Special Issue

Linking Genomic Changes with Cancer in the NGS Era, 2nd Edition

Message from the Guest Editors

The arrival of next-generation sequencing (NGS) technology has greatly enhanced our ability to read genetic code, starting a new era in identifying disease-causing genetic changes. While detecting individual genetic changes has improved, translating these findings remains complex, particularly in cancer research. Establishing new driver genes or variants is a significant NGS-based screening bottleneck. Only a small fraction of the 10–20% of cancers associated with familial aggregation have known genetic causes, and the genomic profile of the 80–90% of sporadic cancers is highly heterogeneous, complicating the identification of driving versus secondary or progression-associated changes.

In this Special Issue, we invite researchers to submit studies on the identification of new genes or variants linked to cancer development or progression. We welcome evidence from case–control studies, segregation analyses, gene editing (e.g., CRISPR/Cas9), protein structure analyses, functional studies, or other approaches relevant for validating gene–disease associations.

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