# Document details





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## Copy number variation of CNVesv27061 analysis among young adults with high blood pressure using optimized droplet digital polymerase chain reaction (ddPCR) method (Conference Paper)

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### Abstract

Several reports and databases on genomic variants have associated variation in DNA sequences (≥ 1kb), or copy number variation (CNV), with susceptibility to common diseases. However, very few reports are found on hypertension and no study has been reported on CNV in prehypertensive and hypertensive young adult Malaysians. In this comparative cross-sectional study, 133 young adults were recruited, comprising of normotensive (45 subjects), prehypertensive (40 subjects) and mild hypertensive (48 subjects) subjects. DNA for CNV determination was extracted from 3 ml of blood samples collected. CNV esv27061 was analysed using optimized droplet digital polymerase chain reaction (ddPCR) method which has enhanced sensitivity and precision. Frequency distribution patterns of CNV among mild hypertensives showed highest peak copy-number-gain (number of copies more than 2) particularly in copy numbers 3 and 5. The prehypertensive subjects exhibited marked increase in copy number 5 when compared with normotensives. All the subjects in this study showed low frequency distribution pattern for copy numbers 2, 6 and 7. This discovery emphasizes the importance of frequency patterns in determining CNV status of prehypertensive and mild hypertensive subjects. Optimization method in this study showed that the detection of CNV esv27061 is possible in our sample population. 

### SciVal Topic Prominence

Topic: Genome | Polymorphism, Single Nucleotide | CNV regions

Prominence percentile: 91.704

### Author keywords

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