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Next-Generation Sequencing Technologies in Solid Tumor

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Message from the Guest Editor

The application of next-generation sequencing (NGS) technologies in investigations of solid tumors has allowed us to obtain the maximum genomic evaluation of the tumor. Furthermore, the application of NGS technologies on the genome/exome of affected subjects and with a positive family history of cancer has allowed the identification of a large number of genes responsible for familial/hereditary forms of cancer. NGS approaches involve DNA and RNA analysis. DNA sequencing deals with revealing nucleotide variants on a selection of genes of interest for a specific tumor area. RNA sequencing allows detection of alternative genetic transcripts, post-transcriptional modifications, gene fusion, single nucleotide mutations/polymorphisms, small and long non-coding RNAs, and changes in gene expression. Most of the applications are in the field of cancer research, but NGS technology is also widely used in molecular diagnostics.

In this Special Issue, we would like to collect recent diagnostic/predictive clinical findings obtained from NGS applications to various solid tumors and on the genome/germinal exome of subjects affected by familial/hereditary cancers.

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Message from the Editor-in-Chief

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