

## **“Target Enrichment and Single Molecule Sequencing for Genomic Analysis of Human Tumors”**

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**Abstract:** Prostate cancer is a complex disease with a wide range of clinical outcomes. In many patients, the disease is indolent and does not require aggressive treatment. However, in other cases, the disease will be life-threatening. Especially given the significant morbidity associated with some treatments, this presents a dilemma for both patients and physicians. Our goal ultimately is to provide more useful information in terms of molecular characterization of individual prostate cancers to enable physicians and patients to make more informed discussion about how aggressive a course of therapy to pursue. We propose to do this by combining the outstanding prostate cancer sample collection from Memorial Sloan-Kettering Cancer Center and their ability to carry out 454 sequencing, with the Cold Spring Harbor Laboratory group’s expertise in Illumina sequencing and advanced methods of exon capture. We propose to sequence the transcriptome of a number of prostate samples as well as to optimize methods to capture the exons from genomic DNA from these same samples. We will then in a complimentary fashion sequence the genomic DNA from these samples using the optimized method we developed. This will give us a wealth of data to use in classifying prostate tumors based on their molecular profile. Ultimately, this should allow a significant improvement in the quality of care for this disease by better informing patients and physicians the likely outcome of an individual patient’s disease.