Reviewer Report

Title: Genome-wide analysis of the H3K27me3 epigenome and transcriptome in Brassica rapa

Version: Original Submission **Date:** 9/1/2019

Reviewer name: Jingyu Zhang

Reviewer Comments to Author:

In this MS, the author demonstrates the profile of H3K27me3 in different organ of Brassica rapa, and uncover its role in plant development with mutant analysis. Though the analysis of H3K27me3 has been done in B. rapa before, it focused only on specific region (Genes Genet Syst. 2016, 91:1-10). This study provides a genomic-wide view of this type of histone modification, enable us to get a comprehensive understanding of its function.

There are also some suggestions listed as below:

1. For high-throughput data, three independent biological repeats are required. Although the author demonstrates the reproducibility of the Epigenomic Analysis pipeline, please make it clear whether the replicate tests has been performed to ensure the accuracy of the results.
2. The H3K27me3 modification analysis has been done in both leaves and inflorescences. The Chip-seq data for inflorescences also deserves a figure to show its details.
3. For figure 5, the mutant and the wild type are in different pictures with different bars. If they are in the same picture, it would be much easier for the comparison. At least their bars should be the same.

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.

Reporting Standards

Does the manuscript adhere to the journal's guidelines on minimum standards of reporting? Choose an item.

Choose an item.

Statistics

Are you able to assess all statistics in the manuscript, including the appropriateness of statistical tests used? Choose an item.

Quality of Written English

Please indicate the quality of language in the manuscript: Choose an item.

Declaration of Competing Interests

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