Reviewer’s report

Title: CVE: an R package for interactive variant prioritisation in precision oncology

Version: 0 Date: 27 Dec 2016

Reviewer: Hua Zhong

Reviewer's report:

This manuscript developed an interactive R package Cancer Variant Explorer (CVE). It integrated multiple analyses of SNV functional annotation, tumor-specific pathway/co-expression module mapping and the druggability assessment to help narrow down and/or find out tumor-driven genes from high-throughput sequencing datasets. Importantly, the tool provides interactive and flexible features so that more researchers will be able to use it independently. The manuscript used melanomas to demonstrate the tool's functionality well. The manuscript is well written, and will be of interest to most cancer researchers.

Are the methods appropriate and well described?
If not, please specify what is required in your comments to the authors.

Yes

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Yes

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