd suggest a straightforward title like "Developing best practices for genotyping-by-sequencing analysis in the construction of linkage maps" or something like this..

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