Reviewer Report

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

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Reviewer Comments to Author:

In this MS, the authors tried to develop a framework for using GBS data for downstream analysis and reduce the impact of sequence errors caused by GBS. However, sequence error is an issue not specific to GBS, it is also for whole genome sequences. Actually, I think the major issue for GBS is the missing data. However, in this MS, the authors did not test the impact of missing data on downstream analysis.The authors also mentioned that sequencing error may cause distortion segregation in linkage map construction, however, distortion segregation in linkage map construction can also happen for correct genotyping data. The distortion segregation can be caused by individual selection during the construction of the population. So I don't think it is correct to use distortion segregation to correct sequence errors.The authors need to clear the major question of this MS, in the abstract, the authors highlight the sequence errors, while in the introduction, the authors highlight the package for linkage map construction (the last paragraph). Actually, from the MS, authors were assembling a framework for genotyping-by-sequencing data.Two major reduced-represented sequencing approaches, GBS and RADseq, have specific tools for genotype calling, such as Tassel and Stack. However, the authors used the GATK and Freebayes pipeline for variant calling, authors need to present the reason they were not using TASSEL and Stack.In the genotyping-by-sequencing data, individuals were barcoded and mixed during sequencing, what package/code was used to split the individuals (demultiplex) from the fastq for GATK and Freebayes pipeline?The maximum missing data was allowed at 25% for markers data, how about for the individual missing rate?On page 6, the authors mentioned 'seuqnece size of 350', what that means?

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