



## Linking Genomic Changes with Cancer in the NGS Era

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### Message from the Guest Editor

The developing of the next-generation sequencing (NGS) technology has opened a new era in the identification of disease-causing genetic changes. The “translationability” of the identified changes is complex, and the establishment of a new driver gene/variant constitutes the NGS-based genetic screening bottleneck. This is particularly true in cancer, where only a very small fraction of the 10-20% of the cancers associated with familial aggregation have a known underlying genetic cause. Moreover, the profile of genomic changes of the 80-90% of the cancers arising sporadically is highly heterogeneous, making difficult to distinguish driving, secondary and progression-associated genomic variation.

We appreciate the work highlighting or discarding the identification of new genes/variants as a cause of cancer development or progression. Evidences may include case-control studies, segregation analysis, gene/variant specific gene editing, protein structure analysis, functional studies, or other approaches considered relevant for validation of a gene-disease association.





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