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Transcriptional and Genetic Tumor Heterogeneity through ScRNA-seq

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Message from the Guest Editor

With the quick progress of scRNA-seq technologies, including approaches to assess cell-level genetic heterogeneity, the anticipation is that scRNA-seq will soon be incorporated in the clinics. This process will greatly benefit from improved knowledge on tumor heterogeneity, the ability to interpret cell-level genetic and transcriptional variation, and, consequently, to distinguish and characterize sensitive and resistant clones. In the near future, this new knowledge is expected to be translated into better diagnosis and treatment of cancer patients.

We invite submissions of both methodological and original research papers assessing tumor heterogeneity through single-cell RNA sequencing. Special focus will be placed on research integrating genetic and transcriptional heterogeneity and identifying cell-level genetic determinants of phenotype. The overarching aim of this issue is to stimulate emerging and promising single-cell research, pursuing at the same time new exploratory and collaborative venues to address its challenges.



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Special Issue



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Message from the Editor-in-Chief

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