

## **Basic of Single Cell RNA Sequencing and application to cancer studies**

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### **Abstract**

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Transcriptome analysis at single cell resolution enables explicit characterization of heterogeneous cell populations, and became an essential tool to study cellular composition and dynamics in normal and disease conditions. Currently, the transcriptome analysis has been extended to incorporate genetic, epigenetic, and protein expression data as well as spatial contexts. Here, we applied massively parallel single cell RNA sequencing to multiple tumor types to define alterations in cancer cells and associated microenvironment during cancer progression. The results demonstrate alterations in cellular composition and gene expression changes in diverse cells types. Expansion of regulatory T cells and myofibroblasts were commonly observed in many cancer types indicating shared manner of tumor antigen presentation to immune cells as well as activation of tissue remodeling. Alterations in cancer cells reflected a deviation from normal differentiation axis as well as an adaptation to the metastatic microenvironment. Collectively, our study demonstrates the power of single cell RNA sequencing in the characterization of cancer as a complex ecosystem, and also promotes development of treatment strategies targeting different cellular components,

### **Keywords**

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*Single cell RNA sequencing, Cellular atlas, Cancer, Microenvironment*