#297 Design of high-performance tumor-informed molecular residual disease (MRD) panels from low FFPE tumor input

Matt LaBella[1]*, Ashley Acevedo[1]*, Ravi Patel[1]*, Kiefer Haug[1], Sangita Ganesh[1], Elise Buser[1], Nafei Xu[1], Shalee Carlson[1], Kyle Trettin[1], Christopher Battey[1], Sarah Ratzel[1], Kieko Hara[2], Pavlos Msaouel[2], Kanishka Sircar[2], Chad Tang[2], Dale Muzzey[1] and Genevieve Gould[1]

*Authors contributed equally, [1]Myriad Genetics, Inc. Salt Lake City, UT, [2]The University of Texas MD Anderson Cancer Center, Houston, TX

Background

Molecular residual disease (MRD) testing can detect cancer recurrence months to years earlier than the current standard of care, enabling earlier treatment of recurrence and improved patient outcomes. Tumor-informed MRD assays typically utilize formalin-fixed paraffin-embedded (FFPE) **tumor tissue**, which **is available in limited quantities** for some patients, for example, following core needle biopsy (CNB), after neoadjuvant treatment, or when patients need multiple tests from the same tumor sample.

Methods

To assess the lower limit of tissue input, we evaluated our MRD assay performance across a range of extracted tumor volumes. Thirty-seven sections from resected primary and metastatic tumors from 5 patients with renal cell carcinoma were H&E stained and macro-dissected. Tumor gDNA was extracted, quantified, prepared into libraries and sequenced. Sequenced libraries were aligned and evaluated for depth of coverage, variation of coverage and duplication rate. Somatic calling was performed on matched tumor and normal samples and a personalized panel with up to 1000 target sites was designed for each tumor section. The performance of each panel was evaluated by orthogonal validation of somatic target sites.

Conclusions

Patient-specific tumor-informed MRD assays have immense potential for increasingly sensitive treatment response and recurrence monitoring that can inform better treatment decisions. FFPE tumor tissue is a critical input into MRD assays but is a limited resource. **This study supports a minimum DNA input of 10 nanograms**, corresponding to a tissue volume of 0.5mm^3 or two 10µm slide with a 25mm^2 area, representing one of the lowest tissue input requirements for an MRD assay. **Low FFPE tissue requirements expand the patient population that may benefit from MRD testing** by utilizing samples that have low tumor content, are post-neoadjuvant therapy, or do not meet the tumor volume requirements of competing MRD offerings.

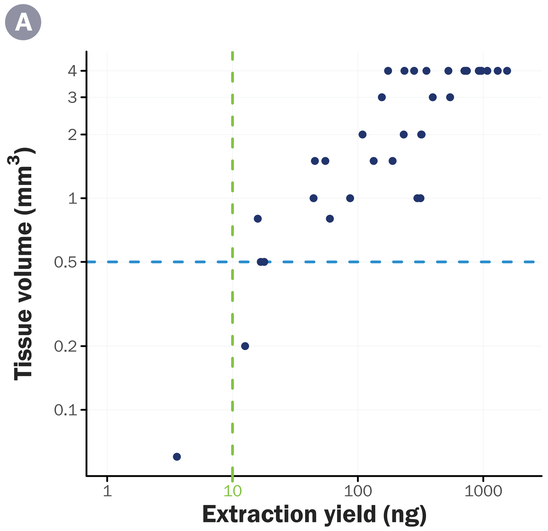
Results

Sufficient DNA quantity is reproducibly extracted from 0.5mm^3 of FFPE tissue

Extracted tumor volumes varied by almost two orders of magnitude, from 0.06mm^3 (equivalent to needle core or fine needle aspirate biopsies) to 4mm^3 (achievable with resected tumor).

