

## **The NanoVelcro CTC-RNA assay: a new method for contemporary genomics and precision medicine via liquid biopsy**

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**Background:** Genome and transcriptome-based analysis has begun to reshape the approach to prostate cancer. Two different gene expression signatures have shown that prostate cancers can be divided into 3 subclasses reflecting luminal basal biology. These subtypes point toward biological drivers that may strongly influence how care should be personalized including optimization of androgen receptor targeted therapy. The majority of work done in this area has been based on tissue-based gene expression. With the advent of newer nanotechnology platforms for isolation of circulating tumor cells (CTCs), profiling of gene expression from blood is now possible

**Methods:** We combined variations of the NanoVelcro assay (thermoreponsive, click-chemistry) allowing for capture and release of CTCs with intact RNA. Gene sets from the PCS and PAM50 signatures were re-reviewed to optimize signal detection in the blood and enrich for genes upregulated in prostate cancer. An nCounter NanoString assay was developed to include the resulting genes. A pilot study was conducted using banked samples available through the Urologic Oncology Program Blood and Biospecimen Bank.

**Results:** The final assay was tested in banked blood samples and provided classifications of patients that associated with clinical responsiveness to therapy. In particular, during emergence of resistance, we see an increase in expression of genes related to the PCS1/Basal phenotypes.

**Conclusions:** This study shows initial proof of principle that genomic classification in blood is possible using contemporary tool for blood component isolation and nanostring. Additional technical and clinical validation are needed prior to widespread implementation, but these methods may make it possible to increase the utilization of genomic classifiers in clinical studies and in practice.

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