Reviewer's report

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

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Reviewer: Xiangyin Kong

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Major Compulsory Revisions
The authors used a new approach named ddPCR to validate the CNVs overlapped with significant genomic regions, which associated with blood pressure in previous GWA studies in two groups of extreme phenotype patients. They identified a deletion of the CNVs 3306 and 64617 were significantly more prevalent in extreme high BP subjects. The results presented here are reasonable and will be a reference for CNVs quantitation.

However, here I have two suggestions:
1. The author selected the CNVs, which overlapped with the reported significant genomic regions using DGV database. However, the boundaries of CNVs may be quite different from the real variant for the method of CNV detecting, which means the overlap between a CNV and a gene may not be accurate. So here I suggest the author consider the CNVs nearby the candidate genomic regions. Moreover, the author mentioned that some genes do not map within the candidate CNV (i.e. CNV 4094) in the newest human genome browser (GRCh37/hg19). Therefore the authors need to use hg19 to annotate the CNVs and genome regions in the selection process.
2. It needs to use some other method to quantify the relative quantity of CNVs as control.

Level of interest: An article of limited interest

Quality of written English: Acceptable

Statistical review: No, the manuscript does not need to be seen by a statistician.

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