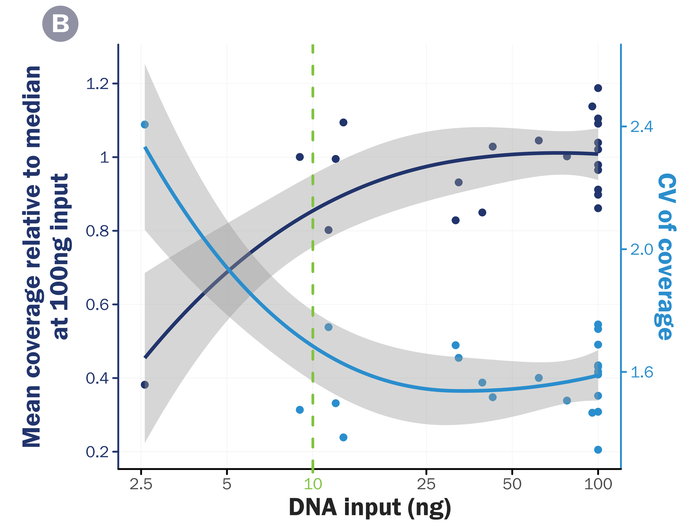
gDNA yield varied linearly (3.6ng to 1549ng) with tumor tissue input (A), indicating the low tissue-to-paraffin ratio did not have an adverse effect on yield.

2 **slide minimum input**
(4 slides recommended)

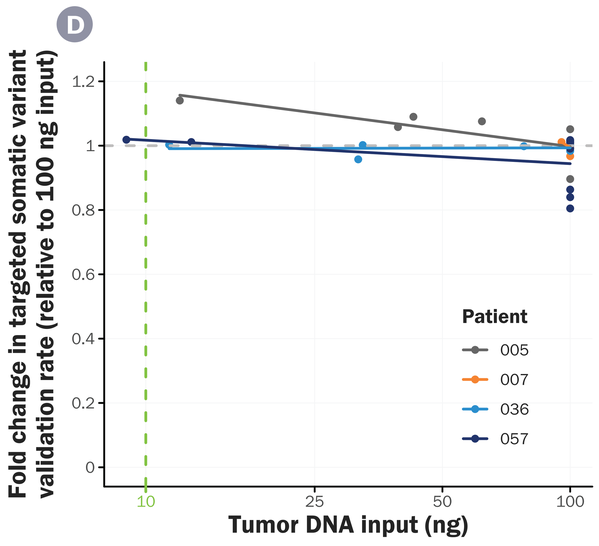


High quality WGS libraries are generated from as little as 10ng of DNA

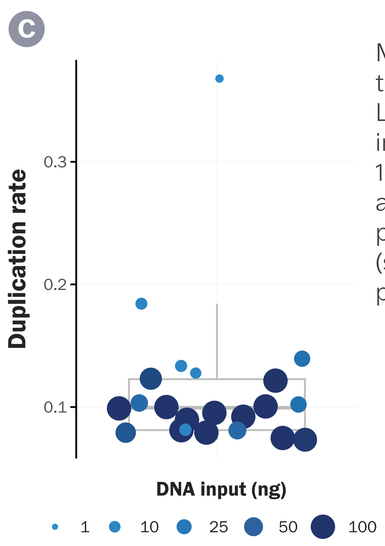
Tumor gDNA input into library prep ranged from 2.5ng to 100ng. Sequence data for each sample was downsampled to 800 million reads to control for flowcell loading differences and aligned to the reference genome.



Personalized target panels show equivalent performance when designed from low DNA input WGS



Results for 4 patients with multiple input DNA amounts are shown in D with best fit lines across the range of inputs. Matched tumor and normal sequence data were paired for somatic variant calling and panel design. Somatic targets from each panel were orthogonally validated by high depth, capture-based sequencing of tumor and normal input DNA. The validation rate of targets selected for each panel was compared to the median validation rate of panels designed for the same patient at 100ng of tumor DNA input.



Mean and coefficient of variation (CV) in coverage are fit by LOESS with 95% confidence intervals shown in B. Below 10ng, mean depth of coverage, CV of coverage and the positional duplication rate (shown in C) indicate poor-quality libraries.