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## Genomic Aberrations in Hematologic Malignancies

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**closed (15 April 2024)**

### Message from the Guest Editors

Recurrent chromosomal abnormalities are very common in a variety of hematological malignancies, such as translocations and/or inversions related to the formation of fusion genes such as t(9;22)(q34.1;q11.2) and related BCR::ABL1; t(8;21)(q22;q22.1) and related RUNX1::RUNX1T1; inv(16)(p13.1q22)/(16;16)(p13.1;q22) and related CBFβ::MYH11; t(15;17)(q24;q21) and related PML::RARA; t(12;21)(p13.2;q22.1) and related ETV6::RUNX1; and a wide spectrum of 11q23 abnormalities/KMT2A(MLL) gene rearrangement and related fusion genes in both myeloid and lymphoid neoplasms. They are widely applied as biomarkers for the diagnosis of specific entities and/or sub-entities of hematological malignancies, targeted therapies, and prognostic predictions in the field of hemato-oncology. Attributed to the widespread application of advanced next-generation sequencing (NGS)-based technologies and genome-wide comprehensive studies, tremendous novel fusion genes as well as chromosomal abnormalities have been identified in hematological malignancies in the past several decades. They all play important roles in the era of precision medicine.



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Special Issue



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## Message from the Editor-in-Chief

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