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Complex Chromosomal Rearrangements in Cancers and Congenital Disorders

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Deadline for manuscript submissions:
closed (15 September 2018)

Message from the Guest Editors

Dear Colleagues,

DNA sequencing of cancer tissues and of individuals with congenital disorders has uncovered many patterns of chromosomal alterations that involve multiple rearrangements. Complex chromosomal rearrangements (CCRs) can result from multiple rounds of mutagenesis due to genome instability. For instance, the breakage–fusion–bridge cycles that can lead to gene amplifications. CCRs can also be generated in a single catastrophic event causing massive mutagenesis, such as chromothripsis and chromoanagenesis. Analysis of CCRs in diseases and their mechanisms have led to new research strategies combining experimental cell biology and DNA sequencing.

We invite colleagues to contribute original analyses and reviews on the general subject of CCRs. Relevant topics include discoveries and descriptions of CCRs in disease, technology and computational approaches for CCR analysis, and experimental studies of CCR mechanisms and their functional impacts. We hope to generate new insight into the aetiology of CCRs and how they contribute to pathogenesis and drive genome evolution.

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Message from the Editorial Board

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