**Reviewer Report**

**Title: rCASC: reproducible Classification Analysis of Single Cell sequencing data**

**Version: Revision 2** **Date:** 7/25/2019

**Reviewer name: Olivier Poirion, Ph.D.**

**Reviewer Comments to Author:**

The authors incorporated additional clustering methods (Scanpy and Griphz) that prove to be scalable for datasets having larger sizes which corresponds to the field needs.
In particular, Scanpy seems to reveal no issue to scale up to 100K cells in the benchmark executed opposite to the other methods.
I recommend accepting this manuscript since I think it is well suited for current and future analytical needs for single cells.
Minor comments: Is there any limitation or trick to use for the preprocessing procedures (low cell quality filter, normalization, annotation, cell cycle removal, matrix creation) executed before the clustering when increasing the sample / feature size?
I presume no because the authors have used them with large dataset. Then, It will be worth metning that in the manuscript with a brief estimate of the computational time / memory needed.
The figure 3 is not updated with Scanpy and griph.
I don't understand the use of the term hierarchical clustering in the manuscript and in the suppl. material.

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