

“Genome Wide Profiling of Single Cells for Diagnosis and Monitoring in Prostate Cancer”

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Funding Category: A

Abstract: We propose a collaborative program to explore the feasibility and utility of applying single cell genomic analysis (SCGA) to the ongoing MSKCC efforts to discover biomarkers that will guide treatment selection in prostate cancer. Genomic biomarkers have potential value in therapeutic guidance and are the subject of current clinical studies at MSKCC. The rationale for applying SCGA is based on studies in breast tumors indicating that genomic heterogeneity could confound the use of molecular markers due to mixing of cell types and that newly available single cell methods could greatly increase the sensitivity of molecular biomarker assays in clinical practice and also provide insight into the etiology of PC. Two of our aims are to examine two important biomarker sources, radical prostatectomy samples and circulating tumor cells (CTCs) from castration-resistant PC cases, for heterogeneity and to compare SCGA to results from microarray based CGH.