Reviewer Report

Title: CNVpytor: a tool for CNV detection and analysis from read depth and allele imbalance in whole genome sequencing

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Reviewer Comments to Author:

In the manuscript, entitled "CNVpytor: a tool for CNV/CNA detection and analysis from read depth and alle imbalance in whole genome sequencing", Suvakov et al., present an extension of CNVnator, a popular CNV caller they previously developed, in Python with significant calculating speed improvement and a newly implemented CNV detection algorithm based on B-allele frequency. Although the current development is based on the original CNVnator, I think the new development in CNVpytor is certainly significant and important. This is not only because of the significant performance improvement and new features in the CNVpytor as pointed out already by the authors, but also because, in my opinion, it is important to re-engineer the classical bioinformatic tools, e.g., CNVnator (developed 10 years ago), with up-to-date programming languages and trim them to work efficiently under modern computational hardware and OS environment. This will save substantial amount of time and effort for their users, and therefore, be significantly useful to the field of research.I have two minor suggestions:1. What is the resolution of CNVpytor for detecting CNAs? This information would be very useful for its users. I suggest the authors at least can provide a comment on the maximum resolution that they recommend. 2. What is the minimum sequencing depth required by CNVpytor, and can it be applied to other types of DNA sequencing data, e.g., whole-exome sequencing? Same as the above, I think these information may also be very useful.

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