

## **Single Cell Expression Profiling – New Insights Into Biology**

A major complexity when studying biological systems is heterogeneity. Tissue extracts or lysates contain cells of many different types, subtypes, and cells in different states and environments. When studying these systems the biology response is confounded by the large cell heterogeneity. While some cells show dramatic and distinct responses to treatment and environmental changes, other may react quite differently or not at all. In classical bulk studies it may be difficult often impossible to deconvolute the critical and biological relevant cellular responses from the measured averages or changes in average expressions. During the last 10 years single cell gene expression profiling techniques has been developed and today efficient and very reliable high throughput approaches are available. In my talk I will describe the high throughput approach we developed including the quality control measures and analysis approaches. I will also present digital PCR, which can be used to validate single cell profiling data. Finally, I will present our most recent efforts on protein profiling using qPCR, which recently was applied for the first time on single cells.