Exploiting single cell transcriptome analyses to track adaptation to endocrine therapies

Synopsis

Endocrine therapies have been used for the past 40 years as they are very effective in lowering relapse rates in women with luminal breast cancer. The effect of endocrine therapies on single cells have not been yet studied. Here I will discuss how single cell transcriptomics can be used to map non-genetic evolution of cancer cells under acute endocrine treatment. Our data show that transcriptional heterogeneity and reprogramming both play a central role during the early phases of endocrine treatment.