



Advances in Basic and Clinical Research of Copy Number Variants

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Deadline for manuscript submissions:

closed (15 September 2017)

Message from the Guest Editors

Dear Colleagues,

DNA Copy Number Variations (CNVs) make genomes highly dynamic and, therefore, are a key mechanism for cells to adapt and evolve. The increased resolution of genomic analyses has revealed that CNVs are abundant and diverse across human populations and therefore can be reliably used as disease susceptibility markers for many complex disorders. The availability of large-scale population studies combining multiple “omics” analyses together with sophisticated mathematical and statistical methodologies provide a unique opportunity to further characterize the underlying mechanisms of CNV formation, the role of CNVs as gene regulators and the use of CNVs as disease biomarkers. In this Special Issue of *Microarrays* we are looking for contributions that deepen our current understanding of CNVs in the context of basic and clinical research. Experimental and theoretical studies are welcome.

