Reviewer's report

Title: Measurement of absolute copy number variation reveals association with essential hypertension

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Reviewer: Alexandre Stewart

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The manuscript by Marques et al., “Measurement of absolute copy number variation reveals association with essential hypertension”, is of interest to the readership of BMC Molecular Genomics. In this manuscript the authors used a technique of droplet digital PCR to quantify copy number variants in the vicinity of genes previously identified by GWAS to associate with blood pressure using a sample of phenotypic extreme cases and controls.

The question posted by the authors is well defined and the methods are appropriate and well described. The data seem straightforward and relatively sound.

Major concerns

In addition to providing blood pressures after “adjustment” using some factor to account for antihypertensive medication in their extreme cases of hypertension, the authors should provide actual blood pressure measurements before and after initiation of medication (where possible) or actual blood pressure measurements even on antihypertensive meds. Also, the nomenclature for copy number variants seems outdated. The authors must provide genomic landmark (start and end of CNV and chromosome number) and preferably should use the esv or essv identifiers so that readers can readily refer to their sequences in the genome browser.

Minor revisions: none

Otherwise the manuscript adheres to the relevant standards for reporting and data deposition. The discussion is fine and the limitations are clearly stated. The authors acknowledge work upon which their study builds and the title and abstract appropriately reflect the content.

Level of interest: An article of importance in its field

Quality of written English: Acceptable

Statistical review: Yes, but I do not feel adequately qualified to assess the statistics.

Declaration of competing interests:
I declare that I have no competing interests